

		TCGAC TT TTTCCCCG		
		A TG__		
GAM1115	LLGL2	3' GCTTCCACAATGCAGCTG 15752	G	AAA
		CAGCTGCA TGTG GGGGC		
		GTCGACGT ACAC CTTCG		
		A ____		
GAM1115	MAGE-E1	5' GCCCCCTCCCCCTGCAGCTG 47946		TGT AA
		CAGCTGCAG GA GGGGC		
		GTCGACGTC CT CCCCCG		
		CCC C_		
GAM1115	MCF2L	3' GCCCCTGCCTCACTGCACTG 60845	C	TGAA
		CAG TGCAGTG AGGGGC		
		GTC ACGTCAC TCCCCG		
		_ TCCG		
GAM1115	MGC10981	3' CCCCACACTGCAGC 51015		AAA
		GCTGCAGTGTG GGG		
		CGACGTCACAC CCC		
		_____		
GAM1115	MGC12760	3' GCTCCCCACACTGCA 51175		AAA
		TGCAGTGTG GGGGC		
		ACGTCACAC CCTCG		
		C__		
GAM1115	MGC12904	3' GCCCCTTCTTTCTCCACAGCT 48334	C__	TGT A
		AGCTG AG GAA GGGGC		
		TCGAC TC CTT CCCCCG		
		ACC TTT _		
GAM1115	MGC16025	5' GCCCCCTCTGGCTGCACTG 51922	C	GT AA
		CAG TGCAGT GA GGGGC		
		GTC ACGTCG CT CCCCCG		
		_ GT C_		
GAM1115	MGC16179	3' GCCCCTCCCAGTTCTGCGGCTG 51303		TG_ AA
		CAGCTGCAG TG AGGGGC		
		GTCGGCGTC AC TCCCCG		
		TTG CC		
GAM1115	MGC16703	3' CCCCTTTTCACGTCAGCT 73099	CA	T
		AGCTG GTG GAAAGGGG		
		TCGAC CAC TTTTCCCC		
		TG _		
GAM1115	MGC3035	5' GCCCCTGCTCATGCAGCTG 44151		GTG A_
		CAGCTGCA TGA AGGGGC		



		GTCGACGT ACT TCCCCG		
		___ CG		
GAM1115	MGC3113	3' CCCCCTTCGCCAGCAGCT 43844	AGT	A
		AGCTGC GTGAA GGGG		
		TCGACG CGCTT CCCC		
		AC_ C		
GAM1115	MGC3130	3' GCCCCCTCATCTCTGCGCTG 43821	T	T_ AA
		CAGC GCAG GTGA GGGGC		
		GTCG CGTC TACT CCCCCG		
		_ TC C_		
GAM1115	MGC4604	3' GCCCCCTTTCTCTACTGAGCT 48979	G	T_
		AGCT CAGTG GAAAGGGGC		
		TCGA GTCAT CTTTCCCCG		
		_ CT		
GAM1115	MGC4701	5' CCCCCGTCTTCTGCAGCT 64557	TGT	AA
		AGCTGCAG GA GGGG		
		TCGACGTC CT CCCC		
		TT_ GC		
GAM1115	MRPS2	3' GCCCCTTGGCTGCAGTT 32091	GTGA	
		AGCTGCAGT AAGGGGC		
		TTGACGTCG TTCCCCG		
		G__		
GAM1115	NFAT5	5' CCCCTCCGCGCCTGCGCTG 56942	T	T AA_
		CAGC GCAG GTG AGGGG		
		GTCG CGTC CGC TCCCC		
		_ _ GCC		
GAM1115	NICE-1	3' CCCCCAGCGCTGCGCT 38803	T	GAAA
		AGC GCAGTGT GGGG		
		TCG CGTCGCG CCCC		
		_ AC_		
GAM1115	NMT1	3' GCCCCTTTCCAAGATACAGC 40785	CAG_	T
		GCTG TG GAAAGGGGC		
		CGAC AC CTTTCCCCG		
		ATAGA _		
GAM1115	P17.3	5' CCCCAGTGCAGCTG 38795	GTGAAA	_
		CAGCTGCAGT GGG G		
		GTCGACGTCA CCC C		
		_____ A		
GAM1115	PIP5K2B	5' CCTCTTTCGCCGCCGC 56893	T	AGT
		GC GC GTGAAAGGGG		

CG CG CGCTTTCTCC  
C C\_\_

GAM1115 PIP5K2B 5' CCTCTTTTCGCCGCCGC 13071 T AGT  
GC GC GTGAAAGGGG  
|| || |||||  
CG CG CGCTTTCTCC  
C C\_\_

GAM1115 PLEKHA3 5' GCCCCCAAGCTCCACGCTG 38862 \_ C G AAA  
CAGC TG AGT TG GGGGC  
|||| ||| || ||||  
GTCG AC TCG AC CCCCCG  
C C A \_\_\_\_

GAM1115 PP1057 5' GCCCCCTCCAAACTGCAGCTG 48434 G AAA  
CAGCTGCAGT TG GGGGC  
||||||| || ||||  
GTCGACGTCA AC CCCCCG  
A CTC

GAM1115 PPM1G 3' CTCCACACTGCAGC 10710 AAA  
GCTGCAGTGTG GGG  
||||||| |||  
CGACGTCACAC CTC

GAM1115 PPP1R10 3' CCCCTGTGGACTGCAGC 10730 G GAA  
GCTGCAGT T AGGGG  
||||||| | ||||  
CGACGTCA G TCCCC  
G TG\_

GAM1115 PRO2405 3' CCCCCCGTGCAGCTG 37799 G TGAAA  
CAGCTGCA TG GGGG  
||||||| || ||||  
GTCGACGT GC CCCC  
\_ C \_\_\_\_

GAM1115 PRO2605 3' GCCCCTGTGCCTGCTACT 94857 CT T GAA  
AG GCAG GT AGGGGC  
|| ||| || |||||  
TC CGTC CG TCCCCG  
AT \_ TG\_

GAM1115 RGS19 5' CCCCTTTCGGCAGC 19650 AGTG  
GCTGC TGAAAGGGG  
|||| |||||  
CGACG GCTTCCCC

GAM1115 RNPC1 5' GCCCCCATGCTGCTGCAGC 33990 \_ AAA  
GCTGCAGT GTG GGGGC  
||||||| ||| ||||  
CGACGTCG CGT CCCCCG  
T ACC

GAM1115 SFXN5 3' GCCCCTTTGGACCTGCAGTTG 58036 T G\_  
CAGCTGCAG GT AAAGGGGC  
||||||| || |||||

GTTGACGTC CA TTTCCCCG  
 \_ GG  
 GAM1115 SH3BGL3 5' CCCGGCAGTGCAGCTG 48437 G GAAAG  
 CAGCTGCA TGT GGG  
 ||||| || ||  
 GTCGACGT ACG CCC  
 G G\_\_\_\_  
 GAM1115 SNX10 3' GCCCCTTTTAAAGCATCT 25265 C AGTG  
 AG TGC TGAAAGGGGC  
 || || |||||  
 TC ACG ATTTTCCCCG  
 T AA\_\_\_\_  
 GAM1115 SR-BP1 3' GCCCCTTCACCTGCAGCT 19634 T A  
 AGCTGCAG GTGAA GGGGC  
 ||||| |||| ||||  
 TCGACGTC CACTT CCCCCG  
 \_ C  
 GAM1115 SRCRB4D 3' CCCCTCCCTGCAGCTG 54955 TGTGAA  
 CAGCTGCAG AGGGG  
 ||||| ||||  
 GTCGACGTC TCCCC  
 CC\_\_\_\_  
 GAM1115 ST13 3' CCCCTCTCCCCAAATGCAGCT 14115 GTGT\_\_\_\_ A  
 G CAGCTGCA GA AGGGG  
 ||||| || ||||  
 GTCGACGT CT TCCCC  
 AAACCCC C  
 GAM1115 STX4A 3' CCCCTTCCTCACACTG 16016 \_\_\_\_  
 CAGTGTGA AAGGGG  
 ||||| ||||  
 GTCACACT TTCCCC  
 CC  
 GAM1115 TNFRSF19L 3' GCCCCTGGCCCTGCTGC 51777 T T GAA  
 GC GCAG GT AGGGGC  
 || |||| || ||||  
 CG CGTC CG TCCCCG  
 T C G\_\_\_\_  
 GAM1115 TRAP25 5' GCCCCTTCGGCCTGAAGCTG 54676 G TG A  
 CAGCT CAG TG AAGGGGC  
 |||| || || |||||  
 GTCGA GTC GC TTCCCCG  
 A CG C  
 GAM1115 TUBB5 3' CCCCTCCCTCCGAGCTG 20298 GCAG T A\_\_\_\_  
 CAGCT TG GA AGGGG  
 |||| || || ||||  
 GTCGA GC CT TCCCC  
 \_\_\_\_ \_ CCC  
 GAM1115 ZF 3' GCCCCTCACAAATGCAGCTG 41088 G AA  
 CAGCTGCA TGTGA GGGGC  
 ||||| |||| ||||

GTCGACGT AACT CCCC  
 A \_  
 GAM1115 LOC112885 3' CCCCTTTCTGTCAGT 56521 \_ GTGT  
 GCTG CA GAAAGGGG  
 ||| || |||||  
 TGAC GT CTTTCCCC  
 T \_  
 GAM1115 LOC113220 3' CTCCACCTGCAGCTG 56551 T AAA  
 CAGCTGCAG GTG GGG  
 ||||| ||| |||  
 GTCGACGTC CAC CTC  
 \_ \_  
 GAM1115 LOC121793 5' GCCCCTTCATCTGTCAGCTG 74114 \_ T A  
 CAGCTG CAG GTGAA GGGG  
 ||||| ||| ||||| |||||  
 GTCGAC GTC TACTT CCCC  
 T \_ \_  
 GAM1115 LOC124842 5' GCCCCTTGAGATCTTGCAGCT 75659 T GA\_  
 G CAGCTGCAG GT AAGGGG  
 ||||| || |||||  
 GTCGACGTT TA TTCCCC  
 C GAGG  
 GAM1115 LOC124930 3' CCCCTTCCACCAGCTGCTGCT 74356 T \_ A\_  
 AGC GCAGT GTG AAGGGG  
 ||| ||||| ||| |||||  
 TCG CGTCG CAC TTCCCC  
 T AC CC  
 GAM1115 LOC124977 5' TCCCTTCCTCACTGCAGC 76065 TGA  
 GCTGCAGTG AAGGGG  
 ||||| |||||  
 CGACGTCAC TTCCCT  
 TCC  
 GAM1115 LOC128402 3' GCCCCTTTCCACCAGC 75782 CA T  
 GCTG GTG GAAAGGGG  
 ||| ||| |||||  
 CGAC CAC CTTTCCCC  
 \_ \_  
 GAM1115 LOC130639 3' CCTGACACTGCACTG 74968 C GAAAG  
 CAG TGCAGTGT GGG  
 ||| ||||| |||  
 GTC ACGTCACA TCC  
 \_ G\_  
 GAM1115 LOC130644 3' CCCCCACACCCATTGCAGCTG 75753 \_ AAA  
 CAGCTGCA GTGTG GGGG  
 ||||| ||||| |||||  
 GTCGACGT CACAC CCCC  
 TACC \_  
 GAM1115 LOC138399 5' CCCCTTTCCCTGCAGGCT 75326 \_ TGT  
 AGC TGCAG GAAAGGGG  
 ||| ||||| |||||

TCG ACGTC CTTTCCCC  
 G C\_\_  
 GAM1115 LOC143451 3' CTCCTCCCCACTGCAGC 76563 TGAA  
 GCTGCAGTG AGGGG  
 ||||| ||||  
 CGACGTCAC TCCTC  
 CCC\_  
 GAM1115 LOC144110 3' GCCCCTTTTCACAGGCCCT 76673 CT AG  
 AG GC TGTGAAAGGGGC  
 || || |||||  
 TC CG ACACTTTCCCCG  
 CC G\_  
 GAM1115 LOC144483 3' GCCCCTCCCACCTGCA 60178 T AA  
 TGCAG GTG AGGGGC  
 |||| || ||||  
 ACGTC CAC TCCCCG  
 \_ CC  
 GAM1115 LOC145125 3' CTCCTCCCCACTGCAGC 77005 TGAA  
 GCTGCAGTG AGGGG  
 ||||| ||||  
 CGACGTCAC TCCTC  
 CCC\_  
 GAM1115 LOC145623 3' GCCAGGCACCCTGCAGCTG 83396 T AAAGG  
 CAGCTGCAG GTG GGC  
 ||||| || |||  
 GTCGACGTC CAC CCG  
 C GGA\_\_  
 GAM1115 LOC146287 5' CCCAGAGGCCATTGCAGCTG 83651 TGAAAG  
 CAGCTGCAGTG GGG  
 ||||| || |||  
 GTCGACGTTAC CCC  
 CGGAGA  
 GAM1115 LOC146823 3' GCCCCTATTCCGCACGCTG 83799 TGCA \_ \_  
 CAGC GTGTG AA AGGGGC  
 ||| |||| || |||||  
 GTCG CACGC TT TCCCCG  
 \_ \_ C A  
 GAM1115 LOC146988 3' CCCCTCAAAATCACCCCAGCTG 83893 CA TGAA\_\_  
 CAGCTG GTG AGGGG  
 |||| || ||||  
 GTCGAC CAC TCCCC  
 CC TAAAC  
 GAM1115 LOC147136 5' CCCCTCCACTCAGC 78262 C T AA  
 GCTG AGTG GA GGGG  
 ||| |||| || ||||  
 CGAC TCAC CT CCCC  
 \_ \_ C\_  
 GAM1115 LOC148758 5' GCCCTAGGCAACTGCAGCTG 78971 G AAA  
 CAGCTGCAGT TG GGGGC  
 ||||| || ||||

	GTCGACGTCA AC TCCCG	
	_ GGA	
GAM1115 LOC150848 5'	GCCCCTTTCCTTGCA 85129	TGT
	CTGCAG GAAAGGGGC	
	GACGTT CTTTCCCCG	
	C_	
GAM1115 LOC151391 3'	CCCCTTTATTTGCAGTTG 85331	TGTG
	CAGCTGCAG AAAGGGG	
	GTTGACGTT TTTCCCC	
	TA_	
GAM1115 LOC155179 3'	GCCCCTTTTTACACAGCTG 81316	GCA _
	CAGCT GTGTGAAA GGGGC	
	GTCGA CACATTTT CCCCC	
	_ T	
GAM1115 LOC157869 3'	GCCCCTTTCATTTGTGAAGT 81626	_ T
	GCT GCAG GTGAAAGGGGC	
	TGA TGTT TACTTTCCCCG	
	AG _	
GAM1115 LOC158373 5'	CCCCAGCACTGCAGGC 71043	_ GAAA
	GC TGCAGTGT GGGG	
	CG ACGTCACG CCCC	
	G A_	
GAM1115 LOC158886 3'	CCCCTCTCCCCCAAATGCAGCT 82833	GTGT_ A
G	CAGCTGCA GA AGGGG	
	GTCGACGT CT TCCCC	
	AAACCCC C	
GAM1115 LOC158972 3'	CCCCTCCCATGAAGCGCTG 86947	T AG AA
	CAGC GC TGTG AGGGG	
	GTCG CG GTAC TCCCC	
	_ AA CC	
GAM1115 LOC159184 5'	CCCCTTCATGCAGCAGCT 60046	A A
	AGCTGC GTGTGAA GGGG	
	TCGACG CGTACTT CCCC	
	A _	
GAM1115 LOC161048 5'	GCCATGGACATGCAGCTG 82259	G GAAAGG
	CAGCTGCA TGT GGC	
	GTCGACGT ACA CCG	
	_ GGT_	
GAM1115 LOC164945 5'	GCCCCCGAGCAGCTGCAGC 87186	_ GAAA
	GCTGCAG TGT GGGGC	

	CGACGTC ACG CCCCCG	
	G AGCC	
GAM1115 LOC170395 3'	GCCCCTCAGTTTGCAG 76371	TG AA
	CTGCAG TGA GGGGC	
	GACGTT ACT CCCCCG	
	TG _	
GAM1115 LOC197285 3'	CCCAACATGCAGCTG 87790	G GAAAG
	CAGCTGCA TGT GGG	
	GTCGACGT ACA CCC	
	_ A _	
GAM1115 LOC197285 3'	CCCCCATCCTGCAGCTG 87791	TG AAA
	CAGCTGCAG TG GGGG	
	GTCGACGTC AC CCCC	
	CT _	
GAM1115 LOC197358 3'	GCCCCTTTCCACTCACCTG 88038	C C T
	CAG TG AGTG GAAAGGGGC	
	GTC AC TCAC CTTTCCCCG	
	C _ _	
GAM1115 LOC199906 5'	CCCCTTTCTCTGGGACAGT 88478	_ TGT
	GCTG CAG GAAAGGGG	
	TGAC GTC CTTTCCCC	
	AGG T_	
GAM1115 LOC199989 3'	GCCCCTCCCCTGCAGC 89894	T AA
	GCTGCAGTG GA GGGGC	
	CGACGTCGC CT CCCCCG	
	C _	
GAM1115 LOC200035 5'	GCCCATTCAGTGCAGCT 73254	TGAAAG
	AGCTGCAGTG GGGC	
	TCGACGTCAC CCGG	
	TTA_	
GAM1115 LOC200301 5'	CCCTCCATTGCAGC 88740	T AA
	GCTGCAGTG GA GGG	
	CGACGTTAC CT CCC	
	_ _	
GAM1115 LOC200958 3'	GCCCCCACCAGACTGCAGC 65925	G AAA_
TG	CAGCTGCAGT TG GGGGC	
	GTCGACGTCA AC CCCCCG	
	G AGCCAC	
GAM1115 LOC202025 5'	GCCCCTTTGTGCTGTA 90292	TG G
	TGCAG T AAAGGGGC	

ATGTC G TTTCCCCG  
 GT \_  
 GAM1115 LOC202126 3' GCCCCTTTGGGTTCCAGC 90314 C TG G  
 GCTG AG T AAAGGGGC  
 ||| || | |||||  
 CGAC TT G TTTCCCCG  
 C GG \_  
 GAM1115 LOC202284 5' GCCCCTTTACCCCTGC 90329 T  
 GCAG GTGAAAGGGGC  
 ||| |||||  
 CGTC CACTTTCCCCG  
 C  
 GAM1115 LOC204970 3' GCCCCTTGGCTGCAGC 89410 GTGA  
 GCTGCAGT AAGGGGC  
 ||||| |||||  
 CGACGTCG TTCCCCG  
 G \_  
 GAM1115 LOC219920 5' GCCCCGCTCCTGCAGCTG 93314 TGT AA  
 CAGCTGCAG GA GGGGC  
 ||||| || |||||  
 GTCGACGTC CT CCCCCG  
 \_ CG  
 GAM1115 LOC220827 3' TTTTCACACTACACT 91247 C C  
 AG TG AGTGTGAAAG  
 || || |||||  
 TC AC TCACACTTTT  
 \_ A  
 GAM1115 LOC245718 3' CCCCTCTCCCCCAAATGCAGCT 90719 GTGT \_ A  
 G CAGCTGCA GA AGGGG  
 ||||| || |||||  
 GTCGACGT CT TCCCC  
 AAACCCC C  
 GAM1115 LOC254105 3' GCCCCTGGGCCTGCACTG 94770 C T GAA  
 CAG TGCAG GT AGGGGC  
 || ||||| || |||||  
 GTC ACGTC CG TCCCCG  
 \_ \_ GG\_  
 GAM1115 LOC254263 3' CCCCCAAACTGCTGCTG 94717 T G AAA  
 CAGC GCAGT TG GGGG  
 ||| ||||| || |||||  
 GTCG CGTCA AC CCCC  
 T A \_  
 GAM1115 LOC254440 3' CTCCTCCCCACTGCAGC 97065 TGAA  
 GCTGCAGT AGGGG  
 ||||| |||||  
 CGACGTCAC TCCTC  
 CCC\_  
 GAM1115 LOC254873 3' TTCCTTTCCTCTGCAGC 94574 TGT  
 GCTGCAG GAAAGGGG  
 ||||| |||||



	CGACGTC CTTTCCTT		
	TC_		
GAM1115 LOC256158 5'	CCCACACGCTGCAGCTG 97656	AAA	
	CAGCTGCAGTGTG GGG		
	GTCGACGTCGCAC CCC		
	A__		
GAM1115 LOC256158 5'	CCCAGCCTGCAGCTG 97657	T GAAAG	
	CAGCTGCAG GT GGG		
	GTCGACGTC CG CCC		
	_ A__		
GAM1115 LOC256598 5'	GCCCCTCGTGGCTGCAGC 96352	GTGAA	
	GCTGCAGT AGGGGC		
	CGACGTCG TCCCCG		
	GTGC_		
GAM1115 LOC257203 5'	GCCCCCTGGCGCCAGCTG 96931	CA GAAA	
	CAGCTG GTGT GGGGC		
	GTCGAC CGCG CCCCCG		
	C_ GTC_		
GAM1115 LOC257319 3'	GCCCCTTATACATGCTG 95774	TGCA A	
	CAGC GTGTG AAGGGGC		
	GTCG CACAT TTCCCCG		
	TA__ A		
GAM1115 LOC257476 3'	CCCCTTCCTCTCCACTGCAGGC 61252	_ T ____	
	GC TGCAGTG GA AAGGGG		
	CG ACGTCAC CT TTCCCC		
	G _ CTCC		
GAM1115 LOC257539 3'	CCCCTTCCTCACACTG 97700	__	
	CAGTGTGA AAGGGG		
	GTCACACT TTCCCC		
	CC		
GAM1115 LOC257578 3'	CCCCTTCCTCACACTG 97820	__	
	CAGTGTGA AAGGGG		
	GTCACACT TTCCCC		
	CC		
GAM1115 LOC51195 3'	GCCCCCTCCCTGCTACTG 32945	CT TGT AA	
	CAG GCAG GA GGGGC		
	GTC CGTC CT CCCCCG		
	AT C_ C_		
GAM1115 LOC54103 5'	GCCCCTAGGGCCACTACACTG 94214	C C TGAA_	
	CAG TG AGTG AGGGGC		

		GTC AC TCAC TCCCCG	
		_ A CGGGA	
GAM1115	LOC55971	3' GCCCCTTTATTACAGC 38129	C TGA
		GCTG AGTG AAGGGGC	
		CGAC TTAT TTCCCCG	
		A _	
GAM1115	LOC84570	5' GCCCCTTTTCGCGCTGCGCTG 50711	T
		CAGC GCAGTGTGAAAGGGGC	
		GTCG CGTCGCGCTTTCCCCG	
		-	
GAM1115	LOC85414	3' GCCCCTTAACCTGCAGCT 52398	T GA
		AGCTGCAG GT AAGGGGC	
		TCGACGTC CA TTCCCCG	
		- A _	
GAM1115	LOC87769	5' CCTGGGTTCTCACTGCAGCTG 71321	T AG_
		CAGCTGCAGTG GAA GGG	
		GTCGACGTCAC CTT TCC	
		T GGG	
GAM1115	LOC90024	3' GCCCCTCTCCCCGACCAACTG 61112	C CAG T_ A
		CAG TG TG GA AGGGGC	
		GTC AC GC CT TCCCCG	
		A CA_ CC C	
GAM1115	LOC90719	3' GCAGAATCTCACTGCAGCTG 63884	T AAGGG
		CAGCTGCAGTG GA GC	
		GTCGACGTCAC CT CG	
		T AAGA_	
GAM1115	LOC90768	5' GCCCCTGGTGGGCACTGCAGC 63956	GAA_
		GCTGCAGTGT AGGGGC	
		CGACGTCACG TCCCCG	
		GGTGG	
GAM1115	LOC91464	5' CCCCTCAAGCTGCAGT 66138	G AA
		GCTGCAGT TGA GGGG	
		TGACGTCG ACT CCCC	
		A _	
GAM1115	LOC91526	5' CCCCTCTGCATGCTGCAGC 66336	AA_
		GCTGCAGTGTG AGGGG	
		CGACGTCGTAC TCCCC	
		GTC	
GAM1115	LOC91917	3' CCCAACATGCAGCTG 67528	G GAAAG
		CAGCTGCA TGT GGG	

GTCGACGT ACA CCC  
 \_ A\_  
 GAM1115 LOC92148 5' GCCCCTGACCACACTGCCACT 68333 CT AA\_  
 AG GCAGTGTG AGGGGC  
 || ||||| |||||  
 TC CGTCACAC TCCCCG  
 AC CAG  
 GAM1115 LOC92299 3' GCCATCACACTGCAGC 68811 AAGG  
 GCTGCAGTGTGA GGC  
 ||||| |||  
 CGACGTCACACT CCG  
 A\_  
 GAM1115 LOC92573 5' CCCCTTTCTGTCAGCT 69804 \_ GTGT  
 AGCTG CA GAAAGGGG  
 |||| || |||||  
 TCGAC GT CTTTCCCC  
 T \_  
 GAM1115 LOC92840 3' CCGAGATCACCTGCAGCTG 56431 T AA\_  
 CAGCTGCAG GTGA GG  
 ||||| ||| ||  
 GTCGACGTC CACT CC  
 \_ AGAG  
 GAM1115 LOC93070 5' GCCCCTTTGCAGCCGCTG 71293 T AG G  
 CAGC GC TGT AAAGGGGC  
 |||| || || |||||  
 GTCG CG ACG TTTCCCCG  
 C \_ \_  
 GAM1115 LOC93320 3' GCCAAGCCCACTGCAGCTG 72051 TGAAAGG  
 CAGCTGCAGTG GGC  
 ||||| |||  
 GTCGACGTCAC CCG  
 CCGAA\_  
 GAM1116 AKAP13 3' GGAAGCACTCACCCCCCA 89684 AA T TCTGT \_  
 TG GG GTGAGT GCT CC  
 || || ||||| ||| ||  
 AC CC CACTCA CGA GG  
 CC \_ \_ \_ A  
 GAM1116 H3F3B 3' AGGAGCACAAAACTCCAGCC 18019 GT C  
 GGT GAGTT TGTGCTCCT  
 ||| |||| |||||  
 CCG CTCAA ACACGAGGA  
 AC A  
 GAM1116 RASD1 3' AGGAACACAAAACAAAACCTTGC 32220 A GTGA C C  
 A TG AGGT GTT TGTG TCCT  
 || |||| ||| |||||  
 AC TTCA CAA ACAC AGGA  
 G AAA\_ A A  
 GAM1116 SLC6A3 5' GAGCACAGAATTCCTCA 6449 T\_ C  
 TG GAGTTCTGTGCT C  
 || ||||| ||||| |

AC CTTAAGACACGA G  
 TC A  
 GAM1116 SLC9A6 3' GAGCACAGAACAATTTCTCA 21004 A T GA  
 TGA GG GT GTTCTGTGCTC  
 ||| ||| |||||  
 ACT CT TA CAAGACACGAG  
 \_ T A\_  
 GAM1116 AF311304 3' ACAAAACTCACACTCTCA 48329 AG C  
 TGA GTGTGAGTT TGT  
 ||| ||||| |||  
 ACT CACACTCAA ACA  
 CT A  
 GAM1116 DKFZp434O0320 3' AGGAGCACAGAAAGGTTTACAT 83692 \_\_\_\_  
 C GGTGTGAG TTCTGTGCTCCT  
 ||||| |||||  
 CTACATT AAGACACGAGGA  
 GGA  
 GAM1116 FLJ11125 3' CATCTGTGCCACCACCTTCA 59579 \_ A TCT\_  
 TGAAGGTG TG GT GTG  
 ||||| ||| |||  
 ACTTCCAC AC CG TAC  
 C \_ TGTC  
 GAM1116 FLJ11286 3' AGGAACACAGAGTCACAGCTTC 37215 G G C  
 A TGAAG TGTGA TTCTGTG TCCT  
 |||| |||| ||||| ||||  
 ACTTC AACT GAGACAC AGGA  
 G \_ A  
 GAM1116 FLJ13110 3' AGGAGCACCTGTGGCTCACACC 43297 CT\_  
 TTC GAAGGTGTGAGTT GTGCTCCT  
 ||||| |||||  
 CTTCCACACTCGG CACGAGGA  
 TGTC  
 GAM1116 FLJ13912 3' GAACACAGAATGGCTCCTCA 42861 A T GA C  
 TGA GG GT GTTCTGTG TC  
 ||| ||| ||||| |||  
 ACT CC CG TAAGACAC AG  
 \_ T G\_ A  
 GAM1116 FLJ20013 3' AGGAGCACAGAACAGGGCCT 34328 GTGA  
 AGGT GTTCTGTGCTCCT  
 ||| |||||  
 TCCG CAAGACACGAGGA  
 GGA\_  
 GAM1116 KIAA0182 3' GAGCCACACCTTCA 72027 AGTTCTGT  
 TGAAGGTGTG GCTC  
 ||||| |||  
 ACTTCCACAC CGAG  
 C\_\_\_\_\_  
 GAM1116 KIAA1666 3' AGAAGCAAGCGTTTCAGACCCTC 65248 A G TT G C  
 A TGA GGT TGAG CT TGCT CT  
 ||| ||| ||| ||| ||| |||

			ACT CCA ACTT GA ACGA GA			
			C G GC _ A			
GAM1116	MFN2	3'	GAGCTGGCTCATACCCCA	29600	AA	CTGT
			TG GGTGTGAGTT GCTC			
			AC CCATACTCGG CGAG			
			CC T__			
GAM1116	SCYA11	5'	GCCAAAGCTCACACCTTCA	11455		C T
			TGAAGGTGTGAGTT TG GC			
			ACTTCCACACTCGA AC CG			
			A _			
GAM1116	SIRPB1	3'	AGAACTCTCACACTCTCA	20240	AG	__
			TGA GTGTGAG TTCT			
			ACT CACACTC AAGA			
			CT TCA			
GAM1116	TREX1	5'	AGAAGCACAGAACCTGGCATT	53275	AG	G _ C
	A		TGA GTGT AG TTCTGTGCT CT			
			ACT TACG TC AAGACACGA GA			
			_ G C A			
GAM1116	TREX1	5'	AGAAGCACAGAACCTGGCATT	53286	AG	G _ C
	A		TGA GTGT AG TTCTGTGCT CT			
			ACT TACG TC AAGACACGA GA			
			_ G C A			
GAM1116	LOC120105	5'	AGCACAGGTCACCATCA	75512	A	TGAGT
			TGA GGTG TCTGTGCT			
			ACT CCAC GGACACGA			
			A T__			
GAM1116	LOC146443	5'	AGGGGCACCACCCCA	77881	AA	TGAGTTCT
			TG GGTG GTGCTCCT			
			AC CCAC CACGGGGA			
			CC			
GAM1116	LOC150095	5'	AGGAGGCAGCCACCACCTT	84853		A T_ G
	C		GAAGGTGTG GT CTGT CTCCT			
			CTTCCACAC CA GACG GAGGA			
			C CC _			
GAM1116	LOC150221	3'	AGAAGCAAGCGTTCAGACCCTC	65274	A	G TT G C
	A		TGA GGT TGAG CT TGCT CT			
			ACT CCA ACTT GA ACGA GA			
			C G GC _ A			
GAM1116	LOC221263	3'	AGAGCCCCACCACCTTCA	93612		_ A_
			TGAAGGTG TG GTTCT			

ACTTCCAC AC CGAGA  
 C CC  
 GAM1116 LOC257396 5' GGAGCATCTCAGACCTTCA 97138 G TTCT  
 TGAAGGT TGAG GTGCTCC  
 ||||| ||| |||||  
 ACTTCCA ACTC TACGAGG  
 G \_\_\_\_  
 GAM1116 LOC54516 3' AGAACCTCACACTCCCA 38758 AA \_  
 TG GGTGTGAG TTCT  
 || ||||| |||  
 AC TCACACTC AAGA  
 CC C  
 GAM1116 LOC96652 3' AGCTCAGAACTCCACCTCCA 65463 A T T  
 TG AGGTG GAGTTCTG GCT  
 || ||| ||||| |||  
 AC TCCAC CTCAAGAC CGA  
 C \_ T  
 GAM1117 AKAP1 3' AGGTCGACCTCATCATCTGGGA 57709 TAAACA CA\_\_  
 TCCCAGATG GAG ACCT  
 ||||| ||| |||  
 AGGGTCTAC CTC TGGA  
 TA\_\_ CAGC  
 GAM1117 ANXA9 5' CTCTCCCACATCTGGGA 13103 AAAC  
 TCCCAGATGT AGAG  
 ||||| |||  
 AGGGTCTACA TCTC  
 CCC\_  
 GAM1117 BLVRB 3' CTCTGTCCCCATCTGGGA 5546 TAA  
 TCCCAGATG ACAGAG  
 ||||| |||||  
 AGGGTCTAC TGTCTC  
 CCC  
 GAM1117 ENTPD1 5' TGCTCTGTTCTTCTGG 8348 TGTA  
 CCAGA AACAGAGCA  
 ||| |||||  
 GGTCT TTGTCTCGT  
 TC\_  
 GAM1117 FUT8 3' GGTGCCTATATCTGAGA 15591 C AAAC A A  
 TC CAGATGT AG GCA CC  
 || ||||| || ||| ||  
 AG GTCTATA TC CGT GG  
 A \_\_\_\_ \_ \_  
 GAM1117 MKI67 3' GGTTGCTCTCACCTGAGA 10046 C A TAAAC  
 TC CAG TG AGAGCAACC  
 || ||| || |||||  
 AG GTC AC TCTCGTTGG  
 A C \_\_\_\_  
 GAM1117 ORC2L 3' TGTTGTGTTTACATCTG 20549 G  
 CAGATGTAAACA AGCA  
 ||||| ||||| |||

		GTCTACATTTGT TTGT		
		G		
GAM1117	SNTB1	5' AGGTTGCTCCACCCCGGTCAGG 40702	CA	GTAAACA
	A	TCC GAT GAGCAACCT		
		AGG CTG CTCGTTGGA		
		A_ GCCCCAC		
GAM1117	APOL4	5' CTTTGTCTGCTGCATCTGG 47624	A__	
		CCAGATGTA ACAGAG		
		GGTCTACGT TGTTTC		
		CTGC		
GAM1117	CNOT7	3' AGGCTGCTCTGTGACTG 25332	ATGTAA	A
		CAG ACAGAGCA CCT		
		GTC TGTCTCGT GGA		
		AG__ C		
GAM1117	DKFZP564M182	3' TGCAGTGGCTTACATCTG 78046	A_ GA	
		CAGATGTAA CA GCA		
		GTCTACATT GT CGT		
		CG GA		
GAM1117	FLJ10081	3' AGGTCACCTGTGTTCAATCTGG 35798	GTA	G CA_
	GA	TCCCAGAT AACA AG ACCT		
		AGGGTCTA TTGT TC TGGA		
		AC_ G CAC		
GAM1117	FLJ10716	3' AGGTTGTTTTTTTCCACATCTG 36480	A_ C	
	GGA	TCCCAGATGT AA AGAGCAACCT		
		AGGGTCTACA TT TTTTGTGGA		
		CC T		
GAM1117	FLJ10786	3' TTTGTCTATATCTGGGA 36643	A	
		TCCCAGATGTA ACAGA		
		AGGGTCTATAT TGTTT		
		C		
GAM1117	FLJ13194	3' TTGCTGTTACATCTG 47133	ACAG	
		CAGATGTAA AGCAA		
		GTCTACATT TCGTT		
		G__		
GAM1117	FLJ13912	3' GCCTGCATTACATCTGG 42863	A_ A	
		CCAGATGTAA CAG GC		
		GGTCTACATT GTC CG		
		AC _		
GAM1117	FLJ14525	3' GCCTCTGTTTCATCTGGGA 51417	T	_
		TCCCAGATG AAACAGAG C		

AGGGTCTAC TTTGTCTC G  
 \_ C  
 GAM1117 FLJ20070 3' GCCTTATTATACATCTGAGA 34476 C AAC\_\_ A  
 TC CAGATGTA AG GC  
 || ||||| ||  
 AG GTCTACAT TC CG  
 A ATTAT \_  
 GAM1117 FLJ20188 3' GCCTAGTTCCACATCTGG 34698 A\_\_ \_ A  
 CCAGATGT AAC AG GC  
 ||||| ||||  
 GGTCTACA TTG TC CG  
 CCC A \_  
 GAM1117 GOLGB1 3' GCTTCTGCTTAATCTGAGA 15633 C G A \_  
 TC CAGAT TAA CAGA GC  
 || |||| |||||  
 AG GTCTA ATT GTCT CG  
 A \_ C T  
 GAM1117 KIAA1323 3' AGGTTGCTTTTTTTTAATC 63037 G C  
 GAT TAAA AGAGCAACCT  
 ||| ||| |||||  
 CTA ATTT TTTCGTTGGA  
 \_ T  
 GAM1117 KIAA1363 3' TTGCTCCATCTGGG 69268 TAAACA  
 CCCAGATG GAGCAA  
 ||||| |||||  
 GGGTCTAC CTCGTT  
 \_\_\_\_\_  
 GAM1117 KIAA1671 3' GCCTTTTACACCTGGGA 65678 A C A  
 TCCCAG TGTAAG AG GC  
 ||||| ||||| ||  
 AGGGTC ACATTT TC CG  
 C \_ \_  
 GAM1117 KIAA1855 3' CTGCCTACATCTGGGG 92340 AA  
 TCCCAGATGTA CAG  
 ||||| |||||  
 GGGGTCTACAT GTC  
 CC  
 GAM1117 OSBPL10 3' GTTGCTTCTTTTACATC 35049 CA  
 GATGTAAA GAGCAAC  
 ||||| |||||  
 CTACATTT TTCGTTG  
 TC  
 GAM1117 STIM2 3' GCTATTTACATCCTGG 40476 \_ CAG  
 CCAG ATGTAAA AGC  
 ||| ||||| ||  
 GGTC TACATTT TCG  
 C A\_\_  
 GAM1117 TRIM2 3' TGCAGTTTTACATCTGTGA 30946 C CAGA  
 TC CAGATGTAAA GCA  
 || ||||| |||



AG GTCTACATTT CGT  
 T TGA\_  
 GAM1117 LOC142941 5' TTTTGTTTAATCTGAGA 82887 C G  
 TC CAGAT TAAACAGAG  
 || |||| |||||  
 AG GTCTA ATTTGTTTT  
 A \_  
 GAM1117 LOC144631 5' GGTGCTCTCCATCGG 83164 A TAAAC  
 CC GATG AGAGCAACC  
 || ||| |||||  
 GG CTAC TCTCGTTGG  
 \_ C\_\_  
 GAM1117 LOC152829 3' GGTCTCTGTACATCTGGGA 80693 AA CA  
 TCCCAGATGT ACAGAG ACC  
 ||||| |||| ||  
 AGGGTCTACA TGTCTC TGG  
 C\_ \_  
 GAM1117 LOC157858 3' GTTGCTCTGGCTGTTTGGA 86601 TAAA  
 TCCCAGATG CAGAGCAAC  
 ||||| |||||  
 AGGGTTTGT GTCTCGTTG  
 CG\_\_  
 GAM1117 LOC158431 3' AGGCTGCCCTTGTTACATCT 86829 AC A A  
 AGATGTAA AG GCA CCT  
 ||||| || |||  
 TCTACATT TC CGT GGA  
 GT C C  
 GAM1117 LOC158777 3' CTGTCAACATCTGGGA 82001 AA  
 TCCCAGATGT ACAG  
 ||||| |||  
 AGGGTCTACA TGTC  
 AC  
 GAM1117 LOC199907 3' GCTTCTATTTACATTTG 88467 C \_  
 CAGATGTAAA AGA GC  
 ||||| ||| ||  
 GTTTACATTT TCT CG  
 A T  
 GAM1117 LOC200597 5' GGGGATCCCGCACATCTGGGA 88842 AAACA GCAA  
 TCCCAGATGT GA CCT  
 ||||| || |||  
 AGGGTCTACA CT GGG  
 CGCC\_ AG\_\_  
 GAM1117 LOC221296 3' TTGCTCTGACAAATTGG 91974 A\_ AAA  
 CCAG TGT CAGAGCAA  
 ||| || |||||  
 GGTT ACA GTCTCGTT  
 AA \_  
 GAM1117 LOC255565 3' GTTGCTCTGAATGTCTGGGA 95100 AAA  
 TCCCAGATGT CAGAGCAAC  
 ||||| |||||

			AGGGTCTGTA	GTCTCGTTG			
			A__				
GAM1117	LOC255862	3'	GGATGCCTACGTCTG	94487	AAAC	A	A
			CAGATGT	AG GCA CC			
			GTCTGCA	TC CGT GG			
			_____	A			
GAM1117	LOC90010	3'	GTTGCTCTGAATGTCTGGGA	61085	AAA		
			TCCCAGATGT	CAGAGCAAC			
			AGGGTCTGTA	GTCTCGTTG			
			A__				
GAM1118	ADH1B	3'	CTTAGACATAAAGTAAAT	72644	C	CAC	
			ATTT ACTTT	TGTCTGAG			
			TAAA TGAAA	ACAGATTC			
			A	T__			
GAM1118	AHR	3'	ATCTCAGATGTTAAAATAAATG	7875	CAC	C	T
			CATTT	TTT AC GTCTGAGAT			
			GTAAG	AAA TG TAGACTCTA			
			TA_	T _			
GAM1118	FDFT1	3'	TAGGAAAGTGAAATG	15518	A		
			CATTTCACTTTC	CTG			
			GTAAAGTGAAAG	GAT			
			—				
GAM1118	JTB	3'	ATCTCAGACAGTGAAAGTGAAA	21959			
	TG		CATTTCACTTTTCACTGTCTGAGAT				
			GTAAAGTGAAAGTGACAGACTCTA				
GAM1118	KLF4	3'	TCCCAGACAGTGGATATG	14891	CT	A	
			CA TTCACTGTCTG	GA			
			GT	AGGTGACAGAC	CT		
			AT	C			
GAM1118	PHYH	3'	ACAGTAAAAGTGAAAT	20608	C		
			ATTTCACTTT	ACTGT			
			TAAAGTGAAA	TGACA			
			A				
GAM1118	PKD2	3'	TCCAGGTTGAAAGTGAAA	60096	CTG	A	
			TTTCACTTTCA	TCTG GA			
			AAAGTGAAAGT	GGAC CT			
			T__	—			
GAM1118	WRN	3'	GGGCAGTGAAAATGAAA	5098	C		
			TTTCA	TTTCACTGTCT			

AAAGT AAAGTGACGGG  
 A  
 GAM1118 ZNF216 3' ATCTGCACAGCAAAGTGAAA 20017 CA CTG  
 TTTCAC TTT CTGT AGAT  
 ||||| ||| |||  
 AAAGTGAAA GACA TCTA  
 C\_ CG\_  
 GAM1118 CG012 5' CTCAC TCTGAAAAGTGAA 83218 CT CT  
 TTCAC TTTCA GT GAG  
 ||||| || |||  
 AAGTGAAAGT CA CTC  
 CT \_  
 GAM1118 EIF2C2 3' ATCTTCTGAGAGTGAAAG 71946 G T\_  
 CTTTCACT TC GAGAT  
 ||||| || |||  
 GAAAGTGA AG TTCTA  
 G TC  
 GAM1118 FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802 ACTTTCAC T  
 G CATTTC GTCTGAGAT  
 |||| | |||||  
 GTAAAG CAGACTCTA  
 AAACATTT\_  
 GAM1118 FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281 CTT  
 CATTTCA TCACTGTCTGAGAT  
 |||| | |||||  
 GTAAAGT AGTGACAGACTCTA  
 C\_  
 GAM1118 KIAA0984 3' TTTGTCCAGTGAAAATGAA 65534 C TC  
 TTCA TTTCAC TGAG  
 ||| ||||| |||  
 AAGT AAAGTGAC GTTT  
 A CT  
 GAM1118 KLHL6 3' ATCTCAGAGCAGGAAA 55299 A \_  
 TTTC CTG TCTGAGAT  
 ||| ||| |||||  
 AAAG GAC AGACTCTA  
 \_ G  
 GAM1118 NIR3 3' GCAGTGAAAAGTGCAAT 66242 T  
 ATT CACTTTCACTGT  
 || |||||  
 TAA GTGAAAAGTGACG  
 C  
 GAM1118 PORIMIN 3' ATCTCAGAGGGCCAAAGTGAA 53598 CA G  
 TTCACTTT CT TCTGAGAT  
 ||||| || |||||  
 AAGTGAAA GG AGACTCTA  
 CC G  
 GAM1118 PP35 3' ATCTCAGACTGAAA 22814 CT  
 TTTC A GTCTGAGAT  
 |||| | |||||

AAAGT CAGACTCTA

GAM1118 PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148 TCAC C\_  
CATTTCACCTT TGT TGAG  
||||||| ||| |||  
GTAAAGTGAA ACG ACTC  
TA\_\_ TT

GAM1118 SEP15 3' TCCTACAGTAAGAGTGAAA 14934 C CT  
TTTCACTTT ACTGT GA  
||||||| ||||| ||  
AAAGTGAGA TGACA CT  
A TC

GAM1118 SFXN2 3' CTCAGGGGAAAAAAGTGAAA 73941 CACTG  
TTTCACTTT TCTGAG  
||||||| |||||  
AAAGTGAAA GGA CTC  
AAAGG

GAM1118 LOC149703 3' ATCTCAGACAGCCGTTTGAAA 84647 ACTTTCA  
TTTC CTGTCTGAGAT  
||| |||||  
AAAG GACAGACTCTA  
GTTTGCC

GAM1118 LOC154007 3' ATCTCAAACCCTTTAGTGAAA 81015 TTCACT C  
TTTCACT GT TGAGAT  
||||| || |||||  
AAAGTGA CA ACTCTA  
TTTCC\_ A

GAM1118 LOC155004 3' TCATTTAAGTGAAAGGAAA 81226 A GTC\_  
TTTC CTTTCACT TGA  
||| ||||| |||  
AAAG GAAAGTGA ACT  
\_ ATTT

GAM1118 LOC222134 5' ACAGTGAAGTGAAATG 94136 T  
CATTTCACCTT CACTGT  
||||||| |||||  
GTAAAGTGAA GTGACA

GAM1119 AKT1 3' AGGACTTCTACAGCTATGCGC 17696 TGGT A  
GCGC GTTGTAGAA TCCT  
||| ||||| |||  
CGCG CGACATCTT AGGA  
TAT\_ C

GAM1119 ASPH 3' ATTTCTACATTAGC 50614 TGT  
GCTGGTGT AGAAAT  
||||| |||||  
CGATTACA TCTTTA

GAM1119 ASPH 3' ATTTCTACATTAGC 50627 TGT  
GCTGGTGT AGAAAT  
||||| |||||

CGATTACA TCTTTA

GAM1119 CELL 3' GAGGACTTCTACAAGCTGGT 8410 TG G A  
GC GT TTGTAGAA TCCTC  
|| || ||||| ||||  
TG CG AACATCTT AGGAG  
GT \_ C

GAM1119 CTLA1 5' AGGAGTCAACACCAACAGC 53073 GC\_ TAGAAA  
GC TGGTGTG TCCT  
|| ||||| ||||  
CG ACCACAAC AGGA  
ACA TG\_\_\_\_

GAM1119 FS 3' CTGCAGCCACCAGTGCT 41816 \_  
AGCGCTGGTG TTGTAG  
||||||| |||||  
TCGTGACCAC GACGTC  
C

GAM1119 GABPA 3' AGGATCTCCACAATGTCTGC 8979 T TG A A  
GC GG TTGT GA ATCCT  
|| || |||| |||||  
CG CT AACA CT TAGGA  
T GT C C

GAM1119 LPP 3' AGGACTTCCACATTTTTCG 18744 CT TGTA A  
GCG GGTGT GAA TCCT  
|| |||| |||||  
CGT TTACA CTT AGGA  
TT C\_\_ C

GAM1119 PAPP A 3' GAATTCCCAACGCCAG 10423 TA A  
CTGGTGTG GAA TC  
||||||| |||||  
GACCGCAAC CTT AG  
C\_ A

GAM1119 PART1 3' GAGAACTTTCTAAAAGACCAGC 33435 C G G TC\_  
ACT AG GCTGGT TT TAGAAA CTC  
|| ||||| ||||| |||||  
TC CGACCA AA ATCTTT GAG  
A G A CAA

GAM1119 PDE4C 3' TTTTCAGCACCAAAGCT 6239 GC T  
AGC TGGTGTG AGAA  
|| ||||| |||||  
TCG ACCACGAC TTTT  
AA \_

GAM1119 SELL 3' GAAGATTTCTACCTGACCAACA 5392 GT\_ \_ C  
GT GCTG GTT GTAGAAATC TC  
|||| ||||| ||||| |||||  
TGAC CAG CATCTTTAG AG  
AAC TC A

GAM1119 SLC7A6 3' GAGGATCCCTACAGCACTCAAG 14308 GCT AA  
CT AGC GGTGTTGTAG ATCCTC  
|| ||||| ||||| |||||

TCG TCACGACATC TAGGAG  
AAC CC  
GAM1119 ZNF35 3' AGGATTGATGGACACCA 12777 G GA  
TGGTGT TA AATCCT  
||||| || |||||  
ACCACAG GT TTAGGA  
\_ AG  
GAM1119 APOARGC 3' GAGGATCCTTCCAAACCAGC 44421 G T AA  
GCTGGT TTG AG ATCCTC  
||||| ||| || |||||  
CGACCA AAC TT TAGGAG  
\_ C CC  
GAM1119 DKFZp434O0320 3' AGGACTTCTCTCCAGGC 83691 G TGTTGT A  
GC CTGG AGAA TCCT  
|| ||| ||| |||  
CG GACC TCTT AGGA  
\_ TC\_ C  
GAM1119 DKFZP564O0423 3' GGACCACACCAGTGC 91696 T TAGAAA  
GCGCTGGTGT G TCC  
||||||| | |||  
CGTGACCACA C AGG  
C \_  
GAM1119 DNAJA3 3' GAGGATTCCAGAACAGCAGCAC 60486 C G GTA A  
T AG GCTG TGTT GAA TCCTC  
|| ||| ||| ||| |||||  
TC CGAC ACAA CTT AGGAG  
A G GAC \_  
GAM1119 FLJ12572 3' AGAATTTTACCCATCAGCACT 43245 C TT C  
AG GCTGGTG GTAGAAAT CT  
|| ||||| ||||| ||  
TC CGACTAC CATTTTGA GA  
A C\_ A  
GAM1119 GRIP1 5' GAGAACTTCTGGTCTCAAGCGC 70626 GGTGTTG ATC  
T AGCGCT TAGAA CTC  
||||| ||||| |||  
TCGCGA GTCTT GAG  
ACTCTG\_ CAA  
GAM1119 HSPC023 3' GAGGACCCTGTCCCCCAGCACT 25910 C TGTTG AAA  
AG GCTGG TAG TCCTC  
|| |||| ||| |||||  
TC CGACC GTC AGGAG  
A CCCT\_ CC\_  
GAM1119 KIAA0350 3' GAGGATTTCTATAACCAGGGC 61174 G GT \_  
T AGC CTGGT TGTAAG AAATCCTC  
||| |||| ||||| |||||  
TCG GACCA ATATC TTTAGGAG  
G \_ C  
GAM1119 KIAA1280 5' GAGGACCCCCACCAGCCAGCGC 69717 GTT AGAAA  
T AGCGCTGGT GT TCCTC  
||||||| || |||||

		TCGCGACCG CA AGGAG		
		AC_ CCCCC		
GAM1119	MAC30	5' GGATTTCTCCAAAGCC 62679	G T	
		GGT TTG AGAAATCC		
		CCG AAC TCTTTAGG		
		A C		
GAM1119	MGC33345	3' GATGCCCACAGCACCAGC 58276		AGAA
		GCTGGTGTGTG ATC		
		CGACCACGACA TAG		
		CCCG		
GAM1119	P11	5' AGGATCTGGAGACACCAGC 20070	G_ AA	
		GCTGGTGTG TAGA TCCT		
		CGACCACAG GTCT AGGA		
		AG _		
GAM1119	P66	3' AGGATTTCTCTTCCAACAGT 40363	G TTGT	
		GCTG TG AGAAATCCT		
		TGAC AC TCTTTAGGA		
		A CTTC		
GAM1119	phorbolin-1	5' TCTTAACACCACGC 88784	C T	
		GCG TGGTGTG AGA		
		CGC ACCACAAT TCT		
		- -		
GAM1119	RAB3GAP	3' GACTTCCCAGCACCAAGCT 66949	GC TA A	
		AGC TGGTGTG GAA TC		
		TCG ACCACGAC CTT AG		
		A_ C_ C		
GAM1119	RSP3	5' GAGAATGGCGCCAACACCAGCC 49173	C TAGAA C	
	CT	AG GCTGGTGTG AT CTC		
		TC CGACCACAAC TA GAG		
		C CGCGG A		
GAM1119	TCL6	5' AGGACCCCCACAGCACCAGGC 26990	G AGAAA	
		GC CTGGTGTGTG TCCT		
		CG GACCACGACA AGGA		
		- CCCCC		
GAM1119	TCL6	5' AGGACCCCCACAGCACCAGGC 40079	G AGAAA	
		GC CTGGTGTGTG TCCT		
		CG GACCACGACA AGGA		
		- CCCCC		
GAM1119	TCL6	5' AGGACCCCCACAGCACCAGGC 40092	G AGAAA	
		GC CTGGTGTGTG TCCT		

CG GACCACGACA AGGA  
 \_ CCCCC  
 GAM1119 TCL6 5' AGGACCCCCACAGCACCAGGC 24974 G AGAAA  
 GC CTGGTGTGT TCCT  
 || ||||| |||  
 CG GACCACGACA AGGA  
 \_ CCCCC  
 GAM1119 TTYH2 3' GAGTTCACAACACCAGAGC 50995 G A A  
 GC CTGGTGTGT GAA TC  
 || ||||| |||  
 CG GACCACAACA CTT AG  
 A \_ G  
 GAM1119 ZNF213 3' GGACCTGCCAGCGCT 65103 TGTT AAA  
 AGCGCTGG GTAG TCC  
 ||||| ||| |||  
 TCGCGACC CGTC AGG  
 \_ C\_  
 GAM1119 LOC149832 5' GAGGACTCCTAGGGGCAGCAGC 84700 G \_ G AAA  
 GCTG TGT T TAG TCCTC  
 ||| ||| ||| |||  
 CGAC ACG G ATC AGGAG  
 G G G CTC  
 GAM1119 LOC150630 5' TCTTAACAACAGCACT 85115 C G T  
 AG GCTG TGTTG AGA  
 || ||| |||| |||  
 TC CGAC ACAAT TCT  
 A A \_  
 GAM1119 LOC151981 5' AGGATTTCTGGCCAGCCGCT 87256 \_ GTTG  
 AGCG CTGGT TAGAAATCCT  
 ||| |||| |||||  
 TCGC GACCG GTCTTTAGGA  
 C \_  
 GAM1119 LOC202126 3' GAGGACTCCTCACCCCAGGC 90313 G T T TA AA  
 GC CTGG GT G GA TCCTC  
 || ||| || | |||||  
 CG GACC CA C CT AGGAG  
 \_ C \_ TC C\_  
 GAM1119 LOC220827 3' TCTACCACCA GTGC 91245 TT  
 GCGCTGGTG GTAGA  
 ||||| |||||  
 CGTGACCAC CATCT  
 \_  
 GAM1119 LOC256145 5' TTCCACAACACCCACGC 96545 CT A  
 GCG GGTGTTGT GAA  
 ||| ||||| |||  
 CGC CCACAACA CTT  
 AC C  
 GAM1119 LOC257482 3' TCTGCAGCCACCAACAGT 94240 GC\_ \_  
 GC TGGTG TTGTAGA  
 || |||| |||||



			TG ACCAC GACGTCT		
			ACA C		
GAM1119	LOC90917	3'	TTCTCAGCCACAGCACT	64342	C GT T
			AG GCTG GTTG AGAA		
			TC CGAC CGAC TCTT		
			A AC _		
GAM1119	LOC91431	5'	TTTATCCCACCAGCCT	56928	C TT
			AG GCTGGTG GTAGA		
			TC CGACCAC TATTT		
			_ CC		
GAM1120	ADAM12	3'	TGAACCTATTTCTTAAACACTT	12973	C C _
	G		CAAGTG TT AGAA TAGGTTCA		
			G TTCAC AA TCTT ATCCAAGT		
			A T T		
GAM1120	ADD1	3'	TGAACCTTCAGAAGCACTCGG	26381	A A AT
			TC AGTGCTTC GA AGGTTCA		
			GG TCACGAAG CT TCCAAGT		
			C A _		
GAM1120	GAB2	3'	AGCCTTCAAAGCACTTGA	54441	CA AT
			TCAAGTGCTT GA AGGTT		
			AGTTCACGAA CT TCCGA		
			A_ _		
GAM1120	GAB2	3'	AGCCTTCAAAGCACTTGA	24484	CA AT
			TCAAGTGCTT GA AGGTT		
			AGTTCACGAA CT TCCGA		
			A_ _		
GAM1120	MCM2	3'	AACCAGAGCACTTGA	67926	CAGAATA
			TCAAGTGCTT GGTT		
			AGTTCACGAG CCAA		
			A_ _ _		
GAM1120	MMP15	3'	GGATCCCCAAGGCACTTGA	10076	CAGAATA
			TCAAGTGCTT GGTT		
			AGTTCACGGA CTAGG		
			ACCC_ _		
GAM1120	PHKG1	5'	GAGCCTGCAAGCACTT	20606	CAGAA
			AAGTGCTT TAGGTT		
			TTCACGAA GTCCGAG		
			C_ _ _		
GAM1120	PRKG1	3'	TGAACCTAAAATAGCAGTTGA	20750	G TCAGAA
			TCAA TGCT TAGGTTCA		

		AGTT ACGA ATCCAAGT	
		G TAAA__	
GAM1120	RELA	3' TGAACAATCAAAGCACTTGG 41756	CA ATAG
		TCAAGTGCTT GA GTTCA	
		GGTTCACGAA CT CAAGT	
		A_ AA__	
GAM1120	STXBP1	3' TGTACTAAAGCACTTGA 12051	C A
		TCAAGTGCTT AG ATA	
		AGTTCACGAA TC TGT	
		A A	
GAM1120	AGXT2L1	3' TTCTGAAGCTACCTGA 48398	A _
		TCA GT GCTTCAGAA	
		AGT CA CGAAGTCTT	
		C T	
GAM1120	BNIP-S	3' TGAATCCCTGAAACATCTGA 56270	AG C AATA
		TCA TG TTCAG GGTTC	
		AGT AC AAGTC CTAAGT	
		CT A C__	
GAM1120	C17orf26	3' GTTCTTCCGAAGCACTGA 57544	A _
		TCA GTGCTTC AGAAT	
		AGT CACGAAG TCTTG	
		_ CCT	
GAM1120	C3IP1	3' TGAACCTAGAACAGCACTGA 41286	A TCAGAA
		TCA GTGCT TAGGTTCA	
		AGT CACGA ATCCAAGT	
		_ CAAG__	
GAM1120	FLJ10352	5' TGGATCCAATGCACTTGA 49562	TTCAGAATA
		TCAAGTGC GGTTC	
		AGTTCACG CTAGGT	
		TAAC_____	
GAM1120	FLJ13231	3' TGAACCCTATTTTAAAACAC 43555	C C _
		GTG TT AGAATAGG TTCA	
		CAC AA TTTTATCC AAGT	
		A A C	
GAM1120	KIAA1349	3' TGAACCTAAAAAGCACT 70760	CAGAA
		AGTGCTT TAGGTTCA	
		TCACGAA ATCCAAGT	
		AA__	
GAM1120	MCPR	3' TGAACCTACCCTGAAACGTGA 42648	A GC AA
		TCA GT TTCAG TAGGTTCA	

AGT CA AAGTC ATCCAAGT  
 G \_ CC  
 GAM1120 MGC20235 3' GGCCTCCCAAAGCACTTGG 58900 CAGAAT  
 TCAAGTGCTT AGGTT  
 ||||| ||||  
 GGTTCACGAA TCCGG  
 ACCC\_  
 GAM1120 MGC2488 3' TGAAGTAGGCTGAAGCATCTGA 43877 AG AA G  
 TCA TGCTTCAG TAG TTCA  
 || ||||| || ||||  
 AGT ACGAAGTC ATC AAGT  
 CT GG \_  
 GAM1120 NOL4 3' GACCTCTGAAGTACTTGA 13695 ATA  
 TCAAGTGCTTCAGA GGTT  
 ||||| ||||  
 AGTTCATGAAGTCT CCAG  
 \_  
 GAM1120 OR2C3 3' TGTTCTGAAGTACCTGA 75451 A  
 TCA GTGCTTCAGAATA  
 || ||||| ||||  
 AGT CATGAAGTCTTGT  
 C  
 GAM1120 PRAM-1 3' GTTGCTGAAGCAGCTGA 69381 AG \_  
 TCA TGCTTCAG AAT  
 || ||||| ||||  
 AGT ACGAAGTC TTG  
 CG G  
 GAM1120 RNF40 3' GAGCCCAGAGCACTTGA 28714 CAGAATA  
 TCAAGTGCTT GGTT  
 ||||| ||||  
 AGTTCACGAG CCGAG  
 AC\_  
 GAM1120 SAC2 3' AACCTAGGAGCATT 30054 AGAA  
 AGTGCTTC TAGGTT  
 ||||| ||||  
 TTACGAGG ATCCAA  
 \_  
 GAM1120 SIAT9 3' GCCCTTTCAAAGCACTT 13991 CA TA  
 AAGTGCTT GAA GGT  
 ||||| || ||||  
 TTCACGAA CTT CCG  
 A\_ TC  
 GAM1120 USP25 3' GAATCCCAAAGTACTTGA 25440 CAGAATA  
 TCAAGTGCTT GGTT  
 ||||| ||||  
 AGTTCATGAA CTAAG  
 ACC\_  
 GAM1120 LOC123036 3' TGAACCTACTCTGAAACAT 74194 C A  
 GTG TTCAGA TAGGTTCA  
 || ||||| |||||

TAC AAGTCT ATCCAAGT  
 A C  
 GAM1120 LOC144438 3' TGAAGTGTAGTGAAGCAT 76839 GAATA  
 GTGCTTCA GGTTC  
 ||||| |||||  
 TACGAAGT TCAAGT  
 GATG\_  
 GAM1120 LOC152765 5' GCCTCTGAAGCACCTG 80659 A ATA  
 CA GTGCTTCAGA GGT  
 || ||||| |||  
 GT CACGAAGTCT CCG  
 C \_  
 GAM1120 LOC219654 3' ACCCTCTGAGCACTT 91296 T ATA  
 AAGTGCT CAGA GGT  
 ||||| ||| |||  
 TTCACGA GTCT CCA  
 \_ C\_  
 GAM1120 LOC221122 3' TGAACCTATCCCGGCCCTCTTG 93442 T\_\_ TCA A  
 G TCAAG GCT GA TAGGTTCA  
 |||| ||| || |||||  
 GGTTT CGG CT ATCCAAGT  
 TCC CC\_ \_  
 GAM1120 LOC56920 3' AACCAGAAGCACTGA 39378 A AGAATA  
 TCA GTGCTTC GGT  
 || ||||| |||  
 AGT CACGAAG CCAA  
 \_ A\_\_\_\_  
 GAM1120 LOC90408 5' GGCCTCCAAAGCACTT 62663 CA ATA  
 AAGTGCTT GA GGTT  
 ||||| || |||  
 TTCACGAA CT CCGG  
 AC \_  
 GAM1121 SLC1A2 3' AGCAAATTCTTGAATAAACTCC 61927 A \_ T\_ A  
 CCA TG GGAGTTTGT CAA ATTT CT  
 || ||||| ||| ||| ||  
 AC CCTCAAATA GTT TAAA GA  
 C A CT C  
 GAM1121 C11orf25 3' AGTAAATACTGACAGCCCCT 48636 A T A  
 AGG GTT GTCA TATTTACT  
 ||| ||| ||| |||||  
 TCC CGA CAGT ATAAATGA  
 C \_ C  
 GAM1121 FLJ12519 3' TAAATATTAACAACTTT 70726 C  
 GGAGTTTGT AATATTTA  
 ||||| |||||  
 TTTCAAACA TTATAAAT  
 A  
 GAM1121 KIAA0534 3' AGTACTCTTAACAAGCTCCTCA 71427 CAATATT  
 TGAGGAGTTTGT TACT  
 ||||| |||

			ACTCCTCGAACA	ATGA		
			ATTCTC_			
GAM1121	KIAA1244	3'	ATTGAAA	ACTCCTCA	71988	G
			TGAGGAGTTT	TCAAT		
			ACTCCTCAAA	AGTTA		
			-			
GAM1121	RAE1	5'	GTTGCGCAA	ACTCCTCA	13216	C
			TGAGGAGTTTGT	AAT		
			ACTCCTCAAACG	TTG		
			C			
GAM1122	GNAI2	3'	AGCACAAGAAGCGT	GAGA	67544	GA_ C
			TCT	GCTTCTTG GCT		
			AGA	CGAAGAAC CGA		
			GTG	A		
GAM1122	HUNK	3'	AGCATAACTCAGATGG		27438	CTTC C
			CCATCTGAG	TTG GCT		
			GGTAGACTC	AAT CGA		
			_____	A		
GAM1122	IKBKB	3'	GAGCACAAAATGAGTTCAGATG		63208	C_ C
			CATCTGAGCTT	TTG GCTC		
			GTAGACTTGAG	AAC CGAG		
			TAA	A		
GAM1122	OSR1	3'	AGCACAGCCTCAGATGGA		17564	CTTC C
			TCCATCTGAG	TTG GCT		
			AGGTAGACTC	GAC CGA		
			C_	A		
GAM1122	PODXL	3'	GGCCAAAAGCTCAGA		18235	C C
			TCTGAGCTT	TTG GCT		
			AGACTCGAA	AAC CGG		
			-	-		
GAM1122	RGS2	3'	GAACGCAAGAAGGGAATAGGTG		11327	AG_ C
			CATCTG	CTTCTTGCG TC		
			GTGGAT	GAAGAACGC AG		
			AAGG	A		
GAM1122	UGT2B28	3'	GCTGGAAAACCAGATAGATG		53841	C AGC T
			CATC ATCTG	TTCT GC		
			GTAG TAGAC	AAGG CG		
			A	CAA T		
GAM1122	ABCA8	5'	CAAGGAGCTCAGTGGAT		23150	T
			ATCCA CTGAGCTTCTTG			

TAGGT GACTCGAGGAAC

GAM1122 CREG 3' TGATGAAACTCAGATGGA 13896 C TTG  
TCCATCTGAG TTC CG  
||||||| ||  
AGGTAGACTC AAG GT  
A TA\_  
GAM1122 FLJ12409 3' GAGCGCAAAGGATAGTGGA 47048 T AG C  
TCCA CTG CTT TTGCGCTC  
||| ||| ||| |||||  
AGGT GAT GGA AACGCGAG  
\_ A\_ \_  
GAM1122 FLJ32784 3' GAGAAGCTCAAGTGGA 58227 TC  
TCCA TGAGCTTCTT  
||| |||||  
AGGT ACTCGAAGAG  
GA  
GAM1122 HSPC065 3' AGCACAAGAGGCAGAGG 26288 A GA C  
CC TCT GCTTCTTG GCT  
|| ||| ||||| |||  
GG AGA CGGAGAAC CGA  
\_ \_ A  
GAM1122 KIAA0318 3' AGCACGCAGCTCAAATG 68945 C TCT C  
CAT TGAGCT TG GCT  
||| ||||| || |||  
GTA ACTCGA GC CGA  
A C\_ A  
GAM1122 KIAA0321 3' AGCACAAGAAGTCCTGGA 62385 TCT G C  
TCCA GA CTTCTTG GCT  
||| || ||||| |||  
AGGT CT GAAGAAC CGA  
C\_ \_ A  
GAM1122 KIAA0561 5' CGCAGCTCAGAGAATG 65879 CCA TCTT  
CAT TCTGAGCT GCG  
||| ||||| |||  
GTA AGACTCGA CGC  
AG\_ \_  
GAM1122 KIAA0963 5' GCGAGAAGCCCAGATAGA 30317 C A  
TC ATCTG GCTTCTTGC  
|| |||| |||||  
AG TAGAC CGAAGAGCG  
A C  
GAM1122 MGC4293 3' AGCGCTGCCAGATGGA 48520 A TTCTT  
TCCATCTG GC GCGCT  
||||| || |||||  
AGGTAGAC CG CGCGA  
C T\_\_\_\_  
GAM1122 PILR(BETA) 5' AAGAAGCCAGATGGAT 25551 A  
ATCCATCTG GCTTCTT  
||||||| |||||

TAGGTAGAC CGAAGAA

GAM1122 RNAHP 3' CGCAAGAAAAGTCGATG 23762 T GC\_  
CATC GA TTCTTGCG  
||||| || |||||  
GTAG CT AAGAACGC  
\_ GAA

GAM1122 ZNF313 3' AGCACAAAAAATCCTCAGATG 37938 C\_\_ C C  
CATCTGAG TT TTG GCT  
||||| || ||| |||  
GTAGACTC AA AAC CGA  
CTA A A

GAM1122 LOC148545 3' GAGACCAATGCCCAGATGGA 78898 A TTC CG  
TCCATCTG GC TTG CTC  
||||| || ||| |||  
AGGTAGAC CG AAC GAG  
C T\_\_ CA

GAM1122 LOC152698 5' GAGAAGCTCAGAAGATG 60425 CA  
CATC TCTGAGCTTCTT  
||| |||||  
GTAG AGACTCGAAGAG  
A\_

GAM1122 LOC200681 3' TGTGAAGCTCAAATGGAT 90108 C TT  
ATCCAT TGAGCTTC GCG  
||||| ||||| |||  
TAGGTA ACTCGAAG TGT  
A \_

GAM1122 LOC221463 3' AGCACAAGCCATGATGGATG 92064 \_ A TCT C  
CATCCATC TG GCT TG GCT  
||||| || ||| ||| |||  
GTAGGTAG AC CGA AC CGA  
T \_ \_ A

GAM1123 CEACAM1 3' CTCTCAGTGTCAATAGATGAA 8148 TA A A  
TTCAT CTGT GATA CTGAGAG  
||||| ||| ||| |||||  
AAGTA GATA CTGT GACTCTC  
\_ A \_

GAM1123 FTSJ2 3' TGTCTACAAAAATGAA 25436 AC  
TTCATT TG TAGATA  
||||| |||||  
AAGTAA ACATCTGT  
AA

GAM1123 NOV 3' TATCTACAGTAATGAA 10243  
TTCATTACTGTAGATA  
||||| |||||  
AAGTAATGACATCTAT

GAM1123 20D7-FC4 5' CTCTCAGTCACCCAGGCTGGA 60899 TTA TAGATA  
TTCA CTG ACTGAGAG  
||| ||| |||||

			AGGT GAC TGA	CTCTC	
			CG_ CCAC__		
GAM1123	HCNGP	3'	CTCTGAAATCACAGTAAT	25152	A AACT
			ATTACTGT GAT GAG		
			TAATGACA CTA CTC		
			_ AAGT		
GAM1123	KIAA1634	3'	GTTTCCACAGTAATGAA	63392	A T
			TTCATTACTGT GA AAC		
			AAGTAATGACA CT TTG		
			C _		
GAM1123	PIK3C2G	5'	CTCTCAGTTACATAAAATAA	15881	CTG GA
			TTA TA TAACTGAGAG		
			AAT AT ATTGA	CTCTC	
			AAA AC		
GAM1123	RPH3A	3'	CTCTCAGTTTGGGTAA	30243	G TAGAT
			TTACT AACTGAGAG		
			AATGG TTGA	CTCTC	
			GT__		
GAM1123	LOC130507	5'	CTCTCAGTTAAATGCAGCGA	74949	TA GA
			T CTGTA TAACTGAGAG		
			A GACGT ATTGA	CTCTC	
			GC AA		
GAM1123	LOC143970	3'	CTCCCAGTCAGATATAGTGA	83001	GATA A
			TTACTGTA ACTG GAG		
			AGTGATAT TGAC CTC		
			AGAC C		
GAM1124	CASQ2	3'	CTGATGCCCTGAGGCACTG	6936	AGATTC
			CAGTGCCTCA TCAG		
			GTCACGGAGT AGTC		
			CCCGT_		
GAM1124	LMAN1	3'	AGAACTAAGACATTGTGAA	18732	C CA A
			TTCACAGTG CT AG TTCT		
			AAGTGTTAC GA TC AAGA		
			A A_ _		
GAM1124	MUTYH	3'	CTGAGAATCCTGTTGTTAGT	24232	AGT CT A
			AC GC CA GATTCTCAG		
			TG TG GT CTAAGAGTC		
			AT_ TT C		
GAM1124	PDE4C	3'	CTGAGAATCCCAGCTACTCAGA	6233	AC C CAA
	A		TTC AGTG CT GATTCTCAG		



AAG TCAT GA CTAAGAGTC  
 AC C CC\_  
 GAM1124 TIMP3 3' TGAGTGTGAGGCACCTGAA 4520 CA AGATT  
 TTCA GTGCCTCA CTCA  
 ||| ||||| |||  
 AAGT CACGGAGT GAGT  
 C\_ GT\_  
 GAM1124 TRPS1 3' GGTCTTGAGACCTGTGAA 26076 TGC  
 TTCACAG CTCAAGATT  
 ||||| |||||  
 AAGTGTC GAGTTCTGG  
 CA\_  
 GAM1124 XKRY 3' CTGAAAATCATCCAGAAGCACT 60017 C AA\_\_ C  
 GTGA TCACAGTGC TC GATT TCAG  
 ||||| || ||| |||  
 AGTGTCACG AG CTAA AGTC  
 A ACCTA A  
 GAM1124 XKRY 3' CTGAAAATCATCCAGAAGCACT 16256 C AA\_\_ C  
 GTGA TCACAGTGC TC GATT TCAG  
 ||||| || ||| |||  
 AGTGTCACG AG CTAA AGTC  
 A ACCTA A  
 GAM1124 DKFZP727M111 3' TGGGCTGAGGCATATGAA 31415 CA AGATT  
 TTCA GTGCCTCA CTCA  
 ||| ||||| |||  
 AAGT TACGGAGT GGGT  
 A\_ C\_  
 GAM1124 DKFZp761D221 3' CTGAGAATTATCCAGCATATGA 50163 CA CTCAA  
 A TTCA GTGC GATTCTCAG  
 ||| ||| |||||  
 AAGT TACG TTAAGAGTC  
 A\_ ACCTA  
 GAM1124 FLJ12704 3' CTGATTGTTAGAAACACTGTGA 46534 CC AA TC  
 A TTCACAGTG TC GAT TCAG  
 ||||| || ||| |||  
 AAGTGTCAC AG TTG AGTC  
 AA A\_ TT  
 GAM1124 FLJ14213 3' CTGAGAATTTCTAGCATGTGAA 45794 G CTCA  
 TTCACA TGC AGATTCTCAG  
 ||||| ||| |||||  
 AAGTGT ACG TTAAAGAGTC  
 \_ ATC\_  
 GAM1124 GOLPH2 3' GAATACTGAAAACACTGTGAA 33321 GCC AG  
 TTCACAGT TCA ATTC  
 ||||| ||| |||  
 AAGTGTC A AGT TAAG  
 AA\_ CA  
 GAM1124 KIAA0326 3' GAGTCTGGAAGGCACTGTG 64328 \_ A  
 CACAGTGCCT C AGATTC  
 ||||| ||| |||

	GTGTCACGGA G TCTGAG	
	A G	
GAM1124 KIAA0757	3' GAATCCTGAGGCCACTGTGAA 20131	_ A
	TTCACAGTG CCTCA GATTC	
	AAGTGTAC GGAGT CTAAG	
	C C	
GAM1124 OSBPL6	5' CTGAGGATAAATCACTGTGAA 50715	CCTCAAG
	TTCACAGTG ATTCTCAG	
	AAGTGTAC TAGGAGTC	
	TAAA__	
GAM1124 SEC15B	3' TCTGAAACACTGTGAA 66688	CC A
	TTCACAGTG TCA GA	
	AAGTGTAC AGT CT	
	AA _	
GAM1124 TDP1	3' AATCTTGAGGCACTGTGAA 37043	
	TTCACAGTGCCTCAAGATT	
	AAGTGTACGGAGTTCTAA	
GAM1124 LOC148823	5' CTGAGAAACCGAGTCACTGTGA 59208	C AAGA
A	TTCACAGTG CTC TTCTCAG	
	AAGTGTAC GAG AAGAGTC	
	T CCA_	
GAM1124 LOC157858	3' CTGAAAATCCTGGCACAGCTGT 86589	___ TCAA C
GAA	TTCACAGT GCC GATT TCAG	
	AAGTGTG CGG CTAA AGTC	
	ACA TC__ A	
GAM1124 LOC163509	5' TGAGAATCCTCATCATGAA 82142	CA CCTCAA
	TTCA GTG GATTCTCA	
	AAGT TAC CTAAGAGT	
	AC TC__	
GAM1124 LOC220980	5' ATCACTGAGGCACTGTGA 93144	A_
	TCACAGTGCCTCA GAT	
	AGTGTACGGAGT CTA	
	CA	
GAM1124 LOC54499	3' GACTCTCAAGGCACTGTG 70631	CA T
	CACAGTGCCT AGA TC	
	GTGTCACGGA TCT AG	
	AC C	
GAM1124 LOC58512	3' AGCGTCGAGGTCACTGTGAA 64656	_ AA T
	TTCACAGTG CCTC GAT CT	

			AAGTGTAC GGAG CTG GA		
			T _ C		
GAM1125	BCRP2	3'	TCTCTTGTGTATATGCAA 62408	A	
			TTGCATATGCACAA AGG		
			AACGTATATGTGTT TCT		
			C		
GAM1125	DYRK1A	5'	TTGGCCAACATATGCAA 55253	CACAAAA	
			TTGCATATG GGTAA		
			AACGTATAC CCGGTT		
			AA_____		
GAM1125	EPHA3	3'	ACCCTGTACATATGTAA 17864	C AAA	
			TTGCATATG ACA GGT		
			AATGTATAC TGT CCA		
			A C_		
GAM1125	FUS2	5'	AACCTGGATCCTGTGCATAGGC 24114	A	AA_____
	AA		TTGC TATGCACA AGGTT		
			AACG ATACGTGT TCCAA		
			G CCTAGG		
GAM1125	GRB14	3'	AATAGTTTGTGCATTGCAA 15673	T	AG
			TTGCA ATGCACAAA GTT		
			AACGT TACGTGTTT TAA		
			_ GA		
GAM1125	IRTA1	3'	TCTTCTCATGCATATGCA 48422	CAA_	
			TGCATATGCA AAGG		
			ACGTATACGT TTCT		
			ACTC		
GAM1125	TKTL1	3'	AACTGTCACTGCATATGCAA 24295	CAAAA	
			TTGCATATGCA GGT		
			AACGTATACGT TCAA		
			CACTG		
GAM1125	FLJ10276	3'	AATTAACCTTTTGGTTGTTTGT 35959	T _	
	GCAA		TTGCATA GCA CAAAAGGTTAATT		
			AACGTGT TGT GTTTTCCAATTAA		
			T TG		
GAM1125	FLJ11011	3'	ACCTTTTCACATATGCAA 36975	CAC	
			TTGCATATG AAAAGGT		
			AACGTATAC TTTTCCA		
			AC_		
GAM1125	FLJ22655	3'	TAACCTTTGTATGCAA 45313	GCACA	
			TTGCATAT AAAGGTTA		

AACGTATG TTTCCAAT

GAM1125 HSPC067 5' AGCCTTTTGTACTATATGCAA 26333 C\_  
TTGCATATG ACAAAGGTT  
||||||| |||||||  
AACGTATAT TGTTTTCCGA  
CA

GAM1125 KIAA1203 3' AATTAACACACATATGCA 71632 CACAAAA  
TGCATATG GGTTAATT  
||||||| |||||||  
ACGTATAC TCAATTAA  
ACAACA\_

GAM1125 KIAA1971 3' GCCTTCTGTGCATATGGAA 74220 G A  
TT CATATGCACA AAGGT  
|| ||||||| |||||  
AA GTATACGTGT TTCCG  
G C

GAM1125 KLF5 3' TTTTGTAATATGCAA 8187 GC  
TTGCATAT ACAAAA  
||||||| |||||  
AACGTATA TGTTTT  
AA

GAM1125 TEB4 3' AATTTTTTAACATATGCAA 60652 CAC  
TTGCATATG AAAAGGTT  
||||||| |||||||  
AACGTATAC TTTTTTAA  
AA\_

GAM1125 LOC144347 3' AGCCTTTTCGCACACATGCA 76811 A\_\_ AC  
TGCAT TGC AAAAGGTT  
||||| ||| |||||||  
ACGTA ACG TTTTCCGA  
CAC C\_

GAM1125 LOC146952 5' TGGCTTTTATGCATATACA 83877 C CA  
TG ATATGCA AAAGGTTA  
|| ||||||| |||||||  
AC TATACGT TTTTCGGT  
A A\_

GAM1125 LOC81034 3' AATTAACCTTTGTGCA 47840 A  
TGCACAAA GGTTAATT  
||||||| |||||||  
ACGTGTTT CCAATTAA

GAM1126 AVPR1A 5' ACCAACACAACACAGCTTTCA 5532 ACA G A  
TGAAAG TGTTGTGT TG GT  
||||| ||||||| || ||  
ACTTTC ACAACACA AC CA  
GAC \_ \_

GAM1126 BCLG 3' GACTCACAGCTTCCACCCTTTC 56987 ACATGTT G  
A TGAAAG GT TGTGAGTC  
||||| || |||||||

ACTTTC CG ACACTCAG  
 CCACCTT \_  
 GAM1126 CACNA2D2 3' GACTCACATTCGACAT 20086 T  
 ATGTTG GTGTGAGTC  
 ||||| |||||  
 TACAGC TACACTCAG  
 T  
 GAM1126 CKTSF1B1 3' GACCCAGCTGAACATGTCTT 25367 GT G A  
 AAGACATGTT GT TG GTC  
 ||||| || || ||  
 TTCTGTACAA CG AC CAG  
 GT \_ C  
 GAM1126 GPR81 5' ACCCACACACACAGGACCCGCA 50747 AAAGACA T A  
 TG TGT GTGTGTG GT  
 || || ||||| ||  
 AC ACA CACACAC CA  
 GCCCAGG \_ C  
 GAM1126 HD 3' TTTACACACACCTCTCA 9196 A CA T  
 A AGA TGT GTGTGTGAG  
 | || || |||||  
 A TCT ACA CACACATTT  
 C CC \_  
 GAM1126 KLF7 3' GACCCACACACATACACACTGT 13541 \_ \_ A  
 C GACA TGT TGTGTGTG GTC  
 ||| || ||||| ||  
 CTGT ACA ACACACAC CAG  
 C CAT C  
 GAM1126 PSME3 3' TCACATACCTTTCA 19377 ACATGTT  
 TGAAAG GTGTGTGA  
 |||| |||||  
 ACTTTC CATACT  
  
 GAM1126 DNAJC6 3' ACTCCAGTAACATGTTTTCA 28840 A G T  
 TGAA GACATGTTGT TG GAGT  
 ||| ||||| || |||  
 ACTT TTGTACAATG AC CTCA  
  
 GAM1126 FLJ11164 3' GACTCACAGGCCAACATGTGTT 37123 A G \_ G  
 CCA TG AA ACATGTTG T TGTGAGTC  
 || || ||||| | |||||  
 AC TT TGTACAAC G ACACTCAG  
 C G C G  
 GAM1126 HIP-55 3' ACACAACATGTTCTC 25925 AA  
 GA GACATGTTGTGT  
 || |||||  
 CT TTGTACAACACA  
 CC  
 GAM1126 KIAA1275 3' GACTCAATCACACGCTCTTCA 61547 A CAT T \_  
 TGAA GA GT GTGTG TGAGTC  
 ||| || || ||| |||||

ACTT CT CG CACAC ACTCAG  
 — — — TA  
 GAM1126 KIAA1301 3' ACCCAACCGTCTTTCA 66339 AT T  
 TGAAAGAC GTTG GT  
 ||||| |||  
 ACTTTCTG CAAC CA  
 C\_ C  
 GAM1126 KIAA1915 5' ACTCTTACATGCCTTTCA 73271 A TGTGTGT  
 TGAAAG CATGT GAGT  
 ||||| |||  
 ACTTTC GTACA CTCA  
 C TT\_\_\_\_  
 GAM1126 MGC20255 3' ACCCACACACACCACCATCTCA 53437 A CA\_ T A  
 A AGA TG TGTGTGTG GT  
 | || || ||||| ||  
 A TCT AC ACACACAC CA  
 C ACC C C  
 GAM1126 PAL 3' ACTCACACACCTGCCTG 31549 T T\_  
 CA GT GTGTGTGAGT  
 || || |||||  
 GT CG CACACACTCA  
 C TC  
 GAM1126 PRO0365 5' CACACACACACCTTTCA 26149 ACA T  
 TGAAAG TGT GTGTGTG  
 ||||| || |||||  
 ACTTTC ACA CACACAC  
 C\_\_ \_  
 GAM1126 RASSF2 3' CACACAACACACTTCCA 28429 A ACA  
 TG AAG TGTTGTGTG  
 || || |||||  
 AC TTC ACAACACAC  
 C AC\_  
 GAM1126 STX1B2 3' ACTCACACTCAGATTCTCA 53514 A C T T  
 A AGA ATGT G GTGTGAGT  
 | || |||| | |||||  
 A TCT TACA C CACACTCA  
 C \_ \_ T  
 GAM1126 LOC121219 3' GCACAACCTGCCTCTCA 74047 A A T  
 TGA AG CA GTTGTGT  
 ||| || |||||  
 ACT TC GT CAACACG  
 C C \_  
 GAM1126 LOC123242 5' GACTACAGACAACATGGCCTTC 75599 AGA G G  
 A TGAA CATGTTGT TGT AGTC  
 ||| ||||| || |||  
 ACTT GTACAACA ACA TCAG  
 CCG G \_  
 GAM1126 LOC124753 3' ACTCACACCCCTCTCTCA 74317 A CATGTTGT  
 TGA AGA GTGTGAGT  
 ||| || |||||

		ACT TCT	CACACTCA		
		C	CCC_____		
GAM1126	LOC144453 3'	ACACAACATGGCTTTCA	76843	A	
		TGAAAG CATGTTGTGT			
		ACTTTC GTACAACACA			
		G			
GAM1126	LOC149706 5'	GACTCACACAAGACCCCTC	84642	CAT	G
		GA GTT TGTGTGAGTC			
		CT CAG ACACACTCAG			
		CCC A			
GAM1126	LOC151201 3'	ATTCATAACATGTCCTTCA	85272	A	T
		TGAA GACATGTTGTG GT			
		ACTT CTGTACAATAC TA			
		C T			
GAM1126	LOC196955 3'	GACTACAGACAACATGGCCTTC	77375	AGA	G G
	A	TGAA CATGTTGT TGT AGTC			
		ACTT GTACAACA ACA TCAG			
		CCG G _			
GAM1126	LOC200782 5'	GACTCACAGCCACACGTC	89507	A T	G
		GAC TGT GT TGTGAGTC			
		CTG ACA CG ACACTCAG			
		C C _			
GAM1126	LOC200982 5'	GACCCACACGGTTGCATGACCT	90221	AGA	TG_ A
	TCA	TGAA CATGT TGTGTG GTC			
		ACTT GTACG GCACAC CAG			
		CCA TTG C			
GAM1126	LOC253001 5'	GACTACAGACAACATGGCCTTC	96257	AGA	G G
	A	TGAA CATGTTGT TGT AGTC			
		ACTT GTACAACA ACA TCAG			
		CCG G _			
GAM1126	LOC51157 3'	ACCCACACAGCGTCACTCA	32487	AA AT	TGA
		TGA GAC GTTGTGTG GT			
		ACT CTG CGACACAC CA			
		CA _ C_			
GAM1127	ACVR1 5'	ACTGCAGCCTCCACCTC	6599	A	
		GAGGT GAGGTTGCAGT			
		CTCCA CTCCGACGTCA			
		C			
GAM1127	AGTR1 5'	AACTCACTGATGCCATCC	5469	TAGA	TG
		GG GGT CAGTGAGTT			

CC CCG GTCACTCAA  
 TA\_\_ TA  
 GAM1127 AGTR1 5' AACTCACTGATGCCATCC 49004 TAGA TG  
 GG GGT CAGTGAGTT  
 || ||| |||||  
 CC CCG GTCACTCAA  
 TA\_\_ TA  
 GAM1127 AHR 3' GCTCACTGCAACCTCTACCTC 7879  
 GAGGTAGAGGTTGCAGTGAGT  
 |||||  
 CTCCATCTCCAACGTCACCTCG  
  
 GAM1127 AIM1 3' ACTGCAGCCTCTACCTC 91813  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCATCTCCGACGTCA  
  
 GAM1127 ALDH1B1 3' ACTGCAACCTCCGCCTC 5486 TA  
 GAGG GAGGTTGCAGT  
 ||| |||||  
 CTCC CTCCAACGTCA  
 GC  
 GAM1127 AP3B2 5' GCCGCAACCTCCTCCTC 16189 TA A  
 GAGG GAGGTTGC GT  
 ||| ||||| ||  
 CTCC CTCCAACG CG  
 TC C  
 GAM1127 APPBP2 3' ACTGCAACCTCCGCCTC 21069 TA  
 GAGG GAGGTTGCAGT  
 ||| |||||  
 CTCC CTCCAACGTCA  
 GC  
 GAM1127 AQP6 3' GCTCACTGCAACCTCTACCTC 7954  
 GAGGTAGAGGTTGCAGTGAGT  
 |||||  
 CTCCATCTCCAACGTCACCTCG  
  
 GAM1127 AQP6 3' GCTCACTGCAACCTCTACCTC 53930  
 GAGGTAGAGGTTGCAGTGAGT  
 |||||  
 CTCCATCTCCAACGTCACCTCG  
  
 GAM1127 ARCN1 3' ACTGCAACCTCCGCCTC 7967 TA  
 GAGG GAGGTTGCAGT  
 ||| |||||  
 CTCC CTCCAACGTCA  
 GC  
 GAM1127 ATP8B2 3' AGCTCACTGCAACCTCCACCTC 65210 A  
 GAGGT GAGGTTGCAGTGAGTT  
 |||||



			CTCCA CTCCAACGTC	ACTCGA		
			C			
GAM1127	BRIP1	3'	ACTGCAACCTTCACCTC	49394	AG	
			GAGGT AGGTTGCAGT			
			CTCCA TCCAACGTCA			
			CT			
GAM1127	C7	3'	CTGCAACCTCCGCCTC	5162	TA	
			GAGG GAGGTTGCAG			
			CTCC CTCCAACGTC			
			GC			
GAM1127	CAMLG	3'	ACCGCAACCTCCACCTT	8229	A	A
			GAGGT GAGGTTGC GT			
			TTCCA CTCCAACG CA			
			C C			
GAM1127	CCNF	3'	AACTCACTGTAACCTCCGCCTC	8309	TA	
			GAGG GAGGTTGCAGTGAGTT			
			CTCC CTCCAATGTCACTCAA			
			GC			
GAM1127	CDH17	3'	ACTGCAACCTCCGCCTC	14498	TA	
			GAGG GAGGTTGCAGT			
			CTCC CTCCAACGTCA			
			GC			
GAM1127	CIAS1	5'	ACTGCAGCCTCCACCTC	16896	A	
			GAGGT GAGGTTGCAGT			
			CTCCA CTCCGACGTCA			
			C			
GAM1127	COX15	3'	ACTCTGCAACCTCCACTTC	54309	A	GT
			GAGGT GAGGTTGCA GAGT			
			CTTCA CTCCAACGT CTCA			
			C			
			—			
GAM1127	CRTAP	3'	ACTGCAACCTCCGCCTC	21029	TA	
			GAGG GAGGTTGCAGT			
			CTCC CTCCAACGTCA			
			GC			
GAM1127	CSNK2A2	5'	AGCTCACTGCAACCTCCACCTC	8559	A	
			GAGGT GAGGTTGCAGTGAGTT			
			CTCCA CTCCAACGTC	ACTCGA		
			C			
GAM1127	CXCL16	3'	GCTCACTGCAACCCCCATCTC	41920	AGA	
			GAGGT GGTTCAGTGAGT			

			CTCTA CCAACGTC	ACTCG		
			CCC			
GAM1127	CYLN2	3'	CTGCAGCCTCCACCTC	12633	A	
			GAGGT GAGGTTGCAG			
			CTCCA CTCCGACGTC			
			C			
GAM1127	CYP1A2	3'	ACTACAACCTCCGCCTC	5670	TA	C
			GAGG GAGGTTG AGT			
			CTCC CTCCAAC TCA			
			GC A			
GAM1127	CYP1A2	3'	ACTGCAACCTCTGCCTC	5672		
			GAGGTAGAGGTTGCAGT			
			CTCCGTCTCCAACGTCA			
GAM1127	CYP1A2	3'	AGCTCACTGCAACCTCCACCTC	5674	A	
			GAGGT GAGGTTGCAGTGAGTT			
			CTCCA CTCCAACGTC	ACTCGA		
			C			
GAM1127	CYP1A2	3'	ACTACAACCTCCGCCTC	69089	TA	C
			GAGG GAGGTTG AGT			
			CTCC CTCCAAC TCA			
			GC A			
GAM1127	CYP1A2	3'	ACTGCAACCTCTGCCTC	69091		
			GAGGTAGAGGTTGCAGT			
			CTCCGTCTCCAACGTCA			
GAM1127	CYP1A2	3'	AGCTCACTGCAACCTCCACCTC	69093	A	
			GAGGT GAGGTTGCAGTGAGTT			
			CTCCA CTCCAACGTC	ACTCGA		
			C			
GAM1127	CYP2B6	3'	GCTCACTGCAACCTCCACC	5733	A	
			GGT GAGGTTGCAGTGAGT			
			CCA CTCCAACGTC	ACTCG		
			C			
GAM1127	CYP4F3	3'	ATTGCAACCTCCGCCTC	6108	TA	
			GAGG GAGGTTGCAGT			
			CTCC CTCCAACGTTA			
			GC			
GAM1127	CYP8B1	3'	ACTACAACCTCTGCCTC	15251		C
			GAGGTAGAGGTTG AGT			

			CTCCGTCTCCAAC TCA	
			A	
GAM1127	CYP8B1	3'	ACTGCAACCTCTGCCTC 15253	
			GAGGTAGAGGTTGCAGT	
			CTCCGTCTCCAACGTCA	
GAM1127	DFFB	3'	ACTGCAACCTCCGCCTC 87373	TA
			GAGG GAGGTTGCAGT	
			CTCC CTCCAACGTCA	
			GC	
GAM1127	DISC1	3'	GCTCACTGCAACCTCTACCTC 37881	
			GAGGTAGAGGTTGCAGTGAGT	
			CTCCATCTCCAACGTCACTCG	
GAM1127	DSCR3	3'	AGCTCACTGCAACCTCCACCTC 20171	A
			GAGGT GAGGTTGCAGTGAGTT	
			CTCCA CTCCAACGTCACTCGA	
			C	
GAM1127	EHD2	3'	AGCTCACTGCAACCTCCACCTC 27485	A
			GAGGT GAGGTTGCAGTGAGTT	
			CTCCA CTCCAACGTCACTCGA	
			C	
GAM1127	EPB72	3'	ACTGCAACCTCCGCCTC 14596	TA
			GAGG GAGGTTGCAGT	
			CTCC CTCCAACGTCA	
			GC	
GAM1127	F2RL2	3'	ATTGCAACCTCTGCCTC 14618	
			GAGGTAGAGGTTGCAGT	
			CTCCGTCTCCAACGTTA	
GAM1127	FEZ1	3'	GCTCACTGCAACCTCCACCTC 42573	A
			GAGGT GAGGTTGCAGTGAGT	
			CTCCA CTCCAACGTCACTCG	
			C	
GAM1127	FGF5	3'	GCTCACTGCAACCTCCAACTC 15542	GTA
			GAG GAGGTTGCAGTGAGT	
			CTC CTCCAACGTCACTCG	
			AAC	
GAM1127	FGF5	3'	GCTCACTGCAACCTCCAACTC 52488	GTA
			GAG GAGGTTGCAGTGAGT	

			CTC CTCCAACGTCACTCG	
			AAC	
GAM1127 FHL2	5'	AGCTCACTGCAAGCTCTACCTC 7560		G
		GAGGTAGAG TTGCAGTGAGTT		
		CTCCATCTC AACGTCACTCGA		
		G		
GAM1127 FZD4	3'	ACTGCAACCTCTGCCTC 24121		
		GAGGTAGAGGTTGCAGT		
		CTCCGTCTCCAACGTCA		
GAM1127 G6PC	3'	ACTGCAACCTCTTCCTC 3817	T	
		GAGG AGAGGTTGCAGT		
		CTCC TCTCCAACGTCA		
		T		
GAM1127 GHR	3'	ACTCACTGCAATCTCCACCTC 3873	A	
		GAGGT GAGGTTGCAGTGAGT		
		CTCCA CTCTAACGTCACTCA		
		C		
GAM1127 GM2A	3'	ACTGCAACCTCCGCCTC 67767	TA	
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		GC		
GAM1127 GPR4	3'	ACTGCAGCCTCCACCTC 59898	A	
		GAGGT GAGGTTGCAGT		
		CTCCA CTCCGACGTCA		
		C		
GAM1127 GPR81	3'	ACTGCAACCTCTGCCTC 50750		
		GAGGTAGAGGTTGCAGT		
		CTCCGTCTCCAACGTCA		
GAM1127 GRAF	3'	ACTGCAACCTCCGCCTC 30548	TA	
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		GC		
GAM1127 HTR1E	5'	ATTGCAACCTCCGCCTC 6009	TA	
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTTA		
		GC		
GAM1127 IL11	3'	TAAGTCAAGCTCCACCTC 5335	A G	
		GAGGT GAG TTGCAGTGA		

			CTCCA CTC AACGTCACT		
			C G		
GAM1127	ITGAM	3'	ACTGCAACCTCCGCCTC 71833	TA	
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	KMO	3'	ACTGCAACCTCTGCCTC 13440		
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	LANCL1	3'	ACTCACTGCATGACCCT 20207	A	—
			AG GGT TGCAGTGAGT		
			TC CCA ACGTCACTCA		
			— GT		
GAM1127	LILRA3	3'	ACTGCAACCTCCGCCTC 95304	TA	
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	LNK	3'	ACTGCAACCTCCACCTT 18454	A	
			GAGGT GAGGTTGCAGT		
			TTCCA CTCCAACGTCA		
			C		
GAM1127	LSS	3'	CTCAACCTCTATCTC 9818	C	
			GAGGTAGAGGTTG AG		
			CTCTATCTCCAAC TC		
GAM1127	LYZ	3'	GCTCACTGCAACCTCCACCTC 4103	A	
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACTCG		
			C		
GAM1127	MAK	3'	ACTGCAACCTCCACCTC 19753	A	
			GAGGT GAGGTTGCAGT		
			CTCCA CTCCAACGTCA		
			C		
GAM1127	MEF2A	5'	ACTGCAACCTCCGCCTC 18777	TA	
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	MEFV	3'	ACTGCAACCTCCGCCTC 4122	TA	
			GAGG GAGGTTGCAGT		

CTCC CTCCAACGTCA  
 GC  
 GAM1127 MEFV 3' AGCTCACTGCAACCTCCACCTC 4125 A  
 GAGGT GAGGTTGCAGTGAGTT  
 ||||| |||||  
 CTCCA CTCCAACGTCACTCGA  
 C  
 GAM1127 MHC2TA 3' ACTGCAACCTCCGCCTC 4159 TA  
 GAGG GAGGTTGCAGT  
 ||||| |||||  
 CTCC CTCCAACGTCA  
 GC  
 GAM1127 MICB 3' ACTGCAACCTCTGCCTC 19817  
 GAGGTAGAGGTTGCAGT  
 ||||| |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 MPL 3' ACTGCAACCTCTGCCTC 18128  
 GAGGTAGAGGTTGCAGT  
 ||||| |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 MPL 3' AGCTCACTGCAACCTCCACCTC 18131 A  
 GAGGT GAGGTTGCAGTGAGTT  
 ||||| |||||  
 CTCCA CTCCAACGTCACTCGA  
 C  
 GAM1127 MRPL49 3' ACTGCAACTTCCACCTC 69563 A  
 GAGGT GAGGTTGCAGT  
 ||||| |||||  
 CTCCA CTCAACGTCA  
 C  
 GAM1127 MYCL2 3' ACTGCAACCTCTGCCTC 18171  
 GAGGTAGAGGTTGCAGT  
 ||||| |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 NQO1 3' ACTGCAACCTCTGCCTC 6149  
 GAGGTAGAGGTTGCAGT  
 ||||| |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 PCDHB11 3' ACTGCAACCTCTGCCTC 38408  
 GAGGTAGAGGTTGCAGT  
 ||||| |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 PCDHB16 3' ACTGCAACCTCTGCCTC 40546  
 GAGGTAGAGGTTGCAGT  
 ||||| |||||

CTCCGTCTCCAACGTCA

GAM1127 PCDHB9 3' ACTGCAACCTCCGCCTC 38933 TA  
GAGG GAGGTTGCAGT  
|||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 PDCL 3' GCTCACTGCAACCTCCACCTC 18214 A  
GAGGT GAGGTTGCAGTGAGT  
|||| |||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1127 PDE6B 3' AGCTCACTGCAACCTCCACCTC 4271 A  
GAGGT GAGGTTGCAGTGAGTT  
|||| |||||  
CTCCA CTCCAACGTCACTCGA  
C

GAM1127 PER2 3' ACTGCAACCTCTGCCTC 43025  
GAGGTAGAGGTTGCAGT  
|||| |||||  
CTCCGTCTCCAACGTCA

GAM1127 PIGR 3' ACTGCAACCTCCGCCTC 72589 TA  
GAGG GAGGTTGCAGT  
|||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 PON1 3' ACTGCAACTTCTACCTC 4798  
GAGGTAGAGGTTGCAGT  
|||| |||||  
CTCCATCTTCAACGTCA

GAM1127 PPP1R12B 3' ACTCACTTCCCTCCTC 49477 T A TTGC  
GAGG AG GG AGTGAGT  
|||| || |||||  
CTCC TC CC TCACTCA  
\_ \_ T\_

GAM1127 PRKWNK3 3' ACTGCTGCAACCTCCCCCTC 61550 TA G  
GAGG GAGGTTGCAGT AGT  
|||| ||||| |||  
CTCC CTCCAACGTCTG TCA  
CC \_

GAM1127 PSMB2 3' ACTGCAACCTCCGCCTC 10945 TA  
GAGG GAGGTTGCAGT  
|||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 RHD 3' ACTGCAACCTCCGCCTC 32291 TA  
GAGG GAGGTTGCAGT  
|||| |||||

		CTCC CTCCAACGTCA	
		GC	
GAM1127 RHD	3'	GCTCACTGCAACCTCTACCTC 32308	
		GAGGTAGAGGTTGCAGTGAGT	
		CTCCATCTCCAACGTCACTCG	
GAM1127 RHD	3'	ACTGCAACCTCCGCCTC 32600	TA
		GAGG GAGGTTGCAGT	
		CTCC CTCCAACGTCA	
		GC	
GAM1127 RHD	3'	GCTCACTGCAACCTCTACCTC 32617	
		GAGGTAGAGGTTGCAGTGAGT	
		CTCCATCTCCAACGTCACTCG	
GAM1127 RPH3AL	3'	GCTCACTGCAACCTCCACCTC 22748	A
		GAGGT GAGGTTGCAGTGAGT	
		CTCCA CTCCAACGTCACTCG	
		C	
GAM1127 SAS	3'	ACCGCAACCTCTGCCTC 19947	A
		GAGGTAGAGGTTGC GT	
		CTCCGTCTCCAACG CA	
		C	
GAM1127 SEDL	3'	ACTGCAACCTCCGCCTC 27320	TA
		GAGG GAGGTTGCAGT	
		CTCC CTCCAACGTCA	
		GC	
GAM1127 SEDL	3'	GCTCACTGCAACCTCCACCTC 27342	A
		GAGGT GAGGTTGCAGTGAGT	
		CTCCA CTCCAACGTCACTCG	
		C	
GAM1127 SEDL	3'	GCTCACTGCAACCTCCACCTC 27343	A
		GAGGT GAGGTTGCAGTGAGT	
		CTCCA CTCCAACGTCACTCG	
		C	
GAM1127 SEPN1	3'	GCTCACTGCAACCTCCACCTC 66371	A
		GAGGT GAGGTTGCAGTGAGT	
		CTCCA CTCCAACGTCACTCG	
		C	
GAM1127 SERPINB9	3'	ACTGCAACCTCCTCCTC 14745	TA
		GAGG GAGGTTGCAGT	



			CTCC CTCCAACGTCA		
			TC		
GAM1127	SHOX	3'	ACTGCAACCTCCGCCTC	22527	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	SIL	3'	ACTGCAACCTCTGCCTC	11679	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	SLA2	3'	AGCTCACTGCAACCTCCATCTC	49889	A
			GAGGT GAGGTTGCAGTGAGTT		
			CTCTA CTCCAACGTCACTCGA		
			C		
GAM1127	SLC14A2	5'	GCTCACTGCAACCTCCACCTC	23134	A
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACTCG		
			C		
GAM1127	SLC15A1	3'	ACTGCAACCTCCGCCTC	17394	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	SMAC	5'	ACTGCAACCTCTGCCTC	57201	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	SNAP23	3'	ACTGCAACCTCCGCCTC	55455	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	SNAP23	3'	ACTGCAACCTCCGCCTC	13802	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	SNX15	3'	GCTCACTGCAACCTCCACCTC	73742	A
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACTCG		
			C		
GAM1127	SPN	3'	ACTGCAACCTCTGCCTC	11912	
			GAGGTAGAGGTTGCAGT		

CTCCGTCTCCAACGTCA

GAM1127 SS18 3' ACTGCAACCTCCGCCTC 18879 TA  
GAGG GAGGTTGCAGT  
|||| ||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 STAU 5' CTGCAACCTCCACCTC 16003 A  
GAGGT GAGGTTGCAG  
|||| ||||||||  
CTCCA CTCCAACGTC  
C

GAM1127 STAU 5' GCTCACTGCAACCTCCACCTC 16005 A  
GAGGT GAGGTTGCAGTGAGT  
|||| ||||||||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1127 SULT2B1 5' ACTGCAACCTCCGCCTC 16018 TA  
GAGG GAGGTTGCAGT  
|||| ||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 TAPBP 3' ACTGCAACCTCCGCCTC 12117 TA  
GAGG GAGGTTGCAGT  
|||| ||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 TAT 3' GCTCACTGCAACCTCCACCTC 4470 A  
GAGGT GAGGTTGCAGTGAGT  
|||| ||||||||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1127 TBXA2R 3' ACTGCAACCTCCGCCTC 6475 TA  
GAGG GAGGTTGCAGT  
|||| ||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 TBXA2R 3' AGCTCACTGCAACCTCCACCTC 6480 A  
GAGGT GAGGTTGCAGTGAGTT  
|||| ||||||||||  
CTCCA CTCCAACGTCACTCGA  
C

GAM1127 TMC1 5' CTGCAACCTCCGCCTC 56903 TA  
GAGG GAGGTTGCAG  
|||| ||||||||  
CTCC CTCCAACGTC  
GC

GAM1127 TPMT 3' ACTGCAACCTCTGCCTC 4531  
GAGGTAGAGGTTGCAGT  
||||||||||||

CTCCGTCTCCAACGTCA

GAM1127	TRIM9	5'	ACTGCAACCTCCGCCTC	30745	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	TRPM6	3'	ACTGCAACCTCTGCCTC	34528	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	TRPV1	3'	ACTGCAACCTCTGCCTC	38069	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	TRPV1	3'	CTGCAACCTCCGCCTC	38081	TA
			GAGG GAGGTTGCAG		
			CTCC CTCCAACGTC		
			GC		
GAM1127	TRPV1	3'	ACTGCAACCTCTGCCTC	54788	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	TRPV1	3'	CTGCAACCTCCGCCTC	54802	TA
			GAGG GAGGTTGCAG		
			CTCC CTCCAACGTC		
			GC		
GAM1127	TRPV1	3'	ACTGCAACCTCTGCCTC	54823	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	TRPV1	3'	CTGCAACCTCCGCCTC	54835	TA
			GAGG GAGGTTGCAG		
			CTCC CTCCAACGTC		
			GC		
GAM1127	TRPV1	3'	ACTGCAACCTCTGCCTC	54855	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	TRPV1	3'	CTGCAACCTCCGCCTC	54867	TA
			GAGG GAGGTTGCAG		

			CTCC CTCCAACGTC		
			GC		
GAM1127	TUBA3	5'	GCAACAACCTCTCCTC	20024	T CA
			GAGG AGAGGTTG GT		
			CTCC TCTCCAAC CG		
			— AA		
GAM1127	TUFT1	3'	ACTGCAACCTCTGCCTC	39247	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	VENTX2	3'	ACTGCAACCTCCGCCTC	27104	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	VHL	3'	ACTGCAACCTCTGCCTC	5053	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	ZNF133	5'	AACTCACTGCAACCTCCACC	12828	A
			GGT GAGGTTGCAGTGAGTT		
			CCA CTCCAACGTCACTCAA		
			C		
GAM1127	ZNF264	3'	ACTGCAACCTCCGCCTC	12742	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	ZNF264	3'	CTGCAACCTCTGCCTC	12754	
			GAGGTAGAGGTTGCAG		
			CTCCGTCTCCAACGTC		
GAM1127	20D7-FC4	5'	ACTGCAGCCTCCACCTC	60892	A
			GAGGT GAGGTTGCAGT		
			CTCCA CTCCGACGTCA		
			C		
GAM1127	ARHF	3'	GCTCACTGCAAGCTCCACCTC	38745	A G
			GAGGT GAG TTGCAGTGAGT		
			CTCCA CTC AACGTCACTCG		
			C G		
GAM1127	ARPP-19	3'	ACTGCAACCTCTGCCTC	21784	
			GAGGTAGAGGTTGCAGT		

CTCCGTCTCCAACGTCA

GAM1127 ASB16 5' ACTGCAACCTCCGCCTC 69929 TA  
GAGG GAGGTTGCAGT  
|||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 ASE-1 3' ACTGCAACCTCCGCCTC 23941 TA  
GAGG GAGGTTGCAGT  
|||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 ATP1B4 3' GCTCACTGCAACCTCCACCTC 23821 A  
GAGGT GAGGTTGCAGTGAGT  
|||| |||||||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1127 BA108L7.2 3' ACTGCAACCTCTGCCTC 48250  
GAGGTAGAGGTTGCAGT  
|||||||||||  
CTCCGTCTCCAACGTCA

GAM1127 BAG5 3' AGCTCACTGCAACCTCCACCTC 16837 A  
GAGGT GAGGTTGCAGTGAGTT  
|||| |||||||||  
CTCCA CTCCAACGTCACTCGA  
C

GAM1127 BNIP-S 3' ACTGCAACCTCCGCCTC 56254 TA  
GAGG GAGGTTGCAGT  
|||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 BTN3A1 3' CTGCAACCTCCACCTC 22919 A  
GAGGT GAGGTTGCAG  
|||| |||||||||  
CTCCA CTCCAACGTC  
C

GAM1127 C1orf24 3' ACTGCAACCTCCGCCTC 53703 TA  
GAGG GAGGTTGCAGT  
|||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 C1QTNF6 3' ACTGCAACCTCTGCCTC 49134  
GAGGTAGAGGTTGCAGT  
|||||||||||  
CTCCGTCTCCAACGTCA

GAM1127 C21orf25 3' ACTGCAACCTCCACCTC 63540 A  
GAGGT GAGGTTGCAGT  
|||| |||||||||

			CTCCA CTCCAACGTCA		
			C		
GAM1127	C3F	3'	AGCTCACGCAACCTCCACCTC 19283	A	A
			GAGGT GAGGTTGC GTGAGTT		
			CTCCA CTCCAACG CACTCGA		
			C C		
GAM1127	C9orf9	3'	ACTGCAACCTCCGCCTC 38501	TA	
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	C9orf9	3'	GCTCACTGCAACCTCCACCTC 38516	A	
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACTCG		
			C		
GAM1127	CAMKK1	3'	ACCCAGCCTCTCCTC 50169	T	CA
			GAGG AGAGGTTG GT		
			CTCC TCTCCGAC CA		
			- C -		
GAM1127	CEACAM8	3'	AACTCACTGCAAGCTCCGCCTC 8419	TA	G
			GAGG GAG TTGCAGTGAGTT		
			CTCC CTC AACGTCACTCAA		
			GC G		
GAM1127	CENPH	3'	ACTGCAACCTCTGCCTC 43268		
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	CHRA1	3'	ACTGCAACCTCCGCCTC 33862	TA	
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	CLSTN2	3'	AACTCACTGTGCGTCTCCTC 42118	T	G T
			GAGG AGA GT GCAGTGAGTT		
			CTCC TCT CG TGTCCTCAA		
			- G -		
GAM1127	CPSF2	3'	ACCGCAACCTCTGCCTC 61567		A
			GAGGTAGAGGTTGC GT		
			CTCCGTCTCCAACG CA		
			C		
GAM1127	DBR1	3'	ACCGCAACCTCCGCCTC 32525	TA	A
			GAGG GAGGTTGC GT		

		CTCC CTCCAACG CA		
		GC C		
GAM1127	DKFZp434A2417 3'	ACTGCAACTTCCACCTC	66092	A
		GAGGT GAGGTTGCAGT		
		CTCCA CTTCAACGTCA		
		C		
GAM1127	DKFZP434C212 3'	GCTCACTGCAACCTCCACCTC	68913	A
		GAGGT GAGGTTGCAGTGAGT		
		CTCCA CTCCAACGTCACTCG		
		C		
GAM1127	DKFZp434E2220 5'	ACTGCAACCTCCGCCTC	34291	TA
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		GC		
GAM1127	DKFZp547H025 3'	AGCTCACTGCAACCTCCACCTC	39349	A
		GAGGT GAGGTTGCAGTGAGTT		
		CTCCA CTCCAACGTCACTCGA		
		C		
GAM1127	DKFZP564O0523 3'	GCTCACTGCAACCTCCACCTC	49516	A
		GAGGT GAGGTTGCAGTGAGT		
		CTCCA CTCCAACGTCACTCG		
		C		
GAM1127	DKFZp761J139 5'	ACTGCAACGTCCACCTC	50103	A G
		GAGGT GA GTTGCAGT		
		CTCCA CT CAACGTCA		
		C G		
GAM1127	DKFZp761N1114 3'	ACTGCAACCTCCGCCTC	79011	TA
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		GC		
GAM1127	DKFZp762P2111 3'	ACTGCAACCTCCGCCTC	86348	TA
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		GC		
GAM1127	DSCR6 3'	ACTGCAACCTCCACTTC	38539	A
		GAGGT GAGGTTGCAGT		
		CTTCA CTCCAACGTCA		
		C		
GAM1127	EREG 3'	GCTCACTGCAACCTCACCTC	7503	A
		GAGGT GAGGTTGCAGTGAGT		

CTCCA CTCCAACGTCACTCG

GAM1127 FBP17 3' GCTCACTACAACCTCCACCTC 72796 A C  
GAGGT GAGGTTG AGTGAGT  
||||| ||||| |||||  
CTCCA CTCCAAC TCACTCG  
C A

GAM1127 FER1L4 3' ACTGCAACCTCCACCTC 47326 A  
GAGGT GAGGTTGCAGT  
||||| |||||  
CTCCA CTCCAACGTCA  
C

GAM1127 FER1L4 3' ACTGCAACCTCCACCTC 47328 A  
GAGGT GAGGTTGCAGT  
||||| |||||  
CTCCA CTCCAACGTCA  
C

GAM1127 FLJ00024 5' ACTGCAACCTCTGCCTC 63745  
GAGGTAGAGGTTGCAGT  
||||| |||||  
CTCCGTCTCCAACGTCA

GAM1127 FLJ10232 3' ACTGCAACCTCCGCCTC 35918 TA  
GAGG GAGGTTGCAGT  
||||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 FLJ10346 5' GCTCACTGCAAGCTCCACCTC 36045 A G  
GAGGT GAG TTGCAGTGAGT  
||||| ||| |||||  
CTCCA CTC AACGTCACTCG  
C G

GAM1127 FLJ10535 3' ACTGCAACCTCTGCCTC 36231  
GAGGTAGAGGTTGCAGT  
||||| |||||  
CTCCGTCTCCAACGTCA

GAM1127 FLJ10922 3' ACTGCAACCTCCGCCTC 36865 TA  
GAGG GAGGTTGCAGT  
||||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 FLJ11004 5' GCTCACTGCAACCTCTACCTC 36969  
GAGGTAGAGGTTGCAGTGAGT  
||||| |||||  
CTCCATCTCCAACGTCACTCG

GAM1127 FLJ11106 5' TCTTGCAACCTCACCTC 37057 A T  
GAGGT GAGGTTGCAG GA  
||||| ||||| ||



CTCCA CTCCAACGTT CT

GAM1127 FLJ12363 3' AGCTCACTGCAACCTCCACCTC 49669 A  
GAGGT GAGGTTGCAGTGAGTT  
||||| |||||||||  
CTCCA CTCCAACGTCACTCGA  
C

GAM1127 FLJ12409 3' ACTGCAACCTCCGCCTC 47041 TA  
GAGG GAGGTTGCAGT  
||||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 FLJ12572 5' ACTGCAACCTCTGCCTC 43243  
GAGGTAGAGGTTGCAGT  
||||| |||||||||  
CTCCGTCTCCAACGTCA

GAM1127 FLJ12649 3' ACTGCAACCTCCGCCTC 44772 TA  
GAGG GAGGTTGCAGT  
||||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 FLJ12668 3' ACTGCAACCTCCATCTC 46511 A  
GAGGT GAGGTTGCAGT  
||||| |||||||||  
CTCTA CTCCAACGTCA  
C

GAM1127 FLJ12687 3' ACTGCAACCTCCGCCTC 46183 TA  
GAGG GAGGTTGCAGT  
||||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 FLJ12747 3' ACTGCAACCTCTGCCTC 49707  
GAGGTAGAGGTTGCAGT  
||||| |||||||||  
CTCCGTCTCCAACGTCA

GAM1127 FLJ12973 3' ACCGCAACCTCCGCCTC 46099 TA A  
GAGG GAGGTTGC GT  
||||| ||||| ||  
CTCC CTCCAACG CA  
GC C

GAM1127 FLJ13072 5' ACTGCAACCTCTGCCTC 89799  
GAGGTAGAGGTTGCAGT  
||||| |||||||||  
CTCCGTCTCCAACGTCA

GAM1127 FLJ13197 3' GCTCACTGCAACCTCTACCTC 44856  
GAGGTAGAGGTTGCAGTGAGT  
||||| |||||||||

CTCCATCTCCAACGTCACCTCG

GAM1127 FLJ14950 3' GCTCACTGCAACCTCCACCTC 51721 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||||||  
CTCCA CTCCAACGTCACCTCG  
C

GAM1127 FLJ14957 3' ACTGCAACCTCTGCCTC 51735  
GAGGTAGAGGTTGCAGT  
|||||||||||  
CTCCGTCTCCAACGTCA

GAM1127 FLJ20004 3' ATTGCAACCTCCGCCTC 95288 TA  
GAGG GAGGTTGCAGT  
||| |||||||  
CTCC CTCCAACGTTA  
GC

GAM1127 FLJ20034 3' ACTGCAACCTCTGCCTC 34353  
GAGGTAGAGGTTGCAGT  
|||||||||||  
CTCCGTCTCCAACGTCA

GAM1127 FLJ20045 3' ACTGCAACCTCTGCCTC 34410  
GAGGTAGAGGTTGCAGT  
|||||||||||  
CTCCGTCTCCAACGTCA

GAM1127 FLJ20079 3' GCTCACCGCAACCTCCACCTC 34496 A A  
GAGGT GAGGTTGC GTGAGT  
||||| ||||| |||||  
CTCCA CTCCAACG CACTCG  
C C

GAM1127 FLJ20342 3' ACTGCAACCTCTGCCTC 34983  
GAGGTAGAGGTTGCAGT  
|||||||||||  
CTCCGTCTCCAACGTCA

GAM1127 FLJ20344 3' ACTGCAACCTCCGCCTC 35003 TA  
GAGG GAGGTTGCAGT  
||| |||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 FLJ20507 3' ACTGCAACCTCTGCCTC 35270  
GAGGTAGAGGTTGCAGT  
|||||||||||  
CTCCGTCTCCAACGTCA

GAM1127 FLJ20507 3' ACTGCAACCTCTGCCTC 60206  
GAGGTAGAGGTTGCAGT  
|||||||||||

CTCCGTCTCCAACGTCA

GAM1127 FLJ20511 3' GCTCACTGCAAGCTCCACCTC 35327 A G  
GAGGT GAG TTGCAGTGAGT  
||||| ||| |||||  
CTCCA CTC AACGTCACTCG  
C G

GAM1127 FLJ20542 3' AACTCACCCAGCCGCCACCTC 49779 AGA CA  
GAGGT GGTG GTGAGTT  
||||| ||||| |||||  
CTCCA CCGAC CACTCAA  
CCG C\_

GAM1127 FLJ20813 3' ACTGCAACTCCACCTC 35677 A G  
GAGGT GAG TTGCAGT  
||||| ||| |||||  
CTCCA CTC AACGTCA  
C \_

GAM1127 FLJ21302 3' ACTGCAACCTCCGCCTC 43208 TA  
GAGG GAGGTTGCAGT  
||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 FLJ22002 3' ACTGCAACCTCCGCCTC 45765 TA  
GAGG GAGGTTGCAGT  
||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 FLJ22531 5' GCTCACTGCAACCTCCACCTC 45031 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1127 FLJ22794 3' ACTGCAACTTCCACCTC 91599 A  
GAGGT GAGGTTGCAGT  
||||| |||||  
CTCCA CTTCAACGTCA  
C

GAM1127 FLJ22965 3' ACTGCAACCTCCGCCTC 42046 TA  
GAGG GAGGTTGCAGT  
||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 FLJ22969 3' ACTGCAACCTCTGCCTC 68642  
GAGGTAGAGGTTGCAGT  
|||||  
CTCCGTCTCCAACGTCA

GAM1127 FLJ23024 3' ACTGCAACCTCTGCCTC 46263  
GAGGTAGAGGTTGCAGT  
|||||

CTCCGTCTCCAACGTCA

GAM1127 FLJ23392 3' ACTGCAACCTCTGCCTC 45524  
GAGGTAGAGGTTGCAGT  
|||||||  
CTCCGTCTCCAACGTCA

GAM1127 FLJ23563 3' ACTGCAACCTCTGCCTC 67583  
GAGGTAGAGGTTGCAGT  
|||||||  
CTCCGTCTCCAACGTCA

GAM1127 FLJ30213 5' AACGAGAGACAACCTCTGCC 58765 CAGTGA  
GGTAGAGGTTG GTT  
||||||| |||  
CCGTCTCCAAC CAA  
AGAGAG

GAM1127 FLJ31101 3' ACTGCAACCTCTGCCTC 35703  
GAGGTAGAGGTTGCAGT  
|||||||  
CTCCGTCTCCAACGTCA

GAM1127 FLJ32865 3' ACTGCAACCTCTGCCTC 58163  
GAGGTAGAGGTTGCAGT  
|||||||  
CTCCGTCTCCAACGTCA

GAM1127 GAL3ST-4 3' ACTGCAACCTCTGCCTC 44930  
GAGGTAGAGGTTGCAGT  
|||||||  
CTCCGTCTCCAACGTCA

GAM1127 GMPPB 5' GCTCACTGCAACCTCCACCTC 95743 A  
GAGGT GAGGTTGCAGTGAGT  
|||| |||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1127 GNG4 3' AGCTCACTGCGACCTCCACCTC 15607 A  
GAGGT GAGGTTGCAGTGAGTT  
|||| |||||  
CTCCA CTCCAGCGTCACTCGA  
C

GAM1127 GP5 3' ACGGGCCCGCAACCCCTCCTC 15638 T A A\_ GA  
GAGG AG GGTTGC GT GT  
||| || ||| || ||  
CTCC TC CCAACG CG CA  
\_ C CC GG

GAM1127 GREB1 3' ACTGCAACCTCTGCCTC 27860  
GAGGTAGAGGTTGCAGT  
|||||||

CTCCGTCTCCAACGTCA

GAM1127 GRWD 3' ACTGCAACCTCCGCCTC 48959 TA  
GAGG GAGGTTGCAGT  
|||| ||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 GTF2E1 3' ACTGCAACCTCTGCCTC 18607  
GAGGTAGAGGTTGCAGT  
||||||||||||  
CTCCGTCTCCAACGTCA

GAM1127 GTPBG3 3' ACTGCAACCTCCACCTC 50893 A  
GAGGT GAGGTTGCAGT  
|||| ||||||||  
CTCCA CTCCAACGTCA  
C

GAM1127 GTPBG3 3' GCTCACTGCAACCTCCATCTC 50901 A  
GAGGT GAGGTTGCAGTGAGT  
|||| ||||||||||  
CTCTA CTCCAACGTCACTCG  
C

GAM1127 H-plk 5' ACTCACTGCAACCTCCACCTC 31800 A  
GAGGT GAGGTTGCAGTGAGT  
|||| ||||||||||  
CTCCA CTCCAACGTCACTCA  
C

GAM1127 HRH4 3' ACTGCAACCTCTGCCTC 41244  
GAGGTAGAGGTTGCAGT  
||||||||||||  
CTCCGTCTCCAACGTCA

GAM1127 HSPC065 3' GCTCACTGCAACCTCCACCTC 26307 A  
GAGGT GAGGTTGCAGTGAGT  
|||| ||||||||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1127 HSPC065 3' GCTGCAACCTCCTCCTC 26311 TA  
GAGG GAGGTTGCAGT  
|||| ||||||||  
CTCC CTCCAACGTCTG  
TC

GAM1127 ICK 3' CTGCAACCTCTGCCTC 29928  
GAGGTAGAGGTTGCAG  
||||||||||||  
CTCCGTCTCCAACGTC

GAM1127 JAM1 5' ACTGCAACCTCCTCCTC 57910 TA  
GAGG GAGGTTGCAGT  
|||| ||||||||

			CTCC CTCCAACGTCA		
			TC		
GAM1127	JM11	3'	ACTGCAACCTCTGCCTC 53249		
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	KCNMB3L	5'	AACCCACGGTGGCCTCTCCTC 26956	T	TG A A
			GAGG AGAGGT C GTG GTT		
			CTCC TCTCCG G CAC CAA		
			— GT G C		
GAM1127	KIAA0063	3'	GCTCACTGCAACCTCCACCTC 29631	A	
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACTCG		
			C		
GAM1127	KIAA0335	3'	AACTCACTACAGTTACACCTC 28989	AGA	GT C
			GAGGT G TG AGTGAGTT		
			CTCCA T AC TCACTCAA		
			CA_ TG A		
GAM1127	KIAA0391	3'	ACTGCAACCTCTGCCTC 27900		
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	KIAA0426	3'	ACTGCAACCTCCGCCTC 28252	TA	
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	KIAA0459	3'	GCTCACTGCAACCTCCACCTC 60999	A	
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACTCG		
			C		
GAM1127	KIAA0469	3'	ACTGCAGCCTCCACCTC 29318	A	
			GAGGT GAGGTTGCAGT		
			CTCCA CTCCGACGTCA		
			C		
GAM1127	KIAA0513	3'	ACTCACTGCAACCTCCACCTC 28328	A	
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACTCA		
			C		
GAM1127	KIAA0513	5'	ACTGCAGCCTCCACCTC 28334	A	
			GAGGT GAGGTTGCAGT		

			CTCCA CTCCGACGTCA		
			C		
GAM1127	KIAA0527	3'	ACTGCAACCTCTGCCTC	95789	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	KIAA0544	3'	ACTGCAACCTCCGCCTC	70884	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	KIAA0561	3'	ACTGCAACCTCCGCCTC	65870	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	KIAA0562	3'	CTGCAACCTCCGCCTC	28153	TA
			GAGG GAGGTTGCAG		
			CTCC CTCCAACGTC		
			GC		
GAM1127	KIAA0563	5'	ACTGCAACCTCTGCCTC	29180	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	KIAA0594	3'	ACTGCAACCTCCGCCTC	64891	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	KIAA0599	3'	ACTGCAACCTCCGCCTC	77161	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	KIAA0599	3'	ACTGCAACCTCCGCCTC	77163	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	KIAA0663	5'	CTGCAACCTCCGCCTC	29127	TA
			GAGG GAGGTTGCAG		
			CTCC CTCCAACGTC		
			GC		
GAM1127	KIAA0720	3'	ACTGCAACCTCTGCCTC	62315	
			GAGGTAGAGGTTGCAGT		

CTCCGTCTCCAACGTCA

GAM1127 KIAA0841 3' ACTGCAACCTCCGCCTC 71367 TA  
GAGG GAGGTTGCAGT  
|||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 KIAA0841 3' AGCTCACTGCAACCTCTGCCTC 71373  
GAGGTAGAGGTTGCAGTGAGTT  
|||||||  
CTCCGTCTCCAACGTCACTCGA

GAM1127 KIAA1041 3' ACTGCAACCTCCGCCTC 30122 TA  
GAGG GAGGTTGCAGT  
|||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 KIAA1054 3' ACTGCAACCTCCGCCTC 68425 TA  
GAGG GAGGTTGCAGT  
|||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 KIAA1161 5' ACTGCAACCCCTCCTC 81729 T A  
GAGG AG GGTTCAGT  
|||| |||||  
CTCC TC CCAACGTCA  
\_ C

GAM1127 KIAA1170 3' ACTGCAACCTCCGCCTC 69841 TA  
GAGG GAGGTTGCAGT  
|||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 KIAA1193 3' ACTGCAACCTCCGCCTC 67625 TA  
GAGG GAGGTTGCAGT  
|||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 KIAA1198 3' ACCGCAACCTCCGCCTC 63281 TA A  
GAGG GAGGTTGC GT  
|||| |||||  
CTCC CTCCAACG CA  
GC C

GAM1127 KIAA1198 3' ACTGCAACCTCCACTTC 63283 A  
GAGGT GAGGTTGCAGT  
|||| |||||  
CTTCA CTCCAACGTCA  
C

GAM1127 KIAA1198 3' GCGCAACCTCTGCCTC 63310 A  
GAGGTAGAGGTTGC GT  
||||||| ||



CTCCGTCTCCAACG CG

GAM1127 KIAA1209 3' ACTGCAGCCTCCACCTC 60746 A  
GAGGT GAGGTTGCAGT  
||||| |||||||||  
CTCCA CTCCGACGTCA  
C

GAM1127 KIAA1257 3' ACCGCAACCTCCGCCTC 62721 TA A  
GAGG GAGGTTGC GT  
||||| ||||||| ||  
CTCC CTCCAACG CA  
GC C

GAM1127 KIAA1320 5' ACTGCAACCTCTGCCTC 69292  
GAGGTAGAGGTTGCAGT  
||||| |||||||||  
CTCCGTCTCCAACGTCA

GAM1127 KIAA1373 3' AGCTCACTGCAACCTCCACCTC 70927 A  
GAGGT GAGGTTGCAGTGAGTT  
||||| |||||||||  
CTCCA CTCCAACGTCACTCGA  
C

GAM1127 KIAA1497 5' ACTGCAACCTCTGCCTC 67501  
GAGGTAGAGGTTGCAGT  
||||| |||||||||  
CTCCGTCTCCAACGTCA

GAM1127 KIAA1508 3' ACTGCAACCTCCGCCTC 61872 TA  
GAGG GAGGTTGCAGT  
||||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 KIAA1571 3' AGCTCACCGCAACCTCCACCTC 60950 A A  
GAGGT GAGGTTGC GTGAGTT  
||||| ||||||| |||||||  
CTCCA CTCCAACG CACTCGA  
C C

GAM1127 KIAA1615 3' TCACTGCAACCTCCACCTC 68728 A  
GAGGT GAGGTTGCAGTGA  
||||| |||||||||  
CTCCA CTCCAACGTCACT  
C

GAM1127 KIAA1655 3' ACTGTAACCTCCACCTC 66585 A  
GAGGT GAGGTTGCAGT  
||||| |||||||||  
CTCCA CTCCAATGTCA  
C

GAM1127 KIAA1655 3' ATTGCAACCTCCGCCTC 66594 TA  
GAGG GAGGTTGCAGT  
||||| |||||||||

			CTCC CTCCAACGTTA		
			GC		
GAM1127	KIAA1737	3'	ACTGCAACCTCCGCCTC	67346	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	KIAA1784	3'	ACTGCAACCTCCGCCTC	65141	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	KIAA1922	5'	ACTGCAACCTCCGCCTC	73612	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	KIAA1956	3'	ACTGCAGCCTCCACCTC	78426	A
			GAGGT GAGGTTGCAGT		
			CTCCA CTCCGACGTCA		
			C		
GAM1127	KIAA1971	3'	ACTGCAACCTCCACCTC	74213	A
			GAGGT GAGGTTGCAGT		
			CTCCA CTCCAACGTCA		
			C		
GAM1127	KLK7	3'	ACTGCAACCTCCGCCTC	17282	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	KLK7	3'	ACTGCAACCTCCGCCTC	57722	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	MCLC	3'	GCTCACTGCAACCTCCACCTC	30686	A
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACTCG		
			C		
GAM1127	MEF-2	3'	ACTGCAACCTCCGCCTC	64375	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	MGC10818	3'	AACTCAGCCACCTGCTACCTC	47532	_ T AG
			GAGGTAG AGGT GC TGAGTT		

CTCCATC TCCA CG ACTCAA  
 G C \_\_\_\_  
 GAM1127 MGC13138 3' ACTGCAACCTCTGCCTC 53012  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1127 MGC14836 3' ACTGCAACCTCCGCCTC 53033 TA  
 GAGG GAGGTTGCAGT  
 ||| |||||  
 CTCC CTCCAACGTCA  
 GC

GAM1127 MGC1842 3' ACTACAACCTCCGCCTC 65638 TA C  
 GAGG GAGGTTG AGT  
 ||| ||||| ||  
 CTCC CTCCAAC TCA  
 GC A

GAM1127 MGC2474 3' ACTGCAACTTCCACCTC 43709 A  
 GAGGT GAGGTTGCAGT  
 |||| |||||  
 CTCCA CTTCAACGTCA  
 C

GAM1127 MGC29891 3' ACTGCAACCTCCGCCTC 58195 TA  
 GAGG GAGGTTGCAGT  
 ||| |||||  
 CTCC CTCCAACGTCA  
 GC

GAM1127 MGC3113 3' ACTGCAGCCTCCACCTC 43837 A  
 GAGGT GAGGTTGCAGT  
 |||| |||||  
 CTCCA CTCCGACGTCA  
 C

GAM1127 MGC3329 3' ACTGCAACCCCCGCCTC 44010 AGA  
 GAGGT GGTTCAGT  
 |||| |||||  
 CTCCG CCAACGTCA  
 CCC

GAM1127 MGC5149 3' ACTGCAACCTCTGCCTC 72282  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1127 MGC9912 3' GCTCACTGCAACCTCCACCTC 54719 A  
 GAGGT GAGGTTGCAGTGAGT  
 |||| |||||  
 CTCCA CTCCAACGTCACTCG  
 C

GAM1127 MLZE 5' ACTGCAACCTCTGCCTC 48612  
 GAGGTAGAGGTTGCAGT  
 |||||

CTCCGTCTCCAACGTCA

GAM1127 MMPL1 3' ACTGCAGCCTCCACCTC 14714 A  
GAGGT GAGGTTGCAGT  
||||| |||||  
CTCCA CTCCGACGTCA  
C

GAM1127 moblak 3' ACTGCATCCTCCACCTC 55485 A T  
GAGGT GAGG TGCAGT  
||||| |||||  
CTCCA CTCC ACGTCA  
C T

GAM1127 MOCS3 3' ACTGCAACCTCCGCCTC 27146 TA  
GAGG GAGGTTGCAGT  
||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 MRPL44 3' GCTCACTGCAACCTCCACCTC 43321 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1127 MtFMT 3' ACTGCAACCTCCGCCTC 57646 TA  
GAGG GAGGTTGCAGT  
||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 NDUFB1 5' ACTGCAACCTCTGCCTC 15812  
GAGGTAGAGGTTGCAGT  
|||||  
CTCCGTCTCCAACGTCA

GAM1127 NDUFC2 3' GCTCACTGCAACCTCCACCTC 15836 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1127 Nup43 3' GCTCACTGCAACCTCCACCTC 45003 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1127 OSBPL2 3' ACCGCAACCTCCGCCTC 29196 TA A  
GAGG GAGGTTGC GT  
||| ||||| ||  
CTCC CTCCAACG CA  
GC C

GAM1127 OSBPL2 3' ACCGCAACCTCCGCCTC 57847 TA A  
GAGG GAGGTTGC GT  
||| ||||| ||

CTCC CTCCAACG CA  
 GC C  
 GAM1127 PASK 5' ACTGCAACCTCTGCCTC 30708  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1127 PELI1 5' ACTGCAACCTCCTCCTC 40246 TA  
 GAGG GAGGTTGCAGT  
 ||| |||||  
 CTCC CTCCAACGTCA  
 TC

GAM1127 PELI1 5' ACTGCAACCTCTGCCTC 40249  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1127 PIP3-E 3' ACTGCAACCTCTGCCTC 66794  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1127 PRO0365 5' AGCTCACTGCAACCTCCACCTC 26148 A  
 GAGGT GAGGTTGCAGTGAGTT  
 |||| |||||  
 CTCCA CTCCAACGTCACTCGA  
 C

GAM1127 PRO1992 5' ACTGCAACCTCTGCCTC 26049  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1127 PRO2955 3' ACTGCAACCTCTGCCTC 37628  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1127 PSTPIP2 3' ACTGCAACCTCTGCCTC 44379  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1127 RAB21 3' GCTCACTGCAAGCTCCACCTC 30388 A G  
 GAGGT GAG TTGCAGTGAGT  
 |||| ||| |||||  
 CTCCA CTC AACGTCACTCG  
 C G

GAM1127 RAB33B 3' ACTGCAACCTCCGCCTC 48484 TA  
 GAGG GAGGTTGCAGT  
 ||| |||||

			CTCC CTCCAACGTCA		
			GC		
GAM1127	RAI	5'	ACTGCAACCTCCGCCTC	21869	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	RAI16	3'	AACTCAGTGACCTCTGCCTC	42750	TG AG
			GAGGTAGAGGT C TGAGTT		
			CTCCGTCTCCA G ACTCAA		
			GT _		
GAM1127	RNF20	3'	AACCACCAAACCTCTACCTC	38962	GCA A
			GAGGTAGAGGT GTG GTT		
			CTCCATCTCAA CAC CAA		
			AC _ _		
GAM1127	RNF8	3'	AGCTCACTGCAACCTCCACCTC	14215	A
			GAGGT GAGGTTGCAGTGAGTT		
			CTCCA CTCCAACGTCACTCGA		
			C		
GAM1127	RNO2	5'	ACTGCAACCTCCACCTT	52760	A
			GAGGT GAGGTTGCAGT		
			TTCCA CTCCAACGTCA		
			C		
GAM1127	SC4MOL	3'	ACTGCAACCTCTGCCTC	22148	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	SCAMP-4	3'	ACTGCAACCTCTGCCTC	54387	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	SCYA16	3'	ACTGTAACCTCCACCTC	15952	A
			GAGGT GAGGTTGCAGT		
			CTCCA CTCCAATGTCA		
			C		
GAM1127	SCYA22	3'	ACCCATCCTCTGCCTC	90936	T CA
			GAGGTAGAGG TG GT		
			CTCCGTCTCC AC CA		
			T C _		
GAM1127	SCYA22	3'	GCTCACTACAACCTCGACCTC	90946	A C
			GAGGT GAGGTTG AGTGAGT		

			CTCCA CTCCAAC TCACTCG		
			G A		
GAM1127	SERF1B	3'	ACTGCAACCTCCGCCTC	43406	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	SIRPB1	3'	ACTGCAACCCCGCCTC	20238	AGA
			GAGGT GGTTCAGT		
			CTCCG CCAACGTCA		
			CCC		
GAM1127	SLC11A1	3'	AACTCATTGCAACCTCCACCTT	59449	A
			GAGGT GAGGTTGCAGTGAGTT		
			TTCCA CTCCAACGTTACTCAA		
			C		
GAM1127	SLC26A9	3'	AACTCACTCTCCCCTACT	56173	A TTGC
			GGTAG GG AGTGAGTT		
			TCATC CC TCACTCAA		
			C TC__		
GAM1127	SLC26A9	3'	AACTCACTCTCCCCTACT	53612	A TTGC
			GGTAG GG AGTGAGTT		
			TCATC CC TCACTCAA		
			C TC__		
GAM1127	SLC2A10	3'	ACTGCAACCTCCACTTC	47814	A
			GAGGT GAGGTTGCAGT		
			CTTCA CTCCAACGTCA		
			C		
GAM1127	SP2	3'	GCCACAACCTCTCCTC	11890	T CA
			GAGG AGAGGTTG GT		
			CTCC TCTCCAAC CG		
			— AC		
GAM1127	STAF65(gamma)	3'	ACTGCAACCTCTGCCTC	29422	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	SUN1	3'	ACTGCAGCCTCCACCTC	47152	A
			GAGGT GAGGTTGCAGT		
			CTCCA CTCCGACGTCA		
			C		
GAM1127	SYT13	3'	ACTGCAACCTCCGCCTC	93446	TA
			GAGG GAGGTTGCAGT		

CTCC CTCCAACGTCA  
 GC  
 GAM1127 TNRC4 3' ACTCACTGCCTCCCCC 23219 TA GTT  
 GG GAG GCAGTGAGT  
 || ||| |||||  
 CC CTC CGTCACTCA  
 CC \_\_\_\_  
 GAM1127 TOR1B 3' AACTCACTGCAACCTCCGCT 27194 TA  
 GG GAGGTTGCAGTGAGTT  
 || |||||  
 TC CTCCAACGTCACTCAA  
 GC  
 GAM1127 TRIM5 3' ACTGCAACCTCCACCTC 52290 A  
 GAGGT GAGGTTGCAGT  
 |||||  
 CTCCA CTCCAACGTCA  
 C  
 GAM1127 TRIM6 3' ACTGCAACCTCTGCCTC 54128  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 TU12B1-TY 3' ACTGCAACCTCTGCCTC 33366  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 TUCAN 3' ACTGCAACCTCTGCCTC 30266  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 UBF-fl 3' ACTGCAACCTCTGCCTC 51546  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 USP22 3' GCTCACTGCAACCTCCACCTC 68015 A  
 GAGGT GAGGTTGCAGTGAGT  
 |||||  
 CTCCA CTCCAACGTCACTCG  
 C  
 GAM1127 VDU1 3' ACTGCAGCCTCCACCTC 30407 A  
 GAGGT GAGGTTGCAGT  
 |||||  
 CTCCA CTCCGACGTCA  
 C  
 GAM1127 VPS33A 3' CTCCTGCAACCTCCACCTC 43339 A  
 GAGGT GAGGTTGCAGTGAG  
 |||||



		CTCCA CTCCAACGTCACTC		
		C		
GAM1127	WBSCR20A	5' ACCGCAACCTCTGCCTC	49645	A
		GAGGTAGAGGTTGC GT		
		CTCCGTCTCCAACG CA		
		C		
GAM1127	ZTL1	3' ACTGCAACCTCTGCCTC	43908	
		GAGGTAGAGGTTGCAGT		
		CTCCGTCTCCAACGTCA		
GAM1127	LOC112724	5' GCTCACTGCAACCTCCACCTC	56499	A
		GAGGT GAGGTTGCAGTGAGT		
		CTCCA CTCCAACGTCACTCG		
		C		
GAM1127	LOC113675	5' ACTGCAACCTCCGCCTC	56567	TA
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		GC		
GAM1127	LOC115219	5' ACTGCAACCTCCGCCTC	73292	TA
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		GC		
GAM1127	LOC116411	5' GCTACAACCTCCACCTC	73867	A C
		GAGGT GAGGTTG AGT		
		CTCCA CTCCAAC TCG		
		C A		
GAM1127	LOC119392	3' ACTGCAACCTCTGCCTC	59129	
		GAGGTAGAGGTTGCAGT		
		CTCCGTCTCCAACGTCA		
GAM1127	LOC120114	3' AGCTCACTGCAATCTCCACCTC	75518	A
		GAGGT GAGGTTGCAGTGAGTT		
		CTCCA CTCTAACGTCACTCGA		
		C		
GAM1127	LOC120939	3' ACTGTAACCTCCACCTC	76243	A
		GAGGT GAGGTTGCAGT		
		CTCCA CTCCAATGTCA		
		C		
GAM1127	LOC126364	3' ACTGCAACCTCCGCCTC	75679	TA
		GAGG GAGGTTGCAGT		

		CTCC CTCCAACGTCA		
		GC		
GAM1127	LOC126526 3'	ACCCACTTTTCTACCTC	74530	TTGC A
		GAGGTAGAGG AGTG GT		
		CTCCATCTTT TCAC CA		
		_____ C		
GAM1127	LOC126661 3'	ACTGCAACCTCCGCCTC	74541	TA
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		GC		
GAM1127	LOC128077 3'	ACTGCAACCTCCGCCTC	74700	TA
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		GC		
GAM1127	LOC128077 3'	ACTGCAACCTCTGCCTC	74703	
		GAGGTAGAGGTTGCAGT		
		CTCCGTCTCCAACGTCA		
GAM1127	LOC128387 3'	ACTGCAACCTCCACTTC	74745	A
		GAGGT GAGGTTGCAGT		
		CTTCA CTCCAACGTCA		
		C		
GAM1127	LOC128989 3'	ACTGCAACCTCCGCCTC	74802	TA
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		GC		
GAM1127	LOC130813 3'	ACCGCAACCTCCGCCTC	75759	TA A
		GAGG GAGGTTGC GT		
		CTCC CTCCAACG CA		
		GC C		
GAM1127	LOC132625 3'	GCTCACTGCAACCTCCACCTC	75909	A
		GAGGT GAGGTTGCAGTGAGT		
		CTCCA CTCCAACGTCACTCG		
		C		
GAM1127	LOC133686 3'	CTGCAACCTCCATCTC	75121	A
		GAGGT GAGGTTGCAG		
		CTCTA CTCCAACGTC		
		C		
GAM1127	LOC135154 3'	AACTCACTGCAACTTCCGCC	75210	TA
		GG GAGGTTGCAGTGAGTT		

[illegible]

		C CCA CTCCAACGTCA		
		— C		
GAM1127	LOC145725 3'	ACTGCAGCCTCCACCTC	77397	A
		GAGGT GAGGTTGCAGT		
		CTCCA CTCCGACGTCA		
		C		
GAM1127	LOC145732 3'	ACTGCAGCCTCCACCTC	77419	A
		GAGGT GAGGTTGCAGT		
		CTCCA CTCCGACGTCA		
		C		
GAM1127	LOC145757 5'	ACTACAACCTCTGCCTC	77449	C
		GAGGTAGAGGTTG AGT		
		CTCCGTCTCCAAC TCA		
		A		
GAM1127	LOC146229 3'	CTGCAACCTCCACCTC	77750	A
		GAGGT GAGGTTGCAG		
		CTCCA CTCCAACGTC		
		C		
GAM1127	LOC146229 3'	GCTCACTGCAACCTCCACCTC	77754	A
		GAGGT GAGGTTGCAGTGAGT		
		CTCCA CTCCAACGTCACTCG		
		C		
GAM1127	LOC146784 5'	GCTCACTGCAACCTCCACCTC	78119	A
		GAGGT GAGGTTGCAGTGAGT		
		CTCCA CTCCAACGTCACTCG		
		C		
GAM1127	LOC146901 3'	ATTGCAACCTCCACCTT	83831	A
		GAGGT GAGGTTGCAGT		
		TTCCA CTCCAACGTTA		
		C		
GAM1127	LOC146909 3'	ACTGCAACCTCCGCCTC	78163	TA
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		GC		
GAM1127	LOC146952 5'	AGCTCACTGCAACCTCCACCTC	83856	A
		GAGGT GAGGTTGCAGTGAGTT		
		CTCCA CTCCAACGTCACTCGA		
		C		
GAM1127	LOC147071 5'	ACTGCAACCTCTGCCTC	72991	
		GAGGTAGAGGTTGCAGT		

CTCCGTCTCCAACGTCA

GAM1127 LOC147407 3' ACTGCAACCTCCGCCTC 76320 TA  
GAGG GAGGTTGCAGT  
|||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 LOC147817 3' GCTCACTGCAACCTCCACCTC 78500 A  
GAGGT GAGGTTGCAGTGAGT  
|||| |||||||||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1127 LOC147990 3' ACTACAACCTCTGCCTC 84087 C  
GAGGTAGAGGTTG AGT  
||||||||| |||  
CTCCGTCTCCAAC TCA  
A

GAM1127 LOC148137 3' ACGGCAACCTCCACCTC 58418 A A  
GAGGT GAGGTTGC GT  
|||| ||||||| ||  
CTCCA CTCCAACG CA  
C G

GAM1127 LOC148189 5' GCTCACTGCAACCTCCACCTC 78712 A  
GAGGT GAGGTTGCAGTGAGT  
|||| |||||||||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1127 LOC148198 3' AGCTCACTGCAACCTCCATCTC 70675 A  
GAGGT GAGGTTGCAGTGAGTT  
|||| |||||||||||  
CTCTA CTCCAACGTCACTCGA  
C

GAM1127 LOC148709 3' ACTACAACCTCCGCCTC 78932 TA C  
GAGG GAGGTTG AGT  
||| ||||| |||  
CTCC CTCCAAC TCA  
GC A

GAM1127 LOC148918 5' AACTCAGCTTCTTCTACCTC 79051 TT AG  
GAGGTAGAGG GC TGAGTT  
||||||| || |||||  
CTCCATCTTC CG ACTCAA  
TT \_

GAM1127 LOC148918 5' ACTGCAGCCTCCACCTC 79057 A  
GAGGT GAGGTTGCAGT  
|||| |||||||||  
CTCCA CTCCGACGTCA  
C

GAM1127 LOC149271 3' AACCCACTGCCCTGTAACC 79235 \_ G TT A  
GGT A AGG GCAGTG GTT  
||| ||| ||||| |||

	CCA T TCC CGTCAC CAA	
	A G _ C	
GAM1127 LOC149506 3'	ACTGCAACCTCTGCCTC 84444	
	GAGGTAGAGGTTGCAGT	
	CTCCGTCTCCAACGTCA	
GAM1127 LOC149506 3'	ACTGCAACTTCCACCTC 84448	A
	GAGGT GAGGTTGCAGT	
	CTCCA CTTCAACGTCA	
	C	
GAM1127 LOC150397 3'	ATTGCAACCTCCGCCTC 79840	TA
	GAGG GAGGTTGCAGT	
	CTCC CTCCAACGTTA	
	GC	
GAM1127 LOC150519 3'	CTGCAACCTGCCACCTC 79917	AG_
	GAGGT AGGTTGCAG	
	CTCCA TCCAACGTC	
	CCG	
GAM1127 LOC150696 3'	ACTGCAGCCTCCACCTC 58475	A
	GAGGT GAGGTTGCAGT	
	CTCCA CTCCGACGTCA	
	C	
GAM1127 LOC150960 3'	GCTGCAACCTCCGCCTC 80066	TA
	GAGG GAGGTTGCAGT	
	CTCC CTCCAACGTCTG	
	GC	
GAM1127 LOC151057 3'	ACTGCAACCTCTGCCTC 85203	
	GAGGTAGAGGTTGCAGT	
	CTCCGTCTCCAACGTCA	
GAM1127 LOC151201 3'	AGCTCACTGCAACCTCCACCTC 85271	A
	GAGGT GAGGTTGCAGTGAGTT	
	CTCCA CTCCAACGTCACTCGA	
	C	
GAM1127 LOC151475 5'	ACTGCAACCTCTGCCTC 85385	
	GAGGTAGAGGTTGCAGT	
	CTCCGTCTCCAACGTCA	
GAM1127 LOC151475 5'	GCTCACTGCAACCTCCACCTC 85409	A
	GAGGT GAGGTTGCAGTGAGT	

CTCCA CTCCAACGTCACTCG  
 C  
 GAM1127 LOC151826 3' ACTGCAACCTCCGCCTC 80351 TA  
 GAGG GAGGTTGCAGT  
 |||| |||||  
 CTCC CTCCAACGTCA  
 GC  
 GAM1127 LOC151877 3' GCTCACTACAACCACCACCTC 85506 AGA C  
 GAGGT GGTG AGTGAGT  
 |||| |||| |||||  
 CTCCA CCAAC TCACTCG  
 CCA A  
 GAM1127 LOC152445 3' ACTGCAACCTCTGCCTC 85739  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 LOC152582 5' ACCGCAACCTCTGCCTC 85786 A  
 GAGGTAGAGGTTGC GT  
 ||||| ||  
 CTCCGTCTCCAACG CA  
 C  
 GAM1127 LOC152620 3' ACTACAACCTCTGCCTC 60077 C  
 GAGGTAGAGGTTG AGT  
 ||||| ||  
 CTCCGTCTCCAAC TCA  
 A  
 GAM1127 LOC152719 5' ACTGCAACCTCTGCCTC 85844  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 LOC152794 5' CTCAGTCAACCTCTACCTC 80675  
 GAGGTAGAGGTTGCAGTGAG  
 |||||  
 CTCCATCTCCAACGTCACTC  
  
 GAM1127 LOC152851 3' GCTGCAACCTCCACCC 80713 A A  
 G GGT GAGGTTGCAGT  
 | || |||||  
 C CCA CTCCAACGTCG  
 \_ C  
 GAM1127 LOC153077 3' ACTGCAACCTCCGCCTC 85902 TA  
 GAGG GAGGTTGCAGT  
 |||| |||||  
 CTCC CTCCAACGTCA  
 GC  
 GAM1127 LOC153688 3' GCTCACTGCAACCTCCACCTC 86113 A  
 GAGGT GAGGTTGCAGTGAGT  
 |||| |||||

CTCCA CTCCAACGTCACCTCG  
 C  
 GAM1127 LOC154075 3' ACTGCAACCTCCGCCTC 81041 TA  
 GAGG GAGGTTGCAGT  
 |||| |||||  
 CTCC CTCCAACGTCA  
 GC  
 GAM1127 LOC154282 5' GCTCACTGCAACCTCCACCTC 86202 A  
 GAGGT GAGGTTGCAGTGAGT  
 |||| |||||  
 CTCCA CTCCAACGTCACCTCG  
 C  
 GAM1127 LOC154877 3' AGCTCACTGCAACCTCTACCTC 86278  
 GAGGTAGAGGTTGCAGTGAGTT  
 |||||  
 CTCCATCTCCAACGTCACCTCGA  
  
 GAM1127 LOC155100 5' AACCCACGGTGGCCTCTCCTC 73022 T TG A A  
 GAGG AGAGGT C GTG GTT  
 |||| |||| | ||||  
 CTCC TCTCCG G CAC CAA  
 \_ GT G C  
 GAM1127 LOC157247 5' AGCTCACTGCAACCTCCACC 81357 A  
 GGT GAGGTTGCAGTGAGTT  
 || |||||  
 CCA CTCCAACGTCACCTCGA  
 C  
 GAM1127 LOC157798 5' ACTGCAACCTCCGCCTC 86544 TA  
 GAGG GAGGTTGCAGT  
 |||| |||||  
 CTCC CTCCAACGTCA  
 GC  
 GAM1127 LOC157858 5' ACTGCAACCTCTGCCTC 86579  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 LOC158191 3' AACCCACGATCTCTCCCCTC 81766 T\_ GCA A  
 GAGG AGAGGTT GTG GTT  
 |||| |||| || ||  
 CTCC TCTCTAG CAC CAA  
 CC \_ C  
 GAM1127 LOC158668 3' ACTGCAACCTCTGCCTC 69361  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 LOC158865 5' ACTGCAACCTCTGCCTC 86928  
 GAGGTAGAGGTTGCAGT  
 |||||



CTCCGTCTCCAACGTCA

GAM1127 LOC161829 3' ACTGCAACCTCCGCCTC 82309 TA  
GAGG GAGGTTGCAGT  
|||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 LOC162461 3' AACTCACTGCACCCACCC 82356 A AGA T  
G GGT GG TGCAGTGAGTT  
| || || |||||  
C CCA CC ACGTCACTCAA  
\_ \_ C

GAM1127 LOC196047 5' ACTGCAACCTCCGCCTC 89588 TA  
GAGG GAGGTTGCAGT  
|||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 LOC196264 3' ACTGCAACCTCTGCCTC 87599  
GAGGTAGAGGTTGCAGT  
|||||||  
CTCCGTCTCCAACGTCA

GAM1127 LOC196411 3' ACTGCAACCTCCGCCTC 87663 TA  
GAGG GAGGTTGCAGT  
|||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1127 LOC196529 3' GCTCACTGCAACCTCCACCTC 87776 A  
GAGGT GAGGTTGCAGTGAGT  
|||| |||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1127 LOC196761 3' AACCCACAACACCTCTGCC 89549 T CA A  
GGTAGAGGT G GTG GTT  
||||| | |||  
CCGTCTCCA C CAC CAA  
\_ AA C

GAM1127 LOC196957 3' ACTGCAGCCTCCACCTC 87814 A  
GAGGT GAGGTTGCAGT  
|||| |||||  
CTCCA CTCCGACGTCA  
C

GAM1127 LOC196961 3' ACTGCAGCCTCCACCTC 87835 A  
GAGGT GAGGTTGCAGT  
|||| |||||  
CTCCA CTCCGACGTCA  
C

GAM1127 LOC197138 3' ACTGCAGCCTCCACCTC 87908 A  
GAGGT GAGGTTGCAGT  
|||| |||||

CTCCA CTCCGACGTCA  
 C  
 GAM1127 LOC197358 3' CTGCAACCTCCGCCTC 88033 TA  
 GAGG GAGGTTGCAG  
 |||| |||||  
 CTCC CTCCAACGTC  
 GC  
 GAM1127 LOC199699 3' AGCTCACTGCAAGCTCCACCTC 88298 A G  
 GAGGT GAG TTGCAGTGAGTT  
 |||| || |||||  
 CTCCA CTC AACGTCACTCGA  
 C G  
 GAM1127 LOC199786 3' ACTGCAACCTCCGCCTC 88363 TA  
 GAGG GAGGTTGCAGT  
 |||| |||||  
 CTCC CTCCAACGTCA  
 GC  
 GAM1127 LOC200014 3' GCTGCAACCCCCACCTC 88534 AGA  
 GAGGT GGTTCAGT  
 |||| |||||  
 CTCCA CCAACGTCG  
 CCC  
 GAM1127 LOC200169 3' AATGAGCTGCAACTCCACC 89936 A G GA  
 GGT GAG TTGCAGT GTT  
 || || ||||| ||  
 CCA CTC AACGTCG TAA  
 C \_ AG  
 GAM1127 LOC200169 5' ACTGCAACCTCTGCCTC 89939  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 LOC200268 3' ACTGCAACCTCTGCCTC 88672  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1127 LOC200310 3' ACTACAACCTCTGCCTC 65727 C  
 GAGGTAGAGGTTG AGT  
 ||||| ||  
 CTCCGTCTCCAAC TCA  
 A  
 GAM1127 LOC200314 3' GCTCACTGCAACCTCCACCTC 90011 A  
 GAGGT GAGGTTGCAGTGAGT  
 |||| |||||  
 CTCCA CTCCAACGTCACTCG  
 C  
 GAM1127 LOC200339 3' ACTGCAACCTCTGCCTC 90027  
 GAGGTAGAGGTTGCAGT  
 |||||

CTCCGTCTCCAACGTCA

GAM1127	LOC200845	5'	ACTGCAACCTCCGCCTC	88893	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	LOC200860	3'	ACTGCAACCTCCACCTC	90156	A
			GAGGT GAGGTTGCAGT		
			CTCCA CTCCAACGTCA		
			C		
GAM1127	LOC201173	5'	ACTGCAACCTCTGCCTC	87321	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	LOC201220	5'	ACTGCAACCTCTGCCTC	87341	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	LOC201294	3'	ACTGCAACCTCCGCCTC	88196	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	LOC201294	3'	ACTGCAACCTCCGCCTC	88198	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	LOC201411	3'	ACTGCAACCTCTGCCTC	62949	
			GAGGTAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1127	LOC201627	3'	ACTGCAACCTCCACCTC	89004	A
			GAGGT GAGGTTGCAGT		
			CTCCA CTCCAACGTCA		
			C		
GAM1127	LOC202025	3'	ACTGCAACCTCCGCCTC	90278	TA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			GC		
GAM1127	LOC202934	3'	ACTACAACCTCTGCCTC	90398	C
			GAGGTAGAGGTTG AGT		

	CTCCGTCTCCAAC TCA		
	A		
GAM1127 LOC203297 5'	ACTGCAACCTCTGCCTC 75346		
	GAGGTAGAGGTTGCAGT		
	CTCCGTCTCCAACGTCA		
GAM1127 LOC203350 3'	AACTGACTGCAACCTCCGCCTC 90555	TA	G
	GAGG GAGGTTGCAGT AGTT		
	CTCC CTCCAACGTCA TCAA		
	GC G		
GAM1127 LOC204804 3'	GCTCACTGCAACCTCGACCTC 89476	A	
	GAGGT GAGGTTGCAGTGAGT		
	CTCCA CTCCAACGTCACTCG		
	G		
GAM1127 LOC204804 3'	GCTCACTGCCACCTCCACCTC 89478	A	T
	GAGGT GAGGT GCAGTGAGT		
	CTCCA CTCCA CGTCACTCG		
	C C		
GAM1127 LOC219735 3'	ACTGCAACCTCTGCCTC 93103		
	GAGGTAGAGGTTGCAGT		
	CTCCGTCTCCAACGTCA		
GAM1127 LOC219894 3'	ACTGCAAGCTCCACCTC 93275	A	G
	GAGGT GAG TTGCAGT		
	CTCCA CTC AACGTCA		
	C G		
GAM1127 LOC220662 3'	ACTGCAACCTCCACCTC 91158	A	
	GAGGT GAGGTTGCAGT		
	CTCCA CTCCAACGTCA		
	C		
GAM1127 LOC220662 3'	ACTGCAACCTCCACTTC 91161	A	
	GAGGT GAGGTTGCAGT		
	CTTCA CTCCAACGTCA		
	C		
GAM1127 LOC221035 3'	ACTACAACCTCTGCCTC 93160		C
	GAGGTAGAGGTTG AGT		
	CTCCGTCTCCAAC TCA		
	A		
GAM1127 LOC221174 5'	AGCTCACTGCGACCTCCACCTC 93498	A	
	GAGGT GAGGTTGCAGTGAGTT		

CTCCA CTCCAGCGTCACTCGA  
 C  
 GAM1127 LOC221271 3' ACTGCAACCTCTGCCTC 91841  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1127 LOC221296 3' GCTCACTGCAACCTCCACCTC 91965 A  
 GAGGT GAGGTTGCAGTGAGT  
 |||||  
 CTCCA CTCCAACGTCACTCG  
 C

GAM1127 LOC221415 5' ACTCACTCATCCTCCTC 93872 TAG T C  
 GAGG AGG TG AGTGAGT  
 ||| ||| |||||  
 CTCC TCC AC TCACTCA  
 \_ T \_

GAM1127 LOC221663 5' GCTCACTGCAACCTCCACCTC 93818 A  
 GAGGT GAGGTTGCAGTGAGT  
 |||||  
 CTCCA CTCCAACGTCACTCG  
 C

GAM1127 LOC221715 5' AACCCAAATGCCTCTACCTT 93746 TGCAG A  
 GAGGTAGAGGT TG GTT  
 ||||| |||||  
 TTCCATCTCCG AC CAA  
 TAA\_ C

GAM1127 LOC221787 3' AACTTATAAACCTCTACTTC 92465 GCA  
 GAGGTAGAGGTT GTGAGTT  
 |||||  
 CTTCATCTCCAA TATTCAA  
 A\_

GAM1127 LOC222070 5' ACTGCAACCTCTGCCTC 94147  
 GAGGTAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1127 LOC222709 5' AACTCACTGCCCCGCGCCTC 92856 AGA TT  
 GAGGT GG GCAGTGAGTT  
 |||||  
 CTCCG CC CGTCACTCAA  
 CG\_ \_

GAM1127 LOC253612 5' ACTGCAACCTCCGCCTC 96737 TA  
 GAGG GAGGTTGCAGT  
 |||||  
 CTCC CTCCAACGTCA  
 GC

GAM1127 LOC253664 3' ATTGCAACCTCTGCCTC 94807  
 GAGGTAGAGGTTGCAGT  
 |||||

CTCCGTCTCCAACGTTA

GAM1127 LOC253666 5' ACTGCAACCTCCGCCTC 95057 TA  
GAGG GAGGTTGCAGT  
|||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 LOC253779 3' ACTGCAACCTCCGCCTC 97142 TA  
GAGG GAGGTTGCAGT  
|||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 LOC254755 3' AACTCAGTGACCTCTGCCTC 97364 TG AG  
GAGGTAGAGGT C TGAGTT  
||||||| | |||||  
CTCCGTCTCCA G ACTCAA  
GT \_

GAM1127 LOC255497 3' ACTGCAACCTCCGCCTC 97184 TA  
GAGG GAGGTTGCAGT  
|||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 LOC255919 3' CTGCAACCTCTGCCTC 95032  
GAGGTAGAGGTTGCAG  
|||||||||||  
CTCCGTCTCCAACGTC

GAM1127 LOC256267 3' ACTGCAACCTCCGCCTC 96794 TA  
GAGG GAGGTTGCAGT  
|||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 LOC256306 3' AGCTCACTGCAACCTCCACCTC 96677 A  
GAGGT GAGGTTGCAGTGAGTT  
|||| |||||||||  
CTCCA CTCCAACGTCACTCGA  
C

GAM1127 LOC51200 3' ACCACAACCTCTGCCTC 32987 CA  
GAGGTAGAGGTTG GT  
||||||| ||  
CTCCGTCTCCAAC CA  
AC

GAM1127 LOC51219 5' ACCGCAACCTCCGCCTC 33109 TA A  
GAGG GAGGTTGC GT  
|||| ||||| ||  
CTCC CTCCAACG CA  
GC C

GAM1127 LOC51696 3' ACTGCAACCTCTGCCTC 32540  
GAGGTAGAGGTTGCAGT  
|||||||||||

CTCCGTCTCCAACGTCA

GAM1127 LOC57107 3' ACTGCAACCTCCGCCTC 39824 TA  
GAGG GAGGTTGCAGT

|||| ||||||||

CTCC CTCCAACGTCA

GC

GAM1127 LOC57146 3' GCTCACTGCAACCTCCAACTC 39923 GTA  
GAG GAGGTTGCAGTGAGT

||| ||||||||||

CTC CTCCAACGTCACTCG

AAC

GAM1127 LOC64102 5' TTGCAACTCCACCTC 42175 A G  
GAGGT GAG TTGCAG

|||| ||| |||||

CTCCA CTC AACGTT

C \_

GAM1127 LOC81034 3' AGCTCACTGCAACCTCCACCTC 47843 A  
GAGGT GAGGTTGCAGTGAGTT

|||| ||||||||||

CTCCA CTCCAACGTCACTCGA

C

GAM1127 LOC89932 3' GCTCACTGCAACCTCCACCTC 60804 A  
GAGGT GAGGTTGCAGTGAGT

|||| ||||||||||

CTCCA CTCCAACGTCACTCG

C

GAM1127 LOC90288 3' CTCCTGCAACCTCCACCTC 62090 A  
GAGGT GAGGTTGCAGTGAG

|||| ||||||||||

CTCCA CTCCAACGTCACTC

C

GAM1127 LOC90333 5' ACTGCAACCTCCACTTC 62276 A  
GAGGT GAGGTTGCAGT

|||| ||||||||

CTTCA CTCCAACGTCA

C

GAM1127 LOC90333 3' ACTGCAACCTCCTCCTC 62278 TA  
GAGG GAGGTTGCAGT

||| ||||||||

CTCC CTCCAACGTCA

TC

GAM1127 LOC90371 5' GCTCACTGCAACCTCCACCTC 62500 A  
GAGGT GAGGTTGCAGTGAGT

|||| ||||||||||

CTCCA CTCCAACGTCACTCG

C

GAM1127 LOC90408 5' GCTCACTGCAACCTCTACCTC 62661  
GAGGTAGAGGTTGCAGTGAGT

||||||||||||||

CTCCATCTCCAACGTCACCTCG

GAM1127 LOC90459 3' ACTGCAACCTCCGCCTC 62878 TA  
GAGG GAGGTTGCAGT  
|||||  
CTCC CTCCAACGTCA  
GC

GAM1127 LOC90485 3' ACTGCAACCTCCGCCTC 63005 TA  
GAGG GAGGTTGCAGT  
|||||  
CTCC CTCCAACGTCA  
GC

GAM1127 LOC90591 3' ACTGCCACCTCCACCTC 63410 A T  
GAGGT GAGGT GCAGT  
|||||  
CTCCA CTCCA CGTCA  
C C

GAM1127 LOC90591 3' AGCTCACTGCAAGCTCCACCTC 63412 A G  
GAGGT GAG TTGCAGTGAGTT  
|||||  
CTCCA CTC AACGTCACCTCGA  
C G

GAM1127 LOC91115 3' ACTGCAACCTCCGCCTC 64919 TA  
GAGG GAGGTTGCAGT  
|||||  
CTCC CTCCAACGTCA  
GC

GAM1127 LOC91115 3' GCTCACTGCAACCTCCACCTC 64940 A  
GAGGT GAGGTTGCAGTGAGT  
|||||  
CTCCA CTCCAACGTCACCTCG  
C

GAM1127 LOC91291 5' AGCTCACTGCAACCTCGACCTC 65476 A  
GAGGT GAGGTTGCAGTGAGTT  
|||||  
CTCCA CTCCAACGTCACCTCGA  
G

GAM1127 LOC91308 3' CTGCAACCTCCACCTC 65559 A  
GAGGT GAGGTTGCAG  
|||||  
CTCCA CTCCAACGTC  
C

GAM1127 LOC92267 3' AGCTCACTGCAACCTCCACCTC 68603 A  
GAGGT GAGGTTGCAGTGAGTT  
|||||  
CTCCA CTCCAACGTCACCTCGA  
C

GAM1127 LOC92303 3' AACTCACTGCAACCTCTGCC 68818  
GGTAGAGGTTGCAGTGAGTT  
|||||



CCGTCTCCAACGTCACCTCAA

GAM1127 LOC92466 3' ACTGCAACCTCCGCCTC 69419 TA  
GAGG GAGGTTGCAGT  
|||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 LOC92661 5' GCTCACTGCAAGCTCCACCTC 70082 A G  
GAGGT GAG TTGCAGTGAGT  
|||| ||| |||||||||  
CTCCA CTC AACGTCACTCG  
C G

GAM1127 LOC92689 3' ACTGCAACCTCCGCCTC 70212 TA  
GAGG GAGGTTGCAGT  
|||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 LOC92697 5' ACCGCAACCTCCGCCTC 70258 TA A  
GAGG GAGGTTGC GT  
|||| |||||| ||  
CTCC CTCCAACG CA  
GC C

GAM1127 LOC92697 5' GCTACAACCTCCACCTC 70274 A C  
GAGGT GAGGTTG AGT  
|||| |||||| ||  
CTCCA CTCCAAC TCG  
C A

GAM1127 LOC92841 3' ACCGCAACCTCCTCCTC 70703 TA A  
GAGG GAGGTTGC GT  
|||| |||||| ||  
CTCC CTCCAACG CA  
TC C

GAM1127 LOC93132 5' ACTGCAACCTCCGCCTC 71478 TA  
GAGG GAGGTTGCAGT  
|||| |||||||||  
CTCC CTCCAACGTCA  
GC

GAM1127 LOC93349 3' ACTGCAACCTCTGCCTC 56448  
GAGGTAGAGGTTGCAGT  
|||||||||||  
CTCCGTCTCCAACGTCA

GAM1127 LOC93408 5' ACTGCAACCTCTGCCTC 56473  
GAGGTAGAGGTTGCAGT  
|||||||||||  
CTCCGTCTCCAACGTCA

GAM1128 OXTR 3' CAACTTAACAAAACAAGTGCAA 6204 CCAGGCT\_  
GA TCTTGCACTTGT GTTG  
||||||||| |||

			AGAACGTGAACA	CAAC	
			AAACAATT		
GAM1128	PPP2CA	5'	CAACAGCCGCCAGAAGTACACG	10742	T C GTCCA
	A		TC TG ACTT GGCTGTTG		
			AG AC TGAA CCGACAAC		
			C A GACCG		
GAM1128	RARB	5'	CAACAGCCTACGTGC	6371	TT CC
			GCAC GT AGGCTGTTG		
			CGTG CA TCCGACAAC		
			— —		
GAM1128	CYYR1	3'	CAACAGCCGCTTGAAGCCAAGA	53671	CA GTCCA
			TCTTG CTT GGCTGTTG		
			AGAAC GAA CCGACAAC		
			C_ GTTCG		
GAM1128	FGD3	3'	CAACAGCCCAGAGCTCAGGA	72896	CA GTCCA
			TCTTG CTT GGCTGTTG		
			AGGAC GAG CCGACAAC		
			TC AC_		
GAM1128	KIAA1350	5'	AACAGCCTTATGCAATGA	72703	_ CTTGTCC
			TC TTGCA AGGCTGTT		
			AG AACGT TCCGACAA		
			T AT_		
GAM1128	KIAA1564	5'	CCTGAACCAGTGCAAGA	63866	T C
			TCTTGCACT GT CAGG		
			AGAACGTGA CA GTCC		
			C A		
GAM1128	P8	3'	CAACCCTAGCAAAAGTGCAAGA	24743	GTCC_ CT
			TCTTGCACTT AGG GTTG		
			AGAACGTGAA TCC CAAC		
			AACGA _		
GAM1128	STK33	3'	CAGTGTTGGACAGTACAA	62897	C T _
			TTG ACT GTCCAG GCTG		
			AAC TGA CAGGTT TGAC		
			A _ G		
GAM1128	LOC145757	5'	CAACAGACCCAGGTGCAA	77455	TCCA _
			TTGCACTTG GG CTGTTG		
			AACGTGGAC CC GACAAC		
			_ A		
GAM1128	LOC152283	3'	CCCGGACAAGTACAAGA	85681	C A
			TCTTG ACTTGTCC GG		

AGAAC TGAACAGG CC  
 A C  
 GAM1128 LOC196528 3' AACAGCCTAGGAGAAG 87760 G \_  
 CTT TCC AGGCTGTT  
 ||| ||| |||||  
 GAA AGG TCCGACAA  
 G A  
 GAM1128 LOC219540 3' CAATTTCTTAAACAAATGCAAG 93595 C CC CT  
 CTTGCA TTGT AGG GTTG  
 ||||| ||| || |||  
 GAACGT AACA TTC TAAC  
 A AA TT  
 GAM1128 LOC256440 3' CAACAGTACAGGAAGAAGTGCA 95567 G\_ AG\_  
 AGA TCTTGCACCTT TCC GCTGTTG  
 ||||| ||| |||||  
 AGAACGTGAA AGG TGACAAC  
 GA ACA  
 GAM1128 LOC91464 3' CAACAGCCCCACAGGATGCAA 66136 \_ CCA  
 TTGCA CTTGT GGCTGTTG  
 ||||| ||| |||||  
 AACGT GGACA CCGACAAC  
 A C\_  
 GAM1129 SMP1 3' CACAGTTTGAAATGTCTTTCA 26697 C GGTGT  
 TGAAAGAC AT ACTGTG  
 ||||| || |||||  
 ACTTTCTG TA TGACAC  
 \_ AAGTT  
 GAM1129 FLJ10852 3' ATCACAGTACACCATGGTCTTT 38734  
 CA TGAAAGACCATGGTGTACTGTGAT  
 ||||| ||||| |||||  
 ACTTTCTGGTACCACATGACACTA  
 GAM1129 FLJ20291 3' GCGTACACCAGACCCTTCA 34867 AGACCA T  
 TGAA TGGTGTAC GT  
 ||| ||||| ||  
 ACTT ACCACATG CG  
 CCCAG\_ \_  
 GAM1129 KIAA0644 3' ATCACAGCCCCGGGTCTTTCA 29060 A TGTA  
 TGAAAGACC TGG CTGTGAT  
 ||||| ||| |||||  
 ACTTTCTGG GCC GACACTA  
 \_ CC\_  
 GAM1129 KIAA1536 3' ATGGACATCATGGCCTCTCA 40491 A A A  
 TGA AG CCATGGTGT CTGT  
 ||| || ||||| |||  
 ACT TC GGTACTACA GGTA  
 C C \_  
 GAM1129 LOC122830 3' CACAGTACTCAGCCTTTCA 74163 ACCA T  
 TGAAAG TGG GTACTGTG  
 ||||| ||| |||||

		ACTTTC ACT CATGACAC	
		CG__ _	
GAM1129	LOC143154 3'	ATCACAGTATTGTGATTTTCA 76478	AC TG GT
		TGAAAG CA GT ACTGTGAT	
		ACTTTT GT TA TGACACTA	
		A_ GT _	
GAM1129	LOC145761 5'	ATCACAGTGACGGTGACCTTCA 83473	A AC G G
		TGAA G CAT GT TACTGTGAT	
		ACTT C GTG CA GTGACACTA	
		_ CA G _	
GAM1129	LOC157653 5'	CACAGTGTTCTTGCCCTTCA 81524	AGA T TG
		TGAA CCA GG TACTGTG	
		ACTT GGT TC GTGACAC	
		CCC _ TT	
GAM1129	LOC163231 5'	CACAGTACAAACCTCTTCA 82437	A CCATGG
		TGAA GA TGTACTGTG	
		ACTT CT ACATGACAC	
		_ CCAA_	
GAM1129	LOC219294 3'	ATCACAGTATTGTGATTTTCA 93004	AC TG GT
		TGAAAG CA GT ACTGTGAT	
		ACTTTT GT TA TGACACTA	
		A_ GT _	
GAM1129	LOC221405 5'	TCACAGTACCATCATTC 93888	CC _
		GA ATGGTG TACTGTGA	
		CT TACTAC ATGACACT	
		_ C	
GAM1130	ADCY3 3'	GAGAACAGAAAGTGCAAT 14457	__ _
		ATTGCACT TGT CTC	
		TAACGTGA ACA GAG	
		AAG A	
GAM1130	CD59 3'	TGGACAAACCGAGTGCAATG 5216	TC__
		CATTGCACTTG TCCA	
		GTAACGTGAGC AGGT	
		CAAAC	
GAM1130	CNR1 3'	GCAGTGGATACGTGTCAATG 32215	_ TT C
		CATTG CAC GT TCCACTGC	
		GTAAC GTG CA AGGTGACG	
		T _ T	
GAM1130	EDNRA 5'	GCAGCACAAAGTGCAAT 64110	CTCCA
		ATTGCACTTGT CTGC	

			TAACGTGAACA	GACG		
			C_____			
GAM1130	GNPI	3'	TGGTCAGTAACAAGTGCAATG	18450	CTCC	C
			CATTGCACTTGT	ACTG CCA		
			GTAACGTGAACA	TGAC GGT		
			A_____	T		
GAM1130	GTF2E2	3'	CAGTTTACAAAACAAGTGCAA	9144	CTCC_____	
			TTGCACTTGT	ACTG		
			AACGTGAACA	TGAC		
			AAACATT			
GAM1130	GYPC	3'	GGGCAGTGCAGGACAA	9163	C_	
			TTGTCT	CACTGCCC		
			AACAGG	GTGACGGG		
			AC			
GAM1130	GYPC	3'	GGGCAGTGCAGGACAA	33653	C_	
			TTGTCT	CACTGCCC		
			AACAGG	GTGACGGG		
			AC			
GAM1130	MAP3K7IP2	3'	TGAGCAGTGGGTGACA	30663	_	C
			TGTC	TCCACTGC CA		
			ACAG	GGGTGACG GT		
			T	A		
GAM1130	MCL1	3'	CAGTGGAACAAGTGCA	41714	C	
			TGCACTTGT	TCCACTG		
			ACGTGAACA	AGGTGAC		
			A			
GAM1130	MMP15	3'	TGGGCAGTGGATGGCCGTGAAT	10079	G	TT _
	G		CATT CAC	GTC TCCACTGCCCA		
			GTAA GTG	CGG AGGTGACGGGT		
			_	C_ T		
GAM1130	Nrap	3'	TGAGCAGTGGAAGGGGC	43348	A	GTC C
			GC CTT	TCCACTGC CA		
			CG GGG	AGGTGACG GT		
			_	AA_ A		
GAM1130	Nrap	3'	TGAGCAGTGGAAGGGGC	55442	A	GTC C
			GC CTT	TCCACTGC CA		
			CG GGG	AGGTGACG GT		
			_	AA_ A		
GAM1130	Nrap	3'	TGAGCAGTGGAAGGGGC	57637	A	GTC C
			GC CTT	TCCACTGC CA		

			CG GGG AGGTGACG GT		
			_ AA_ A		
GAM1130	P2RY6	3'	GGCAGTGGGAAGCCAATG 14742	CACTTG T	
			CATTG TC CCACTGCC		
			GTAAC AG GGTGACGG		
			CGA___ _		
GAM1130	PIAS3	3'	GGCAGTGGGAGGCAAATG 20341	C _	
			CA TTGTCTCC ACTGCC		
			GT AACGGAGG TGACGG		
			A G		
GAM1130	POLK	3'	TAGTGAAGGCAAGTGCAAT 32570	C	
			ATTGCACTTGTCT CACTG		
			TAACGTGAACGGA GTGAT		
			A		
GAM1130	RNTRE	3'	GCAAAACAAGTGCAGTG 28037	CTCCAC	
			CATTGCACTTGT TGC		
			GTGACGTGAACA ACG		
			AA___		
GAM1130	SPTBN4	5'	GCAGCGGAGACAGCGA 47387	ACT A	
			TTGC TGTCTCC CTGC		
			AGCG ACAGAGG GACG		
			___ C		
GAM1130	TCFL4	3'	CAGGGAGACAAGTGAATG 63459	G A	
			CATT CACTTGTCTCC CTG		
			GTAA GTGAACAGAGG GAC		
			___ _		
GAM1130	TNS	3'	GGAGGAGAGAAGAAAGTGCAA 42629	G___ CA G	
			TTGCACTT TCTC CT CC		
			AACGTGAA AGAG GA GG		
			AGA AG _		
GAM1130	XDH	3'	TGGAAGACAAGTGAATG 59416	G _	
			CATT CACTTGTCT CCA		
			GTAA GTGAACAGA GGT		
			___ A		
GAM1130	XDH	3'	TGGAAGACAAGTGAATG 4595	G _	
			CATT CACTTGTCT CCA		
			GTAA GTGAACAGA GGT		
			___ A		
GAM1130	C15orf5	5'	TGGAGACAAATACAATG 48200	CAC	
			CATTG TTGTCTCCA		

GTAAC AACAGAGGT  
 ATA  
 GAM1130 C20orf11 3' GGCAGTGGAAAACCTTGCAA 35441 CTTGTC  
 TTGCA TCCACTGCC  
 ||||| |||||  
 AACGT AGGTGACGG  
 TCAA\_

GAM1130 CDC14B 3' GGCAGTGGGAAACAAATG 52836 C C\_  
 CA TTGT TCCACTGCC  
 || ||||| |||||  
 GT AACA GGGTGACGG  
 A AA

GAM1130 CHODL 3' GTGGAGACAAGCACAG 46313 CA  
 TTG CTTGTCTCCAC  
 ||| |||||  
 GAC GAACAGAGGTG  
 AC

GAM1130 COLEC12 3' TGGGCAGTGGAACGATTTCCAA 47876 CAC\_ C  
 TG CATTG TTGT TCCACTGCCCA  
 ||||| ||| |||||  
 GTAAC AGCA AGGTGACGGGT  
 CTTT \_

GAM1130 DKFZP434J1813 3' GGCAACAGTAAGTGCA 61789 T CCAC C  
 TGCACTTG CT TGC C  
 ||||| || |||  
 ACGTGAAT GA ACG G  
 \_ CA\_ A

GAM1130 DKFZp547I224 5' CAGTGGGCGCAAGTCAATG 39554 C C  
 CATTG ACTTGT TCCACTG  
 ||||| ||||| |||||  
 GTAAC TGAACG GGGTGAC  
 \_ C

GAM1130 FLJ12891 3' GGCAGTTGTAACGCAATG 46345 ACTT CTCC  
 CATTGC GT ACTGCC  
 ||||| || |||||  
 GTAACG CA TGACGG  
 \_ ATGT

GAM1130 FLJ12998 3' GGCAGCAGAGGGACAAGTG 42838 CA\_  
 CACTTGTCTC CTGCC  
 ||||| ||||| |||||  
 GTGAACAGGG GACGG  
 AGAC

GAM1130 FLJ13081 3' GGCAGCGGAATAGAGTGCAAGTG 45751 GTC A  
 CATTGCACTT TCC CTGCC  
 ||||| ||||| |||||  
 GTGACGTGAG AGG GACGG  
 ATA C

GAM1130 FLJ13710 3' GCAGTGGGAAGTACA 45681 C GTC  
 TG ACTT TCCACTGC  
 || ||||| |||||

AC TGAA GGGTGACG  
 A \_\_\_\_  
 GAM1130 FLJ23584 5' GGCAGTGGCTGTGAATG 44741 G TTGTCT  
 CATT CAC CCACTGCC  
 ||||| ||| |||||  
 GTAA GTG GGTGACGG  
 \_ TC\_\_\_\_  
 GAM1130 HRH4 3' GGCAGTGGTCACCAATG 41255 CACTT CT  
 CATTG GT CCACTGCC  
 ||||| || |||||  
 GTAAC CA GGTGACGG  
 \_\_\_\_\_ CT  
 GAM1130 KIAA0218 3' GGCAGCAAAGAAGAAAGAGTGC 28622 G\_ \_ CA\_  
 GAT ATTGCACTT TCT C CTGCC  
 ||||| ||| |||||  
 TAGCGTGAG AGA G GACGG  
 AA A AAAC  
 GAM1130 KIAA0258 3' CAGGATGCAGACAGGTGCAATG 28810 C \_\_\_\_  
 CATTGCACTTGTCT CA CTG  
 ||||| ||||| |||  
 GTAACGTGGACAGA GT GAC  
 C AG  
 GAM1130 KIAA0286 3' GGCAGTGGAGATGGCAAT 68328 ACT  
 ATTGC TGTCTCCACTGCC  
 ||||| |||||  
 TAACG GTAGAGGTGACGG  
 \_\_\_\_\_  
 GAM1130 KIAA0992 3' CAGTGAACCAAGTGCAAT 32205 TC C  
 ATTGCACTTG TC ACTG  
 ||||| || |||||  
 TAACGTGAAC AG TGAC  
 CA \_  
 GAM1130 KIAA1257 3' GGCAGTGGAGTTAAGAGCAATG 62751 A T  
 CATTGC CTTG CTCCACTGCC  
 ||||| ||| |||||  
 GTAACG GAAT GAGGTGACGG  
 A T  
 GAM1130 KIAA1887 3' TGGACAGTGGAGACGTTGTGAT 76779 TG CT C  
 G CAT CA TGTCTCCACTG CCA  
 ||| || ||||| |||  
 GTA GT GCAGAGGTGAC GGT  
 GT T\_ A  
 GAM1130 MGC13061 3' TGGGCAGTGAAGCATGCCAATG 50311 \_ CT T C  
 CATTG CA TG CT CACTGCCCA  
 ||||| || || |||||  
 GTAAC GT AC GA GTGACGGGT  
 C \_ \_ A  
 GAM1130 MMEL2 3' TGAGCAGTGTCCAGTGCAGT 53096 TGTCTC C  
 ATTGCACT CACTGC CA  
 ||||| ||||| ||



			TGACGTGA	GTGACG GT		
			CCT__	A		
GAM1130	MPZL1	3'	GGCAAGGACAAGTACA	14204	C	CCAC
			TG ACTTGTCT	TGCC		
			AC TGAACAGG	ACGG		
			A	A__		
GAM1130	NPD009	5'	GCAGGCGCCAAGTGCTATG	95049	T	TCTCCA
			CAT GCACTTG	CTGC		
			GTA CGTGAAC	GACG		
			T	CGCG__		
GAM1130	PXMP4	3'	GGGCAGTGGGTTGTAA	23377		CTTGTC
			TTGCA	TCCACTGCCC		
			AATGT	GGGTGACGGG		
			T__			
GAM1130	RANBP6	3'	CAGTGGGGACTGTGCA	61636		TT
			TGCAC	GTCTCCACTG		
			ACGTG	CAGGGGTGAC		
			T_			
GAM1130	SLC17A6	3'	GCAATAAGTGCAATG	39743		CTCCAC
			CATTGCACTTGT	TGC		
			GTAACGTGAATA	ACG		
GAM1130	SMAP1	3'	GGGCAGCACAAGTGTAATG	41653		CTCCA
			CATTGCACTTGT	CTGCCC		
			GTAATGTGAACA	GACGGG		
			C__			
GAM1130	LOC115294	3'	GGGCAATATATGAGTGCAAT	73015		TG CTCCAC
			ATTGCACT T	TGCCC		
			TAACGTGA A	ACGGG		
			GT TATA__			
GAM1130	LOC115294	5'	TGGAAATCAAGTGCAAT	73019		TC_
			ATTGCACTTG	TCCA		
			TAACGTGAAC	AGGT		
			TAA			
GAM1130	LOC151057	3'	TGAGCAGTGGAGAACAGCAA	85219		ACTTG C
			TTGC	TCTCCACTGC CA		
			AACG	AGAGGTGACG GT		
			ACA__	A		
GAM1130	LOC151098	5'	GGGCAGTGCTCAATGAATG	80116		G C TCTC
			CATT CA TTG	CACTGCCC		

GTAA GT AAC GTGACGGG  
 \_ \_ TC\_  
 GAM1130 LOC151146 5' GGCAGTGGGGATGCAGTG 80137 CTTG  
 CATTGCA TCTCCACTGCC  
 ||||| |||||  
 GTGACGT AGGGGTGACGG

\_\_\_\_\_  
 GAM1130 LOC151584 3' GGGCAGTAGAAGCAAATG 85450 C TC C  
 CA TTG TC ACTGCCC  
 || ||| || |||||  
 GT AAC AG TGACGGG  
 A GA A

GAM1130 LOC169026 5' TGGGCAGTGAGTTCAACAACAA 82731 CAC T\_ C  
 TTG TTG CTC ACTGCCCA  
 ||| ||| ||| |||||  
 AAC AAC GAG TGACGGGT  
 AAC TT \_

GAM1130 LOC200132 3' TGAGCAGCATTTCATTAAGTGCA 88585 TCTCCA\_ C  
 AT ATTGCACTTG CTGC CA  
 ||||| ||| ||  
 TAACGTGAAT GACG GT  
 TACTTAC A

GAM1130 LOC219927 3' CAGTGGTCACAGTGCAAT 91536 T CT  
 ATTGCACT GT CCACTG  
 ||||| || |||||  
 TAACGTGA CA GGTGAC  
 \_ CT

GAM1130 LOC220929 5' GACAGTGGAGCAGCAA 91402 ACT T CC  
 TTGC TG CTCCACTG C  
 ||| || ||||| |  
 AACG AC GAGGTGAC G  
 \_ \_ AA

GAM1130 LOC253883 3' GGCAAGGACAAGTACA 96033 C CCAC  
 TG ACTTGTCT TGCC  
 || ||||| |||  
 AC TGAACAGG ACGG  
 A A\_

GAM1130 LOC254986 5' TGGAAATCAAGTGCAAT 96085 TC\_  
 ATTGCACTTG TCCA  
 ||||| |||  
 TAACGTGAAC AGGT  
 TAA

GAM1130 LOC96597 5' GGCAGTGGAGGTTGCAGTG 66916 CTTG  
 CATTGCA TCTCCACTGCC  
 ||||| |||||  
 GTGACGT GGAGGTGACGG  
 T\_

GAM1131 ADAMTS8 5' TCGGGCCGCCAGCACCTG 22886 \_ ATAAG  
 CAG TGCTGGC CTGA  
 ||| ||||| |||

			GTC ACGACCG	GGCT		
			C CCG__			
GAM1131	BAP1	3'	TCAGGGACCCAGCACTGG	16219	CATAAG	
			CCAGTGCTGG	CTGA		
			GGTCACGACC	GA CT		
			CAGG__			
GAM1131	BF	5'	TTCAGCTTGGACACTG	8140	CTGGCA	
			CAGTG TAAGCTGAA			
			GTCAC GTTCGACTT			
			AG__			
GAM1131	C1QB	3'	TTCAACTCTGTGTCCCAGCACT	4923	A _ _ C	
	GGC		G CCAGTGCTGG	CATA AG TGAA		
			C GGTACGACC GTGT TC ACTT			
			_ CT C A			
GAM1131	CHC1	3'	CAGCCCTGAGCACTGTGTC	7020	_ _ CATAA	
			GAC CAGTGCT GG	GCTG		
			CTG GTCACGA CC	CGAC		
			T GT ____			
GAM1131	CMRF35	5'	CAGAGCTGTCAGCACCGG	21929	A TAAG	
			CC GTGCTGGCA	CTG		
			GG CACGACTGT	GAC		
			C CGA_			
GAM1131	EPHB6	3'	TCAGCCCTGGACACTGGTC	15466	_ TG CATAA	
			GACCA GTG C G	GCTGA		
			CTGGTCAC G C	CGACT		
			A GT C__			
GAM1131	EVPL	5'	CAGCCTGAGCCAGCACT	8803	A A	
			AGTGCTGGC TA	GCTG		
			TCACGACCG GT	CGAC		
			A C			
GAM1131	GARP	3'	CAGCCCAGCACTGG	18594	CATAA	
			CCAGTGCTGG	GCTG		
			GGTCACGACC	CGAC		
			_____			
GAM1131	GJB5	3'	CAGCTCGACGGCACTGG	17945	GCATA	
			CCAGTGCTG	AGCTG		
			GGTCACGGC	TCGAC		
			AGC__			
GAM1131	GPR81	3'	CTTACCAGCATTAGTC	50757	C CA	
			GAC AGTGCTGG	TAAG		

CTG TTACGACC ATTG  
 A    \_\_\_\_  
 GAM1131 IFI16    5' AGCAAGCCAGCACTAGTC    71221    C    ATAA  
                   GAC AGTGCTGGC    GCT  
                   ||| |||||    |||  
                   CTG TCACGACCG    CGA  
                   A    AA\_\_\_\_  
 GAM1131 KRT4    3' CAGCTGGGCCCAGCACTGGT    9635    \_ATA  
                   ACCAGTGCTGG C    AGCTG  
                   ||||| ||| | |||||  
                   TGGTCACGACC G    TCGAC  
                   C GG\_  
 GAM1131 MAP3K9    3' TTCAGCTTCCCAAACACCAGT    60709    CA C\_ CAT  
                   AC GTG TGG AAGCTGAA  
                   || ||| ||| |||||  
                   TG CAC ACC TTCGACTT  
                   AC AA C\_\_\_\_  
 GAM1131 MGAT5    5' TCAGCTTACAGTTCCTG    10028    T\_ GCA  
                   CAG GCTG TAAGCTGA  
                   ||| ||| |||||  
                   GTC TGAC ATTCGACT  
                   CT    \_\_\_\_  
 GAM1131 MOCS1    3' TTCAGCTTAACAGTTGCCCGGT    92037    A\_ \_ GCA  
                   C    GACC GTG CTG TAAGCTGAA  
                   |||| ||| ||| |||||  
                   CTGG CGT GAC ATTCGACTT  
                   CC T A\_\_\_\_  
 GAM1131 P23    3' TCAGCTTATACCCGGGCT    21719    G C\_  
                   AGT CTGG ATAAGCTGA  
                   ||| ||| |||||  
                   TCG GGCC TATTCGACT  
                   \_ CA  
 GAM1131 PFKFB4    3' TCAGCCACATGCAACACTGTGT    15874    \_ CTG AA\_  
                   C    GAC CAGTG GCAT GCTGA  
                   ||| |||| ||| |||||  
                   CTG GTCAC CGTA CGACT  
                   T AA\_ CAC  
 GAM1131 PTPRK    3' TTCAGCCTGTGGCCCAGCACTG    11125    \_ A  
                   GTC    GACCAGTGCTGG CATA GCTGAA  
                   ||||| ||| |||||  
                   CTGGTCACGACC GTGT CGACTT  
                   CG C  
 GAM1131 RNPEPL1    3' CGGATGCCAGCACCTG    36676    \_ AAG  
                   CAG TGCTGGCAT CTG  
                   ||| ||||| |||  
                   GTC ACGACCGTA GGC  
                   C    \_\_\_\_  
 GAM1131 UBE2L3    3' TCAGCCCTGGCACTGGC    12507    A TG CATAA  
                   G CCAGTGC G    GCTGA  
                   | ||||| | |||||

C GGTACAG C CGACT  
 \_ GT C\_  
 GAM1131 APXL2 5' CAGCCTCAGCACTCATC 75185 CC CATAA  
 GA AGTGCTGG GCTG  
 || ||||| |||  
 CT TCACGACT CGAC  
 AC C\_  
 GAM1131 ARHGEF9 3' TTCAGCTTACCAAGCA 30824 \_ CA  
 TGCT GG TAAGCTGAA  
 |||| || |||||  
 ACGA CC ATTCGACTT  
 A \_  
 GAM1131 CEGP1 3' TTCAGCTTCCTCTAGCCCGG 40589 AGT CAT  
 CC GCTGG AAGCTGAA  
 || |||| |||||  
 GG CGATC TTCGACTT  
 CC\_ TCC  
 GAM1131 DKFZp547D155 3' CAGCCCTGAGACCACTGGTC 70435 CTGG TAA  
 GACCAGTG CA GCTG  
 ||||| || |||  
 CTGGTCAC GT CGAC  
 CAGA CC\_  
 GAM1131 DKFZP727G051 3' TTCAGCCCATCAACCAGCATTG 69483 CATAA\_  
 GTC GACCAGTGCTGG GCTGAA  
 ||||| |||||  
 CTGGTTACGACC CGACTT  
 AACTACC  
 GAM1131 DUSP14 5' CACTGTCACCAGCACTGCTC 22834 C CATA C  
 GA CAGTGCTGG AG TG  
 || ||||| |||  
 CT GTCACGACC TC AC  
 C ACTG \_  
 GAM1131 FLJ10206 5' CAGCTTATGCCAGGAGTC 35898 CAGTG  
 GAC CTGGCATAAGCTG  
 || |||||  
 CTG GACCGTATTCGAC  
 AG\_  
 GAM1131 FLJ20967 5' GGCGCCCAGCACTGGTT 41962 CATAA  
 GACCAGTGCTGG GCT  
 ||||| |||  
 TTGGTCACGACC CGG  
 CG\_  
 GAM1131 FLJ22569 3' TTCAGCTTACTAACTG 43679 GC CA  
 CAGT TGG TAAGCTGAA  
 |||| || |||||  
 GTCA ATC ATTCGACTT  
 A\_ \_  
 GAM1131 FOXN4 3' TTCAGCTTGGACACACTGG 75574 C GCA  
 CCAGTG TG TAAGCTGAA  
 |||| || |||||

			GGTCAC AC GTTCGACTT		
			_ AG_		
GAM1131	GW112	3'	TTCAACTGAAGCCAGCACTGGT 21194	ATA	C
	T		GACCA GTGCTGGC AG TGAA		
			TTGGTCACGACCG TC ACTT		
			AAG A		
GAM1131	HOOK2	3'	CAGCTCACATGGCGCCCAGCAC 25256	___	A_
	TGG		CCAGTGTGCTGG CAT AGCTG		
			GGTCACGACC GTA TCGAC		
			CGCG CAC		
GAM1131	jdp2	3'	TTCAGCACAGCCAGCAT 55327	ATAA	
			GTGCTGGC GCTGAA		
			TACGACCG CGACTT		
			ACA_		
GAM1131	KIAA0767	3'	TCTGCTGCCAGCACAGG 60632	A	TAA T
			CC GTGCTGGCA GC GA		
			GG CACGACCGT CG CT		
			A ___ T		
GAM1131	KIAA0923	3'	TCAGCTTGATGCATGGTC 25838	G	TGGCA
			GACCA TGC TAAGCTGA		
			CTGGT ACG GTTCGACT		
			_ TA___		
GAM1131	KIAA0982	3'	TTCAGTGTGTTGCCAGCAC 25852	TA_	C
			GTGCTGGCA AG TGAA		
			CACGACCGT TC ACTT		
			TTG _		
GAM1131	KIAA1000	3'	TTCAGCTTTGCAAAGTACTGG 65281	G_	T
			CCAGTGTGCT GCA AAGCTGAA		
			GGTCATGA CGT TTCGACTT		
			AA _		
GAM1131	MAP3K3	3'	TCAGCCTGGGCGCTGGTC 9999	GG	TAA
			GACCA GTGCT CA GCTGA		
			CTGGTCGCGG GT CGACT		
			_ C_		
GAM1131	MGC16037	5'	CTTGTCCAGCACTAGTC 51821	C	C
			GAC AGTGTGCTGG ATAAG		
			CTG TCACGACC TGTTT		
			A _		
GAM1131	MIDORI	3'	TCAGCTTATCCTGCAACT 73792	_	T C
			AGT GC GG ATAAGCTGA		

TCA CG CC TATTCGACT  
 A T \_  
 GAM1131 MtFMT 5' CAGTGGCGAGCACTGG 57651 G ATAA  
 CCAGTGCT GC GCTG  
 ||||| || |||  
 GGTCACGA CG TGAC  
 G G\_\_  
 GAM1131 PCDH16 5' TCAGTTCCAACCACTGG 72826 C\_ CATA  
 CCAGTG TGG AGCTGA  
 ||||| || |||||  
 GGTCAC ACC TTGACT  
 CA \_\_\_\_  
 GAM1131 QKI 3' CAGCTTATCAACTCGTC 65439 C GCTGGC  
 GAC AGT ATAAGCTG  
 ||| ||| |||||  
 CTG TCA TATTCGAC  
 C AC\_\_\_\_  
 GAM1131 TNRC6 3' CAACTTTTAGCACTG 70506 CAT C  
 CAGTGCTGG AAG TG  
 ||||| ||| ||  
 GTCACGATT TTC AC  
 \_\_\_\_ A  
 GAM1131 TOB2 3' CAGCCCAGGCCAGCACTG 95618 ATAA  
 CAGTGCTGGC GCTG  
 ||||| |||  
 GTCACGACCG CGAC  
 GACC  
 GAM1131 TU12B1-TY 3' TCAGCCCACAGCACTGTC 33406 C GCATAA  
 GAC AGTGCTG GCTGA  
 ||| ||||| |||||  
 CTG TCACGAC CGACT  
 \_ ACC\_\_\_\_  
 GAM1131 TUSP 3' TCAGCCTAAGAGCGCAGCACTG 39641 \_ A\_\_ A  
 CAGTGCTG GC TA GCTGA  
 ||||| || |||||  
 GTCACGAC CG AT CGACT  
 G AGA C  
 GAM1131 USP19 3' TCAGCTTATGCATCTGGT 88959 TGCTG  
 ACCAG GCATAAGCTGA  
 |||| |||||  
 TGGTC CGTATTCGACT  
 TA\_\_\_\_  
 GAM1131 ZD52F10 3' CAGCCTGTGCCAGCCCTGG 52819 T A  
 CCAG GCTGGCATA GCTG  
 ||| ||||| |||||  
 GGTC CGACCGTGT CGAC  
 C C  
 GAM1131 LOC145268 3' TCAGCTTACAAGAGCCACTG 77062 \_ GGCA  
 CAGTG CT TAAGCTGA  
 |||| || |||||

		GTCAC GA	ATTCGACT		
		C	GAAC		
GAM1131	LOC149296	5'	CAGCTTATGGGCAGCA	79256	G_
			TGCTG CATAAGCTG		
			ACGAC GTATTCGAC		
			GG		
GAM1131	LOC161877	5'	TCAGGGCAGGCCAGCGCTGG	82326	ATAAG
			CCAGTGCTGGC CTGA		
			GGTCGCGACCG GACT		
			GACGG		
GAM1131	LOC163115	5'	TCAGCCCCTGACAGCACTGG	82413	G TAA
			CCAGTGCTG CA GCTGA		
			GGTCACGAC GT CGACT		
			A CCC		
GAM1131	LOC196500	3'	TCAGCTCACTCAGTGGTC	87744	AGT CATA
			GACC GCTGG AGCTGA		
			CTGG TGA CT TCGACT		
			___ CAC_		
GAM1131	LOC197287	3'	TCAGCTCATGTGTTTTGCACTG	60865	T_ _
			CAGTGC GGCATA AGCTGA		
			GTCACG TTGTGT TCGACT		
			TT AC		
GAM1131	LOC200470	5'	TCAGCCTGCGGCGCTGG	90069	G TAA
			CCAGTGCTG CA GCTGA		
			GGTCGCGGC GT CGACT		
			_ C_		
GAM1131	LOC221584	3'	CAGCTTATGTGGCAC	93828	G
			GTGCTG CATAAGCTG		
			CACGGT GTATTCGAC		
			-		
GAM1131	LOC51716	3'	CAGCTCATGGCCCTAGCA	32787	___ A
			TGCTGG CAT AGCTG		
			ACGATC GTA TCGAC		
			CCG C		
GAM1131	LOC92196	5'	CAGAGCACCAGCACTGGC	68456	A CATAAG
			G CCAGTGCTGG CTG		
			C GGTACGACC GAC		
			_ ACGA_		
GAM1132	FLG	3'	CTTCACCTGTACAGTCAGACT	70877	A
			AGTCTGATTGTGCAGGT AAG		



			TCAGACTGACATGTCCA TTC		
			C		
GAM1132	HTR6	3'	TTACCTGCAGGGATCA 6034 _ G		
			TGAT T TGCAGGTAA		
			ACTA G ACGTCCATT		
			G G		
GAM1132	NUMB	3'	CCTTACAATCAAATGTA 13621 GTC C		
			TACA TGATTGTG AGG		
			ATGT ACTAACAT TCC		
			AA _ _		
GAM1132	PSG1	3'	TTATGTAAACAATCAGAC 22603 GCAG		
			GTCTGATTGT GTAA		
			CAGACTAACA TATT		
			AATG		
GAM1132	TRPM6	3'	CCTCACCCACAGATTGTA 34536 ATT C		
			TACAGTCTG GTG AGG		
			ATGTTAGAC CAC TCC		
			ACC _		
GAM1132	ZNF174	5'	ACCCGCCGGTTAGAGCGTA 12895 AG T A		
			TAC TCTGATTG GC GGT		
			ATG AGATTGGC CG CCA		
			CG _ C		
GAM1132	ATP9A	3'	CTTTACCTGCACAATCAGACTG 62042		
	TA		TACAGTCTGATTGTGCAGGTAAAG		
			ATGTCAGACTAACACGTCCATTTT		
GAM1132	CAMP-GEFII	3'	CCTGTTTTTACAATTAGACT 22827		
			AGTCTGATTGTG CAGG		
			TCAGATTAACAC GTCC		
			TTTT		
GAM1132	FYCO1	3'	ACCTGCACAATGGGGGTG 44485 G G		
			CA TCT ATTGTGCAGGT		
			GT GGG TAACACGTCCA		
			G G		
GAM1132	KIAA0232	3'	TTACCTGCTCTCATACTG 72763 C TTGT		
			CAGT TGA GCAGGTAA		
			GTCA ACT CGTCCATT		
			T CT__		
GAM1132	KIAA1145	3'	CTTTACCTGTGGGCATCAGACT 65622 C T __		
	CA		A AGTCTGAT GT GCAGGTAAAG		

A TCAGACTA CG TGTCCATTTC  
 C \_ GG  
 GAM1132 MGC4638 5' CCCAGCAATCAGACTCA 48940 C GCA  
 A AGTCTGATTGT GG  
 | ||||| ||  
 A TCAGACTAACG CC  
 C AC\_  
 GAM1132 NIT1 3' CTTACCTGAGGTCAGACTG 18808 TGTG A  
 CAGTCTGAT CAGGT AAG  
 ||||| |||||  
 GTCAGACTG GTCCA TTC  
 GA\_ C  
 GAM1132 UNC5D 3' CTTACAGATTCCAGACTGT 55136 A\_\_\_\_\_ C  
 A TACAGTCTG TTGTG AG  
 ||||| |||||  
 ATGTCAGAC GACAC TC  
 CACTTA T  
 GAM1132 LOC146517 3' CTTTACCTGTTGTCAAAC 77945 C TGT  
 AGT TGAT GCAGGTAAAG  
 ||| ||| |||||  
 TCA ACTG TGTCCATTTC  
 A T\_  
 GAM1132 LOC222060 5' TACTTTGTCATATCAGACT 94109 T \_ \_  
 AGTCTGAT GTG CAG GTA  
 ||||| ||| |||  
 TCAGACTA TAC GTT CAT  
 \_ T T  
 GAM1132 LOC255350 5' CTTACCTTATTTCAGATCTGTA 97553 \_ TT C A  
 TACAG TCTGA GTG AGGT AAG  
 ||||| ||||| ||| |||||  
 ATGTC AGACT TAT TCCA TTC  
 T \_ \_ C  
 GAM1132 LOC92230 5' TTACCTGCAGGGATCA 68548 \_ G  
 TGAT T TGCAGGTAA  
 ||||| |||||  
 ACTA G ACGTCCATT  
 G G  
 GAM1133 TFAP2C 3' AATCCTTCTCCACCGCA 12229 T TTGTA  
 TCGCGTGG AGG GATT  
 ||||| ||| |||  
 ACGCCACC TCT CTAA  
 \_ TC\_  
 GAM1133 KIAA1918 3' AAGAATCTACAACCTGGAGC 73158 GG  
 GT TAGGTTGTAGATTCTT  
 || |||||  
 CG GTCCAACATCTAAGAA  
 AG  
 GAM1133 LOC133308 5' AAGAATCCTATCTTCCCACCGC 75084 T\_ TGTA  
 A TCGCGTGG AGGT GATTCTT  
 ||||| ||| |||||

ACGCCACC TCTA CTAAGAA  
 CT TC\_\_  
 GAM1134 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
 GTA GGAT GGGTTGTTT  
 ||| ||| |||||  
 CGT CCTA CCCAACAAA  
 C CGTG\_  
 GAM1134 LCT 3' AACCGTAAAAATCCTT 9697 G  
 AAGGATTTTTA GGTT  
 ||||| |||  
 TTCCTAAAAAT CCAA  
 G  
 GAM1134 RPL15 3' AAACAACCCCTAAAAATCCTTAC 11382  
 GTAAGGATTTT TAGGGTTGTTT  
 |||||  
 CATTCTAAAAATCCCAACAAA  
  
 GAM1134 FBXO30 3' AACTAAAAAATCCTGAC 49573 A AG  
 GT AGGATTTT GGTT  
 || ||||| |||  
 CA TCCTAAAAA TCAA  
 G AA  
 GAM1134 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTT  
 GTAAG AGGGTTGTT  
 ||| |||||  
 CATTCTCCCAACAA  
 AT\_\_\_\_  
 GAM1134 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
 TAAG TTTT GGGTTGTTT  
 ||| ||| |||||  
 GTTC AAAA CCCAACAAA  
 \_\_\_\_ C  
 GAM1134 SMT3H2 3' AACCAACATAAAAAATCCTTGC 22670 GG  
 GTAAGGATTTT GTTGTT  
 ||||| |||  
 CGTTCCTAAAAAT CAACAA  
 A\_  
 GAM1134 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
 GTAAGGATTTT GGGTT  
 ||||| |||  
 CGTTCCTAAAAA TCAA  
 GTA  
 GAM1134 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
 GGAT TT GGGTTGTTT  
 ||| || |||||  
 CCTG AA CCCAACAAA  
 T\_ C  
 GAM1134 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
 C GTA GGATTTT TTGTTT  
 || ||||| |||

		CGT CCTAAAAA AACAAA		
		C GATAA		
GAM1134	LOC148089 3'	GGCCCTAAAAATTCCTAC	78637	A
		GTA GGATTTTTAGGGTT		
		CAT CTTAAAAATCCCGG		
		C		
GAM1134	LOC154547 3'	AACAACATAAAAAATCCTTGC	76050	GG
		GTAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1134	LOC158104 3'	ACAGCCAAAAATCCTTA	60313	AG
		TAAGGATTTTT GTTGT		
		ATTCCTAAAAA CCGACA		
		—		
GAM1134	LOC205880 5'	AAACAACCATCATCCTGAC	90709	A TTTAG
		GT AGGAT GGTGTTT		
		CA TCCTA CCAACAAA		
		G CTA_		
GAM1134	LOC221561 3'	AACAACATAAAAAATCCTTGC	92130	GG
		GTAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1134	LOC257591 3'	AACAACATAAAAAATCCTTGC	97840	GG
		GTAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1134	LOC51145 3'	AGCTAAAATCCTTAC	32393	TAG
		GTAAGGATTTT GTT		
		CATTCCTAAAA TCGA		
		—		
GAM1135	CXorf6 3'	TGCCCACTGCGTTCAACAATGC	18520	C_ G T
	T	AGCATTGT AG GC GTGGGCA		
		TCGTAACA TT CG CACCCGT		
		AC G T		
GAM1135	FGFR1 3'	CCCACAGCCCCTGCTGGGC	5204	ATT CA
		GC GT GGGCTGTGGG		
		CG CG CCCGACACCC		
		GGT TC		
GAM1135	FGFR1 3'	CCCACAGCCCCTGCTGGGC	31797	ATT CA
		GC GT GGGCTGTGGG		

CG CG CCGACACCC  
GGT TC

GAM1135 LETM1 3' GCCCACAGCAGCATGCCCT 24622 A T CAGG  
AG GCAT GT GCTGTGGGC  
|| ||| || |||||  
TC CGTA CG CGACACCCG  
C \_ A\_\_

GAM1135 MARK3 5' GCCCACAGCCCGCGGCGGCCT 9914 A AT A\_  
AG GC TGTC GGGCTGTGGGC  
|| || ||| |||||  
TC CG GCGG CCGACACCCG  
\_ \_ CG

GAM1135 PRX 3' TGCCCACCGTGACAGTGC 40541 G CTG  
GCATTGTCA GG TGGGCA  
||||| || |||||  
CGTGACAGT CC ACCCGT  
G \_

GAM1135 RAB5C 3' TGCCCACAACCCCTCCACCCTC 59837 CAT TCA C  
GAG TG GGG TGTGGGCA  
||| || ||| |||||  
CTC AC CCC ACACCCGT  
CC\_ CTC A

GAM1135 C20orf130 3' GCCCACAAGCAACAGT 61756 CAGG \_  
ATTGT GCT GTGGGC  
|||| ||| |||||  
TGACA CGA CACCCG  
A\_\_ A

GAM1135 C20orf151 3' CCCACCTGGGAAATGCTCT 88698 G\_ GCTG  
AGAGCATT TCAGG TGGG  
||||| |||| |||  
TCTCGTAA GGTCC ACCC  
AG \_

GAM1135 C6orf31 3' GCCCCAGCTCTGACAA 47643 T  
TTGTCAGGGCTG GGGC  
||||||| |||  
AACAGTCTCGAC CCG

GAM1135 CBX6 3' TGCCCACAACCCCTCTTTGTTC 26629 TTGTCA C  
T AGAGCA GGG TGTGGGCA  
|||| ||| |||||  
TCTTGT CCC ACACCCGT  
TTCTC\_ A

GAM1135 CINP 3' TGCCCACAACCCGCGGCCAGC 50940 ATT A\_ C  
GC GTC GGG TGTGGGCA  
|| ||| ||| |||||  
CG CGG CCC ACACCCGT  
AC\_ CG A

GAM1135 DKFZp434C0923 3' CCCACAGCCCTCTGTCCT 34212 AG TTGTC  
AG CA AGGGCTGTGGG  
|| || |||||

TC GT TCCCGACACCC  
 CT C\_\_\_\_  
 GAM1135 DKFZP434F1735 5' CCCACAGCCTCTAATA 31498 C \_  
 TGT AG GGCTGTGGG  
 ||| || |||||  
 ATA TC CCGACACCC  
 A T  
 GAM1135 DKFZP434J1813 5' GCCTTTCCCACAATGCTC 61788 CA CTGT  
 GAGCATTGT GGG GGGC  
 ||||| || |||  
 CTCGTAACA CCC TCCG  
 \_ TT\_  
 GAM1135 DKFZp547N157 5' TGCCATGGTCCCTGGCAA 68941 \_ G  
 TTGTCAGGG CTGTGG CA  
 ||||| ||||| ||  
 AACGGTCCC GGTACC GT  
 T \_  
 GAM1135 HHLA2 3' GCCCACAAAACATTGCTCT 22986 T CAGGGC  
 AGAGCA TGT TGTGGGC  
 ||||| || |||||  
 TCTCGT ACA ACACCCG  
 T AA\_\_\_\_  
 GAM1135 KIAA1297 3' TGCTGGCCCCTGACAATGCCCT 72190 A CT G  
 AG GCATTGTCAGGG GT GGCA  
 || ||||| || |||||  
 TC CGTAACAGTCCC CG TCGT  
 C \_ G  
 GAM1135 KIAA1577 5' CCCAACTTAACCAATGCTCT 64475 TCA CTG  
 AGAGCATTG GGG TGGG  
 ||||| || |||  
 TCTCGTAAC TTC ACCC  
 CAA A\_\_\_\_  
 GAM1135 LEAP-2 3' CACCTCCGACAATGCTC 53741 A CT  
 GAGCATTGTC GGG GTG  
 ||||| || |||  
 CTCGTAACAG CCT CAC  
 \_ C\_  
 GAM1135 MGC13114 3' GCCCACAGCCCTATGC 50416 TGTC  
 GCAT AGGGCTGTGGGC  
 ||| |||||  
 CGTA TCCCGACACCCG  
 \_\_\_\_\_  
 GAM1135 N4BP3 3' GCCCACAGCCCCCATGC 66263 T TCA  
 GCAT G GGGCTGTGGGC  
 |||| | |||||  
 CGTA C CCCGACACCCG  
 \_ C\_  
 GAM1135 PADI1 3' CCCACAGCCCCCAGAGGCTCT 61993 A GTCA  
 AGAGC TT GGGCTGTGGG  
 |||| | |||||

TCTCG AG CCGACACCC  
 G ACC\_  
 GAM1135 PRO0159 5' AGACCCTGACATACTCT 26108 CAT \_  
 AGAG TGTCAGGG CT  
 ||| ||||| ||  
 TCTC ACAGTCCC GA  
 AT\_ A  
 GAM1135 PSR 3' GCCCACAGCCCCCTTGGTTCT 65182 ATTGTCA  
 AGAGC GGGCTGTGGGC  
 ||| |||||  
 TCTTG CCGACACCCG  
 GTTCC\_  
 GAM1135 SCYD1 3' CCTGTCCCCCTGACAACACTC 90928 CA CT TG  
 GAG TTGTCAGGG G GG  
 || ||||| | ||  
 CTC AACAGTCCC T CC  
 AC CC GT  
 GAM1135 TXI1 5' GCCCACAGCTGGACA 37370 AG  
 TGTC GGCTGTGGGC  
 ||| |||||  
 ACAG TCGACACCCG  
 G\_  
 GAM1135 LOC144308 5' GCCCATGGGCCCTGACCACACT 83048 CATT \_  
 C GAG GTCAGGGCT GTGGGC  
 || ||||| |||||  
 CTC CAGTCCCGG TACCCG  
 ACAC G  
 GAM1135 LOC149657 3' GCCCACAGCAATTATTGC 84573 T TCAGG  
 GCA TG GCTGTGGGC  
 ||| || |||||  
 CGT AT CGACACCCG  
 T TAA\_  
 GAM1135 LOC149668 5' TGCCCACAGCTGAACACCTCT 84550 CAT CAG  
 AGAG TGT GGCTGTGGGCA  
 ||| || |||||  
 TCTC ACA TCGACACCCGT  
 C\_ AG\_  
 GAM1135 LOC158629 5' CCCACAGAGGTATTAAACAATG 86876 CAGGG\_\_\_\_  
 CTCT AGAGCATTGT CTGTGGG  
 ||||| |||||  
 TCTCGTAACA GACACCC  
 AATTATGGA  
 GAM1135 LOC163682 5' CCCACAGCCAGCTCT 87029 ATTGTCA  
 AGAGC GGCTGTGGG  
 ||| |||||  
 TCTCG CCGACACCC  
 A\_\_\_\_\_  
 GAM1135 LOC163682 5' CCCACAGCCAATGCT 87028 GTCAG  
 AGCATT GGCTGTGGG  
 |||| |||||

TCGTAA CCGACACCC

GAM1135 LOC196374 3' TGCCCACAGCCCAAGCCAGC 87653 ATT CA  
GC GT GGGCTGTGGGCA  
|| || |||||  
CG CG CCGACACCCGT  
AC\_ AA

GAM1135 LOC205385 5' CCCACAGCCCCTACTTTCTC 89505 CATT CA  
GAG GT GGGCTGTGGG  
||| || |||||  
CTC CA CCGACACCC  
TTT\_ TC

GAM1135 LOC222029 3' GGCCCTGACAACAGTCT 94039 GCA  
AGA TTGTCAGGGCT  
||| |||||  
TCT AACAGTCCCGG  
GAC

GAM1135 LOC51754 5' TGCCCACAGCCCGCCTGCTC 71031 TT A  
GAGCA GTC GGGCTGTGGGCA  
|||| ||| |||||  
CTCGT CGG CCGACACCCGT  
C\_ \_

GAM1136 B3GNT3 3' CCCACCTGGTACTGTT 26517 TACTAA A  
AACAGTATC AG TGGG  
||||| || |||  
TTGTCATGG TC ACCC  
C

GAM1136 CSPG3 3' AGCCCATTGACTTAGAACTGT 15227 A CTAAA  
T AACAGT TCTA GATGGGCT  
||||| ||| |||||  
TTGTCA AGAT TTACCCGA  
A TCAG\_

GAM1136 EVA1 3' AGCCCATCTCTAATGAGGACT 58572 A AC\_ A  
AGT TCT TA AGATGGGCT  
||| ||| || |||||  
TCA GGA AT TCTACCCGA  
\_ GTA C

GAM1136 ID4 3' CTTTAATAGATACTGT 7754 C  
ACAGTATCTA TAAAG  
||||| |||||  
TGTCATAGAT ATTTT  
A

GAM1136 RAD51C 3' TTTAGAGATACTGTT 54255 A  
AACAGTATCT CTAAA  
||||| |||||  
TTGTCATAGA GATTT

GAM1136 RHO 3' AGCCCATCTTCAGCAGTTGCT 5018 T A A  
AGTA CT CT AAGATGGGCT  
||| || || |||||



			TCGT GA GA TTCTACCCGA		
			T C C		
GAM1136	STAR	3'	CTCATTAGTAGACATGTT 4445	GTA	AAG
			AACA TCTACTA ATGGG		
			TTGT AGATGAT TACTC		
			AC_ _		
GAM1136	CD109	3'	AGTGGTCTCAGTAGATACT 56046	AA	GG
			AGTATCTACT AGAT GCT		
			TCATAGATGA TCTG TGA		
			C_ G_		
GAM1136	FLJ00024	3'	AGCCCATCCCTGGGACCTGC 63747	TCTA	AA
			GTA CTA GATGGGCT		
			CGT GGT CTACCCGA		
			CCAG CC		
GAM1136	FLJ20666	3'	GCTTACCACAGATACTGTT 35510	ACTAAAGA	
			AACAGTATCT TGGGC		
			TTGTCATAGA ATTCG		
			CACC_		
GAM1136	FLJ20666	3'	GCTTACCACAGATACTGTT 37089	ACTAAAGA	
			AACAGTATCT TGGGC		
			TTGTCATAGA ATTCG		
			CACC_		
GAM1136	FLJ22969	3'	GGCTCAGCAGATGCTGT 68657	ACTAAAGA	
			ACAGTATCT TGGGCT		
			TGTCGTAGA ACTCGG		
			CG_		
GAM1136	GGTLA1	5'	AGCCCATCTCTGTCCCATTGT 14657	ATCT	TAA
			ACAGT AC AGATGGGCT		
			TGTTA TG TCTACCCGA		
			CCC_ TC_		
GAM1136	KIAA0240	3'	TTTAGTAGATTCTGTT 92443	T	
			AACAG ATCTACTAAA		
			TTGTC TAGATGATTT		
			T		
GAM1136	KIAA1028	3'	TTTATTAGATACTGTT 91952	C	
			AACAGTATCTA TAAA		
			TTGTCATAGAT ATTT		
			T		
GAM1136	KIAA1332	3'	CATCAAAAGATACTGTT 71163	ACTAAA	
			AACAGTATCT GATG		

	TTGTCATAGA	CTAC	
	AAA__		
GAM1136 KIAA1497	3' ATCTTTAGTAGACACT	67503	A
	AGT TCTACTAAAGAT		
	TCA AGATGATTTCTA		
	C		
GAM1136 KIAA1858	3' AGCCCATCTCTAGCACACCTTG	67133	TATCTA A
	CAG CTA AGATGGGCT		
	GTT GAT TCTACCCGA		
	CCACAC C		
GAM1136 p25	3' GCCCATCCAGGACACTCC	22851	C A ACTAAA
	A AGT TCT GATGGGC		
	C TCA AGG CTACCCG		
	C C AC__		
GAM1136 PME-1	3' AGCCCATCTTTTCTGTGACTGT	32351	ATCTACT
	ACAGT AAAGATGGGCT		
	TGTCA TTTCTACCCGA		
	GTGTCT_		
GAM1136 PRO0628	3' AGCCCATCTTCTGTACTGCT	26205	TC TA
	AGTA TAC AAGATGGGCT		
	TCGT ATG TTCTACCCGA		
	C_ TC		
GAM1136 LOC122728	3' AGCCCATCTGCTGTATTACTG	74150	TC TAA
	CAGTA TAC AGATGGGCT		
	GTCAT ATG TCTACCCGA		
	T_ TCG		
GAM1136 LOC130507	3' ATCTCTAGTAAATACTGTT	74948	C A
	AACAGTAT TACTA AGAT		
	TTGTCATA ATGAT TCTA		
	A C		
GAM1136 LOC144110	3' AGCCTGGGGCAGCAGGTA	76672	A AAAGA
	CAGTATCT CT TGGGCT		
	GTCATGGA GA GTCCGA		
	C CGGG_		
GAM1136 LOC145368	3' AGCCCATCTGCTGTATTACTG	77092	TC TAA
	CAGTA TAC AGATGGGCT		
	GTCAT ATG TCTACCCGA		
	T_ TCG		
GAM1136 LOC149830	3' CCCATCTCTAAGGCAGGATGCT	84724	A__ AA_
G	CAGTATCT CT AGATGGG		

GTCGTAGG GA TCTACCC  
 ACG ATC  
 GAM1136 LOC150236 5' AGCCCATCCCCAGTTCACT 79680 ATCT AAA\_  
 AGT ACT GATGGGCT  
 ||| ||| |||||  
 TCA TGA CTACCCGA  
 CT\_\_ CCCC  
 GAM1136 LOC150279 3' CCCATGAGGCTCAGATGCTGTT 79667 ACTAAAG  
 AACAGTATCT ATGGG  
 ||||| |||  
 TTGTCGTAGA TACCC  
 CTCGGAG  
 GAM1136 LOC150423 3' AGCCCATCTCCTGTATTACTG 79863 TC TAA  
 CAGTA TAC AGATGGGCT  
 |||| ||| |||||  
 GTCAT ATG TCTACCCGA  
 T\_ TCC  
 GAM1136 LOC151405 5' AGATGGGCTTTAGTAAAGACTG 85334 ATC ATGGG  
 T ACAGT TACTAAAG CT  
 |||| ||||| ||  
 TGTCA ATGATTTC GA  
 GAA GGGTA  
 GAM1136 LOC151473 3' AGCCCATCTCTAGACTCTCGT 80250 \_ TA CTAA  
 AC AG TCTA AGATGGGCT  
 || || ||| |||||  
 TG TC AGAT TCTACCCGA  
 C TC C\_\_  
 GAM1136 LOC153196 5' AGCCCATCCTTGGGACCCTACT 85953 TCTA\_ A  
 AGTA CTAA GATGGGCT  
 ||| ||| |||||  
 TCAT GGTT CTACCCGA  
 CCCAG C  
 GAM1136 LOC221002 3' AGCCCATTCAGATAAAACTG 91475 \_\_\_\_ ACTAAA  
 CAGT ATCT GATGGGCT  
 ||| ||| |||||  
 GTCA TAGA TTACCCGA  
 AAA C\_\_\_\_  
 GAM1136 LOC255290 5' AGCCCATCTCTGTCCCATTGT 95607 ATCT TAA  
 ACAGT AC AGATGGGCT  
 |||| || |||||  
 TGTTA TG TCTACCCGA  
 CCC\_ TC\_  
 GAM1136 LOC91907 3' ATCTTTAGTAGACACT 67493 A  
 AGT TCTACTAAAGAT  
 ||| |||||  
 TCA AGATGATTCTA  
 C  
 GAM1137 KCND2 5' CATACTGACCCTATATTATCC 24393 C TTA AA  
 GGA AAT AG TCAGTATG  
 ||| ||| || |||||

			CCT TTA TC AGTCATAC		
			A TA_ CC		
GAM1137	MMP8	3'	TTCTTAAAATGTCCTA 10067	A	
			TAGGACA TTTAAGAA		
			ATCCTGT AAATTCTT		
			A		
GAM1137	FLJ10619	3'	ATACTGACTCTTCCCCTG 36348	ACAATTT	A
			TAGG AAGA TCAGTAT		
			GTCC TTCT AGTCATA		
			CC_____ C		
GAM1137	FLJ13081	3'	TTCTTTAATTGTCCTA 45753	T	
			TAGGACAATT AAGAA		
			ATCCTGT TAA TTCTT		
			T		
GAM1137	FLJ20509	3'	TGCTCCTTCTTAAACTGTCCTA 35314	A	TC
			TAGGACA TTTAAGAA AGTA		
			ATCCTGT AAATTCTT TCGT		
			C CC		
GAM1137	LOC254700	5'	TGAATTCTTAAATTACCTA 96222	AC	_
			TAGG AATTTAAGAAT CA		
			ATCC TTAAATTCTTA GT		
			A_ A		
GAM1138	ACN	5'	AACACCCAAGCGCCCC 30367	AAA T	ATCA
			GGGGC G CT GGTGTT		
			CCCCG C GA CCACAA		
			____ AC__		
GAM1138	CLCN6	3'	AAACACCTCTCTCTCCCC 41379	CAA TCTATC	
			GGGG AG AGGTGTTT		
			CCCC TC TCCACAAA		
			____ TCTC__		
GAM1138	CLCN6	3'	AAACACCTCTCTCTCCCC 41394	CAA TCTATC	
			GGGG AG AGGTGTTT		
			CCCC TC TCCACAAA		
			____ TCTC__		
GAM1138	CLCN6	3'	AAACACCTCTCTCTCCCC 7072	CAA TCTATC	
			GGGG AG AGGTGTTT		
			CCCC TC TCCACAAA		
			____ TCTC__		
GAM1138	CNTN3	3'	TATCTGATCAGACTTTGCCCC 66698		_
			GGGGCAAAGTCT ATCAGGTG		

		CCCCGTTTCAGA TAGTCTAT	
		C	
GAM1138 CSRP1	3'	CAAACACCTTTCCCTTTGCCCT 14526	TCTATC
		GGGGCAAAG AGGTGTTTG	
		TCCCGTTTC TCCACAAAC	
		CCTT__	
GAM1138 MYCL2	3'	TGATAGATTTTGCCCC 18191	
		GGGGCAAAGTCTATCA	
		CCCCGTTT TAGATAGT	
GAM1138 NTSR1	3'	ACTTCCTGCCAAACTTTGCCCC 10284	CTAT T_
		GGGGCAAAGT CAGG GT	
		CCCCGTTTCA GTCC CA	
		AACC TT	
GAM1138 RAB26	3'	CAAGTGGACAGACTTTGCC 26822	A AGG_
		GGCAAAGTCT TC TG	
		CCGTTTCAGA AG AC	
		C GTGA	
GAM1138 STK10	3'	CCTGATAGACCTGCCCC 19984	AA
		GGGGCA GTCTATCAGG	
		CCCCGT CAGATAGTCC	
		C_	
GAM1138 TCTA	3'	CAAACACCCACATACCTGGCCC 42234	AAA CTATCA
		GGGC GT GGTGTTTG	
		CCCG CA CCACAAAC	
		GTC TACAC_	
GAM1138 ELKS	3'	CAAACACTACAACTTCATCCC 30502	CA CTATCA
		GGGG AAGT GGTGTTTG	
		CCCT TTCA TCACAAAC	
		AC AACA__	
GAM1138 FLJ23537	3'	CAAACACCTGCCTCTCTTCAAC 46023	GCA TCTAT
CC		GGG AAG CAGGTGTTTG	
		CCC TTC GTCCACAAAC	
		AAC TCTCC	
GAM1138 KIAA0433	5'	CAAACACCTCACCCCTGCCTC 30835	AAGTCTATC
		GGGGCA AGGTGTTTG	
		CTCCGT TCCACAAAC	
		CCCCAC__	
GAM1138 KIAA0450	3'	CACTGCTGATGACTTTGCCCC 27620	T _
		GGGGCAAAGTC ATCAG GTG	

		CCCCGTTTCAG TAGTC CAC			
		_ GT			
GAM1138	LEAP-2	5'	AAATATAAACTTTGCCCC	53739	CTATCAG
			GGGGCAAAGT GTGTTT		
			CCCCGTTTCA TATAAA		
			AA_____		
GAM1138	LOC147077	3'	CACCTCCTAATAGACTTAGCCC	78249	A C_____
	C		GGGGC AAGTCTAT AGGTG		
			CCCCG TTCAGATA TCCAC		
			A ATCC		
GAM1139	ADH1B	3'	CTTAGACATAAAGTAAAAT	72644	C CAC
			ATTT ACTTT TGTCTGAG		
			TAAA TGAAA ACAGATTC		
			A T__		
GAM1139	AHR	3'	ATCTCAGATGTTAAAATAAATG	7875	CAC C T
			CATTT TTT AC GTCTGAGAT		
			GTAAA AAA TG TAGACTCTA		
			TA_ T _		
GAM1139	FDFT1	3'	TAGGAAAGTGAAATG	15518	A
			CATTTCACTTTC CTG		
			GTAAAGTGAAAAG GAT		
			_____		
GAM1139	JTB	3'	ATCTCAGACAGTGAAAGTGAAA	21959	
	TG		CATTTCACTTTTCACTGTCTGAGAT		
			GTAAAGTGAAAGTGACAGACTCTA		
			_____		
GAM1139	KLF4	3'	TCCCAGACAGTGGATATG	14891	CT A
			CA TTCACTGTCTG GA		
			GT AGGTGACAGAC CT		
			AT C		
GAM1139	PHYH	3'	ACAGTAAAAGTGAAAT	20608	C
			ATTTCACTTT ACTGT		
			TAAAGTGAAA TGACA		
			A		
GAM1139	PKD2	3'	TCCAGGTTGAAAGTGAAA	60096	CTG A
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T_ _		
GAM1139	WRN	3'	GGGCAGTGAAAATGAAA	5098	C
			TTTCA TTTCACTGTCT		

			AAAGT AAAGTGACGGG		
			A		
GAM1139	ZNF216	3'	ATCTGCACAGCAAAGTGAAA	20017	CA CTG
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1139	CG012	5'	CTCACTCTGAAAGTGAA	83218	CT CT
			TTCACCTTCA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1139	EIF2C2	3'	ATCTTCTGAGAGTGAAAG	71946	G T_
			CTTTCACCT TC GAGAT		
			GAAAGTGA AG TTCTA		
			G TC		
GAM1139	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT	45802	ACTTTCACCT
	G		CATTTTC GTCTGAGAT		
			GTAAAG CAGACTCTA		
			AAACATTT_		
GAM1139	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG	45281	CTT
			CATTTCA TCACTGTCTGAGAT		
			GTAAAGT AGTGACAGACTCTA		
			C_		
GAM1139	KIAA0984	3'	TTTGTCCAGTGAAAATGAA	65534	C TC
			TTCA TTTCACTG TGAG		
			AAGT AAAGTGAC GTTT		
			A CT		
GAM1139	KLHL6	3'	ATCTCAGAGCAGGAAA	55299	A _
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1139	NIR3	3'	GCAGTGAAAGTGCAAT	66242	T
			ATT CACTTTCACTGT		
			TAA GTGAAAGTGACG		
			C		
GAM1139	PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA	53598	CA G
			TTCACCTT CT TCTGAGAT		
			AAGTGAAA GG AGACTCTA		
			CC G		
GAM1139	PP35	3'	ATCTCAGACTGAAA	22814	CT
			TTTCA GTCTGAGAT		

AAAGT CAGACTCTA

GAM1139 PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148 TCAC C\_  
CATTTCACCTT TGT TGAG  
||||||| ||| |||  
GTAAAGTGAA ACG ACTC  
TA\_\_ TT

GAM1139 SEP15 3' TCCTACAGTAAGAGTGAAA 14934 C CT  
TTTCACTTT ACTGT GA  
||||||| ||||| ||  
AAAGTGAGA TGACA CT  
A TC

GAM1139 SFXN2 3' CTCAGGGGAAAAAAGTGAAA 73941 CACTG  
TTTCACTTT TCTGAG  
||||||| |||||  
AAAGTGAAA GGA CTC  
AAAGG

GAM1139 LOC149703 3' ATCTCAGACAGCCGTTTGAAA 84647 ACTTTCA  
TTTC CTGTCTGAGAT  
||| |||||  
AAAG GACAGACTCTA  
GTTTGCC

GAM1139 LOC154007 3' ATCTCAAACCCTTTAGTGAAA 81015 TTCACT C  
TTTCACT GT TGAGAT  
||||| || |||||  
AAAGTGA CA ACTCTA  
TTTCC\_ A

GAM1139 LOC155004 3' TCATTTAAGTGAAAGGAAA 81226 A GTC\_  
TTTC CTTTCACT TGA  
||| ||||| |||  
AAAG GAAAGTGA ACT  
\_ ATTT

GAM1139 LOC222134 5' ACAGTGAAGTGAAATG 94136 T  
CATTTCACCTT CACTGT  
||||||| |||||  
GTAAAGTGAA GTGACA

GAM1140 AQP3 3' TTCACGATCCACCCTTTC 59593 T\_ \_  
GAAA GTGG TCGTGAA  
||| ||| |||||  
CTTT CACC AGCACTT  
CC T

GAM1140 ARSB 3' TCACGACTCTTGTC 3502 AATGTG  
GACAAGA GTCGTGA  
||||| |||||  
CTGTTCT CAGCACT

GAM1140 B4GALT5 3' TTTTCACAAAAATAGTCCTTTG 16519 AAA\_ GGTC  
TCA TGACAAG TGT GTGAAAA  
||||| ||| |||||



			ACTGTTT	ATA	CACTTTT		
			CCTG	AAAA			
GAM1140	CHRNA3	3'	TCGTTACCCATTCTT	5610	T	CG	
			AAGAAATG	GGT TGA			
			TTCTTTAC	CCA GCT			
			—	TT			
GAM1140	DRD1	3'	TTACAACCACATTCTGGCCA	5840	ACA	C	
			TG	AGAAATGTGGT GTGA			
			AC	TCTTTACACCA CATT			
			CGG	A			
GAM1140	FUT1	3'	TCTGATCACATCCCCTGTC	3798	AGAA	T	
			GACA	ATGTGGTTCG GA			
			CTGT	TACACTAGT CT			
			CCCC	—			
GAM1140	IRF1	3'	GCCACATTTCTGATCA	64345	CA		
			TGA	AGAAATGTGGT			
			ACT	TCTTTACACCG			
			AG				
GAM1140	MAP3K8	5'	TCACGACCACCTCATG	17791	A	AAT	
			CA	GA GTGGTCGTGA			
			GT	CT CACCAGCACT			
			A	C—			
GAM1140	NGFR	3'	TTCTGACCACACTTCCTGTC	10231	A	A	T
			GACA	GAA TGTGGTCG GAA			
			CTGT	CTT ACACCAGT CTT			
			C	C			
			—				
GAM1140	OLR1	3'	TTCACAACAGTTCTTGTTA	10341	ATGTG	C	
			TGACAAGAA	GT GTGAA			
			ATTGTTCTT	CA CACTT			
			GA—	A			
GAM1140	POU4F1	3'	CACTGAAAACATTTTGTCA	20660	A	GG	—
			TGACAAGAA	TGT TC GTG			
			ACTGTTTTT	ACA AG CAC			
			—	AA T			
GAM1140	SMP1	3'	TTTCACATGAATAATTTTGTGTC	26705	A	GGTC	
	A		TGACAAGAA	TGT GTGAAA			
			ACTGTTTTT	ATA CACTTT			
			A	AGTA			
GAM1140	ZNF264	3'	TTCTATTAACATTTCTTTTCA	12769	C	GGTCGT	
			TGA	AAGAAATGT GAA			

			ACT TTCTTTACA	CTT			
			T	ATTAT_			
GAM1140	C20orf175	3'	CGAGCTCCACGTTTCCTGCCA	55063	A A	___	
			TG CA GAAATGTGG	TCG			
			AC GT CTTTGCACC	AGC			
			C C	TCG			
GAM1140	CAPNS2	3'	TTTCACAACCCTACATATTTCT	50323	CA	___	C
	GATCA		TGA AGAAATGT	GGT GTGAAA			
			ACT TCTTTATA	CCA CACTTT			
			AG	CATC A			
GAM1140	CLDN6	3'	TTTACACTCACATTTTTATCA	41041	CA	_	C
			TGA AGAAATGTG	GT GTGAA			
			ACT TTTTACAC	CA CATTT			
			A_	T _			
GAM1140	DKFZP564L0864	3'	GCACCAATTTCTTGCCA	72555	A	G	C
			TG CAAGAAAT	TGGT GT			
			AC GTTCTTTA	ACCA CG			
			C	- -			
GAM1140	DKFZP566B183	3'	TTTCCATAAACATTTCTTTTCA	31330	C		GGTCGT
			TGA AAGAAATGT	GAAA			
			ACT TTCTTTACA	CTTT			
			T	AATAC_			
GAM1140	GTF2E1	3'	TACAGACCTCTTGTC	18616	AATGT	_	
			TGACAAGA	GGTC GTG			
			ACTGTTCT	CCAG CAT			
			_____	A			
GAM1140	KIAA0089	3'	TTTTAATTCACATTTCTT	69967	TCG		
			AAGAAATGTGG	TGAAA			
			TTCTTTACACT	ATTTT			
			TA_				
GAM1140	KIAA0373	5'	TTTTCAAAGTAACATTTCTT	28015	GGTCG		
			AAGAAATGT	TGAAAA			
			TTCTTTACA	ACTTTT			
			ATGAA				
GAM1140	KIAA1813	3'	TTTTCACACTGTAAATTTCTTG	70314	__ TG	C	
	T		ACAAGAAAT	G GT GTGAAAA			
			TGTTCTTTA	T CA CACTTTT			
			AA GT	_			
GAM1140	KIAA1951	3'	TTCCAGGCTTCTCTTGTC	73766	AATGT	GT	
			TGACAAGA	GGTC GAA			

			ACTGTTCT	TCGG	CTT		
			CT__	AC			
GAM1140	MGC4170	3'	TTCACCATTTCTTGTC	44227		TGGTC	
			GACAAGAAATG	GTGAA			
			CTGTTCTTTAC	CACTT			
GAM1140	NRN1	3'	CACTGCACATTTCTCCTCA	33432	CA	GTC	
			TGA AGAAATGTG	GTG			
			ACT TCTTTACAC	CAC			
			CC	GT_			
GAM1140	PLA2G12	3'	TTTTCACAACCACATTT	48028	C		
			AAATGTGGT	GTGAAAA			
			TTTACACCA	CACTTTT			
			A				
GAM1140	PPY2	3'	CACTCCACATTCCTGGCCA	40819	ACA A	TC	
			TG AG AATGTGG	GTG			
			AC TC TTACACC	CAC			
			CGG C	T_			
GAM1140	ZNF31	3'	TTTGTAGACCACATTTCTGTT	64992	A	_TG	
	A		TGACA GAAATGTGGTC	G AA			
			ATTGT CTTTACACCAG	T TT			
			C	A GT			
GAM1140	LOC115219	3'	CACGACAACGGGTCCTCA	73295	CAA AA	G	
			TGA GA TGT GTCGTG				
			ACT CT GCA CAGCAC				
			C_	GG A			
GAM1140	LOC120376	5'	TTCAGAGCATTTCTTTCA	75986	C	GG G	
			TGA AAGAAATGT	TC TGAA			
			ACT TTCTTTACG	AG ACTT			
GAM1140	LOC133418	3'	TTTCATATACATTTTTTGCCA	75094	A	GTC	
			TG CAAGAAATGTG	GTGAAA			
			AC GTTTTTTACAT	TACTTT			
			C	A_			
GAM1140	LOC151199	3'	TTAAAACCACAGCTCTTGCCA	80174	A	AA	CG
			TG CAAGA	TGTGGT	TGA		
			AC GTTCT	ACACCA	ATT		
			C	CG	AA		
GAM1140	LOC152317	5'	TCACACTGACTTTTGTCA	85649	AATG	C	
			TGACAAGA	TGGT	GTGA		

ACTGTTTT GTCA CACT  
 CA\_\_ \_  
 GAM1140 LOC152674 3' TTCAACCCACCCTCTTGTCA 85841 AAT TCG  
 TGACAAGA GTGG TGAA  
 ||||| ||| |||  
 ACTGTTCT CACC ACTT  
 CC\_ CA\_  
 GAM1140 LOC152845 5' CATGACCACATTTTTCA 60330 CAA  
 TGA GAAATGTGGTCGTG  
 || |||||  
 ACT TTTTACACCAGTAC  
 \_  
 GAM1140 LOC154743 3' TTTAGTCCACATTGTCTTGTCA 81118 \_ TCG  
 TGACAAGA AATGTGG TGAA  
 ||||| ||||| |||  
 ACTGTTCT TTACACC ATTT  
 G TG\_  
 GAM1140 LOC165476 5' TTCACGGCACCTTCT 87201 AT G  
 AGAA GTG TCGTGAA  
 ||| |||||  
 TCTT CAC GGCACCT  
 C\_ \_  
 GAM1140 LOC254266 5' TTTTCGGTCACACATCTTATCA 97356 C AA GT T  
 TGA AAGA TGTG CG GAA  
 ||| ||| ||| |||  
 ACT TTCT ACAC GC TTT  
 A AC TG T  
 GAM1140 LOC255919 3' TTTCATTCTTACATTTCTAATC 95043 CA TC  
 A  
 TGA AGAAATGTGG GTGAAA  
 ||| ||||| |||||  
 ACT TCTTTACATT TACTTT  
 AA CT  
 GAM1140 LOC51754 5' CACGGCCACATCTCTGTCA 71027 A A  
 TGACA GA ATGTGGTCGTG  
 ||||| |||||  
 ACTGT CT TACACCGGCAC  
 \_ C  
 GAM1140 LOC55862 3' ACCTCATTTCTTGCCA 37485 A T  
 TG CAAGAAATG GGT  
 || ||||| |||  
 AC GTTCTTTAC CCA  
 C T  
 GAM1140 LOC55954 3' CACGTGGTCACTTTTCTCATCA 38877 CA T GT \_  
 TGA AGAAA GTG C GTG  
 ||| ||||| ||| | |||  
 ACT TCTTT CAC G CAC  
 AC T TG TG  
 GAM1141 BLNK 3' TATTGCCTGACCTGATGAA 25258 C AACT C  
 TTCATCAGG TAG GC ATA  
 ||||| ||| |||

AAGTAGTCC GTC CG TAT  
 A \_\_\_\_ T  
 GAM1141 FGG 3' CAGTTTTATGCTGATGA 4963 G\_  
 TCATCAG C TAGAACTG  
 ||||| | |||||  
 AGTAGTC G ATTTTGAC  
 \_T  
 GAM1141 DKFZP564M182 3' GCACTCCAGCCTGATGA 78036 A AC  
 TCATCAGGCT GA TGC  
 ||||| || ||  
 AGTAGTCCGA CT ACG  
 C C\_  
 GAM1141 FLJ11726 3' CTATAGCAGTTCTACCCCTGA 46410 C\_ C  
 TCAGG TAGAACTGC ATAG  
 |||| ||||| ||||  
 AGTCC ATCTTGACG TATC  
 CC A  
 GAM1141 KIAA0418 5' CTATGGCAGTTCCAAGAGGA 27554 AGG A\_  
 TC CT GAACTGCCATAG  
 || || |||||  
 AG GA CTTGACGGTATC  
 GA\_ AC  
 GAM1141 KIAA1372 3' TAGTCCTCAGCCTGATGAA 91652 \_ A  
 TTCATCAGGCT AG ACTG  
 ||||| || ||||  
 AAGTAGTCCGA TC TGAT  
 C C  
 GAM1141 MGC11082 3' ATGGCAGCTGCAGTGA 51099 G\_ T AA  
 TCA GC AG CTGCCAT  
 ||| || |||||  
 AGT CG TC GACGGTA  
 GA \_ \_  
 GAM1141 TSC22 3' CAGTTCTAACTAATGAA 20063 C GC  
 TTCAT AG TAGAACTG  
 |||| || |||||  
 AAGTA TC ATCTTGAC  
 A A\_  
 GAM1141 LOC145719 3' ATGGCAGTCCCCATGAA 83447 CA CTAGA  
 TTCAT GG ACTGCCAT  
 |||| || |||||  
 AAGTA CC TGACGGTA  
 CC \_\_\_\_  
 GAM1141 LOC145720 3' ATGGCAGTCCCCATGAA 83429 CA CTAGA  
 TTCAT GG ACTGCCAT  
 |||| || |||||  
 AAGTA CC TGACGGTA  
 CC \_\_\_\_  
 GAM1141 LOC154714 3' CTATGGCAGTTCCAGC 60440 A  
 GCT GAACTGCCATAG  
 || |||||

		CGA CTTGACGGTATC		
		C		
GAM1141	LOC197114 3'	ATGGCAGTCCCCATGAA	89699	CA CTAGA
		TTCAT GG ACTGCCAT		
		AAGTA CC TGACGGTA		
		CC ____		
GAM1141	LOC201973 3'	TGGATTCTAGCACTGATGAA	89118	_ CTG
		TTCATCAG GCTAGAA CCA		
		AAGTAGTC CGATCTT GGT		
		A A__		
GAM1141	LOC254209 5'	ATGGCAGTCCTAACCT	96289	C A
		AGG TAG ACTGCCAT		
		TCC ATC TGACGGTA		
		A C		
GAM1141	LOC56906 3'	CTATGGCAATTTTGTACCATGA	39317	CAG T C
	A	TTCAT GC AGAA TGCCATAG		
		AAGTA TG TTTT ACGGTATC		
		CCA _ A		
GAM1142	ADAM19 3'	GGTCACTGCCCTTACCTGACC	52710	C A_ AACA
		GG CAGGTAAGG GG GACC		
		CC GTCCATTCC TC CTGG		
		A CG A__		
GAM1142	ARHGDIA 3'	CCACCAGTGCCTGGCCA	15043	A_ A
		TGGCCAGGTA GG GG		
		ACCGGTCCGT CC CC		
		GA A		
GAM1142	C1QG 3'	CCACCTTACTGGCCA	62482	G A
		TGGCCAG TAAGG GG		
		ACCGGTC ATTCC CC		
		_ A		
GAM1142	CALU 3'	CCTGCCATTACCTGGGCA	6883	G _ _
		TG CCAGGTAA GG AGG		
		AC GGTCCATT CC TCC		
		G A G		
GAM1142	CRY2 3'	CTGTTCTGCAAGCCA	72209	CAG AAGG
		TGGC GT AGGAACAG		
		ACCG CG TCCTTGTC		
		AA_ ____		
GAM1142	CTNS 3'	CTGCTCCTTACCCAGC	17042	CA GAA
		GC GGTAAGGAG CAG		

			CG CCATTCCTC GTC		
			AC     —		
GAM1142 DES	3'	CCATCCCTGCCTGGTCA	72124	A	—
		TGGCCAGGTA GGA GG			
		ACTGGTCCGT CCT CC			
		C A			
GAM1142 GPR86	3'	GGTCCATGAAATATTACCTGGC	43651		GGAGGAACA
CA		TGGCCAGGTAA GACC			
		ACCGGTCCATT CTGG			
		ATAAAGTAC			
GAM1142 GRIK3	3'	TCCTGCCCTTACCTGCCA	5890	C	—
		TGGC AGGTAAGG AGGA			
		ACCG TCCATTCC TCCT			
		— CG			
GAM1142 IMPDH1	3'	CTGCTCCAGCCTGGCC	6082	AA	GAA
		GGCCAGGT GGAG CAG			
		CCGGTCCG CCTC GTC			
		A_ —			
GAM1142 ITGA5	3'	TCTGGAACCTCAGCCTGGCCA	61283	AAG	AA_
		TGGCCAGGT GAGG CAGA			
		ACCGGTCCG CTCC GTCT			
		A_ AAG			
GAM1142 LETM1	5'	GGTCCGCCCTCACCTGGCCA	24623	A A	AACA
		TGGCCAGGT AGG GG GACC			
		ACCGGTCCA TCC CC CTGG			
		C _ GC_			
GAM1142 NOS2A	3'	GTCTGTTCCCCATGGCCA	5270	GGTAA	A
		TGGCCA GG GGAACAGAC			
		ACCGGT CC CCTTGTCTG			
		A_ —			
GAM1142 PAP	3'	TTCCCCAACCTGACCA	57236	C	AA A
		TGG CAGGT GG GGAA			
		ACC GTCCA CC CCTT			
		A AC _			
GAM1142 PAP	3'	TTCCCCAACCTGACCA	57240	C	AA A
		TGG CAGGT GG GGAA			
		ACC GTCCA CC CCTT			
		A AC _			
GAM1142 PAP	3'	TTCCCCAACCTGACCA	10420	C	AA A
		TGG CAGGT GG GGAA			

ACC GTCCA CC CCTT  
 A AC \_  
 GAM1142 PLIN 3' TCTGTTCCCCCTCTGATGAACA 10645 GC GGTA A  
 TG CA AGG GGAACAGA  
 || || ||| |||||  
 AC GT TCC CCTTGTCT  
 AA AGTC C  
 GAM1142 PSME3 3' CTGTTCCCTCTCTGACTCA 19372 A A \_  
 C GGT AG GAGGAACAG  
 | ||| || |||||  
 A TCA TC CTCCTTGTC  
 C G T  
 GAM1142 RXRA 3' CTGGCCTCCCTGGCCA 11410 TAAG AA  
 TGGCCAGG GAGG CAG  
 ||||| ||| ||  
 ACCGGTCC CTCC GTC  
 \_ G\_  
 GAM1142 SYN1 5' GTCCGCCCCCGCGGCTCCTGGC 22710 TAA\_\_ A AACA  
 CA TGGCCAGG GG GG GAC  
 ||||| || || |||  
 ACCGGTCC CC CC CTG  
 TCGGCG C GC\_  
 GAM1142 SYN1 5' GTCCGCCCCCGCGGCTCCTGGC 56054 TAA\_\_ A AACA  
 CA TGGCCAGG GG GG GAC  
 ||||| || || |||  
 ACCGGTCC CC CC CTG  
 TCGGCG C GC\_  
 GAM1142 TCP10 3' GCTGCTCCCCTCTGGTCA 16045 GTA A A A  
 TGGCCAG AGG GGA CAG C  
 ||||| ||| ||| |||  
 ACTGGTC TCC CCT GTC G  
 \_ \_ C C  
 GAM1142 TNFSF12 3' TCTCGACTCCCCCCTGGCCA 13746 TAA GAAC  
 TGGCCAGG GGAG AGA  
 ||||| ||| |||  
 ACCGGTCC CCTC TCT  
 CC\_ AGC\_  
 GAM1142 ACAA2 3' TCCTTACTCTACTTGGCCA 91770 \_ \_  
 TGGCCAGGTA AG GAGGA  
 ||||| || |||||  
 ACCGGTTCAT TC TTCCT  
 C A  
 GAM1142 AIP 3' CCTGCCTTACCTGCCA 14278 C \_  
 TGGC AGGTAAGG AGG  
 ||| ||||| |||  
 ACCG TCCATTCC TCC  
 \_ G  
 GAM1142 APELIN 3' TTGGACCCCTCACCTGGCC 33787 A A AA  
 GGCCAGGT AGG GG CAG  
 ||||| ||| || |||



	CCGGTCCA TCC CC GTT		
	C _ AG		
GAM1142 CSRP2BP 3'	CCTGCCATTACCTGGCC 70111	-- --	
	GGCCAGGT AA GG AGG		
	CCGGTCCA TT CC TCC		
	C A G		
GAM1142 DKFZP434L1435 5'	CCCCTGCCTGGCCA 92170	A A	
	TGGCCAGGTA GG GG		
	ACCGGTCCGT CC CC		
	--		
GAM1142 DKFZP564M082 3'	TCCACCTTCCTGGCCA 25897	T A	
	TGGCCAGG AAGG GGA		
	ACCGGTCC TTCC CCT		
	_ A		
GAM1142 DKFZP586M1120 3'	GCTGCTCCTCCCGGGCC 48462	AGGTAA A A	
	GGCC GGAGGA CAG C		
	CCGG CCTCCT GTC G		
	GC__ C C		
GAM1142 FLJ10081 3'	TCTGGGAGCCTTCCTGGCCA 35803	T AGGAA	
	TGGCCAGG AAGG CAGA		
	ACCGGTCC TTCC GTCT		
	_ GAGG_		
GAM1142 FLJ10900 3'	GGCCTCTTCCCCTCACCTGGCC 65591	A A C A	
	GGCCAGGT AGG GGAA AG CC		
	CCGGTCCA TCC CCTT TC GG		
	C _ C C		
GAM1142 FLJ10932 3'	GTCTGCTCCAGCCTGGCTA 36897	AA GAA	
	TGGCCAGGT GGAG CAGAC		
	ATCGGTCCG CCTC GTCTG		
	A_ _		
GAM1142 FLJ11560 3'	GTGCCTCCTCTCACCTGGCCA 47219	A_ A	
	TGGCCAGGT AGGAGG AC		
	ACCGGTCCA TCCTCC TG		
	CTC G		
GAM1142 FLJ13072 5'	CTGTAATCACTCTGGCCA 89813	TAAG GGA	
	TGGCCAGG GA ACAG		
	ACCGGTCT CT TGTC		
	CA_ AA_		
GAM1142 FLJ13855 3'	GGCCTGTTCCCGGTCTGACCT 43589	A A_ A	
	AGGT AGG GGAACAG CC		

TCCA TCT CCTTGTC GG  
 G GGC C  
 GAM1142 FLJ20371 3' GGCCTATTCCTCCTAGAAC 35064 A\_\_ C A  
 GGT AGGAGGAA AG CC  
 ||| ||||| ||  
 CCA TCCTCCTT TC GG  
 AGA A C  
 GAM1142 FLJ21324 5' TCTGCCAGAACCACCTGGCC 91212 AA A\_\_ AA  
 GGCCAGGT GG GG CAGA  
 ||||| || || |||  
 CCGGTCCA CC CC GTCT  
 \_\_ AAGA \_\_  
 GAM1142 FLJ21709 3' CCTGCACCGACCTGGCCA 77918 AA \_\_\_\_  
 TGGCCAGGT GG AGG  
 ||||| || |||  
 ACCGGTCCA CC TCC  
 G\_ ACG  
 GAM1142 FLJ22578 3' GTTCCTCTTGAACCAAGTCA 45875 CA A\_  
 TGGC GGT AGGAGGAAC  
 ||| || |||||  
 ACTG CCA TTCTCCTTG  
 A\_ AG  
 GAM1142 FLJ22593 5' GGCCTGTCTGAACTCACCTGGC 45227 A GA\_ A A  
 C GGCCAGGT AG GGA CAG CC  
 ||||| || || ||| ||  
 CCGGTCCA TC TCT GTC GG  
 C AAG \_ C  
 GAM1142 FLJ23209 3' TCTACCACACCTGGCCA 46057 AA A  
 TGGCCAGGT GG GGA  
 ||||| || |||  
 ACCGGTCCA CC TCT  
 CA A  
 GAM1142 FLJ23506 3' GGCCTGTTTCCTTTAAGCAACCA 45746 CCAG AA A  
 TGG GT GGAGGAACAG CC  
 || || ||||| ||  
 ACC CG TTTCCTTGTC GG  
 AA\_\_ AA C  
 GAM1142 FLJ31978 3' TCTGTTCTCCTCGAATGACC 58352 C GGTA  
 GG CA AGGAGGAACAGA  
 || || |||||  
 CC GT TCCTCCTTGCT  
 A AAGC  
 GAM1142 GOLGA3 3' GGTCTGCGGCACCCGCCTGGCC 19720 AA AGGAA  
 A TGGCCAGGT GG CAGACC  
 ||||| || |||||  
 ACCGGTCCG CC GTCTGG  
 C\_ ACGGC  
 GAM1142 KIAA0171 3' GGTCTGTTTCCTTTTACTACC 27855 \_\_\_\_  
 GGTA AGGAGGAACAGACC  
 ||| |||||

CCAT TTTTCCTTGTCTGG  
 CA  
 GAM1142 KIAA1402 5' GTCTGTTCCCCCTTCCCC 66399 CCA T A  
 GG GG AAGG GGAACAGAC  
 || ||||| |||||  
 CC CC TTCC CCTTGTCTG  
 \_\_\_\_ \_ C  
 GAM1142 KIAA1464 3' GTCCACTCCTCCTGCCTGGCC 68274 A ACA  
 GGCCAGGTA GGAGGA GAC  
 ||||| ||||| ||  
 CCGGTCCGT CCTCCT CTG  
 \_ CAC  
 GAM1142 KIAA1553 3' GGCCTGCTGTCCTATACCTGG 91920 \_ \_ AACA  
 CCA TGGCCAGGTA AGGA GG GACC  
 ||||| ||||| ||  
 ACCGGTCCAT TCCT TC CTGG  
 A G GTC\_  
 GAM1142 KIAA1855 3' GCTGCTCCTTGCCACCA 92342 CCA GAA A  
 TGG GGTAAGGAG CAG C  
 || ||||| |||  
 ACC CCGTTCCTC GTC G  
 A\_ \_ \_ C  
 GAM1142 KIAA1904 3' CTGCTCCTCCTTCCT 73484 T A  
 AGG AAGGAGGA CAG  
 || ||||| ||  
 TCC TTCCTCCT GTC  
 \_ C  
 GAM1142 KIAA1975 3' GTCTCAGGCCCTCCTGGCCA 73976 TAA A AAC\_  
 TGGCCAGG GG GG AGAC  
 ||||| || || ||  
 ACCGGTCC TC CC TCTG  
 \_ \_ GGAC  
 GAM1142 KIAA1985 3' GGTCCGAGTCCTTACCTGGCC 44714 GGAACA  
 GGCCAGGTAAGGA GACC  
 ||||| || ||  
 CCGGTCCATTCT CTGG  
 GAGC\_  
 GAM1142 MAP2K7 3' CCTCCCCACTTGGCCA 17279 AA  
 TGGCCAGGT GGAGG  
 ||||| ||||  
 ACCGGTTCA CCTCC  
 CC  
 GAM1142 MGC11271 3' GGCCTAGCCTCACCTGGCCA 44242 AAG AACA  
 TGGCCAGGT GAGG GACC  
 ||||| || ||  
 ACCGGTCCA CTCC CTGG  
 \_ GATC  
 GAM1142 MRIP2 3' GTCTCAGGCCCTCCTGGCCA 55977 TAA A AAC\_  
 TGGCCAGG GG GG AGAC  
 ||||| || || ||

ACCGGTCC TC CC TCTG  
 \_\_\_\_ \_ GGAC  
 GAM1142 p25 3' CCTAACCTCTCCTGGCCA 22849 TA \_\_\_\_  
 TGGCCAGG AGG AGG  
 ||||| ||| |||  
 ACCGGTCC TCC TCC  
 TC AA  
 GAM1142 PI4KII 3' GGCTGCCTCACCTGGCCA 37345 AAG AA A  
 TGGCCAGGT GAGG CAG CC  
 ||||| ||| ||| ||  
 ACCGGTCCA CTCC GTC GG  
 \_\_\_\_ \_  
 GAM1142 PRDM7 3' GGTCTGTTCTGTTCCACTCTGA 53790 C TAA \_\_\_\_  
 CCA TGG CAGG GGA GGAACAGACC  
 ||| ||| ||| |||||  
 ACC GTCT CCT TCTTGTCTGG  
 A CA\_ TG  
 GAM1142 PRKWNK2 3' GTTCCCCCCCCACCTGCCA 90539 C AA A  
 TGGC AGGT GG GGAAC  
 ||| ||| ||| |||  
 ACCG TCCA CC CCTTG  
 \_ CC C  
 GAM1142 SEZ6 5' GTCCCCTTCCCCGCCTGGCCA 74366 AA AACAA  
 TGGCCAGGT GGAGG GAC  
 ||||| ||| |||  
 ACCGGTCCG CCTTC CTG  
 CC CC\_\_  
 GAM1142 SLC26A1 3' CCCCTCAACCTGGCCA 56217 A\_ A  
 TGGCCAGGT AGG GG  
 ||||| ||| ||  
 ACCGGTCCA TCC CC  
 AC \_  
 GAM1142 SNIP1 5' TCTGTTTTCTTTCGCCAGCCA 45215 CA TA AG  
 TGGC GG AGG GAACAGA  
 ||| || ||| |||||  
 ACCG CC TTT TTTGTCT  
 AC GC CT  
 GAM1142 SPTLC2 3' CTGGATACTTACCTGGCC 16800 GAGGAA  
 GGCCAGGTAAG CAG  
 ||||| |||  
 CCGGTCCATTC GTC  
 ATAG\_\_  
 GAM1142 STAT5A 3' CTATTCCTCCTGGGCC 12011 AGGTA C  
 GGCC AGGAGGAA AG  
 ||| ||||| ||  
 CCGG TCCTCCTT TC  
 G\_\_ A  
 GAM1142 TOLLIP 3' GCTGGCTCACCTGGCCA 38685 AAG GAA A  
 TGGCCAGGT GAG CAG C  
 ||||| ||| ||| |

		ACCGGTCCA CTC GTC G	
		___ G___ C	
GAM1142 TRAF2	3'	GTCTGTGCCACCTTGGCCA 40929	GGTA A A
		TGGCCA AGG GG ACAGAC	
		ACCGGT TCC CC TGTCTG	
		___ A G	
GAM1142 TRIAD3	3'	GGTCTGAAGCCTTCCTGGCCA 94507	T AGGAA
		TGGCCAGG AAGG CAGACC	
		ACCGGTCC TTCC GTCTGG	
		_ GAA_	
GAM1142 VLCS-H2	3'	GGCCTGTGTGAATCCCAGCCTG 24300	AA GGA_ A
		GCCA TGGCCAGGT GGA ACAG CC	
		ACCGGTCCG CCT TGTC GG	
		AC AAGTG C	
GAM1142 LOC115207	3'	CCTACTCTTACCTGGC 56600	--
		GCCAGGTAAG G AGG	
		CGGTCCATTC C TCC	
		T A	
GAM1142 LOC115708	3'	CTGCCCTGCCCTCCTGGCCA 73550	TAA _ AA
		TGGCCAGG GG AGG CAG	
		ACCGGTCC CC TCC GTC	
		TCC G C_	
GAM1142 LOC118704	3'	GTCTCAGGCCCTCCTGGCCA 73924	TAA A AAC_
		TGGCCAGG GG GG AGAC	
		ACCGGTCC TC CC TCTG	
		___ _ GGAC	
GAM1142 LOC118706	3'	GTCTCAGGCCCTCCTGGCCA 73925	TAA A AAC_
		TGGCCAGG GG GG AGAC	
		ACCGGTCC TC CC TCTG	
		___ _ GGAC	
GAM1142 LOC121219	3'	CTGCCTCCCCAGCCA 74046	CA TAA AA
		TGGC GG GGAGG CAG	
		ACCG CC CCTCC GTC	
		A_ _ _	
GAM1142 LOC125967	3'	TTCCCCTTCCTGGCCA 74426	T A
		TGGCCAGG AAGG GGAA	
		ACCGGTCC TTCC CCTT	
		_ _	
GAM1142 LOC143158	3'	GTCTCAGGCCCTCCTGGCCA 76490	TAA A AAC_
		TGGCCAGG GG GG AGAC	

	ACCGGTCC TC CC TCTG		
	____ _ GGAC		
GAM1142 LOC143465 5'	GGTCCATAATAGCCTTACCTGA 82967	GC	AGGAACA_
ACA	TG CAGGTAAGG GACC		
	AC GTCCATTCC CTGG		
	AA GATAATAC		
GAM1142 LOC144308 3'	GTCTTGGCCCCCTGGCCA 83052	TAA A AAC	
	TGGCCAGG GG GG AGAC		
	ACCGGTCC CC CC TCTG		
	____ _ GGT		
GAM1142 LOC146481 3'	CCATCCCTTGCCTGGGCA 77925	G	A__
	TG CCAGGTAAGG GG		
	AC GGTCCGTTCC CC		
	G CTA		
GAM1142 LOC147160 5'	GTCTGCCACCTGGCCA 83970	AAGGA AA _	
	TGGCCAGGT GG CAGA C		
	ACCGGTCCA CC GTCT G		
	____ C_ C		
GAM1142 LOC147160 5'	TCTGTTCCTCCAGCTCCGCCA 83976	CA AA	
	TGGC GGT GGAGGAACAGA		
	ACCG TCG CCTCCTTGTCT		
	CC A_		
GAM1142 LOC158056 5'	GGTCCTGAGCGCCCCTCCTGGC 81687	TA A AA__ _	
CA	TGGCCAGG AGG GG CAG ACC		
	ACCGGTCC TCC CC GTC TGG		
	____ _ GCGA C		
GAM1142 LOC158125 5'	GCTGCCCCACCTGGCCA 81715	AA A AA A	
	TGGCCAGGT GG GG CAG C		
	ACCGGTCCA CC CC GTC G		
	____ C_ _		
GAM1142 LOC195979 3'	GTCTCAGGCCCTCCTGGCCA 87533	TAA A AAC_	
	TGGCCAGG GG GG AGAC		
	ACCGGTCC TC CC TCTG		
	____ _ GGAC		
GAM1142 LOC197419 5'	GTCTGCCCAAGTCTGGCCA 89756	TAA A AA	
	TGGCCAGG GG GG CAGAC		
	ACCGGTCT CC CC GTCTG		
	GAA _ _		
GAM1142 LOC200310 3'	CCTGCCACAGTTCACTTGGCCA 65732	AA_____ _	
	TGGCCAGGT GG AGG		

ACCGGTTCA CC TCC  
 CTTGACA G  
 GAM1142 LOC200819 3' GGCCATGTTTCCTCACCTGACC 90144 C AAG GA\_  
 GG CAGGT GAGGAACA CC  
 || |||| ||||| ||  
 CC GTCCA CTCCTTGT GG  
 A \_\_\_\_ ACC  
 GAM1142 LOC202038 5' CTGTTCCTCGCGCGCCA 89147 CAG AAG  
 TGGC GT GAGGAACAG  
 ||| || |||||  
 ACCG CG CTCCTTGTG  
 CG\_ \_\_\_\_  
 GAM1142 LOC203378 5' GTCTGTTCCCAGCACCAGCTA 90615 CA AAGGA  
 TGGC GGT GGAACAGAC  
 ||| || |||||  
 ATCG CCA CCTTGTCTG  
 A\_ CGAC\_  
 GAM1142 LOC219294 3' TCCTCCTTGCCTGGCCA 93013  
 TGGCCAGGTAAGGAGGA  
 |||||  
 ACCGGTCCGTTCTCCT  
 GAM1142 LOC219295 3' TCCTCCTTGCCTGGCCA 92998  
 TGGCCAGGTAAGGAGGA  
 |||||  
 ACCGGTCCGTTCTCCT  
 GAM1142 LOC220466 3' GTCTCAGGCCCTCCTGGCCA 73960 TAA A AAC\_  
 TGGCCAGG GG GG AGAC  
 ||||| || || |||  
 ACCGGTCC TC CC TCTG  
 \_\_\_\_ \_ GGAC  
 GAM1142 LOC221490 5' TCTGTTCTCCTCCTGCTCC 93668 C\_ TA  
 GG CAGG AGGAGGAACAGA  
 || ||| |||||  
 CC GTCC TCCTCCTTGTCT  
 TC \_\_\_\_  
 GAM1142 LOC253868 3' CTGCTCCTCCTTCGCCT 95581 \_ A  
 AGGT AAGGAGGA CAG  
 ||| ||||| |||  
 TCCG TTCCTCCT GTC  
 C C  
 GAM1142 LOC254213 3' CTGTATGGTCCTTACCCGCC 95161 CA GGA\_  
 GGC GGTAAGGA ACAG  
 || ||||| |||  
 CCG CCATTCCT TGTC  
 C\_ GGTA  
 GAM1142 LOC255102 3' CTGCTCATCATCCTGGCCA 96082 TAAG G A  
 TGGCCAGG GA GA CAG  
 ||||| || || |||

	ACCGGTCC CT CT GTC		
	TA__ A C		
GAM1142 LOC255319 3'	GTCTCAGGCCCTCCTGGCCA 94517	TAA A AAC_	
	TGGCCAGG GG GG AGAC		
	ACCGGTCC TC CC TCTG		
	__ _ GGAC		
GAM1142 LOC255870 3'	CTCTTATTCTACTTGGCCA 94658	_____	
	TGGCCAGGTA AGGAG		
	ACCGGTTCAT TTCTC		
	CTTA		
GAM1142 LOC257160 3'	GTCTGTTCCCCCTCATCTTGC 94851	C A A	
	GC AGGT AGG GGAACAGAC		
	CG TCTA TCC CCTTGTCTG		
	T C C		
GAM1142 LOC257355 3'	CCCCTCACCTGGCCA 94405	A A	
	TGGCCAGGT AGG GG		
	ACCGGTCCA TCC CC		
	C _		
GAM1142 LOC51172 3'	CCCCTCACCTGGCCA 63347	A A	
	TGGCCAGGT AGG GG		
	ACCGGTCCA TCC CC		
	C _		
GAM1142 LOC55893 5'	CCTAAAGAAGCCCACCTGGCCA 37859	AA _____	
	TGGCCAGGT GG AGG		
	ACCGGTCCA CC TCC		
	C_ GAAGAAA		
GAM1142 LOC90639 3'	TCGCCCTCACCTGGCCA 63662	A AG	
	TGGCCAGGT AGG GA		
	ACCGGTCCA TCC CT		
	C CG		
GAM1142 LOC92340 3'	TCCCCTCCCTGGCCA 68998	TA A	
	TGGCCAGG AGG GGA		
	ACCGGTCC TCC CCT		
	C_ _		
GAM1142 LOC92399 3'	CCTCCTTACCTGGCCA 57075		
	TGGCCAGGTAAGGAGG		
	ACCGGTCCATTCCTCC		
GAM1142 LOC93538 3'	CCTATTGAGTTACCTGGTCA 72560	GG_____	
	TGGCCAGGTAA AGG		



			ACTGGTCCATT	TCC		
			GAGTTA			
GAM1143	ANK1	3'	AAAACAAGCGCAGGAGAGCCGC	60383	T	GAAG CA
			GC GCTCT GT CTTGTTTT			
			CG CGAGA CG GAACAAAA			
			C GGA_ C_			
GAM1143	PRX	5'	AGGTGACCCTCAGGCAGC	40518	T A	
			GCTGC CTGA GGTCACTT			
			CGACG GACT CCAGTGGA			
			_ C			
GAM1143	UNRIP	3'	AAAACAAGCAAGCAGAGAAAAG	23197	G_	AAG TCA
	C		GCT CTCTG G CTTGTTTT			
			CGA GAGAC C GAACAAAA			
			AAA GAA_			
GAM1143	ACAA2	3'	AAAACAAGTGACCTTCAGAGCA	91763		
	GC		GCTGCTCTGAAGGTCACTTGTTTT			
			CGACGAGACTTCCAGTGAACAAAA			
GAM1143	DKFZP434D193	3'	AAAACAAGAGCAGTCAAACAG	88873		CTC AG CA
	C		GCTG TGA GT CTTGTTTT			
			CGAC ACT CG GAACAAAA			
			AAA GA A_			
GAM1143	FBXO9	5'	GACCTTGCAGAGCAGC	53109	_	
			GCTGCTCTG AAGGTC			
			CGACGAGAC TTCCAG			
			G			
GAM1143	FLJ11850	3'	AAACAAGGTCAAAGCAGT	42715	C	AGGTCA
			GCTGCT TGA CTTGTTT			
			TGACGA ACT GAACAAA			
			A G_			
GAM1143	FLJ23816	5'	AGTGCCACAACCTCCAGGGCAG	58327	A	_____
	C		GCTGCTCTG AGGT CACT			
			CGACGGGAC TCCA GTGA			
			C ACACC			
GAM1143	IL14	5'	AAGGAGCCTCCAGAGCAGC	95428	A	CA
			GCTGCTCTG AGGT CTT			
			CGACGAGAC TCCG GAA			
			C AG			
GAM1143	KIAA1265	3'	AAAACAAAACCTTTGAGAGCAGC	70785	G	CAC
			GCTGCTCT AAGGT TTGTTTT			

		CGACGAGA TTTCA AACAAAA	
		G A__	
GAM1143 KIAA1958	3'	AAAACAAGTGAAGGAAGAACAG 81895	C GAAGG
		CTG TCT TCACTTGTTTT	
		GAC AGA AGTGAACAAAA	
		A AGGA_	
GAM1143 LOXL4	3'	AAAACAAGTTTGGCAGAGCA 49867	AA TC
		TGCTCTG GG ACTTGTTTT	
		ACGAGAC TT TGAACAAAA	
		GG _	
GAM1143 NRF	3'	AAACAAGTAAACATGCAGC 34079	TCTGAAG C_
		GCTGC GT ACTTGTTT	
		CGACG CA TGAACAAA	
		TA_____ AA	
GAM1143 SDF1	3'	AAAACAAGGAAGTCAAAGCA 90852	C AGG A
		TGCT TGA TC CTTGTTTT	
		ACGA ACT AG GAACAAAA	
		A GA_ _	
GAM1143 WNT10A	3'	AAAACAAGCCTCAGCCAGGC 47400	GCT A TCA
		GCT CTGA GG CTTGTTTT	
		CGG GACT CC GAACAAAA	
		ACC _ _	
GAM1143 LOC149876	5'	AAACGTCTTCAGAGCA 79525	TCACT
		TGCTCTGAAGG TGTTT	
		ACGAGACTTCC GCAAA	
		T_____	
GAM1143 LOC158014	3'	AAACAGAACCTTCAGACA 81642	C CAC
		TG TCTGAAGGT TTGTTT	
		AC AGACTTCCA GACAAA	
		_ A_	
GAM1143 LOC162083	5'	AGTGACACCCAGAGCAGC 82334	AAG
		GCTGCTCTG GTCCT	
		CGACGAGAC CAGTGA	
		CCA	
GAM1143 LOC196746	3'	AAGGACACTCAGAGCAGC 87509	AG A
		GCTGCTCTGA GTC CTT	
		CGACGAGACT CAG GAA	
		CA _	
GAM1143 LOC255870	3'	AAAACAAGTGACCTTCAGAGCA 94654	
GC		GCTGCTCTGAAGGTCCTTGTTTT	

CGACGAGACTTCCAGTGAACAAAA

GAM1143 LOC90643 5' GGTGACCGCCAGAGCAGC 63691 AA  
GCTGCTCTG GGTCAC  
||||||| |||||  
CGACGAGAC CCAGTGG  
CG

GAM1143 LOC91818 5' GGTGACCGCCAGAGCAGC 67271 AA  
GCTGCTCTG GGTCAC  
||||||| |||||  
CGACGAGAC CCAGTGG  
CG

GAM1144 ACK1 3' TCAGTGCTTCCTCTTC 19345 C TC  
GAAG AG GAGCACTGA  
||| || |||||  
CTTC TC TTCGTGACT  
\_ C\_

GAM1144 C1orf6 3' TCAGCATTTCGTTCTTCTGTC 39286 C GT CA  
GACAGAAG A CGAG CTGA  
||||||| | ||| |||  
CTGTCTTC T GCTT GACT  
\_ TG AC

GAM1144 CFTR 3' CAGTCTGACTGTTTCCATC 4927 CA G C  
GA GAAGCAGTC AG ACTG  
|| ||||| || |||  
CT CTTTGTCAG TC TGAC  
AC \_ \_

GAM1144 EGFL4 5' TCAGTGGGCTCTGCTTCTG 61820 TCGAG  
CAGAAGCAG CACTGA  
||||||| |||||  
GTCTTCGTC GTGACT  
TCGG\_

GAM1144 HSPA1B 3' ACTGCCACCTTCTGTACGA 18075 \_ \_\_\_\_  
TCG ACAGAA GCAGT  
||| ||||| |||||  
AGC TGTCTT CGTCA  
A CCAC

GAM1144 IL1RAP 3' CAGTGCTCAACTATTTG 9312 AGC C  
CAGA AGT GAGCACTG  
||| ||| |||||  
GTTT TCA CTCGTGAC  
A\_ A

GAM1144 LAMC1 3' TCAGTACTCTTGTTTCT 9680 TC C  
AGAAGCAG GAG ACTGA  
||||||| ||| |||||  
TCTTTGTT CTC TGACT  
\_ A

GAM1144 DKFZp762E1511 3' GCAGGAGCTGCTTCAGCCGA 59514 ACA \_ GA  
TCG GAAGCAG TC GC  
||| ||||| || ||

AGC CTTCGTC AG CG  
 CGA G GA  
 GAM1144 FLJ13725 5' CAGCTGCTTCTTCTGTC 68286 CAGTC \_  
 GACAGAAG GAGCA CTG  
 ||||| |||||  
 CTGTCTTC TTCGT GAC  
 C  
 GAM1144 GW112 5' CAGTGCTCTGTTTC 21185 GTC  
 GAAGCA GAGCACTG  
 ||||| |||||  
 CTTTGT CTCGTGAC  
 C  
 GAM1144 KIAA1046 3' CAATGAAATGGCTGTTTC 29993 AG\_ C  
 GAAGCAGTCG CA TG  
 ||||| |||||  
 CTTTGTCCGT GT AC  
 AAA A  
 GAM1144 KIAA1671 3' TGCAACTGCTTCAGTCGA 65698 A CGA  
 TCGAC GAAGCAGT GCA  
 ||||| ||||| |||||  
 AGCTG CTTCGTCA CGT  
 A A\_  
 GAM1144 PTPNS1 3' CTCGACTGCCTCCCCGA 54998 ACA A  
 TCG GA GCAGTCGAG  
 ||| |||||  
 AGC CT CGTCAGCTC  
 CC\_ C  
 GAM1144 SFRS10 3' CAGTGCTTAATGCTTATATC 15974 CAG GTC  
 GA AAGCA GAGCACTG  
 || ||||| |||||  
 CT TTCGT TTCGTGAC  
 ATA AA\_  
 GAM1144 TSPEAR 3' CAGTGCTCGCCCATCTG 58716 AGCA T  
 CAGA G CGAGCACTG  
 ||||| |||||  
 GTCT C GCTCGTGAC  
 ACC\_  
 GAM1144 LOC138389 5' TCAGCGCCACTGCTTCTG 76233 CGA A  
 CAGAAGCAGT GC CTGA  
 ||||| |||||  
 GTCTTCGTCA CG GACT  
 C\_ C  
 GAM1144 LOC145474 5' CAGTGCTTTGAGGCTTCTTC 77210 C AG \_  
 GA AGAAGC TCGA GCACTG  
 || ||||| |||||  
 CT TCTTCG AGTT CGTGAC  
 G\_ T  
 GAM1144 LOC150203 5' AGGTTTGACTGCCTCT 60517 A A  
 AGA GCAGTCGAGC CT  
 ||| ||||| ||||| |||||

TCT CGTCAGTTTG GA  
 C \_  
 GAM1144 LOC152580 5' CAGTTTCTGCTTCTGT 85774 TCGAGC  
 ACAGAAGCAG ACTG  
 ||||| |||  
 TGTCTTCGTC TGAC  
 TT\_\_\_\_  
 GAM1144 LOC161734 3' TCAGTGCTCTTCTTCCATGA 87103 ACA CAGTC  
 TCG GAAG GAGCACTGA  
 || ||| |||||  
 AGT CTTC CTCGTGACT  
 AC\_ TT\_\_\_\_  
 GAM1144 LOC91373 3' TCAATGCCGGCGGCCTCTGTGA 65843 G A A A C  
 TC ACAGA GC GTCG GCA TGA  
 || ||| || ||| |||  
 AG TGTCT CG CGGC CGT ACT  
 \_ C G \_ A  
 GAM1144 LOC92181 3' TCAGTATATTGCTCCTGTC 68407 A CGAGC  
 GACAG AGCAGT ACTGA  
 |||| |||| |||  
 CTGTC TCGTTA TGA CT  
 C TA\_\_\_\_  
 GAM1145 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
 GTA GGAT GGGTTGTTT  
 || ||| |||||  
 CGT CCTA CCCAACAAA  
 C CGTG\_  
 GAM1145 LCT 3' AACCGTAAAAATCCTT 9697 G  
 AAGGATTTTTA GGTT  
 ||||| |||  
 TTCCTAAAAAT CCAA  
 G  
 GAM1145 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
 GTAAGGATTTT TAGGGTTGTTT  
 ||||| |||||  
 CATTCTAAAAATCCCAACAAA  
 GAM1145 FBXO30 3' AACTAAAAAATCCTGAC 49573 A AG  
 GT AGGATTTT GGTT  
 || ||||| |||  
 CA TCCTAAAAA TCAA  
 G AA  
 GAM1145 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTT  
 GTAAG AGGGTTGTT  
 ||| |||||  
 CATT TCCCAACAA  
 AT\_\_\_\_  
 GAM1145 PRO0641 5' AAACAACCCCAAACTTG 26210 GAT A  
 TAAG TTTT GGGTTGTTT  
 ||| ||| |||||

		GTTC AAAA CCCAACAAA		
		___ C		
GAM1145	SMT3H2	3' AACAAACATAAAAAATCCTTGC	22670	GG
		GTAAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1145	LOC120103	3' AACCTATGAAAAATCCTTGC	74002	A__
		GTAAAGGATTTTTT GGGTT		
		CGTTCCTAAAAA TCCAA		
		GTA		
GAM1145	LOC129831	3' AAACAACCCCAATGTCC	74889	TT A
		GGAT TT GGGTTGTTT		
		CCTG AA CCCAACAAA		
		T_ C		
GAM1145	LOC133088	5' AAACAAAATAGAAAAATCCCTG	75075	A AGGG_
	C	GTA GGATTTTTT TTGTTT		
		CGT CCTAAAAA AACAAA		
		C GATAA		
GAM1145	LOC148089	3' GGCCCTAAAAATTCCTAC	78637	A
		GTA GGATTTTTTAGGGTT		
		CAT CTTAAAAATCCCGG		
		C		
GAM1145	LOC154547	3' AACAAACATAAAAAATCCTTGC	76050	GG
		GTAAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1145	LOC158104	3' ACAGCCAAAAATCCTTA	60313	AG
		TAAGGATTTTTT GGTTGT		
		ATTCCTAAAAA CCGACA		
		—		
GAM1145	LOC205880	5' AAACAACCATCATCCTGAC	90709	A TTTTAG
		GT AGGAT GGTGTTT		
		CA TCCTA CCAACAAA		
		G CTA__		
GAM1145	LOC221561	3' AACAAACATAAAAAATCCTTGC	92130	GG
		GTAAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1145	LOC257591	3' AACAAACATAAAAAATCCTTGC	97840	GG
		GTAAAGGATTTTTTA GTTGTT		

CGTTCCTAAAAAT CAACAA  
A\_  
GAM1145 LOC51145 3' AGCTAAAATCCTTAC 32393 TAG  
GTAAGGATTTT GGTT  
||||||| |||  
CATTCCTAAAA TCGA

—  
GAM1146 CTGF 5' CAGCCCCGAGACGACAG 8575 G C  
CTGTCGT TCGGG CTG  
||||| ||| |||  
GACAGCA AGCCC GAC  
G C

GAM1146 LIF 3' CAGCATGCTCCGACACAGCAG 9730 C \_ CTGAC  
CTGT GTGTCGG GC GCTG  
||| ||||| || |||  
GACG CACAGCC CG CGAC  
A T TA—

GAM1146 PK428 5' CAGCACCAGCATTGCATGACAG 13208 CGG C AC  
CTGTCGTGT GC TG GCTG  
||||||| || ||| |||  
GACAGTACG CG AC CGAC  
TTA \_ CA

GAM1146 RAGE 3' CAAGCCCGACCGGGCCAG 26445 \_ T C  
CTG TCG GTCGGGC TG  
||| ||| ||||| ||  
GAC GGC CAGCCCG AC  
CG \_ A

GAM1146 UBE3A 5' CAGGACCCGACACACCAG 55588 TC \_  
CTG GTGTCGGG CCTG  
||| ||||| |||  
GAC CACAGCCC GGAC  
CA A

GAM1146 FLJ20671 3' CAGGCCCGCACAACA 35517 C T  
TGT GTG CGGGCCTG  
||| ||| |||||  
ACA CAC GCCCGGAC  
A \_

GAM1146 GFR 3' AGCATCAAGACAAGACA 24465 G GGGCC C  
TGTC TGTC TGA GCT  
||||| ||| |||  
ACAG ACAG ACT CGA  
A A— A

GAM1146 KIAA0376 3' CAGCATCAGGCCTGAGGTCAG 65597 TCG G C  
CTG T TCGGGCCTGA GCTG  
||| | ||||| |||  
GAC G AGTCCGGACT CGAC  
T\_ G A

GAM1146 KIAA0542 5' CGTCAGGCCCGATGGC 66085 GT  
GTC GTCGGGCCTGACG  
||| ||||| |||||

CGG TAGCCCGGACTGC

GAM1146 KIAA1559 3' CAGGCCTGTCACACAG 73060 C T  
CTGT GTG CGGGCCTG  
||||| ||| |||||  
GACA CAC GTCCGGAC

— T  
GAM1146 LOC255031 5' CAGCGCCAGGGCCACGACAG 97231 GTC G A  
CTGTCTG GG CCTG CGCTG  
||||| || ||| |||||  
GACAGCA CC GGAC GCGAC

— G C  
GAM1147 DPYD 3' TCACCTTCATGATTATAG 60443 A A  
CTATAGTCAT AA GTGG  
||||||| || |||  
GATATTAGTA TT CACT  
C C

GAM1147 TBXA2R 5' ACTGTTTATGACTATA 6477 —  
TATAGTCATAAA AGT  
||||||| |||  
ATATCAGTATTT TCA  
G

GAM1147 DKFZp434A171 5' CCCACTTTTATTTGCTATA 70798 C\_  
TATAGT ATAAAAGTGGG  
||||| |||||  
ATATCG TATTTTCACCC  
TT

GAM1147 DKFZP547N043 3' TCCCACTTTTACTA 49318 CAT  
TAGT AAAAGTGGGA  
||| |||||  
ATCA TTTTCACCCT

—  
GAM1147 SH3BGRL2 3' CCTATTATGATTATAGTAA 48886 AAA  
TTACTATAGTCATA GTGGG  
||||||| |||  
AATGATATTAGTAT TATCC

—  
GAM1147 SLC21A14 3' CCCACTTTAATATATGTAA 33831 \_ GTCATA  
TTAC TATA AAAGTGGG  
||| ||| |||||  
AATG ATAT TTTACCC  
T AA—

GAM1147 LOC149506 3' TCCCATTTAATAACTATAATAA 84482 C CATAA  
TTA TATAGT AAGTGGGA  
|| ||||| |||||  
AAT ATATCA TTTACCCT  
A ATAA\_

GAM1147 LOC219988 3' CCCATATTAATATGACTATAG 91619 \_ A  
CTATAGTCATA AA GTGGG  
||||||| || |||



			GATATCAGTAT TT TACCC		
			AA A		
GAM1147	LOC92223	3'	GTCCCACTTTTATAGGAC 68524	___	
			GTC ATAAAAGTGGGAC		
			CAG TATTTTCACCCTG		
			GA		
GAM1148	CD28	3'	CCATAGGAGAAGTGAGAATACT 20437	GATG___	C
	G		CAG ACTTCTCC ATGG		
			GTC TGAAGAGG TACC		
			ATAAGAG A		
GAM1148	FBXL7	3'	CCATGAAAGAAGTTGAAGGC 24546	AGGA	CC
			GCC TGAATTCT CATGG		
			CGG GTTGAAGA GTACC		
			AA__ AA		
GAM1148	HARS	5'	GGAAGTCATCCTTGCTG 9174	C	
			CAGC AGGATGACTTCT		
			GTCG TCCTACTGAAGG		
			T		
GAM1148	L1CAM	3'	CCACTCCCCAGCCAGCCTGGCT 43753	A A TCTCCCA	
	G		CAGCCAGG TG CT TGG		
			GTCGGTCC AC GA ACC		
			G C CCCCTC_		
GAM1148	L1CAM	3'	CCACTCCCCAGCCAGCCTGGCT 4715	A A TCTCCCA	
	G		CAGCCAGG TG CT TGG		
			GTCGGTCC AC GA ACC		
			G C CCCCTC_		
GAM1148	LILRB4	3'	CATGATGTCTTCCTGGCTG 22433	T TTCTCC	
			CAGCCAGGA GAC CATG		
			GTCGGTCCT CTG GTAC		
			T TA___		
GAM1148	MMP11	3'	CCATGGCCTTCAGCCCTGGCTG 19871	A_ CTTCTC	
			CAGCCAGG TGA CCATGG		
			GTCGGTCC ACT GGTACC		
			CG TCC___		
GAM1148	MUCDHL	3'	CCACAGGAGAAGTCACTGCTTG 48365	C GA	CA
			CAG CAG TGAATTCTCC TGG		
			GTT GTC ACTGAAGAGG ACC		
			C __ AC		
GAM1148	MUCDHL	3'	CCACAGGAGAAGTCACTGCTTG 87299	C GA	CA
			CAG CAG TGAATTCTCC TGG		

GTT GTC ACTGAAGAGG ACC  
 C \_ AC  
 GAM1148 SLC22A2 3' CCATGGGACCAGATCCTG 59530 GA TC  
 CAGGAT CT TCCCATGG  
 ||||| || |||||  
 GTCCTA GA AGGGTACC  
 \_ CC  
 GAM1148 SRGAP1 3' CATGGGACGATCCCAGT 72261 CA TGACT \_  
 GC GGA TC TCCCATG  
 || || || |||||  
 TG CCT AG AGGGTAC  
 AC \_ C  
 GAM1148 C11orf21 3' CACACTGACACCCTGGCTG 26238 A ACT TCCCA  
 CAGCCAGG TG TC TG  
 ||||| || || ||  
 GTCGGTCC AC AG AC  
 C \_ TCAC\_  
 GAM1148 DDX27 3' CTGTGGGAAGTCATCCTGGCTG 35439 TC  
 CAGCCAGGATGACT TCCCATGG  
 ||||| |||||  
 GTCGGTCCTACTGA AGGGTGTC  
 \_  
 GAM1148 DKFZp761D221 3' CATGGGAAAATTCTTACT 50162 CC GACTTC  
 AG AGGAT TCCCATG  
 || |||| |||||  
 TC TCTTA AGGGTAC  
 AT AA\_  
 GAM1148 DYRK4 5' CCTGCTGAAGTCATCCCTGCTG 64226 CA TCC T  
 CAGC GGATGACTTC CA GG  
 ||| ||||| || ||  
 GTCG CCTACTGAAG GT CC  
 TC TC\_  
 GAM1148 FLJ10388 3' CCATGGGAGAGATGCTG 36085 G GAC  
 CAG AT TTCTCCCATGG  
 ||| || |||||  
 GTC TA GAGAGGGTACC  
 G \_  
 GAM1148 FLJ11856 3' CATAGGAGATCCTGGCT 44561 TGACT C  
 AGCCAGGA TCTCC ATG  
 ||||| |||||  
 TCGGTCCT AGAGG TAC  
 \_ A  
 GAM1148 FLJ14494 3' CATGGGAGCACCCTGGC 90869 A ACTT  
 GCCAGG TG CTCCCATG  
 ||||| || |||||  
 CGGTCC AC GAGGGTAC  
 C \_  
 GAM1148 FLJ21613 5' CACGGGAGAAGTAGGC 41639 AGGATG A  
 GCC ACTTCTCCC TG  
 ||| ||||| ||

CGG TGAAGAGGG AC  
 A\_\_\_\_\_ C  
 GAM1148 KIAA0184 3' GAGACCATCCTGGCT 65195 ACT  
 AGCCAGGATG TCTC  
 ||||| ||  
 TCGGTCCTAC AGAG  
 C\_\_\_\_  
 GAM1148 KIAA1751 3' AAGGGCACCTGGCTG 71686 A ACTTCT A\_  
 CAGCCAGG TG CCC T  
 ||||| || || |  
 GTCGGTCC AC GGG A  
 \_\_\_\_\_ AC  
 GAM1148 LIMK2 5' GGAGGAGCCATCCCAGC 33626 CA A  
 GC GGATG CTTCTCC  
 || |||| |||||  
 CG CCTAC GAGGAGG  
 AC C  
 GAM1148 MGC11115 3' ATGAGCTTCCTGGCTG 50235 TGA TCTCC  
 CAGCCAGGA CT CAT  
 ||||| || ||  
 GTCGGTCCT GA GTA  
 TC\_ \_\_\_\_\_  
 GAM1148 MGC3113 3' CCACGTGAAACCTCCTGGCT 43842 TGAC TCCCA  
 AGCCAGGA TTC TGG  
 ||||| || ||  
 TCGGTCCT AAG ACC  
 CCA\_ TGC\_  
 GAM1148 N4BP3 3' CATGGGAGTTCCCAGCTG 66256 CA TGACTT  
 CAGC GGA CTCCCATG  
 ||| || |||||  
 GTCG CCT GAGGGTAC  
 AC T\_\_\_\_  
 GAM1148 NPFF 5' CCATGGGAGGAGATCCCAGGT 13555 A\_ GA  
 GCC GGAT CTTCTCCCATGG  
 || ||| |||||  
 TGG CTA GAGGAGGGTACC  
 AC \_\_\_\_  
 GAM1148 PAT2 3' CATGGGAGAAAGTAACCT 80774 ATG \_  
 AGG ACTT CTCCCATG  
 || ||| |||||  
 TCC TGAA GAGGGTAC  
 AA\_ A  
 GAM1148 PRO2949 3' GAGATCATCCTGGCT 37621 CT  
 AGCCAGGATGA TCTC  
 ||||| ||  
 TCGGTCCTACT AGAG  
 \_\_\_\_\_  
 GAM1148 PTP4A1 5' CCATAAGAGTGGTTATCCTGG 12937 T CC  
 CCAGGATGACT CTC ATGG  
 ||||| || |||

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GGTCCTATTGG GAG TACC
      T AA
GAM1148 TBC1D2 3' CCACAGCCTTCCTCACCCTTGG 37314 _ A CTTCTCCCA
      CTG      CAGCCA GG TGA      TGG
              ||||| || |||      |||
              GTCGGT CC ACT      ACC
              T C CCTTCCGAC
GAM1148 TBC1D2 5' CCACGTCAGAGTCATCCTTGCT 37315 C T CCCA
      G      CAGC AGGATGACT CT TGG
              ||| ||||| ||| |||
              GTCG TCCTACTGA GA ACC
              T _ CTGC
GAM1148 TBC1D2 5' CCACGTCGGAGTCATCCTTGC 37316 C TCCCA
      GC AGGATGACTTC TGG
              || ||||| |||
              CG TCCTACTGAGG ACC
              T CTGC_
GAM1148 TBC1D2 5' CCACGTCGGAGTCATCCTTGCT 37317 C TCCCA
      G      CAGC AGGATGACTTC TGG
              ||| ||||| |||
              GTCG TCCTACTGAGG ACC
              T CTGC_
GAM1148 TBC1D2 5' CCACGTCGGAGTCATCCTTGCT 37318 C TCCCA
      G      CAGC AGGATGACTTC TGG
              ||| ||||| |||
              GTCG TCCTACTGAGG ACC
              T CTGC_
GAM1148 TBC1D2 5' CCATGTCGGAGTCATCCTTGCT 37319 C TCC
      G      CAGC AGGATGACTTC CATGG
              ||| ||||| ||||
              GTCG TCCTACTGAGG GTACC
              T CT_
GAM1148 TIAF1 5' ATGGGGCCATCCTGG 54325 ACTTC
      CCAGGATG TCCCAT
      ||||| |||||
      GGCCTAC GGGGTA
      C_
GAM1148 TRIM4 3' CCATGGGAGGTGGGTCTGGC 52252 ATGACT
      GCCAGG TCTCCCATGG
      ||||| |||||
      CGGTCT GGAGGGTACC
      GGGT_
GAM1148 ZNF282 3' ATGGGAGCTCCTGGT 89209 TGACTT
      GCCAGGA CTCCCAT
      ||||| |||||
      TGGTCCT GAGGGTA
      C_
GAM1148 LOC120772 5' CCACAGGAGGGGGCTCCTGGCT 74023 TGA CA
      G      CAGCCAGGA CTTCTCC TGG
              ||||| ||||| |||

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	GTCGGTCCT GGGGAGG ACC	
	CG_ AC	
GAM1148 LOC139341 5'	CCATAGACTTCCATCCTGGC 75381	ACT_ CCC
	GCCAGGATG TCT ATGG	
	CGGTCCTAC AGA TACC	
	CTTC _	
GAM1148 LOC143286 5'	CCATAAGGTCACCTACCCTGGCT 82946	A_ CTCCC
G	CAGCCAGG TGACTT ATGG	
	GTCGGTCC ACTGGA TACC	
	CATC A_	
GAM1148 LOC145748 3'	CCGACTGAAAATCATCTTGGCT 83465	C C CCA
G	CAGCCAGGATGA TT TC TGG	
	GTCGGTTCTACT AA AG GCC	
	_ A TCA	
GAM1148 LOC147118 5'	CCACAGGAACGTCTCCGGCTG 83951	A T TTC CA
	CAGCC GGA GAC TCC TGG	
	GTCGG CCT CTG AGG ACC	
	_ _ CA_ AC	
GAM1148 LOC151517 5'	CCACGGGCGTCATCCTAGC 85434	C TTCT A
	GC AGGATGAC CCC TGG	
	CG TCCTACTG GGG ACC	
	A C_ C	
GAM1148 LOC157226 5'	CCACGGGAGGAGCCGCAGCTG 63931	CA_ ATGA A
	CAGC GG CTTCTCCC TGG	
	GTCG CC GAGGAGGG ACC	
	ACG _ C	
GAM1148 LOC199991 5'	CACGAGAGCATCCTGGCT 89912	A T CCA
	AGCCAGGATG CT CTC TG	
	TCGGTCCTAC GA GAG AC	
	_ _ C_	
GAM1148 LOC202459 5'	AGAAGCCGCCCTGGCTG 59251	A A
	CAGCCAGG TG CTTCT	
	GTCGGTCC GC GAAGA	
	C C	
GAM1148 LOC205011 3'	CATCAAGACATCCTGGCTG 90650	ACT CCC
	CAGCCAGGATG TCT ATG	
	GTCGGTCCTAC AGA TAC	
	_ AC_	
GAM1148 LOC256158 5'	CCATGGGGATCCCACCTCCAGC 97655	C_ A ACT T
	GC AGG TG TC CCCATGG	

			CG TCC AC AG GGGTACC		
			ACC _ CCT _		
GAM1148	LOC256867	5'	CCACAGGAGGGGGCTCCTGGCT	94862	TGA CA
	G		CAGCCAGGA CTTCTCC TGG		
			GTCGGTCCT GGGGAGG ACC		
			CG_ AC		
GAM1148	LOC51195	3'	CCATAAGTCTGTTTCATCCTGCT	32937	C CTTCTCCC
	G		CAGC AGGATGA ATGG		
			GTCG TCCTACT TACC		
			_ TGTCTGAA		
GAM1148	LOC91069	3'	CATGTTACCACCCTGGCTG	64775	A ACTTCTCC
			CAGCCAGG TG CATG		
			GTCGGTCC AC GTAC		
			C CATT_____		
GAM1149	AICDA	5'	GCCTGAGACTTGCAGGGAGGCA	40329	C ATTTGC_
	AGAA		TTC TGCCTCCCT CAGGC		
			AAG ACGGAGGGA GTCCG		
			A CGTTCAGA		
GAM1149	ANK1	3'	GCCTCCGGCCCAGGGAGGCCAG	40027	CT ATTT _
	AA		TTC GCCTCCCT GCC AGGC		
			AAG CGGAGGGA CGG TCCG		
			AC CC_ CC		
GAM1149	ANK1	3'	GCCTCCGGCCCAGGGAGGCCAG	3473	CT ATTT _
	AA		TTC GCCTCCCT GCC AGGC		
			AAG CGGAGGGA CGG TCCG		
			AC CC_ CC		
GAM1149	EIF2C1	3'	CCCAAATCCAGAGGAAGCAAGG	24170	_ C _ _ CCA
	A		TCCT GC TCC CT ATTTG GG		
			AGGA CG AGG GA TAAAC CC		
			A A A CC _		
GAM1149	IKBKG	3'	CCCGGCACTGGGGAAGTCAAGA	13311	C _ C TT A
	A		TTC TG C TCCCTA TGCC GG		
			AAG AC G AGGGGT ACGG CC		
			A T A C_ C		
GAM1149	IKBKG	3'	CCCGGCACTGGGGAAGTCAAGA	94663	C _ C TT A
	A		TTC TG C TCCCTA TGCC GG		
			AAG AC G AGGGGT ACGG CC		
			A T A C_ C		
GAM1149	LY9	3'	AAATAAAAGGCAGGAA	71680	CCC
			TTCCTGCCT TATTT		

AAGGACGGA ATAAA  
 AA\_  
 GAM1149 MAFF 3' TGGCAAATAGGGAGACAAGGA 24655 GC\_  
 TCCT CTCCTATTTGCCA  
 ||| |||||  
 AGGA GAGGGATAAACGGT  
 ACA  
 GAM1149 MC1R 5' GCCCAGATGGAAGGAGGCAGG 9954 \_ CCA  
 CCTGCCTCC CTATTTG GGC  
 ||||| ||||| ||  
 GGACGGAGG GGTAGAC CCG  
 AA \_  
 GAM1149 MYO15A 3' GCCTGAGGGAGGAGGCAGGAG 32671 \_ ATTTGC  
 TTCCTGCCTCC CT CAGGC  
 ||||| || |||||  
 GAGGACGGAGG GG GTCCG  
 A GA\_  
 GAM1149 NRG1 3' GCAAATAGAAAACAGGAA 25646 CCTCC  
 TTCCTG CTATTTGC  
 ||||| |||||  
 AAGGAC GATAAACG  
 AAAA\_  
 GAM1149 NRG1 3' GCAAATAGAAAACAGGAA 25659 CCTCC  
 TTCCTG CTATTTGC  
 ||||| |||||  
 AAGGAC GATAAACG  
 AAAA\_  
 GAM1149 SEPN1 3' GCCTGGCAGAGGAAGAAGGAA 66369 GC C AT  
 TTCCT CT CCT TTGCCAGGC  
 |||| || || |||||  
 AAGGA GA GGA GACGGTCCG  
 A\_ A \_  
 GAM1149 SMURF1 3' GCCTAACCCGCGGGAGGCGGAA 92453 T TATTTGCC  
 TTCC GCCTCCC AGGC  
 ||| ||||| |||  
 AAGG CGGAGGG TCCG  
 \_ CGCCCAA\_  
 GAM1149 STAT6 3' GCCTAGGACGGATAGGCAGGAA 12021 CCCT \_ \_  
 TTCCTGCCT ATTTG CC AGGC  
 ||||| |||| || ||||  
 AAGGACGGA TAGGC GG TCCG  
 \_ A A  
 GAM1149 TFF3 3' GCCCAGGCCTCAAGGGCAGGAA 63566 CCCTATTT A\_  
 TTCCTGCCT GCC GGC  
 ||||| || |||  
 AAGGACGGG CGG CCG  
 AACTC\_ AC  
 GAM1149 TOP3B 5' GCCCGGCGGCTCAGAAAGGCGG 14129 CC AT\_ A  
 GAA TTCCTGCCT CT TTGCC GGC  
 ||||| || ||||| |||

AAGGGCGGA GA GGCGG CCG  
 AA CTC C  
 GAM1149 VAV1 3' GCCTTGGCAGAGACGAG 18305 C\_ A \_  
 CTC CT TTTGCCA GGC  
 ||| || ||||| |||  
 GAG GA AGACGGT CCG  
 CA G T  
 GAM1149 YWHAB 5' GCTGTGGATAGAGAAGCAGGAA 12692 C C TG CA  
 TTCCTGC TC CTATT C GGC  
 ||||| || |||| | |||  
 AAGGACG AG GATAG G TCG  
 A A GT\_\_  
 GAM1149 AF020591 3' GCCTGGCAAACATGGCA 27141 TCCCTA  
 TGCC TTTGCCAGGC  
 ||| |||||  
 ACGG AAACGGTCCG  
 TAC\_\_  
 GAM1149 BCL2L1 3' CCTCAGGCAGGAAGGGCAGGAA 56804 CC ATT \_  
 TTCCTGCCT CT TGCC AGG  
 ||||| || ||| |||  
 AAGGACGGG GG ACGG TCC  
 AA \_ AC  
 GAM1149 BNIP-S 5' TAAAGAAGGAGGCAGGAA 56263 CTA  
 TTCCTGCCTCC TTTG  
 ||||| |||  
 AAGGACGGAGG AAAT  
 AAG  
 GAM1149 BTBD3 5' GCAAATAAGAGAAACAGGAA 30311 C\_ CC  
 TTCCTG CTC TATTTGC  
 |||| ||| |||||  
 AAGGAC GAG ATAAACG  
 AAA A\_  
 GAM1149 C20orf28 3' GCCTGAGACGGGAGGCAGGAA 31224 TAT GC  
 TTCCTGCCTCCC TT CAGGC  
 ||||| || |||||  
 AAGGACGGAGGG AG GTCCG  
 C\_ A\_  
 GAM1149 CHODL 5' CCCGGCAGGGAGGCAGGGA 46310 ATTT A  
 TTCCTGCCTCCCT GCC GG  
 ||||| ||| ||  
 AGGGACGGAGGGA CGG CC  
 \_ C  
 GAM1149 D2S448 3' CCTGAAGGGAAGCAGG 73519 C ATTTGC  
 CCTGC TCCCT CAGG  
 |||| ||| |||  
 GGACG AGGGA GTCC  
 A A\_\_\_\_  
 GAM1149 DKFZP434K1772 3' GCCTTACTCAGGAAGGCAGGAG 67714 C ATTTGCC  
 TTCCTGCCT CCT AGGC  
 ||||| ||| |||



GAGGACGGA GGA TCCG  
 A CTCAT\_\_  
 GAM1149 DKFZp547l094 3' CCTGGCAACCTGAGGGAGG 49637 AT\_\_  
 CCTCCCT TTGCCAGG  
 ||||| |||||  
 GGAGGGA AACGGTCC  
 GTCC  
 GAM1149 DKFZP547L112 3' CCTGGATATAGCAAGGCAGGAA 66529 CC TTG  
 TTCCTGCCT CTAT CCAGG  
 ||||| ||| ||||  
 AAGGACGGA GATA GGTCC  
 AC TA\_  
 GAM1149 FABP7 5' CAAATAAGAAGGCAGGAG 7542 CCC  
 TTCCTGCCT TATTTG  
 ||||| |||||  
 GAGGACGGA ATAAAC  
 AGA  
 GAM1149 FLJ14957 3' CCCAAAGTGGGAGGCAGGGA 51744 TA CCA  
 TTCCTGCCTCCC TTTG GG  
 ||||| ||| ||  
 AGGGACGGAGGG AAAC CC  
 TG \_\_\_\_  
 GAM1149 FLJ20343 3' CCTGGCAAACCTGACCAG 34998 CC CCTA  
 CTG TC TTTGCCAGG  
 ||| || |||||  
 GAC AG AAACGGTCC  
 C\_ TC\_\_  
 GAM1149 FLJ23185 3' CCTGGCAGGATGAGGCAGAGA 46830 \_ CCTA  
 TC CTGCCTC TTTGCCAGG  
 || ||||| |||||  
 AG GACGGAG GGACGGTCC  
 A TA\_  
 GAM1149 GGA2 3' GCCTGATGGGTGGGAGAAGGAA 56882 GC T GC  
 TTCCT CTCCC ATTT CAGGC  
 |||| |||| ||| ||||  
 AAGGA GAGGG TGGG GTCCG  
 A\_ \_ TA  
 GAM1149 GGA2 3' GCCTGATGGGTGGGAGAAGGAA 30468 GC T GC  
 TTCCT CTCCC ATTT CAGGC  
 |||| |||| ||| ||||  
 AAGGA GAGGG TGGG GTCCG  
 A\_ \_ TA  
 GAM1149 HDAC11 3' GCCCATAGGTCCAGGGAGGCAG 45718 ATTT A\_\_  
 G CCTGCCTCCCT GCC GGC  
 ||||| ||| |||  
 GGACGGAGGGA TGG CCG  
 CC\_\_ ATAC  
 GAM1149 IKKE 5' CACAAGGAGGCAGGGA 25746 CTAT CCA  
 TTCCTGCCTCC TTG G  
 ||||| ||| |

AGGGACGGAGG AAC C  
 \_\_\_\_\_ A\_  
 GAM1149 IL1F10 3' CAAGAAGGAGGCAGGAA 50771 CTA  
 TTCCTGCCTCC TTTG  
 ||||| |||  
 AAGGACGGAGG GAAC  
 AA\_  
 GAM1149 KIAA0370 5' GCCCAGCAAATAGGAGCCTGGA 73209 T\_ CTC CA  
 G TTCC GC CCTATTTGC GGC  
 ||| || ||||| |||  
 GAGG CG GGATAAACG CCG  
 TC A\_ AC  
 GAM1149 KIAA0551 3' GCCTGGTTGAGAAGGAGAG 66839 \_ A\_ T  
 CTC CCT TT GCCAGGC  
 ||| ||| || |||||  
 GAG GGA AG TGGTCCG  
 A AG T  
 GAM1149 KIAA1183 3' CCCGGATGGGAGGAGGAA 62530 G TATTTG A  
 TTCCT CCTCCC CC GG  
 |||| ||||| || |||  
 AAGGA GGAGGG GG CC  
 \_ TA\_ C  
 GAM1149 KIAA1464 3' CCTGACCCATGGAGGCAGGAG 68264 CTATTTGC  
 TTCCTGCCTCC CAGG  
 ||||| ||| |||  
 GAGGACGGAGG GTCC  
 TACCCA\_  
 GAM1149 MAPK8IP3 3' GCCTGGTAGATGAAGCAG 52987 C CCT  
 CTGC TC ATTTGCCAGGC  
 ||| || ||||| |||||  
 GACG AG TAGATGGTCCG  
 A \_  
 GAM1149 MGC2306 3' GCCTGGCAGGGGGTGAAGGCAG 50963 \_ AT  
 GAG TTCCTGCCT CCCT TTGCCAGGC  
 ||||| ||| ||||| |||||  
 GAGGACGGA GGGG GACGGTCCG  
 AGT \_  
 GAM1149 MGC2865 5' GCCTGGCAAACCGAAGCAAGAA 50451 C C CCTA  
 TTC TGC TC TTTGCCAGGC  
 ||| ||| || ||||| |||||  
 AAG ACG AG AAACGGTCCG  
 A A CC\_  
 GAM1149 MGC9753 3' GCCTGATTTTGGGGAGGAGGAA 53049 G TTTGC  
 TTCCT CCTCCCTA CAGGC  
 |||| ||||| ||| |||  
 AAGGA GGAGGGGT GTCCG  
 \_ TTTA\_  
 GAM1149 PALM 3' GCCTGGTAGGAGAGAGACAGGA 10414 C C A  
 TCCTG CTC CT TTTGCCAGGC  
 |||| ||| || ||||| |||||

		AGGAC GAG GA GGATGGTCCG	
		A A _	
GAM1149 PDZD2	5'	CCTGGCACGGAAGGAGGAA 80866	G C TATT
		TTCCT CCT CC TGCCAGG	
		AAGGA GGA GG ACGGTCC	
		_ A C__	
GAM1149 PLPL	3'	CCTGGAGGGGGAGGCAGGAG 39431	ATTTG
		TTCCTGCCTCCCT CCAGG	
		GAGGACGGAGGGG GTCC	
		GA__	
GAM1149 RABEX5	3'	GCCTGGAATGGAAGGCGGGAA 27186	C TATTTG
		TTCCTGCCT CC CCAGGC	
		AAGGGCGGA GG GGTCCG	
		A TAA__	
GAM1149 SHANK3	5'	GCCTGCTCGCAGGGAGGCAGAG 65500	_ ATTT C
A		TC CTGCCTCCCT GC AGGC	
		AG GACGGAGGGA CG TCCG	
		A CGCT _	
GAM1149 SRF	5'	CCGGGCCACAGGGGCAGGAA 11944	CCTATTT A
		TTCCTGCCTC GCC GG	
		AAGGACGGGG CGG CC	
		ACAC__ G	
GAM1149 TREX1	5'	CCCAGCAGAGGGAGGCAG 53280	AT CA
		CTGCCTCCCT TTGC GG	
		GACGGAGGGA GACG CC	
		_ AC	
GAM1149 TREX1	5'	CCCAGCAGAGGGAGGCAG 53290	AT CA
		CTGCCTCCCT TTGC GG	
		GACGGAGGGA GACG CC	
		_ AC	
GAM1149 URG4	3'	GCCCCCAGGGTAGGGAGACA 35506	C GCCA
		TG CTCCCTATTT GGC	
		AC GAGGGATGGG CCG	
		A ACCC	
GAM1149 LOC124222	3'	CCTGACAAACAGGCAGGGA 74271	CCCTA C
		TTCCTGCCT TTTG CAGG	
		AGGGACGGA AAAC GTCC	
		C__ A	
GAM1149 LOC131873	5'	CCCGGAGGAGAGGCAGGGA 75877	_ ATTTG A
		TTCCTGCCTC CCT CC GG	

	AGGGACGGAG GGA GG CC	
	A ____ C	
GAM1149 LOC144348 5'	CCTTCCGTAGAAAGACAGGCA 76806	CC A C__
	TGCCT CT TTTGC AGG	
	ACGGA GA AGATG TCC	
	CA A CCT	
GAM1149 LOC146316 5'	CTTCGAGAGGCAGGAA 60872	CCTAT CC
	TTCCTGCCTC TTG AG	
	AAGGACGGAG AGC TC	
	____ T_	
GAM1149 LOC148529 5'	CCTGGCAGACAGGAAGACA 84167	C C A
	TG CT CCT TTTGCCAGG	
	AC GA GGA AGACGGTCC	
	A A C	
GAM1149 LOC149606 3'	GCCCGCGGAGCAGGGAG 79454	A_ CA
	CTCCCT TTTGC GGC	
	GAGGGA AGGCG CCG	
	CG C_	
GAM1149 LOC151057 3'	CCAGGAAAGAAGGCAGGAA 85209	CCCTA G A
	TTCCTGCCT TTT CC GG	
	AAGGACGGA AAA GG CC	
	AG__ _ A	
GAM1149 LOC153346 5'	CCCAGATGGAAGGCA 86022	CC CCA
	TGCCT CTATTTG GG	
	ACGGA GGTAGAC CC	
	A_ ____	
GAM1149 LOC196418 5'	CCTTCCGTAGAAAGACAGGCA 87696	CC A C__
	TGCCT CT TTTGC AGG	
	ACGGA GA AGATG TCC	
	CA A CCT	
GAM1149 LOC199786 3'	GCCTGGCAGCTGAGGCAGAGA 88386	_ CCTAT
	TC CTGCCTC TTGCCAGGC	
	AG GACGGAG GACGGTCCG	
	A TC__	
GAM1149 LOC200058 3'	CCTGAAGGATGGGAAGCCAGGA 88556	C C GC
A	TTCCTG CT CCTATTT CAGG	
	AAGGAC GA GGGTAGG GTCC	
	C A AA	
GAM1149 LOC204579 5'	CCCGGCTATGAGGCAGGAA 89465	CCTATTT A
	TTCCTGCCTC GCC GG	

		AAGGACGGAG	CGG CC	
		TAT_____ C		
GAM1149	LOC219700 5'	GCCTGGCAGTCCAAAGACCAAG	93064	C CCTCCCTAT
	AA	TTC TG	TTGCCAGGC	
		AAG AC	GACGGTCCG	
		A CAGAAACCT		
GAM1149	LOC253181 5'	GCCTGGCAAACAGCACAGGA	97558	CCTCC A
		TCCTG	CT TTTGCCAGGC	
		AGGAC	GA AAACGGTCCG	
		AC_____ C		
GAM1149	LOC253296 3'	GCCTGGGGGCCACAGGAAAGGCA	94490	C_ ATTTG_
	GGAA	TTCCTGCCT	CCT CCAGGC	
		AAGGACGGA	GGA GGTCCG	
		AA CACCGG		
GAM1149	LOC253298 5'	GCCTGGGGGCCACAGGAAAGGCA	97215	C_ ATTTG_
	GGAA	TTCCTGCCT	CCT CCAGGC	
		AAGGACGGA	GGA GGTCCG	
		AA CACCGG		
GAM1149	LOC254107 5'	CCCAGAGGGGCAGGAA	94384	CCCTA CCA
		TTCCTGCCT	TTTG G	
		AAGGACGGG	AGAC C	
		_____ C_		
GAM1149	LOC255189 5'	CTGACCAAGGCAGGAA	96589	CCCTATT C_
		TTCCTGCCT	TG CAG	
		AAGGACGGA	AC GTC	
		_____ CA		
GAM1149	LOC257160 3'	CCTGACTGGGGAGGAAG	94846	G TTTGC
		CT CCTCCCTA	CAGG	
		GA GGAGGGGT	GTCC	
		A CA_____		
GAM1149	LOC257570 3'	GCCTGGGGGCCACAGGAAAGGCA	97833	C_ ATTTG_
	GGAA	TTCCTGCCT	CCT CCAGGC	
		AAGGACGGA	GGA GGTCCG	
		AA CACCGG		
GAM1149	LOC257571 5'	GCCTGGGGGCCACAGGAAAGGCA	97945	C_ ATTTG_
	GGAA	TTCCTGCCT	CCT CCAGGC	
		AAGGACGGA	GGA GGTCCG	
		AA CACCGG		
GAM1150	ESR2 5'	CCACCCGAGCTGCGACGGGCT	7520	A_ AA A
		AGCCTGTC	GGT GG TGG	

			TCGGGCAG TCG CC ACC		
			CG AG C		
GAM1150 LENG4	5'	CCATCCTTGGCGGCTT	44162	T	GGTA
		AAGCC GTCA AGGATGG			
		TTCGG CGGT TCCTACC			
		— ———			
GAM1150 MAP3K12	3'	CCAATTCACCTGATA	20862	AA	_
		TGTCAGGT GGAT GG			
		ATAGTCCA CTTA CC			
		— A			
GAM1150 NT5E	3'	CCATCTTTACAGGCT	10281	CAGGT	
		AGCCTGT AAGGATGG			
		TCGGACA TTTCTACC			
		—————			
GAM1150 PTK7	3'	GGCCATCCTTACCCCACA	11019	CA	
		TGT GGTAAGGATGGCC			
		ACA CCATTCCTACCGG			
		CC			
GAM1150 SIAT8E	3'	GCCACACCACCCGACAGGTT	59858	A	AA A_
		AGCCTGTC GGT GG TGGC			
		TTGGACAG CCA CC ACCG			
		C _ AC			
GAM1150 TCOF1	3'	GGCCATCCCCATGCCTCTGAC	4486	_	A_
		GTCA GGTA GGATGGCC			
		CAGT CCGT CCTACCGG			
		CT ACC			
GAM1150 TNFRSF9	3'	GGCCACCACACCTGACTAACTT	7791	CCT	AA A
		AAG GTCAGGT GG TGGCC			
		TTC CAGTCCA CC ACCGG			
		AAT CA _			
GAM1150 XRCC3	3'	GGCTGGCACGTGACAGGCT	18343	G	AAGGA
		AGCCTGTCA GT TGGCC			
		TCGGACAGT CA GTCGG			
		G CG_			
GAM1150 AIP	3'	GGCCCTGCCTTACCTGCCAAGC	14279	C T	AT_
		GC TG CAGGTAAGG GGCC			
		CG AC GTCCATTCC CCGG			
		A C GTC			
GAM1150 BAG4	3'	CACACTTCACACAACAGGCTT	16855	CAG	_ GA
		AAGCCTGT GT AAG TG			

		TTCGGACA CA TTC AC	
		ACA C AC	
GAM1150 C16orf5	3'	GCCCTCCTACCCGCAGGCTT 25449	CA A T
		AAGCCTGT GGTA GGA GGC	
		TTCGGACG CCAT CCT CCG	
		C_ _ C	
GAM1150 CABP2	5'	GGCCACCCCCGGGGTTCCAGGC 33035	___ A_ TAA A
		GCCTG TC GG GG TGGCC	
		CGGAC GG CC CC ACCGG	
		CTT GG ___ C	
GAM1150 CABP2	5'	GGCCACCCCCGGGGTTCCAGGC 48303	___ A_ TAA A
		GCCTG TC GG GG TGGCC	
		CGGAC GG CC CC ACCGG	
		CTT GG ___ C	
GAM1150 CTNNBIP1	5'	GGCCCAGGGACCGACAGACTT 39665	C A AAGGAT
		AAG CTGTC GGT GGCC	
		TTC GACAG CCA CCGG	
		A _ GGGAC_	
GAM1150 DKFZp434E2220	5'	GGCTGCTCACCTGACAG 34300	AA GA
		CTGTCAGGT G TGGCC	
		GACAGTCCA C GTCGG	
		___ TC	
GAM1150 DKFZp434M0331	5'	CCACCATGCCTGACAG 34232	A A
		CTGTCAGGTA GG TGG	
		GACAGTCCGT CC ACC	
		A _	
GAM1150 FLJ12697	3'	GCCACGGCGACAGGCT 92570	AG AAGGA
		AGCCTGTC GT TGGC	
		TCGGACAG CG ACCG	
		___ GC___	
GAM1150 FLJ13117	3'	GCCACAGGTGCCTGACAGGTT 43542	AGGA
		AGCCTGTCAGGTA TGGC	
		TTGGACAGTCCGT ACCG	
		GGAC	
GAM1150 FLJ13188	5'	CCACTTCCTGACAGCT 41938	C T GA
		AGC TGTCAGG AAG TGG	
		TCG ACAGTCC TTC ACC	
		_ _ _	
GAM1150 FLJ14326	3'	GGCCATCCCTTTTCCATGGCT 49813	TGTCA TAA__
		AGCC GG GGATGGCC	

TCGG CC CCTACCGG  
TA\_\_ TTTTC  
GAM1150 FLJ14810 3' GGCCATCCCTGACACGAAGCT 51627 C\_\_ TAAG  
AGC TGTCAGG GATGGCC  
||| ||||| |||||  
TCG ACAGTCC CTACCGG  
AAGC \_\_\_\_

GAM1150 FLJ20254 5' GGCCATCCTGCAAGACAAGC 34794 C AG A  
GC TGTC GTA GGATGGCC  
|| ||| ||| |||||  
CG ACAG CGT CCTACCGG  
A AA \_

GAM1150 FLJ20375 3' GGCCACATCACTGACAGCTT 35086 C GTAAGGA  
AAGC TGTCAG TGGCC  
||| ||||| |||||  
TTCG ACAGTC ACCGG  
\_ ACTAC\_\_

GAM1150 FLJ20635 3' TCCCATCTGACAGGCT 35480 AA  
AGCCTGTCAGGT GGA  
||||||| |||  
TCGGACAGTCTA CCT  
C\_

GAM1150 FLJ21709 3' GCCACCTGGTGAAAGCTT 77921 CTG GGTA A  
AAGC TCA AGG TGGC  
||| ||| ||| |||  
TTCG AGT TCC ACCG  
AA\_ GG\_ \_

GAM1150 FLJ21916 3' GCTATTATACCTGACACACT 43644 CC AG  
AG TGTCAGGTA GATGGC  
|| ||||| |||||  
TC ACAGTCCAT TTATCG  
AC A\_

GAM1150 FLJ22215 3' CCAGTCCCTGACAGGTT 96833 TAA GA  
AGCCTGTCAGG G TGG  
||||||| | |||  
TTGGACAGTCC C ACC  
\_\_ TG

GAM1150 HBOA 3' GCCATCCCCCTCAGGACT 22966 \_ TC TAA  
AG CCTG AGG GGATGGC  
|| ||| ||| |||||  
TC GGAC TCC CCTACCG  
A \_ C\_

GAM1150 HSNV1 3' GCCACCGTGCCAGGC 34009 GTCA A A  
GCCT GGTA GG TGGC  
||| ||| ||| |||  
CGGA CCGT CC ACCG  
\_\_ G \_

GAM1150 IL14 5' ATTTTACCTGCAGGC 95429 T  
GCCTG CAGGTAAGGAT  
||||| |||||



CGGAC GTCCATTTTTA

GAM1150 KCNH8 5' CCATCCTTCTGGACAACTT 58253 CC A T  
AAG TGTC GG AAGGATGG  
||| ||| || |||||  
TTC ACAG TC TTCCTACC  
AA G \_

GAM1150 KIAA0141 3' GGCCATCCTCGAGACTAGC 28733 CT AGGTA  
GC GTC AGGATGGCC  
|| ||| |||||  
CG CAG TCCTACCGG  
AT AGC \_

GAM1150 KIAA0247 3' COTTACCTAACAGGGTT 28396 G C  
AA CCTGT AGGTAAGG  
|| ||| |||||  
TT GGACA TCCATTCC  
G A

GAM1150 KIAA0397 3' GCCACCAAAGTCTGGCAGACTT 61674 C TAA\_ A  
AAG CTGTCAGG GG TGGC  
||| ||||| || |||  
TTC GACGGTCT CC ACCG  
A GAAA \_

GAM1150 KIAA0759 3' GGCCATCCCTTTCCCCAGGCTT 67327 TCA T \_  
AAGCCTG GG AAGG ATGGCC  
||||| || ||| |||||  
TTCGGAC CC TTCC TACCGG  
C\_ T C

GAM1150 KIAA1128 3' ATCACCGAACAGGCTT 68472 CA AAG  
AAGCCTGT GGT GAT  
||||| ||| |||  
TTCGGACA CCA CTA  
AG \_

GAM1150 KIAA1266 3' GCCACGTGTGCCAAGCAGGCTT 66121 CA AGGA  
AAGCCTGT GGTA TGGC  
||||| ||| |||  
TTCGGACG CCGT ACCG  
AA GTGC

GAM1150 KIAA1522 3' GCCATCCTCCAGGGC 64975 GTCA TA  
GCCT GG AGGATGGC  
||| || |||||  
CGGG CC TCCTACCG  
A\_ \_

GAM1150 MGC11386 3' GCCCTCCATCCCCTGACAGGC 51953 TAA\_ T  
GCCTGTCAGG GGA GGC  
||||| ||| |||  
CGGACAGTCC CCT CCG  
CCTA C

GAM1150 MGC12921 3' GGCCACCCCTCCCGGAGACAAG 63777 C A\_ TAA A  
C GC TGTC GG GG TGGCC  
|| ||| || |||||

CG ACAG CC CC ACCGG  
 A AGG CTC C  
 GAM1150 MGC15906 5' GGCCAAGTTCCTGACAGCCT 51819 C TAAGGA  
 AG CTGTCAGG TGGCC  
 || ||||| ||||  
 TC GACAGTCC ACCGG  
 C TTGA\_\_  
 GAM1150 N4BP3 3' GCCCCTCCCCAACAGGCTT 66264 CA TA AT  
 AAGCCTGT GG AGG GGC  
 ||||| || ||| |||  
 TTCGGACA CC TCC CCG  
 A\_ CC \_  
 GAM1150 OS4 3' CCTTTCCTAACAGACTT 19180 C C T  
 AAG CTGT AGG AAGG  
 ||| ||| ||| |||  
 TTC GACA TCC TTCC  
 A A T  
 GAM1150 POFUT1 3' GCCATCCCCACTGCCTGGC 70471 A\_\_  
 GTCAGGTA GGATGGC  
 ||||| |||||  
 CGGTCCGT CCTACCG  
 CACC  
 GAM1150 RAB10 5' GGCCATTTTGTCCCGAC 85176 A TA  
 GTC GG AGGATGGCC  
 ||| || |||||  
 CAG CC TTTTACCGG  
 C TG  
 GAM1150 SCAMP-4 3' ATCTCACCTGGCAGGC 54389 AA  
 GCCTGTCAGGT GGAT  
 ||||| |||  
 CGGACGGTCCA TCTA  
 C\_  
 GAM1150 LOC132241 5' GGCCATCTGCGTTCCTGCAGGC 75050 T TAA\_\_  
 TT AAGCCTG CAGG GGATGGCC  
 ||||| ||| |||||  
 TTCGGAC GTCC TCTACCGG  
 \_ TTGCG  
 GAM1150 LOC133686 3' CCTCCCCTAACAGGCTT 75119 C TA  
 AAGCCTGT AGG AGG  
 ||||| ||| |||  
 TTCGGACA TCC TCC  
 A CC  
 GAM1150 LOC143153 3' CCCCACCTGACAGGCT 76464 AA  
 AGCCTGTCAGGT GG  
 ||||| ||| ||  
 TCGGACAGTCCA CC  
 CC  
 GAM1150 LOC143154 3' CCCCACCTGACAGGCT 76480 AA  
 AGCCTGTCAGGT GG  
 ||||| ||| ||

TCGGACAGTCCA CC  
CC  
GAM1150 LOC147353 3' ATTTTTCACATAACAGGCTT 84007 CAG \_  
AAGCCTGT GT AAGGAT  
||||||| || |||||  
TTCGGACA CA TTTTTA  
ATA C  
GAM1150 LOC148114 5' CCATCCCCTCTGACCTGACAGA 78660 \_ AA\_\_\_\_  
GC GC CTGTCAGGT GGATGG  
|| ||||| |||||  
CG GACAGTCCA CCTACC  
A GTCTCC  
GAM1150 LOC150568 5' GCCAGGTCTGACAGACT 85044 C TAAGGA  
AG CTGTCAGG TGGC  
|| ||||| |||  
TC GACAGTCT ACCG  
A GG\_\_\_\_  
GAM1150 LOC151126 3' TATTTTCCTGACAGACTT 80131 C TA  
AAG CTGTCAGG AGGATG  
||| ||||| |||||  
TTC GACAGTCC TTTTAT  
A \_  
GAM1150 LOC158378 5' GCCACATCTAGACAGGCTT 86791 \_ AAGGA  
AAGCCTGTC AGGT TGGC  
||||||| ||| |||  
TTCGGACAG TCTA ACCG  
A C\_\_\_\_  
GAM1150 LOC197201 3' GGCCAGTGGACCTGACAG 87941 AAGGA  
CTGTCAGGT TGGCC  
||||||| |||||  
GACAGTCCA ACCGG  
GGTG\_  
GAM1150 LOC197273 5' GCCATGCACCTGACAGCCT 67399 C AAGG  
AG CTGTCAGGT ATGGC  
|| ||||| |||||  
TC GACAGTCCA TACCG  
C CG\_\_\_\_  
GAM1150 LOC199991 3' GGCCATCCTCTGCCAGATTC 89914 T A \_  
C GTC GGTA AGGATGGCC  
| ||| ||| |||||  
C TAG CCGT TCCTACCGG  
T A C  
GAM1150 LOC200918 3' CCATCCTTATGTAGACA 88939 AG\_  
TGTC GTAAGGATGG  
||| |||||  
ACAG TATTCCTACC  
ATG  
GAM1150 LOC201116 5' GGCCATCCCCCTGCACAGACT 88104 C \_ TAA  
AG CTGT CAGG GGATGGCC  
|| ||| ||| |||||

	TC GACA GTCC CCTACCGG	
	A C C__	
GAM1150 LOC204285 5'	CCATCCCCAAGGAGCAGGTTT 89458	CAGGTAA
	AAGCCTGT GGATGG	
	TTTGGACG CCTACC	
	AGGAACC	
GAM1150 LOC219294 3'	CCCCGCCTGACAGGCT 93006	AA
	AGCCTGTCAGGT GG	
	TCGGACAGTCCG CC	
	CC	
GAM1150 LOC219295 3'	CCCCGCCTGACAGGCT 92990	AA
	AGCCTGTCAGGT GG	
	TCGGACAGTCCG CC	
	CC	
GAM1150 LOC220074 5'	GCCATCAGTGACAGGCT 59274	GGTAAG
	AGCCTGTCA GATGGC	
	TCGGACAGT CTACCG	
	GA__	
GAM1150 LOC220739 3'	GCCATGAGACCCACAGACTT 92931	C CA AAGG
	AAG CTGT GGT ATGGC	
	TTC GACA CCA TACCG	
	A C_ GAG_	
GAM1150 LOC220883 3'	GCCATCCCCCTCAGGACT 91262	_ TC TAA
	AG CCTG AGG GGATGGC	
	TC GGAC TCC CCTACCG	
	A _ C__	
GAM1150 LOC221143 3'	GCCATCGGTGACAGGCT 93569	GGTAAG
	AGCCTGTCA GATGGC	
	TCGGACAGT CTACCG	
	GG__	
GAM1150 LOC222614 5'	GGCCATCCTCAGACACTGAC 94358	_ A__
	GTCAG GT AGGATGGCC	
	CAGTC CA TCCTACCGG	
	A GAC	
GAM1150 LOC222662 5'	GGCACCTGGCAAGCTT 92845	C AAGGATG
	AAGC TGTCAGGT GCC	
	TTCG ACGGTCCA CGG	
	A _____	
GAM1150 LOC254122 3'	GGCTGTTCCCCAACAGGC 94753	CA TAA
	GCCTGT GG GGATGGCC	

CGGACA CC CTTGTCGG  
 AC \_\_\_\_  
 GAM1150 LOC254848 3' GGCCATCCTCCAGACA 97092 A TA  
 TGTC GG AGGATGGCC  
 ||||| || |||||  
 ACAG CC TCCTACCGG  
 A \_\_\_\_  
 GAM1150 LOC257054 3' GCCATCCTGGACAGGC 95662 AGGTA  
 GCCTGTC AGGATGGC  
 ||||| |||||  
 CGGACAG TCCTACCG  
 G\_\_\_\_  
 GAM1151 CASP3 3' ACATACTCCTTCCATCA 15095 C A  
 TG ATGGAA GAGTATGT  
 || ||||| |||||  
 AC TACCTT CTCATACA  
 \_ C  
 GAM1151 CASP3 3' ACATACTCCTTCCATCA 52191 C A  
 TG ATGGAA GAGTATGT  
 || ||||| |||||  
 AC TACCTT CTCATACA  
 \_ C  
 GAM1151 MSL3L1 3' AAGAATACTCAGATTTCCAT 54359 GAGTAT  
 ATGGAAA GTATTCTT  
 ||||| |||||  
 TACCTTT CATAAGAA  
 AGACT\_  
 GAM1151 SACM1L 3' GCATACTTTTCCACACA 25824 CA A  
 TG TGGAA GAGTATGT  
 || ||||| |||||  
 AC ACCTT TTCATACG  
 AC \_  
 GAM1151 SURF6 3' TAAGAATACATACTCTTTCCAT 22192 III  
 GCA GCATGGAAAGAGTATGTATTCTT A  
 ||||| ||||| |||||  
 CGTACCTTTCTCATACATAAGAA T  
 III  
 GAM1151 UCHL1 3' AATATATACCCCCCATGCA 14814 AAAGA  
 TGCATGG GTATGTATT  
 ||||| |||||  
 ACGTACC CATATATAA  
 CCCC\_  
 GAM1151 DYRK4 5' AAGAATACGGTAAGCTTCCCA 64225 A AG \_  
 TGG AAG TAT GTATTCTT  
 ||| ||| ||| |||||  
 ACC TTC ATG CATAAGAA  
 C GA G  
 GAM1151 FLJ10276 3' ACATACTCTGTCCATACA 35961 C A  
 TG ATGGA AGAGTATGT  
 || ||||| |||||

AC TACCT TCTCATACA  
 A G  
 GAM1151 KIAA0678 3' AAGAATATTTCCCTCTCCTGCA 66851 T AA TAT\_  
 TGCA GGA GAG GTATTCTT  
 |||| ||| ||| |||||  
 ACGT CCT CTC TATAAGAA  
 \_ \_ CCTT  
 GAM1151 SGK1 3' AAGAACAAGCATCCCTTCCATG 25138 A\_ \_ A AT  
 TA TGCATGGAA GA GT TGT TCTT  
 ||||| || || ||| |||  
 ATGTACCTT CT CG ACA AGAA  
 CC A A \_  
 GAM1151 LOC148638 3' CACTCTCTTTCCACGCA 78919 A TA  
 TGC TGGAAAGAG TG  
 || ||||| ||  
 ACG ACCTTTCTC AC  
 C TC  
 GAM1151 LOC196385 3' ATCTCTTTCCATACA 87654 C T  
 TG ATGGAAAGAG AT  
 || ||||| ||  
 AC TACCTTTCTC TA  
 A \_  
 GAM1151 LOC221178 3' ATACTCCTTCATGCA 93526 AA  
 TGCATGGA GAGTAT  
 ||||| |||||  
 ACGTACTT CTCATA  
 C\_  
 GAM1151 LOC221405 3' AGAATTGCTTTCCATGCA 93880 AGTATGT  
 TGCATGGAAAG ATTCT  
 ||||| |||||  
 ACGTACCTTTC TAAGA  
 GT\_\_\_\_  
 GAM1152 BAZ2A 5' ACACCAACCTTTACGTG 25588 AC A  
 TACGTAAAG TG TGT  
 ||||| || |||  
 GTGCATTTC AC ACA  
 CA C  
 GAM1152 HIS1 3' ACCCTGTACATCCCCTTGACAC 21310 A\_ ACT  
 GT AAG GATGTACAGGGT  
 || ||| |||||  
 CA TTC CTACATGTCCCA  
 CG CC\_  
 GAM1152 TNC 3' ACCAAAGACATCAGTCTCCAAC 9285 AA\_ ACAG  
 GT AGACTGATGT GGT  
 || ||||| |||  
 CA TCTGACTACA CCA  
 ACC GAAA  
 GAM1152 MGC15875 5' TTGACATCAGTCCCTAC 51912 AA A  
 GTA GACTGATGT CAG  
 || ||||| |||

			CAT CTGACTACA GTT		
			CC _		
GAM1152	SOX6	3'	ACCCTGACATTCACTTAAC 52824	A	_ A
			GT AAGACTGA TGT CAGGGT		
			CA TTCTGACT ACA GTCCCA		
			A T _		
GAM1153	A1BG	3'	GTGATCCTCCACCTCA 55427	A	
			TGAGGT GGAGGATCAT		
			ACTCCA CTCCTAGTG		
			C		
GAM1153	A1BG	3'	GTGATCCTCCCGCCTCA 55428	TA	
			TGAGG GGAGGATCAT		
			ACTCC CTCCTAGTG		
			GC		
GAM1153	AIM1	3'	GTGATCCTCCACCTCA 91825	A	
			TGAGGT GGAGGATCAT		
			ACTCCA CTCCTAGTG		
			C		
GAM1153	ALOX15	3'	ATGATCCTCCACCTCA 6683	A	
			TGAGGT GGAGGATCAT		
			ACTCCA CTCCTAGTA		
			C		
GAM1153	BCL10	3'	GTGATCCTCTCACCTCA 14061	AG	
			TGAGGT GAGGATCAT		
			ACTCCA CTCCTAGTG		
			CT		
GAM1153	EFEMP1	3'	AAATTACCCTCCTACCCA 38152	A	ATCA
			TG GGTAGGAGG TAGTTT		
			AC CCATCCTCC ATTAAA		
			_ C__		
GAM1153	EFEMP1	3'	AAATTACCCTCCTACCCA 14637	A	ATCA
			TG GGTAGGAGG TAGTTT		
			AC CCATCCTCC ATTAAA		
			_ C__		
GAM1153	GCN5L1	3'	CTATCCCTCCTACCTCA 7637		ATC
			TGAGGTAGGAGG ATAG		
			ACTCCATCCTCC TATC		
			C__		
GAM1153	GLTSCR1	5'	GTGATCCTCTCACCTCA 31675	AG	
			TGAGGT GAGGATCAT		

			ACTCCA CTCCTAGTG		
			CT		
GAM1153	HSPA5	3'	GTGATCCTTCCACCTCA	18082	A
			TGAGGT GGAGGATCAT		
			ACTCCA CTCCTAGTG		
			C		
GAM1153	HUNK	3'	GTGATCCTCCCATCTCA	27460	A
			TGAGGT GGAGGATCAT		
			ACTCTA CCTCCTAGTG		
			C		
GAM1153	ICAM1	3'	GTGATCCTCCCACCTCA	71577	A
			TGAGGT GGAGGATCAT		
			ACTCCA CCTCCTAGTG		
			C		
GAM1153	JRK	3'	GTGATCCTCCCGCCCCA	86537	A TA
			TG GG GGAGGATCAT		
			AC CC CTCCTAGTG		
			C GC		
GAM1153	MHC2TA	3'	GTGATCCTCCCACCTCA	4185	A
			TGAGGT GGAGGATCAT		
			ACTCCA CTCCTAGTG		
			C		
GAM1153	MPP3	3'	AAACTATGGCTACGTCA	8634	G GAGGA
			TGA GTAG TCATAGTTT		
			ACT CATC GGTATCAAA		
			G _____		
GAM1153	NQO1	3'	GTGATCCGCCTACCTCA	6164	A
			TGAGGTAGG GGATCAT		
			ACTCCATCC CCTAGTG		
			G		
GAM1153	NR1I2	5'	GCTGTCCTCCTACCCCA	13970	A CAT
			TG GGTAGGAGGAT AGT		
			AC CCATCCTCCTG TCG		
			C _____		
GAM1153	OXTR	3'	GATCCTCCTGACCTCA	6208	—
			TGAGGT AGGAGGATC		
			ACTCCA TCCTCCTAG		
			G		
GAM1153	PCDHA9	3'	ATGATCCTCCCGCCTCA	25758	TA
			TGAGG GGAGGATCAT		



			ACTCC CCTCCTAGTA		
			GC		
GAM1153	PRIM2A	3'	GTGATCCTCCTACCTCA 6273		
			TGAGGTAGGAGGATCAT		
			ACTCCATCCTCCTAGTG		
GAM1153	TAF12	3'	GAATAAAGCCTCCTACCCCA 18919	A	ATCATAGT
			TG GGTAGGAGG TTC		
			AC CCATCCTCC AAG		
			C GAAAT__		
GAM1153	TNFRSF11A	3'	GTGATCCTCCCACCTCA 13855	A	
			TGAGGT GGAGGATCAT		
			ACTCCA CCTCCTAGTG		
			C		
GAM1153	TNFRSF9	3'	GTGATCCTCCTGCCTCA 7792		
			TGAGGTAGGAGGATCAT		
			ACTCCGTCCTCCTAGTG		
GAM1153	TNFSF9	3'	GTGATCCTCCCATCTCA 13756	A	
			TGAGGT GGAGGATCAT		
			ACTCTA CCTCCTAGTG		
			C		
GAM1153	UMPS	3'	GTGATCCTCCCACCTCA 4555	A	
			TGAGGT GGAGGATCAT		
			ACTCCA CCTCCTAGTG		
			C		
GAM1153	VHL	3'	TGTGATCCACCCACCTCA 5091	A A	
			TGAGGT GG GGATCATA		
			ACTCCA CC CCTAGTGT		
			C A		
GAM1153	ANKRD6	3'	GTGATCCTCCTGCCTCA 30088		
			TGAGGTAGGAGGATCAT		
			ACTCCGTCCTCCTAGTG		
GAM1153	C21orf67	5'	GAGCGATCCTCCCGCCTCA 54211	TA	ATA
			TGAGG GGAGGATC GTTT		
			ACTCC CCTCCTAG CGAG		
			GC ____		
GAM1153	C22orf19	3'	GTGATCCTCCCACCTC 13430	A	
			GAGGT GGAGGATCAT		

			CTCCA CCTCCTAGTG		
			C		
GAM1153	C22orf19	3'	GTGATCCTCCTGCCTCA	13431	
			TGAGGTAGGAGGATCAT		
			ACTCCGTCCTCCTAGTG		
GAM1153	CLDN1	3'	TGATCTTCCCACCTCA	40850	A
			TGAGGT GGAGGATCA		
			ACTCCA CTTCTAGT		
			C		
GAM1153	CLSTN3	3'	TATGATCGCCCCACCTCA	28212	A AG
			TGAGGT GG GATCATA		
			ACTCCA CC CTAGTAT		
			C CG		
GAM1153	CPSF2	3'	GTGATTCTCCCACCTCA	61595	A
			TGAGGT GGAGGATCAT		
			ACTCCA CCTCTTAGTG		
			C		
GAM1153	CTPS2	3'	AAACCCATACTACTACCTCA	39081	G GATCATA
			TGAGGTAG AG GTTT		
			ACTCCATC TC CAAA		
			A ATACC__		
GAM1153	DCOHM	3'	GTGATCCTCCCACCTTA	49609	A
			TGAGGT GGAGGATCAT		
			ATTCCA CTCCTAGTG		
			C		
GAM1153	DRIM	3'	GTGATCCTCTCACCTCA	27180	AG
			TGAGGT GAGGATCAT		
			ACTCCA CTCCTAGTG		
			CT		
GAM1153	FLB6421	3'	GTGATCCTCCTACCTCA	39230	
			TGAGGTAGGAGGATCAT		
			ACTCCATCCTCCTAGTG		
GAM1153	FLJ10297	3'	GTGATCCTCCTGCCTCA	35983	
			TGAGGTAGGAGGATCAT		
			ACTCCGTCCTCCTAGTG		
GAM1153	FLJ10535	3'	TGTGATCCACCCACCTCA	36254	A A
			TGAGGT GG GGATCATA		

			ACTCCA CC CCTAGTGT		
			C A		
GAM1153	FLJ10607	3'	ATGATCCTTCCACCTCA	77104	A
			TGAGGT GGAGGATCAT		
			ACTCCA CTCCTAGTA		
			C		
GAM1153	FLJ10607	3'	GTGATCCTCCACCTCA	77124	A
			TGAGGT GGAGGATCAT		
			ACTCCA CCTCCTAGTG		
			C		
GAM1153	FLJ10724	3'	GTCATCCTCCTACTCA	36505	G C
			TGAG TAGGAGGAT AT		
			ACTC ATCCTCCTA TG		
			— C		
GAM1153	FLJ10847	3'	GTGATCCTCCACCTCA	36754	A
			TGAGGT GGAGGATCAT		
			ACTCCA CCTCCTAGTG		
			C		
GAM1153	FLJ14442	3'	TATGATACTCCTACCCCA	51374	A G
			TG GGTAGGAG ATCATA		
			AC CCATCCTC TAGTAT		
			C A		
GAM1153	FLJ20273	3'	TGAAACTATGACCCAGTATTCT	38731	TAGGA A
	TA		TGAGG GG TCATAGTTTCA		
			ATTCT CC AGTATCAAAGT		
			TATGA C		
GAM1153	FLJ23185	3'	GTGATCCTCCACCTC	46834	A
			GAGGT GGAGGATCAT		
			CTCCA CTCCTAGTG		
			C		
GAM1153	FLJ23556	3'	TGTGATCCTCCCGCCTCA	45961	TA
			TGAGG GGAGGATCATA		
			ACTCC CTCCTAGTGT		
			GC		
GAM1153	FLJ23563	3'	GTGATCCTCCACCTC	67596	A
			GAGGT GGAGGATCAT		
			CTCCA CTCCTAGTG		
			C		
GAM1153	HGC6.1.1	3'	TGAAAGGCGCCCTCCTACCT	26832	ATCATAG
			AGGTAGGAGG TTCA		

			TCCATCCTCC	AAAGT		
			CGCGG__			
GAM1153	KIAA0446	5'	GTGATCCTCCCACCTCA	68876	A	
			TGAGGT GGAGGATCAT			
			ACTCCA CCTCCTAGTG			
			C			
GAM1153	KIAA0447	3'	ATGATCCTCCCACCTCA	71666	A	
			TGAGGT GGAGGATCAT			
			ACTCCA CCTCCTAGTA			
			C			
GAM1153	KIAA0894	3'	TGAAACTACTCTCCCACCTTA	29709	A	ATCA
			TGAGGT GGAGG TAGTTTCA			
			ATTCCA CCTCT ATCAAAGT			
			C C__			
GAM1153	KIAA0924	3'	TGTGATCCGCCCACCTCA	29726	A	A
			TGAGGT GG GGATCATA			
			ACTCCA CC CCTAGTGT			
			C G			
GAM1153	KIAA1054	3'	GTGATTCTCCCACCTCA	68446	A	
			TGAGGT GGAGGATCAT			
			ACTCCA CCTCTTAGTG			
			C			
GAM1153	KIAA1280	5'	GTGACCCTCCTGCCTCA	69728	A	
			TGAGGTAGGAGG TCAT			
			ACTCCGTCCTCC AGTG			
			C			
GAM1153	KIAA1373	3'	TGAAACTAAATTCCTACCCA	70955	A	GATCA
			TG GGTAGGAG TAGTTTCA			
			AC CCATCCTT ATCAAAGT			
			_ AA__			
GAM1153	KIAA1649	3'	GTGATCCTCCCACCTCA	50278	A	
			TGAGGT GGAGGATCAT			
			ACTCCA CCTCCTAGTG			
			C			
GAM1153	KIAA1671	3'	GTGATTCTCCCACCTCA	65686	A	
			TGAGGT GGAGGATCAT			
			ACTCCA CCTCTTAGTG			
			C			
GAM1153	KIAA1727	3'	GTGATCCTCCCACCTCA	64062	A	
			TGAGGT GGAGGATCAT			

			ACTCCA CCTCCTAGTG			
			C			
GAM1153	KIAA1727	3'	GTGATCCTCCACCTCA	64061	A	
			TGAGGT GGAGGATCAT			
			ACTCCA CCTCCTAGTG			
			C			
GAM1153	KIAA1762	3'	TGATCCTCCTCCTCA	63793	T	
			TGAGG AGGAGGATCA			
			ACTCC TCCTCCTAGT			
			—			
GAM1153	KIAA1821	3'	GTGATCCTCCACCTCA	71794	A	
			TGAGGT GGAGGATCAT			
			ACTCCA CCTCCTAGTG			
			C			
GAM1153	KRTHA3B	3'	ACTTGATCCTCCTCACCCCA	9644	A	_ T
			TG GGT AGGAGGATCA AGT			
			AC CCA TCCTCCTAGT TCA			
			C C —			
GAM1153	MGC10200	3'	GTGATCCTCCACCTCA	58991	A	
			TGAGGT GGAGGATCAT			
			ACTCCA CCTCCTAGTG			
			C			
GAM1153	MGC13159	3'	GTGATCCTCCTGCCTCA	51930		
			TGAGGTAGGAGGATCAT			
			ACTCCGTCCTCCTAGTG			
GAM1153	MGC2488	3'	GTGATCCTCCTGCCTCA	43875		
			TGAGGTAGGAGGATCAT			
			ACTCCGTCCTCCTAGTG			
GAM1153	MGC3113	3'	TGTGATCCTCCACCTCA	43853	A	
			TGAGGT GGAGGATCATA			
			ACTCCA CCTCCTAGTGT			
			C			
GAM1153	PELI1	5'	GTGATCCTCCTGCCTCA	40278		
			TGAGGTAGGAGGATCAT			
			ACTCCGTCCTCCTAGTG			
GAM1153	PRO0611	3'	TGGGAGTTGATCCTCCACCCCA	26015	A A	TAG TT
			TG GGT GGAGGATCA T CA			

		AC CCA CCTCCTAGT A GT	
		_ C TG_GG	
GAM1153	SARM	3' GTGATCCTCCTGCCTCA 30615	
		TGAGGTAGGAGGATCAT	
		ACTCCGTCCTCCTAGTG	
GAM1153	SCYA1	3' GAAACTACCAGCCCTACACCA 11445	AG A__ ATCA
		TG GTAGG GG TAGTTTC	
		AC CATCC CC ATCAAAG	
		CA CGA ____	
GAM1153	SCYA16	3' GTGATCCTCCCACCCCA 15965	A A
		TG GGT GGAGGATCAT	
		AC CCA CTCCTAGTG	
		C C	
GAM1153	ZNF177	5' GTGATCCTCCTGCCTCA 12901	
		TGAGGTAGGAGGATCAT	
		ACTCCGTCCTCCTAGTG	
GAM1153	LOC113026	3' GTGATCCTCCTGCCCA 55906	A
		TG GGTAGGAGGATCAT	
		AC CCGTCCTCCTAGTG	
		C	
GAM1153	LOC130639	5' GTGATCCTCCCACCTCA 74976	A
		TGAGGT GGAGGATCAT	
		ACTCCA CTCCTAGTG	
		C	
GAM1153	LOC134266	3' GTGATCCTCCCACCTCA 75167	A
		TGAGGT GGAGGATCAT	
		ACTCCA CTCCTAGTG	
		C	
GAM1153	LOC135398	3' GTGATCCTCCCACCTCA 75936	A
		TGAGGT GGAGGATCAT	
		ACTCCA CTCCTAGTG	
		C	
GAM1153	LOC144305	3' TGATCCTCCCACCTCA 83039	A
		TGAGGT GGAGGATCA	
		ACTCCA CTCCTAGT	
		C	
GAM1153	LOC144519	5' GTGATCCTCCTGCCTCA 76873	
		TGAGGTAGGAGGATCAT	

ACTCCGTCCTCCTAGTG

GAM1153 LOC146599 5' GTGATCCTCCTGCCTCA 78026  
TGAGGTAGGAGGATCAT  
|||||  
ACTCCGTCCTCCTAGTG

GAM1153 LOC147343 5' GTGATCCTCCCACCTCA 84002 A  
TGAGGT GGAGGATCAT  
|||||  
ACTCCA CCTCCTAGTG  
C

GAM1153 LOC147935 3' GTGATCCTCCTGCCTCA 84082  
TGAGGTAGGAGGATCAT  
|||||  
ACTCCGTCCTCCTAGTG

GAM1153 LOC148137 3' GAAACCTTGGGCTCCTACCTCA 58429 GA TA  
TGAGGTAGGAG TCA GTTTC  
||||| |||  
ACTCCATCCTC GGT CAAAG  
G\_ TC

GAM1153 LOC149734 3' ATGATCCTCCTGCCTCA 84631  
TGAGGTAGGAGGATCAT  
|||||  
ACTCCGTCCTCCTAGTA

GAM1153 LOC151201 3' TGTGATCCTCCCATCTCA 85297 A  
TGAGGT GGAGGATCATA  
|||||  
ACTCTA CCTCCTAGTGT  
C

GAM1153 LOC151826 3' GTGATCCTCCTGCCTCA 80362  
TGAGGTAGGAGGATCAT  
|||||  
ACTCCGTCCTCCTAGTG

GAM1153 LOC151877 3' ATGATCTTCCCACCCCA 85501 A A  
TG GGT GGAGGATCAT  
|| |||  
AC CCA CCTTCTAGTA  
C C

GAM1153 LOC153443 3' GTGATCCTCCCACCTC 80825 A  
GAGGT GGAGGATCAT  
|||||  
CTCCA CCTCCTAGTG  
C

GAM1153 LOC155434 3' TATGATCCTCCACCCCA 86406 A A  
TG GGT GGAGGATCATA  
|| |||

AC CCA CCTCCTAGTAT  
 C \_  
 GAM1153 LOC162461 5' GTGATCCTCCTACCTCA 82364 A  
 TGAGGTAGGAGGATCAT  
 |||||  
 ACTCCATCCTCCTAGTG

GAM1153 LOC200268 3' GTGATCCTCCCACCTCA 88686 A  
 TGAGGT GGAGGATCAT  
 ||||| |||||  
 ACTCCA CCTCCTAGTG  
 C

GAM1153 LOC200268 3' GTGATCCTCCCACCTCA 88687 A  
 TGAGGT GGAGGATCAT  
 ||||| |||||  
 ACTCCA CCTCCTAGTG  
 C

GAM1153 LOC200845 5' TGACCTGGTGATCCTCCTGCCT 88909 AGTT  
 CA TGAGGTAGGAGGATCAT TCA  
 ||||| ||||| ||  
 ACTCCGTCCTCCTAGTG AGT  
 GTCC

GAM1153 LOC200942 3' TGAAACCTTCCTACCCTACCTA 88949 \_ ATCATA\_  
 CCTCA TGAGGTAGG AGG GTTTCA  
 ||||| || |||||  
 ACTCCATCC TCC CAAAGT  
 A CATCCTTC

GAM1153 LOC203339 3' TGTGATCCACCCACCTCA 90554 A A  
 TGAGGT GG GGATCATA  
 ||||| || |||||  
 ACTCCA CC CCTAGTGT  
 C A

GAM1153 LOC204804 3' GTGATCCTCCCAGCTCA 89483 GTA  
 TGAG GGAGGATCAT  
 |||| |||||  
 ACTC CCTCCTAGTG  
 GAC

GAM1153 LOC219529 5' GTGATCCTCCTGCCTCA 92973  
 TGAGGTAGGAGGATCAT  
 ||||| |||||  
 ACTCCGTCCTCCTAGTG

GAM1153 LOC219673 5' GTGATCCTCCCGCCTCA 93038 TA  
 TGAGG GGAGGATCAT  
 |||| |||||  
 ACTCC CTCCTAGTG  
 GC

GAM1153 LOC221814 5' GTGATCCTCCTGCCTCA 93945  
 TGAGGTAGGAGGATCAT  
 ||||| |||||



ACTCCGTCCTCCTAGTG

GAM1153 LOC221815 5' GTGATCCTCCTGCCTCA 93938  
TGAGGTAGGAGGATCAT  
|||||  
ACTCCGTCCTCCTAGTG

GAM1153 LOC254100 3' GTGATCCTCACACCTCA 96415 AG  
TGAGGT GAGGATCAT  
|||||  
ACTCCA CTCCTAGTG  
CA

GAM1153 LOC254685 3' GTGATCCTCCCGCCTCA 96487 TA  
TGAGG GGAGGATCAT  
|||||  
ACTCC CTCCTAGTG  
GC

GAM1153 LOC51193 3' GAGCAATCCTCCCACTTCA 32905 A CATA  
TGAGGT GGAGGAT GTTT  
|||||  
ACTTCA CCTCCTA CGAG  
C A\_\_

GAM1153 LOC51336 3' GTGATCCTCTCACCTCA 33580 AG  
TGAGGT GAGGATCAT  
|||||  
ACTCCA CTCCTAGTG  
CT

GAM1153 LOC57149 3' AAATATGTACCACTCTCA 39933 \_ A AGGAT  
TGAG GT GG CATAGTTT  
||| |||  
ACTC CA CC GTATCAAA  
T \_ AT\_\_

GAM1153 LOC90485 3' GTGATTCCCCTACCTCA 63023 A  
TGAGGTAGG GGATCAT  
|||||  
ACTCCATCC CTTAGTG  
C

GAM1153 LOC91056 3' GTGATCCTCCCATCTCA 94762 A  
TGAGGT GGAGGATCAT  
|||||  
ACTCTA CCTCCTAGTG  
C

GAM1153 LOC91963 3' TGATCCTCCACCTCA 67701 A  
TGAGGT GGAGGATCA  
|||||  
ACTCCA CCTCCTAGT  
C

GAM1153 LOC92148 5' TGTGATCCTCCCGCCTCA 68338 TA  
TGAGG GGAGGATCATA  
|||||

ACTCC CCTCCTAGTGT  
 GC  
 GAM1153 LOC92609 3' GTGACCCTCCTGCCTCA 72849 A  
 TGAGGTAGGAGG TCAT  
 |||||  
 ACTCCGTCCTCC AGTG  
 C  
 GAM1154 ADH4 3' TGTTTATGAATAGAATCA 5412 C GCAG  
 TGA TCTGTTCA GACA  
 |||||  
 ACT AGATAAGT TTGT  
 A AT\_\_  
 GAM1154 APG5L 3' TTTGCCTGAACAGAATCA 16765 C \_  
 TGA TCTGTTTCAG CAGG  
 |||||  
 ACT AGACAAGTC GTTT  
 A C  
 GAM1154 ATP8A2 3' TGTCTGTCCTGCCTCAGTGCA 93521 ACT TTCA A  
 TG CTG GCAGGACA ACA  
 || |||||  
 AC GAC CGTCCTGT TGT  
 GT\_ TC\_\_ C  
 GAM1154 BSN 3' TGTCTGTCCTGCCTCAGTGCA 12931 A TG CA  
 TG CTC TT GCAGGACA  
 || || |||||  
 AC GAG GA CGTCCTGT  
 \_ GT \_  
 GAM1154 EGFL5 5' TGCTTGCTAAGACAGAGTCA 86629 C\_ A  
 TGACTCTGTT AGCAGG CA  
 ||||| |||||  
 ACTGAGACAG TCGTTC GT  
 AA \_  
 GAM1154 EIF4EBP2 3' TTTGTCCCTCGGGACAGAGCA 14593 A AGCA  
 TG CTCTGTTT GGACAAA  
 ||||| |||||  
 AC GAGACAGG CCTGTTT  
 \_ GCTC  
 GAM1154 EYA3 5' CCCTGGACAGACTCA 8810 C CA  
 TGA TCTGTTTCAG GG  
 ||||| ||  
 ACT AGACAGGTC CC  
 C \_  
 GAM1154 GEMIN5 3' TGCTTATTGAACAGATCA 89167 C C\_ A  
 TGA TCTGTTTCAG AGG CA  
 ||||| |||||  
 ACT AGACAAGTT TTC GT  
 \_ TA \_  
 GAM1154 GJA4 3' TGCCTGAGCACAGACAGAGTCA 59369 CAG\_\_ A  
 TGACTCTGTT CAGG CA  
 ||||| |||||

		ACTGAGACAG	GTCC GT		
		ACACGA	_		
GAM1154	MAGEA10	5'	CCTGCTACCCTGATCAGAGTCA 40736	T	_____
			TGACTCTG TCA GCAGG		
			ACTGAGAC AGT CGTCC		
			T CCCAT		
GAM1154	MAGEA12	5'	CCTGCTGCCCTGACCAGAGTCA 18110	-	_____
			TGACTCTG TT CAGCAGG		
			ACTGAGAC AG GTCGTCC		
			C TCCC		
GAM1154	MAGEA2	5'	TGCCTGCTGCCCTGACCAGAGT 60491	-	_____ A
	CA		TGACTCTG TT CAGCAGG CA		
			ACTGAGAC AG GTCGTCC GT		
			C TCCC		
GAM1154	MAGEA3	5'	CCTGTTGCCCTGACCAGAGTCA 18101	T	_____
			TGACTCTG TCAG CAGG		
			ACTGAGAC AGTC GTCC		
			C CCGTT		
GAM1154	MAGEA4	5'	TGCCTGCTGCCCTGAGCAGAGT 9884	_____	A
	CA		TGACTCTGTTCA GCAGG CA		
			ACTGAGACGAGT CGTCC GT		
			CCCGT		
GAM1154	MBD3	3'	GTCCTCTACAGAGTC 14097	TC	C
			GACTCTGT AG AGGAC		
			CTGAGACA TC TCCTG		
			_____		
GAM1154	PTPRF	3'	TTGTCCTCAGAGCA 11109	A	TTCAGC A
			TG CTCTG AGGACA A		
			AC GAGAC TCCTGT T		
			C		
GAM1154	PTPRF	3'	TTGTCCTCAGAGCA 55271	A	TTCAGC A
			TG CTCTG AGGACA A		
			AC GAGAC TCCTGT T		
			C		
GAM1154	PYGO2	3'	CCTGCTGAGCAGAGCCA 63984	A	
			TG CTCTGTT CAGCAGG		
			AC GAGACGAGTCGTCC		
			C		
GAM1154	TCTA	3'	CTACTGCACAGAGTCA 42237	T	C
			TGACTCTGT CAG AG		

ACTGAGACA GTC TC  
 C A  
 GAM1154 TEP1 3' TCAATTTGAACAGAGCA 23045 A CAG  
 TG CTCTGTTTCAG GA  
 || ||||| ||  
 AC GAGACAAGTT CT  
 \_ TAA  
 GAM1154 VAPB 3' TGGGACTGATGAACAGAGTCA 16442 G GA\_  
 TGA CTCTGTTTCAG CA  
 ||||| || ||  
 ACTGAGACAAGT GTC GT  
 A AGG  
 GAM1154 ZNF134 5' TCTTCTGAACAGAGCA 12848 A C  
 TG CTCTGTTTCAG AGGA  
 || ||||| ||||  
 AC GAGACAAGTC TTCT  
 \_ \_  
 GAM1154 ZNF264 3' CCTGCTGAACATCA 12748 CTC  
 TGA TGTTTCAGCAGG  
 ||| ||||| ||  
 ACT ACAAGTCGTCC  
 \_  
 GAM1154 AP1GBP1 3' TGCCTACGGCTGAACGGAGCCA 23400 A \_ A  
 TG CTCTGTTTCAGC AGG CA  
 || ||||| || ||  
 AC GAGGCAAGTCG TCC GT  
 C GCA \_  
 GAM1154 AP1GBP1 3' TGCCTACGGCTGAACGGAGCCA 54525 A \_ A  
 TG CTCTGTTTCAGC AGG CA  
 || ||||| || ||  
 AC GAGGCAAGTCG TCC GT  
 C GCA \_  
 GAM1154 AP1GBP1 3' TGCCTACGGCTGAACGGAGCCA 54537 A \_ A  
 TG CTCTGTTTCAGC AGG CA  
 || ||||| || ||  
 AC GAGGCAAGTCG TCC GT  
 C GCA \_  
 GAM1154 BTN2A1 3' TGCCCTGCACTCACAGGAGCCA 54344 A \_ TCA\_ A  
 TG CTC TGT GCAGG CA  
 || ||| || |||| ||  
 AC GAG ACA CGTCC GT  
 C G CTCA C  
 GAM1154 C20orf20 3' TGTTTGTCCCGCTGCAAG 36856 GTT A  
 CT CAGC GGACAAACA  
 || |||| ||||| ||  
 GA GTCG CCTGTTTGT  
 AC\_ C  
 GAM1154 DKFZp547I224 5' TTTGTAACTACACAGAGTCA 39561 TC CAGG  
 TGA CTCTGT AG ACAA  
 ||||| || ||||

ACTGAGACA TC TGTTC  
 CA AA\_\_  
 GAM1154 DKFZP586C1324 3' TCCTGTTGTCAACAGAGTC 69800 \_\_\_\_  
 GACTCTGTT CAGCAGGA  
 ||||| |||||  
 CTGAGACAA GTTGTCT  
 CT  
 GAM1154 FLJ10482 3' TCTGCTGAGCAAAGCCA 36166 A C  
 TG CT TGTT CAGCAGG  
 || || |||||  
 AC GA ACGAGTCGTCT  
 C A  
 GAM1154 FLJ14437 3' CTTGCCCCAGCAGAGCA 50827 A CA\_  
 TG CTCTGTT GCAGG  
 || ||||| ||||  
 AC GAGACGA CGTTC  
 \_ CCC  
 GAM1154 GFR 3' TGCTTGCTGAGGTGACAGAGTC 24476 \_\_\_\_ A  
 A TGACTCTGT TCAGCAGG CA  
 ||||| ||||| ||  
 ACTGAGACA AGTCGTTC GT  
 GTGG \_  
 GAM1154 GOLGA3 3' TGCTTACAAAACAGGGTCA 19722 C\_\_\_\_  
 TGACTCTGTT AGCA  
 ||||| ||||  
 ACTGGGACAA TCGT  
 AACAT  
 GAM1154 KIAA0322 3' TGTCTTCTGAGCAGAGCCA 92754 A C  
 TG CTCTGTT CAG AGGACA  
 || ||||| |||||  
 AC GAGACGAGTC TTCTGT  
 C \_  
 GAM1154 KIAA0450 5' TGTCTGTCCCCTGCCCCAGGTC 27654 T TT\_ CA A  
 A TGAC CTG CAG GGACA ACA  
 ||| ||| ||| ||||| |||  
 ACTG GAC GTC CCTGT TGT  
 \_ CCC C\_ C  
 GAM1154 KIAA0916 3' TGTTTGTCTGTATAAGAATTA 30494 C GTTCA  
 TGA TCT GCAGGACAAACA  
 ||| ||| |||||  
 ATT AGA TGTCTGT TTTGT  
 A ATA\_\_  
 GAM1154 KIAA1303 3' TGTTTGT TTTGAGACAAAATCA 66005 CTC CAG  
 TGA TGTT CAGGACAAACA  
 ||| ||| |||||  
 ACT ACAG GTTTTGT TTTGT  
 AAA A\_\_  
 GAM1154 KIAA1649 5' CTGGGCTAAACAGAGTTA 50259 C A\_  
 TGACTCTGTT AGC GG  
 ||||| ||| ||

ATTGAGACAA TCG TC  
 A GG  
 GAM1154 KIAA1922 3' TGTCCATCTAACAGAGTC 73645 C CA  
 GACTCTGTT AG GGACA  
 ||||| || ||||  
 CTGAGACAA TC CCTGT  
 \_ TA  
 GAM1154 MAFB 3' TTTGTCCTGCATCAGA 18418 TTCA  
 TCTG GCAGGACAAA  
 ||| |||||  
 AGAC CGTCCTGTTT  
 TA\_\_  
 GAM1154 MGC11271 5' TGCCCGCCCTGAGCAGAGCA 44243 A CA\_ A  
 TG CTCTGTTTCAG GG CA  
 || ||||| ||  
 AC GAGACGAGTC CC GT  
 \_ CCG C  
 GAM1154 MGC17919 3' TGCTTTCTGAACAGG 58223 C A  
 TCTGTTTCAG AGG CA  
 ||||| ||| ||  
 GGACAAGTC TTC GT  
 T \_  
 GAM1154 NS1-BP 5' TTTGCCACCAACAGAGT 72548 CAGCA A  
 ACTCTGTT GG CAAA  
 ||||| || |||  
 TGAGACAA CC GTTT  
 CCA\_\_ \_  
 GAM1154 P2RXL1 3' TGTCATGGCTGGACAAAGTCA 18386 C AG\_  
 TGACT TGTTTCAGC GACA  
 |||| ||||| |||  
 ACTGA ACAGGTCG CTGT  
 A GTA  
 GAM1154 PLP1 5' TCCAGCTGAACAAAGTCA 5010 C A  
 TGACT TGTTTCAGC GGA  
 |||| ||||| |||  
 ACTGA ACAAGTCG CCT  
 A A  
 GAM1154 SB52 3' TGTCTGCCTGTTTAAAAAGTCA 56364 CTG C A A  
 TGACT TT AGCAGG CA ACA  
 |||| || ||||| || |||  
 ACTGA AA TTGTCC GT TGT  
 AA\_ T \_ C  
 GAM1154 SLC26A1 3' CCTGCTGGTAGGAGCCA 41864 A GT  
 TG CTCT TCAGCAGG  
 || ||| |||||  
 AC GAGG GGTCGTCC  
 C AT  
 GAM1154 SMC1L1 3' TGCTGAGCTGAACAGGGCCA 71963 A A\_ A  
 TG CTCTGTTTCAGC GG CA  
 || ||||| || ||

AC GGGACAAGTCG TC GT  
 C AG \_  
 GAM1154 TGIF2 3' TGTTTGT TTTTGTGAGACAGAG 41461 \_ C  
 TCA TGACTCTGT TCAG AGGACAAACA  
 ||||| ||| |||||  
 ACTGAGACA AGTT TTTTGT TTTGT  
 G T  
 GAM1154 TMLHE 3' CCTGTTGAACAACTCA 36515 CTC  
 TGA TGTTTCAGCAGG  
 || |||||  
 ACT ACAAGTTGTCC  
 CAA  
 GAM1154 LOC124773 3' TTGTCCTGGCTCTCAGAGCA 74333 A TTC \_  
 TG CTCTG AGC AGGACAA  
 || ||| ||| |||||  
 AC GAGAC TCG TCCTGTT  
 \_ TC\_ G  
 GAM1154 LOC126755 3' TCTGTGAACGAACAGAG 74568 \_  
 CTCTGTTTCAG CAGG  
 ||||| |||  
 GAGACAAGTC GTCT  
 AAGT  
 GAM1154 LOC137258 5' TTGTCCTGCTACACCGA 75939 T TC  
 TC GT AGCAGGACAA  
 || || |||||  
 AG CA TCGTCCTGTT  
 C CA  
 GAM1154 LOC139422 5' CTGCACCTGAACAGAGTCA 75839 \_  
 TGACTCTGTTCA GCAG  
 ||||| |||  
 ACTGAGACAAGT CGTC  
 CCA  
 GAM1154 LOC146562 3' TGTTTGCCCCGTGGGAAGAGCA 57535 A G A A A  
 TG CTCT TTC GC GG CAAACA  
 || ||| || || |||||  
 AC GAGA AGG TG CC GTTTGT  
 \_ \_ G C C  
 GAM1154 LOC149111 3' TGCTTGCTAAGGAACAGA 79188 \_ A  
 TCTGTTTC AGCAGG CA  
 ||||| ||||| ||  
 AGACAAG TCGTTC GT  
 GAA \_  
 GAM1154 LOC149670 5' TTGTCCTGGCAGAATC 79495 C TCAG  
 GA TCTGT CAGGACAA  
 || ||| |||||  
 CT AGACG GTCCTGTT  
 A \_  
 GAM1154 LOC149910 5' TCCTCTGAAGCAGAGTCA 79535 \_ C  
 TGACTCTGTT CAG AGGA  
 ||||| ||| |||

		ACTGAGACGA GTC TCCT		
		A _		
GAM1154	LOC154092 3'	TGTTTGCTGGCAACAAATAGAG	86162	CA__ A A
		TCA TGACTCTGTT GC GG CAAACA		
		ACTGAGATAA CG TC GTTTGT		
		ACAA G _		
GAM1154	LOC158288 3'	CTGCTAAACAGGGTCA	86712	C
		TGACTCTGTT AGCAG		
		ACTGGGACAA TCGTC		
		A		
GAM1154	LOC158510 5'	CCTGTTGCCCTGACCAGAGTCA	81941	T ____
		TGACTCTG TCAG CAGG		
		ACTGAGAC AGTC GTCC		
		C CCGTT		
GAM1154	LOC164714 5'	TCTGCTGAATAGAATCA	87239	C
		TGA TCTGTTTCAGCAGG		
		ACT AGATAAGTCGTCT		
		A		
GAM1154	LOC203248 3'	TGTCCTGCAGAGTC	89315	GTTCA
		GA CTCT GCAGGACA		
		CTGAGA CGTCCTGT		
		_____		
GAM1154	LOC205418 5'	CCTGCTGACACCTGTTA	90683	TC_ T
		TGAC TGT CAGCAGG		
		ATTG ACA GTCGTCC		
		TCC _		
GAM1154	LOC220370 3'	TGTCCTCTGAACAGA	92837	C
		TCTGTTTCAG AGGACA		
		AGACAAGTC TCCTGT		
		_____		
GAM1154	LOC221271 3'	TTTATCCTGCTGATCAG	91885	T C
		CTG TCAGCAGGA AAA		
		GAC AGTCGTCCT TTT		
		T A		
GAM1154	LOC221584 3'	CCAGGCTGAACAGCATCA	93829	CT A_
		TGA CTGTTCAGC GG		
		ACT GACAAGTCG CC		
		AC GA		
GAM1154	LOC254100 3'	TCAGGCTGAATAGAGCCA	96418	A AG
		TG CTCTGTTCAGC GA		



AC GAGATAAGTCG CT  
 C GA  
 GAM1154 LOC257451 3' CCTGCTGAGCAGAGCCA 95554 A  
 TG CTCTGTTTCAGCAGG  
 || |||||  
 AC GAGACGAGTCGTCC  
 C  
 GAM1154 LOC51195 3' TGTTTCATCCTGCTGAAGTC 32950 CTGT CA  
 GACT TCAGCAGGA AACA  
 ||| ||||| |||  
 CTGA AGTCGTCCT TTGT  
 AC  
 GAM1154 LOC51285 3' TGTCTATCCTGCTGCCATCAG 33347 TT\_\_ CAA  
 CTG CAGCAGGA ACA  
 ||| ||||| |||  
 GAC GTCGTCCT TGT  
 TACC ATC  
 GAM1154 LOC90141 3' TGTCTGCTGGGCTCCAGT 61632 CT\_  
 ACT GTTCAGCAGGACA  
 ||| |||||  
 TGA CGGGTCGTCCTGT  
 CCT  
 GAM1154 LOC92340 3' CCCCTGAGCAGAGTCA 68991 CA  
 TGA CTCTGTTTCAG GG  
 ||||| ||  
 ACTGAGACGAGTC CC  
 C\_  
 GAM1155 FCMD 3' ACAACTATTCACCCTACCT 22086 C GTTAGT  
 AG TAGGG ATAGTTGT  
 || ||| |||||  
 TC ATCCC TATCAACA  
 C ACT\_\_  
 GAM1155 MPDZ 3' CAACCCAACCCCTAGCT 13817 AGTATA  
 AGCTAGGGGTT GTTG  
 ||||| |||  
 TCGATCCCCAA CAAC  
 CC\_\_  
 GAM1155 C12orf4 3' ACTGGTGATCAACCCCTAACTT 39809 C AGTA\_\_  
 A TAAG TAGGGGTT TAGT  
 ||| ||||| |||  
 ATTC ATCCCCAA GTCA  
 A CTAGTG  
 GAM1155 DKFZP434F0318 3' CAACCATTCCCTAACTCC 48005 T\_\_ A  
 GGGGTTAG AT GTTG  
 ||||| || |||  
 CCTCAATC TA CAAC  
 CCT C  
 GAM1155 U5-100K 3' ACAATCCAACCTCCCTAGC 59678 GTT ATA  
 GCTAGGG AGT GTTGT  
 ||||| || |||

		CGATCCC TCA TAACA		
		___ ACC		
GAM1156 BAZ2A	3'	ATACTTCATACCCCAGGAC	25592	A A CC
		GT CTGGG TA TGAAGTAT		
		CA GACCC AT ACTTCATA		
		G C _		
GAM1156 BCL11B	3'	TACTTCAGGCACAACTCT	56802	AC GGATA
		AGAGT TG CCTGAAGTA		
		TCTCA AC GGA		
		CTTCAT		
		___ AC___		
GAM1156 IFNGR1	3'	CAGTATCCAGTACTC	72012	G C
		GAGTACTGG ATAC TG		
		CTCATGACC TATG AC		
		— —		
GAM1156 RGS6	3'	CAGTTGTATTCCAACACTC	15027	AC _
		GAGT TGGGATAC CTG		
		CTCA ACCTTATG GAC		
		CA TT		
GAM1156 SPON2	3'	ATACCTCAGACCTGGTGCTCT	24908	TG ATAC A
		AGAGTAC GG CTGA GTAT		
		TCTCGTG CC GACT CATA		
		GT A___ C		
GAM1156 SUFU	3'	ACTTCAAGATCACTCT	32404	ACTGG ACC
		AGAGT GAT TGAAGT		
		TCTCA CTA ACTTCA		
		___ GA_		
GAM1156 TLL1	3'	TACTTCAAGGAAGACTCT	24956	A GGGATA _
		AGAGT CT CCT GAAGTA		
		TCTCA GA GGA CTTCAT		
		_ A___ A		
GAM1156 DKFZp434E0519	3'	ACTTATAATCCCAGCACTTT	49980	A ACCTG
		AGAGT CTGGGAT AAGT		
		TTTCA GACCCTA TTCA		
		C ATA___		
GAM1156 FLJ10803	3'	GGTAATCCCAGCACTTT	36669	A _
		AGAGT CTGGGAT ACC		
		TTTCA GACCCTA TGG		
		C A		
GAM1156 FLJ11149	3'	GGTAATCCCAGCACTTT	37111	A _
		AGAGT CTGGGAT ACC		

		TTTCA GACCCTA TGG		
		C A		
GAM1156	FLJ11259	3' GTATTCCCAGCACTTT	37192	A _
		AGAGT CTGGGA TAC		
		TTTCA GACCCT ATG		
		C T		
GAM1156	FLJ14117	3' ACTTGTAATCCCAGCACTTT	42899	A _ CTG
		AGAGT CTGGGAT AC AAGT		
		TTTCA GACCCTA TG TTCA		
		C A _		
GAM1156	FLJ14117	3' ACTTGTAATCCCAGCACTTT	42900	A _ CTG
		AGAGT CTGGGAT AC AAGT		
		TTTCA GACCCTA TG TTCA		
		C A _		
GAM1156	FLJ20045	3' ACCTCTAATCCCAGCACTTT	34408	A ACCT A
		AGAGT CTGGGAT GA GT		
		TTTCA GACCCTA CT CA		
		C AT_ C		
GAM1156	GCN2	3' CTTTAATCCCAGCACTTT	62771	A ACC
		AGAGT CTGGGAT TGAAG		
		TTTCA GACCCTA ATTTC		
		C _		
GAM1156	GW112	3' ACTTCAGGTGCTAAACACTT	21184	ACTG A
		GAGT GG TACCTGAAGT		
		TTCA TC GTGGACTTCA		
		CAAA _		
GAM1156	HZFW1	3' ATACTTCAGACATCTCCAAACT	47457	AC _ AC
	C	GAGT TGG GAT CTGAAGTAT		
		CTCA ACC CTA GACTTCATA		
		A_ T CA		
GAM1156	KIAA0161	5' CAGGCATCCAGTACCCT	28500	A G A
		AG GTACTGG AT CCTG		
		TC CATGACC TA GGAC		
		C _ C		
GAM1156	KIAA0472	3' ATACTTCAAGTACTCTATTCTC	71857	TAC GA C
	T	AGAG TGG TAC TGAAGTAT		
		TCTC ATC ATG ACTTCATA		
		TT_ TC A		
GAM1156	PDE11A	3' ATACTGATCAATCCCAGTTCTC	33775	T ACCTGA
		GAG ACTGGGAT AGTAT		

		CTC TGACCCTA TCATA		
		T ACTAG_		
GAM1156	LOC130535 3'	ACTTGTAATCCCAGCACTTT	76145	A _ CTG
		AGAGT CTGGGAT AC AAGT		
		TTTCA GACCCTA TG TTCA		
		C A _		
GAM1156	LOC155376 3'	ACTTGTAATCCCAGCACTTT	81333	A _ CTG
		AGAGT CTGGGAT AC AAGT		
		TTTCA GACCCTA TG TTCA		
		C A _		
GAM1156	LOC203350 3'	CTTTAATCCCAGCACTTT	90567	A ACC
		AGAGT CTGGGAT TGAAG		
		TTTCA GACCCTA ATTTC		
		C _		
GAM1156	LOC219793 5'	TAGCATCTCAGTACTCT	91374	AC
		AGAGTACTGGGAT CTG		
		TCTCATGACTCTA GAT		
		C _		
GAM1156	LOC220573 3'	ACTTCAAGTATCCTCA	69599	T C
		C GGGATAC TGAAGT		
		A TCCTATG ACTTCA		
		C A		
GAM1156	LOC253532 3'	ACTTGTAATCCCAGCACTTT	96025	A _ CTG
		AGAGT CTGGGAT AC AAGT		
		TTTCA GACCCTA TG TTCA		
		C A _		
GAM1156	LOC254875 3'	ACTTGTAATCCCAGCACTTT	96055	A _ CTG
		AGAGT CTGGGAT AC AAGT		
		TTTCA GACCCTA TG TTCA		
		C A _		
GAM1156	LOC90381 3'	ACCTCAGCAGTGCTCT	62542	GGATAC A
		AGAGTACTG CTGA GT		
		TCTCGTGAC GACT CA		
		_ C		
GAM1156	LOC93206 3'	ATACTTCAGGTTTAGTAGTATC	71725	G GGAT
	T	AGA TACTG ACCTGAAGTAT		
		TCT ATGAT TGGACTTCATA		
		_ GATT		
GAM1157	ADH1B 3'	CTTAGACATAAAGTAAAAT	72644	C CAC
		ATTT ACTTT TGTCTGAG		

			TAAA TGAAA ACAGATTC		
			A T__		
GAM1157 AHR	3'	ATCTCAGATGTTAAATAAATG 7875		CAC C T	
		CATTT TTT AC GTCTGAGAT			
		GTAAA AAA TG TAGACTCTA			
		TA_ T _			
GAM1157 FDFT1	3'	TAGGAAAGTGAAATG 15518		A	
		CATTTCACTTTC CTG			
		GTAAAGTGAAAG GAT			
		-			
GAM1157 JTB	3'	ATCTCAGACAGTGAAAGTGAAA 21959			
TG		CATTTCACTTTCAGTGTCTGAGAT			
		GTAAAGTGAAAGTGACAGACTCTA			
GAM1157 KLF4	3'	TCCCAGACAGTGGATATG 14891	CT	A	
		CA TTCAGTGTCTG GA			
		GT AGGTGACAGAC CT			
		AT C			
GAM1157 PHYH	3'	ACAGTAAAAGTGAAAT 20608		C	
		ATTTCACTTT ACTGT			
		TAAAGTGAAA TGACA			
		A			
GAM1157 PKD2	3'	TCCAGGTTGAAAGTGAAA 60096	CTG	A	
		TTTCACTTTCA TCTG GA			
		AAAGTGAAAGT GGAC CT			
		T__ _			
GAM1157 WRN	3'	GGGCAGTGAAAATGAAA 5098		C	
		TTTCA TTTCACTGTCT			
		AAAGT AAAGTGACGGG			
		A			
GAM1157 ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA	CTG	
		TTTCACTTT CTGT AGAT			
		AAAGTGAAA GACA TCTA			
		C_ CG_			
GAM1157 CG012	5'	CTCACTCTGAAAGTGAA 83218	CT	CT	
		TTCAGTTTCA GT GAG			
		AAGTGAAAGT CA CTC			
		CT _			
GAM1157 EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G	T_	
		CTTTCACT TC GAGAT			

		GAAAGTGA AG TTCTA	
		G TC	
GAM1157	FLJ23462	3' ATCTCAGACTTTACAAAGAAAT 45802	ACTTTCAC
		G CATTTC GTCTGAGAT	
		GTAAAG CAGACTCTA	
		AAACATTT_	
GAM1157	FLJ23510	3' ATCTCAGACAGTGACTGAAATG 45281	CTT
		CATTTC TCACTGTCTGAGAT	
		GTAAAGT AGTGACAGACTCTA	
		C_	
GAM1157	KIAA0984	3' TTTGTCCAGTGAAAATGAA 65534	C TC
		TTCA TTCACTG TGAG	
		AAGT AAAGTGAC GTTT	
		A CT	
GAM1157	KLHL6	3' ATCTCAGAGCAGGAAA 55299	A _
		TTTC CTG TCTGAGAT	
		AAAG GAC AGACTCTA	
		_ G	
GAM1157	NIR3	3' GCAGTGAAAGTGCAAT 66242	T
		ATT CACTTTCACTGT	
		TAA GTGAAAGTGACG	
		C	
GAM1157	PORIMIN	3' ATCTCAGAGGGCCAAAGTGAA 53598	CA G
		TTCACTTT CT TCTGAGAT	
		AAGTGAAA GG AGACTCTA	
		CC G	
GAM1157	PP35	3' ATCTCAGACTGAAA 22814	CT
		TTTCA GTCTGAGAT	
		AAAGT CAGACTCTA	
		—	
GAM1157	PRTD-NY3	3' CTCATTGCAATAAGTGAAATG 48148	TCAC C_
		CATTTCAC TT TGT TGAG	
		GTAAAGTGAA ACG ACTC	
		TA_ TT	
GAM1157	SEP15	3' TCCTACAGTAAGAGTGAAA 14934	C CT
		TTTCACTTT ACTGT GA	
		AAAGTGAGA TGACA CT	
		A TC	
GAM1157	SFXN2	3' CTCAGGGGAAAAAAGTGAAA 73941	CACTG
		TTTCACTTT TCTGAG	

		AAAGTGAAA	GGACTC		
		AAAGG			
GAM1157	LOC149703 3'	ATCTCAGACAGCCGTTTGGAAA	84647	ACTTTCA	
		TTTC CTGTCTGAGAT			
		AAAG GACAGACTCTA			
		GTTTGCC			
GAM1157	LOC154007 3'	ATCTCAAACCCTTTAGTGAAA	81015	TTCACT C	
		TTTCACT GT TGAGAT			
		AAAGTGA CA ACTCTA			
		TTTCC_ A			
GAM1157	LOC155004 3'	TCATTTAAGTGAAAAGGAAA	81226	A GTC_	
		TTTC CTTTCACT TGA			
		AAAG GAAAGTGA ACT			
		_ ATTT			
GAM1157	LOC222134 5'	ACAGTGAAGTGAAATG	94136	T	
		CATTTCAC TT CACTGT			
		GTAAAGTGAA GTGACA			
		-			
GAM1158	CYP1A2 3'	TAGTCTCAAACCTCCTGACCTCA	5702	C T	
		TGAG TCAGGAGTTTG GGCTA			
		ACTC AGTCCTCAAAC CTGAT			
		C T			
GAM1158	CYP1A2 3'	TAGTCTCAAACCTCCTGACCTCA	69122	C T	
		TGAG TCAGGAGTTTG GGCTA			
		ACTC AGTCCTCAAAC CTGAT			
		C T			
GAM1158	DHCR24 3'	TACAAATCCTAAGCTCA	28634	C G	
		TGAGCT AGGA TTTGTG			
		ACTCGA TCCT AAACAT			
		A _			
GAM1158	DIAPH2 3'	CCTCAAACCTCCAGGCTCA	22064	CA T	
		TGAGCT GGAGTTTG GG			
		ACTCGG CCTCAAAC CC			
		AC T			
GAM1158	FABP2 3'	CCTCAAACCTCCTGGACTCA	3742	CT T	
		TGAG CAGGAGTTTG GG			
		ACTC GTCCTCAAAC CC			
		AG T			
GAM1158	IVD 3'	CACAACAGCTCCCAAGCATCA	9458	_ CA _	
		TGA GCT GGAGT TTGTG			

			ACT CGA CCTCG AACAC		
			A AC AC		
GAM1158	MICB	3'	AGTTTCAAACCTCCTGACCTCA 19820	C	TG
			TGAG TCAGGAGTTTG GCT		
			ACTC AGTCCTCAAAC TGA		
			C TT		
GAM1158	NEU3	5'	AGCCTCCAACTCCTGGGCTCA 21845		TGT
			TGAGCTCAGGAGTT GGCT		
			ACTCGGGTCCTCAA CCGA		
			CCT		
GAM1158	NFATC4	5'	GCAGCCTCCTGAACTC 15849	C	T
			GAG TCAGGAG TTGT		
			CTC AGTCCTC GACG		
			A C		
GAM1158	NR1I2	3'	TATAGATCCTGAGCTCA 13972	G	
			TGAGCTCAGGA TTTGTG		
			ACTCGAGTCCT AGATAT		
			—		
GAM1158	NR1I2	3'	TATAGATCCTGAGCTCA 41830	G	
			TGAGCTCAGGA TTTGTG		
			ACTCGAGTCCT AGATAT		
			—		
GAM1158	RFX1	3'	AGCCTGTCCTGGGCCCA 11308	A	GTTTGT
			TG GCTCAGGA GGCT		
			AC CGGGTCCT CCGA		
			C GT_____		
GAM1158	RGS9	5'	TAGCCTCAAACCTCCTGGGCTCA 13836		T
			TGAGCTCAGGAGTTTG GGCTA		
			ACTCGGGTCCTCAAAC CCGAT		
			T		
GAM1158	SHOX	3'	AGCCTCAAACCTCCTGGGCTCA 22529		T
			TGAGCTCAGGAGTTTG GGCT		
			ACTCGGGTCCTCAAAC CCGA		
			T		
GAM1158	DKFZp434C0923	3'	AGCCTCCGCCTCCTGGGCTCA 34210		TTTGT
			TGAGCTCAGGAG GGCT		
			ACTCGGGTCCTC CCGA		
			CGCCT		
GAM1158	FLJ12704	3'	CACAGACTCCTGAACTC 46531	C	
			GAG TCAGGAGTTTGTG		



CTC AGTCCTCAGACAC  
A  
GAM1158 FLJ23047 3' TATAACCTCGAACTCCTGGCTC 44626 T T C  
A TGAGC CAGGAGTTTG GG TATA  
||||| ||||| || ||||  
ACTCG GTCCTCAAGC CC ATAT  
\_ T A  
GAM1158 KIAA0161 3' TCTCAAACCTCTGACCTCA 28514 C T  
TGAG TCAGGAGTTTG GG  
||||| ||||| ||  
ACTC AGTCCTCAAAC CT  
C T  
GAM1158 KIAA0830 3' TATATGTGCAAACCTCCCAAGCC 69703 A CA GC  
A TG GCT GGAGTTTGTG TATA  
|| ||| ||||| ||||  
AC CGA CCTCAAACGT ATAT  
\_ AC GT  
GAM1158 KIAA1102 3' ACAAAATCCCAAGCTCA 69009 CA G  
TGAGCT GGA TTTGT  
||||| ||| |||||  
ACTCGA CCT AAACA  
AC A  
GAM1158 KIAA1530 3' AGCCTCAAACCTCTGGGCTCA 67943 T  
TGAGCTCAGGAGTTTG GGCT  
||||| ||||| |||||  
ACTCGGGTCCTCAAAC CCGA  
T  
GAM1158 KIAA1784 3' CACAAACTCCAGAGCTCA 65143 A  
TGAGCTC GGAGTTTGTG  
||||| ||||| |||||  
ACTCGAG CCTCAAACAC  
A  
GAM1158 KIAA1821 3' CCTTGAACCTCCCAGGCTCA 71781 CA T  
TGAGCT GGAGTTTG GG  
||||| ||||| ||  
ACTCGG CCTCAAGT CC  
AC T  
GAM1158 MGC4655 3' CACAACCTCTCCTGGGCCCA 52798 A T\_\_  
TG GCTCAGGAG TTGTG  
|| ||||| |||||  
AC CGGGTCCTC AACAC  
C TCC  
GAM1158 PRO0245 5' TAGTCTCAAACCTCCCGAGCCCA 26135 A A T  
TG GCTC GGAGTTTG GGCTA  
|| ||| ||||| |||||  
AC CGAG CCTCAAAC CTGAT  
C C T  
GAM1158 SMCR7 3' CATAAACCTGAGCCCA 57506 A A  
TG GCTCAGG GTTTGTG  
|| ||||| |||||

			AC CGAGTCC CAAATAC		
			C _		
GAM1158	USP22	3'	GTCTCAAACCTCCTGACCTCA 68021	C	T
			TGAG TCAGGAGTTTG GGC		
			ACTC AGTCCTCAAAC CTG		
			C       T		
GAM1158	VDU1	3'	TAGTCTCAAACCTCCTGACCTCA 30425	C	T
			TGAG TCAGGAGTTTG GGCTA		
			ACTC AGTCCTCAAAC CTGAT		
			C       T		
GAM1158	LOC138199	3'	CCTCAAACCTCCTGGACTCA 75302	CT	T
			TGAG CAGGAGTTTG GG		
			ACTC GTCCTCAAAC CC		
			AG       T		
GAM1158	LOC139422	5'	TATAGCCTAGAACTCCTGAGCT 75845		GT
	CA		TGAGCTCAGGAGTTT GGCTATA		
			ACTCGAGTCCTCAAG CCGATAT		
			AT		
GAM1158	LOC147935	3'	AGCCTCAAACCTCCTGGGCTCA 84080		T
			TGAGCTCAGGAGTTTG GGCT		
			ACTCGGGTCCTCAAAC CCGA		
			T		
GAM1158	LOC148645	5'	AGCCTCAAACCTCCTGGGCTCA 84177		T
			TGAGCTCAGGAGTTTG GGCT		
			ACTCGGGTCCTCAAAC CCGA		
			T		
GAM1158	LOC149132	5'	TATAGCCTCAAACCTCCCAGGCT 79178	CA	T
	CA		TGAGCT GGAGTTTG GGCTATA		
			ACTCGG CCTCAAAC CCGATAT		
			AC       T		
GAM1158	LOC149711	3'	CACAAACTCCTGACCTCA 84676	C	
			TGAG TCAGGAGTTTGTG		
			ACTC AGTCCTCAAACAC		
			C		
GAM1158	LOC150407	3'	CCTCAAACCTCCTGGGCTCA 79819		T
			TGAGCTCAGGAGTTTG GG		
			ACTCGGGTCCTCAAAC CC		
			T		
GAM1158	LOC150587	3'	AGCCTCAAACCTCCTGGGCTCA 85057		T
			TGAGCTCAGGAGTTTG GGCT		

	ACTCGGGTCCTCAAAC CCGA			
	T			
GAM1158 LOC152804 3'	CCTCAAACCTCCTGGGCTCA 85879		T	
	TGAGCTCAGGAGTTTG GG			
	ACTCGGGTCCTCAAAC CC			
	T			
GAM1158 LOC153443 3'	AGCCTCAAACCTCCTGGGCTCA 80822		T	
	TGAGCTCAGGAGTTTG GGCT			
	ACTCGGGTCCTCAAAC CCGA			
	T			
GAM1158 LOC154007 3'	AGCCTCAAACCTCCTAGGCTCA 81010	TC	T	
	TGAGC AGGAGTTTG GGCT			
	ACTCG TCCTCAAAC CCGA			
	GA T			
GAM1158 LOC158629 5'	TAGCCCCAAACCTCCTGGGCTCA 86883		T	
	TGAGCTCAGGAGTTTG GGCTA			
	ACTCGGGTCCTCAAAC CCGAT			
	C			
GAM1158 LOC169611 3'	AGTCTCAAACCTCCTGACCTCA 82754	C	T	
	TGAG TCAGGAGTTTG GGCT			
	ACTC AGTCCTCAAAC CTGA			
	C T			
GAM1158 LOC196047 5'	TAGTCTCAAACCTCCTGACCTCA 89609	C	T	
	TGAG TCAGGAGTTTG GGCTA			
	ACTC AGTCCTCAAAC CTGAT			
	C T			
GAM1158 LOC202908 5'	TAGCCTCAAACCTCCCAGGCTCA 89246	CA	T	
	TGAGCT GGAGTTTG GGCTA			
	ACTCGG CCTCAAAC CCGAT			
	AC T			
GAM1158 LOC219529 5'	AGCCTCAAACCTCCTGAGCCCA 92966	A	T	
	TG GCTCAGGAGTTTG GGCT			
	AC CGAGTCCTCAAAC CCGA			
	C T			
GAM1158 LOC221463 5'	TACAGCCTCATGAGCCCA 92075	A	G	T
	TG GCTCA GAG TTGTG			
	AC CGAGT CTC GACAT			
	C A C			
GAM1158 LOC221756 3'	CGTGAATCCTGAGCTCA 92138	G	TG	
	TGAGCTCAGGA TT TG			

	ACTCGAGTCCT AA GC		
	A GT		
GAM1158 LOC221960 3'	AGCCTCAACCTCCTGAGCTCA 91080	T	T
	TGAGCTCAGGAG TTG GGCT		
	ACTCGAGTCCTC AAC CCGA		
	C T		
GAM1158 LOC222057 5'	TATAGCCTCAAACCTCCCAGGCT 92782	CA	T
CA	TGAGCT GGAGTTTG GGCTATA		
	ACTCGG CCTCAAAC CCGATAT		
	AC T		
GAM1158 LOC222057 3'	CATAGCCTCCTAAGGCCA 92767	A C_	T
	TG GCT AGGAG TTGTG		
	AC CGG TCCTC GATAC		
	_ AA C		
GAM1158 LOC222183 3'	CACAGCCTCCCCCAAGCTC 94165	CA__	T
	GAGCT GGAG TTGTG		
	CTCGA CCTC GACAC		
	ACCC C		
GAM1158 LOC255458 5'	AGCCTCAAACCTCCTGGGCTCA 97146		T
	TGAGCTCAGGAGTTTG GGCT		
	ACTCGGGTCCTCAAAC CCGA		
	T		
GAM1158 LOC255975 5'	CATAGCCTCCTAAGGCCA 95888	A C_	T
	TG GCT AGGAG TTGTG		
	AC CGG TCCTC GATAC		
	_ AA C		
GAM1158 LOC255975 5'	TATAGCCTCAAACCTCCCAGGCT 95898	CA	T
CA	TGAGCT GGAGTTTG GGCTATA		
	ACTCGG CCTCAAAC CCGATAT		
	AC T		
GAM1158 LOC256878 5'	TATAGCCTCAAACCTCCCAGGCT 96905	CA	T
CA	TGAGCT GGAGTTTG GGCTATA		
	ACTCGG CCTCAAAC CCGATAT		
	AC T		
GAM1158 LOC51193 3'	AGTCTCAAACCTCCTGGACTCA 32902	CT	T
	TGAG CAGGAGTTTG GGCT		
	ACTC GTCCTCAAAC CTGA		
	AG T		
GAM1158 LOC51622 3'	AGCCTCAACCTCCTGAGCTCA 31565	T	T
	TGAGCTCAGGAG TTG GGCT		

			ACTCGAGTCCTC AAC CCGA		
			C T		
GAM1158	LOC57146	3'	TAGTCTCAAACCTCTGACCTCA 39927	C	T
			TGAG TCAGGAGTTTG GGCTA		
			ACTC AGTCCTCAAAC CTGAT		
			C T		
GAM1159	ADCY7	3'	GAGCCTTGCCTTTGA 6640 A C		
			TCAAA GCA AGGCTC		
			AGTTT CGT TCCGAG		
			C _		
GAM1159	CACNA2D2	3'	CCAGTTTGAAGCCTGTGC 20080 _CT		
			GCACAGGCT C GTTGG		
			CGTGTCCGA G TGACC		
			A TT		
GAM1159	CDK10	3'	CCAACAGGAGGCCGTGGCTCTG 53767 AA ACA _		
	A		TCA AGC GGC TCCTGTTGG		
			AGT TCG CCG AGGACAACC		
			C_ GTG G		
GAM1159	CDK10	3'	CCAACAGGAGGCCGTGGCTCTG 53776 AA ACA _		
	A		TCA AGC GGC TCCTGTTGG		
			AGT TCG CCG AGGACAACC		
			C_ GTG G		
GAM1159	CDK10	3'	CCAACAGGAGGCCGTGGCTCTG 13400 AA ACA _		
	A		TCA AGC GGC TCCTGTTGG		
			AGT TCG CCG AGGACAACC		
			C_ GTG G		
GAM1159	CELSR2	3'	TCAGGGGAGCCTGTGC 7411 G		
			GCACAGGCTCCT TTGG		
			CGTGTCCGAGGG GACT		
			-		
GAM1159	CTNNB1	5'	CGGGAGGAGCCTGTTCCCCTGA 8579 AAAGC G		
			TCA ACAGGCTCCT TTG		
			AGT TGTCCGAGGA GGC		
			CCCCT G		
GAM1159	FOSB	5'	TCCTACGGAGCCTGCACTTT 22112 CA T T		
			AAAG CAGGCTCC GT GGA		
			TTTC GTCCGAGG CA CCT		
			AC _ T		
GAM1159	GLB1	3'	CCTGTTGGATGAAAGCCTGTGT 4637 AG T_____ TGTT		
	CTTTGA		A CACAGGC CC GG		

T GTGTCCG    GG   CC  
 CT    AAAGTIIIA TTGT  
 GAM1159 MSN    3' TGAGAGAAGCCTGTGCCCTGA 60255    AAA    C G  
       TCA GCACAGGCT CT TTG  
       ||| ||||| || |||  
       AGT CGTGTCCGA GA AGT  
       CC\_    A G  
 GAM1159 P2RX3    5' GGGAGCCTGTCCCTTT 10369    C\_  
       AAAG ACAGGCTCCT  
       |||| |||||  
       TTTC TGTCCGAGGG  
       CC  
 GAM1159 RBL2    3' TCCAACAGAAGAACTGTGTTT 18830    G\_ C  
       AAGCACAG CT CTGTTGGA  
       ||||| || |||||  
       TTTGTGTC GA GACAACCT  
       AA A  
 GAM1159 SET    3' TCCAACAGACCTGGTGCT 11560    \_ CTC  
       AGCAC AGG CTGTTGGA  
       |||| ||| |||||  
       TCGTG TCC GACAACCT  
       G A\_  
 GAM1159 SIT    3' GAGCCTGGCTTTTGA 27077    A  
       TCAAAAGC CAGGCTC  
       ||||| |||||  
       AGTTTTCG GTCCGAG  
       —  
 GAM1159 ZNF3    3' GGAGCCTGCCTCTTGA 34758    A CA  
       TCAA AG CAGGCTCC  
       |||| || |||||  
       AGTT TC GTCCGAGG  
       C C\_  
 GAM1159 DKFZP434A0225 3' CAAACCCTGCTTTTGA 93908    AC CTCCTG  
       TCAAAAGC AGG TTG  
       ||||| ||| |||  
       AGTTTTCG TCC AAC  
       — CA\_\_\_\_  
 GAM1159 DKFZp547J036 3' TCCAACAGAAGCCACAGGC 50130    ACA\_ C  
       GC GGCT CTGTTGGA  
       || ||| |||||  
       CG CCGA GACAACCT  
       GACA A  
 GAM1159 DKFZP564I052 3' GAGCCTGTATTTTGA 66709    GC  
       TCAAAA ACAGGCTC  
       |||| |||||  
       AGTTTT TGTCCGAG  
       A\_  
 GAM1159 FBX09    5' TCCAGTCTGTCTGTGCT 53110    TCCTG  
       AGCACAGGC TTGGA  
       ||||| ||||

TCGTGTCTG GACCT  
TCT\_\_

GAM1159 FENS-1 3' AGGAGCCTGTCTTTT 40437 C  
AAAAG ACAGGCTCCT  
||||| |||||  
TTTTC TGTCCGAGGA

—  
GAM1159 FIGNL1 5' CCAGACCCTGTGCTCTT 42087 A C CTGT  
AA AGCACAGG TC TGG  
|| ||||| || |||  
TT TCGTGTCC AG ACC  
C C \_\_\_\_

GAM1159 FLJ10898 5' CCAACAGGTCCTGCTCT 59425 CA CT  
AG CAGG CCTGTTGG  
|| ||| |||||  
TC GTCC GGACAACC  
TC T\_

GAM1159 FLJ20113 3' CCAACAGGAGCAGGTTT 34574 ACAG  
AAGC GCTCCTGTTGG  
||| |||||  
TTTG CGAGGACAACC  
GA\_\_

GAM1159 FLJ20511 3' TCCAACAGAAGCCTAGTCCT 35331 C \_ C  
AG AC AGGCT CTGTTGGA  
|| ||| |||||  
TC TG TCCGA GACAACCT  
C A A

GAM1159 FLJ22659 3' TCAGCAGGAACCTAGACTCCTG 46262 AA CAC C  
A TCA AG AGG TCCTGTTGG  
||| || ||| |||||  
AGT TC TCC AGGACGACT  
CC AGA A

GAM1159 KIAA0632 3' CCAAGGTGCCTGTGCT 31423 T GT  
AGCACAGGC CCT TGG  
||||| ||| |||  
TCGTGTCCG GGA ACC  
T \_\_\_\_

GAM1159 KIAA0747 3' TCCAAGGGCAGAGCCTGTGC 30967 \_\_ G  
GCACAGGCTC CT TTGGA  
||||| || |||  
CGTGTCCGAG GG AACCT  
AC G

GAM1159 KIAA0871 3' GGAAGATCCTGTGCTCTTGA 30302 A C\_\_  
TCAA AGCACAGG TCC  
||| ||||| |||  
AGTT TCGTGTCC AGG  
C TAGA

GAM1159 KIAA1189 3' CAAGAGCCTGTATTTTGA 72040 GC C  
TCAAAA ACAGGCTC TG  
||||| ||||| ||

AGTTTT TGTCCGAG AC  
 A\_ A  
 GAM1159 MGC20258 5' CCAATCCCTGTGCTCCTG 58151 AA CTCCT  
 CA AGCACAGG GTTGG  
 || ||||| ||||  
 GT TCGTGTCC TAACC  
 CC C\_\_\_\_  
 GAM1159 MGC861 3' TCTTGCAGAGCCTGTGTCTTT 43904 \_ C T  
 AAAG CACAGGCTC TGT GGA  
 ||| ||||| ||| |||  
 TTTC GTGTCCGAG ACG TCT  
 T \_ T  
 GAM1159 PTDSS1 3' TAGGAGCCTCGCTTCCGA 28572 AA AC  
 TC AAGC AGGCTCCTG  
 || ||| |||||  
 AG TTCG TCCGAGGAT  
 CC C\_  
 GAM1159 RAI17 3' CCTGGGAGCCTGTGC 91279 GTT  
 GCACAGGCTCCT GG  
 ||||| ||  
 CGTGTCCGAGGG CC  
 T\_  
 GAM1159 UPLC1 3' CCCACATTTGCCTGTGTCTTG 34722 AA TCC T  
 A TCAA GCACAGGC TGT GG  
 ||| ||||| ||| ||  
 AGTT TGTGTCCG ACA CC  
 CC TTT C  
 GAM1159 USP3 5' TCCAACAAAAGCCCTTGGGTCT 89678 \_ \_ A \_ CC  
 GTTTGA CAAA AG C CA GGCT TGTTGGA  
 ||| ||| ||| |||||  
 GTTT TC G GT CCGA ACAACCT  
 G T G TC AA  
 GAM1159 ZIM2 5' CCAGATACCTGTGTTTTGA 31084 G CTCCTG  
 TCAAAA CACAGG TTGG  
 ||||| ||||| |||  
 AGTTTT GTGTCC GACC  
 \_ ATA\_  
 GAM1159 LOC151176 3' CCCCAGGAGCCAGCTT 85260 ACA TT  
 AAGC GGCTCCTG GG  
 ||| ||||| ||  
 TTCG CCGAGGAC CC  
 AC\_ C\_  
 GAM1159 LOC157740 3' TCCAACACTTGTCATGCTTTT 81565 CA TCC  
 GA TCAAAGCA GGC TGTTGGA  
 ||||| ||| |||||  
 AGTTTTCGT CTG ACAACCT  
 AC TTC  
 GAM1159 LOC158654 3' CCAGACACCTGTGCTCCTGG 81963 AA CTCC \_  
 TCA AGCACAGG TGT TGG  
 ||| ||||| ||| |||



	GGT TCGTGTCC ACA ACC		
	CC ____ G		
GAM1159 LOC168359 5'	CCAAATCCCGTGCTTTT 87275	A	CTCCTG
	AAAAGCAC GG TTGG		
	TTTTCGTG CC AACC		
	C TA____		
GAM1159 LOC200014 3'	CCAGCTCTGCCTGTGCCTT 88520	A	TCCT
	AAA GCACAGGC GTTGG		
	TTT CGTGTCCG CGACC		
	C TCT_		
GAM1159 LOC200213 5'	CCAAGGCCCTGTGCT 88631	CT	GT
	AGCACAGG CCT TGG		
	TCGTGTCC GGA ACC		
	CC ____		
GAM1159 LOC203276 3'	CAAGAGAAGCCTGTGCTT 90474	C	G
	AAGCACAGGCT CT TTG		
	TTCGTGTCCGA GA AAC		
	A G		
GAM1159 LOC203305 3'	CAAGAGAAGCCTGTGCTT 90518	C	G
	AAGCACAGGCT CT TTG		
	TTCGTGTCCGA GA AAC		
	A G		
GAM1159 LOC219690 3'	CCCAGTGCCTGTGCCTCTGA 93071	AAA	TC TT
	TCA GCACAGGC CTG GG		
	AGT CGTGTCCG GAC CC		
	CTC T_ ____		
GAM1159 LOC253263 3'	CCTGTTGGACCCATGCCTGTGC 97030	AA	_____ TGTT
	CCATGA GCACAGGC TCC GG		
	CGTGTCCG AGG CC		
	CC TACCC    TTGT		
GAM1159 LOC254243 3'	CAAGAGAAGCCTGTGCTT 97403	C	G
	AAGCACAGGCT CT TTG		
	TTCGTGTCCGA GA AAC		
	A G		
GAM1159 LOC255230 5'	TCCAACAGATCTCTTGCTTTT 97455	C	CTC
	AAAAGCA AGG CTGTTGGA		
	TTTTCGT TCT GACAACCT		
	_ CTA		
GAM1159 LOC90038 3'	CAAGAGAAGCCTGTGCTT 61147	C	G
	AAGCACAGGCT CT TTG		

TTCGTGTCCGA GA AAC  
 A G  
 GAM1160 ALX3 3' ACTCCTGCCATGTGCCTGC 21416 \_\_\_\_ TTAC  
 GCA CATATGGC AGT  
 ||| ||||| |||  
 CGT GTGTACCG TCA  
 CC TCC\_  
 GAM1160 FGA 3' TACTGTAGCTAAATGT 4962 A T  
 ACAT TGGCT ACAGTA  
 |||| |||| ||||  
 TGTA ATCGA TGTCAT  
 A \_  
 GAM1160 GAS7 3' CTGTCACATGCTTGTG 13321 CATA GCTT  
 TACAAGCA TG ACAG  
 ||||| || |||  
 GTGTTCTG AC TGTC  
 \_\_\_\_ AC\_  
 GAM1160 ITGA4 3' TACTACTTACCATATGTGCTTG 6086 CTTAC  
 CAAGCACATATGG AGTA  
 ||||| ||||  
 GTTCGTGTATACC TCAT  
 ATTCA  
 GAM1160 SMARCA2 3' ACTGTAAACATTGCTT 11782 CAT GC  
 AAGCA ATG TTACAGT  
 |||| || |||||  
 TTCGT TAC AATGTCA  
 \_\_\_\_ A\_  
 GAM1160 YES1 3' ACTGTGAGTATTGCTT 18348 CATATG  
 AAGCA GCTTACAGT  
 |||| |||||  
 TTCGT TGAGTGTCA  
 TA\_\_\_\_  
 GAM1160 ASPN 3' TACTGTAAATGGAATGCTTG 34602 CA\_ GGC  
 CAAGCA TAT TTACAGTA  
 |||| || |||||  
 GTTCGT GTA AATGTCAT  
 AAG \_\_\_\_  
 GAM1160 DCLRE1A 3' TACTGTAAATGTGGGC 69167 A GGC  
 GC CATAT TTACAGTA  
 || |||| |||||  
 CG GTGTA AATGTCAT  
 G \_\_\_\_  
 GAM1160 FLJ10350 3' TACTGTAAATAGCTTGTGCT 95510 TAT \_\_\_\_  
 AGCACA GGCT TACAGTA  
 |||| || |||||  
 TCGTGT TCGA ATGTCAT  
 \_\_\_\_ TAA  
 GAM1160 FLJ13611 3' TACTGTAATGGTTTGTGTCTGT 46295 AG T GGC  
 A  
 TACA CACA AT TTACAGTA  
 |||| ||| || |||||

ATGT GTGT TG AATGTCAT  
 CT T GT\_  
 GAM1160 HCGIV.9 3' ACTGTGTTACTATATGTTGTA 38611 AGC CT\_  
 TACA ACATATGG TACAGT  
 ||| ||||| |||||  
 ATGT TGTATATC GTGTCA  
 \_\_\_\_ ATT  
 GAM1160 KIAA0210 3' TACTGTAAGCCAGTTTTAGCT 28483 ACATA\_  
 AGC TGGCTTACAGTA  
 ||| |||||  
 TCG ACCGAATGTCAT  
 ATTTTG  
 GAM1160 KIAA0515 3' ACTGCAAGCGGCTGCTTGTG 63801 CATATG A  
 TACAAGCA GCTT CAGT  
 ||||| ||| |||  
 GTGTTCTG CGAA GTCA  
 CGG\_\_\_\_ C  
 GAM1160 KIAA1078 3' TACTGTAATTTATGTTCTT 65122 C TGGC  
 AAG ACATA TTACAGTA  
 ||| ||| |||||  
 TTC TGTAT AATGTCAT  
 T TT\_  
 GAM1160 KIAA1185 3' ACTGTACAGTCATGTGCCACGT 62602 AA\_ TA \_  
 A TAC GCACA TGGCT TACAGT  
 ||| ||| ||| |||||  
 ATG CGTGT ACTGA ATGTCA  
 CAC \_\_\_\_ C  
 GAM1160 KIAA1348 3' ACTGTAAGCATGCTTG 68570 CATATG  
 CAAGCA GCTTACAGT  
 ||||| |||||  
 GTTCGT CGAATGTCA  
 A\_\_\_\_  
 GAM1160 MGC3248 3' TACTGTCTTGCCATGTGGC 50657 A TT\_  
 GC CATATGGC ACAGTA  
 || ||||| |||||  
 CG GTGTACCG TGTCAT  
 \_ TTC  
 GAM1160 PP5395 3' TACTGTAAACCATGGTTCCAGC 72109 ACA\_\_\_\_ C  
 GC TATGG TTACAGTA  
 || ||| |||||  
 CG GTACC AATGTCAT  
 ACCTTG A  
 GAM1160 SSFA2 3' ACTGTAAGCCTTGTTGCTTTA 73767 C C T  
 A AAGCA ATA GGCTTACAGT  
 | |||| ||| |||||  
 A TTCGT TGT CCGAATGTCA  
 T \_ T  
 GAM1160 SV2 3' ACTGTAGCTGTGACGTGTTGTA 29302 G A\_ T  
 TACAA CAC TATGGCT ACAGT  
 ||||| ||| ||||| |||||

		ATGTT GTG GTGTCGA TGTCA	
		_ CA _	
GAM1160	LOC122786 3'	TACTGTAAACAGGTA CTGCTTT 74159	C CATA_ GC
	A	A AAGCA TG TTACAGTA	
		A TTCGT AC AATGTCAT	
		T CATGG A_	
GAM1160	LOC154792 3'	TACTGTATTGCATTTGCTT 86249	CATATG T_
		AAGCA GC TACAGTA	
		TTCGT CG ATGTCAT	
		TTA__ TT	
GAM1160	LOC203411 3'	TACTGTAAATATATGT 90630	GC
		ACATATG TTACAGTA	
		TGTATAT AATGTCAT	
		A_	
GAM1160	LOC221596 5'	TACTGTAAAGATCAATACTTGT 91982	CACATA _
		ACAAG TGG CTTACAGTA	
		TGTTC ACT GAATGTCAT	
		ATA__ A	
GAM1160	LOC254100 3'	ACTGTGGCTCACGCCTGTA 96411	A ACATAT T
		TACA GC GGCT ACAGT	
		ATGT CG TCGG TGTCA	
		C CAC__ _	
GAM1160	LOC58489 3'	TACTGTAAGCCTCAGATCGTTG 72529	GCACATAT
	TA	TACAA GGCTTACAGTA	
		ATGTT CCGAATGTCAT	
		GCTAGACT	
GAM1160	LOC91351 3'	ACTAAATGCATATGTGCT 65704	G TTAC
		AGCACATATG C AGT	
		TCGTGTATAC G TCA	
		_ TAAA	
GAM1160	LOC93380 3'	GCCATTGTA CTGTA 72201	C T
		TACAAG ACA ATGGC	
		ATGTTT TGT TACCG	
		A _	
GAM1161	ALX3 3'	ACACTGGCTCCTCAGCTCCAGC 21415	_ ACT
		GCTGGAG TGAGGAGC TGT	
		CGACCTC ACTCCTCG ACA	
		G GTC	
GAM1161	CDH5 3'	AGTGA CTCCCAGCCCAGC 8383	AG A _
		GCTGG TG GGAG CACT	

			CGACC AC CCTC GTGA			
			CG C A			
GAM1161	GRAF	3'	GCCCCTGCACTCCAGC	30561	_	A
			GCTGGAGTG AGG GC			
			CGACCTCAC TCC CG			
			G C			
GAM1161	IFIT4	3'	GCCCCTGCACTCCAGC	70922	_	A
			GCTGGAGTG AGG GC			
			CGACCTCAC TCC CG			
			G C			
GAM1161	NHLH1	3'	AGTGCTCCTCCCCAGC	18796	AGT	
			GCTGG GAGGAGCACT			
			CGACC CTCCTCGTGA			
			CC_			
GAM1161	20D7-FC4	3'	GGGTCTCCTACCCCAGC	60905	A	C
			GCTGG GTGAGGAG ACTT			
			CGACC CACTCCTC TGGG			
			C _			
GAM1161	C20orf28	3'	TGCTTCTCACCCCAGC	31231	A	
			GCTGG GTGAGGAGCA			
			CGACC CACTCTTCGT			
			C			
GAM1161	CSMD1	5'	GCGAGGCTCCTCACTGCAGC	73123	G	A
			GCTG AGTGAGGAGC CTTGT			
			CGAC TCACTCCTCG GAGCG			
			G _			
GAM1161	DKFZP727G051	3'	TGACTCCCCACCCCAGC	69481	A	A _
			GCTGG GTG GGAG CA			
			CGACC CAC CCTC GT			
			C C A			
GAM1161	DMTF1	5'	CGTCGCGCTCGCTCACTCCAGC	40938	_	ACT T
			GCTGGAGTGAG GAGC TG CG			
			CGACCTCACTC CTCG GC GC			
			G C_ T			
GAM1161	FLJ10305	3'	TGCCCCTCCTCCAGC	68360	T	A
			GCTGGAG GAGG GCA			
			CGACCTC CTCC CGT			
			_ C			
GAM1161	FLJ10842	3'	TGCCCCCACTCCAGC	36724	A	A
			GCTGGAGTG GG GCA			

CGACCTCAC CC CGT  
 \_ C  
 GAM1161 FLJ13868 3' AGGCTCCTCACCCCA 42728 A\_ A  
 TGG GTGAGGAGC CT  
 ||| ||||| ||  
 ACC CACTCCTCG GA  
 CC \_

GAM1161 FLJ20294 3' ACACCTCCTCACCCAGC 34868 A CACT  
 GCTGG GTGAGGAG TGT  
 |||| ||||| ||  
 CGACC CACTCCTC ACA  
 C C\_

GAM1161 FLJ20413 3' GCAATCTCCCCACTCCAGC 35133 A CAC  
 GCTGGAGTG GGAG TTGT  
 ||||| ||| |||  
 CGACCTCAC CCTC AACG  
 C T\_

GAM1161 FLJ23360 3' CGCCACCCACTCCAGC 43567 A AGCACT T  
 GCTGGAGTG GG TG CG  
 ||||| || |||  
 CGACCTCAC CC AC GC  
 \_ \_ C

GAM1161 FLJ23878 3' AGTCTCCTCACCCCA 58709 A C  
 TGG GTGAGGAG ACT  
 ||| ||||| |||  
 ACC CACTCCTC TGA  
 C \_

GAM1161 HIC2 3' GCAGAGGCCCTCACTC 65263 A AC  
 GAGTGAGG GC TTGT  
 ||||| || |||  
 CTCACTCC CG GACG  
 C GA

GAM1161 KIAA0574 3' ACAAGTGCCGATTCCCAGC 69277 AGT GA\_  
 GCTGG GAG GCACTTGT  
 |||| ||| |||||  
 CGACC CTT CGTGAACA  
 \_ AGC

GAM1161 KIAA1372 5' TGCCCTCACCCAGC 91653 A A  
 GCTGG GTGAGG GCA  
 |||| ||||| |||  
 CGACC CACTCC CGT  
 C \_

GAM1161 KIAA1538 3' GCAAGTCTCCTCATCCAGC 71547 G C  
 GCTGGA TGAGGAG ACTTGT  
 ||||| ||||| |||||  
 CGACCT ACTCCTC TGAACG

GAM1161 KIAA1871 3' GCAACAAGTGCGAACTCCA 61232 GAGGA C  
 TGGAGT GCACTTGT GC  
 ||||| ||||| ||

ACCTCA CGTGAACA CG  
 AAG\_\_ A  
 GAM1161 MGC2752 5' GCAACAAGTGCTGAGATCAGC 78447 AGTGAGG C  
 GCTGG AGCACTTGT GC  
 |||| ||||| ||  
 CGACT TCGTGAACA CG  
 AGAG\_\_ A  
 GAM1161 PMX2B 5' CACATCTCCCCACTCCAGC 14077 A CACT C  
 GCTGGAGTG GGAG TGT G  
 ||||| ||| |||  
 CGACCTCAC CCTC ACA C  
 C T\_\_ \_  
 GAM1161 PTK6 3' AGCGCCCCTCACTCCTGC 19933 T A A  
 GC GGAGTGAGG GC CT  
 || ||||| || ||  
 CG CCTCACTCC CG GA  
 T C C  
 GAM1161 SLC26A7 3' ACAAATGCTTCTTCCAG 56150 GTG C  
 CTGGA AGGAGCA TTGT  
 |||| ||||| ||||  
 GACCT TCTTCGT AACA  
 \_\_ A  
 GAM1161 SPTLC2 3' TGCACCCCTGCACTCCAGC 16812 \_ A\_\_  
 GCTGGAGTG AGG GCA  
 ||||| ||| |||  
 CGACCTCAC TCC CGT  
 G CCA  
 GAM1161 LOC124976 3' GCCTCCACCCCCACTCCAGC 74382 A\_\_\_\_ \_  
 GCTGGAGTG GGAG C  
 ||||| |||||  
 CGACCTCAC CCTC G  
 CCCC A C  
 GAM1161 LOC143677 5' GACACTGCCCCACCCCAGC 82977 A A A CT  
 GCTGG GTG GG GCA TGTC  
 |||| ||| || ||||  
 CGACC CAC CC CGT ACAG  
 C \_ \_ C\_  
 GAM1161 LOC148056 3' GTACTCCTCACCCCAGC 84109 A C  
 GCTGG GTGAGGAG AC  
 |||| ||||| ||  
 CGACC CACTCCTC TG  
 C A  
 GAM1161 LOC158428 3' ACACTTCATCCTCACTCCA 70557 GCACT  
 TGGAGTGAGGA TGT  
 ||||| |||  
 ACCTCACTCCT ACA  
 ACTTC  
 GAM1161 LOC253296 5' GCGACAAGGTAGCCACCCCCGC 94491 T A AGGA A  
 GC GG GTG GC CTTGTCGC  
 || ||| || |||||

CG CC CAC TG GAACAGCG  
 C C CGA\_ \_  
 GAM1161 LOC257570 5' GCGACAAGGTAGCCACCCCCGC 97834 T A AGGA A  
 GC GG GTG GC CTTGTGCG  
 || ||| || |||||  
 CG CC CAC TG GAACAGCG  
 C C CGA\_ \_  
 GAM1162 AGL 3' ATTCTTAGAATACAGTGCTCAC 3449 A GAATT  
 GT AGCATTGTATTT GAAT  
 || ||||| |||  
 CA TCGTGACATAAG CTTA  
 C ATT\_  
 GAM1162 AGL 3' ATTCTTAGAATACAGTGCTCAC 5344 A GAATT  
 GT AGCATTGTATTT GAAT  
 || ||||| |||  
 CA TCGTGACATAAG CTTA  
 C ATT\_  
 GAM1162 AGL 3' ATTCTTAGAATACAGTGCTCAC 5356 A GAATT  
 GT AGCATTGTATTT GAAT  
 || ||||| |||  
 CA TCGTGACATAAG CTTA  
 C ATT\_  
 GAM1162 AGL 3' ATTCTTAGAATACAGTGCTCAC 5363 A GAATT  
 GT AGCATTGTATTT GAAT  
 || ||||| |||  
 CA TCGTGACATAAG CTTA  
 C ATT\_  
 GAM1162 AGL 3' ATTCTTAGAATACAGTGCTCAC 5369 A GAATT  
 GT AGCATTGTATTT GAAT  
 || ||||| |||  
 CA TCGTGACATAAG CTTA  
 C ATT\_  
 GAM1162 AGL 3' ATTCTTAGAATACAGTGCTCAC 5377 A GAATT  
 GT AGCATTGTATTT GAAT  
 || ||||| |||  
 CA TCGTGACATAAG CTTA  
 C ATT\_  
 GAM1162 SPG3A 3' TTAAAAACAAATGCTTAC 31916 \_ A  
 GTAAGCATT GT TTTGA  
 ||||| || |||  
 CATTGTA CA AAATT  
 A A  
 GAM1162 FLJ20671 3' TCAATTCAAATGTGTTGC 35530 T GT  
 GCA T ATTTGAATTGA  
 ||| | |||||  
 CGT G TAACTTAACT  
 T TG  
 GAM1162 POLYDOM 3' TCAAATACAATACTTAT 44429 C  
 GTAAG ATTGTATTTGA  
 |||| |||||



		TATTC TAACATAAACT		
		A		
GAM1162 SYNJ2	3'	TTTAAATCAATGCTTAC 61770	TA	
		GTAAGCATTG TTTGAA		
		CATTCGTAAC AAATTT		
		TA		
GAM1162 LOC256979	5'	ATTCTAAGTACAATGCTTAC 96045	—	
		GTAAGCATTGTATTT GAAT		
		CATTCGTAACATGAA CTTA		
		T		
GAM1163 ACT	5'	CAGGAAGAAGCGGCTTTAA 40040	CAACGG C	
		TTAAAGCTGC CT CCTG		
		AATTTGCGCG GA GGAC		
		AA___ A		
GAM1163 ATP11A	3'	AGGCCACGCCGGCAGCTT 77017	AAC TC__	
		AAGCTGCC GGC CCT		
		TTCGACGG CCG GGA		
		___ CACC		
GAM1163 CLASP2	3'	CAGGAATGCTTAAAGCTTTAA 64592	GCCAAC TC__	
		TTAAAGCT GGC CCTG		
		AATTTCGA TCG GGAC		
		AAT___ TAA		
GAM1163 LTB4R	3'	GCTCCCACAGGCAGCTTTAA 5648	AAC___	
		TTAAAGCTGCC GGC		
		AATTTGACGG TCG		
		ACACCC		
GAM1163 POU3F1	3'	GCAGGAAATAGCCAAAGCTTTA 59310	GCCAAC C___	
A		TTAAAGCT GGCT CCTGC		
		AATTTCGA CCGA GGACG		
		AA___ TAAA		
GAM1163 RAP1B	3'	CAGGGAGCCACAGTATTTAA 31598	— CCAAC	
		TTAAA GCTG GGCTCCCTG		
		AATTT TGAC CCGAGGGAC		
		A A___		
GAM1163 RBBP2	3'	GCAAGGAGCCGTTTTTTGGCTT 17323	CC_ C	
TGA		TTAAAGCTG AACGGCTCC TGC		
		AGTTTCGGT TTGCCGAGG ACG		
		TTT A		
GAM1163 SLC21A9	3'	CAGGGAGCCACCAGCAGT 23418	CAAC	
		GCTGC GGCTCCCTG		

		TGACG CCGAGGGAC	
		ACCA	
GAM1163	UCP2	5' AGCCACTGGCAGCTTTGA 12531	AC
		TTAAAGCTGCCA GGCT	
		AGTTTCGACGGT CCGA	
		CA	
GAM1163	CDC42BPB	3' CAGAAGACGGCAGTTTTAA 20099	AACGG CC
		TTAAAGCTGCC CT CTG	
		AATTTTGACGG GA GAC	
		CA__ A_	
GAM1163	CLDN4	3' GCAGGGAGGAGGGGACAGCTT 7137	_ AACGG
		AAGCTG CC CTCCCTGC	
		TTCGAC GG GAGGGACG	
		A GGAG_	
GAM1163	CXYorf1	3' CAGGGAGCCACCGGTCGC 82038	T AAC
		GC GCC GGCTCCCTG	
		CG TGG CCGAGGGAC	
		C CCA	
GAM1163	DKFZP434J193	3' CAGAAGCCTGGCAGCT 71001	AC CC
		AGCTGCCA GGCT CTG	
		TCGACGGT CCGA GAC	
		_ A_	
GAM1163	DKFZp586H0623	3' CAGGGAGCAGAGACTGCTTTAA 34066	TGCCAACG
		TTAAAGC GCTCCCTG	
		AATTTCG CGAGGGAC	
		TCAGAGA_	
GAM1163	FLJ20034	3' CAGGGAGCCCGGTCAGCT 34362	_ AAC
		AGCTG CC GGCTCCCTG	
		TCGAC GG CCGAGGGAC	
		T C_	
GAM1163	FLJ22031	3' CAGGGAGACAGCTTTAG 46886	CCAACGG
		TTAAAGCTG CTCCCTG	
		GATTTCGAC GAGGGAC	
		A_____	
GAM1163	GOLPH2	3' GCAAAGTAGCAACAGCTTTAA 33322	CCAACG CCC_
		TTAAAGCTG GCT TGC	
		AATTTTCGAC CGA ACG	
		AA_____ TGAA	
GAM1163	GPR	3' GCAGGGAGCAGGAGC 23333	G AACG
		GCT CC GCTCCCTGC	

		CGA GG CGAGGGACG		
		— A —		
GAM1163	KIAA0335	3' GCAGTAGATGGGCAGCTT 28992		AACGG CC
		AAGCTGCC CT CTGC		
		TTCGACGG GA GACG		
		GTA__ T_		
GAM1163	KIAA0355	3' CAAGGGTGGTTGGCAGCT 28023		G T C
		AGCTGCCAAC GC CC TG		
		TCGACGGTTG TG GG AC		
		G _ A		
GAM1163	KIAA1211	3' AGGGACTTGGCAGTTT 68890		AC C
		AAGCTGCCA GG TCCCT		
		TTTGACGGT TC AGGGA		
		— —		
GAM1163	MGC4251	3' CAGGGAGCCACTGAGGGT 50456		GC AC
		GCT CA GGCTCCCTG		
		TGG GT CCGAGGGAC		
		GA CA		
GAM1163	SFRS10	5' GCAAGAGGTTGGCAGCTTCGA 15977	TA	GG CC
		T AAGCTGCCAAC CTC TGC		
		A TTCGACGGTTG GAG ACG		
		GC _ A_		
GAM1163	TFPT	5' AGAAAGACGTTGGCAACT 25318	C	G CC
		AG TGCCAACG CT CT		
		TC ACGGTTGC GA GA		
		A A AA		
GAM1163	LOC146669	5' CAGAGAGAGCAGCTTT 78054		CAACGG C
		AAAGCTGC CTC CTG		
		TTTCGACG GAG GAC		
		A__ A		
GAM1163	LOC149076	3' GCAGAGGGGTGCGGCAGCTT 79153		AACG _
		AAGCTGCC GCTCC CTGC		
		TTCGACGG TGGGG GACG		
		CG__ A		
GAM1163	LOC151475	5' AGACATTGACAGCTTTAA 85388		C CGG
		TTAAAGCTG CAA CT		
		AATTCGAC GTT GA		
		A ACA		
GAM1163	LOC153416	3' CAGGGAGCCACAGTATTTAA 60539	_	CCAAC
		TTAAA GCTG GGCTCCCTG		

AATTT TGAC CCGAGGGAC  
 A A\_\_\_\_  
 GAM1163 LOC153768 3' CCCCTGCACAGTGTGGCAGCT 56714 G\_\_\_\_\_ TCCCT  
 T AAGCTGCCAAC GC G  
 ||||| || |  
 TTCGACGGTTG CG C  
 TGACAI|| TCCCT  
 GAM1163 LOC51760 3' CAGGGAAGGCAGCTTT 33265 AACGGC  
 AAAGCTGCC TCCCTG  
 ||||| |||||  
 TTTCGACGG AGGGAC  
 A\_\_\_\_  
 GAM1163 LOC91040 3' CAGGGAGCCACCGGTGCG 64709 T AAC  
 GC GCC GGCTCCCTG  
 || ||| |||||  
 CG TGG CCGAGGGAC  
 C CCA  
 GAM1163 LOC92181 3' CAAAGAGCCAGGCTTTGA 68401 GCCAAC CC  
 TTAAAGCT GGCTC TG  
 ||||| ||||| ||  
 AGTTTCGG CCGAG AC  
 A\_\_\_\_ AA  
 GAM1164 ADM 3' CCTGTGTGGAAGAAGGAAACAC 6663 \_\_\_\_ TT\_  
 C GGTGTTTCC TCC TAGG  
 ||||| ||| ||||  
 CCACAAAGG AGG GTCC  
 AAGA TGT  
 GAM1164 RAB7L1 5' CCTCCCTAAAACGCACACCC 14106 TTCCTCC  
 GGGTGT TTTAGGGAGG  
 ||||| |||||  
 CCCACA AAATCCCTCC  
 CGCA\_\_\_\_  
 GAM1164 SERPINB9 3' CTCTAAAAGGAAACCCCA 14754 T CC  
 TGGG GTTTCCT TTTAGGG  
 ||| ||||| |||||  
 ACCC CAAAGGA AAATCTC  
 - -  
 GAM1164 AF053356\_CDS3 3' CCTCCCTGACAAAAACACCCA 43751 CCTCCT  
 TGGGTGTTT TTAGGGAGG  
 ||||| |||||  
 ACCCACAAA AGTCCCTCC  
 AAAC\_\_\_\_  
 GAM1164 C21orf42 3' TAAAGAAGAAAACACCC 54206 C C  
 GGGTGTTC CT CTTA  
 ||||| || |||||  
 CCCACAAA GA GAAAT  
 A A  
 GAM1164 D2S448 3' CTCCCAAGGAGACACCCA 73521 CCTTTA  
 TGGGTGTTTCCT GGGAG  
 ||||| |||||

		ACCCACAGAGGA	CCCTC		
		A_____			
GAM1164	KCND1	5'	CTCCCTGGAGACACCCA	17141	TTC TTT
			TGGGTGT CTCC AGGGAG		
			ACCCACA GAGG TCCCTC		
			CA_ ____		
GAM1164	KIAA0040	3'	CCCAGGGATGAAACACCCA	27783	C TA
			TGGGTGTTTC TCCTT GGG		
			ACCCACAAAG AGGGA CCC		
			T ____		
GAM1164	KIAA0057	3'	CCTCCCCCATTAGAGAACACCC	24419	TC CCTTTA
	A		TGGGTGTT CT GGGAGG		
			ACCCACAA GA CCCTCC		
			GA TTACC_		
GAM1164	KIAA0672	3'	CCTCCATGCCAGAAAACACCCA	29406	C CCTTTAG
			TGGGTGTTT CT GGAGG		
			ACCCACAAA GA CCTCC		
			A CCGTA_		
GAM1164	KIAA1246	3'	CCCCCTACCCCGCAACACCCA	92053	TCCTCCTT A
			TGGGTGTT TAGGG GG		
			ACCCACAA ATCCC CC		
			CGCCCC_ _		
GAM1164	KIAA1677	3'	CCTCCCTAAAAAAGAGGCA	67064	CTCC
			TGTTTC TTTAGGGAGG		
			ACGGAG AAATCCCTCC		
			AAAA		
GAM1164	LOC143958	5'	CCCTAGAGAAAAAACCCA	76635	G CCTC
			TGGGT TTT CTTTAGGG		
			ACCCA AAA GAGATCCC		
			A A_		
GAM1164	LOC163682	5'	CCCAGGAGGAAAGACCCA	87030	G TTA
			TGGGT TTTCTCCT GGG		
			ACCCA AAAGGAGGA CCC		
			G ____		
GAM1164	LOC54466	3'	CCTATGAGAAGGAAACATCCA	38652	C _
			TGGGTGTTTCCT CTT TAGG		
			ACCTACAAAGGA GAG ATCC		
			A T		
GAM1165	CD68	3'	GGGCGACAGAGCCAGA	59800	_
			TTTGGCTCTGT GTCT		

		AGACCGAGACA CGGG	
		G	
GAM1165 CIAO1	3'	TTGGGTAGAAGTGCAGAGCCA 72549	TC C
		TGGCTCTGTG TC ACCCAA	
		ACCGAGACGT AG TGGGTT	
		GA A	
GAM1165 CIAO1	3'	TTGGGTAGAAGTGCAGAGCCA 16652	TC C
		TGGCTCTGTG TC ACCCAA	
		ACCGAGACGT AG TGGGTT	
		GA A	
GAM1165 ELL	3'	AGACAGCTGCTCAGAGCCAAG 21521	_____
		TTTGGCTCTG TGTCT	
		GAACCGAGAC ACAGA	
		TCGTCTG	
GAM1165 EPB49	3'	GGTAGAGTGGGGGGCCAAA 8789	G T C
		TTTGGCTCT TG CTC ACC	
		AAACCGGGG GT GAG TGG	
		G _ A	
GAM1165 GRAF	3'	TGGGTGACAGAGCCAGA 30580	GTCTC
		TTTGGCTCTGT CACCCA	
		AGACCGAGACA GTGGGT	
		_____	
GAM1165 IGJ	3'	TTTGGGTGATGTAAAACCAA 58318	CTC TG TCC
		TTGG TG TC ACCCAA	
		AACC AT AG TGGGTTT	
		AAA GT _____	
GAM1165 LRRC2	3'	TGGGTGACAGAGCCAGA 44480	GTCTC
		TTTGGCTCTGT CACCCA	
		AGACCGAGACA GTGGGT	
		_____	
GAM1165 LZTR1	5'	TGGGCAAAGCGAGCCAAA 22245	GTCTCCA
		TTTGGCTCTGT CCA	
		AAACCGAGGCG GGGT	
		AAAC_____	
GAM1165 PCMT1	3'	GAGGCACAGAGCCAAA 18222	
		TTTGGCTCTGTGTCTC	
		AAACCGAGACACGGAG	
		_____	
GAM1165 SUPT6H	5'	TTGGGTGTCAAAGTCAAA 60397	C TGTCTC
		TTTGGCT TG CACCCA	

			AAACTGA AC	GTGGGTT	
			A T_____		
GAM1165	ATF3	3'	GGCTGGAAGAGCCAAA	14433	GTGTC C
			TTTGGCTCT TCCA CC		
			AAACCGAGA AGGT GG		
			_____ C		
GAM1165	CBCIP2	3'	GGGCGACAGAGCCAGA	51592	_
			TTTGGCTCTGT GTCT		
			AGACCGAGACA CGGG		
			G		
GAM1165	DIS3	3'	TTTGGGTGAGGACACAGAGCCA	30238	TC
			TGGCTCTGTGTC CACCCAAA		
			ACCGAGACACAG GTGGGTTT		
			GA		
GAM1165	DJ37E16.5	3'	TGGGTGGACCAATCCAAA	39732	CTCTG TC
			TTTGG TG TCCACCCA		
			AAACC AC AGGTGGGT		
			TA__ C_		
GAM1165	DKFZp434E0519	3'	TTTGGGTGGGAACACAGAGCCA	49994	CT
	AA		TTTGGCTCTGTGT CCACCCAAA		
			AAACCGAGACACA GGTGGGTTT		
			AG		
GAM1165	DKFZp434I099	5'	GAGCAGTGCAGAGTCAAA	50083	TG__
			TTTGGCTCTG T CTC		
			AAACTGAGAC G GAG		
			GT AC		
GAM1165	DKFZP564O0423	3'	TGTAGACACAGAACAAA	91704	GC C
			TTTG TCTGTGTCT CA		
			AAAC AGACACAGA GT		
			A_ T		
GAM1165	DKFZP586D0623	5'	TGGGTCACAGAGCC	71977	TCTCC
			GGCTCTGTG ACCCA		
			CCGAGACAC TGGGT		
			_____		
GAM1165	DKFZP667C165	3'	TTTGGGTGGGGACACAGAGCCA	67897	
	AA		TTTGGCTCTGTGTCTCCACCCAAA		
			AAACCGAGACACAGGGGTGGGTTT		
GAM1165	DKFZP727G051	3'	GTGTACACACACAGAGCCA	69478	CTC__
			TGGCTCTGTGT CAC		

		ACCGAGACACA	GTG		
		CACAT			
GAM1165 DOCK3	3'	TTTGAGTGGAGGTATGGAGCCA	66508	GT	C
	GA	TTTGGCTCTGT CTCCAC CAAA			
		AGACCGAGGTA GAGGTG GTTT			
		TG A			
GAM1165 ECG2	3'	TGGGTGGGGGACAGAGCCAGA	50795	G	
		TTTGGCTCTGT TCTCCACCCA			
		AGACCGAGACA GGGGGTGGGT			
		—			
GAM1165 FLJ13241	3'	TGGGTGGCAGAGCCAGA	46969	TGTCT	
		TTTGGCTCTG CCACCCA			
		AGACCGAGAC GGTGGGT			
		—			
GAM1165 FLJ14775	5'	GGCTGCGAGAGCCAAG	51603	G CT	
		TTTGGCTCT TGT CC			
		GAACCGAGA GCG GG			
		— TC			
GAM1165 FLJ31455	3'	GGGCGACAGAGCCAGA	58630	—	
		TTTGGCTCTGT GTCT			
		AGACCGAGACA CGGG			
		G			
GAM1165 KIAA0446	3'	AGGCCAGCAGAGCCAAA	68850	—	
		TTTGGCTCTGT GTCT			
		AAACCGAGACG CGGA			
		AC			
GAM1165 KIAA0446	5'	GTGGGGATTGACAGAGCCAGA	68877	—	
		TTTGGCTCTGT GTCTCCAC			
		AGACCGAGACA TAGGGGTG			
		GT			
GAM1165 KIAA0570	3'	TTTGGGTGGAGACACGGCCAAA	28182	CT	
		TTTGGCT GTGTCTCCACCCAAA			
		AAACCGG CACAGAGGTGGGTTT			
		—			
GAM1165 KIAA0748	3'	TTTGGGTGAGGACACAGATCCA	28946	C TC	
	AA	TTTGG TCTGTGTC CACCCAAA			
		AAACC AGACACAG GTGGGTTT			
		T GA			
GAM1165 KIAA0794	3'	GGACCACAGAGCCAAA	80412	TC	
		TTTGGCTCTGTG TCC			



		AAACCGAGACAC AGG		
		C_		
GAM1165 KIAA1056	3'	TGGGTGACAGAGCCAGA	29699	GTCTC
		TTTGGCTCTGT CACCCA		
		AGACCGAGACA GTGGGT		
		_____		
GAM1165 KIAA1203	3'	GAGCACAGAGGCAAA	71639	G T
		TTTG CTCTGTG CTC		
		AAAC GAGACAC GAG		
		G _		
GAM1165 MGC20235	3'	GGAAAAACAGAGCCAAA	58898	GTC
		TTTGGCTCTGT TCC		
		AAACCGAGACA AGG		
		AAA		
GAM1165 MGC2749	3'	AGACACCAGAGCCAGA	43955	_
		TTTGGCTCTG TGTCT		
		AGACCGAGAC ACAGA		
		C		
GAM1165 MGC29891	3'	TGGGCAACAGAGCCAGA	58219	GTCTCCA
		TTTGGCTCTGT CCCA		
		AGACCGAGACA GGGT		
		AC_____		
GAM1165 MGC4663	3'	TGGGCAACAGAGCCAGA	44509	GTCTCCA
		TTTGGCTCTGT CCCA		
		AGACCGAGACA GGGT		
		AC_____		
GAM1165 MYOZ2	3'	GTGGAATCTAGAATCAAA	33461	GC T C
		TTTG TCTG GT TCCAC		
		AAAC AGAT TA AGGTG		
		TA C _		
GAM1165 PMX2B	5'	GTGGAAAGAGCCAAG	14085	GTGTC
		TTTGGCTCT TCCAC		
		GAACCGAGA AGGTG		
		A_____		
GAM1165 PRO0529	5'	TTGAGTGGCAGAGCCAAG	26003	TGTCT C
		TTTGGCTCTG CCAC CAA		
		GAACCGAGAC GGTG GTT		
		_____ A		
GAM1165 PRO1787	3'	TGGAGGGCAAGAGCCAAA	37769	G _
		TTTGGCTCT TGTC TCCA		

		AAACCGAGA ACGG AGGT		
		— G		
GAM1165	SQV7L	5' GGTGGGCATAGCCAAA 70578	CT	CT
		TTTGGCT GTGT CCACC		
		AAACCGA TACG GGTGG		
		— —		
GAM1165	THEA	3' TTGGAAAAGACACAGAGACA 66303	G	CAC_
	AA	TTTG CTCTGTGTCTC CCAA		
		AAAC GAGACACAGAG GGTT		
		A AAAA		
GAM1165	UBN1	3' GGTAGTAGCAAAAGAGCCAAA 33733	G_	CTCC
		TTTGGCTCT TGT ACC		
		AAACCGAGA ACG TGG		
		AA ATGA		
GAM1165	WBSCR23	5' GGGCGACAGAGCCAGA 46768		—
		TTTGGCTCTGT GTCT		
		AGACCGAGACA CGGG		
		G		
GAM1165	WIRE	3' GGGCGACAGAGCCAGA 78306		—
		TTTGGCTCTGT GTCT		
		AGACCGAGACA CGGG		
		G		
GAM1165	LOC128454	5' TGGAGAAAGGAGCCAAA 75785		GTG
		TTTGGCTCT TCTCCA		
		AAACCGAGG AGAGGT		
		AA_		
GAM1165	LOC137492	3' TGGGACACAAAACCAAA 75269	CTC	T
		TTTGG TGTGTC CCA		
		AAACC ACACAG GGT		
		AAA _		
GAM1165	LOC143279	5' GGACAGAGGAGCCAAA 76510		G_
		TTTGGCTCT TGTCT		
		AAACCGAGG ACAGG		
		AG		
GAM1165	LOC145195	3' TGGGTGGAGACCCCA 83275	CTCTGT	
		TGG GTCTCCACCCA		
		ACC CAGAGGTGGGT		
		C_____		
GAM1165	LOC147837	3' GGGCGACAGAGCCAGA 78518		—
		TTTGGCTCTGT GTCT		

AGACCGAGACA CGGG		
G		
GAM1165 LOC148529 5'	TGGGTGGAATATGAAGCCA 84174	CT C
	TGGCT GTGT TCCACCCA	
	ACCGA TATA AGGTGGGT	
	AG A	
GAM1165 LOC149113 5'	TGGGCTACAAGAGCCAAA 79171	G CTCCA
	TTTGGCTCT TGT CCCA	
	AAACCGAGA ACA GGGT	
	_ TC__	
GAM1165 LOC149302 5'	TGGGTGGAGGGGAGCC 79273	GTG
	GGCTCT TCTCCACCCA	
	CCGAGG GGAGGTGGGT	
_____		
GAM1165 LOC152313 3'	TTTGGGCGGGGACACAACCAAA 85671	CTC A
	TTTGG TGTGTCTCC CCCAAA	
	AAACC ACACAGGGG GGGTTT	
	A__ C	
GAM1165 LOC154403 5'	TGGGCTACAAGAGCCAAA 81077	G CTCCA
	TTTGGCTCT TGT CCCA	
	AAACCGAGA ACA GGGT	
	_ TC__	
GAM1165 LOC158267 3'	GGGTGGGGACACAGAGCCAAA 81837	
	TTTGGCTCTGTGTCTCCACCC	
	AAACCGAGACACAGGGGTGGG	
_____		
GAM1165 LOC158471 3'	TTTGGGTGAAAACACTATGCTA 57184	TCT CTC
A	TTGGC GTGT CACCCAAA	
	AATCG CACA GTGGGTTT	
	TAT AAA	
GAM1165 LOC199733 3'	TGGGCAACAGAGCCAGA 89851	GTCTCCA
	TTTGGCTCTGT CCCA	
	AGACCGAGACA GGGT	
	AC_____	
GAM1165 LOC201868 5'	TGGGCTACAAGAGCCAAA 89083	G CTCCA
	TTTGGCTCT TGT CCCA	
	AAACCGAGA ACA GGGT	
	_ TC__	
GAM1165 LOC255196 3'	TGGGCAACAGAGCCAGA 97177	GTCTCCA
	TTTGGCTCTGT CCCA	

AGACCGAGACA GGGT  
 AC\_\_\_\_  
 GAM1165 LOC255650 5' GGGCAGAAGAGCCACAGAGCCA 96714 T CA\_\_\_\_  
 AA TTTGGCTCTGTG CTC CCC  
 ||||| ||| |||  
 AAACCGAGACAC GAG GGG  
 C AAGAC  
 GAM1165 LOC256520 3' GGGCGACAGAGCCAGA 95980 \_  
 TTTGGCTCTGT GTCT  
 ||||| |||  
 AGACCGAGACA CGGG  
 G  
 GAM1165 LOC81501 3' GAGTTTACAGAGCCAA 47905 T\_  
 TTGGCTCTGTG CTC  
 ||||| |||  
 AACCGAGACAT GAG  
 TT  
 GAM1165 LOC90155 3' TTTGGGTGGAGACACAGCCAAA 61699 CT  
 TTTGGCT GTGTCTCCACCCAAA  
 ||||| |||||  
 AAACCGA CACAGAGGTGGGTTT  
 \_  
 GAM1166 GRINL1A 3' TAACATAGTTTGTGGTATTTCA 69518 \_ ATGTG  
 TGAGA AC AAACATATGTTA  
 ||||| || |||||  
 ACTTT TG TTTGATACAAT  
 A GTG\_  
 GAM1166 ILF1 3' AACATAGTTTTGTTTTTGT TTT 15715 T\_\_ TG  
 CA TGAGAACAA G AAACATATGTT  
 ||||| | |||||  
 ACTTTTGT T TTTGATACAA  
 TTT GT  
 GAM1166 IRTA2 3' GTTTCACATGTCCTCA 48409 A  
 TGAG ACATGTGAAAC  
 ||| |||||  
 ACTC TGTACACTTTG  
 C  
 GAM1166 SCN3A 3' AGTTCACATGTTCCA 22629 A A  
 TG GAACATGTGAA CT  
 || ||||| ||  
 AC CTTGTACACTT GA  
 \_ \_  
 GAM1166 DIS3 3' TAACATAGTTTCACATGTTCTC 30236  
 A TGAGAACATGTGAAACTATGTTA  
 ||||| |||||  
 ACTCTTGTACACTTTGATACAAT  
 \_ \_  
 GAM1166 FBXO26 3' AACATAGTGAAACCGTCTC 46091 ACAT GAA  
 GAGA GT ACTATGTT  
 ||| || |||||

CTCT CA TGATACAA  
 GC\_\_ AAG  
 GAM1166 FLJ13842 3' TAACATATTTAGCACATGTTCT 44987 AAAC\_  
 AGAACATGTG TATGTTA  
 ||||| |||||  
 TCTTGTACAC ATACAAT  
 GATTT  
 GAM1166 FLJ23499 3' TAACACAGTTTCACTCTC 42828 ACAT A  
 GAGA GTGAAACT TGTTA  
 ||| ||||| |||||  
 CTCT CACTTTGA ACAAT  
 \_\_\_\_ C  
 GAM1166 KIAA0979 3' AACATAGTTTTTCATCA 30439 C T  
 A ATG GAAACTATGTT  
 | ||| ||||| |||||  
 A TAC TTTTGATACAA  
 C T  
 GAM1166 KR18 3' AACATAGTTTTATCCTGTCTCA 52736 ACAT  
 TGAGA GTGAAACTATGTT  
 |||| ||||| |||||  
 ACTCT TATTTTGATACAA  
 GTCC  
 GAM1166 PRC1 3' AACATAGTGTAATGGTTCTCA 14289 ATGTGAA  
 TGAGAAC ACTATGTT  
 ||||| |||||  
 ACTCTTG TGATACAA  
 GTAAATG  
 GAM1166 PSKH1 3' TGGTTTCACACATTCCCA 68244 A CA  
 TG GAA TGTGAAACTA  
 || ||| ||||| |||||  
 AC CTT ACACTTTGGT  
 C AC  
 GAM1166 SPINLW1 3' AACAGTCCACGTGTTCTCA 39869 AAATA  
 TGAGAACATGTG TGTT  
 ||||| ||||| |||||  
 ACTCTTGTGCAC ACA  
 CTG\_\_  
 GAM1166 LOC144571 3' TAACATAGGACACATCACTC 83156 AAC AAA  
 GAG ATGTG CTATGTTA  
 ||| ||||| ||||| |||||  
 CTC TACAC GATACAAT  
 AC\_ AG\_  
 GAM1166 LOC145899 3' AGCTTCACTGTTCTCA 83567 T A  
 TGAGAAC A GTGAA CT  
 ||||| ||||| |||||  
 ACTCTTGT CACTT GA  
 \_ C  
 GAM1166 LOC149448 3' AGCTTCTCATGTTCTCA 84419 T A  
 TGAGAACATG GAA CT  
 ||||| ||||| ||||| ||||| ||||| |||||

		ACTCTTGTAC CTT GA			
		T C			
GAM1166	LOC160119	5' AGTATCCACATGTTCCCA	87060	A	AA_
		TG GAACATGTG ACT			
		AC CTTGTACAC TGA			
		C CTA			
GAM1166	LOC219790	3' TAACATAGTTTTTCCTGCCCTC	91358	AA	TGT
		GAG CA GAAACTATGTTA			
		CTC GT TTTTGATACAAT			
		CC CCT			
GAM1166	LOC254848	5' GGCCTCAATGTTCTCA	97093	G	AA
		TGAGAACAT TGA CT			
		ACTCTTGTA ACT GG			
		_ CC			
GAM1166	LOC51308	3' AGTGCCACATGTTCCCA	33490	A	AA
		TG GAACATGTG ACT			
		AC CTTGTACAC TGA			
		C CG			
GAM1166	LOC56267	3' TAACTGAAATCTCACTGTTCTC	39013	T	AACTAT_
	A	TGAGAACA GTGA GTTA			
		ACTCTTGT CACT CAAT			
		_ CTAAAGT			
GAM1167	ARHGEF7	5' TTGGATCACAGTCTTTGCACA	14014	T	CAAAA
		TGTGCAAAG CTG CGA			
		ACACGTTTC GAC GTT			
		T ACTAG			
GAM1167	KIAA1813	5' ATTGTGCAGACTCTGCCA	70291	T A	AAA
		TG GCA AGTCTGC ACGAT			
		AC CGT TCAGACG TGTTA			
		_ C _			
GAM1168	ARHGEF6	3' CAAACTTGAAGCCAGGC	68197	ACCA	
		GCCTGG CAAGTTTG			
		CGGACC GTTCAAAC			
		GAA_			
GAM1168	CNTN2	3' GTCACAACCCAGGTGA	17411	ACCACAA _	
		TGCCTGG GTT TGAC			
		AGTGGACC CAA ACTG			
		_ _ _ C			
GAM1168	CORO2A	3' AAAGTGTGGTCCAGAGA	12642	GC	A
		TC CTGGACCACA GTTT			

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AG GACCTGGTGT CAAA
A_ _
GAM1168 CORO2A 3' AAACGTGTGGTCCAGAGA 53398 GC A
TC CTGGACCACA GTTT
|| ||||| |||
AG GACCTGGTGT CAAA
A_ _
GAM1168 GRLF1 3' AGGTCAGAAAGTGGCCCAGG 78551 A AAG
CCTGG CCAC TTTGACCT
||||| ||| |||||
GGACC GGTG AGACTGGA
C AA_
GAM1168 LAPTM5 3' AGGCTTGTGGTCAAGC 22199 CTG
GC GACCACAAGTTT
|| ||||| |||
CG CTGGTGTTTCGGA
AA_
GAM1168 POU2AF1 3' AGATTTACAGTCCAGGC 20647 CAC
GCCTGGAC AAGTTT
||||| |||
CGGACCTG TTTAGA
ACA
GAM1168 PTGS1 3' GTCTCCTGTCTTATGGTCCAG 6355 C TTT__
CTGGACCA AAG GAC
||||| ||| |||
GACCTGGT TTC CTG
A TGCCT
GAM1168 PTGS1 3' GTCTCCTGTCTTATGGTCCAG 54574 C TTT__
CTGGACCA AAG GAC
||||| ||| |||
GACCTGGT TTC CTG
A TGCCT
GAM1168 TRIM34 5' AGGTCAAGTTGAGCCCAG 55224 ACCA G
CTGG CAA TTTGACCT
||| ||| |||||
GACC GTT GAACTGGA
CGA_ _
GAM1168 TRIM9 5' AGGCCAGGCAAGTCCAGGC 30749 CACAA A
GCCTGGAC GTTTG CCT
||||| ||| |||
CGGACCTG CGGAC GGA
AA__ C
GAM1168 ABLIM 5' GATATGTAACCCAGGCGG 22030 ACC A
TCGCTGG ACA GTT
||||| ||| |||
GGCGGACC TGT TAG
CAA A
GAM1168 AMOT 3' AGGCATCTTCATGGTCCAGGGA 55716 G C_ TT A
TC CCTGGACCA AAG TG CCT
|| ||||| ||| |||

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		AG GGACCTGGT TTC AC GGA		
		— AC T_ _		
GAM1168	DKFZp434D177 5'	TTAGACCCAGGCGA	50056	ACCACAA
		TCGCCTGG GTTTGA		
		AGCGGACC CAGATT		
		—		
GAM1168	DKFZp434D177 5'	TTAGACCCAGGCGA	79443	ACCACAA
		TCGCCTGG GTTTGA		
		AGCGGACC CAGATT		
		—		
GAM1168	FLJ23420 3'	CAAGTGGGTCCAGGC	46845	A AG
		GCCTGGACC CA TTTG		
		CGGACCTGG GT GAAC		
		— —		
GAM1168	HSA249128 5'	GGCGCGGTCCAGGCGG	34152	ACAA
		TCGCCTGGACC GTT		
		GGCGGACCTGG CGG		
		CG_		
GAM1168	MGC15668 5'	AGACCCGGTGGTCCAGACG	51277	C AA_
		CG CTGGACCAC GTTT		
		GC GACCTGGTG CAGA		
		A GCC		
GAM1168	MGC22014 3'	AGGTCCCGAGTGTAACCCAGGT	64486	ACC AGTTT
	GA	TCGCCTGG ACA GACCT		
		AGTGGACC TGT CTGGA		
		CAA GAGCC		
GAM1168	SDCCAG10 5'	AGAGTTGTGGTCCAAAGA	19641	GCC G
		TC TGGACCACAA TTT		
		AG ACCTGGTGTT AGA		
		AA_ G		
GAM1168	LOC115442 3'	AGGTCAGGGATGGTCCAG	72676	CAAG
		CTGGACCA TTTGACCT		
		GACCTGGT GGA CTGGA		
		AG_		
GAM1168	LOC129011 5'	AGACCTGCGGTCCAGGC	74862	A A
		GCCTGGACC CA GTTT		
		CGGACCTGG GT CAGA		
		C C		
GAM1168	LOC130536 5'	GCAAAGTCCAGGCG	75746	CACAAG A
		CGCCTGGAC TTTG C		



GCGGACCTG    AAAC G  
                       C  
 GAM1168 LOC149108 3' AGACTTCACTGTGGTCCA    84357    \_\_\_\_\_  
                       TGGACCACA    AGTTT  
                       |||||||    |||||  
                       ACCTGGTGT    TCAGA  
                       CACT  
 GAM1168 LOC221688 5' AGACTCGGGCCCCAGACGA    93674    C    A    ACA  
                       TCG CTGG CC    AGTTT  
                       ||| ||| ||    |||||  
                       AGC GACC GG    TCAGA  
                       A    C    GC\_  
 GAM1168 LOC256228 5' AGACTTGTGGTCAAAGC    96233    CTG  
                       GC    GACCACAAGTTT  
                       ||    |||||||||  
                       CG    CTGGTGTTTCAGA  
                       AAA  
 GAM1168 LOC257441 5' TTAGACCCAGGCGA    95566    ACCACAA  
                       TCGCCTGG    GTTTGA  
                       |||||||    |||||  
                       AGCGGACC    CAGATT  
  
 GAM1168 LOC91960 3' AGGTGCCTCTCGTGGTCCAAGC 67657    C    A    TTTG  
                       GC TGGACCAC AG    ACCT  
                       ||    ||||||| ||    |||||  
                       CG ACCTGGTG TC    TGGA  
                       A    C    TCCG  
 GAM1168 LOC92840 3' GTCCCTCGGGTCCAGGC    56435    ACA    TTT  
                       GCCTGGACC AG    GAC  
                       ||||||| ||    |||  
                       CGGACCTGG TC    CTG  
                       GC\_ C\_\_  
 GAM1169 AARS    3' TTGCTGCAGAGAATAAAAAG    7833    CAG    TATT  
                       CTTT TCTT    TGCAGCAA  
                       ||| |||    |||||||  
                       GAAA AGAG    ACGTCGTT  
                       ATA    \_\_\_\_\_  
 GAM1169 ADRA2B    3' TTGCTGCAGGGAGATGAAAG    5466    G    AT  
                       CTTTCA TCTTT    TTGCAGCAA  
                       ||||| |||||    |||||||  
                       GAAAGT AGAGG    GACGTCGTT  
  
 GAM1169 AGRN    3' CTGTGAAATAAAGTCTGAAA    78836    T    \_  
                       TTTCAG CTTTATTT GCAG  
                       ||||| ||||||| |||  
                       AAAGTC GAAATAAA TGTC  
                       T    G  
 GAM1169 BECN1    3' TTTGCTGCAGTCTGAAAAGTGA 13650    C    T\_  
                       AA    TTTCAGT TTTA    TTGCAGCAAA  
                       ||||||| |||    |||||||

		AAAGTCA AAGT GACGTCGTTT	
		A CT	
GAM1169 CLASP1	3'	CTGCAACTGCTAGGACTGAAAG 65302	TAT__
		CTTTCAGTCTT TTGCAG	
		GAAAGTCAGGA AACGTC	
		TCGTC	
GAM1169 DNMT3L	5'	CTGCAAACCGGCACTGAAGG 25358	_ TTA
		CTTTCAGT CT TTTGCAG	
		GGAAGTCA GG AAACGTC	
		C CC_	
GAM1169 ENC1	3'	TTTGCTGCACAAACATGAAA 13287	GTCTTTATT
		TTTCA TGCAGCAAA	
		AAAGT ACGTCGTTT	
		ACAAAC__	
GAM1169 FLRT3	3'	CTGCAAAACACTGGAA 25216	CTTTA
		TTTCAGT TTTGCAG	
		AAGGTCA AAACGTC	
		CA__	
GAM1169 FSTL3	3'	AAATAAAGACTCAAAG 19605	C
		CTTT AGTCTTTATTT	
		GAAA TCAGAAATAAA	
		C	
GAM1169 KCNK10	3'	CTGTGCCATAAACAACACTGAAAG 40969	C_ TT_
		CTTTCAGT TTTAT GCAG	
		GAAAGTCA AAATA TGTC	
		AC CCG	
GAM1169 KCNK10	3'	CTGTGCCATAAACAACACTGAAAG 56338	C_ TT_
		CTTTCAGT TTTAT GCAG	
		GAAAGTCA AAATA TGTC	
		AC CCG	
GAM1169 KCNK10	3'	CTGTGCCATAAACAACACTGAAAG 56343	C_ TT_
		CTTTCAGT TTTAT GCAG	
		GAAAGTCA AAATA TGTC	
		AC CCG	
GAM1169 RP2	3'	TTTGATAAAACTAAGACTGAAA 22622	TA GCAG
		TTTCAGTCTT TTT CAAA	
		AAAGTCAGAA AAA GTTT	
		TC ATA_	
GAM1169 SCA1	5'	TGCTGCAAGGAACACTGATAG 4401	T CTTTA
		CT TCAGT TTTGCAGCA	

			GA AGTCA	GAACGTCGT		
			T	AG__		
GAM1169	VSX1	3'	CTGTCAAAGGCTGAAA	27466	ATTT	
			TTTCAGTCTTT	GCAG		
			AAAGTCGGAAA	TGTC		
			C__			
GAM1169	DKFZP586C1324	3'	CTGCATTGGGTGAAGACTAAAA	69797	C	__
			TTT AGTCTTTATT	TGCAG		
			AAA TCAGAAAGTGG	ACGTC		
			A	GTT		
GAM1169	DNAH7	3'	TGAAATAAATAAAGACTAAAG	38159	C	CAG
			CTTT AGTCTTTATTTG	CA		
			GAAA TCAGAAATAAAT	GT		
			-	AAA		
GAM1169	EDR1	3'	TGCTGCAGGGACTAAAAG	15385	C	TTAT
			CTTT AGTCT	TTGCAGCA		
			GAAA TCAGG	GACGTCGT		
			A	__		
GAM1169	FLJ10305	5'	CTGCAGCCAGCACTGAAAG	68359	_	TTAT
			CTTTCAGT CT	TTGCAG		
			GAAAGTCA GA	GACGTC		
			C	CC__		
GAM1169	FLJ10460	3'	TTTGCTGCTGGTAATACTGAAA	36135	CT	TT
	G		CTTTCAGT	TTAT GCAGCAAA		
			GAAAGTCA AATG	CGTCGTTT		
			T_	GT		
GAM1169	FLJ20340	3'	TTTGCTACAAAGGGGCTGCAAA	34981	_	TA C
	G		CTTT CAGTCTT	TTTG AGCAAA		
			GAAA GTCGGGG	AAAC TCGTTT		
			C	_ A		
GAM1169	FLJ22557	3'	TGTTGAAAAGACTGAAAG	45256	ATTG	
			CTTTCAGTCTTT	CAGCA		
			GAAAGTCAGAAA	GTTGT		
			A__			
GAM1169	FLJ22940	5'	TGCTGCAGACCAGAAAG	44698	A_	TTATTT
			CTTTC GTCT	GCAGCA		
			GAAAG CAGA	CGTCGT		
			AC	_____		
GAM1169	GBTS1	3'	TTGCTGTTGCAAGACTGAAGG	59066	TATTT	
			CTTTCAGTCTT	GCAGCAA		

			GGAAGTCAGAA	TGTCGTT	
			CGT__		
GAM1169	GT650	3'	CTGCTATTCAAAA	ACTGAGAG	53455 C ATTT_
			CTTTCAGT	TTT GCAG	
			GAGAGTCA	AAA CGTC	
			A	CTTAT	
GAM1169	KIAA0537	3'	GCTGTGACAAC	AGACTGAAA	29250 TTAT TG
			TTTCAGTCT	T CAGC	
			AAAGTCAGA	A GTCG	
			CAAC	GT	
GAM1169	KIAA1165	3'	CTGCCTTAAAG	ATTGAAA	67406 TTT
			TTTCAGTCTTTA	GCAG	
			AAAGTTAGAAAT	CGTC	
			TC_		
GAM1169	KIAA1464	3'	TTGCTACAAATA	AAGGA	68278 C
			TCTTTATTTG	AGCAA	
			AGGAATAAAC	TCGTT	
			A		
GAM1169	MAP2K4	3'	TGCCACAAACC	ACCAGGACTGA	11553 TA__ CA
	AAG		CTTTCAGTCTT	TTTG GCA	
			GAAAGTCAGGA	AAAC CGT	
			CCACC	AC	
GAM1169	NYD-SP15	3'	GAATAAATACT	GAAAG	48110 C
			CTTTCAGT	TTTATTT	
			GAAAGTCA	AAATAAG	
			T		
GAM1169	PEX11A	3'	TTTGCTGAATGAATA	AAAAATTG	13890 C G__
	AAAG		CTTTCAGT	TTTATTT CAGCAAA	
			GAAAGTTA	AAATAAG GTCGTTT	
			A	TAA	
GAM1169	PIGM	5'	TGCTGCAAAGA	ACCGAAGG	59047 A CTTTA
			CTTTC	GT TTTGCAGCA	
			GGAAG	CA AAACGTCGT	
			C	AG__	
GAM1169	PPIL3	5'	GCTGTAAGACT	GAGA	55656 TTATT
			TTTCAGTCT	TGCAGC	
			AGAGTCAGA	ATGTCG	
			_____		
GAM1169	PPIL3	5'	GCTGTAAGACT	GAGA	55658 TTATT
			TTTCAGTCT	TGCAGC	

AGAGTCAGA ATGTCG

GAM1169 PPIL3 5' GCTGTAAGACTGAGA 50645 TTATT  
TTTCAGTCT TGCAGC  
||||||| |||||  
AGAGTCAGA ATGTCG

GAM1169 SLC17A6 3' TTGCTGTAAAAATGAAA 39749 GTCTTTA  
TTTCA TTTGCAGCAA  
||||| |||||  
AAAGT AAATGTCGTT  
AA\_\_\_\_\_

GAM1169 TBLR1 3' CTGCCAATTAAAGACTAGAAG 45101 TC T \_  
CTT AGTCTTTA TTG CAG  
||| ||||| ||| |||  
GAA TCAGAAAT AAC GTC  
GA T C

GAM1169 ZNF304 3' TTGCTAGGAAAGACTGAAA 40319 ATTT  
TTTCAGTCTTT GCAG  
||||||| |||  
AAAGTCAGAAA CGTT  
GGAT

GAM1169 LOC113115 5' TGCTGTAAGACAGAAAG 56547 A TTATT  
CTTTC GTCT TGCAGCA  
||||| ||| |||||  
GAAAG CAGA ATGTCGT  
A \_\_\_\_\_

GAM1169 LOC115004 3' TGCTGCTCAGACTGAA 73176 TTATTT  
TTCAGTCT GCAGCA  
||||||| |||||  
AAGTCAGA CGTCGT  
CT\_\_\_\_\_

GAM1169 LOC145845 3' CAGATAAAGACTAAAA 83552 C  
TTT AGTCTTTATTTG  
||| |||||  
AAA TCAGAAATAGAC  
A

GAM1169 LOC160897 3' GCAGTACCAAGACTGAAA 82246 TAT\_  
TTTCAGTCTT TTGC  
||||||| |||  
AAAGTCAGAA GACG  
CCAT

GAM1169 LOC162333 5' CTCAGATAAAGACTGAA 87129 C  
TTCAGTCTTTATTTG AG  
||||||| |||  
AAGTCAGAAATAGAC TC

GAM1169 LOC223073 5' TTGCCTGAAGACTGAAA 94381 TTT  
TTTCAGTCTTTA GCAG  
||||||| |||

		AAAGTCAGAAAGT CGTT		
		C__		
GAM1169	LOC255177 3'	CTGGGATTACAGAGACTGAAA	96604	AT__ G
		TTTCAGTCTTT TT CAG		
		AAAGTCAGAGA AG GTC		
		CATT G		
GAM1169	LOC256730 3'	TTGCAGCAAGACTGAAA	95236	TTATT A
		TTTCAGTCT TGC GCAA		
		AAAGTCAGA ACG CGTT		
		_____ A		
GAM1169	LOC257469 3'	CTGCTGGTGAAGACTG	95714	TT
		CAGTCTTTAT GCAG		
		GTCAGAAGTG CGTC		
		GT		
GAM1169	LOC90529 3'	TGCCGCAGACTGAAGG	63165	TTATTT A
		CTTTCAGTCT GC GCA		
		GGAAGTCAGA CG CGT		
		_____ C		
GAM1170	KHK 3'	CTGGATTCAAATCTGCCA	4032	CA
		TGGCA ATTTGAATTCAG		
		ACCGT TAAACTTAGGTC		
		C_		
GAM1170	KHK 3'	CTGGATTCAAATCTGCCA	21402	CA
		TGGCA ATTTGAATTCAG		
		ACCGT TAAACTTAGGTC		
		C_		
GAM1170	NRXN3 5'	GCTGGAATTCAAAGTCC	57280	CAA _
		GGCA TTTGAATTC AGT		
		CCGT AAAGTTAAG TCG		
		C_ G		
GAM1170	PRSS16 3'	CTGGTTCAAATTCTGCCA	19629	C T
		TGGCA AATTTGAAT CAG		
		ACCGT TTAACTTG GTC		
		C _		
GAM1170	PXF 3'	ATTCAAGATTGTGCCA	11149	_
		TGGCACAATTT GAAT		
		ACCGTGTTAGA CTTA		
		A		
GAM1170	RAG1 3'	TTACTGAAACATTTTGCCA	4819	C TTGAA
		TGGCA AAT TTCAGTAA		

ACCGT TTA AAGTCATT  
 T CA\_\_\_\_  
 GAM1170 SLC25A15 3' ACTGAAATTGTGCCA 26507 TGAAT  
 TGGCACAATT TCAGT  
 ||||| ||||  
 ACCGTGTTAA AGTCA

\_\_\_\_\_  
 GAM1170 TPM1 3' CTGGTTCAAATGTGCCA 4526 A T  
 TGGCACA TTTGAAT CAG  
 ||||| ||||| |||  
 ACCGTGT AAACCTTG GTC

- -  
 GAM1170 DKFZP434E2135 5' TTACTGAGATCAGCCA 47959 ACAATT A  
 TGGC TGA TTCAGTAA  
 ||| ||| |||||  
 ACCG ACT GAGTCATT  
 \_\_\_\_\_ A

GAM1170 FLJ10824 3' ACTGAATTCTGAGGGTGCC 72574 AA T  
 GGCAC TT GAATTCAGT  
 |||| || |||||  
 CCGTG AG CTTAAGTCA  
 GG T

GAM1170 FLJ22282 3' TGGACCAAATTGTGCC 45594 AA  
 GGCACAATTTG TTCA  
 ||||| ||||  
 CCGTGTTAAAC AGGT  
 C\_

GAM1170 H2AV 3' CTAGATTCAAATTATGC 56848 C TC  
 GCA AATTTGAAT AG  
 ||| ||||| ||  
 CGT TTAACTTA TC  
 A GA

GAM1170 HPCL2 3' TACTGTTAAAATTGTGC 24323 GAATT  
 GCACAATTT CAGTA  
 ||||| ||||  
 CGTGTAAA GTCAT  
 ATT\_

GAM1170 KIAA0256 3' TTTACTGAACTCATTGGGACTA 64425 CA\_ TT A  
 TGG CAA TGA TTCAGTAAA  
 ||| ||| ||| |||||  
 ATC GTT ACT AAGTCATTT  
 AGG \_ C

GAM1170 KIAA0265 3' TTAGGTTCAAATTATGCCA 69888 C TC  
 TGGCA AATTTGAAT AG  
 |||| ||||| ||  
 ACCGT TTAACTTG TT  
 A GA

GAM1170 KRTAP2-4 3' TTTTACTGCTCAAACGTGCACC 52592 C\_ A ATT  
 A TGG ACA TTTGA CAGTAAAA  
 ||| ||| |||| |||||

			ACC TGT AAAC T GTCATTTT		
			AC C C__		
GAM1170	SGKL	3'	ACTGAAATTGTGCCA	25139	TGAAT
			TGGCACAATT TCAGT		
			ACCGTGTAA AGTCA		
GAM1170	Spir-1	5'	TACTGAATCAGATGCACCA	64702	CACA A
			TGG ATTTGA TTCAGTA		
			ACC TAGACT AAGTCAT		
			ACG_ _		
GAM1170	LOC149566	3'	TTGGTTTAAATTATGCCA	84498	C T
			TGGCA AATTTGAAT CAG		
			ACCGT TTAAATTTG GTT		
			A _		
GAM1170	LOC158490	3'	TTTACTGAAAATCCTGCCA	81936	CA GAAT
			TGGCA ATTT TCAGTAAA		
			ACCGT TAAA AGTCATTT		
			CC _		
GAM1170	LOC201183	5'	TTTACTGCTGAATTGTCCA	89759	C AATT
			TGG ACAATTTG CAGTAAA		
			ACC TGTAAAGT GTCATTT		
			_ C__		
GAM1170	LOC253725	3'	ACTGAATTCTGAGGGTGCC	94700	AA T
			GGCAC TT GAATTCAGT		
			CCGTG AG CTTAAGTCA		
			GG T		
GAM1170	LOC254268	3'	GAATTCAAATTAACCA	95408	CAC
			TGG AATTTGAATTC		
			ACC TTAAACTTAAG		
			AA_		
GAM1170	LOC51133	3'	TTTACTGAATTTTCAGT	32286	T
			ATT GAATTCAGTAAA		
			TGA TTAAAGTCATTT		
			C		
GAM1170	LOC54466	3'	TTACTGAACTCAGGTACAGC	38656	ACA A
			GC ATTTGA TTCAGTAA		
			CG TGGACT AAGTCATT		
			ACA C		
GAM1171	KHK	3'	CTGGATTCAAATCTGCCA	4032	CA
			TGGCA ATTTGAATTCAG		



		ACCGT TAAACTTAGGTC		
		C_		
GAM1171	KHK	3' CTGGATTCAAATCTGCCA	21402	CA
		TGGCA ATTTGAATTCAG		
		ACCGT TAAACTTAGGTC		
		C_		
GAM1171	NRXN3	5' GCTGGAATTCAAACTGCC	57280	CAA _
		GGCA TTTGAATTC AGT		
		CCGT AAACTTAAG TCG		
		C_ G		
GAM1171	PRSS16	3' CTGGTTCAAATTCTGCCA	19629	C T
		TGGCA AATTTGAAT CAG		
		ACCGT TTAAACTTG GTC		
		C _		
GAM1171	PXF	3' ATTCAAGATTGTGCCA	11149	_
		TGGCACAATTT GAAT		
		ACCGTGTTAGA CTTA		
		A		
GAM1171	RAG1	3' TTAAGTAAACATTTTGCCA	4819	C TTGAA
		TGGCA AAT TTCAGTAA		
		ACCGT TTA AAGTCATT		
		T CA_		
GAM1171	SLC25A15	3' ACTGAAATTGTGCCA	26507	TGAAT
		TGGCACAATT TCAGT		
		ACCGTGTTAA AGTCA		
		_____		
GAM1171	TPM1	3' CTGGTTCAAATGTGCCA	4526	A T
		TGGCACA TTTGAAT CAG		
		ACCGTGT AAAGTTG GTC		
		_____		
GAM1171	DKFZP434E2135	5' TTAAGTGAATCAGCCA	47959	ACAATT A
		TGGC TGA TTCAGTAA		
		ACCG ACT GAGTCATT		
		_____ A		
GAM1171	FLJ10824	3' ACTGAATTCTGAGGGTGCC	72574	AA T
		GGCAC TT GAATTCAGT		
		CCGTG AG CTTAAGTCA		
		GG T		
GAM1171	FLJ22282	3' TGGACCAAATTGTGCC	45594	AA
		GGCACAATTTG TTCA		

CCGTGTTAAAC AGGT  
 C\_  
 GAM1171 H2AV 3' CTAGATTCAAATTATGC 56848 C TC  
 GCA AATTTGAAT AG  
 ||| ||||| ||  
 CGT TTAAACTTA TC  
 A GA  
 GAM1171 HPCL2 3' TACTGTAAAAATTGTGC 24323 GAATT  
 GCACAATTT CAGTA  
 ||||| ||||  
 CGTGTTAAA GTCAT  
 ATT\_  
 GAM1171 KIAA0256 3' TTTACTGAACTCATTGGGACTA 64425 CA\_ TT A  
 TGG CAA TGA TTCAGTAAA  
 ||| ||| ||| |||||  
 ATC GTT ACT AAGTCATTT  
 AGG \_ C  
 GAM1171 KIAA0265 3' TTAGGTTCAAATTATGCCA 69888 C TC  
 TGGCA AATTTGAAT AG  
 |||| ||||| ||  
 ACCGT TTAAACTTG TT  
 A GA  
 GAM1171 KRTAP2-4 3' TTTTACTGCTCAAACGTGCACC 52592 C\_ A ATT  
 A TGG ACA TTTGA CAGTAAAA  
 ||| ||| |||| |||||  
 ACC TGT AAAC TGCATTTT  
 AC C C\_  
 GAM1171 SGKL 3' ACTGAAATTGTGCCA 25139 TGAAT  
 TGGCACAATT TCAGT  
 ||||| ||||  
 ACCGTGTTAA AGTCA  
 \_\_\_\_\_  
 GAM1171 Spir-1 5' TACTGAATCAGATGCACCA 64702 CACA A  
 TGG ATTTGA TTCAGTA  
 ||| |||| |||||  
 ACC TAGACT AAGTCAT  
 ACG\_ \_  
 GAM1171 LOC149566 3' TTGGTTTAAATTATGCCA 84498 C T  
 TGGCA AATTTGAAT CAG  
 |||| ||||| |||  
 ACCGT TTAAATTTG GTT  
 A \_  
 GAM1171 LOC158490 3' TTTACTGAAAATCCTGCCA 81936 CA GAAT  
 TGGCA ATTT TCAGTAAA  
 |||| ||| |||||  
 ACCGT TAAA AGTCATTT  
 CC \_\_\_\_  
 GAM1171 LOC201183 5' TTTACTGCTGAATTGTCCA 89759 C AATT  
 TGG ACAATTTG CAGTAAA  
 ||| ||||| |||||

ACC TGTTAAGT GTCATTT  
 \_ C\_  
 GAM1171 LOC253725 3' ACTGAATTCTGAGGGTGCC 94700 AA T  
 GGCAC TT GAATTCAGT  
 |||| || |||||  
 CCGTG AG CTTAAGTCA  
 GG T  
 GAM1171 LOC254268 3' GAATTCAAATTAACCA 95408 CAC  
 TGG AATTTGAATTC  
 || |||||  
 ACC TTAAACTTAAG  
 AA\_  
 GAM1171 LOC51133 3' TTTACTGAATTTTCAGT 32286 T  
 ATT GAATTCAGTAAA  
 || |||||  
 TGA TTTAAGTCATTT  
 C  
 GAM1171 LOC54466 3' TTAAGTCAAGTACAGC 38656 ACA A  
 GC ATTTGA TTCAGTAA  
 || |||||  
 CG TGGACT AAGTCATT  
 ACA C  
 GAM1172 LYPLA1 3' ACAATATTAAGAATGCAT 20919 \_ \_  
 GTGCATTCT AGTGT GT  
 ||||| |||||  
 TACGTAAGA TTATA CA  
 A A  
 GAM1172 MPP1 3' AAATGACACATCTGTGCA 10110 TCTA  
 TGCAT GTGTGTCATTT  
 |||| |||||  
 ACGTG TACACAGTAAA  
 TC\_  
 GAM1172 EPB41L1 3' TGAGCACACTGAACAC 70599 CA T \_  
 GTG TTC AGTGTG TCA  
 || || ||||| ||  
 CAC AAG TCACAC AGT  
 \_ \_ G  
 GAM1172 HRIHFB2072 3' AAATCATGTACTAAATGCAC 50723 C TG C  
 GTGCATT TAGTG T ATTT  
 ||||| ||||| |||||  
 CACGTAA ATCAT A TAAA  
 \_ GT C  
 GAM1172 KIAA0417 3' ACACACTGAACGCAC 71240 A T  
 GTGC TTC AGTGTGT  
 |||| || |||||  
 CACG AAG TCACACA  
 C \_  
 GAM1172 KIAA1940 3' GGGTGGTACACACTAGAATGC 79987 \_  
 GCATTCTAGTGTGT CATT  
 ||||| |||||

CGTAAGATCACACA GTGGG  
TG  
GAM1172 MGC1842 3' TGGTCTTCACACCAGATTGCAC 65663 T A TCATT  
GTGCA TCT GTGTG TCA  
||||| ||| ||||| |||  
CACGT AGA CACAC GGT  
T C TTCT\_  
GAM1172 STIP-1 3' GAATTTCAACACTAGAATG 69664 GTCAT  
CATTCTAGTGT TTC  
||||||| |||  
GTAAGATCACA AAG  
ACTTT  
GAM1172 LOC257464 5' TTGAAACAATACAATGAATGCA 89675 TAG CA  
C GTGCATTG TGTGT TTTCAA  
||||||| ||||| |||||  
CACGTAAG ACATA AAAGTT  
TA\_ AC  
GAM1173 THBS1 3' GGAAAACCTACCATCTC 12283 A  
GAGGT GTAGGTTTTCT  
||||| ||||| |||||  
CTCTA CATCCAAAAGG  
C  
GAM1173 ESM1 3' ACAACCAGAAAACCCCT 22874 TAGTA A  
AGG GGTTTTCTG TTGT  
||| ||||| |||||  
TCC CCAAAGAC AACA  
C  
GAM1174 AQP3 3' TTCACGATCCACCCTTTC 59593 T\_ \_  
GAAA GTGG TCGTGAA  
||||| ||||| |||||  
CTTT CACC AGCACTT  
CC T  
GAM1174 ARSB 3' TCACGACTCTTGTC 3502 AATGTG  
GACAAGA GTCGTGA  
||||||| |||||  
CTGTTCT CAGCACT  
GAM1174 B4GALT5 3' TTTTCACAAAAATAGTCCTTTG 16519 AAA\_ GGTC  
TCA TGACAAG TGT GTGAAAA  
||||||| ||| |||||  
ACTGTTT ATA CACTTTT  
CCTG AAAA  
GAM1174 CHRNA3 3' TCGTTACCCATTTCTT 5610 T CG  
AAGAAATG GGT TGA  
||||||| ||| |||  
TTCTTTAC CCA GCT  
\_ TT  
GAM1174 DRD1 3' TTACAACCACATTTCTGGCCA 5840 ACA C  
TG AGAAATGTGGT GTGA  
|| ||||| ||||| |||||

AC TCTTTACACCA CATT  
 CGG A  
 GAM1174 FUT1 3' TCTGATCACATCCCCTGTC 3798 AGAA T  
 GACA ATGTGGTTCG GA  
 ||| ||||| ||  
 CTGT TACACTAGT CT  
 CCCC \_  
 GAM1174 IRF1 3' GCCACATTTCTGATCA 64345 CA  
 TGA AGAAATGTGGT  
 ||| |||||  
 ACT TCTTTACACCG  
 AG  
 GAM1174 MAP3K8 5' TCACGACCACCTCATG 17791 A AAT  
 CA GA GTGGTTCGTGA  
 || || |||||  
 GT CT CACCAGCACT  
 A C\_  
 GAM1174 NGFR 3' TTCTGACCACACTTCCTGTC 10231 A A T  
 GACA GAA TGTGGTCG GAA  
 ||| || ||||| |||  
 CTGT CTT ACACCAGT CTT  
 C C \_  
 GAM1174 OLR1 3' TTCACAACAGTTCTTGTTA 10341 ATGTG C  
 TGACAAGAA GT GTGAA  
 ||||| || |||  
 ATTGTTCTT CA CACTT  
 GA\_ A  
 GAM1174 POU4F1 3' CACTGAAAACATTTTGTCA 20660 A GG \_  
 TGACAAGAA TGT TC GTG  
 ||||| || |||  
 ACTGTTTTT ACA AG CAC  
 \_ AA T  
 GAM1174 SMP1 3' TTTCACATGAATAATTTTGTGTC 26705 A GGTC  
 A TGACAAGAA TGT GTGAAA  
 ||||| || |||  
 ACTGTTTTT ATA CACTTT  
 A AGTA  
 GAM1174 ZNF264 3' TTCTATTAACATTTCTTTTCA 12769 C GGTCGT  
 TGA AAGAAATGT GAA  
 ||| ||||| |||  
 ACT TTCTTTACA CTT  
 T ATTAT\_  
 GAM1174 C20orf175 3' CGAGCTCCACGTTTCCTGCCA 55063 A A \_  
 TG CA GAAATGTGG TCG  
 || || ||||| |||  
 AC GT CTTTGCACC AGC  
 C C TCG  
 GAM1174 CAPNS2 3' TTTCACAACCCTACATATTCT 50323 CA \_ C  
 GATCA TGA AGAAATGT GGT GTGAAA  
 ||| ||||| ||| |||||

ACT TCTTTATA CCA CACTTT  
 AG CATC A  
 GAM1174 CLDN6 3' TTTACACTCACATTTTATCA 41041 CA \_ C  
 TGA AGAAATGTG GT GTGAA  
 ||| ||||| || |||||  
 ACT TTTTACAC CA CATT  
 A\_ T \_  
 GAM1174 DKFZP564L0864 3' GCACCAATTTCTTGCCA 72555 A G C  
 TG CAAGAAAT TGGT GT  
 || ||||| ||| ||  
 AC GTTCTTTA ACCA CG  
 C \_ \_  
 GAM1174 DKFZP566B183 3' TTTCCATAAACATTTCTTTTCA 31330 C GGTCGT  
 TGA AAGAAATGT GAAA  
 ||| ||||| |||  
 ACT TTCTTTACA CTTT  
 T AATAC\_  
 GAM1174 GTF2E1 3' TACAGACCTCTTGTCA 18616 AATGT \_  
 TGACAAGA GGTC GTG  
 ||||| ||| |||  
 ACTGTTCT CCAG CAT  
 \_ A  
 GAM1174 KIAA0089 3' TTTTAATTCACATTTCTT 69967 TCG  
 AAGAAATGTGG TGAAA  
 ||||| |||  
 TTCTTTACACT ATTTT  
 TA\_  
 GAM1174 KIAA0373 5' TTTTCAAAGTAACATTTCTT 28015 GGTCG  
 AAGAAATGT TGAAAA  
 ||||| |||  
 TTCTTTACA ACTTTT  
 ATGAA  
 GAM1174 KIAA1813 3' TTTTCACACTGTAAATTTCTTG 70314 \_ TG C  
 T ACAAGAAAT G GT GTGAAAA  
 ||||| | |||||  
 TGTTCTTTA T CA CACTTTT  
 AA GT \_  
 GAM1174 KIAA1951 3' TTCCAGGCTTCTCTTGTC 73766 AATGT GT  
 TGACAAGA GGTC GAA  
 ||||| ||| |||  
 ACTGTTCT TCGG CTT  
 CT\_ AC  
 GAM1174 MGC4170 3' TTCACCATTTCTTGTC 44227 TGGTC  
 GACAAGAAATG GTGAA  
 ||||| |||  
 CTGTTCTTTAC CACTT  
 \_  
 GAM1174 NRN1 3' CACTGCACATTTCTCCTCA 33432 CA GTC  
 TGA AGAAATGTG GTG  
 ||| ||||| |||

ACT TCTTTACAC CAC  
 CC GT\_  
 GAM1174 PLA2G12 3' TTTTCACAACCACATTT 48028 C  
 AAATGTGGT GTGAAAA  
 ||||| |||||  
 TTTACACCA CACTTTT  
 A  
 GAM1174 PPY2 3' CACTCCACATTCCTGGCCA 40819 ACA A TC  
 TG AG AATGTGG GTG  
 || ||||| |||  
 AC TC TTACACC CAC  
 CGG C T\_  
 GAM1174 ZNF31 3' TTTGTAGACCACATTTCTGT 64992 A \_TG  
 A TGACA GAAATGTGGTC G AA  
 |||| ||||| |||  
 ATTGT CTTTACACCAG T TT  
 C A GT  
 GAM1174 LOC115219 3' CACGACAACGGGTCCTCA 73295 CAA AA G  
 TGA GA TGT GTCGTG  
 ||| || |||||  
 ACT CT GCA CAGCAC  
 C\_ GG A  
 GAM1174 LOC120376 5' TTCAGAGCATTTCTTTCA 75986 C GG G  
 TGA AAGAAATGT TC TGAA  
 ||| ||||| || ||||  
 ACT TTCTTTACG AG ACTT  
 \_ \_  
 GAM1174 LOC133418 3' TTTTCATATACATTTTGTGCCA 75094 A GTC  
 TG CAAGAAATGTG GTGAAA  
 || ||||| |||||  
 AC GTTTTACAT TACTTT  
 C A\_  
 GAM1174 LOC151199 3' TTAAAACACAGCTCTTGCCA 80174 A AA CG  
 TG CAAGA TGTGGT TGA  
 || |||| ||||| |||  
 AC GTTCT ACACCA ATT  
 C CG AA  
 GAM1174 LOC152317 5' TCACACTGACTTTTGTCA 85649 AATG C  
 TGACAAGA TGGT GTGA  
 ||||| |||||  
 ACTGTTTT GTCA CACT  
 CA\_ \_  
 GAM1174 LOC152674 3' TTCAACCCACCCTCTTGTC 85841 AAT TCG  
 TGACAAGA GTGG TGAA  
 ||||| ||| ||||  
 ACTGTTCT CACC ACTT  
 CC\_ CA\_  
 GAM1174 LOC152845 5' CATGACCACATTTTCA 60330 CAA  
 TGA GAAATGTGGTCGTG  
 ||| |||||

ACT TTTTACACCAGTAC

GAM1174 LOC154743 3' TTTAGTCCACATTGTCTTGTCA 81118 \_ TCG  
TGACAAGA AATGTGG TGAA  
||||||| ||||| ||||  
ACTGTTCT TTACACC ATTT  
G TG\_

GAM1174 LOC165476 5' TTCACGGCACCTTCT 87201 AT G  
AGAA GTG TCGTGAA  
|||| ||| |||||  
TCTT CAC GGCACCT  
C\_ \_

GAM1174 LOC254266 5' TTTTCGGTCACACATCTTATCA 97356 C AA GT T  
TGA AAGA TGTG CG GAA  
||| |||| |||| ||||  
ACT TTCT ACAC GC TTT  
A AC TG T

GAM1174 LOC255919 3' TTTTCATTCTTACATTTCTAATC 95043 CA TC  
A TGA AGAAATGTGG GTGAAA  
||| ||||| |||||  
ACT TCTTTACATT TACTTT  
AA CT

GAM1174 LOC51754 5' CACGGCCACATCTCTGTCA 71027 A A  
TGACA GA ATGTGGTCGTG  
||||| || |||||  
ACTGT CT TACACCGGCAC  
\_ C

GAM1174 LOC55862 3' ACCTCATTTCTTGCCA 37485 A T  
TG CAAGAAATG GGT  
|| ||||| |||||  
AC GTTCTTTAC CCA  
C T

GAM1174 LOC55954 3' CACGTGGTCACTTTTCTCATCA 38877 CA T GT \_  
TGA AGAAA GTG C GTG  
||| ||||| ||| | |||  
ACT TCTTT CAC G CAC  
AC T TG TG

GAM1175 ADAMTS8 5' TCGGGCCGCCAGCACCTG 22886 \_ ATAAG  
CAG TGCTGGC CTGA  
||| ||||| |||||  
GTC ACGACCG GGCT  
C CCG\_

GAM1175 BAP1 3' TCAGGGACCCAGCACTGG 16219 CATAAG  
CCAGTGCTGG CTGA  
||||||| |||||  
GGTCACGACC GACT  
CAGG\_

GAM1175 BF 5' TTCAGCTTGGGACACTG 8140 CTGGCA  
CAGTG TAAGCTGAA  
||||| |||||



GTCAC GTTCGACTT  
 AG\_\_\_\_  
 GAM1175 C1QB 3' TTCAACTCTGTGTCCCACT 4923 A \_ \_ C  
 GGC G CCAGTGCTGG CATA AG TGAA  
 | ||||| ||| || |||  
 C GGTACGACC GTGT TC ACTT  
 \_ CT C A  
 GAM1175 CHC1 3' CAGCCCTGAGCACTGTGTC 7020 \_ \_ CATAA  
 GAC CAGTGCT GG GCTG  
 ||| ||||| || |||  
 CTG GTCACGA CC CGAC  
 T GT \_\_\_\_\_  
 GAM1175 CMRF35 5' CAGAGCTGTCAGACCGG 21929 A TAAG  
 CC GTGCTGGCA CTG  
 || ||||| |||  
 GG CACGACTGT GAC  
 C CGA\_  
 GAM1175 EPHB6 3' TCAGCCCTGGACACTGGTC 15466 \_ TG CATAA  
 GACCAGTG C G GCTGA  
 ||||| | | |||||  
 CTGGTCAC G C CGACT  
 A GT C\_\_\_\_  
 GAM1175 EVPL 5' CAGCCTGAGCCAGCACT 8803 A A  
 AGTGCTGGC TA GCTG  
 ||||| || |||  
 TCACGACCG GT CGAC  
 A C  
 GAM1175 GARP 3' CAGCCCAGCACTGG 18594 CATAA  
 CCAGTGCTGG GCTG  
 ||||| |||  
 GGTACGACC CGAC  
 \_\_\_\_\_  
 GAM1175 GJB5 3' CAGCTCGACGGCACTGG 17945 GCATA  
 CCAGTGCTG AGCTG  
 ||||| |||  
 GGTACGGC TCGAC  
 AGC\_  
 GAM1175 GPR81 3' CTTACCAGCATTAGTC 50757 C CA  
 GAC AGTGCTGG TAAG  
 ||| ||||| |||  
 CTG TTACGACC ATTC  
 A \_  
 GAM1175 IFI16 5' AGCAAGCCAGCACTAGTC 71221 C ATAA  
 GAC AGTGCTGGC GCT  
 ||| ||||| |||  
 CTG TCACGACCG CGA  
 A AA\_  
 GAM1175 KRT4 3' CAGCTGGGCCCACTGGT 9635 \_ ATA  
 ACCAGTGCTGG C AGCTG  
 ||||| | |||||

TGGTCACGACC G TCGAC  
 C GG\_  
 GAM1175 MAP3K9 3' TTCAGCTTCCCAAACACCAGT 60709 CA C\_ CAT  
 AC GTG TGG AAGCTGAA  
 || ||| ||| |||||  
 TG CAC ACC TTCGACTT  
 AC AA C\_  
 GAM1175 MGAT5 5' TCAGCTTACAGTTCCTG 10028 T\_ GCA  
 CAG GCTG TAAGCTGA  
 ||| ||| |||||  
 GTC TGAC ATTCGACT  
 CT \_\_\_\_  
 GAM1175 MOCS1 3' TTCAGCTTAACAGTTGCCCGGT 92037 A\_ \_ GCA  
 C GACC GTG CTG TAAGCTGAA  
 ||| ||| ||| |||||  
 CTGG CGT GAC ATTCGACTT  
 CC T A\_  
 GAM1175 P23 3' TCAGCTTATACCCGGGCT 21719 G C\_  
 AGT CTGG ATAAGCTGA  
 ||| ||| |||||  
 TCG GGCC TATTCGACT  
 \_ CA  
 GAM1175 PFKFB4 3' TCAGCCACATGCAACACTGTGT 15874 \_ CTG AA\_  
 C GAC CAGTG GCAT GCTGA  
 ||| ||| ||| |||  
 CTG GTCAC CGTA CGACT  
 T AA\_ CAC  
 GAM1175 PTPRK 3' TTCAGCCTGTGGCCAGCACTG 11125 \_ A  
 GTC GACCAGTGCTGG CATA GCTGAA  
 ||||| ||| |||||  
 CTGGTCACGACC GTGT CGACTT  
 CG C  
 GAM1175 RNPEPL1 3' CGGATGCCAGCACCTG 36676 \_ AAG  
 CAG TGCTGGCAT CTG  
 ||| ||||| |||  
 GTC ACGACCGTA GGC  
 C \_\_\_\_  
 GAM1175 UBE2L3 3' TCAGCCCTGGCACTGGC 12507 A TG CATAA  
 G CCAGTGC G GCTGA  
 | ||||| | |||  
 C GGTACG C CGACT  
 \_ GT C\_  
 GAM1175 APXL2 5' CAGCCTCAGCACTCATC 75185 CC CATAA  
 GA AGTGCTGG GCTG  
 || ||||| |||  
 CT TCACGACT CGAC  
 AC C\_  
 GAM1175 ARHGEF9 3' TTCAGCTTACCAAGCA 30824 \_ CA  
 TGCT GG TAAGCTGAA  
 ||| || |||||

ACGA CC ATTCGACTT  
 A \_  
 GAM1175 CEGP1 3' TTCAGCTTCCTCTAGCCCGG 40589 AGT CAT  
 CC GCTGG AAGCTGAA  
 || |||| |||||  
 GG CGATC TTCGACTT  
 CC\_ TCC  
 GAM1175 DKFZp547D155 3' CAGCCCTGAGACCACTGGTC 70435 CTGG TAA  
 GACCAGTG CA GCTG  
 ||||| || |||  
 CTGGTCAC GT CGAC  
 CAGA CC\_  
 GAM1175 DKFZP727G051 3' TTCAGCCCATCAACCAGCATTG 69483 CATAA\_  
 GTC GACCAGTGCTGG GCTGAA  
 ||||| |||||  
 CTGGTTACGACC CGACTT  
 AACTACC  
 GAM1175 DUSP14 5' CACTGTCACCAGCACTGCTC 22834 C CATA C  
 GA CAGTGCTGG AG TG  
 || ||||| |||  
 CT GTCACGACC TC AC  
 C ACTG \_  
 GAM1175 FLJ10206 5' CAGCTTATGCCAGGAGTC 35898 CAGTG  
 GAC CTGGCATAAGCTG  
 || |||||  
 CTG GACCGTATTCGAC  
 AG\_  
 GAM1175 FLJ20967 5' GGCGCCCAGCACTGGTT 41962 CATAA  
 GACCAGTGCTGG GCT  
 ||||| |||  
 TTGGTCACGACC CGG  
 CG\_  
 GAM1175 FLJ22569 3' TTCAGCTTACTAACTG 43679 GC CA  
 CAGT TGG TAAGCTGAA  
 ||| || |||||  
 GTCA ATC ATTCGACTT  
 A\_ \_  
 GAM1175 FOXN4 3' TTCAGCTTGGACACACTGG 75574 C GCA  
 CCAGTG TG TAAGCTGAA  
 ||||| || |||||  
 GGTCAC AC GTTCGACTT  
 \_ AG\_  
 GAM1175 GW112 3' TTCAACTGAAGCCAGCACTGGT 21194 ATA C  
 T GACCAGTGCTGGC AG TGAA  
 ||||| || |||||  
 TTGGTCACGACCG TC ACTT  
 AAG A  
 GAM1175 HOOK2 3' CAGCTCACATGGCGCCCAGCAC 25256 \_ A\_  
 TGG CCAGTGCTGG CAT AGCTG  
 ||||| || |||||

GGTCACGACC GTA TCGAC  
CGCG CAC  
GAM1175 jdp2 3' TTCAGCACAGCCAGCAT 55327 ATAA  
GTGCTGGC GCTGAA  
||||||| |||||  
TACGACCG CGACTT  
ACA\_  
GAM1175 KIAA0767 3' TCTGCTGCCAGCACAGG 60632 A TAA T  
CC GTGCTGGCA GC GA  
|| ||||| || ||  
GG CACGACCGT CG CT  
A \_ T  
GAM1175 KIAA0923 3' TCAGCTTGATGCATGGTC 25838 G TGGCA  
GACCA TGC TAAGCTGA  
||||| ||| |||||  
CTGGT ACG GTTCGACT  
\_ TA\_  
GAM1175 KIAA0982 3' TTCACTGTTTGCCAGCAC 25852 TA\_ C  
GTGCTGGCA AG TGAA  
||||||| || |||  
CACGACCGT TC ACTT  
TTG \_  
GAM1175 KIAA1000 3' TTCAGCTTTGCAAAGTACTGG 65281 G\_ T  
CCAGTGCT GCA AAGCTGAA  
||||||| ||| |||||  
GGTCATGA CGT TTCGACTT  
AA \_  
GAM1175 MAP3K3 3' TCAGCCTGGGCGCTGGTC 9999 GG TAA  
GACCAGTGCT CA GCTGA  
||||||| || |||  
CTGGTCGCGG GT CGACT  
\_ C\_  
GAM1175 MGC16037 5' CTTGTCCAGCACTAGTC 51821 C C  
GAC AGTGCTGG ATAAG  
||| ||||| |||||  
CTG TCACGACC TGTTC  
A \_  
GAM1175 MIDORI 3' TCAGCTTATCCTGCAACT 73792 \_ T C  
AGT GC GG ATAAGCTGA  
||| || |||||  
TCA CG CC TATTCGACT  
A T \_  
GAM1175 MtFMT 5' CAGTGGCGAGCACTGG 57651 G ATAA  
CCAGTGCT GC GCTG  
||||||| || |||  
GGTCACGA CG TGAC  
G G\_  
GAM1175 PCDH16 5' TCAGTTCCAACCACTGG 72826 C\_ CATA  
CCAGTG TGG AGCTGA  
||||| ||| |||||

GGTCAC ACC TTGACT  
CA \_\_\_\_

GAM1175 QKI 3' CAGCTTATCAACTCGTC 65439 C GCTGGC  
GAC AGT ATAAGCTG  
||| ||| |||||  
CTG TCA TATTCGAC  
C AC\_\_\_\_

GAM1175 TNRC6 3' CAACTTTTAGCACTG 70506 CAT C  
CAGTGCTGG AAG TG  
||||||| ||| ||  
GTCACGATT TTC AC  
\_\_\_\_ A

GAM1175 TOB2 3' CAGCCCAGGCCAGCACTG 95618 ATAA  
CAGTGCTGGC GCTG  
||||||| |||  
GTCACGACCG CGAC  
GACC

GAM1175 TU12B1-TY 3' TCAGCCCACAGCACTGTC 33406 C GCATAA  
GAC AGTGCTG GCTGA  
||| ||||| |||  
CTG TCACGAC CGACT  
\_ ACC\_\_\_\_

GAM1175 TUSP 3' TCAGCCTAAGAGCGCAGCACTG 39641 \_ A\_\_ A  
CAGTGCTG GC TA GCTGA  
||||||| || |||||  
GTCACGAC CG AT CGACT  
G AGA C

GAM1175 USP19 3' TCAGCTTATGCATCTGGT 88959 TGCTG  
ACCAG GCATAAGCTGA  
||||| |||||  
TGGTC CGTATTCGACT  
TA\_\_\_\_

GAM1175 ZD52F10 3' CAGCCTGTGCCAGCCCTGG 52819 T A  
CCAG GCTGGCATA GCTG  
||||| ||||| |||  
GGTC CGACCGTGT CGAC  
C C

GAM1175 LOC145268 3' TCAGCTTACAAGAGCCACTG 77062 \_ GGCA  
CAGTG CT TAAGCTGA  
||||| || |||||  
GTCAC GA ATTCGACT  
C GAAC

GAM1175 LOC149296 5' CAGCTTATGGGCAGCA 79256 G\_  
TGCTG CATAAGCTG  
||||| |||||  
ACGAC GTATTCGAC  
GG

GAM1175 LOC161877 5' TCAGGGCAGGCCAGCGCTGG 82326 ATAAG  
CCAGTGCTGGC CTGA  
||||||| |||

		GGTCGCGACCG GACT		
		GACGG		
GAM1175	LOC163115 5'	TCAGCCCCTGACAGCACTGG 82413	G	TAA
		CCAGTGCTG CA GCTGA		
		GGTCACGAC GT CGACT		
		A CCC		
GAM1175	LOC196500 3'	TCAGCTCACTCAGTGGTC 87744	AGT	CATA
		GACC GCTGG AGCTGA		
		CTGG TGA CT TCGACT		
		___ CAC_		
GAM1175	LOC197287 3'	TCAGCTCATGTGTTTTGCACTG 60865	T_	___
		CAGTGC GGCATA AGCTGA		
		GTCACG TTGTGT TCGACT		
		TT AC		
GAM1175	LOC200470 5'	TCAGCCTGCGGCGCTGG 90069	G	TAA
		CCAGTGCTG CA GCTGA		
		GGTCGCGGC GT CGACT		
		_ C_		
GAM1175	LOC221584 3'	CAGCTTATGTGGCAC 93828	G	
		GTGCTG CATAAGCTG		
		CACGGT GTATTGAC		
		-		
GAM1175	LOC51716 3'	CAGCTCATGGCCCTAGCA 32787	___	A
		TGCTGG CAT AGCTG		
		ACGATC GTA TCGAC		
		CCG C		
GAM1175	LOC92196 5'	CAGAGCACCAGCACTGGC 68456	A	CATAAG
		G CCAGTGCTGG CTG		
		C GGTCACGACC GAC		
		_ ACGA_		
GAM1176	LARGE 3'	AAGGGTAGGCAACCACCTTCA 16432	C	A G
		TG AGGT GTTGCTTGCT CTT		
		AC TCCA CAACGGATGG GAA		
		T C _		
GAM1176	LARGE 3'	AAGGGTAGGCAACCACCTTCA 56106	C	A G
		TG AGGT GTTGCTTGCT CTT		
		AC TCCA CAACGGATGG GAA		
		T C _		
GAM1176	YWHAZ 3'	CTAAGCAAAGAAAAGTGCCTAC 12700	C	GC GC
A		TG AGGTAGTT TT TGCTTAG		

				AC TCCGTCAA AG ACGAATC		
				A A_ AA		
GAM1176	KIAA0286	3'	AGTGACAACTACCTCA	68318	C	C TG
			TG AGGTAGTTG T CT			
			AC TCCATCAAC A GA			
			_ _GT			
GAM1176	KIAA0998	3'	CAAACAACACTACATGCA	30585	G	C
			TGCA GTAGTTG TTG			
			ACGT CATCAAC AAC			
			A A			
GAM1176	LOC149319	3'	AAGCAGCAGGGACACCGGCA	79289	A	A G
			TGC GGT GTT CTTGCTGCTT			
			ACG CCA CAG GGACGACGAA			
			G _ _			
GAM1176	LOC151414	5'	AGCAGTAACCATCTGCA	80234	A	T
			TGCAGGT GTTGCT GCT			
			ACGTCTA CAATGA CGA			
			C _			
GAM1177	ADH1B	3'	CTTAGACATAAAGTAAAT	72644	C	CAC
			ATTT ACTTT TGTCTGAG			
			TAAA TGAAA ACAGATTC			
			A T__			
GAM1177	AHR	3'	ATCTCAGATGTTAAATAAATG	7875	CAC	C T
			CATTT TTT AC GTCTGAGAT			
			GTAAA AAA TG TAGACTCTA			
			TA_ T _			
GAM1177	FDFT1	3'	TAGGAAAGTGAAATG	15518	A	
			CATTTCACTTTC CTG			
			GTAAAGTGAAAG GAT			
			_			
GAM1177	JTB	3'	ATCTCAGACAGTGAAAGTGAAA	21959		
	TG		CATTTCACTTTCACTGTCTGAGAT			
			GTAAAGTGAAAGTGACAGACTCTA			
GAM1177	KLF4	3'	TCCCAGACAGTGGATATG	14891	CT	A
			CA TTCACTGTCTG GA			
			GT AGGTGACAGAC CT			
			AT C			
GAM1177	PHYH	3'	ACAGTAAAAGTGAAAT	20608	C	
			ATTTCACTTT ACTGT			

			TAAAGTGAAA TGACA		
			A		
GAM1177	PKD2	3'	TCCAGGTTGAAAAGTGAAA 60096	CTG	A
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T__ _		
GAM1177	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1177	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA	CTG
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1177	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT	CT
			TTCAC TTTCA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1177	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G	T_
			CTTTCACT TC GAGAT		
			GAAAGTGA AG TTCTA		
			G TC		
GAM1177	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT 45802	ACTTTCACT	
	G		CATTTT GTCTGAGAT		
			GTAAAG CAGACTCTA		
			AAACATTT_		
GAM1177	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281	CTT	
			CATTTCA TCACTGTCTGAGAT		
			GTAAAGT AGTGACAGACTCTA		
			C_		
GAM1177	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C	TC
			TTCA TTTCACTG TGAG		
			AAGT AAAGTGAC GTTT		
			A CT		
GAM1177	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A	_
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1177	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T	
			ATT CACTTTCACTGT		



		TAA GTGAAAGTGACG		
		C		
GAM1177	PORIMIN	3' ATCTCAGAGGGCCAAAGTGAA	53598	CA G
		TTCACTTT CT TCTGAGAT		
		AAGTGAAA GG AGACTCTA		
		CC G		
GAM1177	PP35	3' ATCTCAGACTGAAA	22814 CT	
		TTTCA GTCTGAGAT		
		AAAGT CAGACTCTA		
		—		
GAM1177	PRTD-NY3	3' CTCATTGCAATAAGTGAAATG	48148	TCAC C_
		CATTTCACTT TGT TGAG		
		GTAAAGTGAA ACG ACTC		
		TA__ TT		
GAM1177	SEP15	3' TCCTACAGTAAGAGTGAAA	14934	C CT
		TTTCACTTT ACTGT GA		
		AAAGTGAGA TGACA CT		
		A TC		
GAM1177	SFXN2	3' CTCAGGGGAAAAAAGTGAAA	73941	CACTG
		TTTCACTTT TCTGAG		
		AAAGTGAAA GGA CTC		
		AAAGG		
GAM1177	LOC149703	3' ATCTCAGACAGCCGTTTGAAAA	84647	ACTTTCA
		TTTC CTGTCTGAGAT		
		AAAG GACAGACTCTA		
		GTTTGCC		
GAM1177	LOC154007	3' ATCTCAAACCCTTTAGTGAAA	81015	TTCACT C
		TTTCACT GT TGAGAT		
		AAAGTGA CA ACTCTA		
		TTTCC_ A		
GAM1177	LOC155004	3' TCATTTAAGTGAAAGGAAA	81226	A GTC_
		TTTC CTTTCACT TGA		
		AAAG GAAAGTGA ACT		
		_ ATTT		
GAM1177	LOC222134	5' ACAGTGAAGTGAAATG	94136	T
		CATTTCACTT CACTGT		
		GTAAAGTGAA GTGACA		
		—		
GAM1178	SLC17A4	3' CAACAGTTCTTCATGTAGC	18525	CAGT
		GCTGC TGAAGAACTGTTG		

		CGATG ACTTCTTGACAAC		
		T__		
GAM1178	CITED1	5' CAACAGCTCCAGCTGGCAGC 14729	AA	A
		GCTGCCAGTTG GA CTGTTG		
		CGACGGTCGAC CT GACAAC		
		__ C		
GAM1178	FLJ10900	5' CAACAGTTCTTGCTGAAGCAGT 65590	__	TG
	T	AGCTGC CAGT AAGAACTGTTG		
		TTGACG GTCG TTCTTGACAAC		
		AA __		
GAM1178	HS6ST	3' CAACAGTTCCTTTGCCAGCAGC 62025	CA	T A
		GCTGC GT GA GAACTGTTG		
		CGACG CG TT CTTGACAAC		
		AC T C		
GAM1178	MGC4638	3' CAACAGTTCCTTCAAGTG 48939	G	
		CA TTGAAGAACTGTTG		
		GT AACTTCTTGACAAC		
		G		
GAM1178	ZNF262	3' TTCCCCAATGGCAGCTT 17492	G	AA
		AAGCTGCCA TTG GAA		
		TTCGACGGT AAC CTT		
		_ CC		
GAM1178	LOC115051	3' CAACAGTTCCTTTGCCAGCAGC 60036	CA	T A
		GCTGC GT GA GAACTGTTG		
		CGACG CG TT CTTGACAAC		
		AC T C		
GAM1178	LOC143153	3' CAGCCTCAAGCTGGCAGC 76463	GA	AA
		GCTGCCAGTT AG CTG		
		CGACGGTCGA TC GAC		
		AC C_		
GAM1178	LOC168512	5' CAACAGCCTCTCTGGCAGCTT 82714	TTGA	A_
		AAGCTGCCAG AGA CTGTTG		
		TTCGACGGTC TCT GACAAC		
		__ CC		
GAM1178	LOC199923	3' AACAGTTCCAGACCAGC 88494	CCA	GAA
		GCTG GTT GAACTGTT		
		CGAC CAG CTTGACAA		
		__ AC_		
GAM1178	LOC199926	3' TAGTCCTTCAACTCACAGCTT 89880	CC	A
		AAGCTG AGTTGAAG ACTG		

		TTCGAC TCAACTTC TGAT		
		AC C		
GAM1178	LOC202316	3' TAGTCCTTCAACTCACAGCTT 90340	CC	A
		AAGCTG AGTTGAAG ACTG		
		TTCGAC TCAACTTC TGAT		
		AC C		
GAM1178	LOC221479	3' CAACAACTACAGCAGCAGC 92222	CA	A AAC
		GCTGC GTTG AG TGTG		
		CGACG CGAC TC ACAAC		
		A_ A A__		
GAM1179	CNP	3' AACCTCAGCAACCTGTAAGA 52441	AC	AA TT
		TCTTACAG TG TG GGTT		
		AGAATGTC AC AC CCAA		
		CA G_ T_		
GAM1179	ADNP	3' GGCCAGCCACGTAAGATA 31049	AGAC	AAT
		TATCTTAC TG GTTGGTT		
		ATAGAATG AC CGACCGG		
		C__ _		
GAM1179	DJ328E19.C1.1	3' AACCTGTGCTCAGTCTGAAGA 31150	A	AT TT
		TCTT CAGACTGA G GGTT		
		AGAA GTCTGACT T CCAA		
		_ CG GT		
GAM1179	DKFZP434F091	3' TGGTGTTCAGCCTATAAGA 31283	C A	TT
		TCTTA AG CTGAATG G		
		AGAAT TC GACTTGT T		
		A C GG		
GAM1179	SDCCAG3	3' AACATCAGTTGTAAGATA 21817	A	A
		TATCTTACAG CTGA TGTT		
		ATAGAATGTT GACT ACAA		
		- -		
GAM1179	SSH1	3' AACCAACATGCAGCACAAGA 38609	ACAGA	A
		TCTT CTG ATGTTGGTT		
		AGAA GAC TACAACCAA		
		CAC__ G		
GAM1179	TBLR1	3' TCATGTCAATCTGTAAGA 45106	C	ATGT
		TCTTACAGA TGA TGG		
		AGAATGTCT ACT ACT		
		A GT__		
GAM1179	LOC149013	3' AACCTGTGCTCAGTCTGAAGA 79129	A	AT TT
		TCTT CAGACTGA G GGTT		

		AGAA GTCTGACT T CCAA		
		— CG GT		
GAM1179	LOC161742 3'	AACACTATCTGTCTGTAAAATA 82287	C	T A__
		TAT TTACAGAC GA TGTT		
		ATA AATGTCTG CT ACAA		
		A T ATC		
GAM1179	LOC220638 3'	AACCTGTGCTCAGTCTGAAGA 73908	A	AT TT
		TCTT CAGACTGA G GGTT		
		AGAA GTCTGACT T CCAA		
		— CG GT		
GAM1179	LOC257031 3'	AACCTGTGCTCAGTCTGAAGA 94607	A	AT TT
		TCTT CAGACTGA G GGTT		
		AGAA GTCTGACT T CCAA		
		— CG GT		
GAM1180	BACH2 5'	GCAAAGTTCTCCGGCGA 41488	A TA	
		TC C GAGAACTTTGC		
		AG G CTCTTGAAACG		
		C GC		
GAM1180	CAV1 3'	CTGAGCTACAGAGTCTGGTGA 8260	GAA C	
		TCACTAGA CTTTG AGCTCAG		
		AGTGGTCT GAGAC TCGAGTC		
		— A		
GAM1180	CDKN3 3'	CTGAAATGTCAGTTCTCTAG 17768	TT GC	
		CTAGAGAACT GCA TCAG		
		GATCTCTTGA TGT AGTC		
		C_ AA		
GAM1180	CLTCL1 3'	CTGAGCTGGTGTTCCCTCTATGA 63672	C _ TTTG	
		TCA TAGAG AAC CAGCTCAG		
		AGT ATCTC TTG GTCGAGTC		
		— C TG__		
GAM1180	F2R 3'	CTGAGCATAAGTCCTCTAGTGA 8836	A TGCA	
		TCACTAGAG ACTT GCTCAG		
		AGTGATCTC TGAA CGAGTC		
		C TA__		
GAM1180	GAD2 3'	AGCTGTTCCACTTCTCTAGAGA 5877	A CTTT_	
		TC CTAGAGAA GCAGCT		
		AG GATCTCTT TGTCGA		
		A CACCT		
GAM1180	ITGA2 3'	CTGAGCCCCACATTCTCTAGG 9374	A CTTTGCA	
	A	TC CTAGAGAA GCTCAG		

AG GATCTCTT CGAGTC  
 \_ ACACCCC  
 GAM1180 TCEB1L 3' CTGAACTGTGGTTCTCTA 12146 T TG C  
 TAGAGAAC T CAG TCAG  
 ||||| | ||| |||  
 ATCTCTTG G GTC AGTC  
 \_GT A  
 GAM1180 DKFZP434P106 3' TGAGCTGCAAACCTT 68088 AAC  
 GAG TTTGCAGCTCA  
 || |||||  
 TTC AAACGTCGAGT  
 C\_  
 GAM1180 FLJ10922 3' CTGAGCTGACACTCTC 36876 ACTT \_  
 GAGA TG CAGCTCAG  
 ||| || |||||  
 CTCT AC GTCGAGTC  
 C\_ A  
 GAM1180 KIAA0869 3' CTGAGTCACAAAGTCCTCTAGTG 70856 A T CA  
 CACTAGAG ACTT G GCTCAG  
 ||||| ||| | |||||  
 GTGATCTC TGAA C TGAGTC  
 C \_AC  
 GAM1180 KIAA1464 3' GAGCTGCAGCCTAGGA 68265 A AGAACT  
 TC CTAG TTGCAGCTC  
 || ||| |||||  
 AG GATC GACGTCGAG  
 \_ C\_  
 GAM1180 RARRES2 3' CTGAGCTGCGTGCGTCCAG 11255 A A A\_ T  
 GA TC CT GAG ACT TGCAGCTCAG  
 || ||| || |||||  
 AG GA CTC TGG GCGTCGAGTC  
 \_ C CG T  
 GAM1180 SPEC1 3' CTGAGATAGGAGTTCTCTAGGA 39609 A GCAG  
 TC CTAGAGAACTTT CTCAG  
 || ||||| |||  
 AG GATCTCTTGAGG GAGTC  
 \_ ATA\_  
 GAM1180 YEA 3' TGAGCTGATTCCCACTGA 51537 AGA CTTTG  
 TCACT GAA CAGCTCA  
 |||| || |||||  
 AGTGA CTT GTCGAGT  
 CC\_ A\_  
 GAM1180 ZID 3' CTGAGCCATAGTTCTCTA 21776 T CA  
 TAGAGAACT TG GCTCAG  
 ||||| || |||||  
 ATCTCTTGA AC CGAGTC  
 T \_  
 GAM1180 LOC143310 5' CTGAGCTGCTTACTTTAATGA 76531 C AACTTT  
 TCA TAGAG GCAGCTCAG  
 || |||| |||||

		AGT AT TTC	CGTCGAGTC	
		A	ATT___	
GAM1180	LOC145725	3'	GCAATGTCCTCTGGTGA 77407	A T
			TCACTAGAG AC TTGC	
			AGTGGTCTC TG AACG	
			C T	
GAM1180	LOC145732	3'	GCAATGTCCTCTGGTGA 77429	A T
			TCACTAGAG AC TTGC	
			AGTGGTCTC TG AACG	
			C T	
GAM1180	LOC151283	3'	CTGGAAAGTTCTACAGT 80199	AG G
			ACT AGAACTTT CAG	
			TGA TCTTGAAA GTC	
			CA G	
GAM1180	LOC196957	3'	GCAATGTCCTCTGGTGA 87823	A T
			TCACTAGAG AC TTGC	
			AGTGGTCTC TG AACG	
			C T	
GAM1180	LOC196961	3'	GCAATGTCCTCTGGTGA 87844	A T
			TCACTAGAG AC TTGC	
			AGTGGTCTC TG AACG	
			C T	
GAM1180	LOC197138	3'	GCAATGTCCTCTGGTGA 87917	A T
			TCACTAGAG AC TTGC	
			AGTGGTCTC TG AACG	
			C T	
GAM1180	LOC203078	3'	TGCAAAACTCTCTGGTGA 89277	AC
			TCACTAGAGA TTTGCA	
			AGTGGTCTCT AAACGT	
			CA	
GAM1180	LOC219594	3'	CTGAACTGTGGGTTCTCTA 90778	T TG C
			TAGAGAAC T CAG TCAG	
			ATCTCTTG G GTC AGTC	
			_ GT A	
GAM1180	LOC91397	5'	GCAAGGTTCCCTAAAGA 65909	AC A
			TC TAG GAACTTTGC	
			AG ATC CTTGGAACG	
			AA C	
GAM1181	ANXA5	3'	CTGTAAAATTATGATG 6716	—
			CATCATGAT TACAG	

			GTAGTATTA ATGTC		
			AA		
GAM1181	APBA1	3'	ATCTGTGGGAATGTGGTAGTA 69915	C	CATGA
			TAC ACCACAT TTACAGAT		
			ATG TGGTGTA GGTGTCTA		
			A AG__		
GAM1181	CENTD1	3'	GTACAGTGATGTGGTGGTA 57563		GAT
			TACCACCACATCAT TAC		
			ATGGTGGTGTAGTG ATG		
			AC_		
GAM1181	CENTD1	3'	GTACAGTGATGTGGTGGTA 30853		GAT
			TACCACCACATCAT TAC		
			ATGGTGGTGTAGTG ATG		
			AC_		
GAM1181	HNRPD	3'	GTGTCATGATGTAGTAGTG 48577	C C	T
			TAC AC ACATCATGAT AC		
			GTG TG TGTAGTACTG TG		
			A A _		
GAM1181	HNRPD	3'	GTGTCATGATGTAGTAGTG 9246	C C	T
			TAC AC ACATCATGAT AC		
			GTG TG TGTAGTACTG TG		
			A A _		
GAM1181	PTGS2	3'	ATCTGTAACCAAGATG 6359	A A	
			CATC TG TTACAGAT		
			GTAG AC AATGTCTA		
			A C		
GAM1181	SGCB	3'	TTGTTCAACAATGTGGTGG 4068	CA	TT
			CCACCACAT TGA ACAG		
			GGTGGTGTA ACT TGTT		
			AC _		
GAM1181	FLJ12949	3'	ATCTCTACAAAATGTGGTG 43441	CA	AT C
			CACCACAT TG TA AGAT		
			GTGGTGTA AC AT TCTA		
			AA _ C		
GAM1181	FLJ21369	3'	TAGCCAGATGTGGTGG 45637	A	AT
			CCACCACATC TG TA		
			GGTGGTGTAG AC AT		
			_ CG		
GAM1181	FLJ23514	3'	ATCTGTAATGAATAGTGG 41542	CACA	GAT
			CCAC TCAT TACAGAT		

GGTG AGTA ATGTCTA  
ATA\_ \_  
GAM1181 FLJ23556 3' ATCATGATTGTGATGG 45942 C \_  
CCA CACA TCATGAT  
||| ||| |||||  
GGT GTGT AGTACTA  
A T  
GAM1181 FPGT 3' ATCTGTGGGGGAAGTGGTAGTA 13845 C A ATGA  
TAC ACCAC TC TTACAGAT  
||| ||||| || |||||  
ATG TGGTG AG GGTGTCTA  
A A GG\_  
GAM1181 HSPC043 3' TAGCCATGTGTGGTGG 67722 T AT  
CCACCACA CATG TA  
||||||| ||| ||  
GGTGGTGT GTAC AT  
\_ CG  
GAM1181 KIAA0721 3' TGATCATGTGTGGTG 95975 T  
CACCACA CATGATTA  
||||||| |||||  
GTGGTGT GTACTAGT  
\_  
GAM1181 KIAA0721 3' TGATCATGTGTGGTG 41347 T  
CACCACA CATGATTA  
||||||| |||||  
GTGGTGT GTACTAGT  
\_  
GAM1181 LAT1-3TM 5' ATCTGTAATGCAGCTTGTAATG 68598 CC TCA \_  
CA ACA TG ATTACAGAT  
|| ||| || |||||  
GT TGT AC TAATGTCTA  
AA TCG G  
GAM1181 LAT1-3TM 3' ATCTGTAATGCAGCTTGTAATG 48312 CC TCA \_  
CA ACA TG ATTACAGAT  
|| ||| || |||||  
GT TGT AC TAATGTCTA  
AA TCG G  
GAM1181 MGC4268 3' ATCTGTTTTCCATGATGTGTTG 48743 C \_TT  
CA CACATCATG A ACAGAT  
|| ||||| || |||||  
GT GTGTAGTAC T TGTCTA  
T C TT  
GAM1181 PCANAP7 5' ATCTGTAAAATGATG 93363 GA  
CATCAT TTACAGAT  
||||| |||||  
GTAGTA AATGTCTA  
A\_  
GAM1181 PRIC285 3' CTGTAATCACTCTGGATGGTG 61435 \_ CATCA  
TACCA CCA TGATTACAG  
||||| ||| |||||



		GTGGT GGT ACTAATGTC	
		A CTC__	
GAM1181	UBPH 3'	ATCTGAGGTGATGTGGTG 38917	GATTA
		CACCACATCAT CAGAT	
		GTGGTGTAGTG GTCTA	
		GA__	
GAM1181	LOC146957 3'	TGATCTAATATGGTGGTG 78208	C CAT
		TACCACCA AT GATTA	
		GTGGTGGT TA CTAGT	
		A AT_	
GAM1181	LOC197003 5'	ATCCATAAGCATGACTGGTGGT 87868	CA A CA
	A	TACCACCA TCATG TTA GAT	
		ATGGTGGT AGTAC AAT CTA	
		C_ G AC	
GAM1181	LOC197423 5'	ATCTGTAATGCAGCTTGTAATG 77856	CC TCA _
		CA ACA TG ATTACAGAT	
		GT TGT AC TAATGTCTA	
		AA TCG G	
GAM1181	LOC200310 3'	CTGGCCTGATGTGGAGTA 65735	CA TGATTA
		TAC CCACATCA CAG	
		ATG GGTGTAGT GTC	
		A_ CCG__	
GAM1181	LOC220565 5'	ATCTGTAATGCAGCTTGTAATG 90743	CC TCA _
		CA ACA TG ATTACAGAT	
		GT TGT AC TAATGTCTA	
		AA TCG G	
GAM1181	LOC255328 3'	TGTAGTCATAATATATGGTA 96568	CCAC C
		TACCA AT ATGATTACA	
		ATGGT TA TACTGATGT	
		ATA_ A	
GAM1181	LOC256273 3'	ATCTATAAAGTTGTGGTGG 96403	TCATGA C
		CCACCACA TTA AGAT	
		GGTGGTGT AAT TCTA	
		TGA__ A	
GAM1181	LOC51026 3'	ATCTGTGAAAATGGGATG 32168	CA GA
		CA TCAT TTACAGAT	
		GT GGTA AGTGTCTA	
		AG AA	
GAM1181	LOC54516 3'	ATCTGTAATCATGATGTGGTGG 38760	
	TA	TACCACCACATCATGATTACAGAT	

ATGGTGGTGTAGTACTAATGTCTA

GAM1181 LOC91408 3' TCTGTAGACATGAAGG 65928 ACA A  
CC TCATG TTACAGA  
|| |||| |||||  
GG AGTAC GATGTCT  
A\_\_ A

GAM1182 CABC1 5' GCACAAACAGACGCTC 39654 CTGGC  
GAGC TCTGTTTGTGC  
||| |||||  
CTCG AGACAAACACG  
C\_\_

GAM1182 CEACAM5 3' AACAGAGCAAGACTCCA 15153 C G  
TGGAG CT GCTCTGTT  
|||| || |||||  
ACCTC GA CGAGACAA  
A A

GAM1182 F2R 3' AACAGAGCAAGACTCCA 8831 C G  
TGGAG CT GCTCTGTT  
|||| || |||||  
ACCTC GA CGAGACAA  
A A

GAM1182 FGFR2 3' GACAGAGCGAGACTCCA 43377 C G  
TGGAG CT GCTCTGTT  
|||| || |||||  
ACCTC GA CGAGACAG  
A G

GAM1182 FGFR2 3' GACAGAGCGAGACTCCA 43383 C G  
TGGAG CT GCTCTGTT  
|||| || |||||  
ACCTC GA CGAGACAG  
A G

GAM1182 FUT6 3' GACAGAGCAAGACTCCA 3812 C G  
TGGAG CT GCTCTGTT  
|||| || |||||  
ACCTC GA CGAGACAG  
A A

GAM1182 GCLM 5' GGCGCAGACCAGGCTCCA 9026 C TTGT \_  
TGGAGCCTGG TCTGT GC C  
||||||| ||| ||  
ACCTCGGACC AGACG CG G  
\_ \_\_ A

GAM1182 GPC1 3' GGCTGCAGAGCCCGGCCCA 9103 A T TTGT  
TGG GCC GGCTCTGT GCC  
||| ||| ||||| |||  
ACC CGG CCGAGACG CGG  
C C T\_\_

GAM1182 HPSE 3' CAAACAGGCCAGGCTCCA 21890 T  
TGGAGCCTGGC CTGTTTG  
||||||| |||||

ACCTCGGACCG GACAAAC

GAM1182 IFIT4 3' AACAGAGCAAGACTCCA 70918 C G  
TGGAG CT GCTCTGTT  
||||| || |||||  
ACCTC GA CGAGACAA  
A A

GAM1182 KCNJ5 3' GACAGAGCGAGACTCCA 6091 C G  
TGGAG CT GCTCTGTT  
||||| || |||||  
ACCTC GA CGAGACAG  
A G

GAM1182 LY94 3' GACAGAGCGAGACTCCA 16705 C G  
TGGAG CT GCTCTGTT  
||||| || |||||  
ACCTC GA CGAGACAG  
A G

GAM1182 LZTS1 3' ACAGAGCCTGGCCCCA 40676 A T  
TGG GCC GGCTCTGT  
||| ||| |||||  
ACC CGG CCGAGACA  
C T

GAM1182 MSH3 3' AACAGAGCAAGACTCCA 10116 C G  
TGGAG CT GCTCTGTT  
||||| || |||||  
ACCTC GA CGAGACAA  
A A

GAM1182 POLH 3' AACAGAGCGAGACTCCA 21461 C G  
TGGAG CT GCTCTGTT  
||||| || |||||  
ACCTC GA CGAGACAA  
A G

GAM1182 PRKAB1 3' GCACACCACCAGGCTCCA 20736 CTC TT  
TGGAGCCTGG TG TGTGC  
||||||| || |||||  
ACCTCGGACC AC ACACG  
\_\_\_\_ C\_

GAM1182 SIGLEC6 3' AACAGAGCGAGACTCCA 59925 C G  
TGGAG CT GCTCTGTT  
||||| || |||||  
ACCTC GA CGAGACAA  
A G

GAM1182 SLC10A2 5' AGCAGAGCCAGGGCCCCA 4840 AG  
TGG CCTGGCTCTGTT  
||| |||||  
ACC GGACCGAGACGA  
CG

GAM1182 SNRPN 5' CAAGCAAAAACCAGGCTCCA 42998 CTC\_  
TGGAGCCTGG TGTTTG  
||||||| |||||

			ACCTCGGACC	ACGAAC		
			AAAA			
GAM1182	SNRPN	5'	CAAGCAAAAACCAGGCTCCA	43005	CTC_	
			TGGAGCCTGG	TGTTTG		
			ACCTCGGACC	ACGAAC		
			AAAA			
GAM1182	SNRPN	5'	CAAGCAAAAACCAGGCTCCA	43013	CTC_	
			TGGAGCCTGG	TGTTTG		
			ACCTCGGACC	ACGAAC		
			AAAA			
GAM1182	SNRPN	5'	CAAGCAAAAACCAGGCTCCA	42991	CTC_	
			TGGAGCCTGG	TGTTTG		
			ACCTCGGACC	ACGAAC		
			AAAA			
GAM1182	TNFSF11	5'	CAGGAGCCAAAGCCGGGCTCCA	13512	CT_	G
			TGGAGCCTGGCT	GTTT TG		
			ACCTCGGGCCGA	CGAG AC		
			AAC	G		
GAM1182	TSNAX	3'	GGTAACAGAGCAAGACTCCA	20002	C G	TTG
			TGGAG CT	GCTCTGT TGCC		
			ACCTC GA	CGAGACA ATGG		
			A A	_____		
GAM1182	UBE2L3	3'	GCCTTTGCAGAGTCAAGCTCCA	12503	C	TTGT
			TGGAGC	TGGCTCTGT GC		
			ACCTCG	ACTGAGACG CG		
			A	TTTC		
GAM1182	ZNF264	3'	AACAGAGCGAGACTCCA	12738	C G	
			TGGAG CT	GCTCTGTT		
			ACCTC GA	CGAGACAA		
			A G			
GAM1182	ARNTL2	3'	GACAGAGCGAGACTCCA	39466	C G	
			TGGAG CT	GCTCTGTT		
			ACCTC GA	CGAGACAG		
			A G			
GAM1182	C22orf5	3'	GGATCAGAGCCAGACACCA	24344	AGC	TTTGTG
			TGG	CTGGCTCTG CC		
			ACC	GACCGAGAC GG		
			ACA	TA_____		
GAM1182	DKFZp547C176	3'	GACAGAGCAAGACTCCA	67223	C G	
			TGGAG CT	GCTCTGTT		

		ACCTC GA CGAGACAG			
		A A			
GAM1182	DKFZp564K142	3' AACAGAGCGAGACTCCA	49522	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAA			
		A G			
GAM1182	FADS1	3' GACAGAGCAAGACTCCA	25477	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAG			
		A A			
GAM1182	FLJ12298	3' AACAGAGCGAGACTCCA	49664	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAA			
		A G			
GAM1182	FLJ14117	3' AACAGAGCAAGACTCCA	42896	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAA			
		A A			
GAM1182	FLJ14251	3' GGTAACAGAGCGAGACTCCA	45977	C G	TTG
		TGGAG CT GCTCTGT TGCC			
		ACCTC GA CGAGACA ATGG			
		A G _			
GAM1182	FLJ14327	3' AACAGAGCTAGACTCCA	46127	C	
		TGGAG CTGGCTCTGTT			
		ACCTC GATCGAGACAA			
		A			
GAM1182	FLJ14566	5' GGCCACAGAGCCAGCCCCA	51446	A C	TT T
		TGG GC TGGCTCTGT G GCC			
		ACC CG ACCGAGACA C CGG			
		C _ _			
GAM1182	FLJ20084	3' AACAGAGCGAGACTCCA	34511	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAA			
		A G			
GAM1182	FLJ20306	3' GACAGAGCAAGACTCCA	34917	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAG			
		A A			
GAM1182	FLJ20456	3' GGTAACAGAGCTAGACTCCA	35215	C	TTG
		TGGAG CTGGCTCTGT TGCC			

ACCTC GATCGAGACA ATGG  
 A     —  
 GAM1182 FLJ22054 3' AACAGAGCAAGACTCCA 94391 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAA  
 A A  
 GAM1182 FLJ22393 5' AGCAGGAACCAGGCTCCA 47058 C\_  
 TGGAGCCTGG TCTGTT  
 ||||| || |||||  
 ACCTCGGACC GGACGA  
 AA  
 GAM1182 FLJ23598 3' GCCAAGAGCCAGCTCCA 45522 C GTT T  
 TGGAGC TGGCTCT TG GC  
 ||||| ||||| || ||  
 ACCTCG ACCGAGA AC CG  
 —     —     —  
 GAM1182 FLJ31168 3' GACAGAGCGAGACTCCA 58502 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAG  
 A G  
 GAM1182 GP5 3' GACAGAGCGAGACTCCA 15646 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAG  
 A G  
 GAM1182 GTPBP5 3' GACAGAGCAAGACTCCA 65357 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAG  
 A A  
 GAM1182 HIC 3' AACAGAGCGAGACTCCA 67444 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAA  
 A G  
 GAM1182 ING1-like 3' GACAGAGCGAGACTCCA 54156 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAG  
 A G  
 GAM1182 KBRAS2 3' AACAGAGCAAGACTCCA 34191 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAA  
 A A  
 GAM1182 KIAA0189 3' CAGGAGCAGAGCCAGGCCCA 28273 A G  
 TGG GCCTGGCTCTGTTT TG  
 ||| ||||| ||||| ||

			ACC CGGACCGAGACGAG AC		
			— G		
GAM1182	KIAA0472	3'	AGCAGAGCAAGACTCCA 71853	C G	
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACGA		
			A A		
GAM1182	KIAA0563	3'	GACAGAGCAAGACTCCA 29188	C G	
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A A		
GAM1182	KIAA0565	3'	GACAGAGCAAGACTCCA 66890	C G	
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A A		
GAM1182	KIAA0648	3'	CAACAGAAAGCAGGCTCCA 82651		GC
			TGGAGCCTG TCTGTTTG		
			ACCTCGGAC AGACAAAC		
			GA		
GAM1182	KIAA0924	3'	AACAGAGCGAGACTCCA 29712	C G	
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1182	KIAA1028	3'	CAGAGCACAGGCTCCA 91934		—
			TGGAGCCTG GCTCTG		
			ACCTCGGAC CGAGAC		
			A		
GAM1182	KIAA1719	3'	GGCCAGGGGCCAGGCCCA 68169	A	TTTGT
			TGG GCCTGGCTCTG GCC		
			ACC CGGACCGGGAC CGG		
			C		
GAM1182	KIAA1940	3'	GGTCTCAGAACCAAGGCTCCA 79988		— C TTTGT
			TGGAGCCT GG TCTG GCC		
			ACCTCGGA CC AGAC TGG		
			A A TC__		
GAM1182	LGI2	3'	CAAATCAAAGCCAGGCTC 36397	C	—
			GAGCCTGGCT TG TTTG		
			CTCGGACCGA AC AAAC		
			A T		
GAM1182	MGC10200	3'	AACAGAGCGAGACTCCA 58980	C G	
			TGGAG CT GCTCTGTT		

			ACCTC GA CGAGACAA		
			A G		
GAM1182	MGC2705	5'	GCACCAAGCCAGGCTCC	51113	C TTT
			GGAGCCTGGCT TG GTGC		
			CCTCGGACCGA AC CACG		
			— —		
GAM1182	MGC4562	3'	AACAGAGCGAGACTCCA	55908	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1182	MGC4663	3'	AACAGAGCCAGACTCC	44501	C
			GGAG CTGGCTCTGTT		
			CCTC GACCGAGACAA		
			A		
GAM1182	NPTXR	3'	AACAGAGCAAGACTCCA	54171	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A A		
GAM1182	NPTXR	3'	AACAGAGCAAGACTCCA	26635	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A A		
GAM1182	OR7C1	5'	AACAGAGCCAAGTCCA	82428	G C
			TGGA C TGGCTCTGTT		
			ACCT G ACCGAGACAA		
			_A		
GAM1182	POFUT1	3'	AACAGAGCGAGACTCCA	70462	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1182	PTK6	3'	GACAGAGCGAGACTCCA	19936	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A G		
GAM1182	RASGRF2	3'	GCACGAAGCCAGGCTCC	61042	CTGT
			GGAGCCTGGCT TTGTGC		
			CCTCGGACCGA AGCACG		
			—		
GAM1182	SC65	3'	GACAGAGCGAGACTCCA	21289	C G
			TGGAG CT GCTCTGTT		



			ACCTC GA CGAGACAG		
			A G		
GAM1182	SNURF	3'	CAAGCAAAAACCAGGCTCCA	19052	CTC_
			TGGAGCCTGG TGT TTG		
			ACCTCGGACC ACGAAC		
			AAAA		
GAM1182	TMG4	3'	GACAGAGCAAGACTCCA	43989	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A A		
GAM1182	WBSCR23	3'	GACAGAGCAAGACTCCA	46762	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A A		
GAM1182	WIRE	3'	GACAGAGCCAGACTCC	78305	C
			GGAG CTGGCTCTGTT		
			CCTC GACCGAGACAG		
			A		
GAM1182	WSB1	3'	AACAGAGCGAGACTCCA	56144	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1182	WSB1	3'	AACAGAGCGAGACTCCA	56138	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1182	LOC115704	3'	CAGCCAGAGCCAGGCCCC	73541	A T
			GG GCCTGGCTCTG TTG		
			CC CGGACCGAGAC GAC		
			C C		
GAM1182	LOC124220	5'	GGCACAACCAGACGCC	59146	_ T
			GGC TCTG TTGTGCC		
			CCG AGAC AACACGG		
			C C		
GAM1182	LOC127262	3'	GACAGAGCGAGACTCCA	76110	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A G		
GAM1182	LOC129563	3'	AGCAGAGCAGGCCCCA	74878	A G
			TGG GCCTG CTCTGTT		

		ACC CGGAC GAGACGA		
		C _		
GAM1182	LOC129880 3'	AACAGAGCAAGACTCCA	74900	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAA		
		A A		
GAM1182	LOC143196 3'	AACAGAGCGAGACTCCA	82903	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAA		
		A G		
GAM1182	LOC144319 3'	GGCACAAACAGGCGCCCC	83057	A CTG T
		GG GC GC CTGTTTGTGCC		
		CC CG CG GACAAACACGG		
		C _ _		
GAM1182	LOC145216 3'	GACAGAGCAAGACTCCA	83267	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1182	LOC145820 3'	GACAGAGCAAGACTCCA	77514	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1182	LOC146227 3'	GGTCAGAGCCAGACCCC	77711	AGC TTTGT
		GG CTGGCTCTG GCC		
		CC GACCGAGAC TGG		
		CCA _ _ _		
GAM1182	LOC146713 3'	AACAGAGCAAGACTCCA	83720	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAA		
		A A		
GAM1182	LOC147071 3'	GACAGAGCAAGACTCCA	72999	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1182	LOC147649 3'	GACAGAGCGAGACTCCA	78414	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A G		
GAM1182	LOC148936 3'	AACAGAGCAAGACTCCA	84286	C G
		TGGAG CT GCTCTGTT		

		ACCTC GA CGAGACAA		
		A A		
GAM1182	LOC149803 5'	CAGGCAGAGCAAGCTCCA	79538	CTG
		TGGAGC GCTCTGTTTG		
		ACCTCG CGAGACGGAC		
		AA_		
GAM1182	LOC150299 3'	GACAGAGCAAGACTCCA	84970	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1182	LOC151429 3'	GACAGAGCAAGACTCCA	85353	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1182	LOC151904 3'	AACAGAGCGAGACTCCA	80382	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAA		
		A G		
GAM1182	LOC158292 5'	GACAGAGCGAGACTCCA	86730	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A G		
GAM1182	LOC162137 5'	CAAGCAGGCCAAGCCCCA	87111	A C T
		TGG GC TGGC CTGTTTG		
		ACC CG ACCG GACGAAC		
		C A _		
GAM1182	LOC163033 5'	CGACCAGGACCAAGCCCCA	82396	A C CT T
		TGG GC TGG CTG TTG		
		ACC CG ACC GAC AGC		
		C A AG C		
GAM1182	LOC163682 3'	ACACTCAAAGCCGGGCTCCA	87020	C TT
		TGGAGCCTGGCT TG TGT		
		ACCTCGGGCCGA AC ACA		
		A TC		
GAM1182	LOC200261 3'	GCACAAACCTCTGGAGGCCCA	88655	A GGCTCT
		TGG GCCT GTTTGTGC		
		ACC CGGA CAAACACG		
		_ GGTCTC		
GAM1182	LOC201173 3'	GACAGAGCAAGACTCCA	87329	C G
		TGGAG CT GCTCTGTT		

		ACCTC GA CGAGACAG		
		A A		
GAM1182	LOC201182 5'	AACAGAGCAAGACTCCA	89760	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAA		
		A A		
GAM1182	LOC219627 3'	GACAGAGCGAGACTCCA	92178	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A G		
GAM1182	LOC221543 5'	GACAGAGCAAGACTCCA	93742	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1182	LOC221943 5'	GACAGAGCAAGACTCCA	93989	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1182	LOC222160 5'	GACAGAGCAAGACTCCA	94127	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1182	LOC253039 5'	GGCTCCAAAACCAGGCTCTA	96159	CTCTG T_
		TGGAGCCTGG TTTG GCC		
		ATCTCGGACC AAAC CGG		
		A___ CT		
GAM1182	LOC254659 3'	AAACAGAGCAAGACTCCA	95109	C G
		TGGAG CT GCTCTGTTT		
		ACCTC GA CGAGACAAA		
		A A		
GAM1182	LOC256158 5'	AACATCGAGCCAGGCCCA	97639	A _
		TGG GCCTGGCTC TGTT		
		ACC CGGACCGAG ACAA		
		_ CT		
GAM1182	LOC256207 3'	GACAGAGCAAGACTCCA	95169	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1182	LOC257596 5'	GACAGAGCAAGACTCCA	97935	C G
		TGGAG CT GCTCTGTT		

ACCTC GA CGAGACAG  
 A A  
 GAM1182 LOC56963 3' GCACAAAGCCAGGCTTCA 71455 CTGT  
 TGGAGCCTGGCT TTGTGC  
 ||||| |||||  
 ACTTCGGACCGA AACACG  
  
 GAM1182 LOC91149 3' GCTGAACCAGAGCCAGACTCCA 65079 C \_ T  
 TGGAG CTGGCTCTG TTTG GC  
 |||| ||||| |||| ||  
 ACCTC GACCGAGAC AAGT CG  
 A C \_  
 GAM1182 LOC91409 3' AGGCAAGGCCAGGCCCCA 65951 A TC  
 TGG GCCTGGC TGTTT  
 || ||||| |||||  
 ACC CGGACCG ACGGA  
 C GA  
 GAM1182 LOC91862 3' GGTGACAGAGCGAGACTCCA 53470 C G TGT  
 TGGAG CT GCTCTGTT GCC  
 |||| || ||||| |||  
 ACCTC GA CGAGACAG TGG  
 A G \_  
 GAM1182 LOC92482 3' AACAGAGCAAGACTCCA 69485 C G  
 TGGAG CT GCTCTGTT  
 |||| || |||||  
 ACCTC GA CGAGACAA  
 A A  
 GAM1183 LAMC1 3' GTGGGCTTCTCAACTTTTGA 9678 AA AG  
 TCGAAAGTTGA AAGCT AC  
 ||||| |||| ||  
 AGTTTCAACT TTCGG TG  
 C\_ G\_  
 GAM1183 MEL 3' CTGTCTGATCTTTTCAACTTT 18121 G C\_  
 GGA TC AAAGTTGAAAAAG TAGACAG  
 || ||||| |||||  
 AG TTTCAACTTTTTC GTCTGTC  
 G TA  
 GAM1183 NEDD4 3' CTGTTTACTTCTTCACTTTTCGA 70010 T A C  
 TCGAAAGT GAA AAG TAGACAG  
 ||||| || || |||||  
 AGCTTCA CTT TTC ATTTGTC  
 \_ C \_  
 GAM1183 PYGO2 3' GTGTGTTCTTCAACTTTTCGG 63989 AA T G  
 TCGAAAGTTGAA AGC A AC  
 ||||| || || ||  
 GGCTTCAACTT TTG T TG  
 C\_ \_G  
 GAM1183 RAB4A 3' CTGTCCAGCTCTGTTGATTTT 15922 TG AAA A  
 AAAGT A AGCT GACAG  
 |||| | ||| |||||

		TTTTA T TCGA CTGTC		
		GT GTC C		
GAM1183	TNFAIP1	3' CTGTGTGCATTTTCAACT	40919	_ T G
		AGTTGAAAA GC A ACAG		
		TCAACTTTTT CG T TGTC		
		A _ G		
GAM1183	AUTL1	3' CTGTCTAGCCTCCTGCT	51661	T_ AAAA
		AGT GA GCTAGACAG		
		TCG CT CGATCTGTC		
		TC C__		
GAM1183	C17orf31	3' GTCTAGCTTCCTCTTC	34127	AGTT AA
		GAA GA AAGCTAGAC		
		CTT CT TTCGATCTG		
		__ CC		
GAM1183	C5orf4	3' GCCTTTTCCAAC TTTC	50496	_ A
		GAAAGTTG AAAA GC		
		CTTTCAAC TTTT CG		
		C C		
GAM1183	C5orf4	3' GCCTTTTCCAAC TTTC	32984	_ A
		GAAAGTTG AAAA GC		
		CTTTCAAC TTTT CG		
		C C		
GAM1183	DKFZP586H2123	3' CTGGTGGTCTTCCCCAAC TTTC	61926	AAA _ GA
		GAAAGTTG AAG CTA CAG		
		CTTTCAAC TTC GGT GTC		
		CCC T G_		
GAM1183	DREV1	3' AGTGTTTTCTAAC TTTC	32068	_ A
		GAAAGTT GAAAA GCT		
		CTTTCAA CTTTT TGA		
		T G		
GAM1183	INSM2	3' CTGTGGGGCTTTCTTCAACTT	50865	_ AG
		AAGTTGAA AAAGCT ACAG		
		TTCAACTT TTTCGG TGTC		
		C GG		
GAM1183	KDEL R3	3' CTGCTAGGGTTTCAATT	22458	AG A
		AGTTGAAAA CTAG CAG		
		TTAACTTTT GATC GTC		
		GG _		
GAM1183	KIAA1449	3' CTGTCTCTGTTTCAACTTT	40450	A CT
		AAAGTTGAAA AG AGACAG		

TTTCAACTTT TC TCTGTC  
 G \_  
 GAM1183 LRPPRC 3' CTGCATAACTTTT CGAACTTTTCG 55705 GAA C GA  
 A TCGAAAGTT AAAG TA CAG  
 ||||| ||| || ||  
 AGCTTTCAA TTTC AT GTC  
 GC\_ A AC  
 GAM1183 TFEC 3' TCTTCTCTTCAACTTTTC 24294 AA CT  
 GAAAGTTGAA AG AGA  
 ||||| || ||  
 CTTTCAACTT TC TCT  
 C\_ T\_  
 GAM1183 TSC22 3' CTGTTGCACTTGTCAACTTTTC 20066 AA CTA  
 GAAAGTTGA AAG GACAG  
 ||||| || ||||  
 CTTTCAACT TTC TTGTC  
 G\_ ACG  
 GAM1183 LOC151178 5' CTGTCTAGCTCCCCTCTGC 80149 T AAA\_  
 GT GA AGCTAGACAG  
 || || |||||  
 CG CT TCGATCTGTC  
 T CCCC  
 GAM1183 LOC257451 3' GTGTGTTCTTCAACTTTTCGG 95559 AA T G  
 TCGAAAGTTGAA AGC A AC  
 ||||| ||| ||  
 GGCTTTCAACTT TTG T TG  
 C\_ \_G  
 GAM1183 LOC93097 5' CTGCAAGGACTTTTCAGCCTTC 71361 A AG AGA  
 GAA GTTGAAAA CT CAG  
 || ||||| || ||  
 CTT CGACTTTT GG GTC  
 C CA AAC  
 GAM1184 ATP7A 3' ATTTCTTTGTTAGTTGCA 3518 \_ G  
 TG AA TAACAAAGAAAT  
 || |||||  
 AC TT ATTGTTTCTTTA  
 G G  
 GAM1184 CBFA2T2 3' ATTTCTTTGCCCATTTGGG 17458 AA CAAA  
 CCCAAATG GTAA GAAAT  
 ||||| ||| ||||  
 GGGTTTAC CGTT CTTTA  
 C\_ TC\_  
 GAM1184 DAF 3' TTGTGCTCTTCATTTAGGA 5138 C TA\_  
 TCC AAATGAAG ACAA  
 || ||||| ||  
 AGG TTTACTTC TGTT  
 A TCG  
 GAM1184 HPSE 3' CTGAGTTACTTCCCTTAGGA 21891 C AT AA  
 TCC AA GAAGTAAC AG  
 || || ||||| ||

			AGG TT CTTCATTG TC		
			A CC AG		
GAM1184 LAMA4	3'	ATTTCTTATTTCTCATTTGG	9665	A TAACA	
		CCAAATGA G AAGAAAT			
		GGTTTACT C TTCTTTA			
		_ TTTA _			
GAM1184 MAP2	3'	ATTTCTCTGAGGCCATTTGGGA	48994	AA AA A	
		TCCCAAATG GT CA AGAAAT			
		AGGGTTTAC CG GT TCTTTA			
		_ GA C			
GAM1184 NAGA	3'	TTTTGTTACATCATTT	4240	A	
		AAATGA GTAACAAAG			
		TTTACT CATTGTTTT			
		A			
GAM1184 STK24	3'	CTTTGGCATTTGGGG	13117	AAGTAA	
		TCCCAAATG CAAAG			
		GGGGTTTAC GTTTC			
		G_____			
GAM1184 TBX22	3'	ATTTCTTTGTTATACATTT	33780	AA	
		AAATG GTAACAAAGAAAT			
		TTTAC TATTGTTTCTTTA			
		A_			
GAM1184 TCF12	3'	TTTCTCTGTCATTTGG	12181	AGTAA A	
		CCAAATGA CA AGAAA			
		GGTTTACT GT TCTTT			
		_____ C			
GAM1184 USP14	3'	TGTTTCACCTCATTTGG	17662	A _	
		CCAAATGA GT AACA			
		GGTTTACT CA TTGT			
		C CT			
GAM1184 ZNF146	5'	TTACTCTGCATTTGGGA	23089	A__	
		TCCCAAATG AGTAA			
		AGGGTTTAC TCATT			
		GTC			
GAM1184 BRPF3	3'	TTCTTATACATTTGGGA	92325	AAGTAACA	
		TCCCAAATG AAGAA			
		AGGGTTTAC TTCTT			
		ATA_____			
GAM1184 DKFZP564O0523	3'	TTTCTTTGTTTTTTGGGA	49521	TGAAGT	
		TCCCAA AACAAGAAA			



AGGGTTT TTGTTTCTTT  
 T\_\_\_\_  
 GAM1184 FBXO32 3' TTTGGACACTTCATTTG 54258 AA\_  
 CAAATGAAGT CAAA  
 ||||| |||  
 GTTTACTTCA GTTT  
 CAG  
 GAM1184 FLJ12765 3' TTGTTTACTTCATCAAGGA 45847 CAA \_  
 TCC ATGAAGTAA CAA  
 || ||||| |||  
 AGG TACTTCATT GTT  
 AAC T  
 GAM1184 HRIHFB2436 3' TTTGTTATCTCATCTGG 26800 A AG  
 CCA ATGA TAACAAA  
 || ||| |||||  
 GGT TACT ATTGTTT  
 C CT  
 GAM1184 KIAA0141 3' ATTTTGAGGTCCCCATTTGGGA 28730 AAGTA AAA  
 TCCCAAATG AC GAAAT  
 ||||| || |||||  
 AGGGTTTAC TG TTTA  
 CCC\_\_ GAG  
 GAM1184 KIAA0648 3' ATTTCTTTGTTTTCTTTTGG 82650 T\_ T  
 CCAAA GAAG AACAAAGAAAT  
 |||| ||| |||||  
 GGTTT CTTT TTGTTTCTTTA  
 TC \_  
 GAM1184 KIAA1033 3' TTTGTTACCTCACTTG 64521 A A  
 CAA TGA GTAACAAA  
 || ||| |||||  
 GTT ACT CATTGTTT  
 C C  
 GAM1184 KIAA1239 3' ATTTAAATGGTTACTTCATCTG 71327 A AAAG\_  
 CA ATGAAGTAAC AAAT  
 || ||||| |||  
 GT TACTTCATTG TTTA  
 C GTAAA  
 GAM1184 KIAA1247 3' ATTTCTTTGTTATGTC 61851 A  
 GA GTAACAAAGAAAT  
 || |||||  
 CT TATTGTTTCTTTA  
 G  
 GAM1184 OSBPL6 5' TTCTTTGTTTGTGGATTTGAGA 50716 C GAAGT  
 TC CAAAT AACAAAGAA  
 || ||| |||||  
 AG GTTTA TTGTTTCTT  
 A GGTGT  
 GAM1184 PRO0529 3' ATTTCTTTGTTAAAGTC 25987 AG\_  
 GA TAACAAAGAAAT  
 || |||||

		CT ATTGTTTCTTTA		
		GAA		
GAM1184 SHARP	3'	TCTCCCTTGCTCATTTGG	30398	A CAA
		CCAAATGA GTAA AGA		
		GGTTTACT CGTT TCT		
		_ CCC		
GAM1184 VANG1	3'	TCTGCACTTTATTTGG	57250	AACAA
		CCAAATGAAGT AGA		
		GGTTTATTTCA TCT		
		CG__		
GAM1184 ZNF313	3'	TGTTACCTCTCCATTTGGGA	37945	A T__
		TCCCAAATG AG AACA		
		AGGGTTTAC TC TTGT		
		C TCCAT		
GAM1184 LOC134147	3'	TTGATTATTTCATTTG	57167	_
		CAAATGAAGTAA CAA		
		GTTTACTTTATT GTT		
		A		
GAM1184 LOC139197	5'	TTCTCAGTGCTCATTTGG	75822	A ACAA
		CCAAATGA GTA GAA		
		GGTTTACT CGT CTT		
		_ GACTC		
GAM1184 LOC147639	3'	TTCTGCTACTCATTTGG	78384	A ACAA
		CCAAATGA GTA AGAA		
		GGTTTACT CAT TCTT		
		_ CG__		
GAM1184 LOC151009	3'	ATTTCTTTATCTGTTTCATGGG	85191	AA AC_
	A	TCCCA TGAAGTA AAAGAAAT		
		AGGGT ACTTTGT TTTCTTTA		
		_ CTA		
GAM1184 LOC153222	3'	CTTTGTTACCCCATTTG	80786	AA
		CAAATG GTAACAAAG		
		GTTTAC CATTGTTTC		
		CC		
GAM1184 LOC155434	5'	ATTTCTTTGTTATTTTATTGGG	86401	A
	A	TCCCAA TGAAGTAACAAAGAAAT		
		AGGGTT ATTTTATTGTTTCTTTA		
		_		
GAM1184 LOC160897	3'	TCTTTGTGTTACTTCA	82249	_
		TGAAGTAACA AAGA		

		ACTTCATTGT TTCT		
		GT		
GAM1184	LOC253981	3' TTCTTTTATTTTCATATAGGA 95836	CAA	CA
		TCC ATGAAGTAA AAGAA		
		AGG TACTTTATT TTCTT		
		ATA _		
GAM1185	ALPL	5' CCCACCCACGTCGATTGCATCT 4893	TG GTT	A A A
	CT	AGAGGTG G AC TG GT GG		
		TCTCTAC T TG AC CA CC		
		GT AGC C C C		
GAM1185	FOSB	3' CCTACCCAATGTCTCCACACC 22102	TT	GA_
		GGTGTGGG ACAT GTAGG		
		CCACACCC TGTA CATCC		
		TC ACC		
GAM1185	FPGS	3' CACCCACCCACACCT 17082	TTACA	A A
		AGGTGTGGG TG GT G		
		TCCACACCC AC CA C		
		C_ C C		
GAM1185	HSD17B1	5' CGTGGGAACCCACACCT 4685	A_	
		AGGTGTGGGTT CATG		
		TCCACACCCAA GTGC		
		GG		
GAM1185	KCNK3	3' CCTACTCAGCCCCACTCCCCT 9549	A T	TTACA
		AG GG GTGGG TGAGTAGG		
		TC CC CACCC ACTCATCC		
		C T CG_		
GAM1185	LCP1	3' CCTACTCACATACACACACACC 9694	G _	CA
	T	AGGTGTG GT TA TGAGTAGG		
		TCCACAC CA AT ACTCATCC		
		A C AC		
GAM1185	PEX3	5' CTAGTCAGCCACACCCCT 13267	A	TACA G
		AG GGTGTGGGT TGA TAG		
		TC CCACACCCG ACT ATC		
		C _ G		
GAM1185	PRX	3' CACTCTGCCACACTTC 40522	TACAT	A
		GAGGTGTGGGT GAGT G		
		CTTCACACCCG CTCA C		
		T_ C		
GAM1185	TFAP2A	3' CCCGCTCCCACACCCCT 12228	A	TTACATG TA
		AG GGTGTGGG AG GG		

TC CCACACCC TC CC  
 C \_\_\_\_\_ GC  
 GAM1185 TPK1 3' CCTACTCACACATTAACCCCC 42383 TGT CA\_\_\_\_  
 GG GGGTTA TGAGTAGG  
 || ||||| |||||  
 CC CCAAT ACTCATCC  
 \_\_\_\_\_ TACAC  
 GAM1185 ZNF179 3' CCCACTCCTGGCCCACAGCC 23100 \_ CAT A  
 GG TGTGGGTTA GAGT GG  
 || ||||| ||| ||  
 CC ACACCCGGT CTCA CC  
 G C\_ C  
 GAM1185 A 3' CCTACTCAGCTTCCATCACCCC 27074 A \_ TTACA  
 T AG GGTG TGGG TGAGTAGG  
 || ||| ||| |||||  
 TC CCAC ACCT ACTCATCC  
 C T TCG\_\_\_\_  
 GAM1185 A 3' CCTACTCAGCTTCCATCACCCC 39094 A \_ TTACA  
 T AG GGTG TGGG TGAGTAGG  
 || ||| ||| |||||  
 TC CCAC ACCT ACTCATCC  
 C T TCG\_\_\_\_  
 GAM1185 BCKDK 5' CTACCCACCCACACC 59795 TACAT A  
 GGTGTGGGT G GTAG  
 ||||| | |||  
 CCACACCCA C CATC  
 \_\_\_\_\_ C  
 GAM1185 CAPN6 3' CCCACCCATCCACACACACCT 26602 G TAC A A  
 AGGTGTG GT ATG GT GG  
 ||||| || ||| ||  
 TCCACAC CA TAC CA CC  
 A CC\_ C C  
 GAM1185 DSCR1L1 3' CTA CTACACGCGACACC 19496 \_ G TACAT  
 GGTGT G GT GAGTAG  
 |||| | || ||||  
 CCACA C CA CTCATC  
 G G \_\_\_\_\_  
 GAM1185 FLJ10315 5' CCCACCCACCTCCACACCTC 36018 TTACA A A  
 GAGGTGTGGG TG GT GG  
 ||||| || ||| ||  
 CTCCACACCC AC CA CC  
 TCCC\_ C C  
 GAM1185 FLJ12783 3' CACTCATTCCACACCTCT 48679 TTAC A  
 AGAGGTGTGGG ATGAGT G  
 ||||| ||| |  
 TCTCCACACCT TACTCA C  
 \_\_\_\_\_ C  
 GAM1185 FLJ23416 3' CCTACCCAACCCACACACC 49948 TTACA A  
 GGTGTGGG TG GTAGG  
 ||||| || ||||

		CCACACCC AC CATCC		
		CA__ C		
GAM1185 KIAA0523	3'	CCTGGCCACGAACCCACACCTC 67733	ACA AG	
		GAGGTGTGGGTT TG TAGG		
		CTCCACACCCAA AC GTCC		
		GC_ CG		
GAM1185 KIAA1076	3'	CCCACTCACCCCAACCCACAC 65512	ACA__ A	
	C	GGTGTGGGTT TGAGT GG		
		CCACACCCAA ACTCA CC		
		CCCCC C		
GAM1185 KIAA1303	3'	CCCCTCCCCGCACCTC 66000	TTACAT TA_	
		GAGGTGTGGG GAG G		
		CTCCACGCCC CTC C		
		_____ CCA		
GAM1185 KPTN	3'	CAGCTAACCCACTCCTCT 73410	T CA	
		AGAGG GTGGGTTA TG		
		TCTCC CACCCAAT AC		
		T CG		
GAM1185 NAPA	3'	CCCACCCCAGCCCCACACCT 13816	TTACA A_ A	
		AGGTGTGGG TG GT GG		
		TCCACACCC AC CA CC		
		CG__ CC C		
GAM1185 PSKH1	3'	CCCACCCATGGTGCACACCT 68236	GGTTA A A	
		AGGTGTG CATG GT GG		
		TCCACAC GTAC CA CC		
		GTG__ C C		
GAM1185 SLC5A7	5'	CTCGCACCCACACCCCT 41511	A TACA	
		AG GGTGTGGGT TGAG		
		TC CCACACCCA GCTC		
		C C__		
GAM1185 LOC124753	3'	CTGGGTAACCTCACACCCCT 74322	A ATGAG	
		AG GGTGTGGGTTAC TAG		
		TC CCACACTCAATG GTC		
		C G__		
GAM1185 LOC148709	5'	CCCACTCACCAACAGCCCACAC 78939	G ACA__ A	
	TCT	AGAG TGTGGGTT TGAGT GG		
		TCTC ACACCCGA ACTCA CC		
		_ CCACC C		
GAM1185 LOC148764	5'	CCCACCCACCTTCTCCCACACC 78984	TTACA_ A A	
	T	AGGTGTGGG TG GT GG		

			TCCACACCC	AC CA CC		
			TCTTCC	C C		
GAM1186	AKAP13	3'	GGACGCCCACTGCTCCTC	22143	A	A
			GAG AGCAGTGG	CGTCC		
			CTC TCGTCACC	GCAGG		
			C	C		
GAM1186	AKAP13	3'	GGACGCCCACTGCTCCTC	23247	A	A
			GAG AGCAGTGG	CGTCC		
			CTC TCGTCACC	GCAGG		
			C	C		
GAM1186	AKAP13	3'	GGACGCCCACTGCTCCTC	58579	A	A
			GAG AGCAGTGG	CGTCC		
			CTC TCGTCACC	GCAGG		
			C	C		
GAM1186	APOC4	3'	GTTCACTTCTCCA	7917	CA	
			TGGAGAAG	GTGGAC		
			ACCTCTTC	TACTTG		
			A_			
GAM1186	BRS3	3'	GGAAAAATGCTGCTTCTCC	8178		GACG
			GGAGAAGCAGTG	TCC		
			CCTCTTCGTCGT	AGG		
			AAAA			
GAM1186	CSRP1	3'	GGAGCCCCTGCTTCTCCA	14534		T ACG
			TGGAGAAGCAG	GG TCC		
			ACCTCTTCGTC	CC AGG		
			_ CG_			
GAM1186	FBXL7	3'	GGAAGGACATGCAGTCCTCC	24552	AA A	GAC
			GGAG GC GTG	GTCCTTCC		
			CCTC TG CGT	CAGGAAGG		
			C_ A A_			
GAM1186	GML	3'	GACCCTTATCCACTGCTCCTCT	9050	A	C_____
	A		TGGAG AGCAGTGA	GTC		
			ATCTC TCGTCACCT	CAG		
			C	ATTCC		
GAM1186	NEDD4	3'	GAAAACTGTTTACTTCTTC	70011	C	_ CC
			GAAG AGTGGAC	GT TTC		
			CTTC TCATTTG	CA AAG		
			T	T AA		
GAM1186	PSME3	3'	GGACTGTTCCACTGCCCCTCC	19374	AA	__
			GGAG GCAGTGA	C GTCC		

			CCTC CGTCACCT G CAGG		
			CC TT		
GAM1186	RUNX3	3'	GGAAGGACCTCACTGTCTCCA 15116	AA	AC
			TGGAG GCAGTGG GTCCTTCC		
			ACCTC TGTCACCT CAGGAAGG		
			__ C_		
GAM1186	SIM2	3'	GGAAGGGATGTGCCCGCCTCTC 17386	A AGT	_ _
	CA		TGGAGA GC GG ACGTCC TTCC		
			ACCTCT CG CC TGTAGG AAGG		
			C C__ G G		
GAM1186	SLC22A11	3'	AAGGAGTTGCCTCTTCTCCA 37488	C TG	G
			TGGAGAAG AG GAC TCCTT		
			ACCTCTTC TC TTG AGGAA		
			_ CG _		
GAM1186	TITF1	3'	GACCACCATCCACCGCTGCTCC 12423	A A	C__
	A		TGGAG AGC GTGGA GTC		
			ACCTC TCG CACCT CAG		
			G C ACCAC		
GAM1186	VANGL2	3'	GGAAGGACTCCCACCTCACCA 71651	A AGCA	AC
			TGG GA GTGG GTCCTTCC		
			ACC CT CACC CAGGAAGG		
			A C__ CT		
GAM1186	C5orf4	3'	GAAAAACATCCACTGTAGCT 32983	AA	C CC
			AG GCAGTGGA GT TTC		
			TC TGTCACCT CA AAG		
			GA A AA		
GAM1186	C5orf4	3'	GAAAAACATCCACTGTAGCT 50495	AA	C CC
			AG GCAGTGGA GT TTC		
			TC TGTCACCT CA AAG		
			GA A AA		
GAM1186	CAMKK2	3'	GGAAACTCTGCTTCCCCA 21584	A	T ACG
			TGG GAAGCAG GG TCC		
			ACC CTTCGTC TC AGG		
			C _ AA_		
GAM1186	DUSP10	3'	AAGGATTGCTGCTCTCCA 23278	A	TG ACG
			TGGAGA GCAG G TCCTT		
			ACCTCT CGTC T AGGAA		
			_ GT__		
GAM1186	DUSP10	3'	AAGGATTGCTGCTCTCCA 58559	A	TG ACG
			TGGAGA GCAG G TCCTT		

ACCTCT CGTC T AGGAA  
 \_ GT \_  
 GAM1186 ENDOGLYX1 3' GAAGGACTGGAATGCTTCTCC 45402 GTGGAC  
 GGAGAAGCA GTCCTTC  
 ||||| |||||  
 CCTCTTCGT CAGGAAG  
 AAGGT\_  
 GAM1186 EPB41L1 3' GAAAGAACCAGATGCTCTCCA 70594 A G\_ ACG C  
 TGGAGA GCA TGG TC TTC  
 ||||| ||| ||| |||||  
 ACCTCT CGT ACC AG AAG  
 \_ AG A\_ A  
 GAM1186 FBP17 3' GAAAAGCTCACTGCTGCCCA 72791 AGA AC CC  
 TGG AGCAGTGG GT TTC  
 ||| ||||| || |||  
 ACC TCGTCACT CG AAG  
 CCG \_ AA  
 GAM1186 FLB6421 5' GGAATCCACTGCCCTGCA 39227 G AA CG  
 TG AG GCAGTGGA TCC  
 || || ||||| |||  
 AC TC CGTCACCT AGG  
 G CC A\_  
 GAM1186 FLJ00058 5' GGAAGGACAGGCTGGCCTCTCC 78766 A \_ GGAC  
 GGAGA GC AGT GTCCTTCC  
 ||||| || ||| |||||  
 CCTCT CG TCG CAGGAAGG  
 C G GA\_  
 GAM1186 FLJ11996 3' AAGAACGTCTATCTATCCA 46433 GA CA C  
 TGGA AG GTGGACGT CTT  
 |||| || ||||| |||  
 ACCT TC TATCTGCA GAA  
 A\_ \_ A  
 GAM1186 FLJ20128 3' AAGAGACCCTTCTCCA 34594 CAGTGGAC \_  
 TGGAGAAG GTC CTT  
 ||||| ||| |||  
 ACCTCTTC CAG GAA  
 C\_ \_ A  
 GAM1186 FLJ20371 5' GGAGTCCTCACCATTCTCCA 35062 CA \_ G  
 TGGAGAAG GT GGAC TCC  
 ||||| || ||| |||  
 ACCTCTTC CA CCTG AGG  
 AC CT \_  
 GAM1186 FLJ23420 5' GGCCACCTCTTCTCCA 46848 CA AC  
 TGGAGAAG GTGG GTC  
 ||||| ||| |||  
 ACCTCTTC CACC CGG  
 TC \_  
 GAM1186 KIAA0318 3' AAGGGGCTGCTTTCCA 68943 A GGACG  
 TGGAGA GCAGT TCCTT  
 ||||| ||||| |||||



ACCTTT CGTCG GGGAA

GAM1186 KIAA0323 3' GGAGCCCCTGCTCCTCC 63267 A ACG  
GGAG AGCAGTGG TCC  
||||| ||||| ||  
CCTC TCGTCACC AGG  
C CG\_  
GAM1186 KIAA0522 3' GAATCTCCGCTGCCTCTCCA 71969 A CG\_  
TGGAGA GCAGTGG TC  
||||| ||||| ||  
ACCTCT CGTCGCCT AG  
C CTA  
GAM1186 KIAA1045 3' GAAGAAGTTTTCCGCTTCTCC 71052 AGT GTC  
GGAGAAGC GGAC CTTC  
||||| ||| ||||  
CCTCTTCG TTTG GAAG  
CCT AA\_  
GAM1186 KIAA1054 3' AAGGACACCCAGTAATTCTC 68422 GCAG AC  
GAGAA TGG GTCCTT  
||||| ||| |||||  
CTCTT ACC CAGGAA  
AATG CA  
GAM1186 KIAA1841 3' AAGGCAAAGTCTTCTCC 80043 GGAC T  
GGAGAAGCAGT G CCTT  
||||||| | ||||  
CCTCTTCGTCA C GGAA  
AA\_\_  
GAM1186 KIAA1872 3' GGACCTCACTGCTCCCCCA 62940 AGA AC  
TGG AGCAGTGG GTCC  
||| ||||| ||||  
ACC TCGTCACT CAGG  
CCC C\_  
GAM1186 MGC30052 3' GAAGGAATTGGACACTTCTCCA 58534 AGC GA \_\_  
TGGAGA AGTG CG TCCTTC  
||||| ||| || |||||  
ACCTCT TCAC GT AGGAAG  
\_\_ AG TA  
GAM1186 NXPH3 3' GAAGGACAGGCCTGCCCA 65760 AGAA TGGAC  
TGG GCAG GTCCTTC  
||| ||| |||||  
ACC CGTC CAGGAAG  
\_\_ CGGA\_  
GAM1186 SEC24C 3' GAAACACTGCTTCTCCA 16997 GACG  
TGGAGAAGCAGTG TC  
||||||| ||  
ACCTCTTCGTCAAC AG  
AA\_\_  
GAM1186 TNFRSF19L 3' GGGCCCCACTGCCTGTCCA 51778 GAA AC  
TGGA GCAGTGG GTCC  
||| ||||| ||||

	ACCT CGTCACC CGGG	
	GTC _	
GAM1186 LOC115574 3'	GGACCACCCACTGCTTCTCC 73467	AC_
	GGAGAAGCAGTGG GTCC	
	CCTCTTCGTCACC CAGG	
	CAC	
GAM1186 LOC124871 3'	GGAAAAATTTCTGCTGCCCCA 74348	AGAA TG C CC
	TGG GCAG GA GT TTCC	
	ACC CGTC CT TA AAGG	
	C_ GT T AA	
GAM1186 LOC148696 5'	GAAGGGTGCCACCCCTCCA 84188	AAGCA A GT
	TGGAG GTGG C CCTTC	
	ACCTC CACC G GGAAG	
	CCC_ _TG	
GAM1186 LOC151475 5'	AAGGCCACACTGCCCTCC 85381	AA GAC T
	GGAG GCAGTG G CCTT	
	CCTC CGTCAC C GGAA	
	C_ AC_	
GAM1186 LOC152009 3'	GGAAGTCCACTGCTCTCC 85541	A ACG_
	GGAGA GCAGTGG TCC	
	CCTCT CGTCACC AGG	
	_ GTCA	
GAM1186 LOC152445 3'	AAGGACATGCTTTCCA 85737	A GTGGAC
	TGGAGA GCA GTCCTT	
	ACCTTT CGT CAGGAA	
	_ A_	
GAM1186 LOC197003 3'	AAGAGCTTCCCCTTCTCCA 87863	CAGT C TC
	TGGAGAAG GGA G CTT	
	ACCTCTTC CCT C GAA	
	C_ T GA	
GAM1186 LOC203413 5'	GAGGCCCACTGCTTCCCA 90634	A AC T
	TGG GAAGCAGTGG G CCTT	
	ACC CTTCGTCACC C GGAG	
	_ _	
GAM1186 LOC219942 3'	GGAAGGACACCATTTTCTCC 93347	CA AC
	GGAGAAG GTGG GTCCTTCC	
	CCTCTTT TACC CAGGAAGG	
	_ A_	
GAM1186 LOC221935 3'	GCAGCCACCGCTTCTCCA 92621	A AC
	TGGAGAAGC GTGG GT	

		ACCTCTTCG CACC CG		
		C GA		
GAM1186	LOC253263	3' GACTGACCCACTGCTACCCCA	97032	AGA AC CT
		TGG AGCAGTGG GTC TC		
		ACC TCGTCACC CAG AG		
		CCA _ TC		
GAM1186	LOC51161	3' GAAGGATGCAGCCCCCCA	32512	AGAA AG GA
		TGG GC TG CGTCCTTC		
		ACC CG AC GTAGGAAG		
		CCCC _ _		
GAM1186	LOC92492	5' GGTCTGTCCACTGCCTCCCA	69527	A A T_
		TGG GA GCAGTGGACG CC		
		ACC CT CGTCACCTGT GG		
		_ C CT		
GAM1187	A1BG	3' CACAGCAACCTCTACCTC	55411	A
		GAGGTAGAGGTTGC GTG		
		CTCCATCTCCAACG CAC		
		A		
GAM1187	ACVR1	5' CACTGCAGCCTCCACCTC	6604	A
		GAGGT GAGGTTGCAGTG		
		CTCCA CTCCGACGTCAC		
		C		
GAM1187	ADRB3	3' CTTTCCACAACCTCTACCTT	3436	CAGT
		GAGGTAGAGGTTG GAG		
		TTCCATCTCCAAC TTC		
		ACCT		
GAM1187	AHR	3' CACTGCAACCTCTACCTC	7877	
		GAGGTAGAGGTTGCAGTG		
		CTCCATCTCCAACGTCAC		
GAM1187	AIM1	3' CACTGCAGCCTCTACCTC	91818	
		GAGGTAGAGGTTGCAGTG		
		CTCCATCTCCGACGTCAC		
GAM1187	ALDH1B1	3' CACTGCAACCTCCGCCTC	5491	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCAC		
		GC		
GAM1187	AP3B2	5' CGCCGCAACCTCCTCCTC	16188	TA A
		GAGG GAGGTTGC GTG		

			CTCC CTCCAACG CGC		
			TC C		
GAM1187	APPBP2	3'	CACTGCAACCTCCGCCTC	21074	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	AQP6	3'	CGGCTCACTGCAACCTCTACCT	53922	
	C		GAGGTAGAGGTTGCAGTGAGTTG		
			CTCCATCTCCAACGTCACCTCGGC		
GAM1187	AQP6	3'	CGGCTCACTGCAACCTCTACCT	7947	
	C		GAGGTAGAGGTTGCAGTGAGTTG		
			CTCCATCTCCAACGTCACCTCGGC		
GAM1187	ARCN1	3'	CACTGCAACCTCCGCCTC	7972	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	ATP8B2	3'	CAGCTCACTGCAACCTCCACCT	65215	A
	C		GAGGT GAGGTTGCAGTGAGTTG		
			CTCCA CTCCAACGTCACCTCGAC		
			C		
GAM1187	BRIP1	3'	CACTGCAACCTTCACCTC	49397	AG
			GAGGT AGGTTGCAGTG		
			CTCCA TCCAACGTCAC		
			CT		
GAM1187	C7	3'	CTGCAACCTCCGCCTC	5162	TA
			GAGG GAGGTTGCAG		
			CTCC CTCCAACGTC		
			GC		
GAM1187	CAMLG	3'	CACCGCAACCTCCACCTT	8233	A A
			GAGGT GAGGTTGC GTG		
			TTCCA CTCCAACG CAC		
			C C		
GAM1187	CCNF	3'	CAACTCACTGTAACCTCCGCCT	8314	TA
	C		GAGG GAGGTTGCAGTGAGTTG		
			CTCC CTCCAATGTCACTCAAC		
			GC		
GAM1187	CDH17	3'	CACTGCAACCTCCGCCTC	14501	TA
			GAGG GAGGTTGCAGTG		

			CTCC CTCCAACGTCAC			
			GC			
GAM1187	CIAS1	5'	CACTGCAGCCTCCACCTC	16899	A	
			GAGGT GAGGTTGCAGTG			
			CTCCA CTCCGACGTCAC			
			C			
GAM1187	COX15	3'	ACTCTGCAACCTCCACTTC	54308	A	GT
			GAGGT GAGGTTGCA GAGT			
			CTTCA CTCCAACGT CTCA			
			C			
GAM1187	CRTAP	3'	CACTGCAACCTCCGCCTC	21030	TA	
			GAGG GAGGTTGCAGTG			
			CTCC CTCCAACGTCAC			
			GC			
GAM1187	CSNK2A2	5'	CAGCTCACTGCAACCTCCACCT	8561	A	
	C		GAGGT GAGGTTGCAGTGAGTTG			
			CTCCA CTCCAACGTCACTCGAC			
			C			
GAM1187	CXCL16	3'	CGGCTCACTGCAACCCCCATCT	41919	AGA	
	C		GAGGT GGTTGCAGTGAGTTG			
			CTCTA CCAACGTCACTCGGC			
			CCC			
GAM1187	CYLN2	3'	CTGCAGCCTCCACCTC	12633	A	
			GAGGT GAGGTTGCAG			
			CTCCA CTCCGACGTC			
			C			
GAM1187	CYP1A2	3'	CACTGCAACCTCTGCCTC	5680		
			GAGGTAGAGGTTGCAGTG			
			CTCCGTCTCCAACGTCAC			
GAM1187	CYP1A2	3'	CACTACAACCTCCGCCTC	69098	TA	C
			GAGG GAGGTTG AGTG			
			CTCC CTCCAAC TCAC			
			GC A			
GAM1187	CYP1A2	3'	CACTGCAACCTCTGCCTC	69099		
			GAGGTAGAGGTTGCAGTG			
			CTCCGTCTCCAACGTCAC			
GAM1187	CYP1A2	3'	CAGCTCACTGCAACCTCCACCT	5683	A	
	C		GAGGT GAGGTTGCAGTGAGTTG			

			CTCCA CTCCAACGTCAC		
			C		
GAM1187	CYP1A2	3'	CACTACAACCTCCGCCTC	5679	TA C
			GAGG GAGGTTG AGTG		
			CTCC CTCCAAC TCAC		
			GC A		
GAM1187	CYP1A2	3'	CAGCTCACTGCAACCTCCACCT	69102	A
	C		GAGGT GAGGTTGCAGTGAGTTG		
			CTCCA CTCCAACGTCAC		
			C		
GAM1187	CYP2B6	3'	CGGCTCACTGCAACCTCCACC	5728	A
			GGT GAGGTTGCAGTGAGTTG		
			CCA CTCCAACGTCAC		
			C		
GAM1187	CYP4F3	3'	CATTGCAACCTCCGCCTC	6112	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTTAC		
			GC		
GAM1187	CYP8B1	3'	CACTACAACCTCTGCCTC	15258	C
			GAGGTAGAGGTTG AGTG		
			CTCCGTCTCCAAC TCAC		
			A		
GAM1187	CYP8B1	3'	CACTGCAACCTCTGCCTC	15260	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1187	DFFB	3'	CACTGCAACCTCCGCCTC	87378	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	DISC1	3'	CGGCTCACTGCAACCTCTACCT	37875	
	C		GAGGTAGAGGTTGCAGTGAGTTG		
			CTCCATCTCCAACGTCAC		
GAM1187	DSCR3	3'	CAGCTCACTGCAACCTCCACCT	20174	A
	C		GAGGT GAGGTTGCAGTGAGTTG		
			CTCCA CTCCAACGTCAC		
			C		
GAM1187	EHD2	3'	CAGCTCACTGCAACCTCCACCT	27490	A
	C		GAGGT GAGGTTGCAGTGAGTTG		

			CTCCA CTCCAACGTC	ACTCGAC	
			C		
GAM1187 EPB72	3'	CACTGCAACCTCCGCCTC	14600	TA	
		GAGG GAGGTTGCAGTG			
		CTCC CTCCAACGTCAC			
		GC			
GAM1187 F2RL2	3'	CATTGCAACCTCTGCCTC	14620		
		GAGGTAGAGGTTGCAGTG			
		CTCCGTCTCCAACGTTAC			
GAM1187 FANCF	3'	CAGTGCAACCTCTGCCTC	42671	G	
		GAGGTAGAGGTTGCA TG			
		CTCCGTCTCCAACGT AC			
		G			
GAM1187 FEZ1	3'	CACTGCAACCTCCACCTC	42567	A	
		GAGGT GAGGTTGCAGTG			
		CTCCA CTCCAACGTCAC			
		C			
GAM1187 FGF5	3'	CGGCTCACTGCAACCTCCAACT	15538	GTA	
C		GAG GAGGTTGCAGTGAGTTG			
		CTC CTCCAACGTC	ACTCGGC		
		AAC			
GAM1187 FGF5	3'	CGGCTCACTGCAACCTCCAACT	52484	GTA	
C		GAG GAGGTTGCAGTGAGTTG			
		CTC CTCCAACGTC	ACTCGGC		
		AAC			
GAM1187 FHL1	3'	AACTCACTGCTCACCTC	7556	TT__	
		GAGG GCAGTGAGTT			
		CTCC CGTCACTCAA			
		CACT			
GAM1187 FHL2	5'	CAGCTCACTGCAAGCTCTACCT	7562	G	
C		GAGGTAGAG TTGCAGTGAGTTG			
		CTCCATCTC AACGTCACTCGAC			
		G			
GAM1187 FZD4	3'	CACTGCAACCTCTGCCTC	24129		
		GAGGTAGAGGTTGCAGTG			
		CTCCGTCTCCAACGTCAC			
GAM1187 G6PC	3'	CACTGCAACCTCTTCCTC	3822	T	
		GAGG AGAGGTTGCAGTG			

			CTCC TCTCCAACGTCAC		
			T		
GAM1187	GHR	3'	GA	3883	A
			CTCACTGCAATCTCCACCTC		
			GAGGT GAGGTTGCAGTGAGTT		
			CTCCA CTCTAACGTC		
			ACTCAG		
			C		
GAM1187	GM2A	3'	CA	67774	TA
			CTGCAACCTCCGCCTC		
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	GNE	3'	CA	18476	G
			ATGCAACCTCTGCC		
			GGTAGAGGTTGCA TG		
			CCGTCTCCAACGT AC		
			A		
GAM1187	GPR4	3'	CA	59901	A
			CTGCAAGCCTCCACCTC		
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1187	GPR56	5'	CA	19066	A A
			TCGTAACCTCCACCTC		
			GAGGT GAGGTTGC GTG		
			CTCCA CTCCAATG TAC		
			C C		
GAM1187	GPR81	3'	CA	50754	
			CTGCAACCTCTGCCTC		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1187	GRAF	3'	CA	30551	TA
			CTGCAACCTCCGCCTC		
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	HTR1E	5'	CA	6012	TA
			ATTGCAACCTCCGCCTC		
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTTAC		
			GC		
GAM1187	IL11	3'	CA	5325	A G
			CTGCAAGCTCCACCTC		
			GAGGT GAG TTGCAGTG		
			CTCCA CTC AACGTCAC		
			C G		
GAM1187	ITGAM	3'	CA	71836	TA
			CTGCAACCTCCGCCTC		
			GAGG GAGGTTGCAGTG		



			CTCC CTCCAACGTCAC		
			GC		
GAM1187 KMO	3'	CACTGCAACCTCTGCCTC	13447		
		GAGGTAGAGGTTGCAGTG			
		CTCCGTCTCCAACGTCAC			
GAM1187 LANCL1	3'	AACTCACTGCATGACCCT	20203	A	—
		AG GGT TGCAGTGAGTT			
		TC CCA ACGTCACTCAA			
		— GT			
GAM1187 LILRA3	3'	CACTGCAACCTCCGCCTC	95308	TA	
		GAGG GAGGTTGCAGTG			
		CTCC CTCCAACGTCAC			
		GC			
GAM1187 LNK	3'	CACTGCAACCTCCACCTT	18459	A	
		GAGGT GAGGTTGCAGTG			
		TTCCA CTCCAACGTCAC			
		C			
GAM1187 LSS	3'	CAACCCCTCAACCTCTATCTC	9813		C TGA
		GAGGTAGAGGTTG AG GTTG			
		CTCTATCTCCAAC TC CAAC			
		— CC—			
GAM1187 LYZ	3'	CGGCTCACTGCAACCTCCACCT	4099	A	
C		GAGGT GAGGTTGCAGTGAGTTG			
		CTCCA CTCCAACGTCACCTCGGC			
		C			
GAM1187 MAK	3'	CTTACTGCAACCTCCACCTC	19760	A	
		GAGGT GAGGTTGCAGTGAG			
		CTCCA CTCCAACGTCATTC			
		C			
GAM1187 MEF2A	5'	CACTGCAACCTCCGCCTC	18781	TA	
		GAGG GAGGTTGCAGTG			
		CTCC CTCCAACGTCAC			
		GC			
GAM1187 MEFV	3'	CAGCTCACTGCAACCTCCACCT	4130	A	
C		GAGGT GAGGTTGCAGTGAGTTG			
		CTCCA CTCCAACGTCACCTCGAC			
		C			
GAM1187 MEFV	3'	CACTGCAACCTCCGCCTC	4128	TA	
		GAGG GAGGTTGCAGTG			

CTCC CTCCAACGTCAC  
 GC  
 GAM1187 MHC2TA 3' CACTGCAACCTCCGCCTC 4166 TA  
 GAGG GAGGTTGCAGTG  
 |||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1187 MICB 3' CACTGCAACCTCTGCCTC 19822  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 MPL 3' CACTGCAACCTCTGCCTC 18133  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 MPL 3' CAGCTCACTGCAACCTCCACCT 18135 A  
 C GAGGT GAGGTTGCAGTGAGTTG  
 |||| |||||  
 CTCCA CTCCAACGTCACCTCGAC  
 C  
 GAM1187 MRPL49 3' CACTGCAACTTCCACCTC 69567 A  
 GAGGT GAGGTTGCAGTG  
 |||| |||||  
 CTCCA CTTCAACGTCAC  
 C  
 GAM1187 MSN 3' CAACCCAGGAGCATCCACCTC 60251 AGA T AG\_ A  
 GAGGT GG TGC TG GTTG  
 |||| || || ||||  
 CTCCA CC ACG AC CAAC  
 \_\_\_\_ T AGG C  
 GAM1187 MYCL2 3' CACTGCAACCTCTGCCTC 18177  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 NDRG3 3' CACTGCAACCTCTGCC 49293  
 GGTAGAGGTTGCAGTG  
 |||||  
 CCGTCTCCAACGTCAC  
  
 GAM1187 NQO1 3' CACTGCAACCTCTGCCTC 6154  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 PCDHB11 3' CACTGCAACCTCTGCCTC 38411  
 GAGGTAGAGGTTGCAGTG  
 |||||

CTCCGTCTCCAACGTCAC

GAM1187 PCDHB16 3' CACTGCAACCTCTGCCTC 40551  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 PCDHB9 3' CACTGCAACCTCCGCCTC 38936 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 PDCL 3' CGGCTCACTGCAACCTCCACCT 18212 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||||  
CTCCA CTCCAACGTCACTCGGC  
C

GAM1187 PDE6B 3' CAGCTCACTGCAACCTCCACCT 4275 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||||  
CTCCA CTCCAACGTCACTCGAC  
C

GAM1187 PER2 3' CACTGCAACCTCTGCCTC 43029  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 PIGR 3' CACTGCAACCTCCGCCTC 72592 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 PON1 3' CACTGCAACTTCTACCTC 4802  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCATCTTCAACGTCAC

GAM1187 PPP1R12B 3' AACTCACTTCCCTCCTC 49476 T A TTGC  
GAGG AG GG AGTGAGTT  
||| || |||||  
CTCC TC CC TCACTCAA  
\_ \_ T\_

GAM1187 PRKWNK3 3' ACTGCTGCAACCTCCCCCTC 61549 TA G  
GAGG GAGGTTGCAGT AGT  
||| ||||| |||  
CTCC CTCCAACGTCTG TCA  
CC \_

GAM1187 PSMB2 3' CACTGCAACCTCCGCCTC 10950 TA  
GAGG GAGGTTGCAGTG  
||| |||||

			CTCC CTCCAACGTCAC		
			GC		
GAM1187	PTGIS	3'	CAGCTCACCACAACCTCCACCT 6326	A	CA
	C		GAGGT GAGGTTG GTGAGTTG		
			CTCCA CTCCAAC CACTCGAC		
			C AC		
GAM1187	RAB36	3'	CAGTGCAACCTCTGCCTC 16951	G	
			GAGGTAGAGGTTGCA TG		
			CTCCGTCTCCAACGT AC		
			G		
GAM1187	RAB36	3'	CACGTACACCCACCTC 16948	AGA _ A	
			GAGGT GGT TGC GTG		
			CTCCA CCA ATG CAC		
			CCC C _		
GAM1187	RHD	3'	CACTGCAACCTCCGCCTC 32298	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	RHD	3'	CACTGCAACCTCTACCTC 32609		
			GAGGTAGAGGTTGCAGTG		
			CTCCATCTCCAACGTCAC		
GAM1187	RHD	3'	CACTGCAACCTCCGCCTC 32607	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	RHD	3'	CACTGCAACCTCTACCTC 32300		
			GAGGTAGAGGTTGCAGTG		
			CTCCATCTCCAACGTCAC		
GAM1187	RPH3AL	3'	CGGCTCACTGCAACCTCCACCT 22745	A	
	C		GAGGT GAGGTTGCAGTGAGTTG		
			CTCCA CTCCAACGTCACTCGGC		
			C		
GAM1187	SAS	3'	CACCGCAACCTCTGCCTC 19950	A	
			GAGGTAGAGGTTGC GTG		
			CTCCGTCTCCAACG CAC		
			C		
GAM1187	SEDL	3'	CACTGCAACCTCCGCCTC 27328	TA	
			GAGG GAGGTTGCAGTG		

			CTCC CTCCAACGTCAC		
			GC		
GAM1187	SEDL	3'	CACTGCAACCTCCACCTC	27325	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCAACGTCAC		
			C		
GAM1187	SEDL	3'	CACTGCAACCTCCACCTC	27326	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCAACGTCAC		
			C		
GAM1187	SEPN1	3'	CACTGCAACCTCCACCTC	66363	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCAACGTCAC		
			C		
GAM1187	SERPINB9	3'	CACTGCAACCTCCTCCTC	14749	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			TC		
GAM1187	SHOX	3'	CACTGCAACCTCCGCCTC	22531	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	SIL	3'	CACTGCAACCTCTGCCTC	11686	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1187	SLA2	3'	CAGCTCACTGCAACCTCCATCT	49894	A
	C		GAGGT GAGGTTGCAGTGAGTTG		
			CTCTA CTCCAACGTCACCTCGAC		
			C		
GAM1187	SLC14A2	5'	CACTGCAACCTCCACCTC	23130	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCAACGTCAC		
			C		
GAM1187	SLC15A1	3'	CACTGCAACCTCCGCCTC	17398	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	SMAC	5'	CACTGCAACCTCTGCCTC	57204	
			GAGGTAGAGGTTGCAGTG		

CTCCGTCTCCAACGTCAC

GAM1187 SNAP23 3' CACTGCAACCTCCGCCTC 13806 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 SNAP23 3' CACTGCAACCTCCGCCTC 55459 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 SNX15 3' CGGCTCACTGCAACCTCCACCT 73737 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||||  
CTCCA CTCCAACGTCACTCGGC  
C

GAM1187 SPN 3' CACTGCAACCTCTGCCTC 11917  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 SS18 3' CACTGCAACCTCCGCCTC 18883 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 STAU 5' ACTGCAACCTCCACCTC 15994 A  
GAGGT GAGGTTGCAGT  
|||||  
CTCCA CTCCAACGTCA  
C

GAM1187 STAU 5' CGGCTCACTGCAACCTCCACCT 16000 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||||  
CTCCA CTCCAACGTCACTCGGC  
C

GAM1187 SULT2B1 5' CACTGCAACCTCCGCCTC 16023 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 TAPBP 3' CTTACTGCAACCTCCGCCTC 12125 TA  
GAGG GAGGTTGCAGTGAG  
|||||  
CTCC CTCCAACGTCATTG  
GC

GAM1187 TAT 3' CGGCTCACTGCAACCTCCACCT 4464 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||||

			CTCCA CTCCAACGTCACTCGGC		
			C		
GAM1187	TBXA2R	3'	CAGCTCACTGCAACCTCCACCT 6485	A	
		C	GAGGT GAGGTTGCAGTGAGTTG		
			CTCCA CTCCAACGTCACTCGAC		
			C		
GAM1187	TBXA2R	3'	CACTGCAACCTCCGCCTC 6483	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	TMC1	5'	CTGCAACCTCCGCCTC 56902	TA	
			GAGG GAGGTTGCAG		
			CTCC CTCCAACGTC		
			GC		
GAM1187	TNFRSF10B	3'	CAGTGCAACCTCCGCCTC 13867	TA	G
			GAGG GAGGTTGCA TG		
			CTCC CTCCAACGT AC		
			GC G		
GAM1187	TPMT	3'	CACTGCAACCTCTGCCTC 4534		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1187	TRIM9	5'	CACTGCAACCTCCGCCTC 30755	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	TRPM6	3'	CACTGCAACCTCTGCCTC 34535		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1187	TRPV1	3'	CACTGCAACCTCTGCCTC 54792		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1187	TRPV1	3'	CTGCAACCTCCGCCTC 54802	TA	
			GAGG GAGGTTGCAG		
			CTCC CTCCAACGTC		
			GC		
GAM1187	TRPV1	3'	CACTGCAACCTCTGCCTC 38073		
			GAGGTAGAGGTTGCAGTG		

CTCCGTCTCCAACGTCAC

GAM1187 TRPV1 3' CTGCAACCTCCGCCTC 38081 TA  
GAGG GAGGTTGCAG  
|||| ||||||||  
CTCC CTCCAACGTC  
GC

GAM1187 TRPV1 3' CACTGCAACCTCTGCCTC 54859  
GAGGTAGAGGTTGCAGTG  
||||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1187 TRPV1 3' CACTGCAACCTCTGCCTC 54827  
GAGGTAGAGGTTGCAGTG  
||||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1187 TRPV1 3' CTGCAACCTCCGCCTC 54835 TA  
GAGG GAGGTTGCAG  
|||| ||||||||  
CTCC CTCCAACGTC  
GC

GAM1187 TRPV1 3' CTGCAACCTCCGCCTC 54867 TA  
GAGG GAGGTTGCAG  
|||| ||||||||  
CTCC CTCCAACGTC  
GC

GAM1187 TUFT1 3' CACTGCAACCTCTGCCTC 39252  
GAGGTAGAGGTTGCAGTG  
||||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1187 VENTX2 3' CACTGCAACCTCCGCCTC 27108 TA  
GAGG GAGGTTGCAGTG  
|||| ||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 VHL 3' CACTGCAACCTCTGCCTC 5064  
GAGGTAGAGGTTGCAGTG  
||||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1187 ZNF133 5' CAACTCACTGCAACCTCCACC 12831 A  
GGT GAGGTTGCAGTGAGTTG  
||| ||||||||||||  
CCA CTCCAACGTCACTCAAC  
C

GAM1187 ZNF264 3' CTGCAACCTCTGCCTC 12753  
GAGGTAGAGGTTGCAG  
||||||||||||||



CTCCGTCTCCAACGTC

GAM1187 ZNF264 3' CACTGCAACCTCCGCCTC 12746 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 20D7-FC4 5' CACTGCAGCCTCCACCTC 60896 A  
GAGGT GAGGTTGCAGTG  
|||| |||||||||  
CTCCA CTCCGACGTCAC  
C

GAM1187 ARHF 3' CACTGCAAGCTCCACCTC 38738 A G  
GAGGT GAG TTGCAGTG  
|||| ||| |||||||  
CTCCA CTC AACGTCAC  
C G

GAM1187 ARHGAP5 5' CGGCTCACCACAACCCCCACCT 77073 AGA CA  
C GAGGT GGTTG GTGAGTTG  
|||| |||| |||||||  
CTCCA CCAAC CACTCGGC  
CCC AC

GAM1187 ARPP-19 3' CACTGCAACCTCTGCCTC 21791  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1187 ASB16 5' CACTGCAACCTCCGCCTC 69932 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 ASE-1 3' CACTGCAACCTCCGCCTC 23946 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 ATP1B4 3' CGGCTCACTGCAACCTCCACCT 23816 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||| |||||||||||  
CTCCA CTCCAACGTCAGTCGGC  
C

GAM1187 BA108L7.2 3' CACTGCAACCTCTGCCTC 48259  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1187 BAG5 3' CAGCTCACTGCAACCTCCACCT 16840 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||| |||||||||||

			CTCCA CTCCAACGTC	ACTCGAC		
			C			
GAM1187	BNIP-S	3'	CACTGCAACCTCCGCCTC	56257	TA	
			GAGG	GAGGTTGCAGTG		
			CTCC	CTCCAACGTCAC		
			GC			
GAM1187	BTN3A1	3'	CTGCAACCTCCACCTC	22919	A	
			GAGGT	GAGGTTGCAG		
			CTCCA	CTCCAACGTC		
			C			
GAM1187	C1orf24	3'	CACTGCAACCTCCGCCTC	53710	TA	
			GAGG	GAGGTTGCAGTG		
			CTCC	CTCCAACGTCAC		
			GC			
GAM1187	C1QTNF6	3'	CACTGCAACCTCTGCCTC	49139		
			GAGGTAGAGGTTGCAGTG			
			CTCCGTCTCCAACGTCAC			
GAM1187	C21orf25	3'	CTTACTGCAACCTCCACCTC	63547	A	
			GAGGT	GAGGTTGCAGTGAG		
			CTCCA	CTCCAACGTCATTC		
			C			
GAM1187	C3F	3'	CAGCTCACCGCAACCTCCACCT	19287	A	A
	C		GAGGT	GAGGTTGC GTGAGTTG		
			CTCCA	CTCCAACG CACTCGAC		
			C	C		
GAM1187	C9orf9	3'	CACTGCAACCTCCGCCTC	38506	TA	
			GAGG	GAGGTTGCAGTG		
			CTCC	CTCCAACGTCAC		
			GC			
GAM1187	C9orf9	3'	CACTGCAACCTCCACCTC	38504	A	
			GAGGT	GAGGTTGCAGTG		
			CTCCA	CTCCAACGTCAC		
			C			
GAM1187	CEACAM8	3'	CAACTCACTGCAAGCTCCGCCT	8421	TA	G
	C		GAGG	GAG TTGCAGTGAGTTG		
			CTCC	CTC AACGTC	CACTCAAC	
			GC	G		
GAM1187	CENPH	3'	CACTGCAACCTCTGCCTC	43271		
			GAGGTAGAGGTTGCAGTG			

CTCCGTCTCCAACGTCAC

GAM1187 CHRAC1 3' CACTGCAACCTCCGCCTC 33867 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 CLSTN2 3' CAACTCACTGTGCGTCTCCTC 42125 T G T  
GAGG AGA GT GCAGTGAGTTG  
|||| ||| || |||||||||  
CTCC TCT CG TGTCACTCAAC  
\_ G \_

GAM1187 CPSF2 3' CACCGCAACCTCTGCCTC 61574 A  
GAGGTAGAGGTTGC GTG  
||||||||||| |||  
CTCCGTCTCCAACG CAC  
C

GAM1187 DBR1 3' CACCGCAACCTCCGCCTC 32528 TA A  
GAGG GAGGTTGC GTG  
|||| |||||| |||  
CTCC CTCCAACG CAC  
GC C

GAM1187 DKFZp434A2417 3' CACTGCAACTTCCACCTC 66097 A  
GAGGT GAGGTTGCAGTG  
|||| |||||||||  
CTCCA CTTCAACGTCAC  
C

GAM1187 DKFZP434C212 3' CACTGCAACCTCCACCTC 68906 A  
GAGGT GAGGTTGCAGTG  
|||| |||||||||  
CTCCA CTCCAACGTCAC  
C

GAM1187 DKFZp434E2220 5' CACTGCAACCTCCGCCTC 34294 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 DKFZp547H025 3' CAGCTCACTGCAACCTCCACCT 39353 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||| |||||||||||||  
CTCCA CTCCAACGTCACCTCGAC  
C

GAM1187 DKFZP564O0523 3' CGGCTCACTGCAACCTCCACCT 49514 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||| |||||||||||||  
CTCCA CTCCAACGTCACCTCGGC  
C

GAM1187 DKFZp761J139 5' CACTGCAACGTCCACCTC 50104 A G  
GAGGT GA GTTGCAGTG  
|||| || |||||||||

			CTCCA CT CAACGTCAC		
			C G		
GAM1187	DKFZp761N1114	3'	CACTGCAACCTCCGCCTC	79015	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	DKFZp762P2111	3'	CACTGCAACCTCCGCCTC	86353	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	DRIL2	3'	CAATAAACCTCTACCTC	21323	GCAG
			GAGGTAGAGGTT TG		
			CTCCATCTCCAA AC		
			ATA_		
GAM1187	DSCR6	3'	CACTGCAACCTCCACTTC	38543	A
			GAGGT GAGGTTGCAGTG		
			CTTCA CTCCAACGTCAC		
			C		
GAM1187	EREG	3'	CGGCTCACTGCAACCTCACCTC	7497	A
			GAGGT GAGGTTGCAGTGAGTTG		
			CTCCA CTCCAACGTCACCTCGGC		
			—		
GAM1187	FBP17	3'	CGGCTCACTACAACCTCCACCT	72787	A C
	C		GAGGT GAGGTTG AGTGAGTTG		
			CTCCA CTCCAAC TCACTCGGC		
			C A		
GAM1187	FER1L4	3'	CTGACTGCAACCTCCACCTC	47344	A G
			GAGGT GAGGTTGCAGT AG		
			CTCCA CTCCAACGTCA TC		
			C G		
GAM1187	FER1L4	3'	CTGACTGCAACCTCCACCTC	47343	A G
			GAGGT GAGGTTGCAGT AG		
			CTCCA CTCCAACGTCA TC		
			C G		
GAM1187	FLJ00024	5'	CACTGCAACCTCTGCCTC	63753	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1187	FLJ10232	3'	CACTGCAACCTCCGCCTC	35922	TA
			GAGG GAGGTTGCAGTG		

CTCC CTCCAACGTCAC  
 GC  
 GAM1187 FLJ10346 5' CGGCTCACTGCAAGCTCCACCT 36042 A G  
 C GAGGT GAG TTGCAGTGAGTTG  
 ||||| ||| |||||  
 CTCCA CTC AACGTCACCTCGGC  
 C G  
 GAM1187 FLJ10535 3' CACTGCAACCTCTGCCTC 36235  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 FLJ10922 3' CACTGCAACCTCCGCCTC 36871 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1187 FLJ11004 5' CGGCTCACTGCAACCTCTACCT 36968  
 C GAGGTAGAGGTTGCAGTGAGTTG  
 |||||  
 CTCCATCTCCAACGTCACCTCGGC  
  
 GAM1187 FLJ11106 5' TCTTGCAACCTCACCTC 37056 A T  
 GAGGT GAGGTTGCAG GA  
 ||||| ||||| ||  
 CTCCA CTCCAACGTT CT  
  
 GAM1187 FLJ12363 3' CAGCTCACTGCAACCTCCACCT 49675 A  
 C GAGGT GAGGTTGCAGTGAGTTG  
 ||||| |||||  
 CTCCA CTCCAACGTCACCTCGAC  
 C  
 GAM1187 FLJ12409 3' CACTGCAACCTCCGCCTC 47044 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1187 FLJ12572 5' CACTGCAACCTCTGCCTC 43247  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 FLJ12649 3' CACTGCAACCTCCGCCTC 44777 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1187 FLJ12668 3' CACTGCAACCTCCATCTC 46513 A  
 GAGGT GAGGTTGCAGTG  
 ||||| |||||

		CTCTA CTCCAACGTCAC		
		C		
GAM1187	FLJ12687	3' CACTGCAACCTCCGCCTC	46188	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCAC		
		GC		
GAM1187	FLJ12747	3' CACTGCAACCTCTGCCTC	49712	
		GAGGTAGAGGTTGCAGTG		
		CTCCGTCTCCAACGTCAC		
GAM1187	FLJ12973	3' CACCGCAACCTCCGCCTC	46103	TA A
		GAGG GAGGTTGC GTG		
		CTCC CTCCAACG CAC		
		GC C		
GAM1187	FLJ12975	3' CACCACAACCTCCTCCTC	69577	TA CA
		GAGG GAGGTTG GTG		
		CTCC CTCCAAC CAC		
		TC AC		
GAM1187	FLJ13072	5' CACTGCAACCTCTGCCTC	89804	
		GAGGTAGAGGTTGCAGTG		
		CTCCGTCTCCAACGTCAC		
GAM1187	FLJ13197	3' CGGCTCACTGCAACCTCTACCT	44851	
	C	GAGGTAGAGGTTGCAGTGAGTTG		
		CTCCATCTCCAACGTCACCTCGGC		
GAM1187	FLJ14950	3' CACTGCAACCTCCACCTC	51714	A
		GAGGT GAGGTTGCAGTG		
		CTCCA CTCCAACGTCAC		
		C		
GAM1187	FLJ14957	3' CACTGCAACCTCTGCCTC	51742	
		GAGGTAGAGGTTGCAGTG		
		CTCCGTCTCCAACGTCAC		
GAM1187	FLJ20004	3' CATTGCAACCTCCGCCTC	95291	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTTAC		
		GC		
GAM1187	FLJ20034	3' CACTGCAACCTCTGCCTC	34359	
		GAGGTAGAGGTTGCAGTG		

CTCCGTCTCCAACGTCAC

GAM1187 FLJ20045 3' CACTGCAACCTCTGCCTC 34416  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 FLJ20079 3' CACCGCAACCTCCACCTC 34488 A A  
GAGGT GAGGTTGC GTG  
|||||  
CTCCA CTCCAACG CAC  
C C

GAM1187 FLJ20342 3' CACTGCAACCTCTGCCTC 34987  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 FLJ20344 3' CACTGCAACCTCCGCCTC 35006 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 FLJ20507 3' CACTGCAACCTCTGCCTC 60210  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 FLJ20507 3' CACTGCAACCTCTGCCTC 35275  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 FLJ20511 3' CGGCTCACTGCAAGCTCCACCT 35323 A G  
C GAGGT GAG TTGCAGTGAGTTG  
|||||  
CTCCA CTC AACGTCACTCGGC  
C G

GAM1187 FLJ20542 3' CAACTCACCCAGCCGCCACCTC 49781 AGA CA  
GAGGT GGTG GTGAGTTG  
|||||  
CTCCA CCGAC CACTCAAC  
CCG C\_

GAM1187 FLJ20813 3' CACTGCAACTCCACCTC 35679 A G  
GAGGT GAG TTGCAGTG  
|||||  
CTCCA CTC AACGTCAC  
C \_

GAM1187 FLJ21302 3' CACTGCAACCTCCGCCTC 43212 TA  
GAGG GAGGTTGCAGTG  
|||||

CTCC CTCCAACGTCAC  
 GC  
 GAM1187 FLJ22002 3' CACTGCAACCTCCGCCTC 45768 TA  
 GAGG GAGGTTGCAGTG  
 |||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1187 FLJ22531 5' CGGCTCACTGCAACCTCCACCT 45029 A  
 C GAGGT GAGGTTGCAGTGAGTTG  
 |||| |||||  
 CTCCA CTCCAACGTCACTCGGC  
 C  
 GAM1187 FLJ22794 3' CACTGCAACTTCCACCTC 91603 A  
 GAGGT GAGGTTGCAGTG  
 |||| |||||  
 CTCCA CTTCAACGTCAC  
 C  
 GAM1187 FLJ22965 3' CACTGCAACCTCCGCCTC 42049 TA  
 GAGG GAGGTTGCAGTG  
 |||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1187 FLJ22969 3' CACTGCAACCTCTGCCTC 68646  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 FLJ23024 3' CACTGCAACCTCTGCCTC 46266  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 FLJ23392 3' CACTGCAACCTCTGCCTC 45527  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 FLJ23563 3' CACTGCAACCTCTGCCTC 67592  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 FLJ31101 3' CACTGCAACCTCTGCCTC 35706  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 FLJ32865 3' CACTGCAACCTCTGCCTC 58168  
 GAGGTAGAGGTTGCAGTG  
 |||||



CTCCGTCTCCAACGTCAC

GAM1187 GAL3ST-4 3' CACTGCAACCTCTGCCTC 44934  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 GIT2 3' CAGCTCACAGCCCCACC 54091 AGA TT A  
GGT GG GC GTGAGTTG  
||| || |||  
CCA CC CG CACTCGAC  
\_\_\_ CC A

GAM1187 GIT2 3' CAGCTCACAGCCCCACC 54078 AGA TT A  
GGT GG GC GTGAGTTG  
||| || |||  
CCA CC CG CACTCGAC  
\_\_\_ CC A

GAM1187 GIT2 3' CAGCTCACAGCCCCACC 28756 AGA TT A  
GGT GG GC GTGAGTTG  
||| || |||  
CCA CC CG CACTCGAC  
\_\_\_ CC A

GAM1187 GMPPB 5' CGGCTCACTGCAACCTCCACCT 95732 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||||  
CTCCA CTCCAACGTCACTCGGC  
C

GAM1187 GNG4 3' CAGCTCACTGCGACCTCCACCT 15611 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||||  
CTCCA CTCCAGCGTCACTCGAC  
C

GAM1187 GP5 3' ACGGGCCCGCAACCCCTCCTC 15637 T A A\_ GA  
GAGG AG GGTTGC GT GT  
||||| |||  
CTCC TC CCAACG CG CA  
\_ C CC GG

GAM1187 GREB1 3' CACTGCAACCTCTGCCTC 27865  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 GRWD 3' CACTGCAACCTCCGCCTC 48963 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 GTF2E1 3' CACTGCAACCTCTGCCTC 18611  
GAGGTAGAGGTTGCAGTG  
|||||

CTCCGTCTCCAACGTCAC

GAM1187 GTPBG3 3' CTTACTGCAACCTCCACCTC 50900 A  
GAGGT GAGGTTGCAGTGAG  
||||| |||||||||  
CTCCA CTCCAACGTCATTC  
C

GAM1187 GTPBG3 3' CACTGCAACCTCCATCTC 50895 A  
GAGGT GAGGTTGCAGTG  
||||| |||||||||  
CTCTA CTCCAACGTCAC  
C

GAM1187 H-plk 5' CGACTCACTGCAACCTCCACCT 31806 A  
C GAGGT GAGGTTGCAGTGAGTTG  
||||| |||||||||  
CTCCA CTCCAACGTCACTCAGC  
C

GAM1187 HRH4 3' CACTGCAACCTCTGCCTC 41248  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||  
CTCCGTCTCCAACGTCAC

GAM1187 HSPC065 3' CACTGCAACCTCCACCTC 26290 A  
GAGGT GAGGTTGCAGTG  
||||| |||||||||  
CTCCA CTCCAACGTCAC  
C

GAM1187 HSPC065 3' CGCTGCAACCTCCTCCTC 26293 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCGC  
TC

GAM1187 ICK 3' CTGCAACCTCTGCCTC 29927  
GAGGTAGAGGTTGCAG  
||||| |||||||||  
CTCCGTCTCCAACGTC

GAM1187 JAM1 5' CACTGCAACCTCCTCCTC 57916 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
TC

GAM1187 JM11 3' CACTGCAACCTCTGCCTC 53252  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||  
CTCCGTCTCCAACGTCAC

GAM1187 KCNMB3L 5' CAACCCACGGTGGCCTCTCCTC 26958 T TG A A  
GAGG AGAGGT C GTG GTTG  
||| ||||| | ||| |||

CTCC TCTCCG G CAC CAAC  
 — GT G C  
 GAM1187 KIAA0063 3' CGGCTCACTGCAACCTCCACCT 29622 A  
 C GAGGT GAGGTTGCAGTGAGTTG  
 |||| ||||||||  
 CTCCA CTCCAACGTCACCTCGGC  
 C  
 GAM1187 KIAA0391 3' CACTGCAACCTCTGCCTC 27909  
 GAGGTAGAGGTTGCAGTG  
 |||||||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 KIAA0426 3' CACTGCAACCTCCGCCTC 28255 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1187 KIAA0459 3' CGGCTCACTGCAACCTCCACCT 60989 A  
 C GAGGT GAGGTTGCAGTGAGTTG  
 |||| ||||||||  
 CTCCA CTCCAACGTCACCTCGGC  
 C  
 GAM1187 KIAA0469 3' CACTGCAGCCTCCACCTC 29323 A  
 GAGGT GAGGTTGCAGTG  
 |||| |||||||  
 CTCCA CTCCGACGTCAC  
 C  
 GAM1187 KIAA0513 3' ACTCACTGCAACCTCCACCTC 28326 A  
 GAGGT GAGGTTGCAGTGAGT  
 |||| ||||||||  
 CTCCA CTCCAACGTCACCTCA  
 C  
 GAM1187 KIAA0513 5' CACTGCAGCCTCCACCTC 28343 A  
 GAGGT GAGGTTGCAGTG  
 |||| |||||||  
 CTCCA CTCCGACGTCAC  
 C  
 GAM1187 KIAA0527 3' CACTGCAACCTCTGCCTC 95795  
 GAGGTAGAGGTTGCAGTG  
 |||||||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 KIAA0544 3' CACGCACCTCTACC 70894 T A  
 GGTAGAGGT GC GTG  
 ||||| || ||  
 CCATCTCCA CG CAC  
  
 — —  
 GAM1187 KIAA0544 3' CACTGCAACCTCCGCCTC 70896 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||||

			CTCC CTCCAACGTCAC		
			GC		
GAM1187	KIAA0557	3'	CACCACAACCTCCACCTC	77990	A CA
			GAGGT GAGGTTG GTG		
			CTCCA CTCCAAC CAC		
			C AC		
GAM1187	KIAA0561	3'	CACTGCAACCTCCGCCTC	65875	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	KIAA0562	3'	CTGCAACCTCCGCCTC	28153	TA
			GAGG GAGGTTGCAG		
			CTCC CTCCAACGTC		
			GC		
GAM1187	KIAA0563	5'	CACTGCAACCTCTGCCTC	29184	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1187	KIAA0594	3'	CTTACTGCAACCTCCGCCTC	64897	TA
			GAGG GAGGTTGCAGTGAG		
			CTCC CTCCAACGTCATTC		
			GC		
GAM1187	KIAA0599	3'	CACTGCAACCTCCGCCTC	77169	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	KIAA0599	3'	CTTACTGCAACCTCCGCCTC	77177	TA
			GAGG GAGGTTGCAGTGAG		
			CTCC CTCCAACGTCATTC		
			GC		
GAM1187	KIAA0630	3'	TTTACCACCACCTCTACC	89401	TGCA
			GGTAGAGGT GTGAG		
			CCATCTCCA CATTT		
			CCAC		
GAM1187	KIAA0720	3'	CACTGCAACCTCTGCCTC	62318	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1187	KIAA0841	3'	CACTGCAACCTCCGCCTC	71376	TA
			GAGG GAGGTTGCAGTG		

		CTCC CTCCAACGTCAC		
		GC		
GAM1187	KIAA0841	3' CACTGCAACCTCTGCCTC	71377	
		GAGGTAGAGGTTGCAGTG		
		CTCCGTCTCCAACGTCAC		
GAM1187	KIAA1041	3' CACTGCAACCTCCGCCTC	30128	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCAC		
		GC		
GAM1187	KIAA1054	3' CACTGCAACCTCCGCCTC	68429	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCAC		
		GC		
GAM1187	KIAA1161	5' CACTGCAACCCCTCCTC	81736	T A
		GAGG AG GGTTCAGTG		
		CTCC TC CCAACGTCAC		
		_ C		
GAM1187	KIAA1170	3' CACTGCAACCTCCGCCTC	69846	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCAC		
		GC		
GAM1187	KIAA1193	3' CACTGCAACCTCCGCCTC	67632	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCAC		
		GC		
GAM1187	KIAA1198	3' CACCGCAACCTCCGCCTC	63291	TA A
		GAGG GAGGTTGC GTG		
		CTCC CTCCAACG CAC		
		GC C		
GAM1187	KIAA1198	3' CACTGCAACCTCCACTTC	63293	A
		GAGGT GAGGTTGCAGTG		
		CTTCA CTCCAACGTCAC		
		C		
GAM1187	KIAA1209	3' CACTGCAGCCTCCACCTC	60751	A
		GAGGT GAGGTTGCAGTG		
		CTCCA CTCCGACGTCAC		
		C		
GAM1187	KIAA1257	3' CACCGCAACCTCCGCCTC	62730	TA A
		GAGG GAGGTTGC GTG		

			CTCC CTCCAACG CAC		
			GC C		
GAM1187	KIAA1320	5'	CACTGCAACCTCTGCCTC	69297	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1187	KIAA1373	3'	CAGCTCACTGCAACCTCCACCT	70932	A
		C	GAGGT GAGGTTGCAGTGAGTTG		
			CTCCA CTCCAACGTCAC		
			C		
GAM1187	KIAA1497	5'	CACTGCAACCTCTGCCTC	67505	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1187	KIAA1508	3'	CACTGCAACCTCCGCCTC	61879	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	KIAA1571	3'	CACCGCAACCTCCACCTC	60952	A A
			GAGGT GAGGTTGC GTG		
			CTCCA CTCCAACG CAC		
			C C		
GAM1187	KIAA1615	3'	CAGATCACTGCAACCTCCACCT	68702	A G
		C	GAGGT GAGGTTGCAGTGA TTG		
			CTCCA CTCCAACGTCAC		
			C A		
GAM1187	KIAA1655	3'	CACTGTAACCTCCACCTC	66597	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCAATGTCAC		
			C		
GAM1187	KIAA1655	3'	CATTGCAACCTCCGCCTC	66601	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTTAC		
			GC		
GAM1187	KIAA1737	3'	CACTGCAACCTCCGCCTC	67351	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	KIAA1784	3'	CACTGCAACCTCCGCCTC	65145	TA
			GAGG GAGGTTGCAGTG		

			CTCC CTCCAACGTCAC		
			GC		
GAM1187	KIAA1922	5'	CACTGCAACCTCCGCCTC	73617	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	KIAA1956	3'	CACTGCAGCCTCCACCTC	78431	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1187	KIAA1971	3'	CTTACTGCAACCTCCACCTC	74218	A
			GAGGT GAGGTTGCAGTGAG		
			CTCCA CTCCAACGTCATTC		
			C		
GAM1187	KLK7	3'	CACTGCAACCTCCGCCTC	57729	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	KLK7	3'	CACTGCAACCTCCGCCTC	17289	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	KRT6	3'	CAACTCACCCGTCTCCTCCCTC	82218	TA TT A_
			GAGG GAGG GC GTGAGTTG		
			CTCC CTCC TG CACTCAAC		
			— TC CC		
GAM1187	MCLC	3'	CGGCTCACTGCAACCTCCACCT	30681	A
	C		GAGGT GAGGTTGCAGTGAGTTG		
			CTCCA CTCCAACGTCACTCGGC		
			C		
GAM1187	MEF-2	3'	CACTGCAACCTCCGCCTC	64379	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	MGC12518	3'	TACTGCAACCTCTGCC	64083	
			GGTAGAGGTTGCAGTG		
			CCGTCTCCAACGTCAT		
GAM1187	MGC13138	3'	CACTGCAACCTCTGCCTC	53014	
			GAGGTAGAGGTTGCAGTG		

CTCCGTCTCCAACGTCAC

GAM1187 MGC14836 3' CACTGCAACCTCCGCCTC 53037 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 MGC1842 3' CTTACTACAACCTCCGCCTC 65648 TA C  
GAGG GAGGTTG AGTGAG  
|||| ||||| |||||  
CTCC CTCCAAC TCATTC  
GC A

GAM1187 MGC2474 3' CACTGCAACTTCCACCTC 43714 A  
GAGGT GAGGTTGCAGTG  
|||| |||||||||  
CTCCA CTTCAACGTCAC  
C

GAM1187 MGC29891 3' CACTGCAACCTCCGCCTC 58202 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 MGC3113 3' CACTGCAGCCTCCACCTC 43840 A  
GAGGT GAGGTTGCAGTG  
|||| |||||||||  
CTCCA CTCCGACGTCAC  
C

GAM1187 MGC3329 3' CACTGCAACCCCCGCCTC 44015 AGA  
GAGGT GGTTCAGTG  
|||| |||||||||  
CTCCG CCAACGTCAC  
CCC

GAM1187 MGC5149 3' CACTGCAACCTCTGCCTC 72286  
GAGGTAGAGGTTGCAGTG  
|||||||  
CTCCGTCTCCAACGTCAC

GAM1187 MGC9912 3' CGGCTCACTGCAACCTCCACCT 54716 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||| |||||||||  
CTCCA CTCCAACGTCAGTGGC  
C

GAM1187 MLZE 5' CACTGCAACCTCTGCCTC 48615  
GAGGTAGAGGTTGCAGTG  
|||||||  
CTCCGTCTCCAACGTCAC

GAM1187 MMPL1 3' CACTGCAGCCTCCACCTC 14717 A  
GAGGT GAGGTTGCAGTG  
|||| |||||||||



			CTCCA CTCCGACGTCAC		
			C		
GAM1187	moblak	3'	CACTGCATCCTCCACCTC	55488	A T
			GAGGT GAGG TGCAGTG		
			CTCCA CTCC ACGTCAC		
			C T		
GAM1187	MOCS3	3'	CACTGCAACCTCCGCCTC	27149	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	MRPL44	3'	CGGCTCACTGCAACCTCCACCT	43317	A
	C		GAGGT GAGGTTGCAGTGAGTTG		
			CTCCA CTCCAACGTCAC		
			C		
GAM1187	MtFMT	3'	CACTGCAACCTCCGCCTC	57649	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	NDUFB1	5'	CACTGCAACCTCTGCCTC	15815	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1187	NDUFC2	3'	CGGCTCACTGCAACCTCCACCT	15830	A
	C		GAGGT GAGGTTGCAGTGAGTTG		
			CTCCA CTCCAACGTCAC		
			C		
GAM1187	Nup43	3'	CGGCTCACTGCAACCTCCACCT	44999	A
	C		GAGGT GAGGTTGCAGTGAGTTG		
			CTCCA CTCCAACGTCAC		
			C		
GAM1187	OSBPL2	3'	CACCGCAACCTCCGCCTC	29205	TA A
			GAGG GAGGTTGC GTG		
			CTCC CTCCAACG CAC		
			GC C		
GAM1187	OSBPL2	3'	CACCGCAACCTCCGCCTC	57856	TA A
			GAGG GAGGTTGC GTG		
			CTCC CTCCAACG CAC		
			GC C		
GAM1187	PASK	5'	CACTGCAACCTCTGCCTC	30713	
			GAGGTAGAGGTTGCAGTG		

CTCCGTCTCCAACGTCAC

GAM1187 PELI1 5' CACTGCAACCTCTGCCTC 40257  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 PELI1 5' CACTGCAACCTCCTCCTC 40255 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
TC

GAM1187 PIP3-E 3' CACTGCAACCTCTGCCTC 66801  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 PRO0365 5' CAGCTCACTGCAACCTCCACCT 26153 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||||  
CTCCA CTCCAACGTCACCTCGAC  
C

GAM1187 PRO1992 5' CACTGCAACCTCTGCCTC 26054  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 PRO2955 3' CACTGCAACCTCTGCCTC 37632  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 PSTPIP2 3' CACTGCAACCTCTGCCTC 44384  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 RAB21 3' CGGCTCACTGCAAGCTCCACCT 30386 A G  
C GAGGT GAG TTGCAGTGAGTTG  
||||| |||  
CTCCA CTC AACGTCACCTCGGC  
C G

GAM1187 RAB33B 3' CACTGCAACCTCCGCCTC 48489 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 RAI 5' CACTGCAACCTCCGCCTC 21874 TA  
GAGG GAGGTTGCAGTG  
||| |||||

			CTCC CTCCAACGTCAC		
			GC		
GAM1187	RNF20	3'	CACCAAACCTCTACCTC	38966	GCA
			GAGGTAGAGGTT	GTG	
			CTCCATCTCCAA	CAC	
			AC_		
GAM1187	RNF8	3'	CAGCTCACTGCAACCTCCACCT	14218	A
	C		GAGGT GAGGTTGCAGTGAGTTG		
			CTCCA CTCCAACGTCACTCGAC		
			C		
GAM1187	RNO2	5'	CACTGCAACCTCCACCTT	52764	A
			GAGGT GAGGTTGCAGTG		
			TTCCA CTCCAACGTCAC		
			C		
GAM1187	SC4MOL	3'	CACTGCAACCTCTGCCTC	22151	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1187	SCAMP-4	3'	CACTGCAACCTCTGCCTC	54391	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1187	SCYA16	3'	CACTGTAACCTCCACCTC	15956	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCAATGTCAC		
			C		
GAM1187	SCYA22	3'	CGGCTCACTACAACCTCGACCT	90943	A C
	C		GAGGT GAGGTTG AGTGAGTTG		
			CTCCA CTCCAAC TCACTCGGC		
			G A		
GAM1187	SERF1B	3'	CACTGCAACCTCCGCCTC	43410	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1187	SIRPB1	3'	CACTGCAACCCCCGCCTC	20244	AGA
			GAGGT GGTTCAGTG		
			CTCCG CCAACGTCAC		
			CCC		
GAM1187	SLC11A1	3'	CATTGCAACCTCCACCTT	59453	A
			GAGGT GAGGTTGCAGTG		

TTCCA CTCCAACGTTAC  
 C  
 GAM1187 SLC26A9 3' CAACTCACTCTCCCCTACT 53618 A TTGC  
 GGTAG GG AGTGAGTTG  
 ||||| || |||||  
 TCATC CC TCACTCAAC  
 C TC\_\_  
 GAM1187 SLC26A9 3' CAACTCACTCTCCCCTACT 56179 A TTGC  
 GGTAG GG AGTGAGTTG  
 ||||| || |||||  
 TCATC CC TCACTCAAC  
 C TC\_\_  
 GAM1187 SLC2A10 3' CACTGCAACCTCCACTTC 47817 A  
 GAGGT GAGGTTGCAGTG  
 ||||| |||||  
 CTTCA CTCCAACGTCAC  
 C  
 GAM1187 SP2 3' CGCCACAACCTCTCCTC 11888 T CA  
 GAGG AGAGGTTG GTG  
 ||||| ||||| ||  
 CTCC TCTCCAAC CGC  
 \_ AC  
 GAM1187 STAF65(gamma) 3' CACTGCAACCTCTGCCTC 29428  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 SUN1 3' CACTGCAGCCTCCACCTC 47155 A  
 GAGGT GAGGTTGCAGTG  
 ||||| |||||  
 CTCCA CTCCGACGTCAC  
 C  
 GAM1187 SYT13 3' CACTGCAACCTCCGCCTC 93451 TA  
 GAGG GAGGTTGCAGTG  
 ||||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1187 TOR1B 3' CAACTCACTGCAACCTCCGCT 27196 TA  
 GG GAGGTTGCAGTGAGTTG  
 || |||||  
 TC CTCCAACGTCAC  
 GC  
 GAM1187 TRIM5 3' CACTGCAACCTCCACCTC 52295 A  
 GAGGT GAGGTTGCAGTG  
 ||||| |||||  
 CTCCA CTCCAACGTCAC  
 C  
 GAM1187 TRIM6 3' CACTGCAACCTCTGCCTC 54135  
 GAGGTAGAGGTTGCAGTG  
 |||||

CTCCGTCTCCAACGTCAC

GAM1187 TU12B1-TY 3' CACTGCAACCTCTGCCTC 33371  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 TUCAN 3' CACTGCAACCTCTGCCTC 30271  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 UBF-fl 3' CACTGCAACCTCTGCCTC 51555  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 USP22 3' CGGCTCACTGCAACCTCCACCT 68009 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||||  
CTCCA CTCCAACGTCACTCGGC  
C

GAM1187 VDU1 3' CACTGCAGCCTCCACCTC 30414 A  
GAGGT GAGGTTGCAGTG  
|||||  
CTCCA CTCCGACGTCAC  
C

GAM1187 VPS33A 3' CTCAGTCAACCTCCACCTC 43338 A  
GAGGT GAGGTTGCAGTGAG  
|||||  
CTCCA CTCCAACGTCACTC  
C

GAM1187 WBSCR20A 5' CACCGCAACCTCTGCCTC 49650 A  
GAGGTAGAGGTTGC GTG  
|||||  
CTCCGTCTCCAACG CAC  
C

GAM1187 ZNF364 3' CTTCTCCAACCTCTACC 66772 C T  
GGTAGAGGTTG AG GAG  
|||||  
CCATCTCCAAC TC TTC  
C \_

GAM1187 ZTL1 3' CACTGCAACCTCTGCCTC 43911  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1187 LOC112724 5' CGGCTCACTGCAACCTCCACCT 56496 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||||

CTCCA CTCCAACGTCACCTCGGC  
C  
GAM1187 LOC113675 5' CACTGCAACCTCCGCCTC 56570 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC  
GAM1187 LOC115219 5' CACTGCAACCTCCGCCTC 73298 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC  
GAM1187 LOC116411 5' CGCTACAACCTCCACCTC 73860 A C  
GAGGT GAGGTTG AGTG  
|||||  
CTCCA CTCCAAC TCGC  
C A  
GAM1187 LOC119392 3' CACTGCAACCTCTGCCTC 59132  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC  
  
GAM1187 LOC120114 3' CAGCTCACTGCAATCTCCACCT 75521 A  
C GAGGT GAGGTTGCAGTGAGTTG  
|||||  
CTCCA CTCTAACGTCACCTCGAC  
C  
GAM1187 LOC120939 3' CACTGTAACCTCCACCTC 76248 A  
GAGGT GAGGTTGCAGTG  
|||||  
CTCCA CTCCAATGTCAC  
C  
GAM1187 LOC126364 3' CACTGCAACCTCCGCCTC 75684 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC  
GAM1187 LOC126661 3' CACTGCAACCTCCGCCTC 74545 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC  
GAM1187 LOC128077 3' CACTGCAACCTCCGCCTC 74707 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC  
GAM1187 LOC128077 3' CACTGCAACCTCTGCCTC 74709  
GAGGTAGAGGTTGCAGTG  
|||||

CTCCGTCTCCAACGTCAC

GAM1187	LOC128387	3'	CACTGCAACCTCCACTTC	74747	A	
			GAGGT GAGGTTGCAGTG			
			CTTCA CTCCAACGTCAC			
			C			
GAM1187	LOC128989	3'	CACTGCAACCTCCGCCTC	74806	TA	
			GAGG GAGGTTGCAGTG			
			CTCC CTCCAACGTCAC			
			GC			
GAM1187	LOC130813	3'	CACCGCAACCTCCGCCTC	75764	TA	A
			GAGG GAGGTTGC GTG			
			CTCC CTCCAACG CAC			
			GC C			
GAM1187	LOC132625	3'	CACTGCAACCTCCACCTC	75900	A	
			GAGGT GAGGTTGCAGTG			
			CTCCA CTCCAACGTCAC			
			C			
GAM1187	LOC133686	3'	CTGCAACCTCCATCTC	75120	A	
			GAGGT GAGGTTGCAG			
			CTCTA CTCCAACGTC			
			C			
GAM1187	LOC135154	3'	CAACTCACTGCAACTTCCGCC	75213	TA	
			GG GAGGTTGCAGTGAGTTG			
			CC CTTCAACGTCACTCAAC			
			GC			
GAM1187	LOC135293	3'	CACTGCAACCTCTGCCTC	76175		
			GAGGTAGAGGTTGCAGTG			
			CTCCGTCTCCAACGTCAC			
GAM1187	LOC135763	3'	CACTGCAACCTCCGCCTC	56787	TA	
			GAGG GAGGTTGCAGTG			
			CTCC CTCCAACGTCAC			
			GC			
GAM1187	LOC135818	3'	CACCACAACCTCCGCCTC	75231	TA	CA
			GAGG GAGGTTG GTG			
			CTCC CTCCAAC CAC			
			GC AC			
GAM1187	LOC142913	5'	CACTGCAGCCTCCACCTC	76415	A	
			GAGGT GAGGTTGCAGTG			

		CTCCA CTCCGACGTCAC	
		C	
GAM1187	LOC143187 3'	CACTGCAACCTCCACCTC	59096 A
		GAGGT GAGGTTGCAGTG	
		CTCCA CTCCAACGTCAC	
		C	
GAM1187	LOC143241 5'	CACTGCAACCTCTGCCTC	57174
		GAGGTAGAGGTTGCAGTG	
		CTCCGTCTCCAACGTCAC	
GAM1187	LOC144248 5'	GCTCACTGCAACCTCCACCTC	76738 A
		GAGGT GAGGTTGCAGTGAGT	
		CTCCA CTCCAACGTCACTCG	
		C	
GAM1187	LOC144317 5'	CAACTCACTGCAACCTCTTCCT	76784 T
	C	GAGG AGAGGTTGCAGTGAGTTG	
		CTCC TCTCCAACGTCACTCAAC	
		T	
GAM1187	LOC144524 5'	CAGCTCACTGCAACCTCCACCT	83123 A
	C	GAGGT GAGGTTGCAGTGAGTTG	
		CTCCA CTCCAACGTCACTCGAC	
		C	
GAM1187	LOC145268 5'	CACTGCAACCTCCACCC	77055 A A
		G GGT GAGGTTGCAGTG	
		C CCA CTCCAACGTCAC	
		- C	
GAM1187	LOC145725 3'	CACTGCAGCCTCCACCTC	77400 A
		GAGGT GAGGTTGCAGTG	
		CTCCA CTCCGACGTCAC	
		C	
GAM1187	LOC145732 3'	CACTGCAGCCTCCACCTC	77422 A
		GAGGT GAGGTTGCAGTG	
		CTCCA CTCCGACGTCAC	
		C	
GAM1187	LOC145757 5'	CACTACAACCTCTGCCTC	77457 C
		GAGGTAGAGGTTG AGTG	
		CTCCGTCTCCAAC TCAC	
		A	
GAM1187	LOC146229 3'	CGGCTCACTGCAACCTCCACCT	77739 A
	C	GAGGT GAGGTTGCAGTGAGTTG	



CTCCA CTCCAACGTCACTCGGC  
 C  
 GAM1187 LOC146229 3' CTGCAACCTCCACCTC 77750 A  
 GAGGT GAGGTTGCAG  
 |||| |||||  
 CTCCA CTCCAACGTC  
 C  
 GAM1187 LOC146784 5' CGGCTCACTGCAACCTCCACCT 78109 A  
 C GAGGT GAGGTTGCAGTGAGTTG  
 |||| |||||  
 CTCCA CTCCAACGTCACTCGGC  
 C  
 GAM1187 LOC146839 3' CACCACAACCTCCGCCTC 83808 TA CA  
 GAGG GAGGTTG GTG  
 ||| ||||| ||  
 CTCC CTCCAAC CAC  
 GC AC  
 GAM1187 LOC146901 3' CATTGCAACCTCCACCTT 83835 A  
 GAGGT GAGGTTGCAGTG  
 |||| |||||  
 TTCCA CTCCAACGTTAC  
 C  
 GAM1187 LOC146909 3' CACTGCAACCTCCGCCTC 78168 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1187 LOC146952 5' CAGCTCACTGCAACCTCCACCT 83862 A  
 C GAGGT GAGGTTGCAGTGAGTTG  
 |||| |||||  
 CTCCA CTCCAACGTCACTCGAC  
 C  
 GAM1187 LOC147071 5' CACTGCAACCTCTGCCTC 72995  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 LOC147407 3' CACTGCAACCTCCGCCTC 76324 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1187 LOC147817 3' CACTGCAACCTCCACCTC 78491 A  
 GAGGT GAGGTTGCAGTG  
 |||| |||||  
 CTCCA CTCCAACGTCAC  
 C  
 GAM1187 LOC147990 3' CACTACAACCTCTGCCTC 84090 C  
 GAGGTAGAGGTTG AGTG  
 ||||| |||

		CTCCGTCTCCAAC TCAC		
		A		
GAM1187	LOC148137 3'	CACGGCAACCTCCACCTC	58421	A A
		GAGGT GAGGTTGC GTG		
		CTCCA CTCCAACG CAC		
		C G		
GAM1187	LOC148189 5'	CGGCTCACTGCAACCTCCACCT	78707	A
	C	GAGGT GAGGTTGCAGTGAGTTG		
		CTCCA CTCCAACGTCACTCGGC		
		C		
GAM1187	LOC148198 3'	CAGCTCACTGCAACCTCCATCT	70678	A
	C	GAGGT GAGGTTGCAGTGAGTTG		
		CTCTA CTCCAACGTCACTCGAC		
		C		
GAM1187	LOC148709 3'	CACTACAACCTCCGCCTC	78935	TA C
		GAGG GAGGTTG AGTG		
		CTCC CTCCAAC TCAC		
		GC A		
GAM1187	LOC148918 5'	CAACTCAGCTTCTTCTACCTC	79061	TT AG
		GAGGTAGAGG GC TGAGTTG		
		CTCCATCTTC CG ACTCAAC		
		TT _		
GAM1187	LOC148918 5'	CACTGCAGCCTCCACCTC	79064	A
		GAGGT GAGGTTGCAGTG		
		CTCCA CTCCGACGTCAC		
		C		
GAM1187	LOC149506 3'	CACTGCAACCTCTGCCTC	84453	
		GAGGTAGAGGTTGCAGTG		
		CTCCGTCTCCAACGTCAC		
GAM1187	LOC149506 3'	CACTGCAACTTCCACCTC	84454	A
		GAGGT GAGGTTGCAGTG		
		CTCCA CTTCAACGTCAC		
		C		
GAM1187	LOC149577 3'	CGGCTCACCACAACCTCCACCT	84509	A CA
	C	GAGGT GAGGTTG GTGAGTTG		
		CTCCA CTCCAAC CACTCGGC		
		C AC		
GAM1187	LOC150397 3'	CATTGCAACCTCCGCCTC	79843	TA
		GAGG GAGGTTGCAGTG		

		CTCC CTCCAACGTTAC		
		GC		
GAM1187	LOC150519 3'	CTGCAACCTGCCACCTC	79916	AG_
		GAGGT AGGTTGCAG		
		CTCCA TCCAACGTC		
		CCG		
GAM1187	LOC150696 3'	CACTGCAGCCTCCACCTC	58478	A
		GAGGT GAGGTTGCAGTG		
		CTCCA CTCCGACGTCAC		
		C		
GAM1187	LOC150960 3'	CGCTGCAACCTCCGCCTC	80058	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCGC		
		GC		
GAM1187	LOC151057 3'	CACTGCAACCTCTGCCTC	85208	
		GAGGTAGAGGTTGCAGTG		
		CTCCGTCTCCAACGTCAC		
GAM1187	LOC151201 3'	CAGCTCACTGCAACCTCCACCT	85274	A
	C	GAGGT GAGGTTGCAGTGAGTTG		
		CTCCA CTCCAACGTCACTCGAC		
		C		
GAM1187	LOC151475 5'	CACTGCAACCTCCACCTC	85393	A
		GAGGT GAGGTTGCAGTG		
		CTCCA CTCCAACGTCAC		
		C		
GAM1187	LOC151475 5'	CACTGCAACCTCTGCCTC	85394	
		GAGGTAGAGGTTGCAGTG		
		CTCCGTCTCCAACGTCAC		
GAM1187	LOC151826 3'	CACTGCAACCTCCGCCTC	80354	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCAC		
		GC		
GAM1187	LOC151877 3'	CGGCTCACTACAACCACACCT	85504	AGA C
	C	GAGGT GGTTG AGTGAGTTG		
		CTCCA CCAAC TCACTCGGC		
		CCA A		
GAM1187	LOC152343 3'	CAGTGCAACCTCCGCCTC	80558	TA G
		GAGG GAGGTTGCA TG		

		CTCC CTCCAACGT AC	
		GC G	
GAM1187	LOC152445 3'	CACTGCAACCTCTGCCTC 85749	
		GAGGTAGAGGTTGCAGTG	
		CTCCGTCTCCAACGTCAC	
GAM1187	LOC152582 5'	CACCGCAACCTCTGCCTC 85789	A
		GAGGTAGAGGTTGC GTG	
		CTCCGTCTCCAACG CAC	
		C	
GAM1187	LOC152620 3'	CACTACAACCTCTGCCTC 60078	C
		GAGGTAGAGGTTG AGTG	
		CTCCGTCTCCAAC TCAC	
		A	
GAM1187	LOC152719 5'	CACTGCAACCTCTGCCTC 85848	
		GAGGTAGAGGTTGCAGTG	
		CTCCGTCTCCAACGTCAC	
GAM1187	LOC152794 5'	CACTGCAACCTCTACCTC 80673	
		GAGGTAGAGGTTGCAGTG	
		CTCCATCTCCAACGTCAC	
GAM1187	LOC152851 3'	CGCTGCAACCTCCACCC 80708	A A
		G GGT GAGGTTGCAGTG	
		C CCA CTCCAACGTCGC	
		- C	
GAM1187	LOC153077 3'	CACTGCAACCTCCGCCTC 85907	TA
		GAGG GAGGTTGCAGTG	
		CTCC CTCCAACGTCAC	
		GC	
GAM1187	LOC153688 3'	CGGCTCACTGCAACCTCCACCT 86102	A
	C	GAGGT GAGGTTGCAGTGAGTTG	
		CTCCA CTCCAACGTCAGTCCGGC	
		C	
GAM1187	LOC153883 5'	CACTGCAACCTCCACC 80979	A
		GGT GAGGTTGCAGTG	
		CCA CTCCAACGTCAC	
		C	
GAM1187	LOC154075 3'	CACTGCAACCTCCGCCTC 81044	TA
		GAGG GAGGTTGCAGTG	

CTCC CTCCAACGTCAC  
 GC  
 GAM1187 LOC154282 5' CGGCTCACTGCAACCTCCACCT 86196 A  
 C GAGGT GAGGTTGCAGTGAGTTG  
 |||| ||||||||  
 CTCCA CTCCAACGTCACCTCGGC  
 C  
 GAM1187 LOC154726 5' CACCACAACCTCCGCCTC 81102 TA CA  
 GAGG GAGGTTG GTG  
 ||| ||||| ||  
 CTCC CTCCAAC CAC  
 GC AC  
 GAM1187 LOC154877 3' CAGCTCACTGCAACCTCTACCT 86284  
 C GAGGTAGAGGTTGCAGTGAGTTG  
 ||||||||||||  
 CTCCATCTCCAACGTCACCTCGAC  
  
 GAM1187 LOC155100 5' CAACCCACGGTGGCCTCTCCTC 73024 T TG A A  
 GAGG AGAGGT C GTG GTTG  
 ||| ||||| | ||| ||||  
 CTCC TCTCCG G CAC CAAC  
 \_ GT G C  
 GAM1187 LOC157247 5' CAGCTCACTGCAACCTCCACC 81359 A  
 GGT GAGGTTGCAGTGAGTTG  
 ||| ||||||||  
 CCA CTCCAACGTCACCTCGAC  
 C  
 GAM1187 LOC157798 5' CACTGCAACCTCCGCCTC 86548 TA  
 GAGG GAGGTTGCAGTG  
 ||| ||||||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1187 LOC157858 5' CACTGCAACCTCTGCCTC 86584  
 GAGGTAGAGGTTGCAGTG  
 ||||||||||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 LOC158476 3' CACTGCAACCTCCGCC 86838 TA  
 GG GAGGTTGCAGTG  
 || ||||||||  
 CC CTCCAACGTCAC  
 GC  
 GAM1187 LOC158668 3' CACTGCAACCTCTGCCTC 69365  
 GAGGTAGAGGTTGCAGTG  
 ||||||||||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1187 LOC158865 5' CACTGCAACCTCTGCCTC 86933  
 GAGGTAGAGGTTGCAGTG  
 ||||||||||||

CTCCGTCTCCAACGTCAC

GAM1187	LOC161829	3'	CACTGCAACCTCCGCCTC	82312	TA	
			GAGG GAGGTTGCAGTG			
			CTCC CTCCAACGTCAC			
			GC			
GAM1187	LOC196047	5'	CACTGCAACCTCCGCCTC	89594	TA	
			GAGG GAGGTTGCAGTG			
			CTCC CTCCAACGTCAC			
			GC			
GAM1187	LOC196264	3'	CACTGCAACCTCTGCCTC	87603		
			GAGGTAGAGGTTGCAGTG			
			CTCCGTCTCCAACGTCAC			
GAM1187	LOC196411	3'	CACTGCAACCTCCGCCTC	87668	TA	
			GAGG GAGGTTGCAGTG			
			CTCC CTCCAACGTCAC			
			GC			
GAM1187	LOC196529	3'	CTTACCACAACCTCCACCTC	87773	A	CA
			GAGGT GAGGTTG GTGAG			
			CTCCA CTCCAAC CATTG			
			C AC			
GAM1187	LOC196529	3'	GCTCACTGCAACCTCCACCTC	87775	A	
			GAGGT GAGGTTGCAGTGAGT			
			CTCCA CTCCAACGTCACG			
			C			
GAM1187	LOC196761	3'	CAACCCACAACACCTCTGCC	89552	T CA	A
			GGTAGAGGT G GTG GTTG			
			CCGTCTCCA C CAC CAAC			
			_AA C			
GAM1187	LOC196957	3'	CACTGCAGCCTCCACCTC	87817	A	
			GAGGT GAGGTTGCAGTG			
			CTCCA CTCCGACGTCAC			
			C			
GAM1187	LOC196961	3'	CACTGCAGCCTCCACCTC	87838	A	
			GAGGT GAGGTTGCAGTG			
			CTCCA CTCCGACGTCAC			
			C			
GAM1187	LOC197138	3'	CACTGCAGCCTCCACCTC	87911	A	
			GAGGT GAGGTTGCAGTG			

	CTCCA CTCCGACGTCAC	
	C	
GAM1187 LOC197358 3'	CTGCAACCTCCGCCTC	88033 TA
	GAGG GAGGTTGCAG	
	CTCC CTCCAACGTC	
	GC	
GAM1187 LOC199699 3'	CAGCTCACTGCAAGCTCCACCT	88300 A G
	C GAGGT GAG TTGCAGTGAGTTG	
	CTCCA CTC AACGTCACGTCGAC	
	C G	
GAM1187 LOC199786 3'	CACTGCAACCTCCGCCTC	88370 TA
	GAGG GAGGTTGCAGTG	
	CTCC CTCCAACGTCAC	
	GC	
GAM1187 LOC200014 3'	CGCTGCAACCCCCACCTC	88523 AGA
	GAGGT GGTTCAGTG	
	CTCCA CCAACGTCGC	
	CCC	
GAM1187 LOC200169 5'	CACTGCAACCTCTGCCTC	89945
	GAGGTAGAGGTTGCAGTG	
	CTCCGTCTCCAACGTCAC	
GAM1187 LOC200268 3'	CACTGCAACCTCTGCCTC	88678
	GAGGTAGAGGTTGCAGTG	
	CTCCGTCTCCAACGTCAC	
GAM1187 LOC200310 3'	CACTACAACCTCTGCCTC	65729 C
	GAGGTAGAGGTTG AGTG	
	CTCCGTCTCCAAC TCAC	
	A	
GAM1187 LOC200314 3'	CACTGCAACCTCCACCTC	90003 A
	GAGGT GAGGTTGCAGTG	
	CTCCA CTCCAACGTCAC	
	C	
GAM1187 LOC200339 3'	CACTGCAACCTCTGCCTC	90033
	GAGGTAGAGGTTGCAGTG	
	CTCCGTCTCCAACGTCAC	
GAM1187 LOC200845 5'	CACTGCAACCTCCGCCTC	88896 TA
	GAGG GAGGTTGCAGTG	

	CTCC CTCCAACGTCAC		
	GC		
GAM1187 LOC200860 3'	CACTGCAACCTCCACCTC	90160	A
	GAGGT GAGGTTGCAGTG		
	CTCCA CTCCAACGTCAC		
	C		
GAM1187 LOC201173 5'	CACTGCAACCTCTGCCTC	87325	
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1187 LOC201220 5'	CACTGCAACCTCTGCCTC	87345	
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1187 LOC201294 3'	CACTGCAACCTCCGCCTC	88203	TA
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1187 LOC201294 3'	CACTGCAACCTCCGCCTC	88204	TA
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1187 LOC201411 3'	CACTGCAACCTCTGCCTC	62952	
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1187 LOC201626 3'	CACTGCAACCTCCGCC	88988	TA
	GG GAGGTTGCAGTG		
	CC CTCCAACGTCAC		
	GC		
GAM1187 LOC201627 3'	CTGACTGCAACCTCCACCTC	89012	A G
	GAGGT GAGGTTGCAGT AG		
	CTCCA CTCCAACGTCA TC		
	C G		
GAM1187 LOC202025 3'	CACTGCAACCTCCGCCTC	90284	TA
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1187 LOC202934 3'	CACTACAACCTCTGCCTC	90404	C
	GAGGTAGAGGTTG AGTG		



	CTCCGTCTCCAAC TCAC		
	A		
GAM1187 LOC203297 5'	CACTGCAACCTCTGCCTC 75349		
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1187 LOC203350 3'	CAACTGACTGCAACCTCCGCCT 90563	TA	G
C	GAGG GAGGTTGCAGT AGTTG		
	CTCC CTCCAACGTCA TCAAC		
	GC G		
GAM1187 LOC204804 3'	CGGCTCACTGCCACCTCCACCT 89471	A	T
C	GAGGT GAGGT GCAGTGAGTTG		
	CTCCA CTCCA CGTCACTCGGC		
	C C		
GAM1187 LOC204804 3'	GCTCACTGCAACCTCGACCTC 89474	A	
	GAGGT GAGGTTGCAGTGAGT		
	CTCCA CTCCAACGTCACTCG		
	G		
GAM1187 LOC219735 3'	CACTGCAACCTCTGCCTC 93107		
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1187 LOC219894 3'	CACTGCAAGCTCCACCTC 93277	A	G
	GAGGT GAG TTGCAGTG		
	CTCCA CTC AACGTCAC		
	C G		
GAM1187 LOC220662 3'	CACTGCAACCTCCACCTC 91166	A	
	GAGGT GAGGTTGCAGTG		
	CTCCA CTCCAACGTCAC		
	C		
GAM1187 LOC220662 3'	CACTGCAACCTCCACTTC 91167	A	
	GAGGT GAGGTTGCAGTG		
	CTTCA CTCCAACGTCAC		
	C		
GAM1187 LOC220846 3'	CTTTCCACAACCTCTACCTT 90817		CAGT
	GAGGTAGAGGTTG GAG		
	TTCCATCTCCAAC TTC		
	ACCT		
GAM1187 LOC221035 3'	CACTACAACCTCTGCCTC 93162		C
	GAGGTAGAGGTTG AGTG		

		CTCCGTCTCCAAC TCAC	
		A	
GAM1187	LOC221174 5'	CAGCTCACTGCGACCTCCACCT 93501	A
	C	GAGGT GAGGTTGCAGTGAGTTG	
		CTCCA CTCCAGCGTCACTCGAC	
		C	
GAM1187	LOC221271 3'	CACTGCAACCTCTGCCTC 91850	
		GAGGTAGAGGTTGCAGTG	
		CTCCGTCTCCAACGTCAC	
GAM1187	LOC221296 3'	CGGCTCACTGCAACCTCCACCT 91960	A
	C	GAGGT GAGGTTGCAGTGAGTTG	
		CTCCA CTCCAACGTCACTCGGC	
		C	
GAM1187	LOC221415 5'	AACTCACTCATCCTCCTC 93870	TAG T C
		GAGG AGG TG AGTGAGTT	
		CTCC TCC AC TCACTCAA	
		___ T _	
GAM1187	LOC221663 5'	CACTGCAACCTCCACCTC 93811	A
		GAGGT GAGGTTGCAGTG	
		CTCCA CTCCAACGTCAC	
		C	
GAM1187	LOC221715 5'	CAACCCAAATGCCTCTACCTT 93750	TGCAG A
		GAGGTAGAGGT TG GTTG	
		TTCCATCTCCG AC CAAC	
		TAA__ C	
GAM1187	LOC222070 5'	CACTGCAACCTCTGCCTC 94152	
		GAGGTAGAGGTTGCAGTG	
		CTCCGTCTCCAACGTCAC	
GAM1187	LOC253612 5'	CACTGCAACCTCCGCCTC 96742	TA
		GAGG GAGGTTGCAGTG	
		CTCC CTCCAACGTCAC	
		GC	
GAM1187	LOC253664 3'	CATTGCAACCTCTGCCTC 94809	
		GAGGTAGAGGTTGCAGTG	
		CTCCGTCTCCAACGTTAC	
GAM1187	LOC253666 5'	CACTGCAACCTCCGCCTC 95060	TA
		GAGG GAGGTTGCAGTG	

	CTCC CTCCAACGTCAC		
	GC		
GAM1187 LOC253779 3'	CACTGCAACCTCCGCCTC	97144	TA
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1187 LOC255177 3'	CACCGCATCCTCCACCTC	96602	A T A
	GAGGT GAGG TGC GTG		
	CTCCA CTCC ACG CAC		
	C T C		
GAM1187 LOC255497 3'	CACTGCAACCTCCGCCTC	97188	TA
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1187 LOC255919 3'	CTTTCTGCAACCTCTGCCTC	95035	T
	GAGGTAGAGGTTGCAG GAG		
	CTCCGTCTCCAACGTC TTC		
	T		
GAM1187 LOC256267 3'	CACTGCAACCTCCGCCTC	96798	TA
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1187 LOC256306 3'	CAGCTCACTGCAACCTCCACCT	96683	A
C	GAGGT GAGGTTGCAGTGAGTTG		
	CTCCA CTCCAACGTCACGAC		
	C		
GAM1187 LOC51200 3'	CACCACAACCTCTGCCTC	32991	CA
	GAGGTAGAGGTTG GTG		
	CTCCGTCTCCAAC CAC		
	AC		
GAM1187 LOC51219 5'	CACCGCAACCTCCGCCTC	33112	TA A
	GAGG GAGGTTGC GTG		
	CTCC CTCCAACG CAC		
	GC C		
GAM1187 LOC51696 3'	CACTGCAACCTCTGCCTC	32543	
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1187 LOC57107 3'	CACTGCAACCTCCGCCTC	39831	TA
	GAGG GAGGTTGCAGTG		

		CTCC CTCCAACGTCAC	
		GC	
GAM1187	LOC57146 3'	CGGCTCACTGCAACCTCCAACCT 39918	GTA
	C	GAG GAGGTTGCAGTGAGTTG	
		CTC CTCCAACGTCACCTCGGC	
		AAC	
GAM1187	LOC64102 5'	CACTTGCAACTCCACCTC 42169	A G _
		GAGGT GAG TTGCA GTG	
		CTCCA CTC AACGT CAC	
		C _ T	
GAM1187	LOC81034 3'	CAGCTCACTGCAACCTCCACCT 47846	A
	C	GAGGT GAGGTTGCAGTGAGTTG	
		CTCCA CTCCAACGTCACCTCGAC	
		C	
GAM1187	LOC89932 3'	CACTGCAACCTCCACCTC 60791	A
		GAGGT GAGGTTGCAGTG	
		CTCCA CTCCAACGTCAC	
		C	
GAM1187	LOC90288 3'	CTCACTGCAACCTCCACCTC 62089	A
		GAGGT GAGGTTGCAGTGAG	
		CTCCA CTCCAACGTCACCTC	
		C	
GAM1187	LOC90333 5'	CACTGCAACCTCCACTTC 62283	A
		GAGGT GAGGTTGCAGTG	
		CTTCA CTCCAACGTCAC	
		C	
GAM1187	LOC90333 3'	CACTGCAACCTCCTCCTC 62284	TA
		GAGG GAGGTTGCAGTG	
		CTCC CTCCAACGTCAC	
		TC	
GAM1187	LOC90371 5'	CACTGCAACCTCCACCTC 62494	A
		GAGGT GAGGTTGCAGTG	
		CTCCA CTCCAACGTCAC	
		C	
GAM1187	LOC90408 5'	CACTGCAACCTCTACCTC 62658	
		GAGGTAGAGGTTGCAGTG	
		CTCCATCTCCAACGTCAC	
GAM1187	LOC90459 3'	CACTGCAACCTCCGCCTC 62883	TA
		GAGG GAGGTTGCAGTG	

		CTCC CTCCAACGTCAC		
		GC		
GAM1187	LOC90485 3'	CACTGCAACCTCCGCCTC	63008	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCAC		
		GC		
GAM1187	LOC90591 3'	CAGCTCACTGCAAGCTCCACCT	63418	A G
	C	GAGGT GAG TTGCAGTGAGTTG		
		CTCCA CTC AACGTCACTCGAC		
		C G		
GAM1187	LOC90591 3'	CACTGCCACCTCCACCTC	63416	A T
		GAGGT GAGGT GCAGTG		
		CTCCA CTCCA CGTCAC		
		C C		
GAM1187	LOC90957 3'	GCAGAACCTCTACCTC	64464	—
		GAGGTAGAGGT TGC		
		CTCCATCTCCA ACG		
		AG		
GAM1187	LOC91115 3'	CGGCTCACTGCAACCTCCACCT	64931	A
	C	GAGGT GAGGTTGCAGTGAGTTG		
		CTCCA CTCCAACGTCACTCGGC		
		C		
GAM1187	LOC91115 3'	CACTGCAACCTCCGCCTC	64927	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCAC		
		GC		
GAM1187	LOC91250 5'	CATTACAGCCTCCACCTC	65321	A C
		GAGGT GAGGTTG AGTG		
		CTCCA CTCCGAC TTAC		
		C A		
GAM1187	LOC91291 5'	CAGCTCACTGCAACCTCGACCT	65478	A
	C	GAGGT GAGGTTGCAGTGAGTTG		
		CTCCA CTCCAACGTCACTCGAC		
		G		
GAM1187	LOC92267 3'	CAGCTCACTGCAACCTCCACCT	68607	A
	C	GAGGT GAGGTTGCAGTGAGTTG		
		CTCCA CTCCAACGTCACTCGAC		
		C		
GAM1187	LOC92303 3'	CAACTCACTGCAACCTCTGCC	68820	
		GGTAGAGGTTGCAGTGAGTTG		

CCGTCTCCAACGTCACCTCAAC

GAM1187 LOC92466 3' CACTGCAACCTCCGCCTC 69423 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 LOC92661 5' CACTGCAAGCTCCACCTC 70079 A G  
GAGGT GAG TTGCAGTG  
|||| ||| |||||||  
CTCCA CTC AACGTCAC  
C G

GAM1187 LOC92689 3' CACTGCAACCTCCGCCTC 70219 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 LOC92697 5' CACCGCAACCTCCGCCTC 70262 TA A  
GAGG GAGGTTGC GTG  
|||| |||||| |||  
CTCC CTCCAACG CAC  
GC C

GAM1187 LOC92697 5' CGCTACAACCTCCACCTC 70264 A C  
GAGGT GAGGTTG AGTG  
|||| |||||| |||  
CTCCA CTCCAAC TCGC  
C A

GAM1187 LOC92841 3' CACCGCAACCTCCTCCTC 70706 TA A  
GAGG GAGGTTGC GTG  
|||| |||||| |||  
CTCC CTCCAACG CAC  
TC C

GAM1187 LOC93132 5' CACTGCAACCTCCGCCTC 71485 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1187 LOC93349 3' CACTGCAACCTCTGCCTC 56453  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1187 LOC93408 5' CACTGCAACCTCTGCCTC 56475  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1188 CFTR 3' AACTCCAAACTGACTCTT 4924 CA AT A  
AGGAGTCA GTT TGGA TT  
|||||| ||| ||| ||

		TTCTCAGT CAA ACCT AA	
		— — C	
GAM1188 ED1	3'	CTACTAGTGTGACTCCTT 7368	G T
		AAGGAGTCACA TTA TGG	
		TTCCTCAGTGT GAT ATC	
		— C	
GAM1188 ZIC3	3'	CAATTTTGAACCACTGACTCC 12729	CA_ A TG
TT		AAGGAGTCA GTT T GAATTG	
		TTCCTCAGT CAA G TTTAAC	
		CAC _GT	
GAM1188 ABLIM	3'	CAACTCCAAAGTAGACTCCTT 9758	_ AGTTA A
		AAGGAGTC AC TTGGA TTG	
		TTCCTCAG TG AACCT AAC	
		A A_____ C	
GAM1188 ABLIM	3'	CAACTCCAAAGTAGACTCCTT 22019	_ AGTTA A
		AAGGAGTC AC TTGGA TTG	
		TTCCTCAG TG AACCT AAC	
		A A_____ C	
GAM1188 BHLHB2	3'	CAATTCCATCCTAAAACTCCTT 13377	CAC TTAT
		AAGGAGT AG TGAATTG	
		TTCCTCA TC ACCTTAAC	
		AAA CT__	
GAM1188 LOC114987	3'	CAATATCAAACCATGGCTCCT 59121	CA AT A
		AGGAGTCA GTT TGG ATTG	
		TCCTCGGT CAA ACT TAAC	
		AC _ A	
GAM1188 LOC146452	3'	ATTCTATAACTGATAACTCC 77913	CA_ T
		GGAGT CAGTTAT GGAAT	
		CCTCA GTCAATA TCTTA	
		ATA _	
GAM1188 LOC146513	5'	TAATAACTGCCACTCC 83700	CA
		GGAGT CAGTTATTG	
		CCTCA GTCAATAAT	
		CC	
GAM1188 LOC149153	5'	TGATAACTGTGATCCTT 84369	G
		AAGGA TCACAGTTATTG	
		TTCCT AGTGTCAATAGT	
		—	
GAM1188 LOC221935	3'	AACTCCAATAACTGAGCT 92612	CA A
		AGT CAGTTATTGGA TT	

		TCG GTCAATAACCT AA	
		A_ C	
GAM1188	LOC54557	3' ATAACATGACTCCTT 72827	CA
		AAGGAGTCA GTTAT	
		TTCCTCAGT CAATA	
		A_	
GAM1189	BCL6	5' CACCAAGTCCTCCCCTGCCAC 8125	C A_ A
		GTG CA GGAG ACTTGGTG	
		CAC GT CCTC TGAACCAC	
		C CC C	
GAM1189	HEPH	3' TTCTCCTTGGCAGTGA 28966	G
		TCA TGCCAAGGAGAA	
		AGT ACGGTTCTCTT	
		G	
GAM1189	HEPH	3' TTCTCCTTGGCAGTGA 57034	G
		TCA TGCCAAGGAGAA	
		AGT ACGGTTCTCTT	
		G	
GAM1189	KRT16	5' CACCTCCCTCCTTGGCAC 95196	AACTT
		GTGCCAAGGAG GGTG	
		CACGGTTCCTC CCAC	
		CCT__	
GAM1189	MTCP1	5' CACCAAGGACTTGGTACTGA 26428	GAGAA
		TCAGTGCCAAG CTTGGTG	
		AGTCATGGTTC GAACCAC	
		AG__	
GAM1189	PCOLN3	3' CCTGTCCCCTTGGGCACTGA 10910	_ A ACTT
		TCAGTGCC AAGG GA GG	
		AGTCACGG TTCC CT CC	
		G C GT__	
GAM1189	PTPN7	3' CAGGCCCTCCCTGGCACTG 11064	A AA
		CAGTGCCA GGAG CTTG	
		GTCACGGT CCTC GGAC	
		C CC	
GAM1189	PTPN7	3' CAGGCCCTCCCTGGCACTG 54546	A AA
		CAGTGCCA GGAG CTTG	
		GTCACGGT CCTC GGAC	
		C CC	
GAM1189	PTPN7	3' CAGGCCCTCCCTGGCACTG 54557	A AA
		CAGTGCCA GGAG CTTG	



			GTCACGGT CCTC GGAC		
			C CC		
GAM1189	TBL2	3'	CCACCTGGCACTGA	24925	A AGAACT
			TCAGTGCCA GG TGG		
			AGTCACGGT CC ACC		
GAM1189	TBL2	3'	CCACCTGGCACTGA	52181	A AGAACT
			TCAGTGCCA GG TGG		
			AGTCACGGT CC ACC		
GAM1189	TRPM6	3'	TGGGTTCTCCTAGACACTGA	34551	CCA
			TCAGTG AGGAGAACTTG		
			AGTCAC TCCTCTTGGGT		
			AGA		
GAM1189	BRD4	3'	CACCCCCTCGCTGGCACTGA	54273	AG AACTT
			TCAGTGCCA GAG GGTG		
			AGTCACGGT CTC CCAC		
			CG CC__		
GAM1189	C20orf106	5'	CACCAAGGGCCTGGCAC	55055	A AGAA
			GTGCCA GG CTTGGTG		
			CACGGT CC GAACCAC		
			_ GG__		
GAM1189	CAMKK1	3'	GCCCTCCTTGGCCTGA	50173	T AACTT
			TCAG GCCAAGGAG GGT		
			AGTC CGGTTCTC CCG		
GAM1189	FLJ12294	3'	ACCAGCACTGGCACTGA	47005	A GAGAAC
			TCAGTGCCA G TTGGT		
			AGTCACGGT C GACCA		
			_ AC__		
GAM1189	GPR88	5'	ACTTGCTCCTGGCACTGA	41874	A AACTT
			TCAGTGCCA GGAG GGT		
			AGTCACGGT CCTC TCA		
			_ GT__		
GAM1189	KIAA1086	3'	CAGGCGCCTCCTGGCACTGA	70743	A AA_
			TCAGTGCCA GGAG CTTG		
			AGTCACGGT CCTC GGAC		
			_ CGC		
GAM1189	KIAA1372	5'	GTTTTCTCAGCACTGA	91651	CA
			TCAGTGC AGGAGAAC		

AGTCACG TCCTTTTG  
 AC  
 GAM1189 KIAA1538 5' CACCAAGTTCCTGCTCAC 71533 CCA A  
 GTG AGG GAACTTGGTG  
 ||| ||| |||||  
 CAC TCC CTTGAACCAC  
 TCG \_  
 GAM1189 MAP2K4 3' CTTGGGCCTCCCTGGCACTGA 11548 A AA T  
 TCAGTGCCA GGAG CT GG  
 ||||| ||| ||  
 AGTCACGGT CCTC GG TC  
 C CG T  
 GAM1189 NPTXR 3' GCCTCTCCCCAGCACTGA 26645 CAA ACTT  
 TCAGTGC GGAGA GGT  
 ||||| ||| ||  
 AGTCACG CCTCT CCG  
 ACC \_  
 GAM1189 NPTXR 3' GCCTCTCCCCAGCACTGA 54181 CAA ACTT  
 TCAGTGC GGAGA GGT  
 ||||| ||| ||  
 AGTCACG CCTCT CCG  
 ACC \_  
 GAM1189 SNAP29 3' ACCAAGTTCTTCCAGCA 16536 CAA  
 TGC GGAGAACTTGGT  
 ||| |||||  
 ACG CTTCTTGAACCA  
 AC\_  
 GAM1189 TUBAL2 3' CACCCTGCCCTAGGCACTGA 38447 A AGAACTT  
 TCAGTGCC AGG GGTG  
 ||||| ||| ||  
 AGTCACGG TCC CCAC  
 A CGTC\_  
 GAM1189 UBCE7IP5 3' TTCCTCTTGGAAGCACTGA 30165 GA  
 TCAGTGCCAAG GAA  
 ||||| ||| ||  
 AGTCACGGTTC CTT  
 TC  
 GAM1189 LOC145622 3' CACCACTCAACTGCCTGGCACT 77295 A \_ AACT\_  
 GA TCAGTGCCA GG AG TGGTG  
 ||||| ||| ||  
 AGTCACGGT CC TC ACCAC  
 \_ G AACTC  
 GAM1189 LOC146268 3' CACCAAGTGAAAGCGGCACTGA 77802 G AAGGAGA  
 TCAGT CC ACTTGGTG  
 |||| || |||||  
 AGTCA GG TGAACCAC  
 \_ CGAAAG\_  
 GAM1189 LOC146435 3' CACCAAATGGAGCTTGGCACT 77896 GAGAAC  
 AGTGCCAAG TTGGTG  
 ||||| ||| ||

		TCACGGTTC	AACCAC		
		GAGGTA			
GAM1189	LOC149761 5'	CACCAAGGGCCTGGCAC	79483	A	AGAA
		GTGCCA GG	CTTGGTG		
		CACGGT CC	GAACCAC		
		_ GG_			
GAM1189	LOC155060 3'	GTTCTCCCAGGCACTGA	86332	AA	
		TCAGTGCC	GGAGAAC		
		AGTCACGG	CCTCTTG		
		AC			
GAM1189	LOC220558 5'	CACCAAAGTCCTTGGCACTG	91137		GAAC
		CAGTGCCAAGGA	TTGGTG		
		GTCACGGTTCCT	AACCAC		
		GA_			
GAM1189	LOC222060 5'	CTAAGTCCTCCCTGGCACTGG	94106	A	A
		TCAGTGCCA	GGAG ACTTGG		
		GGTCACGGT	CCTC TGAATC		
		C C			
GAM1190	CERD4 3'	TTGGGCACACTCCACCAG	23859	_	G
		CTGGTGGAGTG	GC CCAG		
		GACCACCTCAC	CG GGTT		
		A _			
GAM1190	HPCAL1 5'	CTGCAGCCCCTCCCCACCAG	56186	_	T GC
		CTGGT	GGAG GGC CAG		
		GACCA	CCTC CCG GTC		
		CC C AC			
GAM1190	MIF 3'	TGCGCTGGCTCCACCC	10035	A	C
		GG GTGG	GCCAGCGCA		
		CC CACC	CGGTGCGT		
		_ T			
GAM1190	APCL 3'	GCGCTGGCCTCTCCCCAG	19677	T	T C
		CTGG	GGAG GG GCCAGCGC		
		GACC	CCTC TC CGGTGCGC		
		- - -			
GAM1190	ARHGDIG 3'	TTGCCGGCCACTCCTCCAG	6783	T	GCCAGC
		CTGG	GGAGTGGC GCAA		
		GACC	CCTCACCG CGTT		
		T GC_			
GAM1190	DGCR6L 3'	TGCACTGGGGCCACCC	52690	A	_ G C
		GG GTGG	C CCAG GCA		

		CC CACC G GGTC CGT	
		_ C G A	
GAM1190 FBXO21	3'	GGAAAGCCACTCCACCAG 53238	G__
		CTGGTGGAGTGGC CC	
		GACCACCTCACCG GG	
		AAA	
GAM1190 FLJ13262	5'	CGCGAGACCCGCTCCACCAG 46156	CGCCA
		CTGGTGGAGTGG GCG	
		GACCACCTCGCC CGC	
		CAGAG	
GAM1190 FLJ14871	5'	TGCGCTGGCGCCCCACC 51669	AGT
		GGTGG GGCGCCAGCGCA	
		CCACC CCGCGGTGCGGT	
		C__	
GAM1190 FLJ22282	3'	GCTGCCTCCTCCACTCAG 45591	_ TG C C
		CTG GTGGAG G GC AGC	
		GAC CACCTC C CG TCG	
		T CT _ _	
GAM1190 GTPBP1	3'	CTGGCCACCACTCCACCAG 15013	C_
		CTGGTGGAGTGG GCCAG	
		GACCACCTCACCC CGGTC	
		AC	
GAM1190 HELO1	5'	TGCGCCGGCTGCCACCC 41498	A _ A
		GG GTGGC GCC GCGCA	
		CC CACCG CGG CGCGT	
		_ T C	
GAM1190 KIAA0379	3'	TTGCGAATGCCACCCCACTA 68151	A CCAG
		TGGTGG GTGGCG CGCAA	
		ATCACC CACCGT GCGTT	
		C AA__	
GAM1190 LTBP4	3'	TGCACTGCTCCCGCCTCCACCA 13113	_ CGC C
G		CTGGTGGAG TGG CAG GCA	
		GACCACCTC GCC GTC CGT	
		C CTC A	
GAM1190 MGC15730	3'	CGCCCCGGCCACTCCATCAG 51800	GCCA
		CTGGTGGAGTGGC GCG	
		GACTACCTCACCG CGC	
		GCCC	
GAM1190 PPFIA4	3'	TGCACTGCAACCTCCACCAG 70334	TGGC C C
		CTGGTGGAG GC AG GCA	

		GACCACCTC	CG TC CGT		
		CAA_ _ A			
GAM1190	LOC126961 3'	GCGCCACCTCCACTAG	74628	_	
		CTGGTGGAG TGGCGC			
		GATCACCTC ACCGCG			
		C			
GAM1190	LOC146433 5'	GCAGCCCAGCCACTCCTCCAG	77876	T	GCCA _
		CTGG GGAGTGGC GC GC			
		GACC CCTCACCG CG CG			
		T ACC_ A			
GAM1190	LOC196872 3'	CGCTGCAACCATTCCACCAG	87796		CGC
		CTGGTGGAGTGG CAGCG			
		GACCACCTTACC GTCGC			
		AAC			
GAM1190	LOC199923 3'	TGCACTAGCGCCGCACC	88500	A	C C
		GG GTGGCGC AG GCA			
		CC CGCCGCG TC CGT			
		A A A			
GAM1190	LOC254263 5'	GCGCTGGCGCCCCCGG	94718	T	AGT
		CTGG GG GCGCCAGCGC			
		GGCC CC CCGCGGTCGCG			
		- - -			
GAM1190	LOC257395 3'	GCGCCACCTCCACTAG	95420	_	
		CTGGTGGAG TGGCGC			
		GATCACCTC ACCGCG			
		C			
GAM1190	LOC56270 5'	CGCCGGCTTCAACCAG	39018	_	_
		CTGGT GGAGT GGCG			
		GACCA CTTCG CCGC			
		A G			
GAM1190	LOC56270 5'	CGCCGGCTTCAACCAG	39019	_	_
		CTGGT GGAGT GGCG			
		GACCA CTTCG CCGC			
		A G			
GAM1190	LOC90133 3'	GGTGCACCAGCTCCACCAG	61607		G__
		CTGGTGGAGT GCGCC			
		GACCACCTCG CGTGG			
		ACCA			
GAM1191	ARHGEF6 3'	CAAACCTGAAGCCAGGC	68198		ACCA
		GCCTGG CAAGTTTG			

		CGGACC GTTCAAAC		
		GAA_		
GAM1191 BIG1	3'	TCAAACCTTGCAACTCCAG	21205	CCA___
		CTGGA CAAGTTTGA		
		GACCT GTTCAAAC		
		CACAAC		
GAM1191 CAB1	5'	TCAAGCTGACCCAGGCGG	39658	ACCACA
		TCGCCTGG AGTTTGA		
		GGCGGACC TCGAACT		
		CAG___		
GAM1191 CORO2A	3'	TCAAACCTGTGGTCCAGAGA	53403	GC A
		TC CTGGACCACA GTTTGA		
		AG GACCTGGTGT CAAACT		
		A_ _		
GAM1191 CORO2A	3'	TCAAACCTGTGGTCCAGAGA	12647	GC A
		TC CTGGACCACA GTTTGA		
		AG GACCTGGTGT CAAACT		
		A_ _		
GAM1191 DISC1	3'	TCAAACCTCCTGACCTCAGGCGA	37892	_AC CA
		TCGCCTG G CA AGTTTGA		
		AGCGGAC C GT TCAAAC		
		T CA CC		
GAM1191 EN2	5'	CGGGCGGCCCGAGGCGG	7459	A ACAA
		TCGCCTGG CC GTTTG		
		GGCGGACC GG CGGGC		
		C ___		
GAM1191 FOXD2	5'	CAGAGGGGGGCCCGAGGCGA	15562	A ACAAG
		TCGCCTGG CC TTTG		
		AGCGGACC GG AGAC		
		C GGG___		
GAM1191 GPX3	5'	TCAGGCAGCGGCTCAGGCGA	9125	GA ACAA
		TCGCCTG CC GTTTGA		
		AGCGGAC GG CGGACT		
		TC CGA_		
GAM1191 HNF3G	3'	AACTCTGGTCCAGGAGA	72339	G CA
		TC CCTGGACCA AGTT		
		AG GGACCTGGT TCAA		
		A C_		
GAM1191 IL13RA1	3'	TCAAACCTTGAGTCACAAAGA	7778	GCC _ CA
		TC TG GAC CAAGTTTGA		

			AG AC CTG GTTCAAAC		
			AA_ A A_		
GAM1191 KCNS2	3'	CAAAC	TTGTATTGAAGGGA	68300	G GGACC
			TC CCT ACAAGTTTG		
			AG GGA TGTTCAAAC		
			_ AGTTA		
GAM1191 LMO4	5'	CAAAC	TTGCAGCAGCGA	22251	_ GACCA
			TCGC CTG CAAGTTTG		
			AGCG GAC GTTCAAAC		
			AC _		
GAM1191 LZTS1	3'	TCAAAC	TTGTGGCCTCAAGC	40695	CT_ A
			GC GG CCACAAGTTTGA		
			CG CC GGTGTTCAAAC		
			AACT _		
GAM1191 MATK	3'	CAAGGAGGGTCCAGGCGG		57816	ACAAG
			TCGCCTGGACC TTTG		
			GGCGGACCTGG GAAC		
			GAG_		
GAM1191 MATK	3'	CAAGGAGGGTCCAGGCGG		57819	ACAAG
			TCGCCTGGACC TTTG		
			GGCGGACCTGG GAAC		
			GAG_		
GAM1191 MATK	3'	CAAGGAGGGTCCAGGCGG		9915	ACAAG
			TCGCCTGGACC TTTG		
			GGCGGACCTGG GAAC		
			GAG_		
GAM1191 MIR16	3'	TCAAAC	TTGTGGCCA	33565	A
			TGG CCACAAGTTTGA		
			ACC GGTGTTCAAAC		
			-		
GAM1191 PIK3C2B	3'	AGCTCGGTCCAGGTGA		10559	ACA
			TCGCCTGGACC AGTT		
			AGTGGACCTGG TCGA		
			C_		
GAM1191 PLCG2	5'	CAAACCCGGGGCAGGCGG		72463	GA ACAA
			TCGCCTG CC GTTTG		
			GGCGGAC GG CAAAC		
			GG CC_		
GAM1191 PLIN	3'	CAAAC	TTGTGGCCAAAAGA	10640	GCC A
			TC TGG CCACAAGTTTG		

AG ACC GGTGTTCAAAC  
 AAA \_  
 GAM1191 POU2AF1 3' CAGATTTACAGTCCAGGC 20648 CAC  
 GCCTGGAC AAGTTTG  
 ||||| |||||  
 CGGACCTG TTTAGAC  
 ACA  
 GAM1191 SLC6A12 3' CGAATGTGCTCCAGGCGA 11734 C AG  
 TCGCCTGGA CACA TTTG  
 ||||| ||| |||  
 AGCGGACCT GTGT AAGC  
 C \_  
 GAM1191 STARD4 3' TCAAACCTGTAGTACTACAGA 57516 GCC \_ C  
 TC TGG AC ACAAGTTTGA  
 || ||| |||||  
 AG ATC TG TGTTCAAAC  
 AC\_ A A  
 GAM1191 TP53 3' TCAAACCTCTGGGCTCAGGCGA 5043 A\_ CA  
 TCGCCTGG CCA AGTTTGA  
 ||||| ||| |||||  
 AGCGGACT GGT TCAAAC  
 CG CC  
 GAM1191 TR2 5' CAAACTTTCCAGGC 72314 CCAC  
 GCCTGGA AAGTTTG  
 ||||| |||||  
 CGGACCT TTCAAAC  
 \_  
 GAM1191 C21orf42 5' TCAAACCTTGTAGCTGTATGA 54207 CC ACC  
 TCG TGG ACAAGTTTGA  
 ||| ||| |||||  
 AGT GTC TGTTCAAAC  
 AT GA\_  
 GAM1191 DAZAP1 3' CAAACTTGTGAACTCGTGA 38536 CT AC  
 TCGC GG CACAAGTTTG  
 ||| || |||||  
 AGTG TC GTGTTCAAAC  
 C\_ AA  
 GAM1191 DBR1 3' AACTCCTGACCTCAGGCGA 32523 \_AC CA  
 TCGCCTG G CA AGTT  
 ||||| | || |||  
 AGCGGAC C GT TCAA  
 T CA CC  
 GAM1191 DC-TM4F2 3' CAAACTTGTGACTGC 48171 CT AC  
 GC GG CACAAGTTTG  
 || || |||||  
 CG TC GTGTTCAAAC  
 \_ A\_  
 GAM1191 DKFZp434N2030 5' TCAAACCTTGTCTCGC 65525 CT CAC  
 GC GGAC AAGTTTGA  
 || ||| |||||



CG CCTG TTCAAACCT  
CT \_\_\_\_

GAM1191 DKFZP564I1171 3' TCAGAAGCTGAGTCCAGGC 71592 \_ CAAG  
GCCTGGAC CA TTTGA  
||||||| || |||||  
CGGACCTG GT AGACT  
A CGA\_

GAM1191 DKFZP564O0423 3' TCAAACCTCCTGGCCTCAGGCGA 91699 \_A CA  
TCGCCTG G CCA AGTTTGA  
||||||| ||| |||||  
AGCGGAC C GGT TCAAACCT  
T C CC

GAM1191 EPN2 5' CAAACTTGTGGACAGG 30321 GA  
CCTG CCACAAGTTTG  
||| |||||  
GGAC GGTGTTCAAAC  
A\_

GAM1191 EREG 3' TCAAACCTTATGGGCAGGGA 7510 G GA C  
TC CCTG CCA AAGTTTGA  
|| ||| ||| |||||  
AG GGAC GGT TTCAAACCT  
\_ G\_ A

GAM1191 FLJ10718 3' TCAAACCTCTTAGGCTCAGGCGA 36496 GA ACA\_  
TCGCCTG CC AGTTTGA  
||||||| || |||||  
AGCGGAC GG TCAAACCT  
TC ATTC

GAM1191 FLJ10803 3' TCAAACCTTGTATGGATGA 36671 \_ TGGACC  
TCG CC ACAAGTTTGA  
||| || |||||  
AGT GG TGTTCAAACCT  
A TA\_\_\_\_

GAM1191 FLJ20312 5' TCAAACCTTGTGTGCTGAGG 34928 \_ AC  
CCT GG CACAAGTTTGA  
||| || |||||  
GGA TC GTGTTCAAACCT  
G GT

GAM1191 FLJ23420 3' CAAGTGGGTCCAGGC 46846 A AG  
GCCTGGACC CA TTTG  
||||||| || |||  
CGGACCTGG GT GAAC

GAM1191 FREQ 3' TCAGCTGCTGGCCCGGGCGA 26585 A CA T  
TCGCCTGG CCA AGTT GA  
||||||| ||| ||| ||  
AGCGGGCC GGT TCGA CT  
C CG \_

GAM1191 H2AV 3' TCAAACCTCCTGACCTCAGGCGA 56858 \_AC CA  
TCGCCTG G CA AGTTTGA  
||||||| | || |||||

AGCGGAC C GT TCAAAC T  
 T CA CC  
 GAM1191 HSA249128 5' GGCGCGGTCCAGGCGG 34153 ACAA  
 TCGCCTGGACC GTT  
 ||||| ||  
 GGCGGACCTGG CGG  
 CG\_\_  
 GAM1191 KIAA0089 5' AAGCACGGTCCAGGCGG 69960 ACAA  
 TCGCCTGGACC GTTT  
 ||||| ||  
 GGCGGACCTGG CGAA  
 CA\_\_  
 GAM1191 KIAA0256 3' CAAACTTGTCTCTGAGTGC 64417 \_ \_ CAC  
 GC CT GGAC AAGTTTG  
 || || || || || || || ||  
 CG GA CCTG TTCAAAC  
 T GT \_  
 GAM1191 KIAA1026 3' TCAACTCCTGACCTCAGGCGA 71207 \_ AC CA T  
 TCGCCTG G CA AGTT GA  
 ||||| | || || || ||  
 AGCGGAC C GT TCAA CT  
 T CA CC \_  
 GAM1191 KIAA1981 3' CAGAGGATGATTCAGGCGA 88341 C CAAG  
 TCGCCTGGA CA TTTG  
 ||||| || ||  
 AGCGGACTT GT AGAC  
 A AGG\_  
 GAM1191 MGC13090 5' TCAAAC TGTCCGCCAAGT 51141 C ACC  
 GC TGG ACAAGTTTGA  
 || || || || || || || ||  
 TG ACC TGTTCAAACT  
 A GCC  
 GAM1191 MGC2452 5' TCAAGGAGATGTGGTCCAGG 50990 AG\_\_  
 CCTGGACCACA TTTGA  
 ||||| || ||  
 GGACCTGGTGT GAACT  
 AGAG  
 GAM1191 MYT1L 5' TCAAAC TGTGGTGG 66825 TGG  
 CC ACCACAAGTTTGA  
 || || || || || || || ||  
 GG TGGTGTTCAAACT  
 \_  
 GAM1191 NUDT13 3' TCAGTTTGTGACCCAGGGA 63215 G AC AGT  
 TC CCTGG CACA TTGA  
 || || || || || || || ||  
 AG GGACC GTGT GACT  
 \_ CA TT\_  
 GAM1191 PCDH17 3' CAAAC TGTATTAGG 27087 ACC  
 CCTGG ACAAGTTTG  
 || || || || || || || ||

GGATT TGTTCAAAC  
A\_\_  
GAM1191 PGRMC1 3' TCAAACCTGTAATTGTGGT 21895 TG CC  
GCC GA ACAAGTTTGA  
||| || |||||  
TGG TT TGTTCAAACT  
TG AA  
GAM1191 PTDSS2 3' CATGGTGTGGTCCAGGC 47884 AGTT  
GCCTGGACCACA TG  
||||||| ||  
CGGACCTGGTGT AC  
GGT\_  
GAM1191 RPS6KB1 3' TCAAACCTTTTCCCAGGC 12038 ACCAC  
GCCTGG AAGTTTGA  
||||| |||||  
CGGACC TTCAAACCT  
CTT\_  
GAM1191 USP22 3' TCAAACCTCCTGACCTCAGGCGA 68023 \_ AC CA  
TCGCCTG G CA AGTTTGA  
||||| | || |||||  
AGCGGAC C GT TCAAACCT  
T CA CC  
GAM1191 LOC129011 5' CAGACCTGCGGTCCAGGC 74865 A A  
GCCTGGACC CA GTTTG  
||||||| || |||||  
CGGACCTGG GT CAGAC  
C C  
GAM1191 LOC130595 5' CAGGCTCAGTCCAGGC 75748 CACA  
GCCTGGAC AGTTTG  
||||||| |||||  
CGGACCTG TCGGAC  
AC\_  
GAM1191 LOC131873 5' CTGGTGGTCCAGGAGA 75879 G A  
TC CCTGGACCAC AG  
|| ||||| ||  
AG GGACCTGGTG TC  
A G  
GAM1191 LOC145978 3' TCAAACCTTTAACAGGTGA 77600 GACCAC  
TCGCCTG AAGTTTGA  
||||| |||||  
AGTGGAC TTCAAACCT  
AAT\_  
GAM1191 LOC146890 5' TCAGAAGTAGTCAGGCGA 83854 G C AAG  
TCGCCTG AC AC TTTGA  
||||| || || |||||  
AGCGGAC TG TG AGACT  
\_ A A\_  
GAM1191 LOC150622 5' CTGGTGGTCCAGGGA 79957 G A  
TC CCTGGACCAC AG  
|| ||||| ||

		AG GGACCTGGTG TC	
		— G	
GAM1191	LOC152002 3'	CAAACCAGCTCCAGGTGA 80431	CCACAA
		TCGCCTGGA GTTTG	
		AGTGGACCT CAAAC	
		CGAC__	
GAM1191	LOC153474 3'	TCAGAAGCTGAGTCCAGGC 80847	_ CAAG
		GCCTGGAC CA TTTGA	
		CGGACCTG GT AGACT	
		A CGA_	
GAM1191	LOC154007 3'	TCAAACCTCCTAGGCTCAGGCGA 81021	GA ACA_
		TCGCCTG CC AGTTTGA	
		AGCGGAC GG TCAAAC	
		TC ATCC	
GAM1191	LOC154789 5'	TCAAACCTTGAGCAGGC 81141	GACCA
		GCCTG CAAGTTTGA	
		CGGAC GTTCAAAC	
		GA__	
GAM1191	LOC158301 3'	CAAACCTGTGGTTCCA 81869	_ A
		TGGA CCACA GTTTG	
		ACCT GGTGT CAAAC	
		T C	
GAM1191	LOC199906 3'	TCAAACCTCCTGACCTCAGGCGA 88487	_ AC CA
		TCGCCTG G CA AGTTTGA	
		AGCGGAC C GT TCAAAC	
		T CA CC	
GAM1191	LOC199991 5'	TCAGAGCGTTCCAGGCGA 89916	CC AAG
		TCGCCTGGA AC TTTGA	
		AGCGGACCT TG AGACT	
		__ CG_	
GAM1191	LOC219529 5'	TCAAACCTCCTGAGCCCAGGTGA 92974	AC_ CA
		TCGCCTGG CA AGTTTGA	
		AGTGGACC GT TCAAAC	
		CGA CC	
GAM1191	LOC220753 3'	CAAACCTTGTAGAGGTGGGC 92941	GG __
		GCCT ACC ACAAGTTTG	
		CGGG TGG TGTCAAAC	
		__ AGA	
GAM1191	LOC221718 3'	TCAAACCTTATTGGTGAAG 93632	GG C_
		CT ACCA AAGTTTGA	

		GA TGGT TTCAAACT			
		AG TA			
GAM1191	LOC253927	3' TCAAACCTTAGACTTCAGGC	95025	CCAC	
		GCCTGGA AAGTTTGA			
		CGGACTT TTCAAACT			
		CAGA			
GAM1191	LOC51028	3' CAAATATGGTCCAGG	32179	CAA	
		CCTGGACCA GTTTG			
		GGACCTGGT TAAAC			
		A_			
GAM1192	ADAM17	3' ATGCCTGTAATCCCAGCACTTG	41553	_ A	A
		CA GT GCTGGGATTACAG CAT			
		GT CA CGACCCTAATGTC GTA			
		T _ C			
GAM1192	ADAM17	3' ATGCCTGTAATCCCAGCACTTG	12081	_ A	A
		CA GT GCTGGGATTACAG CAT			
		GT CA CGACCCTAATGTC GTA			
		T _ C			
GAM1192	ADAT1	3' CTGTAATCCTAGCTACT	23898		
		AGTAGCTGGGATTACAG			
		TCATCGATCCTAATGTC			
GAM1192	AICDA	3' CTGTAATCCCAGCACT	40326	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
GAM1192	AK1	3' ATGCCTGTAATCCCAGCACT	4879	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		_ C			
GAM1192	ALDH3A2	3' ATGCCTGTAATCCCAGCACT	69270	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		_ C			
GAM1192	ALDH3B1	3' ATGCCTGTAATCCCAGCTACT	91520		A
		AGTAGCTGGGATTACAG CAT			
		TCATCGACCCTAATGTC GTA			
		C			
GAM1192	ALDH3B1	3' CTGTAATCCCAGCACT	91524	A	
		AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

GAM1192 ALDH8A1 3' ATGCCTATAATCCCAGCACT 42607 A C A  
AGT GCTGGGATTA AG CAT  
||| ||||| || |||  
TCA CGACCCTAAT TC GTA  
A C  
GAM1192 ANKH 3' ATGCCTGTAATCCCAACACT 53987 AGC A  
AGT TGGGATTACAG CAT  
||| ||||| |||  
TCA ACCCTAATGTC GTA  
CA\_ C  
GAM1192 ANKH 3' CTGTAATCCCAGCTACT 53989  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC  
  
GAM1192 ARHGEF6 3' CTGTGGTCCCAGCTACTCA 68202 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTGGTGTC  
C  
GAM1192 ATM 3' CTGTAATCCCAGCACT 56295 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC  
  
GAM1192 ATM 3' CTATAATCCCAGCACT 56303 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC  
A  
GAM1192 ATM 3' CTGTAATCCCAGCACT 3511 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC  
  
GAM1192 ATP1A2 3' ATGCCTGTAATCCCAGCACT 5521 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C  
GAM1192 ATP1A2 3' CTGTAATCTCAGCTACTCA 5524 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACTCTAATGTC  
C  
GAM1192 BAAT 3' ATGTCTCCCCAGCTGC 8112 ATTAC  
GTAGCTGGG AGACAT  
||||| |||||

			CGTCGACCC	TCTGTA		
			CC___			
GAM1192	BHMT2	3'	CTGCAATCCCAGCACT	34309	A	A
			AGT GCTGGGATT CAG			
			TCA CGACCCTAA GTC			
			— C			
GAM1192	BRCA1	3'	CTGTAATCCCAGCTACT	23593		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
			—			
GAM1192	BRCA1	3'	CTGTAATCCCAGCACT	23518	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	BRCA1	3'	CTGTAATCCCAGCTACT	23519		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
			—			
GAM1192	BRCA1	3'	CTGTAATCCCAGCACT	23527	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	BRCA1	3'	CTGTAATCCCAGCTACT	23528		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
			—			
GAM1192	BRCA1	3'	CTGTAATCCCAGCACT	23535	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	BRCA1	3'	CTGTAATCCCAGCTACT	23536		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
			—			
GAM1192	BRCA1	3'	CTGTAATCCCAGCACT	23543	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	BRCA1	3'	CTGTAATCCCAGCTACT	23544		
			AGTAGCTGGGATTACAG			

TCATCGACCCTAATGTC

GAM1192 BRCA1 3' CTGTAATCCCAGCACT 23551 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 BRCA1 3' CTGTAATCCCAGCTACT 23552  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1192 BRCA1 3' CTGTAATCCCAGCACT 23559 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 BRCA1 3' CTGTAATCCCAGCTACT 23560  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1192 BRCA1 3' CTGTAATCCCAGCACT 23568 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 BRCA1 3' CTGTAATCCCAGCTACT 23569  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1192 BRCA1 3' CTGTAATCCCAGCACT 23576 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 BRCA1 3' CTGTAATCCCAGCTACT 23577  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1192 BRCA1 3' CTGTAATCCCAGCACT 23584 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 BRCA1 3' CTGTAATCCCAGCTACT 23585  
AGTAGCTGGGATTACAG  
|||||||



TCATCGACCCTAATGTC

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GAM1192 BRCA1  3' CTGTAATCCCAGCACT  23592  A
                AGT GCTGGGATTACAG
                ||| |||||
                TCA CGACCCTAATGTC

GAM1192 BRCA2  3' ATGCCTGTAATCCCAACACTTT 3548  TAGC_  A
                G      CAG  TGGGATTACAG CAT
                ||| ||||| |||
                GTT  ACCCTAATGTC GTA
                TCACA      C

GAM1192 C1orf1  3' CTGTAATCCCAACACT  6859  AGC
                AGT TGGGATTACAG
                ||| |||||
                TCA ACCCTAATGTC
                CA_

GAM1192 C5R1   3' CTGTAATCCCAGAACT  8204  AG
                AGT CTGGGATTACAG
                ||| |||||
                TCA GACCCTAATGTC
                A_

GAM1192 CARKL  3' ATGCCTGTAATCCCAGCTACT 25183  A
                AGTAGCTGGGATTACAG CAT
                ||||| |||||
                TCATCGACCCTAATGTC GTA
                C

GAM1192 CASP10 3' ATGCCTGTAATCCCAGTACTCT 52098  TA_  A
                G      CAG  GCTGGGATTACAG CAT
                ||| ||||| |||
                GTC  TGACCCTAATGTC GTA
                TCA      C

GAM1192 CASP10 3' ATGCCTGTAATCCCAGTACTCT 52116  TA_  A
                G      CAG  GCTGGGATTACAG CAT
                ||| ||||| |||
                GTC  TGACCCTAATGTC GTA
                TCA      C

GAM1192 CASP6  3' ATGCCTGCAATCCCAGCTACTT 52200  _  A  A
                G      CA GTAGCTGGGATT CAG CAT
                || ||||| ||| |||
                GT CATCGACCCTAA GTC GTA
                T      C  C

GAM1192 CASP6  3' CTGTAATCCCAGCACT  52203  A
                AGT GCTGGGATTACAG
                ||| |||||
                TCA CGACCCTAATGTC

GAM1192 CASP6  3' ATGCCTGCAATCCCAGCTACTT 6907  _  A  A
                G      CA GTAGCTGGGATT CAG CAT
                || ||||| ||| |||
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				GT CATCGACCCTAA GTC GTA		
				T C C		
GAM1192	CASP6	3'	CTGTAATCCCAGCACT	6910	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	CASP8	3'	ATGTCTATAATCCCAGCACT	6913	A	C
			AGT GCTGGGATTA AGACAT			
			TCA CGACCCTAAT TCTGTA			
			— A			
GAM1192	CASP8	3'	ATGTCTATAATCCCAGCACT	52919	A	C
			AGT GCTGGGATTA AGACAT			
			TCA CGACCCTAAT TCTGTA			
			— A			
GAM1192	CASP8	3'	ATGTCTATAATCCCAGCACT	52930	A	C
			AGT GCTGGGATTA AGACAT			
			TCA CGACCCTAAT TCTGTA			
			— A			
GAM1192	CASP8	3'	ATGTCTATAATCCCAGCACT	52942	A	C
			AGT GCTGGGATTA AGACAT			
			TCA CGACCCTAAT TCTGTA			
			— A			
GAM1192	CD68	3'	ATGCCTGTAATCCCAGCACT	59797	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	CHRNA5	3'	CTGTAATCCCAGCACT	59755	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	CHST5	3'	ATGCCTGTAATCCCAGCATTTT	24022	TA_	A
	G		CAG GCTGGGATTACAG CAT			
			GTT CGACCCTAATGTC GTA			
			TTA C			
GAM1192	CHST5	3'	CTGTAATCCCAGCTACTTA	24025	C	
			A AGTAGCTGGGATTACAG			
			A TCATCGACCCTAATGTC			
			T			
GAM1192	CNGB1	3'	ATGCCTATAATCCCAGTGCT	7110	G	C A
			AGTA CTGGGATTA AG CAT			

			TCGT GACCCTAAT TC GTA		
			— A C		
GAM1192	COG7	3'	CTGTAATCCCAGCACT 67622	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	COL16A1	3'	CTGTAATCCTAGCTATT 8500		
			AGTAGCTGGGATTACAG		
			TTATCGATCCTAATGTC		
			—		
GAM1192	COPA	3'	CTGTAATCCCAGCACT 15187	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	CORO2A	3'	ATGCCTGTAATCCCAGCACTCT 12644	TA_	A
	G		CAG GCTGGGATTACAG CAT		
			GTC CGACCCTAATGTC GTA		
			TCA C		
GAM1192	CORO2A	3'	ATGCCTGTAATCCCAGCACTCT 53400	TA_	A
	G		CAG GCTGGGATTACAG CAT		
			GTC CGACCCTAATGTC GTA		
			TCA C		
GAM1192	CPT2	3'	ATGCCTGTAATCCCAGCATTTT 3641	TA_	A
	G		CAG GCTGGGATTACAG CAT		
			GTT CGACCCTAATGTC GTA		
			TTA C		
GAM1192	CRACC	3'	CTGTAATCCCAGCACT 41005	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	CTMP	3'	CTGTAATCCCAGCACTTTA 53876	C A	
			TA AGT GCTGGGATTACAG		
			AT TCA CGACCCTAATGTC		
			T _		
GAM1192	CTMP	3'	CTGTAGTCCCAGCTACTCA 53877	C	
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTGATGTC		
			C		
GAM1192	CTNNB1	3'	TCTGTAATGGTACTG 8581	G GGG	
			CAGTA CT ATTACAGA		

GTCAT GG TAATGTCT

GAM1192	CTSS	3'	ATGCCTGTAATCCCAGCTACTT	14540	—	A
	G		CA GTAGCTGGGATTACAG	CAT		
			GT CATCGACCCTAATGTC	GTA		
			T	C		
GAM1192	CTSS	3'	CTGTAATCCCAGTACTTG	14542	C G	
			A AGTA CTGGGATTACAG			
			G TCAT GACCCTAATGTC			
			T	—		
GAM1192	CYP4F3	3'	CTGTAATCCCAGCACTTTA	6115	C A	
			TA AGT GCTGGGATTACAG			
			AT TCA CGACCCTAATGTC			
			T	—		
GAM1192	DAPP1	3'	ATGCCTGTAATCCCAGGACT	26917	AG	A
			AGT CTGGGATTACAG	CAT		
			TCA GACCCTAATGTC	GTA		
			G	C		
GAM1192	DAPP1	3'	TGTAATCCCAGCTACTCA	26920	C	
			A AGTAGCTGGGATTACA			
			A TCATCGACCCTAATGT			
			C			
GAM1192	DBT	3'	CTGTAATCCCAGCACT	8610	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	DCLRE1C	3'	ATGCCTGTAATCCCAGCTAC	42524		A
			GTAGCTGGGATTACAG	CAT		
			CATCGACCCTAATGTC	GTA		
			C			
GAM1192	DDOST	3'	ATGCCTGTAATCCCAGCACT	17816	A	A
			AGT GCTGGGATTACAG	CAT		
			TCA CGACCCTAATGTC	GTA		
			—			
			C			
GAM1192	DFFA	3'	CTGTAATCCCAGCACTG	15302	A	
			CAGT GCTGGGATTACAG			
			GTCA CGACCCTAATGTC			
			—			
GAM1192	DHFR	3'	ATGCCTGTAGTCCCAGCTACTC	5799	C	A
	A		A AGTAGCTGGGATTACAG	CAT		

			A TCATCGACCCTGATGTC GTA		
			C C		
GAM1192 DHFR	3'	CTGTAATCCCAGCGCT	5803	A	
		AGT GCTGGGATTACAG			
		TCG CGACCCTAATGTC			
GAM1192 DMC1	3'	CTGTAATCCCAGCACT	22972	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
GAM1192 DNASE2	3'	ATGCCTGTAGTCCCAGCCACTG	7263	A	A
		CAGT GCTGGGATTACAG CAT			
		GTCA CGACCCTGATGTC GTA			
		C C			
GAM1192 DSC1	3'	CTGTAATCCCAGCTACTCA	44328	C	
		A AGTAGCTGGGATTACAG			
		A TCATCGACCCTAATGTC			
		C			
GAM1192 DSC1	3'	CTGTAATCCCAGCTACTCA	17059	C	
		A AGTAGCTGGGATTACAG			
		A TCATCGACCCTAATGTC			
		C			
GAM1192 DVL3	3'	GTCTGTAATCCCAGCACT	15373	A	
		AGT GCTGGGATTACAGAC			
		TCA CGACCCTAATGTCTG			
GAM1192 DYRK1A	3'	ATGTCTGTAACCAATAATGTA	55198	G	GCTG A
		TACA TA GG TTACAGACAT			
		ATGT AT CC AATGTCTGTA			
		A AA__ _			
GAM1192 DYRK1A	3'	ATGTCTGTAACCAATAATGTA	55240	G	GCTG A
		TACA TA GG TTACAGACAT			
		ATGT AT CC AATGTCTGTA			
		A AA__ _			
GAM1192 DYRK1A	3'	ATGTCTGTAACCAATAATGTA	7349	G	GCTG A
		TACA TA GG TTACAGACAT			
		ATGT AT CC AATGTCTGTA			
		A AA__ _			
GAM1192 EFG2	5'	CTGTAATCCCAGCACT	50476	A	
		AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

—  
GAM1192 EGFL5 3' CTGTAATCCCAGCACT 86618 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 EHHADH 3' CTGTAATCCCAGCACT 8750 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 F2R 3' CTGTAATCCCAGCACT 8837 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 F2RL3 3' CTGCAATCCCAGCACT 14178 A A  
AGT GCTGGGATT CAG  
||| ||||| |||  
TCA CGACCCTAA GTC

— C  
GAM1192 F2RL3 3' CTGTAATCCCAGCACTTTA 14179 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||  
AT TCA CGACCCTAATGTC

T —  
GAM1192 F2RL3 3' TGTAATCCCAGCTACTCA 14197 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1192 FANCD2 3' CTGTAATCCCAGCACT 52355 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 FCMD 3' CTATAGTCCCAGCTAC 22091 C  
GTAGCTGGGATTA AG  
||||||| ||  
CATCGACCCTGAT TC

A  
GAM1192 FGFR1 3' CTGTAATCCCAGCACTTTA 43614 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||  
AT TCA CGACCCTAATGTC

T —  
GAM1192 FGFR1 3' CTGTAATCCCAGCACTTTA 43621 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||

			AT TCA CGACCCTAATGTC		
			T _		
GAM1192	FGFR2	3'	ATGCCTGTAATCCCAGCACT 43382	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			_ C		
GAM1192	FGFR2	3'	ATGCCTGTAATCCCAGCACT 43376	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			_ C		
GAM1192	FKRP	3'	CTGTAATCCCAGCACT 44185	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			_		
GAM1192	FLRT2	5'	GTCTGTAATCCCAGCGCTCTGT 25064	TA_	
			ACAG GCTGGGATTACAGAC		
			TGTC CGACCCTAATGTCTG		
			TCG		
GAM1192	FUT6	3'	CTGTAATCCCAGCACT 3811	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			_		
GAM1192	GALNT7	3'	CTGTAATCCCAGCTACTTG 54018	_	
			CA GTAGCTGGGATTACAG		
			GT CATCGACCCTAATGTC		
			T		
GAM1192	GNE	3'	CTGTAATCCCAGCACT 18478	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			_		
GAM1192	GP2	3'	ATGCCTGTAATCCCAGC 7680	A	
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1192	GP6	3'	ATGTCTGTAATCCTAGCACTGT 33030	A	
	G		TACAGT GCTGGGATTACAGACAT		
			GTGTCA CGATCCTAATGTCTGTA		
			_		
GAM1192	GPRK7	3'	TCTATAATCCCAGTTAC 57629	C	
			GTAGCTGGGATTA AGA		

			CATTGACCCTAAT TCT		
			A		
GAM1192	GRAF	3'	CTATAATCCCAGCACT 30556	A	C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1192	GRM6	3'	CTGTAATCCCAGCACT 5934	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	HFE	3'	CTGTAATCCCAGGGTGCTG 4651	G	—
			CAGTA C TGGGATTACAG		
			GTCGT G ACCCTAATGTC		
			G G		
GAM1192	HIP1	3'	ATGCCTGTAATCCCAGAACT 18055	AG	A
			AGT CTGGGATTACAG CAT		
			TCA GACCCTAATGTC GTA		
			A_ C		
GAM1192	HIP1	3'	CTGTAATCCCAGCACT 18059	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	HIP1	3'	GTAATCCCAGCTACTCA 18065	C	
			A AGTAGCTGGGATTAC		
			A TCATCGACCCTAATG		
			C		
GAM1192	HLA-E	3'	ATGCCTGTAATCCCAGCACT 91021	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	HUNK	3'	CTGTAATCCCAGCACT 27449	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	IAPP	3'	GTGCCTGTAATCCCAGCTACTC 4696	C	A
	A		A AGTAGCTGGGATTACAG CAT		
			A TCATCGACCCTAATGTC GTG		
			C C		
GAM1192	ICA1	3'	TGCAGTCCCAGCTACTCA 42257	C	A
			A AGTAGCTGGGATT CA		



			A TCATCGACCCTGA GT		
			C C		
GAM1192	ICMT	3'	CTGTAATCCCAAAGTGCTG 24812	GC_	
			CAGTA TGGGATTACAG		
			GTCGT ACCCTAATGTC		
			GAA		
GAM1192	IFIT4	3'	ATGCCTGTAATCCCAGCACT 70920	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	IFNAR1	3'	CTGTAATCCCAGCACT 5284	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	IL10	3'	CTGTAATCCCAGCACT 5127	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	IL12RB2	3'	ATGCCTGTAATCCCAGCACT 7768	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	IL17R	3'	CTGTAATCCCAGCAC 26776	A	
			GT GCTGGGATTACAG		
			CA CGACCCTAATGTC		
			—		
GAM1192	IL1R1	3'	CTATAATCCCAGCACT 6057	A	C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1192	IL1R1	3'	CTGTAATCCCAGCTAC 6058		
			GTAGCTGGGATTACAG		
			CATCGACCCTAATGTC		
			—		
GAM1192	IL4R	5'	ATGCCTATAATCCCAGCACT 4699	A	C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1192	IPP	3'	ATGCCTATAATCCCAGCACT 19724	A	C A
			AGT GCTGGGATTA AG CAT		

			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1192	IRAK1	3'	CTGTAATCCCAGCACT 7808 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	ITGAL	3'	CTGTAATCCCAGCACT 9391 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	ITGAL	3'	CTGTAGTCCCAGCTACTCA 9392 C		
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTGATGTC		
			C		
GAM1192	JRK	3'	CTGTAATCCCAGCACTG 86526 A		
			CAGT GCTGGGATTACAG		
			GTCA CGACCCTAATGTC		
			—		
GAM1192	KAI1	3'	CTGTAATCCCAGCACT 9499 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	KCNA7	3'	ATGCCTGTGATCCCAGCTACTC 49049 C		A
	A		A AGTAGCTGGGATTACAG CAT		
			A TCATCGACCCTAGTGTC GTA		
			C C		
GAM1192	KNSL1	3'	ATGCCTGTAATCCCAGCACT 15747 A		A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	LAMP2	3'	CTGTAATCCCAGCACT 25712 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LDLR	3'	CTGTAATCCCAGCACT 4985 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LDLR	3'	CTGTAATCCCAGCACT 4986 A		
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

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GAM1192 LEP    3' CTGTAATCCCAGCACT    4048    A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1192 LRRC2 3' CTATAATCCCAGCACT    44467    A    C
      AGT GCTGGGATTA AG
      ||| ||||| ||
      TCA CGACCCTAAT TC

      -      A
GAM1192 LRRC2 3' CTATAATCCCAGCACT    44468    A    C
      AGT GCTGGGATTA AG
      ||| ||||| ||
      TCA CGACCCTAAT TC

      -      A
GAM1192 LRRC2 3' CTGTAATCCCAGCACT    44469    A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1192 LRRC2 3' GTAATCCCAGCTACTCA    44477    C
      A AGTAGCTGGGATTAC
      | |||||
      A TCATCGACCCTAATG
      C

GAM1192 LUZP1 3' ATGCCTGTAATCGCAGCTACTC 53296    C    G    A
      A
      A AGTAGCTG GATTACAG CAT
      | ||||| ||||| |||
      A TCATCGAC CTAATGTC GTA
      C    G    C

GAM1192 LUZP1 3' CTGTAATCCCAGCACT    53299    A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1192 MAFF 3' TCTGTAATCCCAGCACT    24654    A
      AGT GCTGGGATTACAGA
      ||| |||||
      TCA CGACCCTAATGTCT

      -
GAM1192 MCM4 3' CTGTAATCCCAGCACT    61903    A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1192 MIR16 3' ATGCCTGTATTCCCAGCTACTC 33563    C    T    A
      A
      A AGTAGCTGGGA TACAG CAT
      | ||||| |||| |||
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			A TCATCGACCCT ATGTC GTA		
			C     T     C		
GAM1192	MOG	3'	CTGTAATCCCAGCACT     10102     A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	MSH3	3'	ATGCCTGTAATCCCAGCACT     10118     A     A		
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			—     C		
GAM1192	MTMR8	3'	CTGTAATCCCAGCACT     31292     A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	MTNR1A	3'	CTGTAATCCCAGCTACT     19889		
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
			—		
GAM1192	NFKBIL2	3'	CTGTAATCCCAACACT     25525     AGC		
			AGT TGGGATTACAG		
			TCA ACCCTAATGTC		
			CA_		
GAM1192	NPHP1	3'	CTGTAATCCCAACACT     62479     AGC		
			AGT TGGGATTACAG		
			TCA ACCCTAATGTC		
			CA_		
GAM1192	NPHS1	3'	CTATAATCCCAGCACT     16190     A     C		
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			—     A		
GAM1192	NT5C2	3'	ATGCCTGTAATCCCATCATCTA 24237     C___     A		
	CT		AGTAG TGGGATTACAG CAT		
			TCATC ACCCTAATGTC GTA		
			TACT     C		
GAM1192	NT5C2	3'	CTGTAATCCCAGCACT     24238     A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	OASL	3'	CTGTAATCCCAGAACT     13578     AG		
			AGT CTGGGATTACAG		

			TCA GACCCTAATGTC		
			A_		
GAM1192	OPTN	3'	ATGCCTGTAATCCCAGCACT 41767	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	P2RX7	3'	GTCTGTAATCCCAGCGCT 10374	A	
			AGT GCTGGGATTACAGAC		
			TCG CGACCCTAATGTCTG		
			—		
GAM1192	PA2G4	3'	CTGTAATCCCAGCACT 71299	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	PCDH11X	3'	CTGTAATCCCAGCACT 52007	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	PCDH11X	3'	CTGTAATCCCAGCACT 52008	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	PCDH11Y	3'	CTGTAATCCCAGCACT 52060	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	PCDH11Y	3'	CTGTAATCCCAGCACT 52066	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	PDE4C	3'	ATGCCTATAATCCCAGCACT 6230	A	C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1192	PDE4C	3'	TGCCTGTAATCCCGGTACT 6238	G	A
			AGTA CTGGGATTACAG CA		
			TCAT GGCCCTAATGTC GT		
			— C		
GAM1192	PIK3R2	3'	ATGCCTGTAATCCCAGCACT 17256	A	A
			AGT GCTGGGATTACAG CAT		

				TCA CGACCCTAATGTC GTA		
				— C		
GAM1192	PKD2	3'	CTGTAATCCCAGCACT	60092	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	PLA2G2D	3'	ATGCCTGTAATCCCAACACT	24786	AGC	A
			AGT TGGGATTACAG CAT			
			TCA ACCCTAATGTC GTA			
			CA_ C			
GAM1192	POLK	3'	CTGTAATCCCAGCTACT	32566		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
			—			
GAM1192	PSD	5'	CTGCAATCCCAGCACT	10927	A	A
			AGT GCTGGGATT CAG			
			TCA CGACCCTAA GTC			
			— C			
GAM1192	PSMB2	3'	ATGCCTGTAATCCCAGCACT	10947	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	PSMB9	3'	CTATAATCCCAGCACT	10960	A	C
			AGT GCTGGGATTA AG			
			TCA CGACCCTAAT TC			
			— A			
GAM1192	PSMD5	3'	CTATAATCTCAGCTACTCA	17303	C	C
			A AGTAGCTGGGATTA AG			
			A TCATCGACTCTAAT TC			
			C A			
GAM1192	PTAFR	3'	CTGTAATCCCAGCACT	6294	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	PTAFR	3'	CTGTAGTCCCAGCTACTCA	6295	C	
			A AGTAGCTGGGATTACAG			
			A TCATCGACCCTGATGTC			
			C			
GAM1192	RAB3B	3'	CTGTAATCCCAGCACT	11185	A	
			AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

GAM1192 RAB7L1 3' CTGTAATCCCAGCACT 14107 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 RAB7L1 3' TGCCTGTAATCCCAGC 14110 A  
GCTGGGATTACAG CA  
||| ||||| ||  
CGACCCTAATGTC GT

C  
GAM1192 RAD51L1 5' CTGTAATCCCAGCGCT 56060 A  
AGT GCTGGGATTACAG  
||| |||||  
TCG CGACCCTAATGTC

GAM1192 RBBP5 3' ATGCCTGTAATCCCAGCTAC 17332 A  
GTAGCTGGGATTACAG CAT  
||| ||||| |||  
CATCGACCCTAATGTC GTA

C  
GAM1192 RBBP5 3' CTGTAATCCCAGCACT 17334 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 RBBP9 3' ATGCCTGTAATCCCAGCACTGT 70128 A A  
G TACAGT GCTGGGATTACAG CAT  
||| ||||| |||  
GTGTCA CGACCCTAATGTC GTA

C  
GAM1192 RBL1 3' ATGCCTATAATCCCAGCTACTT 11260 \_ C A  
G CA GTAGCTGGGATTA AG CAT  
|| ||||| || |||  
GT CATCGACCCTAAT TC GTA  
T A C

GAM1192 RBM3 3' CTGTAATCCCAGTGA CT 70487 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA TGACCCTAATGTC  
G

GAM1192 RECQL5 3' ATGTCTGTATTGGCTACTGT 14924 TG GAT  
ACAGTAGC G TACAGACAT  
||| ||| | |||||  
TGTCATCG T ATGTCTGTA  
GT \_

GAM1192 RFC2 3' CTGTAATCCCAACACT 11304 AGC  
AGT TGCGGATTACAG  
||| |||||

			TCA ACCCTAATGTC		
			CA_		
GAM1192	RPN1	5'	ATGCCTGTAATCCCAGCTACT 11389	A	
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1192	SCD	3'	ATGTCTGTTTATTAATACTACTG 17346	C	GATT
			CAGTAG TGG ACAGACAT		
			GTCATC ATT TGTCTGTA		
			A ATT_		
GAM1192	SCN2B	3'	CTGTAATCCCAGCACT 15938	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			-		
GAM1192	SIM2	3'	CTGTAATCCCAGCACT 23783	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			-		
GAM1192	SLC14A1	3'	CTGTAATCCCAGCACT 31839	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			-		
GAM1192	SLC14A2	3'	CTGTAATCCCAGCACT 23132	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			-		
GAM1192	SLC26A4	3'	ATGCCTGTAATCCCAGCACT 4783	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			C		
			-		
GAM1192	SLC28A2	3'	CTGTAATCCCAGCGCT 14869	A	
			AGT GCTGGGATTACAG		
			TCG CGACCCTAATGTC		
			-		
GAM1192	SLC2A3	3'	CTGTAATCCCAGCACT 22660	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			-		
GAM1192	SLC2A6	3'	CTGTAATCCCAGCACT 34157	A	
			AGT GCTGGGATTACAG		



TCA CGACCCTAATGTC

GAM1192 SLC31A1 3' ATGCCTGTAATCCCAGCACT 8511 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1192 SLC31A1 3' TGTAATCCCAGCTACTCA 8515 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT

GAM1192 SMG1 3' CTGTAATCCCAGCACT 30651 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 SRGAP1 5' ATGCCTGTAGTCTCAGCTACTC 72259 C A  
A AGTAGCTGGGATTACAG CAT  
| |||||  
A TCATCGACTCTGATGTC GTA  
C C

GAM1192 STAT3 3' CTGTAATCCCAGCACT 11998 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 STAT3 3' CTGTAATCCCAGCACT 57713 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 SULT1A2 3' ATGTCTGCAATCCCAGCGATTT 72215 TA\_ A  
G CAG GCTGGGATT CAGACAT  
||| |||||  
GTT CGACCCTAA GTCTGTA  
TAG C

GAM1192 SULT1A3 3' ATGTCTGCAATCCCAGCGATTT 12052 TA\_ A  
G CAG GCTGGGATT CAGACAT  
||| |||||  
GTT CGACCCTAA GTCTGTA  
TAG C

GAM1192 SULT2A1 3' ATGCCTGTAATCCCAGCACT 71751 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1192 SULT2A1 3' ATGTCTGTAATCCCAGCACT 71752 A  
AGT GCTGGGATTACAGACAT  
||| |||||

TCA CGACCCTAATGTCTGTA

—  
GAM1192 SUV39H2 3' CTGTAGTCCCAGCTACTCA 45136 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTGATGTC  
C

GAM1192 SWAP70 3' CTGTAATCCCAGCACT 71348 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 TBX6 3' CTGTAATCCCACTACTTG 54964 \_ C  
CA GTAG TGGGATTACAG  
|| ||| |||||  
GT CATC ACCCTAATGTC  
T A

GAM1192 TCF7 3' CTGTAATCCCAGCACT 12161 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 TCTA 3' CTGTAATCCCAACACT 42238 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1192 TEM7 3' CTGTAATCCCAGCACT 39884 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 TKTL1 5' ATGTCTGTCTTTCAGCCAC 24296 A GG TT  
GT GCTG A ACAGACAT  
|| ||| | |||||  
CA CGAC T TGTCTGTA  
C TT C\_

GAM1192 TM7SF3 3' CTGTAATCCCAATACTG 59666 GC  
CAGTA TGGGATTACAG  
|||| |||||  
GTCAT ACCCTAATGTC  
A\_

GAM1192 TNFRSF10A 3' ATGCCTGTAATCCCAGCACT 13886 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
— C

GAM1192 TNFRSF10D 3' ATGCCTGTAATCCCAGCACT 13860 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||

			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	TNFSF15	3'	CTGTAATCCCAACT 17592	AGC	
			AGT TGGGATTACAG		
			TCA ACCCTAATGTC		
			CA_		
GAM1192	TRIM14	3'	CTGTAATCCCAGCGCT 52635	A	
			AGT GCTGGGATTACAG		
			TCG CGACCCTAATGTC		
			—		
GAM1192	TRIM14	3'	ATGCCTGTAATCCCAGCTACT 28851		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1192	TRIM9	5'	ATGCCTGTAATCCCAGCTA 30752		A
			TAGCTGGGATTACAG CAT		
			ATCGACCCTAATGTC GTA		
			C		
GAM1192	TRPM8	3'	TGTAATCCCAGCTACTCA 43987	C	
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1192	TSN	3'	CTGTAATCCCAGCACACTG 16106	A_	
			CAGT GCTGGGATTACAG		
			GTCA CGACCCTAATGTC		
			CA		
GAM1192	TSN	3'	TGCCTGTAATTCAGT 16111	G	A
			GCTGG ATTACAG CA		
			TGACT TAATGTC GT		
			— C		
GAM1192	TSNAX	3'	CTGTAATCCCAGCACT 19998	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	TTF2	3'	TGCCTGTAATCCCGACACT 13176	AGC	A
			AGT TGGGATTACAG CA		
			TCA GCCCTAATGTC GT		
			CA_ C		
GAM1192	UBE2G2	3'	CTGCAATCCCAGCACT 64855	A	A
			AGT GCTGGGATT CAG		

			TCA CGACCCTAA GTC		
			— C		
GAM1192	UBE2G2	3'	CTGTAGTCTCAGCTACTCA 64856	C	
			A AGTAGCTGGGATTACAG		
			A TCATCGACTCTGATGTC		
			C		
GAM1192	UC28	3'	ATGCCTGTAATCCCAGCTACT 41288		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1192	UC28	3'	CTGTAATCCCAGCACT 41290	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	UPK1B	3'	ATGCCTGTAATCCCAGCACT 22715	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			C		
GAM1192	USP14	3'	CTGTAATCCCAGCACT 17658	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	VDR	3'	TGTAATCCCAGCTACTCA 4574	C	
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1192	VHL	3'	ATGCCTGTAATCCCAGC 5058		A
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1192	VHL	3'	ATGCCTGTAATCCCAGCACT 5059	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			C		
			—		
GAM1192	VHL	3'	ATGCCTGTAATCCTAGCTACTC 5060	C	A
	A		A AGTAGCTGGGATTACAG CAT		
			A TCATCGATCCTAATGTC GTA		
			C C		
GAM1192	VHL	3'	CTGTAATCCCAGCACT 5069	A	
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

		—		
GAM1192	VHL	3' TCTGTAATCCTAGCTACT	5090	
		AGTAGCTGGGATTACAGA		
		TCATCGATCCTAATGTCT		
GAM1192	VPS41	3' ATGCCTGTAATCCCAGCTACT	26921	A
		AGTAGCTGGGATTACAG CAT		
		TCATCGACCCTAATGTC GTA		
		C		
GAM1192	WIG1	3' CTGTAATCCCAGCACT	94466	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
GAM1192	WSX1	3' CTGTAATCCCAGCACT	16732	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
GAM1192	ZNF136	3' CTGTAATCCCAGCACT	59888	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
GAM1192	ZNF137	3' CTGTAATCCCAGCACT	12862	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
GAM1192	ZNF14	3' ATGCCTCTAATCCCAGCTACTC	40713	C
	A	A AGTAGCTGGGATTA AG CAT		C A
		A TCATCGACCCTAAT TC GTA		
		C C C		
GAM1192	ZNF36	3' CTGTAATCCCAGCACT	93962	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
GAM1192	ZNF74	3' ATGTCCCTGTGGTCCCAGCTAC	12790	C
	TCA	A AGTAGCTGGGATTACA GACAT		—
		A TCATCGACCCTGGTGT CTGTA		
		C CC		
GAM1192	ZNF74	3' CTGTAATCTTAACACTGTG	12795	AGC
		TACAGT TGGGATTACAG		

GTGTCA ATTCTAATGTC  
 CA\_  
 GAM1192 AF020591 3' ATGCCTGTAATCCCAGCACTCT 27135 TA\_ A  
 G CAG GCTGGGATTACAG CAT  
 ||| |||||  
 GTC CGACCCTAATGTC GTA  
 TCA C  
 GAM1192 AF020591 3' CTGTAATCCCAGCACT 27139 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 -  
 GAM1192 AF020591 3' CTGTAGTCCCAGCTACTCA 27140 C  
 A AGTAGCTGGGATTACAG  
 | |||||  
 A TCATCGACCCTGATGTC  
 C  
 GAM1192 AKAP11 3' CTGTAATCCCAGAACTCTG 57831 TAG\_  
 CAG CTGGGATTACAG  
 ||| |||||  
 GTC GACCCTAATGTC  
 TCAA  
 GAM1192 AKR1D1 3' ATGCCTATAATCCCAGCACT 19972 A C A  
 AGT GCTGGGATTA AG CAT  
 ||| ||||| || |||  
 TCA CGACCCTAAT TC GTA  
 - A C  
 GAM1192 AKR1D1 3' TGTAATCCCAGCTACTCA 19978 C  
 A AGTAGCTGGGATTACA  
 | |||||  
 A TCATCGACCCTAATGT  
 C  
 GAM1192 APOF 3' CTGTAATCCCAGCACTGTG 7909 A  
 TACAGT GCTGGGATTACAG  
 ||||| |||||  
 GTGTCA CGACCCTAATGTC  
 -  
 GAM1192 APXL2 3' CTGTAATCCCAGCACT 75189 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 -  
 GAM1192 ARNTL2 3' ATGCCTGTAATCCCAGCACT 39454 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||  
 TCA CGACCCTAATGTC GTA  
 - C  
 GAM1192 ARNTL2 3' CTGTAATCCCAACTGCT 39462 C  
 AGTAG TGGGATTACAG  
 ||||| |||||

			TCGTC ACCCTAATGTC		
			A		
GAM1192	ARNTL2	3'	CTGTAATCCCAGTACT	39463	G
			AGTA CTGGGATTACAG		
			TCAT GACCCTAATGTC		
			—		
GAM1192	BANP	3'	ATGCCTGTAATCCCAGC	66214	A
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1192	BFAR	3'	CTGTAATCCCAGCTACTTG	60771	—
			CA GTAGCTGGGATTACAG		
			GT CATCGACCCTAATGTC		
			T		
GAM1192	BIA2	3'	CTGTAATCCCAGCACT	71281	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	BIRC1	3'	CTGTAATCCCAGCACT	15788	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	BLOV1	3'	CTGTAATCCCAGCACT	76280	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	BLOV1	3'	CTGTAATCCCAGCTACTTG	76281	—
			CA GTAGCTGGGATTACAG		
			GT CATCGACCCTAATGTC		
			T		
GAM1192	BLOV1	3'	ATGCCTGTAATCCCAGCTACT	76277	A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1192	BNIP-S	3'	GTCTGTAATCCCAGCACT	56274	A
			AGT GCTGGGATTACAGAC		
			TCA CGACCCTAATGTCTG		
			—		
GAM1192	C13orf1	3'	CTGTAATCCCAGCACT	39969	A
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1192 C1orf24 3' CTATAATCCCAGCACT 53714 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC

GAM1192 C1QTNF2 3' ATGCCTATAATCCCAGGACT 49124 AG C A  
AGT CTGGGATTA AG CAT  
||| ||||| || |||  
TCA GACCCTAAT TC GTA

GAM1192 C20orf108 3' CTGTAATCCCAGCACT 55045 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

GAM1192 C20orf12 3' ATGCCTGTAATCCCAGTTACT 36321 A  
AGTAGCTGGGATTACAG CAT  
||||| ||||| |||  
TCATTGACCCTAATGTC GTA  
C

GAM1192 C20orf12 3' CTGTAATCCCAGCACT 36322 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

GAM1192 C20orf130 3' GTGGCTGTCCCAGCCAC 61758 A TTA A  
GT GCTGGGA CAG CAT  
|| ||||| ||| |||  
CA CGACCCT GTC GTG  
C \_ G

GAM1192 C20orf142 3' CTGTAATCCCAGCTACT 74775  
AGTAGCTGGGATTACAG  
||||| ||||| |||||  
TCATCGACCCTAATGTC

GAM1192 C20orf175 3' CTGTAATCCCAACACT 55064 AGC  
AGT TGGGATTACAG  
||| ||||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1192 C20orf177 3' ATGCCTGTAATCCCAGCTACT 62143 A  
AGTAGCTGGGATTACAG CAT  
||||| ||||| ||||| |||  
TCATCGACCCTAATGTC GTA  
C

GAM1192 C20orf177 3' CTGTAATCCCAGCACT 62146 A  
AGT GCTGGGATTACAG  
||| ||||| ||||| |||||



TCA CGACCCTAATGTC

—  
GAM1192 C20orf183 3' CTGTAATCCCAGCACT 47803 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 C20orf29 3' CTGTAATCCCAGCACT 37126 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 C21orf108 3' CTATAATCCCAGCACT 88720 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC  
— A

—  
GAM1192 C22orf19 3' GTCTGTAATCCCAGCACT 13429 A  
AGT GCTGGGATTACAGAC  
||| |||||  
TCA CGACCCTAATGTCTG

—  
GAM1192 C22orf20 3' ATGCCTGTAATCCCAGCTATT 47425 A  
AGTAGCTGGGATTACAG CAT  
||||| |||  
TTATCGACCCTAATGTC GTA  
— C

—  
GAM1192 C2F 3' CTGTAATCCCAGCACT 20928 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 C6orf10 5' CTGTAATCCCATCATTTGCT 22289 C\_\_\_  
AGTAG TGGGATTACAG  
|||| |||||  
TCGTT ACCCTAATGTC  
TACT

—  
GAM1192 C6orf5 3' CTGTAATCCCAGCACT 31346 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 C6orf5 3' CTGTAATCCCAGCACT 31347 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 C8orf2 3' CTGTAATCCCAGCACT 23163 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1192 C9orf5 3' TCTGTAATCCCAGCACT 49284 A  
AGT GCTGGGATTACAGA  
||| |||||  
TCA CGACCCTAATGTCT

GAM1192 CALN1 3' CTATAATCCCAGCACT 48866 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC

GAM1192 CAMKK2 5' CTGTAATCCCAGCACT 21582 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 CBCIP2 3' CTGTAATCCCAGCACT 51590 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 cerk 3' CTGTAATCCCAGCACT 42846 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 CFLAR 3' CTGTAATCCCAGCACT 13929 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 CG012 5' ATGCCTATATTCTAGCTACTCA 83214 C TAC A  
A AGTAGCTGGGAT AG CAT  
| ||||| || |||  
A TCATCGATCTTA TC GTA  
C TA\_ C

GAM1192 CG012 5' ATGCCTGTAATCCCAACACT 83215 AGC A  
AGT TGGGATTACAG CAT  
||| ||||| |||  
TCA ACCCTAATGTC GTA  
CA\_ C

GAM1192 CG012 5' CTGTAATCCCAGCTATTCGGCT 83219  
G CAGT AGCTGGGATTACAG  
||| |||||  
GTCG TCGACCCTAATGTC  
GCTTA

GAM1192 CGI-203 3' TGTAATCCCAGCTACTCA 39904 C  
A AGTAGCTGGGATTACA  
| |||||

A TCATCGACCCTAATGT  
 C  
 GAM1192 CHR7A 3' ATGCTTGTAAATCCCAGCTACTC 95017 C GA  
 A A AGTAGCTGGGATTACA CAT  
 I ||||| ||||| |||  
 A TCATCGACCCTAATGT GTA  
 C TC  
 GAM1192 CLDN15 3' ATGCCTGTAATCCCAGCACT 56558 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| ||||| |||  
 TCA CGACCCTAATGTC GTA  
 C  
 GAM1192 CNNM4 3' TCTGTTGTCAACTGCTGTA 39484 CTGG T  
 TACAGTAG GAT ACAGA  
 ||||| ||| |||||  
 ATGTCGTC CTG TGTCT  
 AA\_ T  
 GAM1192 COE2 3' ATGCCTGTAATCCCAGCTACTT 64247 \_ A  
 G CA GTAGCTGGGATTACAG CAT  
 || ||||| ||||| |||  
 GT CATCGACCCTAATGTC GTA  
 T C  
 GAM1192 COE2 3' CTGTAATCCCAGCACT 64251 A  
 AGT GCTGGGATTACAG  
 ||| ||||| |||||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1192 CPR2 3' CTGTAATCCCAGCACT 48095 A  
 AGT GCTGGGATTACAG  
 ||| ||||| |||||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1192 CPR2 3' CTGTAATCCCAGCTACTCA 48096 C  
 A AGTAGCTGGGATTACAG  
 I ||||| ||||| |||||  
 A TCATCGACCCTAATGTC  
 C  
 GAM1192 CSAD 3' CTGTAATCCCAGCACT 32028 A  
 AGT GCTGGGATTACAG  
 ||| ||||| |||||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1192 D21S2056E 3' ATGCCTGTAATCCCAGCTACT 13467 A  
 AGTAGCTGGGATTACAG CAT  
 ||||| ||||| ||||| |||  
 TCATCGACCCTAATGTC GTA  
 C  
 GAM1192 D21S2056E 3' CTGTAATCCCAGCACT 13470 A  
 AGT GCTGGGATTACAG  
 ||| ||||| |||||

TCA CGACCCTAATGTC

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GAM1192 DCOHM  3' CTGTAATCCCTGCACT    49600  A T
      AGT GC GGGATTACAG
      ||| || |||||
      TCA CG CCCTAATGTC
      - T
GAM1192 DDX34  3' CTGTAATCCCAGCACT    27982  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1192 DEGS  3' ATGCCTGTAATCCCAGCTACAT 58613  _      A
      G      CA GTAGCTGGGATTACAG CAT
      || ||||| |||
      GT CATCGACCCTAATGTC GTA
      A      C
GAM1192 DEGS  3' ATGCCTATAATCCCAGCACT    13409  A      C A
      AGT GCTGGGATTA AG CAT
      ||| ||||| || |||
      TCA CGACCCTAAT TC GTA
      -      A C
GAM1192 DEGS  3' ATGCCTGTAATCCCAGCTACAT 13410  _      A
      G      CA GTAGCTGGGATTACAG CAT
      || ||||| |||
      GT CATCGACCCTAATGTC GTA
      A      C
GAM1192 DIS3  3' ATGCCTGTAATCCCAGCTACTT 30227  _      A
      G      CA GTAGCTGGGATTACAG CAT
      || ||||| |||
      GT CATCGACCCTAATGTC GTA
      T      C
GAM1192 DKFZP434B168 3' CTGTAATCCCAGCACT    31253  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1192 DKFZP434C171 3' CTGTAATCCCAGCACT    31553  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1192 DKFZP434C1715 3' CTGTAATCCCAGCAC    86148  A
      GT GCTGGGATTACAG
      || |||||
      CA CGACCCTAATGTC

      -
GAM1192 DKFZp434E0519 3' CTATAATCCCAGCACT    49986  A      C
      AGT GCTGGGATTA AG
      ||| ||||| ||
```

TCA CGACCCTAAT TC  
 — A  
 GAM1192 DKFZp434E2220 5' TGTAATCCCAGCTACTCA 34304 C  
 A AGTAGCTGGGATTACA  
 | |||||  
 A TCATCGACCCTAATGT  
 C  
 GAM1192 DKFZP434F091 3' TGTAATCCCAACTACTCA 31284 C C  
 A AGTAG TGGGATTACA  
 | |||| |||||  
 A TCATC ACCCTAATGT  
 C A  
 GAM1192 DKFZp434G171 3' ATGCCTGTAATCCCAGCACT 79431 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||  
 TCA CGACCCTAATGTC GTA  
 — C  
 GAM1192 DKFZp434G171 3' TGTAATCCCAGCTACTCA 79440 C  
 A AGTAGCTGGGATTACA  
 | |||||  
 A TCATCGACCCTAATGT  
 C  
 GAM1192 DKFZP434I1735 3' CTGTAATCCCAGCTACT 87801  
 AGTAGCTGGGATTACAG  
 |||||  
 TCATCGACCCTAATGTC  
  
 GAM1192 DKFZP434L187 5' CTGTAATCCCAGCTACT 68804  
 AGTAGCTGGGATTACAG  
 |||||  
 TCATCGACCCTAATGTC  
  
 GAM1192 DKFZP434N1511 3' ATGCCTGTAATCCCAGCACT 91415 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||  
 TCA CGACCCTAATGTC GTA  
 — C  
 GAM1192 DKFZP434N161 3' GTCTGTAATCCCAGCACT 78522 A  
 AGT GCTGGGATTACAGAC  
 ||| |||||  
 TCA CGACCCTAATGTCTG  
 —  
 GAM1192 DKFZp547C176 3' CTGTAATCCCAGCACT 67222 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1192 DKFZp547I094 3' CTGTAATCCCAGCACT 49639 A  
 AGT GCTGGGATTACAG  
 ||| |||||

TCA CGACCCTAATGTC

—  
GAM1192 DKFZp547I094 3' CTGTAGTCACAGCTACT 49640 G  
AGTAGCTG GATTACAG  
||||||| |||||||  
TCATCGAC CTGATGTC

A

GAM1192 DKFZP564B1023 3' ATGCCTGTAATCCCAGCTACT 48536 A  
AGTAGCTGGGATTACAG CAT  
||||||| |||||  
TCATCGACCCTAATGTC GTA

C

GAM1192 DKFZP564B1023 3' CTGTAATCCCAGCACT 48538 A  
AGT GCTGGGATTACAG  
||| |||||||  
TCA CGACCCTAATGTC

—  
GAM1192 DKFZP564I052 3' CTGTAATCCCAGCACT 66707 A  
AGT GCTGGGATTACAG  
||| |||||||  
TCA CGACCCTAATGTC

—  
GAM1192 DKFZP564M182 3' CTGTAATCCCAGCACT 78033 A  
AGT GCTGGGATTACAG  
||| |||||||  
TCA CGACCCTAATGTC

—  
GAM1192 DKFZP564M182 3' CTGTAATCCCAGCTACT 78034  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1192 DKFZp566H0824 3' CTGTAATCCCAGCACTTTA 34050 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||||  
AT TCA CGACCCTAATGTC

T —

GAM1192 DKFZP586C1324 3' ATGCCTGTAATCCCAGCACT 69796 A A  
AGT GCTGGGATTACAG CAT  
||| ||||||| |||  
TCA CGACCCTAATGTC GTA

C

—  
GAM1192 DKFZP586M1120 3' CTGTAATCCCAGCACT 48457 A  
AGT GCTGGGATTACAG  
||| |||||||  
TCA CGACCCTAATGTC

—  
GAM1192 DKFZP667O116 3' TGCCTATAATCCCGGCACT 94287 A C A  
AGT GCTGGGATTA AG CA  
||| ||||||| || ||

			TCA CGGCCCTAAT TC GT			
			— A C			
GAM1192	DKFZP761E2110	3'	ATGCCTGTAATCCCAGCAC	48224	A	A
			GT GCTGGGATTACAG CAT			
			CA CGACCCTAATGTC GTA			
			— C			
GAM1192	DKFZP761G1913	3'	ATGCCTGTAATCCCAGCACT	48909	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	DKFZP761G1913	3'	CTGTAATCCCAGCTACTTG	48913	—	
			CA GTAGCTGGGATTACAG			
			GT CATCGACCCTAATGTC			
			T			
GAM1192	DKFZp761J139	5'	CTGTAATCCCAGCACT	50108	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	DRF1	3'	CTATAATCCCAGCACT	47030	A	C
			AGT GCTGGGATTA AG			
			TCA CGACCCTAAT TC			
			— A			
GAM1192	DRF1	3'	CTGTAATCCCAGCACT	47032	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	DRF1	3'	TGTAATCCCAGCTACTCA	47038	C	
			A AGTAGCTGGGATTACA			
			A TCATCGACCCTAATGT			
			C			
GAM1192	FADS1	3'	ATGCCTGTAATCCCAACACT	25473	AGC	A
			AGT TGGGATTACAG CAT			
			TCA ACCCTAATGTC GTA			
			CA_ C			
GAM1192	FADS1	3'	CTGTAATCCCAGCTAC	25476		
			GTAGCTGGGATTACAG			
			CATCGACCCTAATGTC			
GAM1192	FBXO27	3'	ATGCCTGTAATCCCAGCACT	74504	A	A
			AGT GCTGGGATTACAG CAT			

TCA CGACCCTAATGTC GTA  
 — C  
 GAM1192 FBXO27 3' CTGTAATCCCTGCACT 74508 A T  
 AGT GC GGGATTACAG  
 ||| || |||||  
 TCA CG CCCTAATGTC  
 — T  
 GAM1192 FBXO6 3' CTGTAATCCCAGCACT 37383 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1192 FBXO9 3' ATGCCTATAATCCCAGCACT 53100 A C A  
 AGT GCTGGGATTA AG CAT  
 ||| ||||| || |||  
 TCA CGACCCTAAT TC GTA  
 — A C  
 GAM1192 FBXO9 3' CTATAATCCCAATACT 53102 GC C  
 AGTA TGGGATTA AG  
 ||| ||||| ||  
 TCAT ACCCTAAT TC  
 A\_ A  
 GAM1192 FKBP14 3' ATGCCTGTAATCCCAGCACT 35622 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||  
 TCA CGACCCTAATGTC GTA  
 — C  
 GAM1192 FKBP14 3' ATGCCTGTAATCCCAGCACT 35623 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||  
 TCA CGACCCTAATGTC GTA  
 — C  
 GAM1192 FKSG17 3' CTGTAATCCCAGTTACTCA 49329 C  
 A AGTAGCTGGGATTACAG  
 | |||||  
 A TCATTGACCCTAATGTC  
 C  
 GAM1192 FLJ00060 3' ATGTCTGTAATCCCAGCACTCT 61091 TA\_  
 G CAG GCTGGGATTACAGACAT  
 ||| |||||  
 GTC CGACCCTAATGTCTGTA  
 TCA  
 GAM1192 FLJ10008 3' GTCTGTAATCCCAGCACT 35729 A  
 AGT GCTGGGATTACAGAC  
 ||| |||||  
 TCA CGACCCTAATGTCTG  
 —  
 GAM1192 FLJ10043 3' CTGTAATCCCAGCACT 35758 A  
 AGT GCTGGGATTACAG  
 ||| |||||



TCA CGACCCTAATGTC

GAM1192 FLJ10043 3' CTGTAATCCCAGCTACT 35759  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1192 FLJ10058 3' ATGCCTGTAATCCCAGCACT 35782 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1192 FLJ10244 3' ATGCCTGTAATCCCAGCTGCT 35940 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCGTCGACCCTAATGTC GTA

GAM1192 FLJ10460 3' CTGTAATCCCAACACT 36127 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1192 FLJ10460 3' CTGTAATCCCAGCACT 36128 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 FLJ10460 3' CTGTAATCCCAGCTACTTG 36129 \_  
CA GTAGCTGGGATTACAG  
|| |||||  
GT CATCGACCCTAATGTC  
T

GAM1192 FLJ10547 3' CTGTAATCCCAGCACT 36267 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 FLJ10607 3' CTGTAATCCCAGCACT 77113 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 FLJ10607 3' CTGTAATCCCAGCTACTCA 77114 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
C

GAM1192 FLJ10613 3' GTCTGTAATCCCAGCACT 38825 A  
AGT GCTGGGATTACAGAC  
||| |||||

TCA CGACCCTAATGTCTG

—  
GAM1192 FLJ10650 3' CTGTAATCCCAGCACT 36382 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 FLJ10704 3' ATGCCTGTAATCCCAGCTACT 36449 A  
AGTAGCTGGGATTACAG CAT  
||||||| |||  
TCATCGACCCTAATGTC GTA

C  
GAM1192 FLJ10781 3' CTGTAATCCCAGCACT 36631 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 FLJ10781 3' TGTAATCCCAGCTACTCA 36638 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1192 FLJ10803 3' CTGTAATCCCAGCACT 36664 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 FLJ10826 3' ATGCCTGTAATCCCAGCTACT 36700 A  
AGTAGCTGGGATTACAG CAT  
||||||| |||  
TCATCGACCCTAATGTC GTA  
C

GAM1192 FLJ10830 3' ATGCCTGTAGTCCCAGCCACTC 36717 C A A  
A A AGT GCTGGGATTACAG CAT  
| ||| ||||| |||  
A TCA CGACCCTGATGTC GTA  
C C C

GAM1192 FLJ10830 3' ATGCCTGTAGTTCCAGCTACTC 36718 C A  
A A AGTAGCTGGGATTACAG CAT  
| ||||| |||  
A TCATCGACCTTGATGTC GTA  
C C

GAM1192 FLJ10989 3' CTGTAATCCCAGCACT 36949 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 FLJ10997 3' TGCCTGACCACCTACTGTA 36957 C GATTA A  
TACAGTAG TGG CAG CA  
||||| ||| ||| ||

			ATGTCATC ACC	GTC GT		
			C A	C		
GAM1192	FLJ11029	3'	CTGTAATCCCAGCACT	60975	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	FLJ11036	3'	CTGCGGTTCCAGCTACTCA	36998	C	TA
			A AGTAGCTGGGAT CAG			
			A TCATCGACCTTG GTC			
			C GC			
GAM1192	FLJ11042	3'	ATGCCTGTAATCCCAGCACT	37004	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	FLJ11126	3'	ATGCCTATAATCCCAGCAC	37083	A	C A
			GT GCTGGGATTA AG CAT			
			CA CGACCCTAAT TC GTA			
			— A C			
GAM1192	FLJ11136	3'	CTGTAATCCCAGCACT	37093	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	FLJ11151	3'	CTGTAATCCCAGCACT	67874	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	FLJ11151	3'	CTGTAATCCCAGCTACT	67875		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
			—			
GAM1192	FLJ11267	3'	ATGCCTGTAATCCCAGCACT	39003	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	FLJ11370	3'	ATGCCTGTAATCCCAGCTACT	46370		A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1192	FLJ11637	3'	CTGTAATCCCAGCACT	46380	A	
			AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

GAM1192 FLJ11700 3' CTGTAATCCCAGCACT 46038 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 FLJ11700 3' CTGTAATCCCAGCTACTCA 46039 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
C

GAM1192 FLJ11710 5' ATGCCTGTAGTCCCAGCTACTC 45825 C A  
A AGTAGCTGGGATTACAG CAT  
| ||||| |||  
A TCATCGACCCTGATGTC GTA  
C C

GAM1192 FLJ11722 3' ATGCCTGTAATCCCAGGACT 46389 AG A  
AGT CTGGGATTACAG CAT  
||| ||||| |||  
TCA GACCCTAATGTC GTA  
G\_ C

GAM1192 FLJ11722 3' CTGTAATCCCAGCTACT 46391  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1192 FLJ11722 3' TGTAATCCCAGCTACTCA 46401 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1192 FLJ11726 3' CTGTAATCCCAGCACT 46411 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 FLJ11996 3' ATGCCTGTAATCCCAGCTACT 46434 A  
AGTAGCTGGGATTACAG CAT  
||||||| |||  
TCATCGACCCTAATGTC GTA  
C

GAM1192 FLJ12056 3' ATGCCTATAATCCCAACACT 46251 AGC C A  
AGT TGGGATTA AG CAT  
||| ||||| |||  
TCA ACCCTAAT TC GTA  
CA\_ A C

GAM1192 FLJ12056 3' ATGCCTGTAATCCCAGCTATT 46252 A  
AGTAGCTGGGATTACAG CAT  
||||||| |||

TTATCGACCCTAATGTC GTA  
 C  
 GAM1192 FLJ12122 3' CTGTAATCCCAGCACT 46462 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1192 FLJ12178 3' GTCTGTAATCCCAGCACT 47103 A  
 AGT GCTGGGATTACAGAC  
 ||| |||||  
 TCA CGACCCTAATGTCTG  
 —  
 GAM1192 FLJ12294 3' CTATAATCCCAGCTACT 47012 C  
 AGTAGCTGGGATTA AG  
 ||||| ||  
 TCATCGACCCTAAT TC  
 A  
 GAM1192 FLJ12294 3' CTGTAATCCCAGCACT 47013 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1192 FLJ12331 3' CTATAATCCCAGCACTTTA 46478 C A C  
 TA AGT GCTGGGATTA AG  
 || ||| ||||| ||  
 AT TCA CGACCCTAAT TC  
 T \_ A  
 GAM1192 FLJ12363 3' CTGTAATCCCAGCACT 49679 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1192 FLJ12547 3' CTGTAATCCCAGCACTGTG 46491 A  
 TACAGT GCTGGGATTACAG  
 ||||| |||||  
 GTGTCA CGACCCTAATGTC  
 —  
 GAM1192 FLJ12606 3' CTGTAATCCCAGCACT 45640 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1192 FLJ12618 3' ATGCCTGTAATCTCAGCTACTC 45994 C A  
 A  
 A AGTAGCTGGGATTACAG CAT  
 | ||||| |||  
 A TCATCGACTCTAATGTC GTA  
 C C  
 GAM1192 FLJ12660 3' CTGTAATCCCAGCACT 47141 A  
 AGT GCTGGGATTACAG  
 ||| |||||

TCA CGACCCTAATGTC

—  
GAM1192 FLJ12660 3' CTGTAATCCCAGCTACT 47142  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1192 FLJ12666 3' CTGTAATCCCAGCACT 44767 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 FLJ12800 3' CTGTAATCCCAGCACT 43232 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 FLJ12949 3' ATGCCTGTAGTCCCAGCTACTC 43442 C A  
A A AGTAGCTGGGATTACAG CAT  
| ||||| |||  
A TCATCGACCCTGATGTC GTA  
C C

GAM1192 FLJ12949 3' CTGTAATCCCAGCACT 43445 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 FLJ12985 3' CTGTAATCCCAGCACT 46240 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 FLJ13117 3' ATGCCTGTAATCCCAGCACT 43539 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

—  
GAM1192 FLJ13162 3' ATGCCTGTAATCCCAGCTACT 46550 A  
AGTAGCTGGGATTACAG CAT  
||||| |||  
TCATCGACCCTAATGTC GTA  
C

GAM1192 FLJ13162 3' CTGTAATCCCAGCACT 46556 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 FLJ13193 3' ATGCCTATAATCCCGGCTACT 49758 C A  
AGTAGCTGGGATTA AG CAT  
||||| |||

			TCATCGGCCCTAAT TC GTA		
			A C		
GAM1192	FLJ13193	3'	CTGTAATCCCAACACTTTA 49765	C	AGC
			TA AGT TGGGATTACAG		
			AT TCA ACCCTAATGTC		
			T CA_		
GAM1192	FLJ13193	3'	CTGTAATCCCAGCACT 49766	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	FLJ13305	3'	ATGCCTGTAATCCCAGC 90125	A	
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1192	FLJ13448	3'	CTGTAATCCCAGTTACT 47135		
			AGTAGCTGGGATTACAG		
			TCATTGACCCTAATGTC		
			—		
GAM1192	FLJ13456	3'	CTGTAATCCCAGCACT 65936	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	FLJ13456	3'	CTGTAATCCCAGCTACTCA 65937	C	
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTAATGTC		
			C		
GAM1192	FLJ13614	3'	CTGTAATCCCAGCACT 57451	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	FLJ13659	3'	ATGCCTGTAATCCCAGCTACT 47243	A	
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1192	FLJ13659	3'	CTGTAATCCCAGCACT 47246	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	FLJ13769	3'	ATGCCTATAATCCCAGCACT 46600	A	C A
			AGT GCTGGGATTA AG CAT		

				TCA CGACCCTAAT TC GTA		
				— A C		
GAM1192	FLJ13769	3'	CTGTAATCCCAGCACT	46608	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	FLJ13848	3'	CTGTAATCCCAGCACT	45465	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	FLJ13910	3'	CTGCATTTTAGCTCTG	42927	T	TA
			CAG AGCTGGGAT CAG			
			GTC TCGATTTTA GTC			
			— C_			
GAM1192	FLJ13952	3'	ATGCCTGTAACCCCAGCTACT	45613	A	A
			AGTAGCTGGG TTACAG CAT			
			TCATCGACCC AATGTC GTA			
			C C			
GAM1192	FLJ13952	3'	ATGCCTGTAATCCCAGCACT	45614	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	FLJ13984	3'	CTGTGGTCCCAGCTACTCA	45448	C	
			A AGTAGCTGGGATTACAG			
			A TCATCGACCCTGGTGTC			
			C			
GAM1192	FLJ14100	3'	CTGTAATCCCAGCACT	46679	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	FLJ14107	3'	ATGCCTGTAATCCCAGCACT	46689	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	FLJ14117	3'	ATGCCTGTAGTCCCAGCTACTC	42901	C	A
	A		A AGTAGCTGGGATTACAG CAT			
			A TCATCGACCCTGATGTC GTA			
			C C			
GAM1192	FLJ14117	3'	CTGTAATACCAGCTACTCA	42907	C	G
			A AGTAGCTGG ATTACAG			



			A TCATCGACC TAATGTC		
			C A		
GAM1192	FLJ14117	3'	CTGTAATCCCAGCACT	42908	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	FLJ14225	3'	CTGTAATCCCAGCACT	45902	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	FLJ14251	3'	CTGTAATCCCAGCACT	45970	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	FLJ14326	3'	ATGCCTATAATCCCAGCTACT	49799	C A
			AGTAGCTGGGATTA AG CAT		
			TCATCGACCCTAAT TC GTA		
			A C		
GAM1192	FLJ14326	3'	ATGCCTGTAATCCCAGC	49800	A
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1192	FLJ14327	3'	ATGCCTGTAATCCCAGCACT	46129	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			C		
			—		
GAM1192	FLJ14345	3'	CTGTAATCCCAGCACT	45334	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	FLJ14345	3'	CTGTAATCCCAGCTACT	45335	
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
			—		
GAM1192	FLJ14346	3'	CTGTAATCCCAGCACT	46709	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	FLJ14346	3'	CTGTAATCCCAGCACT	46710	A
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

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      -
GAM1192 FLJ14397 3' ATGCCTGTAACCCCAGCTACT 51323      A      A
      AGTAGCTGGG TTACAG CAT
      ||||| ||||| |||
      TCATCGACCC AATGTC GTA
      C      C
GAM1192 FLJ14397 3' CTATAATCCCAGCACT 51325      A      C
      AGT GCTGGGATTA AG
      || ||||| ||
      TCA CGACCCTAAT TC
      -      A
GAM1192 FLJ14621 3' CTGTAATCCCAGCACT 51470      A
      AGT GCTGGGATTACAG
      || ||||| |||
      TCA CGACCCTAATGTC
      -
GAM1192 FLJ14642 3' ATGCCTGTAATCCCAGCACT 51493      A      A
      AGT GCTGGGATTACAG CAT
      || ||||| |||
      TCA CGACCCTAATGTC GTA
      -      C
GAM1192 FLJ14642 3' CTGTAATCCCAGCACT 51499      A
      AGT GCTGGGATTACAG
      || ||||| |||
      TCA CGACCCTAATGTC
      -
GAM1192 FLJ14888 3' ATGCCTGTAATCCCAGCACT 51679      A      A
      AGT GCTGGGATTACAG CAT
      || ||||| |||
      TCA CGACCCTAATGTC GTA
      -      C
GAM1192 FLJ20004 3' ATGCCTGTAATCCCAGCACT 34312      A      A
      AGT GCTGGGATTACAG CAT
      || ||||| |||
      TCA CGACCCTAATGTC GTA
      -      C
GAM1192 FLJ20004 3' CTGTAATCCCAGCACT 95292      A
      AGT GCTGGGATTACAG
      || ||||| |||
      TCA CGACCCTAATGTC
      -
GAM1192 FLJ20004 3' TGCCTGTAATCCCAGCTACT 95301      A
      AGTAGCTGGGATTACAG CA
      ||||| ||| ||
      TCATCGACCCTAATGTC GT
      C
GAM1192 FLJ20006 3' CTGTAATCCCAGCACT 34320      A
      AGT GCTGGGATTACAG
      || ||||| |||
```

TCA CGACCCTAATGTC

—  
GAM1192 FLJ20006 3' CTGTAATCCCAGCTACT 34321  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1192 FLJ20034 3' CTGTAATCCCAGCACT 34371 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 FLJ20055 3' CTGAAGTCCCAGCTACTCA 34440 C A  
A AGTAGCTGGGATT CAG  
| ||||| |||  
A TCATCGACCCTGA GTC  
C A

GAM1192 FLJ20055 3' CTGTAATCCCAGCACTTTA 34441 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||  
AT TCA CGACCCTAATGTC  
T —

GAM1192 FLJ20059 3' ATGCCTGTAATCCCAGCACT 34446 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
— C

GAM1192 FLJ20071 3' ATGCCTATAATCCCAGCTACTT 34479 — C A  
G CA GTAGCTGGGATTA AG CAT  
|| ||||| || |||  
GT CATCGACCCTAAT TC GTA  
T A C

GAM1192 FLJ20081 3' CTGTAATCCCAGCACT 34507 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 FLJ20139 3' CTGTAATCCCAACACT 34624 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1192 FLJ20174 3' CTGTAATCCCAAAGTGCTG 34688 GC\_  
CAGTA TGGGATTACAG  
|||| |||||  
GTCGT ACCCTAATGTC  
GAA

GAM1192 FLJ20200 3' TGCCTGTAATCCCTGCACT 34729 A T A  
AGT GC GGGATTACAG CA  
||| || ||||| ||

				TCA CG CCCTAATGTC GT		
				— T C		
GAM1192	FLJ20211	3'	CTGTAATCCCAGCACT	34751	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	FLJ20280	3'	CTGTAATCCCAGCACT	34849	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	FLJ20280	3'	CTGTAATCCCTGCTACT	34850	T	
			AGTAGC GGGATTACAG			
			TCATCG CCCTAATGTC			
			T			
GAM1192	FLJ20340	3'	ATGCCTGTAATCCCAGCATTTT	34972	TA_	A
	G		CAG GCTGGGATTACAG CAT			
			GTT CGACCCTAATGTC GTA			
			TTA C			
GAM1192	FLJ20340	3'	TGTAATCCCAGCTACTCA	34979	C	
			A AGTAGCTGGGATTACA			
			A TCATCGACCCTAATGT			
			C			
GAM1192	FLJ20359	3'	ATGCCTGTAATCCCAGCACT	35035	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			C			
GAM1192	FLJ20452	3'	ATGCCTGTAATCCCAGCACT	35196	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			C			
GAM1192	FLJ20464	3'	ATGCCTATAATCCGAGCTACT	35228	G	C A
			AGTAGCT GGATTA AG CAT			
			TCATCGA CCTAAT TC GTA			
			G A C			
GAM1192	FLJ20464	3'	ATGCCTGTAATCCCAGCACT	35229	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			C			
GAM1192	FLJ20464	3'	ATGCCTGTAATCTCAGCTACT	35230		A
			AGTAGCTGGGATTACAG CAT			

[illegible]

TCA CGACCCTAATGTC

GAM1192 FLJ21144 3' ATGCCTGTAATCCCAGCACT 42875 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1192 FLJ21162 3' ATGCCTATAATCCCAGCACT 45892 A C A  
AGT GCTGGGATTA AG CAT  
||| ||||| ||  
TCA CGACCCTAAT TC GTA

GAM1192 FLJ21162 3' CTATAAACCCAGCTACTCA 45894 C A C  
A AGTAGCTGGG TTA AG  
| ||||| ||  
A TCATCGACCC AAT TC  
C A A

GAM1192 FLJ21240 3' ATGCCTGTAATATCAGCTACTC 45837 C GG A  
A A AGTAGCTG ATTACAG CAT  
| ||||| ||||| ||  
A TCATCGAC TAATGTC GTA  
C TA C

GAM1192 FLJ21272 3' ATGCCTGTAATCCCAGC 46735 A  
GCTGGGATTACAG CAT  
||| ||||| ||  
CGACCCTAATGTC GTA  
C

GAM1192 FLJ21551 3' CTGTAATCCCAGCTAC 45628  
GTAGCTGGGATTACAG  
||| ||||| ||  
CATCGACCCTAATGTC

GAM1192 FLJ21657 3' CTGTAATCCCAACACT 42509 AGC  
AGT TGGGATTACAG  
||| ||||| ||  
TCA ACCCTAATGTC  
CA\_

GAM1192 FLJ21687 3' CTGTAATCCCAGCACT 45857 A  
AGT GCTGGGATTACAG  
||| ||||| ||  
TCA CGACCCTAATGTC

GAM1192 FLJ21870 3' ATGCCTGTAATCCCAGCACT 43458 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| ||  
TCA CGACCCTAATGTC GTA

GAM1192 FLJ22054 3' CTGTAATCCAAGCTGC 94395 G  
GTAGCT GGATTACAG  
||| ||||| ||

			CGTCGA CCTAATGTC			
			A			
GAM1192	FLJ22054	3'	CTGTAATCCCAGCACT	94396	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	FLJ22167	3'	ATGCCTGTAATCCCAGCATTTT	44565	TA_	A
	G		CAG GCTGGGATTACAG CAT			
			GTT CGACCCTAATGTC GTA			
			TTA C			
GAM1192	FLJ22167	3'	CTGTAATCCCAGCTACTTA	44572	C	
			A AGTAGCTGGGATTACAG			
			A TCATCGACCCTAATGTC			
			T			
GAM1192	FLJ22313	3'	GTCTGTAATCCCAGCACT	42344	A	
			AGT GCTGGGATTACAGAC			
			TCA CGACCCTAATGTCTG			
			—			
GAM1192	FLJ22692	3'	CTGTAATCCCAGCACT	46802	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	FLJ23022	3'	TGCCTGTAATCCCTGCACT	46814	A T	A
			AGT GC GGGATTACAG CA			
			TCA CG CCCTAATGTC GT			
			_ T C			
GAM1192	FLJ23042	3'	ATGCCTGTAATCCCAGCTACT	47170		A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1192	FLJ23042	3'	CTGTAATCCCAGCACT	47172	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	FLJ23120	3'	CTGTAATCCCAGCTACTCA	85148	C	
			A AGTAGCTGGGATTACAG			
			A TCATCGACCCTAATGTC			
			C			
GAM1192	FLJ23235	3'	ATGCCTGTAATCCCAGCACT	46305	A	A
			AGT GCTGGGATTACAG CAT			

			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	FLJ23323	3'	CTGTAATCCCAAAGTGCTG 45051	GC_		
			CAGTA TGGGATTACAG			
			GTCGT ACCCTAATGTC			
			GAA			
GAM1192	FLJ23447	3'	ATGCCTGTAATCCCAGCACT 45710	A	A	
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	FLJ23476	3'	ATGCCTGTAATCCCAACATTCT 44958	TAGC_	A	
	G		CAG TGGGATTACAG CAT			
			GTC ACCCTAATGTC GTA			
			TTACA C			
GAM1192	FLJ23499	3'	ATGCCTGTAATCCCAGCACT 42816	A	A	
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	FLJ23499	3'	ATGCCTGTAATCCCAGCACT 42817	A	A	
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	FLJ23499	3'	CTGTAATCCCAGCTACT 42821			
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
			— C			
GAM1192	FLJ23537	3'	ATGCCTGCAATCCCAGCTACTT 46021	_	A	A
	G		CA GTAGCTGGGATT CAG CAT			
			GT CATCGACCCTAA GTC GTA			
			T C C			
GAM1192	FLJ25012	3'	ATGCCTGTAATCCAGTACT 58088	G	G	A
			AGTA CTGG ATTACAG CAT			
			TCAT GACC TAATGTC GTA			
			— — C			
GAM1192	FLJ25012	3'	CTATGGTCCCAGCTACTCA 58089	C	C	
			A AGTAGCTGGGATTA AG			
			A TCATCGACCCTGGT TC			
			C A			
GAM1192	FLJ25012	3'	CTGTAATCCCAGCACT 58090	A		
			AGT GCTGGGATTACAG			



TCA CGACCCTAATGTC

GAM1192 FLJ25179 3' ATGCCTGTAATCCCAGCACT 58354 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

GAM1192 FLJ30046 3' CTGCAATGTTTGCTACTGTA 58100 TG G A  
TACAGTAGC G ATT CAG  
||||||| | ||| |||  
ATGTCATCG T TAA GTC

TT G C  
GAM1192 FLJ30092 3' CTGTAATCCCAGCACT 58689 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

GAM1192 FLJ30681 3' CTGTAATCCCAGCTACT 91786  
AGTAGCTGGGATTACAG  
||||||| |||  
TCATCGACCCTAATGTC

GAM1192 FLJ31455 3' CTGTAATCCCAGCACT 58623 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

GAM1192 FLJ31737 3' CTGTAATCCCAGCACT 58694 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

GAM1192 FUSIP1 3' ATGCCTGTAATCTCAGCTACTC 53955 C A  
A AGTAGCTGGGATTACAG CAT  
| ||||| ||||| |||  
A TCATCGACTCTAATGTC GTA  
C C

GAM1192 FUSIP1 3' CTGTAATCCCAGCACT 53957 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

GAM1192 GALNT6 3' ATGCCTGTAGTCGCAGCTACTC 23290 C G A  
A AGTAGCTG GATTACAG CAT  
| ||||| ||||| |||  
A TCATCGAC CTGATGTC GTA  
C G C

GAM1192 GCN2 3' ATGCCTGTAGTCCCAGCTACT 62768 A  
AGTAGCTGGGATTACAG CAT  
||||||| ||||| |||

			TCATCGACCCTGATGTC	GTA		
			C			
GAM1192	GLTP	3'	CTGTAATCCCAGCACT	33159	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	GLTP	3'	CTGTAGTTCAGCTACTCA	33160	C	
			A AGTAGCTGGGATTACAG			
			A TCATCGACCTTGATGTC			
			C			
GAM1192	GP5	3'	CTGTAATCCCAGCACT	15645	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	HES2	3'	CTGTAATCCCAGCACT	38854	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	HSD17B7	3'	TGTAGTCCCAGCTACTCA	33037	C	
			A AGTAGCTGGGATTACA			
			A TCATCGACCCTGATGT			
			C			
GAM1192	HSH2	3'	ATGCCTGTAATCCCAGCTACTT	51671	—	A
	G		CA GTAGCTGGGATTACAG			
			GT CATCGACCCTAATGTC			
			T C			
GAM1192	HSMPP8	3'	CTATAATCCCAGCGCT	93474	A	C
			AGT GCTGGGATTA AG			
			TCG CGACCCTAAT TC			
			— A			
GAM1192	HSPC043	3'	ATGCCTGTAATCCCAGCACT	67719	A	A
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			— C			
GAM1192	HSPC043	3'	CTGTAATCCCAGCTACT	67720		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
			—			
GAM1192	ICAM4	3'	CTGTAATCCCAGCACT	42353	A	
			AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

GAM1192 ICAM4 3' CTGTAATCCCAGCACT 7749 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 IL10RB 3' ATGCCTATAATCCCAGCTACT 5275 C A  
AGTAGCTGGGATTA AG CAT  
||||| |||  
TCATCGACCCTAAT TC GTA  
A C

GAM1192 IMAGE:4907098 3' CTGTAATCCCAGCACT 91658 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 INE1 3' CTGTAATCCCAGCTCTTTGT 13374 T\_  
ACAG AGCTGGGATTACAG  
||| |||||  
TGTT TCGACCCTAATGTC  
TC

GAM1192 ING1-like 3' CTGTAATCCCAGCACT 54155 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 JAM1 3' ATGCCTGTAATCCCAGCTGCT 33749 A  
AGTAGCTGGGATTACAG CAT  
||||| |||  
TCGTCGACCCTAATGTC GTA  
C

GAM1192 JAM1 3' CTATAATCCCAGAGGCTG 33756 AG C  
CAGT CTGGGATTA AG  
||| ||||| ||  
GTCG GACCCTAAT TC  
GA A

GAM1192 JAM1 3' ATGCCTGTAATCCCAGCTGCT 57887 A  
AGTAGCTGGGATTACAG CAT  
||||| |||  
TCGTCGACCCTAATGTC GTA  
C

GAM1192 JAM1 3' CTATAATCCCAGAGGCTG 57894 AG C  
CAGT CTGGGATTA AG  
||| ||||| ||  
GTCG GACCCTAAT TC  
GA A

GAM1192 JAM1 3' ATGCCTGTAATCCCAGCTGCT 57915 A  
AGTAGCTGGGATTACAG CAT  
||||| |||

			TCGTCGACCCTAATGTC GTA		
			C		
GAM1192	JAM1	3'	CTATAATCCCAGAGGCTG 57923	AG	C
			CAGT CTGGGATTA AG		
			GTCG GACCCTAAT TC		
			GA A		
GAM1192	JAM1	3'	ATGCCTGTAATCCCAGCTGCT 57942		A
			AGTAGCTGGGATTACAG CAT		
			TCGTCGACCCTAATGTC GTA		
			C		
GAM1192	JAM1	3'	CTATAATCCCAGAGGCTG 57949	AG	C
			CAGT CTGGGATTA AG		
			GTCG GACCCTAAT TC		
			GA A		
GAM1192	KALI	3'	CTGTAATCCCAGTACT 53592	G	
			AGTA CTGGGATTACAG		
			TCAT GACCCTAATGTC		
			—		
GAM1192	KATII	3'	CTATAATCCCAGCACT 32646	A	C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			A		
GAM1192	KBRAS2	3'	ATGCCTGTAATCCCAGCTAC 34192		A
			GTAGCTGGGATTACAG CAT		
			CATCGACCCTAATGTC GTA		
			C		
GAM1192	KIAA0042	3'	CTGTAATCCCAGCACT 29610	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	KIAA0090	3'	ATGCCTGTAATCCCAGC 88438		A
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1192	KIAA0159	3'	CTGTAATCCCAGCACT 29507	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	KIAA0159	3'	TGTAATCCCAGCTACTCA 29511	C	
			A AGTAGCTGGGATTACA		

			A TCATCGACCCTAATGT			
			C			
GAM1192	KIAA0184	3'	CTGTAATCCCAGCACT	65194	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	KIAA0226	3'	CTGTAATCCCAGCACT	63514	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	KIAA0226	3'	CTGTAATCCCAGCTACTTG	63515	—	
			CA GTAGCTGGGATTACAG			
			GT CATCGACCCTAATGTC			
			T			
GAM1192	KIAA0252	3'	CTGTAATCCCAGCACT	62791	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	KIAA0266	3'	CTGTAATCCCAGCACT	41331	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	KIAA0266	3'	CTGTAATCCCAGCACT	41332	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	KIAA0268	3'	CTGTGTTTTAGCTAATGTA	70002	G	T
			TACA TAGCTGGGAT ACAG			
			ATGT ATCGATTTTG TGTC			
			A			
			—			
GAM1192	KIAA0355	3'	CTGTAATCCCAGCACT	28025	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	KIAA0391	3'	ATGCCTGTGGTCCCAGCTACTC	27904	C	A
	A		A AGTAGCTGGGATTACAG CAT			
			A TCATCGACCCTGGTGTC GTA			
			C C			
GAM1192	KIAA0420	3'	ATGCCTATAATCCCAACACT	63352	AGC	C A
			AGT TGGGATTA AG CAT			

			TCA ACCCTAAT TC GTA			
			CA_ A C			
GAM1192	KIAA0441	3'	ATGCCTGTAATCCCAGCACT	28952	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	KIAA0445	5'	CTGTAATCCCAGCACT	27953	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	KIAA0471	3'	TCTGTAATCCCAGCACT	29400	A	
			AGT GCTGGGATTACAGA			
			TCA CGACCCTAATGTCT			
			—			
GAM1192	KIAA0472	3'	ATGCCTGTAATCCAAGATACTC	71859	C	G G A
	A		A AGTA CT GGATTACAG CAT			
			A TCAT GA CCTAATGTC GTA			
			C A A C			
GAM1192	KIAA0514	3'	ATGCCTGTAATCCCAGCACT	28077	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	KIAA0547	3'	TGTAATCCCAGCTACTCA	28918	C	
			A AGTAGCTGGGATTACA			
			A TCATCGACCCTAATGT			
			C			
GAM1192	KIAA0563	3'	CTGTAATCCCAGCACT	29187	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	KIAA0565	3'	TCTGTAATTGCTATTG	66900	TGG	
			CAGTAGC GATTACAGA			
			GTTATCG TTAATGTCT			
			—			
GAM1192	KIAA0618	3'	ATGCCTGTAATCCCAGC	29161	A	
			GCTGGGATTACAG CAT			
			CGACCCTAATGTC GTA			
			C			
GAM1192	KIAA0635	3'	CTGTAATCCCAGCACT	27696	A	
			AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

GAM1192 KIAA0694 3' ATGCCTATAATCCCAATACTTT 72579 C GC C A  
A TA AGTA TGGGATTA AG CAT

|| ||| ||||| || |||  
AT TCAT ACCCTAAT TC GTA  
T A\_ A C

GAM1192 KIAA0694 3' CTGTAATCCCAGCACT 72580 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 KIAA0752 3' ATGCCTGCAATCCCAGCTACT 67048 A A  
AGTAGCTGGGATT CAG CAT  
||||||| ||| |||  
TCATCGACCCTAA GTC GTA  
C C

GAM1192 KIAA0794 3' ATGCCTGTAATCCCAACACT 80409 AGC A  
AGT TGGGATTACAG CAT  
||| ||||| ||| |||  
TCA ACCCTAATGTC GTA  
CA\_ C

GAM1192 KIAA0794 3' CTGTAATCCCAGCTACTCA 80411 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
C

GAM1192 KIAA0795 3' CTATAATCCCAGCACT 46590 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC  
A

GAM1192 KIAA0825 3' CTGTAATCCCAGCACT 61025 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 KIAA0825 3' GTGCCTGCAATCCCAGCTACTC 61027 C A A  
A AGTAGCTGGGATT CAG CAT  
| ||||| ||| |||  
A TCATCGACCCTAA GTC GTG  
C C C

GAM1192 KIAA0831 3' CTGTAATCCCAGCTACT 29972  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1192 KIAA0831 3' CTGTAATCCCGGCACT 29973 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGGCCCTAATGTC

GAM1192 KIAA0852 5' CTGTAATCCCAGCACT 30077 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

GAM1192 KIAA0853 3' ATGTCTGTAGTCACAGCTACTC 30537 C G  
A AGTAGCTG GATTACAGACAT  
| ||||||| |||||||||  
A TCATCGAC CTGATGTCTGTA  
C A

GAM1192 KIAA0872 3' ATGCCTGTAATCCCAGCACT 30061 A A  
AGT GCTGGGATTACAG CAT  
||| ||||||||| |||  
TCA CGACCCTAATGTC GTA  
C

GAM1192 KIAA0872 3' CTGTAATCCCAGCACT 30062 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

GAM1192 KIAA0889 3' ATGCCTGTAATCCCAGCACT 31129 A A  
AGT GCTGGGATTACAG CAT  
||| ||||||||| |||  
TCA CGACCCTAATGTC GTA  
C

GAM1192 KIAA0907 3' CTGTAATCCCAGCACT 30173 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

GAM1192 KIAA0907 3' CTGTAATCCCAGCACT 30174 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

GAM1192 KIAA0912 3' CTGTAATCCCAGCACT 64409 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

GAM1192 KIAA0918 3' TCTGTAAGATGGGGCTACTGT 73136 GGGA\_  
ACAGTAGCT TTACAGA  
||||||| |||||||  
TGTCATCGG AATGTCT  
GGTAG

GAM1192 KIAA0930 3' CTGTAATCCCAGCACT 70542 A  
AGT GCTGGGATTACAG  
||| |||||||||



TCA CGACCCTAATGTC

GAM1192 KIAA1032 3' ATGCCTGTAGTCCCAGCTACTC 66151 C A  
A AGTAGCTGGGATTACAG CAT  
I ||||||||||||| III  
A TCATCGACCCTGATGTC GTA  
C C

GAM1192 KIAA1056 3' CTGTAATCCCAGCACT 29695 A  
AGT GCTGGGATTACAG  
III |||||||||||  
TCA CGACCCTAATGTC

GAM1192 KIAA1056 3' CTGTAATCCCAGCTGCT 29696  
AGTAGCTGGGATTACAG  
|||||||||||||  
TCGTCGACCCTAATGTC

GAM1192 KIAA1086 3' CTATAATCCCAGCACT 70744 A C  
AGT GCTGGGATTA AG  
III ||||||||| II  
TCA CGACCCTAAT TC  
A

GAM1192 KIAA1086 3' CTGTAATCCCAGCACT 70745 A  
AGT GCTGGGATTACAG  
III |||||||||||  
TCA CGACCCTAATGTC

GAM1192 KIAA1130 3' ATGCCTGTAATCCCAGCACT 62412 A A  
AGT GCTGGGATTACAG CAT  
III ||||||||||| III  
TCA CGACCCTAATGTC GTA  
C

GAM1192 KIAA1130 3' ATGCCTGTAATCCCAGTGCT 62413 G A  
AGTA CTGGGATTACAG CAT  
III ||||||||||| III  
TCGT GACCCTAATGTC GTA  
C

GAM1192 KIAA1130 3' TGTAATCCCAGCTACTCA 62428 C  
A AGTAGCTGGGATTACA  
I |||||||||||||  
A TCATCGACCCTAATGT  
C

GAM1192 KIAA1164 3' ATGCCTGTAATCCCAGTACT 69503 G A  
AGTA CTGGGATTACAG CAT  
III ||||||||||| III  
TCAT GACCCTAATGTC GTA  
C

GAM1192 KIAA1191 3' CTGTAATCCCAGCACT 39954 A  
AGT GCTGGGATTACAG  
III |||||||||||

TCA CGACCCTAATGTC

GAM1192 KIAA1204 3' TCTGTAATCCCAACACT 69220 AGC  
AGT TGGGATTACAGA  
||| |||||  
TCA ACCCTAATGTCT  
CA\_

GAM1192 KIAA1228 3' CTGTAATCCCAGCACT 65041 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 KIAA1244 3' CTGTAATCCCAGCACT 71989 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 KIAA1244 3' CTGTAATCCCAGCTACTTA 71990 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
T

GAM1192 KIAA1253 3' ATGCCTGTGGTCCCAGCTACTG 91896 A  
CAGTAGCTGGGATTACAG CAT  
||||||| |||  
GTCATCGACCCTGGTGTC GTA  
C

GAM1192 KIAA1271 3' CTGTAATCCCAGCACT 69542 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 KIAA1271 3' GTCTGTAATCCCAGCTATT 69551  
AGTAGCTGGGATTACAGAC  
|||||||  
TTATCGACCCTAATGTCTG

GAM1192 KIAA1276 3' CTGTAATCCCATCACT 66430 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CT\_

GAM1192 KIAA1277 3' ATGCCTATAATCCCAGCACT 64450 A C A  
AGT GCTGGGATTA AG CAT  
||| ||||| || |||  
TCA CGACCCTAAT TC GTA

GAM1192 KIAA1328 3' CTGTAATCCCAGGCTTTG 61646 T \_  
CAG AGC TGGGATTACAG  
||| ||| |||||

			GTT TCG ACCCTAATGTC		
			— G		
GAM1192	KIAA1348	3'	ATGCCTGTAATCCCAGCTACT 68571	A	
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1192	KIAA1348	3'	CTGTAATCCCAGCACTGTG 68575	A	
			TACAGT GCTGGGATTACAG		
			GTGTCA CGACCCTAATGTC		
			—		
GAM1192	KIAA1364	3'	ATGCCTGTAATCCCAGCACT 63586	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			C		
GAM1192	KIAA1364	3'	CTGTAATCCCAGCTACTTG 63593	—	
			CA GTAGCTGGGATTACAG		
			GT CATCGACCCTAATGTC		
			T		
GAM1192	KIAA1377	3'	ATGCCTGTAATCCCAGCACT 67174	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			C		
GAM1192	KIAA1404	3'	CTGTAATCCCAGCACT 61987	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	KIAA1423	3'	TAGTCCCAGCTACTCA 61728	C	
			A AGTAGCTGGGATTA		
			A TCATCGACCCTGAT		
			C		
GAM1192	KIAA1456	3'	ATGCCTGTAATCCCAGCACT 66988	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			C		
GAM1192	KIAA1456	3'	ATGCCTGTAATCCCAGCCACTT 66989	— A	A
	G		CA GT GCTGGGATTACAG CAT		
			GT CA CGACCCTAATGTC GTA		
			T C C		
GAM1192	KIAA1473	3'	ATGCCTGTAATCCCAGCTACT 70663	A	
			AGTAGCTGGGATTACAG CAT		

			TCATCGACCCTAATGTC GTA		
			C		
GAM1192	KIAA1473	3'	CTGTAATCCCAGCACT 70667 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	KIAA1486	3'	CTGTAATCCCAGCACTCTG 67379 TA_		
			CAG GCTGGGATTACAG		
			GTC CGACCCTAATGTC		
			TCA		
GAM1192	KIAA1554	3'	CTGTAATCCCAGCTACCTG 95152 _		
			CAG TAGCTGGGATTACAG		
			GTC ATCGACCCTAATGTC		
			C		
GAM1192	KIAA1559	3'	ATGCCTGTAATCCCAGCACT 73057 A A		
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	KIAA1559	3'	ATGCCTGTAATCCCAGCTACTT 73058 _ A		
	G		CA GTAGCTGGGATTACAG CAT		
			GT CATCGACCCTAATGTC GTA		
			T C		
GAM1192	KIAA1559	3'	CTGTAATCCCAGCACT 73064 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	KIAA1586	5'	CTGTAATCCCAGCACT 92329 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	KIAA1614	3'	ATGCCTATAATCCCAGCTACTT 70117 _ C A		
	G		CA GTAGCTGGGATTA AG CAT		
			GT CATCGACCCTAAT TC GTA		
			T A C		
GAM1192	KIAA1614	3'	ATGCCTGTAATCCCAGAACT 70118 AG A		
			AGT CTGGGATTACAG CAT		
			TCA GACCCTAATGTC GTA		
			A_ C		
GAM1192	KIAA1630	3'	ATGCCTGTAATCCCAGCACT 38030 A A		
			AGT GCTGGGATTACAG CAT		

			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	KIAA1656	5'	CTGTAATCCCAGCACT 65794	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	KIAA1674	3'	CTGTAATCCCAGCACT 68777	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	KIAA1715	3'	ATGCCTGTAATCCTAGCTACTC 68117	C	A
	A		A AGTAGCTGGGATTACAG CAT		
			A TCATCGATCCTAATGTC GTA		
			C C		
GAM1192	KIAA1735	3'	CTGTAGTCCCAGCTACTCA 87627	C	
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTGATGTC		
			C		
GAM1192	KIAA1751	3'	ATGCCTGTAATCCCAGAACT 71688	AG	A
			AGT CTGGGATTACAG CAT		
			TCA GACCCTAATGTC GTA		
			A_ C		
GAM1192	KIAA1811	5'	CTGTAATCCCAGCACT 64796	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	KIAA1829	3'	TGTAATCCCAGCTACTCA 61958	C	
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1192	KIAA1872	3'	ATGCCTGTAATCCCAGCACTCT 62923	TA_	A
	G		CAG GCTGGGATTACAG CAT		
			GTC CGACCCTAATGTC GTA		
			TCA C		
GAM1192	KIAA1872	3'	ATGCCTGTAATCCCAGCTACT 62924		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1192	KIAA1872	3'	CTATAATCCCAGCACT 62929	A	C
			AGT GCTGGGATTA AG		

TCA CGACCCTAAT TC  
 — A  
 GAM1192 KIAA1872 3' CTGTAATCCCAGACTTTG 62931 T \_  
 CAG AG CTGGGATTACAG  
 ||| || |||||  
 GTT TC GACCCTAATGTC  
 — A  
 GAM1192 KIAA1941 3' CTGTAATCCCAGCACT 74838 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1192 KIAA1948 5' ATGCCTATAATCCCAGCTACT 82399 C A  
 AGTAGCTGGGATTA AG CAT  
 ||||| || |||  
 TCATCGACCCTAAT TC GTA  
 A C  
 GAM1192 KIAA1951 3' CTGTAATCCCAGCACT 73761 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1192 KIAA1954 3' CTGTAATCCCAGCACT 77719 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1192 KIAA1958 3' CTATAATCCCAGCACT 81902 A C  
 AGT GCTGGGATTA AG  
 ||| ||||| ||  
 TCA CGACCCTAAT TC  
 — A  
 GAM1192 KIAA1979 3' CTGTAATCCCAGCACT 88278 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1192 KIAA1979 3' CTGTAATCCCAGCTACTCA 88279 C  
 A AGTAGCTGGGATTACAG  
 | |||||  
 A TCATCGACCCTAATGTC  
 C  
 GAM1192 KLHL6 3' CTGTAATCCCAGCCCTATG 55303 GTA\_  
 CA GCTGGGATTACAG  
 || |||||  
 GT CGACCCTAATGTC  
 ATCC  
 GAM1192 KLHL8 3' CTGTAATCCAGCTACTCA 62854 C  
 A AGTAGCTGGGATTACAG  
 | |||||

			A TCATCGACCTTAATGTC		
			C		
GAM1192	KR18	3'	CTGTAATCCCAGTACT	52745	G
			AGTA CTGGGATTACAG		
			TCAT GACCCTAATGTC		
			—		
GAM1192	KREMEN	3'	ATGCCTGTAATCCCAGCACT	49404	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			—		
			C		
GAM1192	KREMEN	3'	CTGTAATCCCAGCTACT	49406	
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
			—		
GAM1192	LHPP	5'	CTGTAATCCCAGCACT	42101	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LIAS	3'	CTGTAATCCCAGCACTTTA	70635	C A
			TA AGT GCTGGGATTACAG		
			AT TCA CGACCCTAATGTC		
			T —		
GAM1192	LIM	3'	CTGTAATCCCAGCACT	21302	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LIM	3'	CTGTAATCCCAGCTACTCA	21303	C
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTAATGTC		
			C		
GAM1192	LRG	3'	CTGTAATCCCAGCACT	53750	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LRRFIP1	3'	TGCCTGTAATCTCAGTAC	16420	G A
			GTA CTGGGATTACAG CA		
			CAT GACTCTAATGTC GT		
			—		
			C		
GAM1192	LRRFIP1	3'	TGTAATCCCAGCCACT	16421	A
			AGT GCTGGGATTACA		

			TCA CGACCCTAATGT			
			C			
GAM1192	LSR68	3'	TGCCTATAATCCCAGCTACTCA 37937	C		C A
			A AGTAGCTGGGATTA AG CA			
			I			
			A TCATCGACCCTAAT TC GT			
			C A C			
GAM1192	LYSAL1	3'	CTGTAATCCCAGCACT 16918	A		
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	MACF1	3'	CTGTAATCCCAGCACT 52316	A		
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	MAWBP	3'	ATGCCTGTAATCCCAGCACT 42106	A		A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			C			
GAM1192	MCAM	3'	CTGTAATCCCAGCACT 21454	A		
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	MESDC2	3'	CTGTAATCCCAGTACT 72492	G		
			AGTA CTGGGATTACAG			
			TCAT GACCCTAATGTC			
			—			
GAM1192	MESDC2	3'	TGTAATCCCAGCTACTCA 72503	C		
			A AGTAGCTGGGATTACA			
			I			
			A TCATCGACCCTAATGT			
			C			
GAM1192	METL	3'	ATGCCTGTAATCCCAGCCACT 37253	A		A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			C C			
GAM1192	MGC10765	3'	ATGCCTGTAATCCCAGCACT 44299	A		A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			C			
			—			
GAM1192	MGC10765	3'	CTGTAATCCCAGCTAC 44301			
			GTAGCTGGGATTACAG			



CATCGACCCTAATGTC

GAM1192 MGC10771 3' ATGCCTGTAATCCCAGCACT 44451 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

— C

GAM1192 MGC10814 5' ATGCCTGTAATCCCAGCACT 51036 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

— C

GAM1192 MGC10814 3' CTGTAATCCCAGCACT 51038 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—

GAM1192 MGC10999 3' ATGCCTGTAATCCCAGCACTGT 50225 A A  
G TACAGT GCTGGGATTACAG CAT  
||||| |||||  
GTGTCA CGACCCTAATGTC GTA

— C

GAM1192 MGC11287 5' GTCTATAATCCCAGCACTGTG 48834 A C  
TACAGT GCTGGGATTA AGAC  
||||| |||||  
GTGTCA CGACCCTAAT TCTG

— A

GAM1192 MGC11386 3' CTATAATCCCAGCACT 51950 A C  
AGT GCTGGGATTA AG  
||| |||||  
TCA CGACCCTAAT TC

— A

GAM1192 MGC13017 3' TCTGTAATCCCAGCTACT 54694  
AGTAGCTGGGATTACAGA  
|||||  
TCATCGACCCTAATGTCT

GAM1192 MGC13053 3' CTGTAATCCCAGTACT 51131 G  
AGTA CTGGGATTACAG  
|||||  
TCAT GACCCTAATGTC

—

GAM1192 MGC13523 3' TGCCTGTAATTTCACTA 53031 C GG A  
TAG TG ATTACAG CA  
||| || |||||  
ATC AC TAATGTC GT

— TT C

GAM1192 MGC14126 3' CTGTAATCCCAGCACT 51854 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

—  
GAM1192 MGC14817 3' CTGTAATCCCAGCACT 50336 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 MGC15397 3' CTGTAATCCCAGCACT 54679 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 MGC15631 3' ATGCCTGTAATCCCAGTGCT 51259 G A  
AGTA CTGGGATTACAG CAT  
||| ||||| |||  
TCGT GACCCTAATGTC GTA

— C  
GAM1192 MGC15631 3' CTGTCATCCCAGCTAC 51263 T  
GTAGCTGGGAT ACAG  
||| ||||| |||  
CATCGACCCTA TGTC

C  
GAM1192 MGC16142 3' ATGCCTATAATCCCAGCACT 51291 A C A  
AGT GCTGGGATTA AG CAT  
||| ||||| || |||  
TCA CGACCCTAAT TC GTA

— A C  
GAM1192 MGC16142 3' ATGCCTATAATCCCAGCTACT 51292 C A  
AGTAGCTGGGATTA AG CAT  
||| ||||| || |||  
TCATCGACCCTAAT TC GTA

A C  
GAM1192 MGC16332 3' ATGCCTGTAATCCCAACACT 56774 AGC A  
AGT TGGGATTACAG CAT  
||| ||||| |||  
TCA ACCCTAATGTC GTA  
CA\_ C

GAM1192 MGC16385 3' CTGTAATCCCAGCACT 58887 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 MGC16703 3' ATGCCTGTAATCCCAGCACT 73098 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

— C  
GAM1192 MGC20235 3' CTGTAATCCCAGTACT 58894 G  
AGTA CTGGGATTACAG  
||| |||||

TCAT GACCCTAATGTC

GAM1192 MGC20235 3' CTGTAGTCCCAGCTACTCA 58895 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTGATGTC  
C

GAM1192 MGC22805 3' ATGCCTGTAATCCCAGCTACTT 58080 \_ A  
G CA GTAGCTGGGATTACAG CAT  
|| |||||  
GT CATCGACCCTAATGTC GTA  
T C

GAM1192 MGC2396 3' ATGCCTGTAATCCCAGCTACT 53460 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1192 MGC2562 3' CTATAATCCCAGCACT 50437 A C  
AGT GCTGGGATTA AG  
||| |||||  
TCA CGACCCTAAT TC  
\_ A

GAM1192 MGC2562 3' CTGTAATCCCAGCACT 50438 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 MGC26641 3' CTGTAATCCCAACTACTCA 58657 C C  
A AGTAG TGGGATTACAG  
| |||||  
A TCATC ACCCTAATGTC  
C A

GAM1192 MGC2731 3' ATGCCTGTAATCCCAGCTACT 43948 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1192 MGC29762 3' CTGTAATCCCAGCACT 58472 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 MGC29891 3' CTGTAATCCCAACACT 58204 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1192 MGC29891 3' CTGTAATCCCAGCACT 58205 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1192 MGC29937 3' ATGCCTGTAATCCCAGCACT 58110 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1192 MGC29937 3' ATGCCTGTAATCCCAGTTACTC 58111 C A  
A AGTAGCTGGGATTACAG CAT  
| |||||  
A TCATTGACCCTAATGTC GTA

GAM1192 MGC3207 3' CTGTAATCCCAGCACT 62558 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 MGC39350 3' CTGTAATCCCCAGCACT 58654 A \_  
AGT GCTGGG ATTACAG  
||| |||||  
TCA CGACCC TAATGTC

GAM1192 MGC4248 3' CTGTAATCCCAGCACT 50327 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 MGC4663 3' CTATAATCCCAGCACTTTA 44505 C A C  
TA AGT GCTGGGATTA AG  
|| ||| |||||  
AT TCA CGACCCTAAT TC

GAM1192 MGC5254 3' CTGTAATCCCAGCACT 50410 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 MGC5384 3' ATGCCTGTAATCCCAGCACT 48269 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1192 MKRN4 3' CTGTAATCCCAGCACT 47746 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 MOST2 5' ATGCCTGTAGTCCCAGCTACTC 39674 C A  
A AGTAGCTGGGATTACAG CAT  
| |||||

				A TCATCGACCCTGATGTC GTA		
				C C		
GAM1192	MOST2	5'	CTGTAATCCCAGCACT	39684	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
GAM1192	MRP63	3'	CTGTAATCCCAACACTTTA	43807	C AGC	
			TA AGT TGGGATTACAG			
			AT TCA ACCCTAATGTC			
			T CA_			
GAM1192	MRPL56	3'	CTGTAATCCCAACACT	51688	AGC	
			AGT TGGGATTACAG			
			TCA ACCCTAATGTC			
			CA_			
GAM1192	MRPS10	3'	CTGTAATCCCAGCACT	36292	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
GAM1192	MRPS10	3'	GTGCCTGTAATCCCAGCTACTC	36298	C	A
	A		A AGTAGCTGGGATTACAG CAT			
			A TCATCGACCCTAATGTC GTG			
			C C			
GAM1192	MT-ACT48	3'	ATGCCTGTAATCCCAGCACT	24686	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
GAM1192	N4BP2	3'	CTGTAATCCCAGCACT	36403	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
GAM1192	NDUFC2	3'	ATGCCTGTAATCCCAGCACT	15825	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
GAM1192	NDUFC2	3'	CTGCAATCCCAGCTACTCA	15832	C	A
			A AGTAGCTGGGATT CAG			
			A TCATCGACCCTAA GTC			
			C C			
GAM1192	NMNAT	3'	CTGTAATCCCAGCACT	42956	A	
			AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

GAM1192 NMT2 3' CTGTAATCCCAGCACT 16664 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 NPTXR 3' CTGTAATCCCAGCACT 54178 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 NPTXR 3' CTGTAATCCCAGCACT 26642 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 OCLM 5' ATGCCTATAATCCCAGCACT 42347 A C A  
AGT GCTGGGATTAG CAT  
||| ||||| || |||  
TCA CGACCCTAAT TC GTA

GAM1192 ORC6L 3' ATGCCTGTAATCCCAGCTCCT 26722 T A  
AG AGCTGGGATTACAG CAT  
|| ||||| |||  
TC TCGACCCTAATGTC GTA  
C C

GAM1192 ORC6L 3' CTGTAATCCCAGCACT 26724 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 PAFAH2 3' ATGCCTGTAATCCCAGCACT 4760 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

GAM1192 PAFAH2 3' CTATAATCCCAGCTACTCA 4762 C C  
A AGTAGCTGGGATTAG  
| ||||| ||  
A TCATCGACCCTAAT TC  
C A

GAM1192 PB1 3' CTGTAATCCCAGCACT 37021 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 PDCD7 3' CTGTAATCCCAACACT 72138 AGC  
AGT TGGGATTACAG  
||| |||||

			TCA ACCCTAATGTC			
			CA_			
GAM1192	phorbolin-1	3'	CTGTAATCCCAGCACT	88778	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	PILR(ALPHA)	3'	CTGTAATCCCAGCTACT	25546		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
GAM1192	PIWIL2	3'	CTGTAGTCCCAGCTACTCA	36055	C	
			A AGTAGCTGGGATTACAG			
			A TCATCGACCCTGATGTC			
			C			
GAM1192	PNPASE	3'	ATGCCTGTAATCCTAGCTACTC	70870	C	A
	A		A AGTAGCTGGGATTACAG CAT			
			A TCATCGATCCTAATGTC GTA			
			C C			
GAM1192	POFUT1	3'	ATGCCTGTAATCCCAGCACT	70465	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	POLYDOM	3'	ATGCCTGTAATTCCAGCTACTC	44424	C	A
	A		A AGTAGCTGGGATTACAG CAT			
			A TCATCGACCTTAATGTC GTA			
			C C			
GAM1192	POLYDOM	3'	CTGTAATCCCAGCACT	44425	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	PPP1R3B	3'	ATGCCTGTAATCCCAGCACT	44815	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	PPP1R3B	3'	TGCCTGTAATCCCTGCACT	44826	A T	A
			AGT GC GGGATTACAG CA			
			TCA CG CCCTAATGTC GT			
			— T C			
GAM1192	PRDM14	3'	ATGCCTGTGGTTCCAGCCACTC	44444	C A	A
	A		A AGT GCTGGGATTACAG CAT			

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          A TCA CGACCTTGGTGTC GTA
            C C      C
GAM1192 PRDM14 3' CTGTAATCCCAGCACT 44447 A
          AGT GCTGGGATTACAG
          ||| |||||
          TCA CGACCCTAATGTC

          —
GAM1192 PRO0038 3' ATGCCTATAATCCCAACACCCT 26090 TAGC_ C A
          G          CAG TGGGATTA AG CAT
          ||| ||||| || |||
          GTC ACCCTAAT TC GTA
          CCACA A C
GAM1192 PRO0255 3' CTGTAATCTCAGCACT 26141 A
          AGT GCTGGGATTACAG
          ||| |||||
          TCA CGACTCTAATGTC

          —
GAM1192 PRO0478 3' ATGCCTGTAATCCCAGCACT 26183 A A
          AGT GCTGGGATTACAG CAT
          ||| ||||| |||
          TCA CGACCCTAATGTC GTA
          C
GAM1192 PRO0478 5' CTGTAATCCCAGCACT 26187 A
          AGT GCTGGGATTACAG
          ||| |||||
          TCA CGACCCTAATGTC

          —
GAM1192 PRO0478 3' CTGTAATCCCAGCCTG 26188 TA
          CAG GCTGGGATTACAG
          ||| |||||
          GTC CGACCCTAATGTC

          —
GAM1192 PRO0478 5' CTGTAATCCCAGGTACT 26189 G
          AGTA CTGGGATTACAG
          ||| |||||
          TCAT GACCCTAATGTC
          G
GAM1192 PRO0478 3' TGTAATCCCAGCTACTCA 26198 C
          A AGTAGCTGGGATTACA
          | |||||
          A TCATCGACCCTAATGT
          C
GAM1192 PRO0611 3' ATGCCTGTAATCCCAGCACT 26007 A A
          AGT GCTGGGATTACAG CAT
          ||| ||||| |||
          TCA CGACCCTAATGTC GTA
          C
GAM1192 PRO0618 3' CTGTAATCCCAGCACTTTA 26200 C A
          TA AGT GCTGGGATTACAG
          || ||| |||||

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			AT TCA CGACCCTAATGTC			
			T _			
GAM1192	PRO1048	5'	TCTGTAATCCCAGCACT	37525	A	
			AGT GCTGGGATTACAGA			
			TCA CGACCCTAATGTCT			
			—			
GAM1192	PRO1496	3'	ATGCCTGTAATCCCAGCACT	37757	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	PRO1580	5'	ATGCCTTGTCCCAGCTTCT	37530	T	TAC A
			AG AGCTGGGAT AG CAT			
			TC TCGACCCTG TC GTA			
			T T_ C			
GAM1192	PRO1777	3'	ATGCCTGTAATCCCAGCATTCT	37762	TA_	A
	G		CAG GCTGGGATTACAG CAT			
			GTC CGACCCTAATGTC GTA			
			TTA C			
GAM1192	PRO1853	3'	ATGCCTGTAATCCCAGCACT	37771	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	PRO2015	3'	CTGTAATCCCAGCACT	37557	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	PRO2198	5'	CTGTAATCCCGGCACT	37791	A	
			AGT GCTGGGATTACAG			
			TCA CGGCCCTAATGTC			
			—			
GAM1192	PRO2730	3'	CTGTAATCCCAGCACT	47415	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	PRO2859	3'	ATGCCTGTAATCCCAGCACT	37614	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	PRO2949	3'	ATGCCTGTAATCCCAGCACT	37619	A	A
			AGT GCTGGGATTACAG CAT			

			TCA CGACCCTAATGTC GTA			
			- C			
GAM1192	PSR	3'	CTGTAATCCCAGCACT	65180	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			-			
GAM1192	PTD012	3'	ATGCCTATAATCCCAGCACT	25890	A	C A
			AGT GCTGGGATTA AG CAT			
			TCA CGACCCTAAT TC GTA			
			- A C			
GAM1192	PTK6	3'	ATGCCTGTAATCCCAGCACT	19934	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			- C			
GAM1192	PTRF	3'	ATGCCTGTAATCCCGACTACT	63497		A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1192	RAB4B	5'	ATGCCTGTAATCCCAGCACT	32372	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			- C			
GAM1192	RAB4B	5'	ATGCCTGTAATCCCAGCTACT	32373		A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1192	RHOBTB3	3'	CTGTAATCCCAGCTACT	29744		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
			C			
GAM1192	RNO2	5'	CTGTAATCCCAGCACT	52769	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			-			
GAM1192	RoXaN	3'	ATGCCTGTAATCCCAGC	46632		A
			GCTGGGATTACAG CAT			
			CGACCCTAATGTC GTA			
			C			
GAM1192	RoXaN	3'	CTATAATCCCAGCACTCTG	46641	TA_	C
			CAG GCTGGGATTA AG			

			GTC CGACCCTAAT TC		
			TCA A		
GAM1192	RoXaN	3'	TCTGTAATCCCAGCTACTCA 46659 C		
			A AGTAGCTGGGATTACAGA		
			A TCATCGACCCTAATGTCT		
			C		
GAM1192	Rpo1-2	3'	ATGCCTGTAGTTCCAGCTACTC 38697 C		A
	A		A AGTAGCTGGGATTACAG CAT		
			A TCATCGACCTTGATGTC GTA		
			C C		
GAM1192	RRP4	3'	CTATAATCCCAGCACT 26563 A C		
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1192	SAMHD1	3'	ATGCCTGTAATCCCAGCACT 61308 A A		
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	SC65	3'	CTGTAATCCCAGCACTG 21288 A		
			CAGT GCTGGGATTACAG		
			GTCA CGACCCTAATGTC		
			—		
GAM1192	SCIN	3'	CTGTAATCCCAGCACT 52424 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	SCYA5	3'	CTGTAATCCCAGCTACT 11450		
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
			—		
GAM1192	SEMA3E	3'	CTGTAATCCCAGCACT 24881 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	SEMA5A	3'	ATGCCTATAATCCCAGCACT 14252 A C A		
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1192	SGKL	3'	ATGCCTATAATCCCAGCTACTT 25140 — C A		
	G		CA GTAGCTGGGATTA AG CAT		

			GT CATCGACCCTAAT TC GTA		
			T A C		
GAM1192	SGKL	3'	ATGCCTTTAGTCCCAGCTACTC 25141	C	C A
	A		A AGTAGCTGGGATTA AG CAT		
			I		
			A TCATCGACCCTGAT TC GTA		
			C T C		
GAM1192	SGKL	3'	CTGTAATCCCAGCACT 25142	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	SLC7A11	3'	TCTGTAATCATATCTAC 26757	C G	
			GTAG TG GATTACAGA		
			CATC AT CTAATGTCT		
			T A		
GAM1192	SLC7A11	3'	TCTGTAATCCCAGCACT 26758	A	
			AGT GCTGGGATTACAGA		
			TCA CGACCCTAATGTCT		
			—		
GAM1192	SMAP-5	3'	CTGTAATCCCAGCACT 47931	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	SNAPC1	3'	ATGCCTGTAATCCCAGC 11838	A	
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1192	SPTLC2	3'	ATGCCTGTAATCCCAGCTAC 16797	A	
			GTAGCTGGGATTACAG CAT		
			CATCGACCCTAATGTC GTA		
			C		
GAM1192	SS18L1	3'	CTGTAATCCCAGCACT 65344	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	SS18L1	3'	CTGTAATCCCAGCTACT 65345		
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
			—		
GAM1192	TA-LRRP	3'	ATGCCTATAATCCCAGCACT 31068	A	C A
			AGT GCTGGGATTA AG CAT		

			TCA CGACCCTAAT TC GTA				
			— A C				
GAM1192	TACTILE	3'	CTGTAATCCCAGCACT	19469	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1192	THEA	3'	CTGTAATCCCAGCACT	66282	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1192	TIP47	3'	CTGTAATCCCAGCACT	19479	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1192	TMG4	3'	ATGCCTGTAATCCCAGCACT	43988	A	A	
			AGT GCTGGGATTACAG CAT				
			TCA CGACCCTAATGTC GTA				
			— C				
GAM1192	TRIAD3	3'	ATGCCTATAATCCCAGGTACTC	94500	C	G	C A
	A		A AGTA CTGGGATTA AG CAT				
			A TCAT GACCCTAAT TC GTA				
			C G A C				
GAM1192	TRIM38	3'	CTGTAATCCCAGAACTATGT	20986		GTAG_	
			ACA CTGGGATTACAG				
			TGT GACCCTAATGTC				
			ATCAA				
GAM1192	UBF-fl	3'	CTGTAATCCCAGCACT	51564	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1192	VPS4B	3'	ATGCCTGTAATCCCAGCACT	16821	A	A	
			AGT GCTGGGATTACAG CAT				
			TCA CGACCCTAATGTC GTA				
			— C				
GAM1192	VPS4B	3'	TGTAATCCCAGCTACTCA	16826	C		
			A AGTAGCTGGGATTACA				
			A TCATCGACCCTAATGT				
			C				
GAM1192	WBSCR21	3'	CTGTAATCCCAGCTACT	48476			
			AGTAGCTGGGATTACAG				

TCATCGACCCTAATGTC

GAM1192 WBSCR23 3' CTGTAATCCCAGCACT 46759 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 WBSCR23 3' CTGTAATCCCAGCTACT 46760  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1192 WBSCR23 3' GTCTGTAGTCCCAGCTACTCA 46770 C  
A AGTAGCTGGGATTACAGAC  
| |||||  
A TCATCGACCCTGATGTCTG  
C

GAM1192 YEA 3' ATGCCTGTAATCCCAGCTACTT 51528 — A  
G CA GTAGCTGGGATTACAG CAT  
|| |||||  
GT CATCGACCCTAATGTC GTA  
T C

GAM1192 YME1L1 3' CTGTAATCCCAGCACT 57778 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 YME1L1 3' TCTGTAATCCCAGCACT 57781 A  
AGT GCTGGGATTACAGA  
||| |||||  
TCA CGACCCTAATGTCT

—  
GAM1192 YME1L1 3' CTGTAATCCCAGCACT 26528 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 YME1L1 3' TCTGTAATCCCAGCACT 26531 A  
AGT GCTGGGATTACAGA  
||| |||||  
TCA CGACCCTAATGTCT

—  
GAM1192 ZAK 3' CTGTAATCCCAGCACT 56125 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 ZFP106 3' CTGTAATCCCAGCACT 42466 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1192 ZFP106 3' CTGTAATCCCAGCTCT 42467 T  
AG AGCTGGGATTACAG  
|| |||||  
TC TCGACCCTAATGTC

GAM1192 ZIM3 3' ATGCCTGTAATCCCAGTACT 53536 G A  
AGTA CTGGGATTACAG CAT  
|||| |||||  
TCAT GACCCTAATGTC GTA

GAM1192 ZNF197 3' ATGCCTGTAATCCCAGCACT 22763 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1192 ZNF197 3' GTAATCCCAGCTACTCA 22766 C  
A AGTAGCTGGGATTAC  
| |||||  
A TCATCGACCCTAATG  
C

GAM1192 ZNF271 3' CTGTAATCCCAACACT 95250 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1192 ZNF297B 5' ATGCCTATAATCCCAACACTTT 25774 C AGC C A  
A TA AGT TGGGATTA AG CAT  
|| ||| ||||| || |||  
AT TCA ACCCTAAT TC GTA  
T CA\_ A C

GAM1192 ZNF297B 5' CTGTAATCCCAGCACT 25781 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 ZNF297B 3' CTGTAATCCCAGCACT 25782 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 ZNF297B 3' CTGTAATCCCAGCTACT 25783  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1192 ZNF33A 3' ATGCCTGTAATCCCAGCACT 91344 A A  
AGT GCTGGGATTACAG CAT  
||| |||||

			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	ZNF347	3'	ATGCCTGTAATCCCAACACT 50845	AGC	A
			AGT TGGGATTACAG CAT		
			TCA ACCCTAATGTC GTA		
			CA_ C		
GAM1192	LOC112687	3'	CTATAATCCCAGCACT 72859	A	C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1192	LOC113201	3'	ATGCCTATAGTCCCAGCTACT 56549		C A
			AGTAGCTGGGATTA AG CAT		
			TCATCGACCCTGAT TC GTA		
			A C		
GAM1192	LOC115129	5'	CTATAATCCCAGCACT 73229	A	C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1192	LOC115129	5'	CTGTAATCCCAGCTACT 73231		
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
GAM1192	LOC115129	5'	CTGTAATCCCAGGTACT 73232	G	
			AGTA CTGGGATTACAG		
			TCAT GACCCTAATGTC		
			G		
GAM1192	LOC115273	3'	ATGCCTGTAATCCCAGTTACT 73357		A
			AGTAGCTGGGATTACAG CAT		
			TCATTGACCCTAATGTC GTA		
			C		
GAM1192	LOC115761	3'	ATGCCTGTAATCCCAGCACTGT 91737	A	A
	G		TACAGT GCTGGGATTACAG CAT		
			GTGTCA CGACCCTAATGTC GTA		
			— C		
GAM1192	LOC116228	3'	CTGTAATCCCAGCACT 73798	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC116349	3'	CTGTAATCCCAGCACT 73830	A	
			AGT GCTGGGATTACAG		



TCA CGACCCTAATGTC

GAM1192 LOC119504 5' ATGCCTGTAATCCCAGCTACT 73989 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA

C

GAM1192 LOC119504 5' CTGTAATCCCAGCACT 73990 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC122704 3' CTGTAATCCCAGCACT 74139 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC122704 3' TGTAATCCCAGCTACTCA 74145 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1192 LOC122970 3' CTGTAATCCCAGTACT 74178 G  
AGTA CTGGGATTACAG  
||| |||||  
TCAT GACCCTAATGTC

GAM1192 LOC126282 3' CTGTAATCCCAGCACT 74472 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC126282 3' CTGTAATCCCAGCACT 74473 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC127262 3' ATGCCTGTAATCCCAGC 76107 A  
GCTGGGATTACAG CAT  
|||||  
CGACCCTAATGTC GTA

C

GAM1192 LOC127428 3' ATGCCTATAATCCCAGCGCT 74662 A C A  
AGT GCTGGGATTA AG CAT  
||| ||||| |||  
TCG CGACCCTAAT TC GTA

A C

GAM1192 LOC130162 3' ATGTCTGTAATCCCAGCACT 74909 A  
AGT GCTGGGATTACAGACAT  
||| |||||

TCA CGACCCTAATGTCTGTA

GAM1192 LOC130535 3' ATGCCTGTAATCCCAGC 76147 A  
GCTGGGATTACAG CAT  
||||||| |||  
CGACCCTAATGTC GTA

C

GAM1192 LOC130535 3' CTGTAGTCCCAGCTACTCA 76151 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTGATGTC

C

GAM1192 LOC130589 3' CTGTAATCCCAGCACT 57132 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC130951 3' CTGTAATCCCAACACTTTG 57143 TAGC\_  
CAG TGGGATTACAG  
||| |||||  
GTT ACCCTAATGTC  
TCACA

GAM1192 LOC131744 3' ATGCCTGTAATCCCAGCACTGT 75868 A A  
A TACAGT GCTGGGATTACAG CAT  
||||| ||||| |||  
ATGTCA CGACCCTAATGTC GTA

C

GAM1192 LOC131965 3' ATGCCTGTAATCCCAGCACT 75027 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

C

GAM1192 LOC131965 3' TGTAATCCCAGCTACTCA 75034 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT

C

GAM1192 LOC132625 3' ATGCCTGTAATCCCAACACTTT 75898 TAGC\_ A  
GT ACAG TGGGATTACAG CAT  
||||| ||||| |||  
TGTT ACCCTAATGTC GTA  
TCACA C

GAM1192 LOC132625 3' CTGTGTTCCCAGCTACTCA 75906 C T  
A AGTAGCTGGGA TACAG  
| ||||| |||||  
A TCATCGACCCT GTGTC

C T

GAM1192 LOC133926 3' ATGCCTGTAATCCCAGCGCT 75131 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||

		TCG CGACCCTAATGTC GTA		
		— C		
GAM1192	LOC134147 3'	CTGTAATCCCAGCACT 57161	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC134147 3'	GTGCCTGTAATCCCAGCTACTC 57166	C	A
	A	A AGTAGCTGGGATTACAG CAT		
		A TCATCGACCCTAATGTC GTG		
		C C		
GAM1192	LOC137362 3'	ATGCCTGTAATCCCAACACTTT 75263	TAGC_	A
	G	CAG TGGGATTACAG CAT		
		GTT ACCCTAATGTC GTA		
		TCACA C		
GAM1192	LOC138241 3'	CTGTAATCCCAACACT 75308	AGC	
		AGT TGGGATTACAG		
		TCA ACCCTAATGTC		
		CA_		
GAM1192	LOC138428 3'	ATGCCTGTAATCCCTGCTACT 75331	T	A
		AGTAGC GGGATTACAG CAT		
		TCATCG CCCTAATGTC GTA		
		T C		
GAM1192	LOC138428 3'	CTATAATCCCAGCACT 75335	A	C
		AGT GCTGGGGATTA AG		
		TCA CGACCCTAAT TC		
		— A		
GAM1192	LOC143310 3'	CTGTAATCCCAGCACT 76532	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC143888 3'	CTGTAATCCCAGCACT 76659	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC143943 3'	ATGCCTGTAATCCCAGCACT 82994	A	A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		— C		
GAM1192	LOC144289 3'	CTGTAATCCCAGCTACT 83024		
		AGTAGCTGGGATTACAG		

TCATCGACCCTAATGTC

GAM1192 LOC144289 3' TCTGTAATCCCAGCACT 83029 A  
AGT GCTGGGATTACAGA  
||| |||||  
TCA CGACCCTAATGTCT

—  
GAM1192 LOC144465 3' ATGCCTGTAATCCCAAACT 76852 AGC A  
AGT TGGGATTACAG CAT  
||| |||||  
TCA ACCCTAATGTC GTA  
AA\_ C

GAM1192 LOC144465 3' ATGCCTGTAATCCCAGCTACT 76853 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1192 LOC144465 3' TGTAATCCCAGCTACTCA 76857 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1192 LOC144481 3' ATGCCTGTAATCCCAATACT 83093 GC A  
AGTA TGGGATTACAG CAT  
||| |||||  
TCAT ACCCTAATGTC GTA  
A\_ C

GAM1192 LOC144481 3' ATGCCTGTAATCCCAGCTACT 83094 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1192 LOC144486 3' CTGTAATCCCAGCACGCTG 83083 A\_  
CAGT GCTGGGATTACAG  
||| |||||  
GTCG CGACCCTAATGTC  
CA

GAM1192 LOC144524 3' ATGCCTGTAGTCCCAGCTACTT 83121 C A  
A A AGTAGCTGGGATTACAG CAT  
| |||||  
A TCATCGACCCTGATGTC GTA  
T C

GAM1192 LOC144817 3' CTGTAATCCCAGCACT 76967 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 LOC145216 3' CTGTAATCCCAGCACT 83265 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1192 LOC145216 3' CTGTAATCCCAGCTACTCA 83266 C  
A AGTAGCTGGGATTACAG  
I |||||  
A TCATCGACCCTAATGTC  
C

GAM1192 LOC145231 3' ATGCCTATAATCCCAGCACT 83278 A C A  
AGT GCTGGGATTA AG CAT  
||| ||||| || |||  
TCA CGACCCTAAT TC GTA  
A C

GAM1192 LOC145231 3' ATGCCTGTAATCCCAGCACT 83279 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

GAM1192 LOC145231 3' ATGCCTGTAATCCCAGCTACTT 83280 \_ A  
G CA GTAGCTGGGATTACAG CAT  
|| ||||| |||  
GT CATCGACCCTAATGTC GTA  
T C

GAM1192 LOC145299 3' CTGTAATCCCAGCACT 83314 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC145333 3' CTGTAATCCCAGCACT 83326 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC145387 3' CTGTAATCCCAGCACT 83354 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC145438 3' ATGCCTGTAGCCCCAGCTACTC 83334 C AT A  
A A AGTAGCTGGG TACAG CAT  
I ||||| |||| |||  
A TCATCGACCC ATGTC GTA  
C CG C

GAM1192 LOC145438 3' CTGTAATCCCAGCACT 83336 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC145453 3' CTGTAATCTGAGCAC 77140 A G  
GT GCT GGATTACAG  
|| ||| |||||

		CA CGA TCTAATGTC			
		— G			
GAM1192	LOC145482 3'	CTGTAATCCCAGCTACT	77229		
		AGTAGCTGGGATTACAG			
		TCATCGACCCTAATGTC			
GAM1192	LOC145483 3'	CTGTAATCCCAACACT	77242	AGC	
		AGT TGGGATTACAG			
		TCA ACCCTAATGTC			
		CA_			
GAM1192	LOC145663 3'	CTGTAATCCCAGCAATTG	83413	A	
		CAGT GCTGGGATTACAG			
		GTTA CGACCCTAATGTC			
		A			
GAM1192	LOC145757 3'	ATGCCTGTAATCCCAGCACT	77454	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		— C			
GAM1192	LOC145757 3'	GTAGTCCCAGCTACTCA	77470	C	
		A AGTAGCTGGGATTAC			
		A TCATCGACCCTGATG			
		C			
GAM1192	LOC145820 3'	CTGTAATCCCAGCACT	77513	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1192	LOC145824 3'	ATGCCTGTAATCCCAGCACT	77523	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		— C			
GAM1192	LOC145955 3'	ATGCCTGTAATCCCAACACT	83588	AGC	A
		AGT TGGGATTACAG CAT			
		TCA ACCCTAATGTC GTA			
		CA_ C			
GAM1192	LOC146059 3'	ATGCCTGTAATCCCAGCACT	77619	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		— C			
GAM1192	LOC146059 3'	TGTAATCCCAGCTACTCA	77623	C	
		A AGTAGCTGGGATTACA			

A TCATCGACCCTAATGT  
 C  
 GAM1192 LOC146229 3' CTGTAATCCCAGCACTCTG 77751 TA\_  
 CAG GCTGGGATTACAG  
 ||| |||||  
 GTC CGACCCTAATGTC  
 TCA  
 GAM1192 LOC146272 5' CTGTAATCCCAGCACT 77787 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1192 LOC146332 3' CTGTAATCCCAACACT 77824 AGC  
 AGT TGGGATTACAG  
 ||| |||||  
 TCA ACCCTAATGTC  
 CA\_  
 GAM1192 LOC146540 3' ATGCCTGTAGTCCCAGCTACTC 77970 C A  
 A A AGTAGCTGGGATTACAG CAT  
 | ||||| |||  
 A TCATCGACCCTGATGTC GTA  
 C C  
 GAM1192 LOC146540 3' CTGTAATCCCAGCACT 77974 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1192 LOC146667 3' ATGCCTGTAATCCCAGCACT 83702 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||  
 TCA CGACCCTAATGTC GTA  
 C  
 GAM1192 LOC146669 3' CTGTAATCCAGCACTGTG 78058 A G  
 TACAGT GCTGG ATTACAG  
 ||||| |||| |||||  
 GTGTCA CGACC TAATGTC  
 — —  
 GAM1192 LOC146713 3' CTGTAATCCCAGCACT 83725 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1192 LOC146723 3' CTGTAATCCCAGCTACT 78083  
 AGTAGCTGGGATTACAG  
 ||||| |||||  
 TCATCGACCCTAATGTC  
 —  
 GAM1192 LOC146728 3' ATGCCTGTGGTCCCAGCTACTC 83746 C A  
 A A AGTAGCTGGGATTACAG CAT  
 | ||||| |||

			A TCATCGACCCTGGTGTC GTA		
			C C		
GAM1192	LOC146756	3'	CTGTAATCCCAGCACT 83776	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC146756	3'	CTGTAATCCCAGCACT 83777	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC146780	3'	ATGCCTGTAATCCCTGCACTTA 83786	C A T	A
			A AGT GC GGGATTACAG CAT		
			A TCA CG CCCTAATGTC GTA		
			T _ T C		
GAM1192	LOC146901	3'	ATGCCTATAATCCCAGCTACT 83829		C A
			AGTAGCTGGGATTA AG CAT		
			TCATCGACCCTAAT TC GTA		
			A C		
GAM1192	LOC146901	3'	CTGTAATCCCCGCACT 83839	A T	
			AGT GC GGGATTACAG		
			TCA CG CCCTAATGTC		
			_ C		
GAM1192	LOC146923	3'	CTGTAATCCCAGCACT 78192	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC146975	5'	CTATAATCCCAGCACT 78223	A	C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			_ A		
GAM1192	LOC147057	3'	ATGCCTGTAATCCCAGCACT 83909	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			_ C		
GAM1192	LOC147071	3'	CTGTAATCCCAGCACT 72998	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC147599	3'	ATGCCTGTAATCCCAGCACCCT 84040	TA_	A
	G		CAG GCTGGGATTACAG CAT		



		GTC CGACCCTAATGTC GTA		
		CCA C		
GAM1192	LOC147660 3'	CTGTAATCCCAGCAC	78392	A
		GT GCTGGGATTACAG		
		CA CGACCCTAATGTC		
		—		
GAM1192	LOC147664 3'	ATGCCTGTAATCCCAGCTACTT	78403	— A
	G	CA GTAGCTGGGATTACAG CAT		
		GT CATCGACCCTAATGTC GTA		
		T C		
GAM1192	LOC147664 3'	CTGTAATCCCAACACT	78408	AGC
		AGT TGGGATTACAG		
		TCA ACCCTAATGTC		
		CA_		
GAM1192	LOC147669 3'	CTGTAATCCCAGCACT	84061	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC147700 3'	ATGCCTGTAATCCCAGCTACT	59193	A
		AGTAGCTGGGATTACAG CAT		
		TCATCGACCCTAATGTC GTA		
		C		
GAM1192	LOC147700 3'	CTGTAATCCCAACACT	59197	AGC
		AGT TGGGATTACAG		
		TCA ACCCTAATGTC		
		CA_		
GAM1192	LOC147727 5'	CTATAATCCCAGCTACTCA	78467	C C
		A AGTAGCTGGGATTA AG		
		A TCATCGACCCTAAT TC		
		C A		
GAM1192	LOC147837 3'	ATGCCTGTAATCCCAGCTACT	78512	A
		AGTAGCTGGGATTACAG CAT		
		TCATCGACCCTAATGTC GTA		
		C		
GAM1192	LOC147837 3'	CTGTAATCCCAGCACT	78515	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC147990 3'	CTGTAATCCCAGCACT	84092	A
		AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

—  
GAM1192 LOC147990 3' CTGTAATCTCAGCTACTCA 84093 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACTCTAATGTC  
C

GAM1192 LOC148147 3' CTGTAATCCCAGCACT 78680 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 LOC148198 3' ATGCCTGTAATCCCAGCTACT 70676 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1192 LOC148198 3' CTGTAATCCCAGCACT 70681 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 LOC148254 3' TGCCTGTAATCCCTGCACT 78760 A T A  
AGT GC GGGATTACAG CA  
||| || ||||| ||  
TCA CG CCCTAATGTC GT  
— T C

GAM1192 LOC148343 3' TGCCTGTAATCCCCGCACT 78796 A T A  
AGT GC GGGATTACAG CA  
||| || ||||| ||  
TCA CG CCCTAATGTC GT  
— C C

GAM1192 LOC148397 3' ATGCCTGTAATCCTAGCTATT 78812 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TTATCGATCCTAATGTC GTA  
C

GAM1192 LOC148397 3' CTGTAATCCCGGCACTGTG 78817 A  
TACAGT GCTGGGATTACAG  
||||| |||||  
GTGTCA CGGCCCTAATGTC

—  
GAM1192 LOC148534 3' ATGCCTGTAATCCCAGCACT 78894 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
— C

GAM1192 LOC148734 3' CTGTAATCCCAGCACT 78954 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1192 LOC148749 3' CTGTAATCCCAGCACT 78960 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC148758 5' ATGCCTATAATCCCAGCTACTT 78965 \_ C A  
G CA GTAGCTGGGATTA AG CAT  
|| ||||| || |||  
GT CATCGACCCTAAT TC GTA  
T A C

GAM1192 LOC148758 5' ATGCCTGTAATCCCAGAACT 78966 AG A  
AGT CTGGGATTACAG CAT  
||| ||||| |||  
TCA GACCCTAATGTC GTA  
A\_ C

GAM1192 LOC148809 3' ATGCCTATAATCCCAGCTTCT 79000 T C A  
AG AGCTGGGATTA AG CAT  
|| ||||| || |||  
TC TCGACCCTAAT TC GTA  
T A C

GAM1192 LOC148809 5' CTGTAATCCCAGCACT 79003 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC148918 5' CTGTAATCCCAGCACT 79071 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC148936 3' CTGTAATCCCAGCACT 84290 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC148938 3' CTGTAATCCCAGCACT 84270 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC149073 3' CTATAATCCCAGCACT 84324 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC

GAM1192 LOC149073 3' GTGCCTGTAATCCCAGCTACTC 84331 C A  
A A AGTAGCTGGGATTACAG CAT  
| ||||| |||

			A TCATCGACCCTAATGTC GTG		
			C C		
GAM1192	LOC149113	3'	CTGTAATCCCAGAACTTTA	79164	C AG
			TA AGT CTGGGATTACAG		
			AT TCA GACCCTAATGTC		
			T A_		
GAM1192	LOC149113	3'	CTGTAATCCCAGCACT	79165	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC149194	5'	CTGTAATCCCAGCTACTCA	79225	C
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTAATGTC		
			C		
GAM1192	LOC149194	5'	GTCTGTAATCCCAGCACT	79229	A
			AGT GCTGGGATTACAGAC		
			TCA CGACCCTAATGTCTG		
			—		
GAM1192	LOC149271	3'	CTGTAATCCCAGCACT	79240	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC149319	3'	GTCTGTAATCCCAGCACT	79301	A
			AGT GCTGGGATTACAGAC		
			TCA CGACCCTAATGTCTG		
			—		
GAM1192	LOC149579	5'	CTGTAATCCCAGCACT	71133	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC149606	3'	GTCTGTAGTCCCAGCTACTCA	79455	C
			A AGTAGCTGGGATTACAGAC		
			A TCATCGACCCTGATGTCTG		
			C		
GAM1192	LOC149628	3'	CTATAATCCCAGCTACT	79462	C
			AGTAGCTGGGATTA AG		
			TCATCGACCCTAAT TC		
			A		
GAM1192	LOC149628	3'	CTGTAATCCCAGCACT	79463	A
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

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      —
GAM1192 LOC149668 3' ATGCCTGTAATCCCAGCACT 84534  A      A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      —      C
GAM1192 LOC149705 3' CTGTAATCCCAACACTTTG 84623  TAGC_
      CAG  TGGGATTACAG
      ||| |||||
      GTT  ACCCTAATGTC
      TCACA
GAM1192 LOC149837 3' TGGAAATCCCAGCTAT 84747      A_
      GTAGCTGGGATT CA
      ||||| ||
      TATCGACCCTAA GT
      AG
GAM1192 LOC150139 3' ATGCCTGTAATCCCAGCTG 79584      A
      TAGCTGGGATTACAG CAT
      ||||| |||
      GTCGACCCTAATGTC GTA
      C
GAM1192 LOC150185 3' ATGCCTGTAATCCCAACACT 84905  AGC      A
      AGT TGGGATTACAG CAT
      ||| ||||| |||
      TCA ACCCTAATGTC GTA
      CA_      C
GAM1192 LOC150319 3' ATGCCTGTAATCCCAGCACT 79647  A      A
      AGT GCTGGGATTACAG CAT
      ||| ||||| |||
      TCA CGACCCTAATGTC GTA
      —      C
GAM1192 LOC150319 3' ATGCCTGTAATCCCAGTTACTC 79648  C      A
      A
      A AGTAGCTGGGATTACAG CAT
      | ||||| |||
      A TCATTGACCCTAATGTC GTA
      C      C
GAM1192 LOC150343 3' CTGTAATCCCAGCACT 79672  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC
      —
GAM1192 LOC150358 3' ATGCCTATAATCCCAGCACT 84920  A      C A
      AGT GCTGGGATTA AG CAT
      ||| ||||| || |||
      TCA CGACCCTAAT TC GTA
      —      A C
GAM1192 LOC150358 3' ATGCCTGTAATCCCAGCACT 84921  A      A
      AGT GCTGGGATTACAG CAT
      ||| ||||| |||
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			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	LOC150358	3'	CTGTAATCCCAGGTACTCA	84922	C G
			A AGTA CTGGGATTACAG		
			I		
			A TCAT GACCCTAATGTC		
			C G		
GAM1192	LOC150372	3'	ATGCCTGTAATCCCAGC	79786	A
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1192	LOC150481	3'	CTGTAATCCCAGCACT	79884	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC150622	3'	CTGTAATCCCAACACT	79958	AGC
			AGT TGGGATTACAG		
			TCA ACCCTAATGTC		
			CA_		
GAM1192	LOC150630	3'	ATGCCTATAATCCCAGCTACT	85099	C A
			AGTAGCTGGGATTA AG CAT		
			TCATCGACCCTAAT TC GTA		
			A C		
GAM1192	LOC150630	3'	ATGCCTGTAATCCCAGCACT	85100	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			C		
GAM1192	LOC150889	3'	ATGCCTGTAATCCCAGCACT	80024	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			C		
GAM1192	LOC150935	3'	ATGCCTGTAATCCCAGCGCT	80031	A A
			AGT GCTGGGATTACAG CAT		
			TCG CGACCCTAATGTC GTA		
			C		
GAM1192	LOC150998	3'	CTGTGGTCCCAGCTAC	85183	
			GTAGCTGGGATTACAG		
			CATCGACCCTGGTGTC		
			—		
GAM1192	LOC151196	3'	CTGTAACCCCAGCTACTCA	85265	C A
			A AGTAGCTGGG TTACAG		
			I		

		A TCATCGACCC AATGTC	
		C C	
GAM1192	LOC151196 3'	CTGTAATCCCAGCACT	85266 A
		AGT GCTGGGATTACAG	
		TCA CGACCCTAATGTC	
		—	
GAM1192	LOC151248 3'	CTGTAATCCCAGCACT	80186 A
		AGT GCTGGGATTACAG	
		TCA CGACCCTAATGTC	
		—	
GAM1192	LOC151248 3'	TGTAATCCCAGCTACTCA	80193 C
		A AGTAGCTGGGATTACA	
		A TCATCGACCCTAATGT	
		C	
GAM1192	LOC151429 3'	ATGCCTGTAATCCCAGC	85344 A
		GCTGGGATTACAG CAT	
		CGACCCTAATGTC GTA	
		C	
GAM1192	LOC151429 3'	CTGTAATCCCAGCACT	85352 A
		AGT GCTGGGATTACAG	
		TCA CGACCCTAATGTC	
		—	
GAM1192	LOC151446 3'	ATGCCTGTAATCCCAGCTACTG	85375 A
		CAGTAGCTGGGATTACAG CAT	
		GTCATCGACCCTAATGTC GTA	
		C	
GAM1192	LOC151556 3'	CTGTAATCCCAGTACT	80274 G
		AGTA CTGGGATTACAG	
		TCAT GACCCTAATGTC	
		—	
GAM1192	LOC151556 3'	TGTAATCCCAGCTACTCA	80283 C
		A AGTAGCTGGGATTACA	
		A TCATCGACCCTAATGT	
		C	
GAM1192	LOC151602 3'	CTGTAATCCCAACACT	80294 AGC
		AGT TGGGATTACAG	
		TCA ACCCTAATGTC	
		CA_	
GAM1192	LOC151602 3'	CTGTAATCCCAGCTACTCA	80295 C
		A AGTAGCTGGGATTACAG	

		A TCATCGACCCTAATGTC			
		C			
GAM1192	LOC151614 3'	CTGTAATCCCAGCACT	80304	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1192	LOC151623 3'	ATGCCTGTGGTCTCAGCTACTC	85456	C	A
	A	A AGTAGCTGGGATTACAG CAT			
		A TCATCGACTCTGGTGTC GTA			
		C C			
GAM1192	LOC151904 3'	CTGTAATCCCAGCACT	80390	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1192	LOC152263 3'	CTGTAATCCCAGCACT	85674	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1192	LOC152263 3'	TCCATAATCCTAGCTGCT	85676		CA
		AGTAGCTGGGATTA GA			
		TCGTCGATCCTAAT CT			
		AC			
GAM1192	LOC152316 3'	ATGCCTGTAATCCCAGCACTTT	85609	C A	A
	A	TA AGT GCTGGGATTACAG CAT			
		AT TCA CGACCCTAATGTC GTA			
		T — C			
GAM1192	LOC152426 3'	CTGTAATCCCAGCACT	85714	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1192	LOC152445 3'	ATGCCTGTAATCCCAACTACT	85746	C	A
		AGTAG TGGGATTACAG CAT			
		TCATC ACCCTAATGTC GTA			
		A C			
GAM1192	LOC152453 3'	ATGCCTGTAATCCCAGCACT	80592	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		— C			
GAM1192	LOC152453 3'	ATGCCTGTAATCCCAGCTACT	80593		A
		AGTAGCTGGGATTACAG CAT			



			TCATCGACCCTAATGTC	GTA		
			C			
GAM1192	LOC152453	3'	CTGTAATCCCAACACT	80595	AGC	
			AGT TGGGATTACAG			
			TCA ACCCTAATGTC			
			CA_			
GAM1192	LOC152453	3'	CTGTAATCCCAGCACT	80596	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	LOC152453	3'	CTGTAATCCCAGTTACTCA	80597	C	
			A AGTAGCTGGGATTACAG			
			A TCATTGACCCTAATGTC			
			C			
GAM1192	LOC152627	5'	TGTAATCCCAGCTACTCA	80632	C	
			A AGTAGCTGGGATTACA			
			A TCATCGACCCTAATGT			
			C			
GAM1192	LOC152804	3'	ATGCCTGTAATCCCAGCTACT	85878		A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1192	LOC152860	3'	ATGTCTGTAATCCCAGCTACTG	80696		
			CAGTAGCTGGGATTACAGACAT			
			GTCATCGACCCTAATGTCTGTA			
GAM1192	LOC152860	3'	CTATAATCCCAGCACT	80701	A	C
			AGT GCTGGGATTA AG			
			TCA CGACCCTAAT TC			
			— A			
GAM1192	LOC152926	3'	ATGCCTGTAATCCCAGCACT	80744	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1192	LOC153077	3'	CTATAATCCCAGCTACTCA	85909	C	C
			A AGTAGCTGGGATTA AG			
			A TCATCGACCCTAAT TC			
			C A			
GAM1192	LOC153260	3'	CTGTAATCCCAGCACT	80804	A	
			AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

GAM1192 LOC153561 3' ATGCCTGTAATCCCAGCACT 80888 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
C  
GAM1192 LOC153579 3' CTGTAATCCCAGTACT 80895 G  
AGTA CTGGGATTACAG  
||| |||||  
TCAT GACCCTAATGTC  
GAM1192 LOC153642 3' CTATAGTCTCAGCTACTCA 80907 C C  
A AGTAGCTGGGATTA AG  
| ||||| ||  
A TCATCGACTCTGAT TC  
C A  
GAM1192 LOC153642 3' CTGTAATCCCAGGACT 80908 AG  
AGT CTGGGATTACAG  
||| |||||  
TCA GACCCTAATGTC  
G\_  
GAM1192 LOC153682 3' ATGCCTGTAATCCCAGCACT 86084 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
C  
GAM1192 LOC153688 3' ATGCCTATAATCCCAGCACT 86095 A C A  
AGT GCTGGGATTA AG CAT  
||| ||||| || |||  
TCA CGACCCTAAT TC GTA  
A C  
GAM1192 LOC154092 3' TCTGTAATCCCAGCACT 86161 A  
AGT GCTGGGATTACAGA  
||| |||||  
TCA CGACCCTAATGTCT  
GAM1192 LOC154215 3' ATGTCTGTAATATACACACAC 81053 AGC GG\_  
GT TG ATTACAGACAT  
|| || |||||  
CA AC TAATGTCTGTA  
CAC ATA  
GAM1192 LOC154403 3' CTGTAATCCCAGAACTTTA 81071 C AG  
TA AGT CTGGGATTACAG  
|| ||| |||||  
AT TCA GACCCTAATGTC  
T A\_  
GAM1192 LOC154739 5' ATGTCTATAATTCCAGCTACTC 86225 C C  
A A AGTAGCTGGGATTA AGACAT  
| ||||| |||||

		A TCATCGACCTTAAT TCTGTA		
		C            A		
GAM1192	LOC154791 3'	ATGCCTGTAATCCCAGCTACT	81154	A
		AGTAGCTGGGATTACAG CAT		
		TCATCGACCCTAATGTC GTA		
		C		
GAM1192	LOC154791 3'	CTGTAATCCCAGCACT	81156	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC154992 3'	CTGTAATCCCAGAACTTTA	81215	C AG
		TA AGT CTGGGATTACAG		
		AT TCA GACCCTAATGTC		
		T A_		
GAM1192	LOC155006 3'	ATGCCTGTAATCCCAGCACT	81229	A      A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		C		
GAM1192	LOC155006 3'	ATGCCTGTAATCCCAGCACT	81230	A      A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		C		
GAM1192	LOC155006 3'	CTGTAATCCCAGCTACTTG	81237	—
		CA GTAGCTGGGATTACAG		
		GT CATCGACCCTAATGTC		
		T		
GAM1192	LOC155072 3'	CTGTAATCCCAGCACT	86375	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC155072 3'	CTGTAATCCCAGCACT	86376	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC155438 3'	CTGTAATCCCAGTACCT	86393	TA
		AG GCTGGGATTACAG		
		TC TGACCCTAATGTC		
		CA		
GAM1192	LOC157278 3'	CTGTAATCCCAGCACT	86423	A
		AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

—  
GAM1192 LOC157292 5' CTGTAATCTCAGTTACTCA 86413 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATTGACTCTAATGTC  
C

GAM1192 LOC157464 5' CTGTAATCCCAGCACT 86448 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 LOC157657 3' ATGCCTGTAATCCCACTACT 81516 C A  
AGTAG TGGGATTACAG CAT  
|||| ||||| |||  
TCATC ACCCTAATGTC GTA  
A C

GAM1192 LOC157657 3' CTGTAATCCCAGCACT 81518 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 LOC157660 3' CTGTAATCCCAGCACT 86507 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 LOC158160 3' TGTAGTCCCACTACTCA 73082 C C  
A AGTAG TGGGATTACA  
| |||| |||||  
A TCATC ACCCTGATGT  
C A

GAM1192 LOC158187 3' CTGTAGTCCCAGCTAC 86691  
GTAGCTGGGATTACAG  
|||||||  
CATCGACCCTGATGTC

GAM1192 LOC158191 3' CTGTAATCCCAGCACT 81775 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 LOC158292 5' ATGCCTGTAATCCCAGCACT 86728 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

—  
GAM1192 LOC158292 5' TGTAATCCCAGCTACTCA 86732 C  
A AGTAGCTGGGATTACA  
| |||||

			A TCATCGACCCTAATGT		
			C		
GAM1192	LOC158310	3'	CTGTAATCCCAGCACT	86753	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC158819	5'	ATGCCTGTAATCCCAGCTTCT	86901	T A
			AG AGCTGGGATTACAG CAT		
			TC TCGACCCTAATGTC GTA		
			T C		
GAM1192	LOC158819	3'	CTGTAATCCCAGCACT	86903	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC158819	5'	CTGTAATCCCAGCACT	86904	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC158863	3'	CTGTAATCCCAACACT	86923	AGC
			AGT TGGGATTACAG		
			TCA ACCCTAATGTC		
			CA_		
GAM1192	LOC158987	3'	CTGTAATCCCAACACT	86961	AGC
			AGT TGGGATTACAG		
			TCA ACCCTAATGTC		
			CA_		
GAM1192	LOC159036	3'	ATGCCTGTAATCCCAGCACT	86969	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	LOC159053	3'	CTGTAATCCCAGGACT	86978	AG
			AGT CTGGGATTACAG		
			TCA GACCCTAATGTC		
			G_		
GAM1192	LOC161823	3'	ATGCCTGTAATCCCAGCACT	82300	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	LOC170395	3'	CTGCAGTCCCAGCTACTCA	76368	C A
			A AGTAGCTGGGATT CAG		

			A TCATCGACCCTGA GTC		
			C C		
GAM1192	LOC170395 3'	CTGTAATCCCAGCACT	76369	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1192	LOC196047 5'	CTGTAATCCCAGTACT	89600	G	
		AGTA CTGGGATTACAG			
		TCAT GACCCTAATGTC			
		—			
GAM1192	LOC196528 3'	CTATAATCCCAGCACT	87764	A	C
		AGT GCTGGGATTA AG			
		TCA CGACCCTAAT TC			
		— A			
GAM1192	LOC197196 3'	CTGTAATCCCAGCACT	89733	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1192	LOC197201 3'	ATGCCTGTAATCTCAGCTACTC	87933	C	A
	A	A AGTAGCTGGGATTACAG CAT			
		A TCATCGACTCTAATGTC GTA			
		C C			
GAM1192	LOC197201 3'	CTGTAATCCCAGCACT	87936	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1192	LOC197319 3'	CTGTAATCCCAGCACT	87969	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1192	LOC197319 3'	CTGTAATCCCAGCTCCT	87970	T	
		AG AGCTGGGATTACAG			
		TC TCGACCCTAATGTC			
		C			
GAM1192	LOC199733 3'	CTGAAATCCCAGCTACTG	89849		A
		CAGTAGCTGGGATT CAG			
		GTCATCGACCCTAA GTC			
		A			
GAM1192	LOC199786 3'	CTGTAATCCCAGCACT	88380	A	
		AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

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GAM1192 LOC200014 3' CTGTAATCCCACCACT   88526   AGC
      AGT TGGGATTACAG
      ||| |||||
      TCA ACCCTAATGTC
      CC_
GAM1192 LOC200251 5' CTGTAATCCCAGCTACTCA 88665   C
      A AGTAGCTGGGATTACAG
      | |||||
      A TCATCGACCCTAATGTC
      C
GAM1192 LOC200317 3' CTGTAATCCCAGCTACTTG 88794   _
      CA GTAGCTGGGATTACAG
      || |||||
      GT CATCGACCCTAATGTC
      T
GAM1192 LOC200470 3' CTGTAATCCCAACACT   90062   AGC
      AGT TGGGATTACAG
      ||| |||||
      TCA ACCCTAATGTC
      CA_
GAM1192 LOC200728 3' CTGTAATCCCAGCACT   90115   A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC
      -
GAM1192 LOC200803 3' ATGCCTGTAATCCTAGCTACTC 88879   C           A
      A
      A AGTAGCTGGGATTACAG CAT
      | ||||| |||
      A TCATCGATCCTAATGTC GTA
      C           C
GAM1192 LOC200803 3' TGCCTGTAATCCCACCACT 88881   AGC           A
      AGT TGGGATTACAG CA
      ||| ||||| ||
      TCA ACCCTAATGTC GT
      CC_           C
GAM1192 LOC200918 3' TGTAATCCCAGCTACTTA 88943   C
      A AGTAGCTGGGATTACA
      | |||||
      A TCATCGACCCTAATGT
      T
GAM1192 LOC200940 3' ATGCCTGTAATCCCAGCTACTT 88950   _           A
      G
      CA GTAGCTGGGATTACAG CAT
      || ||||| |||
      GT CATCGACCCTAATGTC GTA
      T           C
GAM1192 LOC201173 3' CTGTAATCCCAGCACT   87328   A
      AGT GCTGGGATTACAG
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TCA CGACCCTAATGTC

GAM1192 LOC201182 5' ATGCCTGTAATCCCAGCTAC 89763 A  
GTAGCTGGGATTACAG CAT  
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CATCGACCCTAATGTC GTA

C

GAM1192 LOC201220 3' CTGTAATCCCAGCACT 87349 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

GAM1192 LOC201252 3' ATGCCTGTAATCCCACTACT 88165 C A  
AGTAG TGGGATTACAG CAT  
|||| |||||  
TCATC ACCCTAATGTC GTA

A C

GAM1192 LOC201252 3' CTGTAATCCCAGAACT 88168 AG  
AGT CTGGGATTACAG  
||| |||||  
TCA GACCCTAATGTC

A\_

GAM1192 LOC201564 3' ATGCCTGTAATCCCAGCTACTT 80435 \_ A  
G CA GTAGCTGGGATTACAG CAT  
|| |||||  
GT CATCGACCCTAATGTC GTA

T C

GAM1192 LOC201685 3' ATGTCTATGGTCCCAGCTACTC 90239 C C  
A A AGTAGCTGGGATTA AGACAT  
| |||||  
A TCATCGACCCTGGT TCTGTA

C A

GAM1192 LOC201685 3' CTGTAATCCCAGCACT 90241 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

GAM1192 LOC201689 3' CTGTAATCCCAGCACT 67144 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

GAM1192 LOC201868 3' CTGTAATCCCAGCACT 89077 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

GAM1192 LOC201868 3' TGTAATCCCAGCTACTCA 89084 C  
A AGTAGCTGGGATTACA  
| |||||



		A TCATCGACCCTAATGT		
		C		
GAM1192	LOC201895 3'	CTGTAATCCCAGCACT	89087	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC201895 3'	GTGCCTGTAATCCCAGCTACTC	89091	C
	A	A AGTAGCTGGGATTACAG CAT		A
		A TCATCGACCCTAATGTC GTG		
		C C		
GAM1192	LOC201911 3'	CTGTAATCCCAGCACT	90261	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC202868 3'	CTGTAATCCCAGCACT	90373	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC202868 3'	CTGTAATCCCAGCACT	90374	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC203025 3'	ATGCCTGTAATCCCAACACTTT	89249	TAGC_ A
	G	CAG TGGGATTACAG CAT		
		GTT ACCCTAATGTC GTA		
		TCACA C		
GAM1192	LOC203246 3'	CTGTAATCCCAGCACT	89304	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC203276 3'	GTCTATAATTCCAGCTACTCA	90487	C C
		A AGTAGCTGGGATTA AGAC		
		A TCATCGACCTTAAT TCTG		
		C A		
GAM1192	LOC203305 3'	GTCTATAATTCCAGCTACTCA	90531	C C
		A AGTAGCTGGGATTA AGAC		
		A TCATCGACCTTAAT TCTG		
		C A		
GAM1192	LOC203350 3'	ATGCCTGTAATCCCAGCACT	90560	A A
		AGT GCTGGGATTACAG CAT		

TCA CGACCCTAATGTC GTA  
 — C  
 GAM1192 LOC203350 3' ATGCCTGTAGTTGCAGCTACTC 90561 C G A  
 A A AGTAGCTG GATTACAG CAT  
 I ||||| ||||| ||  
 A TCATCGAC TTGATGTC GTA  
 C G C  
 GAM1192 LOC203378 3' CTGTAATCCCGGCACT 90602 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGGCCCTAATGTC  
 —  
 GAM1192 LOC203378 3' CTGTAGTTCCAGCTACTG 90603  
 CAGTAGCTGGGATTACAG  
 |||||  
 GTCATCGACCTTGATGTC  
 —  
 GAM1192 LOC219406 3' CTGCAATCCCAGCTACT 93559 A  
 AGTAGCTGGGATT CAG  
 ||||| ||  
 TCATCGACCCTAA GTC  
 C  
 GAM1192 LOC219406 3' CTGTAATCCCAGCACT 93560 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1192 LOC219540 3' CTGTAATCCCAGCTACTTG 93598 —  
 CA GTAGCTGGGATTACAG  
 || |||||  
 GT CATCGACCCTAATGTC  
 T  
 GAM1192 LOC219627 3' ATGCCTGTAATCCCAACACT 92175 AGC A  
 AGT TGGGATTACAG CAT  
 ||| ||||| ||  
 TCA ACCCTAATGTC GTA  
 CA\_ C  
 GAM1192 LOC219627 3' CTGTAATCCCAGCACT 92177 A  
 AGT GCTGGGATTACAG  
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 TCA CGACCCTAATGTC  
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 GAM1192 LOC219627 3' GTGCCTGTAATCCCAGCTACTC 92185 C A  
 A A AGTAGCTGGGATTACAG CAT  
 I ||||| ||  
 A TCATCGACCCTAATGTC GTG  
 C C  
 GAM1192 LOC219649 3' ATGCCTATAATCCCAGC 92950 C A  
 GCTGGGATTA AG CAT  
 ||||| || ||

CGACCCTAAT TC GTA

A C

GAM1192 LOC219649 3' CTGTAATCCCAGCTACT 92956  
AGTAGCTGGGATTACAG  
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TCATCGACCCTAATGTC

GAM1192 LOC219649 3' GTCTGTAATCCCAGCACT 92961 A  
AGT GCTGGGATTACAGAC  
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TCA CGACCCTAATGTCTG

—  
GAM1192 LOC219672 5' ATGCCTGTAATCCCAGCACT 91328 A A  
AGT GCTGGGATTACAG CAT  
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TCA CGACCCTAATGTC GTA

— C  
GAM1192 LOC219673 3' CTGTAATCCCAGCACT 93031 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

—  
GAM1192 LOC219722 5' CTGTAATCCCAGCACT 93081 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

—  
GAM1192 LOC220370 3' ATGCCTGTAATCCCAACACTCT 92824 T C\_\_ A  
G CAG AG TGGGATTACAG CAT  
||| ||| |||||  
GTC TC ACCCTAATGTC GTA

— ACA C  
GAM1192 LOC220506 3' CTATAATCCCAGCACTTTA 74077 C A C  
TA AGT GCTGGGATTA AG  
|| ||| ||||| ||  
AT TCA CGACCCTAAT TC  
T \_ A

GAM1192 LOC220662 3' CTGTAATCCCAGCACT 91169 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 LOC220662 3' CTGTAATCCCAGCACT 91170 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

—  
GAM1192 LOC220662 3' CTGTAATCCCAGCTACTTG 91171 \_  
CA GTAGCTGGGATTACAG  
|| |||||

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GT CATCGACCCTAATGTC
T
GAM1192 LOC220662 3' CTGTCATCCCAGCTACTCA 91172 C T
A AGTAGCTGGGAT ACAG
| ||||| |||
A TCATCGACCCTA TGTC
C C
GAM1192 LOC220906 3' ATGCCTGTAATCCCAACACT 91396 AGC A
AGT TGGGATTACAG CAT
||| ||||| |||
TCA ACCCTAATGTC GTA
CA_ C
GAM1192 LOC221042 3' CTGTAATCCCAGCGCT 93185 A
AGT GCTGGGATTACAG
||| ||||| |||
TCG CGACCCTAATGTC
-
GAM1192 LOC221178 3' ATGCCTGTAATCCCAGCACT 93527 A A
AGT GCTGGGATTACAG CAT
||| ||||| |||
TCA CGACCCTAATGTC GTA
- C
GAM1192 LOC221178 3' ATGCCTGTAATCCCAGCTACTG 93528 A
CAGTAGCTGGGATTACAG CAT
||||| |||
GTCATCGACCCTAATGTC GTA
C
GAM1192 LOC221271 3' CTGTAATCCCAGCACT 91856 A
AGT GCTGGGATTACAG
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TCA CGACCCTAATGTC
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GAM1192 LOC221271 3' CTGTAATCCCAGCTACT 91857
AGTAGCTGGGATTACAG
||||| |||
TCATCGACCCTAATGTC
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GAM1192 LOC221474 3' CTGTAATCCCAGCACT 92381 A
AGT GCTGGGATTACAG
||| ||||| |||
TCA CGACCCTAATGTC
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GAM1192 LOC221474 3' TGTAATCCCAGCTACTCA 92389 C
A AGTAGCTGGGATTACA
| ||||| |||
A TCATCGACCCTAATGT
C
GAM1192 LOC221477 3' CTGTAATCCCAGCTAC 92152
GTAGCTGGGATTACAG
||||| |||

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CATCGACCCTAATGTC

GAM1192 LOC221489 3' CTGTAATCCCAGCACT 93641 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

—  
GAM1192 LOC221490 3' CTGTAATCCCAGCACT 93658 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

—  
GAM1192 LOC221543 3' CTGTAATCCCAGCACT 93740 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 LOC221543 5' CTGTAATCCCAGCACTCTG 93741 TA\_  
CAG GCTGGGATTACAG  
||| |||||  
GTC CGACCCTAATGTC  
TCA

GAM1192 LOC221931 3' ATGCCTGTAATCCCAGCACT 93993 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
C

—  
GAM1192 LOC221954 5' CTGTAATCCCAGCACT 94000 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1192 LOC221962 3' CTGTAATCCCAGCACT 92681 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

—  
GAM1192 LOC222066 3' CTGTAATCCCAGCTATT 92744  
AGTAGCTGGGATTACAG  
|||||||  
TTATCGACCCTAATGTC

GAM1192 LOC222160 5' ATGCCTGTAATCCCAGCACT 94118 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

— C  
GAM1192 LOC222160 3' CTGTAATCCCAGCTACT 94125  
AGTAGCTGGGATTACAG  
|||||||

TCATCGACCCTAATGTC

GAM1192 LOC222182 3' CTGTAATCCCTTAGCTACTCA 94189 C \_\_\_\_  
A AGTAGCT GGGATTACAG  
| ||||| |||||  
A TCATCGA CCCTAATGTC  
C TT

GAM1192 LOC222865 3' CTGTAATCCCAGCACT 92860 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC253612 3' CTGTAATCCCAACACT 96748 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1192 LOC253612 3' GTCTGTAATCCCAGCTACT 96755  
AGTAGCTGGGATTACAGAC  
|||||  
TCATCGACCCTAATGTCTG

GAM1192 LOC253639 3' ATGCCTGTAATCCCAGCTACT 95818 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1192 LOC253927 3' ATGCCTGTAATCCCAGCACT 95023 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
C

GAM1192 LOC254045 3' ATGCCTGTAATCCCAATACT 96502 GC A  
AGTA TGGGATTACAG CAT  
||| |||||  
TCAT ACCCTAATGTC GTA  
A\_ C

GAM1192 LOC254045 3' ATGCCTGTAATCCCAGCTACT 96503 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1192 LOC254243 3' GTCTATAATTCCAGCTACTCA 97416 C C  
A AGTAGCTGGGATTA AGAC  
| |||||  
A TCATCGACCTTAAT TCTG  
C A

GAM1192 LOC254249 5' TGCTTGTCCTCCAGCTACTG 95449 TAC A  
CAGTAGCTGGGAT AG CA  
||||| ||

GTCATCGACCCTG TC GT  
 T\_\_ \_  
 GAM1192 LOC254531 5' ATGCCTGTAATCCCAGCTACTT 94980 \_ A  
 G CA GTAGCTGGGATTACAG CAT  
 || |||||  
 GT CATCGACCCTAATGTC GTA  
 T C  
 GAM1192 LOC254531 5' CTGTAATCCCAGCACT 94985 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1192 LOC255042 3' ATGCCTGTAATCCTAGCTACTC 95312 C A  
 A A AGTAGCTGGGATTACAG CAT  
 | |||||  
 A TCATCGATCCTAATGTC GTA  
 C C  
 GAM1192 LOC255042 3' CTGTAATCCCAGCACT 95315 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1192 LOC255042 3' CTGTAATCCCAGCACT 95316 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1192 LOC255177 3' CTGTAATCCCAGCACT 96605 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1192 LOC255196 3' ATGCCTATAATCCCAGCACT 97164 A C A  
 AGT GCTGGGATTA AG CAT  
 ||| ||||| || |||  
 TCA CGACCCTAAT TC GTA  
 \_ A C  
 GAM1192 LOC255196 5' CTGTAATCCCAGCACT 97169 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1192 LOC255231 3' CTGTAATCCCAGCACT 95373 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1192 LOC255252 3' ATGCCTATAATCCCAGCACT 95006 A C A  
 AGT GCTGGGATTA AG CAT  
 ||| ||||| || |||

			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1192	LOC255326	3'	CTGTAATCCCAGACTGTG 96376	AG	
			TACAGT CTGGGATTACAG		
			GTGTCA GACCCTAATGTC		
			—		
GAM1192	LOC255328	3'	ATGTCTGTAATCCCAGCACT 96557	A	
			AGT GCTGGGATTACAGACAT		
			TCA CGACCCTAATGTCTGTA		
			—		
GAM1192	LOC255461	3'	CTGTAATCCCAGCACT 97319	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC255516	3'	CTGTAATCCCAGCACT 97332	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC255624	3'	CTGTAATCCCAGCACT 94523	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC255671	3'	CTGTAATCCCAGCTGCT 97255		
			AGTAGCTGGGATTACAG		
			TCGTCGACCCTAATGTC		
			—		
GAM1192	LOC255671	3'	TCTGTAATCCCAGCACT 97264	A	
			AGT GCTGGGATTACAGA		
			TCA CGACCCTAATGTCT		
			—		
GAM1192	LOC255937	3'	ATGCCTGTAATCCCAGCTACT 95987		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1192	LOC255937	3'	CTGTAATCCCAGCTCT 95988	T	
			AG AGCTGGGATTACAG		
			TC TCGACCCTAATGTC		
			—		
GAM1192	LOC255971	3'	CTATAATCCCAGCACT 96533	A	C
			AGT GCTGGGATTA AG		



			TCA CGACCCTAAT TC		
			— A		
GAM1192	LOC256073	3'	CTGTAATCCCAATGCT	96664	GC
			AGTA TGGGATTACAG		
			TCGT ACCCTAATGTC		
			A_		
GAM1192	LOC256207	3'	TCTGTAATTGCTATTG	95179	TGG
			CAGTAGC GATTACAGA		
			GTTATCG TTAATGTCT		
			—		
GAM1192	LOC256267	3'	ATGCCTGTAATCCCAGCACT	96797	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	LOC256277	3'	CTGTAATCCCAGCACT	94698	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC256520	3'	TGTAATCCCAGCTACTCA	95981	C
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1192	LOC256980	3'	TCTGTAATCCCAGCACTCTG	95223	TA_
			CAG GCTGGGATTACAGA		
			GTC CGACCCTAATGTCT		
			TCA		
GAM1192	LOC257354	3'	ATGCCTATAATCCCAACACT	95085	AGC C A
			AGT TGGGATTA AG CAT		
			TCA ACCCTAAT TC GTA		
			CA_ A C		
GAM1192	LOC257480	3'	CTGTAATCCCAGCACT	77869	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC257539	3'	ATGCCTGTAATCCCAGCACT	97699	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	LOC257578	3'	ATGCCTGTAATCCCAGCACT	97819	A A
			AGT GCTGGGATTACAG CAT		

				TCA CGACCCTAATGTC GTA		
				— C		
GAM1192	LOC257596	3'	CTGTAATCCCAGCACT	97933	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	LOC257596	5'	CTGTAATCCCAGCACTCTG	97934	TA_	
			CAG GCTGGGATTACAG			
			GTC CGACCCTAATGTC			
			TCA			
GAM1192	LOC51145	3'	TGTAATCCCAGCTACTCA	32400	C	
			A AGTAGCTGGGATTACA			
			A TCATCGACCCTAATGT			
			C			
GAM1192	LOC51333	3'	CTGTAATCCCAGCACT	33567	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1192	LOC51333	3'	CTGTAATCCCAGCTACTG	33568		
			CAGTAGCTGGGATTACAG			
			GTCATCGACCCTAATGTC			
			—			
GAM1192	LOC51652	3'	ATGCCTATAATCCCAGTGCT	32191	G	C A
			AGTA CTGGGATTA AG CAT			
			TCGT GACCCTAAT TC GTA			
			A C			
			—			
GAM1192	LOC51716	3'	TGCCTGTAATCCCTGC	32795	T	A
			GC GGGATTACAG CA			
			CG CCCTAATGTC GT			
			T C			
GAM1192	LOC51759	3'	ATGCCTGTAATCCCAGCTGCT	72812		A
			AGTAGCTGGGATTACAG CAT			
			TCGTCGACCCTAATGTC GTA			
			C			
GAM1192	LOC55974	3'	ATGCCTGTAATCCCAGATACT	38130	G	A
			AGTA CTGGGATTACAG CAT			
			TCAT GACCCTAATGTC GTA			
			A C			
GAM1192	LOC55974	3'	CTGTAATCCCAGCACT	38131	A	
			AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

GAM1192 LOC57118 3' CTGTAATCCCAACACT 39867 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1192 LOC63929 3' ATGCCTGTAATCCTGGCTACT 42041 TG A  
AGTAGC GGATTACAG CAT  
||||| ||||| |||  
TCATCG CCTAATGTC GTA  
GT C

GAM1192 LOC64167 3' CTGTAATCCCAGCACT 42279 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC89890 3' CTGTAATCCCAGCTAC 60578  
GTAGCTGGGATTACAG  
|||||  
CATCGACCCTAATGTC

GAM1192 LOC90038 3' GTCTATAATTCCAGCTACTCA 61159 C C  
A AGTAGCTGGGATTA AGAC  
| ||||| |||  
A TCATCGACCTTAAT TCTG  
C A

GAM1192 LOC90092 3' CTGTAATCCCAGCACT 61405 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC90092 3' CTGTAATCCCAGCACT 61406 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1192 LOC90141 3' ATGCCTACAATCCCAGCACT 61625 A AC A  
AGT GCTGGGATT AG CAT  
||| ||||| |||  
TCA CGACCCTAA TC GTA

GAM1192 LOC90155 5' ATGCCTGTAATCCCAGCACT 61691 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

GAM1192 LOC90321 3' ATGCCTATAATCTCAGCAC 62260 A C A  
GT GCTGGGATTA AG CAT  
|| ||||| |||

		CA CGACTCTAAT TC GTA		
		— A C		
GAM1192	LOC90321	3' ATGCCTGCAATCCCAGCTACT 62261	A	A
		AGTAGCTGGGATT CAG CAT		
		TCATCGACCCTAA GTC GTA		
		C C		
GAM1192	LOC90408	5' ATGCCTGTAATCCCAGCACT 62656	A	A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		— C		
GAM1192	LOC90509	3' CTGTAATCCCAGCACT 63104	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC90538	3' TCTGTAATCCCAGCACT 63196	A	
		AGT GCTGGGATTACAGA		
		TCA CGACCCTAATGTCT		
		—		
GAM1192	LOC90580	3' ATGTCTGTAATCCCAGC 63371		
		GCTGGGATTACAGACAT		
		CGACCCTAATGTCTGTA		
		—		
GAM1192	LOC90591	3' ATGCCTGTAATCCCAGCTACAT 63414	—	A
	G	CA GTAGCTGGGATTACAG CAT		
		GT CATCGACCCTAATGTC GTA		
		A C		
GAM1192	LOC90591	3' CTGTAATCCCAGCACT 63423	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC90591	3' CTGTAATCCCAGCACT 63424	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1192	LOC90624	3' CTGTAATCCCGCACT 63603	A	T
		AGT GC GGGATTACAG		
		TCA CG CCCTAATGTC		
		— —		
GAM1192	LOC90639	3' CTGCAATCCCAGCACTTTA 63656	C	A A
		TA AGT GCTGGGATT CAG		

AT TCA CGACCCTAA GTC  
 T \_ C  
 GAM1192 LOC90777 3' CTATAATCTCAGCAC 63967 A C  
 GT GCTGGGATTA AG  
 || ||||| ||  
 CA CGACTCTAAT TC  
 \_ A  
 GAM1192 LOC90918 5' ATGCCTGTAATCCCAGCTACT 64350 A  
 AGTAGCTGGGATTACAG CAT  
 ||||| ||||| ||  
 TCATCGACCCTAATGTC GTA  
 C  
 GAM1192 LOC90979 3' CTGTAATCCCAGCACT 64526 A  
 AGT GCTGGGATTACAG  
 || ||||| ||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1192 LOC90982 5' ATGTCTCTTTCCAGCTCT 64537 T TTAC  
 AG AGCTGGGA AGACAT  
 || ||||| |||||  
 TC TCGACCTT TCTGTA  
 \_ TC\_  
 GAM1192 LOC91035 3' CTATAATCCCAGCACT 64669 A C  
 AGT GCTGGGATTA AG  
 || ||||| ||  
 TCA CGACCCTAAT TC  
 \_ A  
 GAM1192 LOC91056 3' ATGCCTGTAATCCCAGCACT 94756 A A  
 AGT GCTGGGATTACAG CAT  
 || ||||| ||||| ||  
 TCA CGACCCTAATGTC GTA  
 \_ C  
 GAM1192 LOC91250 5' CTGTAATCCCAGTTACT 65323  
 AGTAGCTGGGATTACAG  
 ||||| ||||| ||  
 TCATTGACCCTAATGTC  
 \_  
 GAM1192 LOC91250 5' TCTGTAATCCCCGCACT 65330 A T  
 AGT GC GGGATTACAGA  
 || || ||||| ||  
 TCA CG CCCTAATGTCT  
 \_ C  
 GAM1192 LOC91286 3' ATGCCTGTAATCCTAGCCACT 65451 A A  
 AGT GCTGGGATTACAG CAT  
 || ||||| ||||| ||  
 TCA CGATCCTAATGTC GTA  
 C C  
 GAM1192 LOC91380 3' CTGTAATCCCAACTAC 65860 C  
 GTAG TGGGATTACAG  
 |||| ||||| ||

			CATC ACCCTAATGTC		
			A		
GAM1192	LOC91380	3'	TGCCTGTAATCCCGGCACT	65864	A A
			AGT GCTGGGATTACAG CA		
			TCA CGGCCCTAATGTC GT		
			— C		
GAM1192	LOC91380	3'	TGTAATCCCAGCTACTCA	65865	C C
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1192	LOC91574	3'	TCTGTAATCCCAGCACT	66521	A A
			AGT GCTGGGATTACAGA		
			TCA CGACCCTAATGTCT		
			—		
GAM1192	LOC91664	3'	CTGTAATCCCAGCACT	66872	A A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC91750	3'	CTGTAATCCCAGCACT	67061	A A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1192	LOC91796	5'	ATGCCTGTAATCCCAGCACT	67210	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1192	LOC91812	3'	GTGCCTGTAATCCCAGCTACTC	67242	C A
	A		A AGTAGCTGGGATTACAG CAT		
			A TCATCGACCCTAATGTC GTG		
			C C		
GAM1192	LOC91813	3'	GTGCCTGTAATCCCAGCTACTC	67259	C A
	A		A AGTAGCTGGGATTACAG CAT		
			A TCATCGACCCTAATGTC GTG		
			C C		
GAM1192	LOC91963	5'	CTGTAATCCCAGCTACTTG	67694	—
			CA GTAGCTGGGATTACAG		
			GT CATCGACCCTAATGTC		
			T		
GAM1192	LOC92078	3'	CTATAATCCCAGCACT	67980	A C
			AGT GCTGGGATTA AG		

			TCA CGACCCTAAT TC			
			- A			
GAM1192	LOC92078	3'	TGTAATCCCAACTACTCA	67990	C	C
			A AGTAG TGGGATTACA			
			A TCATC ACCCTAATGT			
			C A			
GAM1192	LOC92228	3'	CTGTAATCCCAGCACT	68541	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			-			
GAM1192	LOC92267	3'	CTGTAATCCCAGCACT	68613	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			-			
GAM1192	LOC92270	5'	CTGTAATCCCAGCACT	68630	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			-			
GAM1192	LOC92270	5'	TGTAATCCCAGCTACTCA	68637	C	
			A AGTAGCTGGGATTACA			
			A TCATCGACCCTAATGT			
			C			
GAM1192	LOC92283	3'	ATGCCTGTAATCCCAGCACT	68744	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			- C			
GAM1192	LOC92299	3'	CTGTAATCCCAGCACT	68809	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			-			
GAM1192	LOC92405	3'	ATGTCTGTAATCCCAGCTACT	69192		
			AGTAGCTGGGATTACAGACAT			
			TCATCGACCCTAATGTCTGTA			
			-			
GAM1192	LOC92421	3'	ATGCCTATAATCCCAGCACT	69212	A	C A
			AGT GCTGGGATTAG CAT			
			TCA CGACCCTAAT TC GTA			
			- A C			
GAM1192	LOC92465	5'	ATGCCTGTAATCCCAGCACT	69402	A	A
			AGT GCTGGGATTACAG CAT			

			TCA CGACCCTAATGTC GTA		
			- C		
GAM1192	LOC92465	3'	ATGTCTGTAGTCCCAGCCACTC 69403	C A	
	A		A AGT GCTGGGATTACAGACAT		
			A TCA CGACCCTGATGTCTGTA		
			C C		
GAM1192	LOC92465	3'	CTGTAATCCCAGCACT 69406	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			-		
GAM1192	LOC92465	5'	TGTAATCCCAGCTACTCA 69415	C	
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1192	LOC92466	3'	ATGCCTGTAATCCCAGCACT 69422	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			- C		
GAM1192	LOC92482	3'	CTGTAATCCCAGCACT 69488	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			-		
GAM1192	LOC92573	5'	CTGTAATCCCAGCACT 69805	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			-		
GAM1192	LOC92573	5'	TCTGTAATCCCAGCTTCT 69811	T	
			AG AGCTGGGATTACAGA		
			TC TCGACCCTAATGTCT		
			T		
GAM1192	LOC92661	5'	ATGCCTATAATCCCAGC 70078	C A	
			GCTGGGATTA AG CAT		
			CGACCCTAAT TC GTA		
			A C		
GAM1192	LOC92771	3'	TGTAATCCCAGCTACTCA 53078	C	
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1192	LOC93132	5'	CTGTAATCCCAGCACT 71488	A	
			AGT GCTGGGATTACAG		



TCA CGACCCTAATGTC

GAM1192 LOC93613 3' ATGCCTGTAATCCCAGCACT 72694 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

— C  
GAM1192 LOC93613 3' CTGTAATCCCAGCTATT 72698  
AGTAGCTGGGATTACAG  
|||||||  
TTATCGACCCTAATGTC

GAM1192 LOC96597 5' CTGTAATCCCAGCTACTCA 66913 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
C

GAM1193 BAT3 3' CCTTCACAGTATTTAAGA 16160 G GTTT  
TC TAAA CTGTGAAGG  
|| ||| |||||  
AG ATTT GACACTTCC  
A AT\_\_

GAM1193 BAT3 3' CCTTCACAGTATTTAAGA 54780 G GTTT  
TC TAAA CTGTGAAGG  
|| ||| |||||  
AG ATTT GACACTTCC  
A AT\_\_

GAM1193 BAT3 3' CCTTCACAGTATTTAAGA 54783 G GTTT  
TC TAAA CTGTGAAGG  
|| ||| |||||  
AG ATTT GACACTTCC  
A AT\_\_

GAM1193 BTEB1 3' CCCTCACAGAAAGAAACGA 6841 AAAG A  
TCGT TTTCTGTGA GG  
||| ||||| ||  
AGCA AAAGACACT CC  
AAG\_ C

GAM1193 ILF1 3' CCCTCACAGGACCCACCAGG 15717 C AAA T A  
CCT GT GTT CTGTGA GG  
||| || ||| ||||| ||  
GGA CA CAG GACACT CC  
C CC\_ \_ C

GAM1193 RYR2 3' CCTTCACAGAGACACGTGG 6413 T AAA  
CC CGT GTTTCTGTGAAGG  
|| ||| |||||  
GG GCA CAGAGACACTTCC  
T \_

GAM1193 ZFP103 3' CCTAGCAAGACTTTACAAG 19023 C C GA  
CT GTAAAGTTT TGT AGG  
|| ||||| ||| |||

GA CATTTTCAGA ACG TCC  
A \_ A\_  
GAM1193 ENDO180 3' CCCCCACAGGAACCAGAGGTA 20142 GTAAA AA  
TACCTC GTTTCTGTG GG  
||||| ||||||| ||  
ATGGAG CAAGGACAC CC  
AC\_\_ CC  
GAM1193 FLJ20507 3' CTTACATTTCACGAG 35286 A GTTTC  
CTCGT AA TGTGAAG  
||||| || |||||||  
GAGCA TT ACACTTC  
C \_\_\_\_  
GAM1193 FLJ20507 3' CTTACATTTCACGAG 60221 A GTTTC  
CTCGT AA TGTGAAG  
||||| || |||||||  
GAGCA TT ACACTTC  
C \_\_\_\_  
GAM1193 FLJ23120 3' CCTTCACAAAACTTGTAC 85147 \_ C  
GTA AAGTTT TGTGAAGG  
||| ||||||| |||||||  
CAT TTCAAA ACACTTCC  
G A  
GAM1193 KIAA0426 3' CTTACACAAAATGAGATG 28257 AAA C  
CGT GTTT TGTGAAG  
||| ||| |||||||  
GTA TAAA ACACTTC  
GAG A  
GAM1193 KIAA1277 3' CCCTCACAGAAACACAAAAGGG 64451 CGTAAA A  
CCT GTTTCTGTGA GG  
||| ||||||| || ||  
GGG CAAAGACACT CC  
AAAACA C  
GAM1193 MGC10940 3' CCTCTAACAAAACTTTAC 50215 C GA\_  
GTAAAGTTT TGT AGG  
||||||||| ||| |||  
CATTTCAAA ACA TCC  
A ATC  
GAM1193 MGC3251 3' CCCTCACAGAAAGTCATCGAGG 49313 TAAAG A  
CCTCG TTTCTGTGA GG  
||||| ||||||| ||  
GGAGC AAAGACACT CC  
TACTG C  
GAM1193 PCDH10 3' TGTAGAACTTTAGAGG 51998 G GT  
CCTC TAAAGTTTCT G  
||||| ||||||| |  
GGAG ATTTCAAAGA T  
\_ TG  
GAM1193 LOC115708 3' CCCTCACAGAAGCCAAGG 73546 CGTAAA A  
CCT GTTTCTGTGA GG  
||| ||||||| ||

GGA CGAAGACACT CC  
 AC\_\_\_\_\_ C  
 GAM1193 LOC146452 3' CCTCACAGCTGAACTTTA 77914 \_\_\_\_ A  
 TAAAGTTTC TGTGA GG  
 ||||| |||||  
 ATTTCAAAG ACACT CC  
 TCG \_  
 GAM1193 LOC147669 5' CCCTCACAAGATCCTCGAGGTA 84060 TAA TT \_ A  
 TACCTCG AG TCT GTGA GG  
 ||||| || ||| |||||  
 ATGGAGC TC AGA CACT CC  
 \_\_\_\_ CT A C  
 GAM1193 LOC157663 3' CATGAGAACTTTAAAAGGTA 81537 CG \_  
 TACCT TAAAGTTTCT GTG  
 |||| ||||| |||||  
 ATGGA ATTTCAAAGA TAC  
 AA G  
 GAM1193 LOC255019 3' CCTCACAGCTGAACTTTA 95080 \_\_\_\_ A  
 TAAAGTTTC TGTGA GG  
 ||||| |||||  
 ATTTCAAAG ACACT CC  
 TCG \_  
 GAM1194 ADAM19 3' CAGGAAGAAGACTGGCCATTAT 52703 C CTGAG  
 G CATGA GGCT TTCTTCCTG  
 |||| ||| |||||  
 GTATT CCGG AAGAAGGAC  
 A TCAG\_  
 GAM1194 FACL5 5' CAGGAAGAAGCTCAGAGCCG 64186  
 CGGCTCTGAGTTCTTCCTG  
 |||||  
 GCCGAGACTCAAGAAGGAC  
 GAM1194 GNAL 5' CAGGAAAGAGAGGAGCCGTCG 9058 GAG TC  
 TGACGGCTCT T TTCCTG  
 ||||| | |||||  
 GCTGCCGAGG A AAGGAC  
 AG\_ GA  
 GAM1194 KAL1 3' CAGGAAGAAGCTTCTGTCA 4013 CTCT  
 TGACGG GAGTTCTTCCTG  
 |||| |||||  
 ACTGTC TTCAAGAAGGAC  
 \_\_\_\_\_  
 GAM1194 MYO1E 3' CAGGAGGACAAAACCACCATG 17187 AC CTC AGT  
 CATG GG TG TCTTCCTG  
 ||| || || |||||  
 GTAC CC AC AGGAGGAC  
 CA AAA \_\_\_\_  
 GAM1194 PRKAR2B 3' CAGAAAGAAGCTCAGATGT 10804 \_ C  
 GC TCTGAGTTCTT CTG  
 || ||||| |||||

			TG AGACTCAAGAA GAC		
			T      A		
GAM1194	PUM2	3'	AGGATCAAAGCTGTCATG	31014	C GTTCT
			CATGACGGCT TGA TCCT		
			GTACTGTCGA ACT AGGA		
			A _____		
GAM1194	SKI	3'	CAGGAAGTGCAGAGCCGCA	11701	A AGTT
			TG CGGCTCTG CTCCTG		
			AC GCCGAGAC GAAGGAC		
			— GT—		
GAM1194	TEM8	3'	AGGAAGATGCAACCCCATG	36326	AC CTC AGT
			CATG GG TG TCTTCCT		
			GTAC CC AC AGAAGGA		
			C_ A_ GT_		
GAM1194	ARHGEF4	5'	AGAAAAAACTCAGGGC	52207	C C
			GCTCTGAGTT TT CT		
			CGGGACTCAA AA GA		
			A A		
GAM1194	FLJ31978	3'	CAGGAAGGAACAAGCGCC	58348	T GAG
			GGC CT TTCTTCCTG		
			CCG GA AGGAAGGAC		
			C ACA		
GAM1194	HSU24186	5'	AGAACTCAAAGCCGTC	25324	C
			GACGGCT TGAGTTCT		
			CTGCCGA ACTCAAGA		
			A		
GAM1194	KCNT1	3'	AGCTCCAGGGCCGCCA	61825	A —
			TG CGGCTCT GAGTT		
			AC GCCGGGA CTCGA		
			C CC		
GAM1194	KIAA1867	3'	CAGGAAGAACCCAAGAGCTCAT	94822	CG GA_
			ATGA GCTCT GTTCTTCCTG		
			TACT CGAGA CAAGAAGGAC		
			— ACC		
GAM1194	KIAA1878	3'	AATTCAGAGAATCGTCATG	91707	—
			CATGACGG CTCTGAGTT		
			GTACTGCT GAGACTTAA		
			AA		
GAM1194	MFN1	3'	CAGGAAGAACTCATGA	35541	_
			TC TGAGTTCTTCCTG		

AG ACTCAAGAAGGAC  
 T  
 GAM1194 MIDORI 3' CAGGGCCCTTCCAGAGCCTGTC 73784 \_ AGTTCT  
 ATG CATGAC GGCTCTG TCCTG  
 ||||| ||||| |||||  
 GTACTG CCGAGAC GGGAC  
 T CTTCCC  
 GAM1194 MYH7B 3' CAGGAAGAACCTGGCTCGCATG 70530 A \_ CTGA  
 CATG CG GCT GTTCTTCCTG  
 ||||| ||||| |||||  
 GTAC GC CGG CAAGAAGGAC  
 \_ T TC\_  
 GAM1194 RNAHP 3' AGAAAGCAGCAGCCGTCAT 23761 \_ AG  
 ATGACGGCT CTG TTCT  
 ||||| ||||| |||||  
 TACTGCCGA GAC AAGA  
 C GA  
 GAM1194 SLC37A1 3' AGACGGAGCTCAGACCC 38561 C TC  
 GG TCTGAGTTCT CT  
 || ||||| |||||  
 CC AGACTCGAGG GA  
 C CA  
 GAM1194 LOC116236 3' CAGGAAAAGCACAAACCTCAT 73809 C CTC A C  
 ATGA GG TG GTT TTCCTG  
 ||||| ||||| |||||  
 TACT CC AC CGA AAGGAC  
 \_ AA\_ A A  
 GAM1194 LOC124801 3' CAGGAAGAACTCTCTTGCATG 74336 A CTCT  
 CATG CGG GAGTTCTTCCTG  
 ||||| ||||| |||||  
 GTAC GTT CTCAAGAAGGAC  
 \_ CT\_  
 GAM1194 LOC222160 5' AGGAAGAACTCACCCC 94117 CTC  
 GG TGAGTTCTTCCT  
 || ||||| |||||  
 CC ACTCAAGAAGGA  
 CC\_  
 GAM1194 LOC51094 3' CAGGAAGAATAAAGCC 32045 CTGA  
 GGCT GTTCTTCCTG  
 ||||| ||||| |||||  
 CCGA TAAGAAGGAC  
 AA\_  
 GAM1194 LOC92078 3' CAGGAAGAAGAATCGACCGTC 67977 C T G\_  
 GACGG TC GA TTCTTCCTG  
 ||||| ||||| |||||  
 CTGCC AG CT AAGAAGGAC  
 \_ \_ AAG  
 GAM1195 SIRT2 3' AATATAACCCACACC 24259 A A  
 GGT TG GGTTATATT  
 ||||| ||||| |||||

CCA AC CCAATATAA  
 C \_  
 GAM1195 SIRT2 3' AATATAACCCACACC 47589 A A  
 GGT TG GGTTATATT  
 ||| || |||||  
 CCA AC CCAATATAA  
 C \_  
 GAM1195 CSNK1G1 3' GACCAATACCTCATACCTA 41870 TAT A  
 TAGGTATGAGGT ATT GTC  
 ||||| ||| |||  
 ATCCATACTCCA TAA CAG  
 \_ C  
 GAM1196 FCGRT 3' CCTGGAACACTGGCATCTCTGA 14640 TG A  
 G CTCAGAG GTTA TGTTCAGG  
 ||||| ||| |||||  
 GAGTCTC CGGT ACAAGGTCC  
 TA C  
 GAM1196 PTGIR 3' CCTCTACCAAGCCACTCCAAGA 6320 CA AAT TCC  
 TCT GAGTGGTT GT AGG  
 ||| ||||| || |||  
 AGA CTCACCGA CA TCC  
 AC AC\_ TC\_  
 GAM1196 TCF3 3' CAGAACGGCCACTCGAGA 70730 A TAA CA  
 TCTC GAGTGGT TGTTC G  
 ||| ||||| ||| |  
 AGAG CTCACCG GCAAG C  
 \_ \_ AC  
 GAM1196 FLJ12287 3' CCTGGAAACTCCACTCTGA 42312 TTAATG  
 TCAGAGTGG TTCCAGG  
 ||||| |||||  
 AGTCTCACC AAGGTCC  
 TCA\_  
 GAM1196 FLJ14327 3' CCTGGTGTCAACCTCTCTGAGA 46134 T AATGTT  
 TCTCAGAG GGTT CCAGG  
 ||||| ||| |||||  
 AGAGTCTC CCAA GGTCC  
 T CTGT\_  
 GAM1196 KIAA0295 3' CCTGGAACCCTACACTTGAGA 68101 G GTTAAT  
 TCTCA AGTG GTTCCAGG  
 ||||| ||| |||||  
 AGAGT TCAC CAAGGTCC  
 \_ ATCC\_  
 GAM1196 KIAA0326 5' CCTGGAACACTGCAGTCCTGAG 64324 AG G TAA  
 CTCAG T GT TGTTCAGG  
 |||| | || |||||  
 GAGTC G CG ACAAGGTCC  
 CT A TC\_  
 GAM1196 KIAA0430 3' CTGGAACAGACTCAAAGA 38840 CA GGTAA  
 TCT GAGT TGTTCAG  
 ||| |||| |||||

AGA CTCA ACAAGGTC  
 AA G\_\_\_\_  
 GAM1196 KIAA0626 5' CCTGGAACCCCACTC 67439 TAAT  
 GAGTGGT GTTCCAGG  
 ||||| |||||  
 CTCACCA CAAGGTCC  
 CCC\_  
 GAM1196 KIAA1045 3' CCTGGCCACAAAACCACTCCAA 71049 CA AA T\_  
 G CT GAGTGGTT TGT CCAGG  
 || ||||| || ||||  
 GA CTCACCAA ACA GGTCC  
 AC A\_ CC  
 GAM1196 KIAA1970 3' CCTAAGCCAGAACCACTCAGAG 74296 A AAT CC  
 A TCTC GAGTGGTT GTT AGG  
 ||| ||||| || |||  
 AGAG CTCACCAA CGA TCC  
 A GAC A\_  
 GAM1196 SLC26A9 3' CCTGAAACATCACTGCCCTC 53620 T TA\_\_ C  
 GAG GGT ATGTT CAGG  
 ||| ||| ||||| ||||  
 CTC CCG TACAA GTCC  
 \_ TCAC A  
 GAM1196 SLC26A9 3' CCTGAAACATCACTGCCCTC 56181 T TA\_\_ C  
 GAG GGT ATGTT CAGG  
 ||| ||| ||||| ||||  
 CTC CCG TACAA GTCC  
 \_ TCAC A  
 GAM1196 TU12B1-TY 3' CCTGGAACATCAGGTTTCCTGG 33374 AGTGGTTA  
 GA TCTCAG ATGTTCCAGG  
 ||||| |||||  
 AGGGTC TACAAGGTCC  
 CTTTGGAC  
 GAM1196 VILL 3' AGCATCAACCATCTCTGAGA 68409 \_ A  
 TCTCAGAG TGGTT ATGTT  
 ||||| ||||| |||||  
 AGAGTCTC ACCAA TACGA  
 T C  
 GAM1196 LOC149267 3' CCTAGAACATCCTGCTCTGA 56677 TG TTA C  
 TCAGAG G ATGTTC AGG  
 ||||| | ||||| |||  
 AGTCTC C TACAAG TCC  
 GT C\_\_ A  
 GAM1196 LOC221543 3' CTCATTTACCACTCTGA 93739 T TTCC  
 TCAGAGTGGT AATG AG  
 ||||| ||| ||  
 AGTCTCACCA TTAC TC  
 T \_\_\_\_  
 GAM1196 LOC257596 3' CTCATTTACCACTCTGA 97932 T TTCC  
 TCAGAGTGGT AATG AG  
 ||||| ||| ||

AGTCTCACCA TTAC TC  
 T \_\_\_\_  
 GAM1196 LOC93259 5' CTGGAACCACACTTTGAGA 71816 GTTAAT  
 TCTCAGAGTG GTTCCAG  
 ||||| |||||  
 AGAGTTTCAC CAAGGTC  
 AC\_\_\_\_  
 GAM1197 ACP1 5' CTCCCGCGGCTCCTTCC 15032 TAA AA  
 GGAAGG AG GTGGGAG  
 ||||| || |||||  
 CCTTCC TC CGCCCTC  
 \_\_\_\_ GG  
 GAM1197 ACP1 5' CTCCCGCGGCTCCTTCC 23020 TAA AA  
 GGAAGG AG GTGGGAG  
 ||||| || |||||  
 CCTTCC TC CGCCCTC  
 \_\_\_\_ GG  
 GAM1197 ACTC 3' TCTCTCCATCTACCTTCCA 60187 AAGAA GA  
 TGGAAGGTA GTGG GGA  
 ||||| ||| |||  
 ACCTTCCAT TACC TCT  
 C\_\_\_\_ TC  
 GAM1197 ADAM19 3' TCCTCCCACCCTCCTCCA 52713 A TAAAGAA  
 TGGA GG GTGGGAGGA  
 ||| || |||||  
 ACCT CC CACCCTCCT  
 \_ TCC\_\_\_\_  
 GAM1197 AQP6 3' CCCCCAAATCTCCTCCTTCCA 53918 TAA AG A  
 TGGAAGG AGA TGGG GG  
 ||||| ||| ||| ||  
 ACCTTCC TCT ACCC CC  
 TCC AA \_  
 GAM1197 AR 5' CTCCCCCACCCTGCCTTCC 3491 AAGAA A  
 GGAAGGTA GTGGG GGAG  
 ||||| |||| |||  
 CCTTCCGT CACCC CTC  
 CC\_\_\_\_ C  
 GAM1197 ARNT2 3' CCAGCCTCCTTCCCTTCCA 29455 TAAA TG A\_  
 TGGAAGG GAAG GG GG  
 ||||| ||| || ||  
 ACCTTCC CTTC CC CC  
 \_\_\_\_ CT GA  
 GAM1197 ASNS 5' CTCCTCCCCTCTCACCCGCCA 55940 AA\_ AA A T  
 TGG GGT AGA G GGGAGGAG  
 ||| ||| ||| |||||  
 ACC CCA TCT C CCCTCCTC  
 GCC C\_ \_\_  
 GAM1197 B3GALT5 3' CCCTCCACCTCAGTCCCA 52556 AA AAA A GA  
 TGG GGT GA GTGG GG  
 ||| ||| || ||| ||



		ACC TCG CT CACC CC			
		C_ A_ C TC			
GAM1197	B3GALT5	3' CCCTCCACCTCAGCTCCCA	52560	AA AAA A	GA
		TGG GGT GA GTGG GG			
		ACC TCG CT CACC CC			
		C_ A_ C TC			
GAM1197	B3GALT5	3' CCCTCCACCTCAGCTCCCA	52568	AA AAA A	GA
		TGG GGT GA GTGG GG			
		ACC TCG CT CACC CC			
		C_ A_ C TC			
GAM1197	B3GALT5	3' CCCTCCACCTCAGCTCCCA	52576	AA AAA A	GA
		TGG GGT GA GTGG GG			
		ACC TCG CT CACC CC			
		C_ A_ C TC			
GAM1197	B3GALT5	3' CCCTCCACCTCAGCTCCCA	20218	AA AAA A	GA
		TGG GGT GA GTGG GG			
		ACC TCG CT CACC CC			
		C_ A_ C TC			
GAM1197	B4GALT1	3' CTCCCCCACCCTTCTTTCA	7668	TAAAGAA	A
		TGGAAGG GTGGG GGAG			
		ACTTTCT CACCC CCTC			
		TCCCC_ C			
GAM1197	BAZ2A	3' CTTTTCACCTCCACCCCCC	25601	AA AAA A	
	A	TGG GGT GA GTGGGAGGAG			
		ACC CCA CT CACCCTTTTC			
		CC CC_ C			
GAM1197	BCL11B	3' CTCCATCCTTCATCCTCCA	43189	A TAAA	TG_
		TGGA GG GAAG GGAG			
		ACCT CC CTTC CCTC			
		_ TA_ CTA			
GAM1197	BIG1	5' TCCTCCTCCTCCCCTCCA	21206	A TAAA A	TG
		TGGA GG GA G GGAGGA			
		ACCT CC CT C CCTCCT			
		C _ _ CT			
GAM1197	BMP1	3' CTCCCTTTCCTGCACCTCCCA	20419	A AA _ T	
		TGG AGGT AG AAG GGGAG			
		ACC TCCA TC TTT CCCTC			
		C CG C _			
GAM1197	BSG	3' CCTCCCACCCACCGCCA	8182	AA AAAGAA	
		TGG GGT GTGGGAGG			

			ACC CCA CACCCTCC		
			G_ CC_____		
GAM1197	BSG	3'	CCTCCCACCCACCGCCA	67797	AA AAAGAA
			TGG GGT GTGGGAGG		
			ACC CCA CACCCTCC		
			G_ CC_____		
GAM1197	BTG2	3'	CCCACTTCCTCTACCCCA	22212	AA AA_
			TGG GGTA GAAGTGGG		
			ACC CCAT CTTACCC		
			C_ CTC		
GAM1197	CAPN1	3'	CTCCTGTCCCCTCTCCTCCA	17750	A TAA AT _
			TGG AGG AGA G GGGG		
			ACC TCC TCT C CCCT CCTC		
			C _ _ _ GT		
GAM1197	CASP2	3'	CTCCCTTCTTTACCTTC	6897	GT
			GAAGGTAAAGAA GGGAG		
			CTTCCATTTCTT CCCTC		
			—		
GAM1197	CASP2	3'	CTCCCTTCTTTACCTTC	52139	GT
			GAAGGTAAAGAA GGGAG		
			CTTCCATTTCTT CCCTC		
			—		
GAM1197	CASP2	3'	CTCCCTTCTTTACCTTC	52152	GT
			GAAGGTAAAGAA GGGAG		
			CTTCCATTTCTT CCCTC		
			—		
GAM1197	CASP2	3'	CTCCCTTCTTTACCTTC	52167	GT
			GAAGGTAAAGAA GGGAG		
			CTTCCATTTCTT CCCTC		
			—		
GAM1197	CASQ1	5'	CCTCCCACTTGAGCCCC	6930	AA AAAG
			GG GGT AAGTGGGAGG		
			CC CCG TTCACCCTCC		
			_ AG_		
GAM1197	CELSR3	3'	CTCCCCCTATTCCACCCCA	7398	AA AAA GT A
			TGG GGT GAA GGG GGAG		
			ACC CCA CTT CCC CCTC		
			C_ C_ AT _		
GAM1197	CFL1	3'	CCCCTGGATTTTCCTTCT	18570	T GA_ T
			GGAAGG AAA AG GGG		

TCTTCC TTT TC CCC  
 T AGG \_  
 GAM1197 CHC1 3' CTCCCCTTTTCCCTACCTTCCA 7022 A\_\_ T  
 TGGAAGGTA AGAAG GGGAG  
 ||||| |||| ||||  
 ACCTTCCAT TTTTC CCCTC  
 CCC \_  
 GAM1197 CHRN2 5' CTCCTCCCCCTCACCGTCC 5625 A AAA A T  
 GGA GGT GA G GGGAGGAG  
 ||| ||| ||| |||||  
 CCT CCA CT C CCCTCCTC  
 G \_ \_ C  
 GAM1197 CLCN1 3' CCTCCCACGACCTCC 3591 A AAAGAA  
 GGA GGT GTGGGAGG  
 ||| ||| |||||  
 CCT CCA CACCCTCC  
 \_ G\_\_\_\_  
 GAM1197 COL5A1 3' CCTCCCACCTGACTTC 3633 GTAA AA  
 GAAG AG GTGGGAGG  
 ||| || |||||  
 CTTC TC CACCCTCC  
 AG\_\_ \_  
 GAM1197 CTNS 3' CTCCTACCTCCACCTTCT 17041 AAA A  
 GGAAGGT GA GTGGGAG  
 ||||| || |||||  
 TCTTCCA CT CATCCTC  
 C\_ C  
 GAM1197 CYLN2 3' CCTCTCCTCACCTCCCA 12631 A AAA A T  
 TGG AGGT GA G GGGAGG  
 ||| ||| ||| |||||  
 ACC TCCA CT C CTCTCC  
 C \_ \_ \_  
 GAM1197 CYP8B1 3' TCCTCCTCTTTTACCTTC 15274 AAA T  
 GAAGGT GAAG GGGAGGA  
 ||||| ||| |||||  
 CTTCCA CTTT TCCTCCT  
 \_ C  
 GAM1197 DAAM2 3' CCTTCCTTCTCTACCCTC 92286 A A GT  
 GA GGTA AGAA GGGAGG  
 || ||| ||| |||||  
 CT CCAT TCTT CCTTCC  
 C C \_  
 GAM1197 DDX3 3' CCTCCCGCCTACCCCA 7222 AA AAGAA  
 TGG GGTA GTGGGAGG  
 ||| ||| |||||  
 ACC CCAT CGCCCTCC  
 C\_ C\_\_\_\_  
 GAM1197 DFFB 3' TCCTTCCTCAGCCTCCCA 87399 A AAA AGT  
 TGG AGGT GA GGGAGGA  
 ||| ||| || |||||

ACC TCCG CT CCTTCCT  
 C A\_\_ \_\_  
 GAM1197 DLG4 3' CTCCCCCGGCCTCCCTCCCA 7253 A TAAA A \_ A  
 TGG AGG GA GT GGG GGAG  
 ||| ||| || ||| ||||  
 ACC TCC CT CG CCC CCTC  
 C \_\_\_\_ C G C  
 GAM1197 DPYSL2 3' CCCATTATCTTTTCACCTCCCA 7293 A \_ \_  
 TGG AGGT AAAGA AGTGGG  
 ||| |||| |||| ||||  
 ACC TCCA TTTCT TTACCC  
 C CT A  
 GAM1197 DRD2 3' CCTCCACCTCCAGTCCCCC 5843 AA TAAA A  
 GG GG GA GTGGGAGG  
 || || || |||||  
 CC CC CT CACCCTCC  
 C\_ TGAC C  
 GAM1197 DRD2 3' CTCCTGTTTCCCTTCCCTTCCA 5844 T A\_ TG  
 TGGAAGG AA GAAG GGAG  
 ||||| || ||| |||  
 ACCTTCC TT CTTT CCTC  
 C CC GT  
 GAM1197 ELMO1 3' TCCTCCACCTCTCTCCCT 55285 TAA A  
 AGG AGA GTGGGAGGA  
 ||| ||| |||||  
 TCC TCT CACCCTCCT  
 CTC C  
 GAM1197 EN2 3' CTCCCTCTCCTCACCCTCC 7460 A AA A T  
 GGA GGT AG AG GGGAG  
 ||| ||| || ||| ||||  
 CCT CCA TC TC CCCTC  
 C C\_ C T  
 GAM1197 EPHB2 3' TCCTCCACCTGCCACCA 15448 AA AAGAA  
 TGG GGTA GTGGGAGGA  
 ||| |||| |||||  
 ACC CCGT CACCCTCCT  
 A\_ C\_\_\_\_  
 GAM1197 F8 3' CCCCTTCTTGCCCTCCA 3727 A A T  
 TGGA GGTAA GAAG GGG  
 |||| |||| ||| |||  
 ACCT CCGTT CTTC CCC  
 C \_ \_  
 GAM1197 F8 3' CTCCCAGATTACTCCTTCCTTC 3728 TAA\_ \_ G\_  
 CA TGGAAGG AG AA TGGGAG  
 ||||| || || |||||  
 ACCTTCC TC TT ACCCTC  
 TTCC A AG  
 GAM1197 F9 3' CTCTCTCCCTTTTACCCTCCA 3739 A AAGT \_  
 TGGA GGTAAAG GGGAG GAG  
 |||| ||||| |||| |||

		ACCT CCATTTT CCCTC CTC		
		C ____ T		
GAM1197 FXR2	3'	CTCCCCTGCTATCCCTCCTCCC 16785	A	TAAA _ TG A
A		TGG AGG GA AG GG GGAG		
		ACC TCC CT TC CC CCTC		
		C TCC_ A GT _		
GAM1197 FXR2	3'	CTCCTCCCATCCTGTACCCCCC 16786	AA	A AA
A		TGG GGTA AG GTGGGAGGAG		
		ACC CCAT TC TACCCTCCTC		
		CC G C_		
GAM1197 FY	5'	CCTCCCACCTGCCCTCA 8970	AA	AAGAA
		TGG GGTA GTGGGAGG		
		ACT CCGT CACCCTCC		
		CC C_		
GAM1197 G1P3	3'	CTCCTGTCTCAACCTCCCA 8975	A	AAA AG
		TGG AGGT GA TGGGAG		
		ACC TCCA CT GTCCTC		
		C A_ CT		
GAM1197 G1P3	3'	CTCCTGTCTCAACCTCCCA 43150	A	AAA AG
		TGG AGGT GA TGGGAG		
		ACC TCCA CT GTCCTC		
		C A_ CT		
GAM1197 G1P3	3'	CTCCTGTCTCAACCTCCCA 43152	A	AAA AG
		TGG AGGT GA TGGGAG		
		ACC TCCA CT GTCCTC		
		C A_ CT		
GAM1197 GPC1	3'	CTCCTCCCCTGGGACTCCCA 9101	AA	AAAGA
		TGG GGT AGTGGGAGGAG		
		ACC TCA TCACCCTCCTC		
		C_ GGG_		
GAM1197 GPC4	5'	CTCCAACCTCTTCTCCCTCCA 7553	A	TAA TG GA
		TGGA GG AGAAG G GGAG		
		ACCT CC TCTTC C CCTC		
		C ____ CT AA		
GAM1197 GRF2	3'	CTCCCCTCTTGACCTTCCA 17990	A	A T
		TGGAAGGT AAGA G GGGAG		
		ACCTTCCA TTCT C CCCTC		
		G _ _		
GAM1197 GRIK3	3'	TCCTGCCCTTACCTGCCA 5891	A	AAGA T G
		TGG AGGTA AG GG AGGA		

		ACC TCCAT TC CC TCCT	
		G _ _ _ G	
GAM1197 GRM6	3'	CTCCTGCCTCCACCTCCCA	5932 A AAA A TG
		TGG AGGT GA G GGAG	
		ACC TCCA CT C CCTC	
		C C_ C GT	
GAM1197 HDAC5	5'	CCTCCCGTCCCAGCCCCCA	57608 AA AAA AG
		TGG GGT GA TGGGAGG	
		ACC CCG CT GCCCTCC	
		C_ ACC _	
GAM1197 HDAC5	5'	CCTCCCGTCCCAGCCCCCA	18451 AA AAA AG
		TGG GGT GA TGGGAGG	
		ACC CCG CT GCCCTCC	
		C_ ACC _	
GAM1197 HEPH	5'	CCTCCCTCATCCTCCCA	28964 A TAAA AGT
		TGG AGG GA GGGAGG	
		ACC TCC CT CCCTCC	
		C TA_ _	
GAM1197 HEXA	3'	CCTCCCACTCCTGACC	4973 AA A
		GGT AG AGTGGGAGG	
		CCA TC TCACCCTCC	
		G_ C	
GAM1197 HFE	5'	CCCGTTTCCCGCCCCCA	4650 AA AAA
		TGG GGT GAAGTGGG	
		ACC CCG CTTTGCCC	
		CC CCC	
GAM1197 HFE	5'	CCCGTTTCCCGCCCCCA	57319 AA AAA
		TGG GGT GAAGTGGG	
		ACC CCG CTTTGCCC	
		CC CCC	
GAM1197 HFE	5'	CCCGTTTCCCGCCCCCA	57324 AA AAA
		TGG GGT GAAGTGGG	
		ACC CCG CTTTGCCC	
		CC CCC	
GAM1197 HFE	5'	CCCGTTTCCCGCCCCCA	57325 AA AAA
		TGG GGT GAAGTGGG	
		ACC CCG CTTTGCCC	
		CC CCC	
GAM1197 HFE	5'	CCCGTTTCCCGCCCCCA	57326 AA AAA
		TGG GGT GAAGTGGG	

		ACC CCG CTTTGCCC		
		CC CCC		
GAM1197 HFE	5'	CCCGTTTCCCCGCCCCCA	57327	AA AAA
		TGG GGT GAAGTGGG		
		ACC CCG CTTTGCCC		
		CC CCC		
GAM1197 HFE	5'	CCCGTTTCCCCGCCCCCA	57328	AA AAA
		TGG GGT GAAGTGGG		
		ACC CCG CTTTGCCC		
		CC CCC		
GAM1197 HHIP	5'	CTCCTCCCACTTCCCAGCC	42488	AAA
		GGT GAAGTGGGAGGAG		
		CCG CTTACCCCTCCTC		
		ACC		
GAM1197 HMGA2	5'	CTCCTCTTGCTACCTCCACCTC	12998	A AA A_ TG
CA		TGGA GGT AG AG GGAGGAG		
		ACCT CCA TC TC TCTCCTC		
		_ CC CA GT		
GAM1197 HOXC10	3'	CTCCATGTCTTTACCTCCCA	61269	A AGTG
		TGG AGGTAAAGA GGAG		
		ACC TCCATTTCT CCTC		
		C GTA_		
GAM1197 HPCA	3'	CCTCCCGGCTCTTAGCTTCCA	9253	G A AG
		TGGAAG TAA GA TGGGAGG		
		ACCTTC ATT CT GCCCTCC		
		G _ CG		
GAM1197 IFITM2	3'	CCACTTACTCCACCTTCCA	21226	AA _
		TGGAAGGT AG AAGTGG		
		ACCTTCCA TC TTCACC		
		CC A		
GAM1197 IGFBP5	3'	CCTCCCACCCCGAGCCCCG	5191	AA AAAGAA
		TGG GGT GTGGGAGG		
		GCC CCG CACCCTCC		
		_ ACCCC_		
GAM1197 IGSF8	3'	CTTCCCCACTCCTTCCCTCCCA	53505	A TA A A
		TGG AGG AAG AGTGGG GGAG		
		ACC TCC TTC TCACCC CTTC		
		C C_ C _		
GAM1197 IL24	3'	CCCCATGCTTCTTTACCCCTCA	22442	AA _ A
		TGG GGTAAGAAGTG GG GG		

ACT CCATTTCTTCGT CC CC  
 CC A \_  
 GAM1197 IL6R 3' CTCTCTTCTCCACCTCCCA 5119 A AA T  
 TGG AGGT AGAAG GGG  
 ||| ||| ||||| |||  
 ACC TCCA TCTTC CTC  
 C CC T  
 GAM1197 ITGA7 3' TCCTCCCACCCAACTTCC 9382 GTAAAGAA  
 GGAAG GTGGGAGGA  
 ||||| |||||  
 CCTTC CACCCTCCT  
 AACC\_\_\_\_  
 GAM1197 ITS1 3' CTAAGACACTTTTCCACCCTCC 11618 A AA GG\_\_\_\_  
 A TGGG GGT AGAAGTG AG  
 ||||| ||| ||||| ||  
 ACCT CCA TTTTCAC TC  
 C CC AGAA  
 GAM1197 KAI1 3' CTCCTCCAGGCCTGCCTCCCA 9498 A AAGAA G\_  
 TGG AGGTA GT GGAGGAG  
 ||| ||||| || |||||  
 ACC TCGT CG CCTCCTC  
 C C\_\_\_\_ GA  
 GAM1197 KCNA7 3' TCCTCCTGTTTACCCCA 49060 AA AGAA TG  
 TGG GGTA G GGAGGA  
 ||| ||||| | |||||  
 ACC CCATT T CCTCCT  
 \_\_\_\_ GT  
 GAM1197 KCNE1L 3' CCTCTTCACCCCTGCACCTTCC 24403 AA AA \_  
 A TGGGAAGGT AG GTGG GAGG  
 ||||| || ||| |||||  
 ACCTTCCA TC CACT CTCC  
 CG CC T  
 GAM1197 KRTHB1 3' CCTCCCACCTCCTGGCCTCACA 9649 GA AA A  
 TG AGGT AG AGTGGGAGG  
 || |||| || |||||  
 AC TCCG TC TCACCCTCC  
 AC G\_ C  
 GAM1197 LFG 3' CTCACCTTCTCCACCCGCCA 76717 AA AA  
 TGG GGT AGAAGTGGG  
 ||| ||| |||||  
 ACC CCA TCTTCACTC  
 GC CC  
 GAM1197 LRP1 5' CCTCCCCGCTCCTCCCA 9799 A TAAAGAA \_  
 TGG AGG GTGGG AGG  
 ||| ||| ||||| |||  
 ACC TCC CGCCC TCC  
 C TC\_\_\_\_ C  
 GAM1197 MAML1 3' TCCTCCTCCTCCTCCCA 28594 A TAAA A TG  
 TGG AGG GA G GGAGGA  
 ||| ||| ||| |||||



		ACC TCC CT C CCTCCT	
		C ____ _CT	
GAM1197	MAP3K7IP1	3' CTCCTCCCACCATCACCTCCC 20378	A AAA A_
		GG AGGT GA GTGGGAGGAG	
		CC TCCA CT CACCCTCCTC	
		C ____ AC	
GAM1197	MFGE8	3' CTCCTCTTTCCCACCCTCCA 19811	A AAA T
		TGGA GGT GAAG GGGAG	
		ACCT CCA TTTC CCCTC	
		C CCC T	
GAM1197	MGST1	5' CTCCTCCTCGGCCTCACCATTTC 39697	_ AAA A _
	CA	TGGAA GGT GA GT GGGAGGAG	
		ACCTT CCA CT CG TCCTCCTC	
		A ____ C GC	
GAM1197	MMP19	3' CTCCCATGTTCTCCCTCCCTCC 42971	A TAA_ _
		GGA GG AGAA GTGGGAG	
		CCT CC TCTT TACCCTC	
		C TCCC G	
GAM1197	MMP19	3' CTCCCATGTTCTCCCTCCCTCC 10083	A TAA_ _
		GGA GG AGAA GTGGGAG	
		CCT CC TCTT TACCCTC	
		C TCCC G	
GAM1197	MPP2	3' CTCCTCCCACCTCTCACCCC 59821	AA AA A
		GG GGT AGA GTGGGAGGAG	
		CC CCA TCT CACCCTCCTC	
		_ C_ C	
GAM1197	MTCP1	5' CCAAGTCACCTTCTTACCTCCC 26429	A A _ GA_
	A	TGG AGGTAA GAAG TGG GG	
		ACC TCCATT CTTC ACT CC	
		C _ C GAA	
GAM1197	MUC3B	3' TCCTCCTCATTCCTTCCA 94269	TAAA GT
		TGGAAGG GAA GGGAGGA	
		ACCTTCC CTT TCCTCCT	
		____ AC	
GAM1197	NCOA3	3' CTTTTCCTTCCCCACCCCCCA 21530	AA AAA T GG
		TGG GGT GAAG G AGG	
		ACC CCA CTTC C TTC	
		CC CCC _TT	
GAM1197	NDRG1	3' CTCCTCCACAGCCCCAACCTCC 59567	A AAAGAAGTG
	CA	TGG AGGT GGAGGAG	

ACC TCCA      CTCCTC  
           C    ACCCCGACA  
 GAM1197 NHLH1    5' CTCCCCCTTCCTCCCCCTCCCA 18799    A   TAAA\_   T  
                   TGG AGG    GAAG GGGAG  
                   ||| |||    |||| ||||  
                   ACC TCC    CTTC CCCTC  
                   C    CCCTC    C  
 GAM1197 NOTCH3    3' CTCCTCCCCACCCACCTCCC 4745    A   AAAGAA    \_  
                   GG AGGT    GTGGG AGGAG  
                   || ||||    |||| ||||  
                   CC TCCA    CACCC TCCTC  
                   C    CCC\_    C  
 GAM1197 NPY2R    5' CTCCCACCTTCACCCGCC    6184    AA   A   AA  
                   GG GGT AAG GTGGGAG  
                   || ||| |||    |||||  
                   CC CCA TTC CACCCTC  
                   GC    C    \_  
 GAM1197 NRBP    3' TCCTGTCCCTTCCCCCA    25433    AA   TAAA    T    \_  
                   TGG GG    GAAG GGG AGGA  
                   ||| ||    |||| ||| |||  
                   ACC CC    CTTC CCT TCCT  
                   C\_    \_    \_    G  
 GAM1197 NTSR1    3' CTCCCCTCCTCCCTCCCA    10291    A   TAA   A   T  
                   TGG AGG    AG AG GGGAG  
                   ||| |||    || ||| ||||  
                   ACC TCC    TC TC CCCTC  
                   C    C\_    C    \_  
 GAM1197 NUP98    3' CTCCAAAGCATTTCACCCCTC 32861    A   AAA    \_  
                   CA            TGGA GGT    GAAGTG    GGAG  
                   |||| |||    |||||    |||  
                   ACCT CCA    CTTTAC    CCTC  
                   C    CC\_    GAAA  
 GAM1197 NYX    3' CTCCCCTTCCCCTCATCTTCCA 42599    AAA\_    T  
                   TGGAAGGT    GAAG GGGAG  
                   |||||||    ||| |||||  
                   ACCTTCTA    CTTC CCCTC  
                   CTCCC    \_  
 GAM1197 OAS3    3' CTCCCCTGCCTCCCA    20540    A   AAAGA    T  
                   TGG AGGT    AG GGGAG  
                   ||| |||    || |||||  
                   ACC TCG    TC CCCTC  
                   C    \_    \_  
 GAM1197 OGG1    3' CCCAAGGATTCTTCACCTCCC 33658    A   A\_    G\_  
                   A            TGG AGGT    AAGAA    TGGG  
                   ||| |||    |||||    |||  
                   ACC TCCA    TTCTT    ACCC  
                   C    CC    AGGA  
 GAM1197 OPA3    3' CCTCCATCATCCTTCACCTCC 47108    A   A    AAGTG\_  
                   GGA GGT AAG    GGAGG  
                   ||| ||| |||    |||||

			CCT CCA TTC    CCTCC		
			_ C CTACTA		
GAM1197	ORC1L	3'	CCCCCAACCTCATCCTCCCA	14736	A TAA AAG A
			TGG AGG AG TGGG GG		
			ACC TCC TC ACCC CC		
			C TAC CA_ _		
GAM1197	PARG	3'	TCCTCCCACCTCCCACC	13272	AAA A
			GGT GA GTGGGAGGA		
			CCA CT CACCCTCCT		
			CC_ C		
GAM1197	PATE	3'	CTCCCACCCTTACCTCCA	56312	A AGAA
			TGGA GGTA GTGGGAG		
			ACCT CCATT CACCCTC		
			_ CC_		
GAM1197	PAX2	3'	TCCTCCCATCCCCTCCCA	14329	A TAAAGAA
			TGG AGG GTGGGAGGA		
			ACC TCC TACCCTCCT		
			C CC_		
GAM1197	PAX2	3'	TCCTCCCATCCCCTCCCA	14337	A TAAAGAA
			TGG AGG GTGGGAGGA		
			ACC TCC TACCCTCCT		
			C CC_		
GAM1197	PDE4A	5'	CCCTCCGCGGCTCCCCCTTCCA	20582	TAA AA GA
			TGGAAGG AG GTGG GG		
			ACCTTCC TC CGCC CC		
			CCC GG TC		
GAM1197	PDE4A	3'	CTCCATCCCCTTTCCCTTCCA	20584	TAAA T _
			TGGAAGG GAAG GGA GGAG		
			ACCTTCC TTTC CCCT CCTC		
			C_ _ A		
GAM1197	PDE4A	3'	TTCCTCCCTAGCCTTCCA	20589	AAAGAAGT
			TGGAAGGT GGGAGGAG		
			ACCTTCCG CCCTCCTT		
			AT_		
GAM1197	PHF1	3'	CCCTCTTCTCTACCCTCC	44147	A A T
			GGA GGTA AGAAG GGG		
			CCT CCAT TCTTC CCC		
			C C T		
GAM1197	PHF1	3'	CCCTCTTCTCTACCCTCC	10543	A A T
			GGA GGTA AGAAG GGG		

CCT CCAT TCTTC CCC  
 C C T  
 GAM1197 PIGR 3' CCTCTTCTTCTTTCTTCCA 72595 T T  
 TGGAAGG AAAGAAG GGGAGG  
 ||||| ||||| |||||  
 ACCTTCC TTTCTTC TTCTCC  
  
 GAM1197 PITX1 3' CTCCTCCCACTTCCCACTCC 10597 A\_ TAAA  
 GGA GG GAAGTGGGAGGAG  
 ||| || |||||  
 CCT CC CTTACCCCTCCTC  
 CA \_\_\_\_  
 GAM1197 PKD2L1 5' CCCTCTTCAAACCCCCACCTTC 32261 AAA\_\_\_\_\_ T  
 CA TGGAAGGT GAAG GGG  
 ||||| ||| |||  
 ACCTTCCA CTTC CCC  
 CCCCCAA T  
 GAM1197 PKM2 3' TCCACCCTCCACCTTCCA 10603 AAA AGT A  
 TGGAAGGT GA GGG GGA  
 ||||| || ||| |||  
 ACCTTCCA CT CCC CCT  
 C\_ \_ A  
 GAM1197 PML 3' CTCCTATTAGCCCTCCTTCCA 52655 TAAAGA\_  
 TGGAAGG AGTGGGAG  
 ||||| |||||  
 ACCTTCC TTATCCTC  
 TCCCCGA  
 GAM1197 POU2AF1 3' CCTTTCCTTCTTTACCTCCC 20650 A T GG  
 GG AGGTAAAGAAG G AGG  
 || ||||| |||  
 CC TCCATTTCTTC C TCC  
 C \_ TT  
 GAM1197 PPBP 3' CCAAACCTTCTTTAACTCCCA 10702 A G G\_  
 TGG AG TAAAGAAGT GG  
 ||| || ||||| ||  
 ACC TC ATTTCTTCA CC  
 C A AA  
 GAM1197 PPP1R12B 3' CTCTATTCTTCTTCACCTCTCA 49467 GA A TG\_  
 TG AGGT AAGAAG GGAG  
 || ||| ||||| |||  
 AC TCCA TTCTTC TCTC  
 TC C TTA  
 GAM1197 PPP1R12B 3' CTCTATTCTTCTTCACCTCTCA 49478 GA A TG\_  
 TG AGGT AAGAAG GGAG  
 || ||| ||||| |||  
 AC TCCA TTCTTC TCTC  
 TC C TTA  
 GAM1197 PPP2R1A 3' CTCCCCCATTTACTTCTCCACC 26444 A AA \_\_\_\_\_ A  
 TCCC GG AGGT AGAAGT GGG GGAG  
 || ||| ||||| ||| |||

CC TCCA TCTTCA CCC CCTC  
 C CC TTTA \_  
 GAM1197 PReX1 3' CTCCTCCTCATCTTAGCTTCCA 40431 G A AGT  
 TGAAG TAA GA GGGAGGAG  
 ||||| ||| || |||||  
 ACCTTC ATT CT TCCTCCTC  
 G \_ AC\_  
 GAM1197 PRKACA 3' CTCATCCCCTTCACCCTCC 10790 A AAA T G  
 GGA GGT GAAG GGGA GAG  
 ||| ||| ||||| |||  
 CCT CCA CTTC CCCT CTC  
 C \_ \_ A  
 GAM1197 PTK2B 3' CTCCTCTTTCTCTCCCAACCC 14628 AA AAA\_ \_ TG  
 CCA TGG GGT GA AG GGAGGAG  
 ||| ||| ||| |||||  
 ACC CCA CT TC TCTCCTC  
 C\_ ACCC C TT  
 GAM1197 PTK7 3' TCCTCTTCCTCACCTC 11021 A AAA A TG  
 GA GGT GA G GGAGGA  
 || ||| ||| |||||  
 CT CCA CT C TCTCCT  
 C \_ \_ CT  
 GAM1197 PTPRN 3' CTCCTCCCACCACCCTCC 11130 A AAAGAA  
 GGA GGT GTGGGAGGAG  
 ||| ||| |||||  
 CCT CCA CACCCTCCTC  
 C C\_\_\_\_  
 GAM1197 PXN 3' CCCCTTCTTTACTTCCA 11159 A T  
 TGG AGGTAAAGAAG GGG  
 ||| ||||| |||  
 ACC TTCATTTCTTC CCC  
 C \_  
 GAM1197 RAB5B 3' CTCCCCCAGGACTTACCTTCC 11190 AGAAG A  
 A TGAAGGTAA TGGG GGAG  
 ||||| ||| |||  
 ACCTTCCATT ACCC CCTC  
 CAGG\_ C  
 GAM1197 RAI3 3' CTCCCATCTCCATCTCCA 14284 A AAA AG  
 TGG AGGT GA TGGGAG  
 ||| ||| || |||||  
 ACC TCTA CT ACCCTC  
 C C\_ CT  
 GAM1197 RALB 3' CTCCCCTTCTTCCCTCCA 11243 A TA T  
 TGG AGG AAGAAG GGGAG  
 ||| ||| ||||| |||||  
 ACC TCC TTCTTC CCCTC  
 C C\_ \_  
 GAM1197 RGS19IP1 3' CTCCCATCTCTCCTTCCA 62507 TAA AG  
 TGAAGG AGA TGGGAG  
 ||||| ||| |||||

ACCTTCC TCT ACCCTC  
 \_\_\_\_ CT  
 GAM1197 RS1 3' CCTGAAAGCTTCTCACCTCCA 4390 A AA GGG\_  
 TGGA GGT AGAAGT AGG  
 |||| || ||||| ||  
 ACCT CCA TCTTCG TCC  
 C C\_ AAAG  
 GAM1197 RUNX1 3' CTCCCTCTCTTCCCCCA 8263 AA TA A T  
 TGG GG AAGA G GGGAG  
 ||| || |||| | ||||  
 ACC CC TTCT C CCCTC  
 \_\_\_\_ CC \_ T  
 GAM1197 RXRA 3' TCCTCCCCGCGCCCTCCA 11418 A AAAGAA \_  
 TGGA GGT GTGGG AGGA  
 |||| || |||| ||||  
 ACCT CCG CGCCC TCCT  
 C C\_\_\_\_\_ C  
 GAM1197 S100A1 3' TTCCTCTCCACCCTCCA 20777 A TAAAGAA \_  
 TGG AGG GTGG GAGGAG  
 ||| || |||| |||||  
 ACC TCC CACC CTCCTT  
 C \_\_\_\_\_ T  
 GAM1197 S100A11 3' CCCACCCCTTTCTTCCA 18836 T AA\_  
 TGGAAGG AAAG GTGGG  
 ||||| ||| ||||  
 ACCTTCC TTTC CACCC  
 \_ CCC  
 GAM1197 SALL1 3' CTCCTACTCCTTGCCCCCA 11432 AA A A  
 TGG GGTA GA GTGGGAG  
 || |||| | |||||  
 ACC CCGTT CT CATCCTC  
 CC C \_  
 GAM1197 SECTM1 3' CTTCCCCTCCACCCCCCA 11528 AA AAA A T  
 TGG GGT GA G GGGAGG  
 ||| || || | |||||  
 ACC CCA CT C CCCTTC  
 CC C\_ \_  
 GAM1197 SFRP1 3' CCCGCTCCCTTTCCCTCCA 11567 A T A\_  
 TGGA GG AAAG AGTGGG  
 |||| || ||| |||||  
 ACCT CC TTTC TCGCCC  
 C \_ CC  
 GAM1197 SHOX 3' CTCTCACCTCCACCTCCA 22537 A AAA A  
 TGG AGGT GA GTGGGAG  
 ||| ||| || |||||  
 ACC TCCA CT CACTCTC  
 C C\_ C  
 GAM1197 SLC22A12 5' CTCCACATTCCCTACTTTCCA 58070 AA GTG  
 TGGAAGGTA GAA GGAG  
 ||||| || |||

ACCTTTCAT CTT CCTC  
 CC ACA  
 GAM1197 SLC2A4 3' TTCCTCCCCACCTTCC 6443 AAAGAAGT  
 GGAAGGT GGGAGGAG  
 ||||| |||||  
 CCTTCCA CCCTCCTT  
 C\_\_\_\_\_  
 GAM1197 SLC4A1 3' CCACATCCCCACCTTCCA 4424 AAA A  
 TGGAAGGT GA GTGG  
 ||||| || |||  
 ACCTTCCA CT CACC  
 CCC A  
 GAM1197 SLC8A2 3' CCCCCCACTTCACCCCA 66330 AA AAA A  
 TGG GGT GAAGTGGG GG  
 ||| ||| ||||| ||  
 ACC CCA CTTACCC CC  
 \_ \_ C  
 GAM1197 SORD 5' CTCCCAGGCCCCACCTTCCA 11871 AAAGAAG  
 TGGAAGGT TGGGAG  
 ||||| |||||  
 ACCTTCCA ACCCTC  
 CCCC GG\_  
 GAM1197 SPARC 3' CTCCTTTTCTTCACCCTCC 11898 A A T  
 GGA GGT AAGAAG GGGAG  
 ||| ||| ||||| |||||  
 CCT CCA TTCTTT TCCTC  
 C C \_  
 GAM1197 ST14 3' CTCGCTTCCTCAGCCTCCA 41766 A AAA\_  
 TGGA GGT GAAGTGGG  
 ||||| ||| |||||  
 ACCT CCG CTTGCTC  
 \_ ACTC  
 GAM1197 SURF4 3' CTA CTTCCTTACCCCGG 52542 AA A  
 TGG GGTA GAAGTGG  
 ||| ||||| |||||  
 GCC CCATT CTTCATC  
 C\_ C  
 GAM1197 SYT5 3' CCTCCCCCACCTTCCA 12074 AAAGAAGT  
 TGGAAGGT GGGAGG  
 ||||| |||||  
 ACCTTCCA CCCTCC  
 CCC\_\_\_\_\_  
 GAM1197 TEGT 3' CCCAATTAGACTTCCTCTCCTT 64622 TAAA \_\_\_\_\_  
 CCA TGGAAGG GAAGT GGG  
 ||||| ||||| |||  
 ACCTTCC CTTCA CCC  
 TCTC GATTAA  
 GAM1197 TIMP3 3' CCTCTTGCTTCTTCCCCACCTC 4506 A\_ A\_\_ TG  
 ACCA TGG AGGT AAGAAG GGAGG  
 ||| ||||| ||||| |||||

ACC TCCA TTCTTC TCTCC  
 AC CCCC GT  
 GAM1197 TMP21 3' CTCCTCCCACCTTGTACCTC 22402 A AAGAA  
 GA GGTA GTGGGAGGAG  
 || ||| |||||  
 CTCCAT CACCCTCCTC  
 \_ GTTC\_  
 GAM1197 TRIM14 3' CTCCCAGTCCTCATCTTCCA 28854 AAA AG  
 TGGAAGGT GA TGGGAG  
 ||||| || |||||  
 ACCTTCTA CT ACCCTC  
 CTC G\_  
 GAM1197 TSPY 3' CTCCTCGCTTTCCCTTCCA 82106 TAAA \_  
 TGGAAGG GAAGTG GGAG  
 ||||| ||||| |||||  
 ACCTTCC TTTCGC CCTC  
 C\_\_ T  
 GAM1197 UBE2V1 3' CCCATATCTTCTCTCCCCCA 12515 AA TA\_\_ A  
 TGG GG AAGA GTGGG  
 ||| || ||| |||||  
 ACC CC TTCT TACCC  
 CC TCTC A  
 GAM1197 UBE2V1 3' CCCATATCTTCTCTCCCCCA 41790 AA TA\_\_ A  
 TGG GG AAGA GTGGG  
 ||| || ||| |||||  
 ACC CC TTCT TACCC  
 CC TCTC A  
 GAM1197 UBL5 3' CTCCCATCCTCATCCCCCA 44149 AA TAA AA  
 TGG GG AG GTGGGAG  
 ||| || || |||||  
 ACC CC TC TACCCTC  
 C\_ TAC C\_  
 GAM1197 UFD1L 3' CTCCTTCTTCCCTACTCCCCA 73285 AA AA T  
 TGG GGTA GAAG GGGAG  
 ||| ||| ||| |||||  
 ACC TCAT CTTT TCCTC  
 CC CC T  
 GAM1197 WBP2 3' CTCCTGCCTCCCTGCCTCCCA 73029 A AA A TG  
 TGG AGGTA GA G GGAG  
 ||| |||| ||| |||||  
 ACC TCCGT CT C CCTC  
 C CC C GT  
 GAM1197 WNT10B 3' CTCCTCCCACCTTCTCAACTCCA 12674 AG AA  
 TGGA GT AGAAGTGGGAGGAG  
 |||| || ||||| |||||  
 ACCT CA TCTTCACCCTCCTC  
 \_ AC  
 GAM1197 WNT5A 3' CCCCTTTGTCTCCAACCTCCA 12663 A AA\_ AGT A  
 TGGA GGT AGA GGG GG  
 |||| ||| ||| ||| ||



			ACCT CCA TCT TCC CC		
			_ ACC GTT _		
GAM1197	YWHAH	3'	CCTCCCACCTCTTTCTTC	12695	TA A
			GAAGG AAGA GTGGGAGG		
			CTTCT TTCT CACCCTCC		
			_ C		
GAM1197	ZNF216	5'	CCCTCGCTTCCCTCCTCCCA	20019	A TAAA A
			TGG AGG GAAGTGGG GG		
			ACC TCC CTTCGCTC CC		
			C TCC_ _		
GAM1197	ZNF216	5'	CTCCTCCCACCTTCCCGAGCTCC	20020	AGGTAAA
			GGA GAAGTGGGAGGAG		
			CCT CTTCACCCTCCTC		
			CGAGCC_		
GAM1197	ZNF278	3'	CCTCCCACCTTCTCTAGTTC	26727	GG A
			GAA TA AGAAGTGGGAGG		
			CTT AT TCTTCACCCTCC		
			G_ C		
GAM1197	ZNF278	3'	CTCCTTCTCCACCACCCA	26729	AA AA T
			TGG GGT AGAAG GGG		
			ACC CCA TCTTC CTC		
			CA CC _		
GAM1197	ZNF278	3'	CCTCCCACCTTCTCTAGTTC	49434	GG A
			GAA TA AGAAGTGGGAGG		
			CTT AT TCTTCACCCTCC		
			G_ C		
GAM1197	ZNF278	3'	CTCCTTCTCCACCACCCA	49436	AA AA T
			TGG GGT AGAAG GGG		
			ACC CCA TCTTC CTC		
			CA CC _		
GAM1197	ZNF278	3'	CCTCCCACCTTCTCTAGTTC	49442	GG A
			GAA TA AGAAGTGGGAGG		
			CTT AT TCTTCACCCTCC		
			G_ C		
GAM1197	ZNF278	3'	CTCCTTCTCCACCACCCA	49444	AA AA T
			TGG GGT AGAAG GGG		
			ACC CCA TCTTC CTC		
			CA CC _		
GAM1197	ZNF74	5'	CTCCCGCCTCAACCTCCCA	12794	A AAA A
			TGG AGGT GA GTGGGAG		

ACC TCCA CT CGCCCTC  
 C A\_\_ C  
 GAM1197 ACTR3 3' CCACCCCTTCCCCCA 19145 AA TAAA T A  
 TGG GG GAAG GGG GG  
 ||| || ||| ||| ||  
 ACC CC CTTC CCC CC  
 C\_ \_\_\_\_ \_ A  
 GAM1197 AKAP11 3' CCTCCCCTCCTCCCA 32705 A TAAAGA T \_  
 TGG AGG AG GGGAG G  
 ||| ||| || ||||| |  
 ACC TCC TC CCCTC C  
 C \_\_\_\_\_ \_ T  
 GAM1197 AKAP11 3' CTCCTCCCACTGTCTCTCACCT 32706 A AA\_ \_  
 CCC GG AGGT AGA AGTGGGAGGAG  
 || ||| ||| ||||| |||||  
 CC TCCA TCT TCACCCTCCTC  
 C CTC G  
 GAM1197 ARGBP2 3' CCGTCACCATCTCCACCTCCCA 40772 A AAA AG \_ \_  
 TGG AGGT GA TGG GA GG  
 ||| ||| || ||| |||  
 ACC TCCA CT ACC CT CC  
 C C\_\_ CT A G  
 GAM1197 ARHF 3' CCTCCCATCTCCACCCCA 38740 AA AAA AG  
 TGG GGT GA TGGGAGG  
 ||| ||| || |||||  
 ACC CCA CT ACCCTCC  
 \_ C\_\_ CT  
 GAM1197 ARHGEF15 3' CTCCATTTCTTCCTTTACCCCC 30259 AA \_ TG\_\_  
 CA TGG GGTAAG AAG GGAG  
 ||| ||||| ||| |||  
 ACC CCATTTTCTTC CCTC  
 CC C TTTA  
 GAM1197 ASB16 3' CTCCTGCCTCTGCCTCCCA 69935 A AA A TG  
 TGG AGGT AGA G GGAG  
 ||| ||| ||| | |||  
 ACC TCCG TCT C CCTC  
 C \_ C GT  
 GAM1197 BRPF3 3' CTCCCCAGGACACCACCTCCC 92316 A AAAGAAG A  
 A TGG AGGT TGGG GGAG  
 ||| ||| ||| |||  
 ACC TCCA ACCC CCTC  
 C CCACAGG \_  
 GAM1197 BSMAP 3' CCCCCAAATCCTTCTCCTC 23993 A TAAA \_\_\_\_ A  
 CCA TGG AGG GAAG TGGG GG  
 ||| ||| ||| ||| |||  
 ACC TCC CTTC ACCC CC  
 C TCTC CTAA \_  
 GAM1197 C20orf149 3' CCTCCCCACCTCCCACCCCCCA 44172 AA AAA A \_  
 TGG GGT GA GTGGG AGG  
 ||| ||| || ||||| |||

ACC CCA CT CACCC TCC  
 CC CC\_ C C  
 GAM1197 C20orf98 3' CCTCCCTAACCCCTTACCTTC 71514 AGAAGT  
 GAAGGTAA GGGAGG  
 ||||| |||||  
 CTTCCATT CCCTCC  
 CCCAAT  
 GAM1197 CD36L1 3' CCCAGGCTTCCTCCCCTCCA 18566 A TAAA \_  
 TGGA GG GAAGT GGG  
 ||| || ||||| |||  
 ACCT CC CTTCG CCC  
 C CTC\_ GA  
 GAM1197 CDH26 3' CTCCCTATCCCTCTTTCCCCC 41465 AA T AGT \_  
 A TGG GG AAAGA GGGA GGAG  
 ||| ||||| ||| |||||  
 ACC CC TTTCT CCCT CTC  
 CC \_ \_ ATC  
 GAM1197 CGB1 3' TCCCCCAGCCTTCCA 52965 AAAGAAG A  
 TGGAAGGT TGGG GGA  
 ||||| ||| |||  
 ACCTCCG ACCC CCT  
 \_ C  
 GAM1197 CGB2 3' TCCCCCAGCCTTCCA 52966 AAAGAAG A  
 TGGAAGGT TGGG GGA  
 ||||| ||| |||  
 ACCTCCG ACCC CCT  
 \_ C  
 GAM1197 CLSTN3 5' CTCCTCTTCACCCCCA 28208 AA AAA T  
 TGG GGT GAAG GGGAGG  
 ||| ||| ||||| |||||  
 ACC CCA CTTC TCCTCC  
 C\_ \_ \_  
 GAM1197 COL4A3BP 5' TCCTCCTGCTCCCCCCA 19130 AA TAAA A TG  
 TGG GG GA G GGAGGA  
 ||| || ||| |||||  
 ACC CC CT C CTCCT  
 CC \_ \_ GT  
 GAM1197 COP9 3' CTCTCTTTTACCCCCCA 22004 AA AAA T  
 TGG GGT GAAG GGGAG  
 ||| ||| ||||| |||||  
 ACC CCA CTTT CTCTC  
 CC \_ T  
 GAM1197 DDX39 3' CCTCCCACCTCCCTTCC 57312 TAAA A  
 GGAAGG GA GTGGGAGG  
 ||||| || |||||  
 CCTTCC CT CACCCTCC  
 \_ C  
 GAM1197 DEFCAP 5' CTCCTCCCACCCACCTCTTCT 29950 TAAAGAA  
 GGAAGG GTGGGAGGAG  
 ||||| |||||

TCTTCT CACCCTCCTC  
 CCACCC\_  
 GAM1197 DEFCAP 5' CTCCTCCCACCCACCTCTTCT 52230 TAAAGAA  
 GGAAGG GTGGGAGGAG  
 ||||| |||||  
 TCTTCT CACCCTCCTC  
 CCACCC\_  
 GAM1197 DGKD 3' CTCCTCCCGCTCCTCCCTCC 59404 A TAA A  
 GGA GG AG AGTGGGAGGAG  
 ||| || |||||  
 CCT CC TC TCGCCCTCCTC  
 C \_ C  
 GAM1197 DJ159A19.3 3' CCTCCCACCCATCTCCTCCA 31650 A TAA A\_  
 TGGA GG AGA GTGGGAGG  
 ||||| ||| |||||  
 ACCT CC TCT CACCCTCC  
 \_ \_ ACC  
 GAM1197 DJ159A19.3 3' CTCCTGCCCTCTGCCTCCCA 31651 A A AA TG  
 TGG AGGTA AG G GGAG  
 ||| ||||| || | |||||  
 ACC TCCGT TC C CCTC  
 C C CC GT  
 GAM1197 dJ309H15.1 3' TCCTCCCACCTCTTCC 56797 TAAAGAA  
 GGAAGG GTGGGAGGA  
 ||||| |||||  
 CCTTCT CACCCTCCT  
 CC\_\_\_\_\_  
 GAM1197 DKFZp434A1010 3' TCCTCCTCTCCCTCCA 71344 A TAAAGA T  
 TGGA GG AG GGGAGGA  
 ||||| || |||||  
 ACCT CC TC TCCTCCT  
 C \_ \_ \_ \_  
 GAM1197 DKFZp434I1930 3' CTCCCCTTCTTTCCCTTCCA 50033 T T  
 TGGAAGG AAAGAAG GGGAG  
 ||||| ||||| |||||  
 ACCTTCC TTTCTTC CCCTC  
 C \_  
 GAM1197 DKFZP434J037 3' TCCTCCCACAACCCCCCA 48220 AA AAAGAA  
 TGG GGT GTGGGAGGA  
 ||| ||| |||||  
 ACC CCA CACCCTCCT  
 CC A\_\_\_\_\_  
 GAM1197 DKFZP434N014 3' CTCCTGGCTCCTTATCCCCCA 60599 AA A AG  
 TGG GGTAAG GA TGGGAG  
 ||| ||||| || |||||  
 ACC CTATT CT GTCCTC  
 CC C CG  
 GAM1197 DKFZp547H236 3' CTCCTGTCCCCCTACCTCC 78543 A AAGAAGT \_  
 GGA GGTA GGA GGAG  
 ||| ||||| ||| |||||

CCT CCAT    CCCT CCTC  
   \_ CCC\_    GT  
 GAM1197 DKFZP564G092 5' CTCCTCCCTCTTTACCCTCC 31535    A    AGT  
           GGA GGTAAGA GGGAGGAG  
           ||| |||||    |||||  
           CCT CCATTTCT CCCTCCTC  
           C    \_  
 GAM1197 DKFZP566I1024 3' CTCCCACCTCGACCTCCCA 70101    A    AA AA  
           TGG AGGT AG GTGGGAG  
           ||| |||    || |||||  
           ACC TCCA TC CACCCTC  
           C GC \_  
 GAM1197 DKFZP586G1122 3' CCTCCCACCAGTCACCTCCA 61285    A    AAAGAA  
           TGGA GGT GTGGGAGG  
           ||| |||    |||||  
           ACCT CCA CACCCTCC  
           \_ CTGAC\_  
 GAM1197 DKFZP727C091 3' CTCTTACCCCTCCCCTCCCA 66210    A    TAAA A T \_  
           TGG AGG GA G GGG AGGAG  
           ||| |||    || ||| |||||  
           ACC TCC CT C CCC TTCTC  
           C C\_ \_ C A  
 GAM1197 DKFZp761B0514 3' TCCTCCCAGCAGCCTCCA 50160    A    AAAGAAG  
           TGGA GGT TGGGAGGA  
           ||| |||    |||||  
           ACCT CCG ACCCTCCT  
           \_ ACG\_  
 GAM1197 DPCR1 3' CCCATTCTCTCTCCTCCCA 55121    A    TAA \_  
           TGG AGG AGA AGTGGG  
           ||| |||    || |||||  
           ACC TCC TCT TTACCC  
           C TC\_ C  
 GAM1197 DPCR1 3' TCCTCCCACCTTCACCCCA 55124    AA    A AA  
           TGG GGT AAG GTGGGAGGA  
           ||| ||| ||| |||||  
           ACC CCA TTC CACCCTCCT  
           \_ C \_  
 GAM1197 DSCAML1 3' CCTCCTCCTCACCTTCC 40360    AAA    A TG  
           GGAAGGT GA G GGAGG  
           |||||    || |||||  
           CCTTCCA CT C CCTCC  
           \_ \_ CT  
 GAM1197 E1B-AP5 3' CCCACCTCCCCAGCCTTCCA 22898    AAA\_    A  
           TGGAAGGT GA GTGGG  
           |||||    || |||||  
           ACCTTCCG CT CACCC  
           ACCC C  
 GAM1197 E1B-AP5 3' CCTCCTGTTCACTCTCC 22900    AG    AAA G  
           GGA GT GAA TGGGAGG  
           ||| ||    || |||||

CCT CA CTT GTCCTCC  
 CT \_\_\_\_ \_  
 GAM1197 E1B-AP5 3' CCCACCTCCCCAGCCTTCCA 58565 AAA\_ A  
 TGGAAGGT GA GTGGG  
 ||||| || ||||  
 ACCTCCG CT CACCC  
 ACCC C  
 GAM1197 E1B-AP5 3' CCTCCTGTTCACTCTCC 58567 AG AAA G  
 GGA GT GAA TGGGAGG  
 ||| || ||| |||||  
 CCT CA CTT GTCCTCC  
 CT \_\_\_\_ \_  
 GAM1197 ELF4 5' CTCCAGCTCTCTCCACCCCC 7433 AA AA \_ G  
 GG GGT AGA AGT GGAG  
 || ||| ||| ||| |||  
 CC CCA TCT TCG CCTC  
 C\_ CC C A  
 GAM1197 ELOVL2 3' CCTCCCTCCCTCCCA 34958 A TAAA AGT \_  
 TGG AGG GA GGGAG G  
 ||| ||| || |||||  
 ACC TCC CT CCCTC C  
 C \_\_\_\_ \_ T  
 GAM1197 EZF-2 3' CTCCTCCTTCCCTCCCA 37098 A TAAA TG  
 TGG AGG GAAG GGAG  
 ||| ||| ||| |||  
 ACC TCC CTTC CCTC  
 C \_\_\_\_ CT  
 GAM1197 FBXO27 3' CCCTCTCTTCTCCTCCCA 74506 A TAA T A  
 TGG AGG AGAAG GGG GG  
 ||| ||| |||| ||| ||  
 ACC TCC TCTTC CTC CC  
 C \_\_\_\_ T \_  
 GAM1197 FEM-2 3' CCTCCCCTTCCCTCCCA 27574 A TAAAG T  
 TGG AGG AAG GGGAGG  
 ||| ||| ||| |||||  
 ACC TCC TTC CCCTCC  
 C \_\_\_\_ \_  
 GAM1197 FLJ00024 3' CCCCTTCTCTCCCTCCCA 63756 A TAA T  
 TGGA GG AGAAG GGG  
 |||| || |||| |||  
 ACCT CC TCTTC CCC  
 C TC\_ \_  
 GAM1197 FLJ10314 3' CCTCCCCTGTCTCCTCCCA 36011 A TAA \_ T  
 TGG AGG AGA AG GGGAGG  
 ||| ||| ||| ||| |||||  
 ACC TCC TCT TC CCCTCC  
 C \_\_\_\_ G \_  
 GAM1197 FLJ11362 3' CCTTTCCTTCTCCTCCCA 41680 A TAAA T GG  
 TGG AGG GAAG G AGG  
 ||| ||| |||| | |||

ACC TCC CTTC C TCC  
 C TCTC \_TT  
 GAM1197 FLJ11539 3' CTCCCACCTCACCTCCCA 45376 A AAA A\_  
 TGG AGGT GA GTGGGAG  
 ||| ||| || |||||  
 ACC TCCA CT CACCCTC  
 C \_ CC  
 GAM1197 FLJ11618 3' CCTCCCGTTACCTACCA 42393 A AAA G  
 TGG AGGT GAA TGGGAGG  
 ||| ||| || |||||  
 ACC TCCA CTT GCCCTCC  
 A \_ \_  
 GAM1197 FLJ12448 3' CTCCTCCTCTCTACACCCCA 43177 AA AA A T  
 TGG GGT AGA G GGGAGGAG  
 ||| ||| ||| |||||  
 ACC CCA TCT C TCCTCCTC  
 C\_ CA \_ \_  
 GAM1197 FLJ12541 3' TCCCCGGCTCTCCTCCCA 42329 A TAA A G A  
 TGG AGG AGA GT GG GGA  
 ||| ||| ||| ||| |||  
 ACC TCC TCT CG CC CCT  
 C \_ \_ G \_  
 GAM1197 FLJ12650 3' TCTCCCACTACCCTCCA 44529 A AAAGA  
 TGGA GGT AGTGGGAGG  
 |||| ||| |||||  
 ACCT CCA TCACCCTCT  
 C \_ \_ \_  
 GAM1197 FLJ12788 3' CTCCCCCAACCCCTTACCTTT 42545 AGAAG\_ A  
 CA TGGAAGGTAA TGGG GGAG  
 ||||| ||| |||  
 ACTTTCCATT ACCC CCTC  
 CCCCCA \_  
 GAM1197 FLJ12921 3' CCCCTTCCCCCACCTTCC 45909 AAA\_ T  
 GGAAGGT GAAG GGG  
 ||||| ||| |||  
 CCTTCCA CTTC CCC  
 CCCC \_  
 GAM1197 FLJ12921 3' CTCCTCACTCTCTACCTCCC 45910 A A A \_  
 GG AGGTA AGA GTG GGAG  
 || |||| ||| ||| |||  
 CC TCCAT TCT CAC CCTC  
 C C \_ T  
 GAM1197 FLJ13111 3' CTCCTCCCCACCCCCCA 46938 AA TAAAGAA \_  
 TGG GG GTGGG AGGAG  
 ||| || |||| |||||  
 ACC CC CACCC TCCTC  
 CC \_ \_ C  
 GAM1197 FLJ13852 3' CTCCTCTTTCTCCTCCCA 43577 A T AGT  
 TGG AGG AAAGA GGGAG  
 ||| ||| |||| |||||

ACC TCC TTTCT CCCTC  
 C \_ \_ \_  
 GAM1197 FLJ14549 3' CCCACTTCCCTCTCCTTCCA 51441 TAAA\_  
 TGGAAGG GAAGTGGG  
 ||||| |||||  
 ACCTTCC CTTACCC  
 TCTCC  
 GAM1197 FLJ14596 3' CTCCTCCCACCTCTGTCACCAC 51459 AA AA\_ A  
 CA TGG GGT AGA GTGGGAGGAG  
 ||| ||| ||| |||||  
 ACC CCA TCT CACCCTCCTC  
 A\_ CTG C  
 GAM1197 FLJ14681 5' CTCCTATCTCTGCCTTCCA 51524 AA AG  
 TGGAAGGT AGA TGGGAG  
 ||||| ||| |||||  
 ACCTTCCG TCT ATCCTC  
 \_ CT  
 GAM1197 FLJ14721 3' CCTTCCCCTACCCCA 51581 AA AAAGA T  
 TGG GGT AG GGGAGG  
 ||| ||| || |||||  
 ACC CCA TC CCTTCC  
 C\_ \_ \_ C  
 GAM1197 FLJ14800 3' CTCCTTTCTCCCCTTCCA 51612 TAA GT  
 TGGAAGG AGAA GGGAG  
 ||||| ||| |||||  
 ACCTTCC TCTT TCCTC  
 CC\_ \_  
 GAM1197 FLJ14824 3' CTCTTCCTTCTCCCCTCCA 51643 A TAA TG  
 TGG AGG AGAAG GGAG  
 ||| ||| ||||| |||  
 ACC TCC TCTTC TCTC  
 C CC\_ CT  
 GAM1197 FLJ20085 3' CCCCCGCCCCCGCACCTTCCA 34514 AAAGAA A  
 TGGAAGGT GTGGG GG  
 ||||| ||||| ||  
 ACCTTCCA CGCCC CC  
 CGCCCC \_  
 GAM1197 FLJ20207 5' CTCCCGCTTCCTCCCTCCA 34736 A TAAA  
 TGG AGG GAAGTGGGAG  
 ||| ||| |||||  
 ACC TCC CTTCGCCCTC  
 C CTC\_  
 GAM1197 FLJ20344 3' CTCCTGCCTCAACCTCCA 35010 A AAA A TG  
 TGG AGGT GA G GGAG  
 ||| ||| ||| |||  
 ACC TCCA CT C CCTC  
 C A\_ C GT  
 GAM1197 FLJ20359 3' CTCCCACCCTCTCTCCTCCA 35041 A TAA A\_  
 TGG AGG AGA GTGGGAG  
 ||| ||| ||| |||||



ACC TCC TCT CACCCTC  
 C TC\_ CC  
 GAM1197 FLJ20548 3' CCCCTGCCCCTTTTCCTTCCA 35375 T AA TG A  
 TGGAAGG AAAG G GG GG  
 ||||| ||| | ||  
 ACCTTCC TTTC C CC CC  
 T CC GT \_  
 GAM1197 FLJ21313 3' CTTATACTTCCTTCCTCCA 43683 A T A G  
 TGG AGG AA GAAGTG GAG  
 ||| ||| || ||||| |||  
 ACC TCC TT CTTCAT TTC  
 C \_ C A  
 GAM1197 FLJ21596 3' CTCCTCCCACCCCGTAGCTCCA 45700 A G AAGAA  
 TGGA G TA GTGGGAGGAG  
 |||| | || |||||  
 ACCT C AT CACCCTCCTC  
 \_ G GCCC\_  
 GAM1197 FLJ22671 3' CTCCTTCTCCTTCACCTTCCA 45865 AAA TG  
 TGGAAGGT GAAG GGAGGAG  
 ||||| ||| |||||  
 ACCTTCCA CTTC CTCCTC  
 \_ CT  
 GAM1197 FLJ23022 3' TCCTTTCTCCTTCCTTCCA 46813 TA AAGT GG  
 TGGAAGG AAG G AGGA  
 ||||| ||| | |||  
 ACCTTCC TTC C TCCT  
 \_ CT\_ TT  
 GAM1197 FLJ23189 3' CTTATTCACTCCTTTGCCTCCC 46840 A A \_  
 A TGG AGGTAAAG AGTGGG AGG  
 ||| ||||| ||||| |||  
 ACC TCCGTTTC TCACTT TTC  
 C C A  
 GAM1197 FLJ23416 3' TCCTCCCCTCCCCTCCA 49955 A TAAA A T  
 TGG AGG GA G GGGAGGA  
 ||| ||| || | |||||  
 ACC TCC CT C CCCTCCT  
 C C\_ \_  
 GAM1197 FLJ30532 3' CTCCTGCCTCTGCCTCCA 58547 A AA A TG  
 TGG AGGT AGA G GGAG  
 ||| ||| ||| | |||  
 ACC TCCG TCT C CCTC  
 C \_ C GT  
 GAM1197 FOXH1 5' CCTCCCCTCCCCCTTCCA 14072 TAAA A T  
 TGGAAGG GA G GGGAGG  
 ||||| || | |||||  
 ACCTTCC CT C CCCTCC  
 CC\_ \_  
 GAM1197 GBTS1 3' CCCCTGCTCTCTCTCCACCCTC 59053 A AA \_ TG A  
 C GGA GGT AGA AG GG GG  
 ||| ||| ||| || |||

CCT CCA TCT TC CC CC  
 C CC CTC GT \_  
 GAM1197 GOLGA3 3' CTCCCGGCACTTCTACCTTCCA 19716 AA \_\_\_\_  
 TGGAAGGT AGAAGT GGGAG  
 ||||| |||| ||||  
 ACCTTCCA TCTTCA CCCTC  
 \_ CGG  
 GAM1197 GPS2 3' CCTTTTACTCCCCTACCCCA 50574 AA AAGA  
 TGG GGTA AGTGGGAGG  
 ||| ||| |||||  
 ACC CCAT TCATTTTCC  
 \_ CCCC  
 GAM1197 GPS2 3' CCTTTTACTCCCCTACCCCA 87156 AA AAGA  
 TGG GGTA AGTGGGAGG  
 ||| ||| |||||  
 ACC CCAT TCATTTTCC  
 \_ CCCC  
 GAM1197 GRASP1 3' CTCCTCCCCTTCTACCCCC 39301 AA AA T  
 GG GGTA GAAG GGGAGGAG  
 || ||| ||| |||||  
 CC CCAT CTTC CCCTCCTC  
 C\_ C\_ \_  
 GAM1197 HSA011916 3' CCTCCCACCCCTCTCTGCC 31059 A A\_\_  
 GGTA AGA GTGGGAGG  
 |||| ||| |||||  
 CCGT TCT CACCCTCC  
 C CCC  
 GAM1197 HSA011916 3' CCTCCCACCCCTCTCTGCC 60271 A A\_\_  
 GGTA AGA GTGGGAGG  
 |||| ||| |||||  
 CCGT TCT CACCCTCC  
 C CCC  
 GAM1197 HSU79275 3' CTCCTTTCTCTCTCCCCTCCA 66317 A TA A T GG  
 TGGA GG AAG AG G AGGAG  
 |||| || ||| ||| ||||  
 ACCT CC TTC TC C TCCTC  
 \_ CC C \_ TT  
 GAM1197 HU-K4 3' CTCCCACCTCTACCTCCA 24367 A AA A  
 TGGA GGT AGA GTGGGAG  
 |||| ||| ||| |||||  
 ACCT CCA TCT CACCCTC  
 \_ \_ C  
 GAM1197 IL18BP 5' CCTCCCCCACCTTTCA 19106 AAAGAAGT  
 TGGAAGGT GGGAGG  
 ||||| |||||  
 ACTTTCCA CCCTCC  
 CC\_\_\_\_\_  
 GAM1197 KCNH8 5' CTCCTTTCTCCCTCCATCCTT 58256 TAA\_\_\_\_\_ T  
 CCA TGGAAGG AGAAG GGGAG  
 ||||| ||||| |||||

ACCTTCC TCTTT CCCTC  
 TACCTCCC \_  
 GAM1197 KIAA0232 3' CTCCTCCCCATCTCACCCCA 72748 AA AA AGT  
 TGG GGT AGA GGGAGGAG  
 ||| ||| ||| |||||  
 ACC CCA TCT CCCTCCTC  
 C\_ C\_ AC\_  
 GAM1197 KIAA0257 3' CTCCCCTCCCCACCCTCC 70818 A AAA A T  
 GGA GGT GA G GGGAG  
 ||| ||| ||| |||||  
 CCT CCA CT C CCCTC  
 C CCC \_ \_  
 GAM1197 KIAA0285 3' CTCCTCCCACCTTCTCACCTTT 29016 AA \_  
 CA TGAAGGT AGAAG TGGGAGGAG  
 ||||| ||||| |||||  
 ACTTTCCA TCTTC ACCCTCCTC  
 C\_ C  
 GAM1197 KIAA0296 3' TCCTCTCTCTCTCCCCCA 28119 AA TAA A T  
 TGG GG AGA G GGGAGGA  
 ||| || ||| |||||  
 ACC CC TCT C CTCTCCT  
 CC \_ \_ T  
 GAM1197 KIAA0356 3' CTCTGTGTCTCTTTACTCCCC 66191 AA AGTG \_  
 A TGG GGTAAAGA GGA GGAG  
 ||| ||||| ||| |||||  
 ACC TCATTCT CCT TCTC  
 CC \_ \_ GTG  
 GAM1197 KIAA0367 3' CCTCCCACAGCCACCTCCA 67297 A AAAGAA  
 TGGA GGT GTGGGAGG  
 ||||| ||| |||||  
 ACCT CCA CACCCTCC  
 \_ CCCGA\_  
 GAM1197 KIAA0376 3' CCTCCCACATGACCCGTCCA 65599 A\_ AAAGAA  
 TGGA GGT GTGGGAGG  
 ||||| ||| |||||  
 ACCT CCA CACCCTCC  
 GC GTA\_  
 GAM1197 KIAA0446 3' CCACTTCTCTACCTTC 68858 A  
 GAAGGTA AGAAGTGG  
 ||||| |||||  
 CTTCCAT TCTTCACC  
 C  
 GAM1197 KIAA0515 3' CCCTCCGCTCCCTTCCA 63806 TAAA A GA  
 TGGAAGG GA GTGG GG  
 ||||| || ||| ||  
 ACCTTCC CT CGCC CC  
 \_ \_ TC  
 GAM1197 KIAA0515 3' CTCTGGACCTGTCTCCACCTCC 63807 A AA AGT GA\_  
 CA TGG AGGT AGA GG GGAG  
 ||| |||| ||| || |||

ACC TCCA TCT CC TCTC  
 C CC GT\_ AGG  
 GAM1197 KIAA0532 3' CTCCCACCTCCACCTCCCA 70772 A AAA A  
 TGG AGGT GA GTGGGAG  
 ||| ||| || |||||  
 ACC TCCA CT CACCCTC  
 C C\_ C  
 GAM1197 KIAA0552 5' CCTCCCCTCCCCCTCCCA 28312 A TAAA A T  
 TGG AGG GA G GGGAGG  
 ||| ||| || |||||  
 ACC TCC CT C CCCTCC  
 C CCC\_ \_  
 GAM1197 KIAA0620 3' CCTCCCACCTGTCCCA 62120 AA TAA AA  
 TGG GG AG GTGGGAGG  
 ||| || || |||||  
 ACC CC TC CACCCTCC  
 \_ TG\_ \_  
 GAM1197 KIAA0721 3' CTCCCCCTCTCCCTCCCA 41340 A TAA A T  
 TGG AGG AGA G GGGAG  
 ||| ||| ||| |||||  
 ACC TCC TCT C CCCTC  
 C C\_ \_ C  
 GAM1197 KIAA0721 3' CTCCCCCTCTCCCTCCCA 95967 A TAA A T  
 TGG AGG AGA G GGGAG  
 ||| ||| ||| |||||  
 ACC TCC TCT C CCCTC  
 C C\_ \_ C  
 GAM1197 KIAA0773 3' CTCCCCCAATGCCCTGCCTTCC 28053 AAGAAG A  
 A TGGGAAGGTA TGGG GGAG  
 ||||| ||| |||  
 ACCTTCGGT ACCC CCTC  
 CCCGTA \_  
 GAM1197 KIAA0854 3' CCTCCCACACTGCCCCCA 30098 AA AAGAA  
 TGG GGTA GTGGGAGG  
 ||| ||| |||||  
 ACC CCGT CACCCTCC  
 CC CA\_  
 GAM1197 KIAA1026 3' CTCCTCCCACACATTACCTTCC 71193 AGAA  
 A TGGGAAGGTAA GTGGGAGGAG  
 ||||| |||||  
 ACCTTCATT CACCCTCCTC  
 ACA\_  
 GAM1197 KIAA1028 3' CTCCAACCTCCACCTTCCA 91936 AAA A G  
 TGGGAAGGT GA GT GGAG  
 ||||| || |||  
 ACCTTCCA CT CA CCTC  
 C\_ C A  
 GAM1197 KIAA1042 3' CTCCCTCTCTTCCCCCA 30337 AA TA A T  
 TGG GG AAGA G GGGAG  
 ||| || ||| |||||

ACC CC TTCT C CCCTC  
 \_\_ CC \_ T  
 GAM1197 KIAA1046 3' CTCCCCAGCCCCCTTACCTTC 29995 AGAA\_ G A  
 GAAGGTAA GT GG GGAG  
 ||||| || ||||  
 CTTCCATT CG CC CCTC  
 CCCCC A \_  
 GAM1197 KIAA1075 5' CTCCCCACATCCTCCCCCTC 61717 A TAAA\_ A A  
 CA TGGG GG GA GTGGG GGAG  
 ||| || || |||| ||||  
 ACCT CC CT CACCC CCTC  
 C CCCTC A \_  
 GAM1197 KIAA1111 3' CCCTCACCCCTTTACCCCCA 96207 AA AA A  
 TGG GGTAAG GTGGG GG  
 || |||| |||| ||  
 ACC CCATTC CACTC CC  
 C\_ CC \_  
 GAM1197 KIAA1163 3' CTCCTCTTACCCTACCCCA 78900 AA AAGAA  
 TGG GGTA GTGGGAGGAG  
 || ||| |||||  
 ACC CCAT CATTCTCCTC  
 \_\_ CC\_\_  
 GAM1197 KIAA1169 3' CTCCTCGCTTCCCTCCCA 35449 A TAAA \_  
 TGG AGG GAAGTG GGAG  
 || ||| |||| ||||  
 ACC TCC CTTCGC CCTC  
 C C\_\_ T  
 GAM1197 KIAA1184 3' CCCTCTGCTTCACCTCCA 42611 A AAA TG GA  
 TGGA GGT GAAG G GG  
 |||| ||| ||| | ||  
 ACCT CCA CTTC C CC  
 \_ \_\_ GT TC  
 GAM1197 KIAA1193 3' CCACCTGCCTCTTCCCCCTCCA 67634 A TA A TG A  
 TGGA GG AAGA G GG GG  
 |||| || ||| | ||  
 ACCT CC TTCT C CC CC  
 C CC C GT A  
 GAM1197 KIAA1205 3' CCTCCCACTCCTTTTCT 70044 T A  
 AGG AAAG AGTGGGAGG  
 || ||| |||||  
 TCT TTTC TCACCCTCC  
 \_ C  
 GAM1197 KIAA1363 3' CCCCCATCTCCTCCTTCCA 69261 TAAA AG A  
 TGGAAGG GA TGGG GG  
 ||||| || |||| ||  
 ACCTTCC CT ACCC CC  
 TC\_\_ CT \_  
 GAM1197 KIAA1463 3' TTCCTCCCCACTCCTCCA 72279 A TAAAGA \_  
 TGGA GG AGTGGG AGGAG  
 |||| || |||| ||||

ACCT CC TCACCC TCCTT  
 ————— C  
 GAM1197 KIAA1538 5' TCTTCCTCTCCCCCTCCA 71558 A TAA AGTG  
 TGGA GG AGA GGAGGA  
 |||| || || ||||  
 ACCT CC TCT CCTTCT  
 C CC\_ ———  
 GAM1197 KIAA1543 5' CTCCTGTCTTCACCTTCC 70984 AAA \_  
 GGAAGGT GAAG TGGGAG  
 ||||| ||| |||||  
 CCTTCCA CTTC GTCCTC  
 ——— T  
 GAM1197 KIAA1666 3' TTCCTCCCTCACCCTCCA 65252 A\_ AAA AGT  
 TGGA GGT GA GGGAGGAG  
 ||| ||| || |||||  
 ACCT CCA CT CCCTCCTT  
 CA ———  
 GAM1197 KIAA1671 3' TCTTCCTCCTCACCTCCA 65696 A AAA A TG  
 TGGA GGT GA G GGAGGA  
 ||| ||| || |||||  
 ACCT CCA CT C CCTTCT  
 ——— CT  
 GAM1197 KIAA1719 3' CTCCCTTACCCCTCCCCTCCA 68159 A TAA AA A  
 TGGA GG AG GTGGG GGAG  
 |||| || || |||||  
 ACCT CC TC CATTG CCTC  
 C C\_ CC \_  
 GAM1197 KIAA1811 3' CTCCTCCCCTGGTCCTCCCCC 64795 AA TAAAGA T  
 A TGG GG AG GGGAGGAG  
 ||| || || |||||  
 ACC CC TC CCCTCCTC  
 CC TCCTGG \_  
 GAM1197 KIAA1822 3' TCCTCCCCAGCCTCCA 67575 A AAAGAAGT  
 TGGA GGT GGGAGGA  
 |||| || |||||  
 ACCT CCG CCCTCCT  
 — AC\_——  
 GAM1197 KIAA1870 5' CTCTGGCAGACCTTTTACCTTC 51830 AA\_ G  
 CA TGGAAGGTAAAG GT GGAG  
 ||||| || |||  
 ACCTTCCATTTT CG TCTC  
 CCAGA G  
 GAM1197 KIAA1871 3' CTCCTCCCTCCTCAGCCTCCA 61231 A AA AAGT  
 TGG AGGT AG GGGAGGAG  
 ||| ||| || |||||  
 ACC TCG TC CCCTCCTC  
 C AC CT\_  
 GAM1197 KIAA1883 3' CCTCCCCTCCCTACCA 73418 A TAAA A  
 TGG AGG GA GTGGGAGG  
 ||| ||| || |||||

		ACC TCC CT CACCCTCC			
		A C _ _			
GAM1197	KIAA1893	3' CTCAGCACCTCACCTCCCA	73213	A AAA A_ G_	
		TGG AGGT GA GTG GAG			
		ACC TCCA CT CAC CTC			
		C _ CC GA			
GAM1197	KIAA1938	3' CCCTTTTCTCCACTCCCA	92193	AA AA T	
		TGG GGT AGAAG GGG			
		ACC TCA TCTTT CCC			
		C_ CC T			
GAM1197	KIAA1938	3' CCTCCCAATCTCCTTCCA	92194	TAA AG	
		TGGAAGG AGA TGGGAGG			
		ACCTTCC TCT ACCCTCC			
		_ A_			
GAM1197	KIAA1949	5' CCCACCTCTCCCCCTCCA	92081	A TAA A	
		TGGA GG AGA GTGGG			
		ACCT CC TCT CACCC			
		C CC_ C			
GAM1197	KIAA1949	5' CCCTCCACTTCCTCTCCTCCCA	92082	A TAAA GA	
		TGG AGG GAAGTGG GG			
		ACC TCC CTTCACC CC			
		C TCTC TC			
GAM1197	KIAA1949	5' CCCACCTCTCCCCCTCCA	97749	A TAA A	
		TGGA GG AGA GTGGG			
		ACCT CC TCT CACCC			
		C CC_ C			
GAM1197	KIAA1949	5' CCCTCCACTTCCTCTCCTCCCA	97750	A TAAA GA	
		TGG AGG GAAGTGG GG			
		ACC TCC CTTCACC CC			
		C TCTC TC			
GAM1197	KIAA1949	5' CCCACCTCTCCCCCTCCA	97871	A TAA A	
		TGGA GG AGA GTGGG			
		ACCT CC TCT CACCC			
		C CC_ C			
GAM1197	KIAA1949	5' CCCTCCACTTCCTCTCCTCCCA	97872	A TAAA GA	
		TGG AGG GAAGTGG GG			
		ACC TCC CTTCACC CC			
		C TCTC TC			
GAM1197	LRG	3' CCCCTTGTCTTCCTTCCA	53747	T A AGT A	
		TGGAAGG AA GA GGG GG			

ACCTTCC TT CT TCC CC  
 \_ C GT\_ \_  
 GAM1197 LYPLA2 3' CTCCCCCAGCTGTCTCACCCC 23429 AA AA \_ \_ A  
 CA TGG GGT AGA AG TGGG GGAG  
 ||| ||| ||| || |||| ||||  
 ACC CCA TCT TC ACCC CCTC  
 C\_ C\_ G G C  
 GAM1197 MAP2K5 5' CCTCCCCCTCATCCTCCA 10865 A TAAA A T  
 TGGA GG GA G GGGAGG  
 |||| || || || ||||  
 ACCT CC CT C CCCTCC  
 \_ TA\_ \_ C  
 GAM1197 MCF2L 3' CTCCCCACGCGCCCCCTGCCTC 60844 A AAGAA\_ \_ A  
 CCA TGG AGGTA GTG GG GGAG  
 ||| |||| ||| || ||||  
 ACC TCCGT CGC CC CCTC  
 C CCCCCG A \_  
 GAM1197 MEIS3 3' CTCCTGTCCCCCCACCTCC 78280 A AAAGAAGT \_  
 GGA GGT GGGA GGAG  
 ||| ||| ||| ||| ||||  
 CCT CCA CCCT CCTC  
 \_ CCCC\_ GT  
 GAM1197 MGC10540 3' CTCCCTTTACTTCTTACCTCCC 50381 A A GA  
 A TGG AGGTAA GAAGTGG GGAG  
 ||| ||||| ||||| ||||  
 ACC TCCATT CTCATT CCTC  
 C \_ TC  
 GAM1197 MGC10540 3' CTCCTCCCACCCCTTTAGCTGC 50382 A G AA  
 T GG AG TAAAG GTGGGAGGAG  
 || || |||| ||||| |||||  
 TC TC ATTTC CACCCTCCTC  
 G G CC  
 GAM1197 MGC11115 3' CTCCCTCTCTCTTTACCCTCC 50238 A \_ T  
 GGA GGTAAAGA AG GGGAG  
 ||| ||||| || ||||  
 CCT CCATTCT TC CCCTC  
 C C T  
 GAM1197 MGC12966 3' TCATACCCCTTTCCTTCCA 51126 TAAA T AG\_  
 TGGAAGG GAAG GGG GA  
 ||||| ||| ||| ||  
 ACCTTCC TTTC CCC CT  
 \_ \_ ATA  
 GAM1197 MGC13138 3' TCCTTCCTCAGCCTCCCA 53027 A AAA AGT  
 TGG AGGT GA GGGAGGA  
 ||| ||| || |||||  
 ACC TCCG CT CCTTCCT  
 C A\_ \_  
 GAM1197 MGC20235 3' CTCATCACACCCTTACCTCCCA 58893 A AGAA \_  
 TGG AGGTAA GTGG GAG  
 ||| ||||| ||| |||



ACC TCCATT CACT CTC  
 C CCCA A  
 GAM1197 MGC2628 3' CTCCTTTTCTCTCCCTCCA 43973 A TAA T  
 TGGA GG AGAAG GGGAG  
 ||| || |||| ||||  
 ACCT CC TCTTT TCCTC  
 C TC\_ T  
 GAM1197 MGC2803 3' CCCCCCTTCTCACCTCC 43864 A AA T A  
 GGA GGT AGAAG GGG GG  
 ||| ||| |||| ||| ||  
 CCT CCA TCTTC CCC CC  
 \_ C\_ \_ \_  
 GAM1197 MGC3200 3' CTACACTTCCCCTCCTTCCA 50222 TAAA GG  
 TGGAAGG GAAGTG AG  
 ||||| ||||| ||  
 ACCTTCC CTTTAC TC  
 TCCC A\_  
 GAM1197 MGC35558 5' CCTCCCGCCACCCCGCCA 58780 AA\_ AAAGAA  
 TGG GGT GTGGGAGG  
 ||| ||| |||||  
 ACC CCA CGCCCTCC  
 GCC C\_\_\_\_  
 GAM1197 MGC3771 3' CCCACCTTCCCCACCTTC 48243 AAA \_  
 GAAGGT GAAG TGGG  
 ||||| ||| ||||  
 CTTCCA CTTC ACCC  
 CCC C  
 GAM1197 MGC4172 3' CTCCTTCCCTCCCCACCCTTC 44202 TAAAGA T  
 GAAGG AG GGGAGGAG  
 |||| || |||||  
 CTTCC TC CCTTCCTC  
 CACCCC \_  
 GAM1197 MGC4342 3' CCTCCCCGCTCCCTTCCA 44265 TAAA A \_  
 TGGAAGG GA GTGGG AGG  
 ||||| || ||||| |||  
 ACCTTCC CT CGCCC TCC  
 \_ \_ C  
 GAM1197 MGC4549 3' CTCCTTCTCCACCTTCTA 50464 AA T  
 TGGAAGGT AGAAG GGG  
 ||||| ||||| |||  
 ATCTTCCA TCTTC CTC  
 CC \_  
 GAM1197 MGC861 3' CCTCCCACCTCCCACACTC 43903 AG AAA A  
 GA GT GA GTGGGAGG  
 || || || |||||  
 CT CA CT CACCCTCC  
 CA CC\_ \_  
 GAM1197 MOST2 5' CTCCCCCACCTCCCCACCTAC 39683 \_ AAA A A  
 TTCA TGGA AGGT GA GTGGG GGAG  
 ||| ||| || ||||| |||

			ACTT TCCA CT CACCC CCTC		
			CA CCC C C		
GAM1197	NALP2	3'	CTCCTCCCCGGCCCTACCCCT 35315	AA	AAGAAGT
	CA		TGG GGTA GGGAGGAG		
			ACT CCAT CCCTCCTC		
			CC CCCC GGC		
GAM1197	NFAT5	5'	CTCCCAGCCTCCCCCCTCCCA 56943	A	TAAA A _
			TGG AGG GA G TGGGAG		
			ACC TCC CT C ACCCTC		
			C CCCC C G		
GAM1197	NIT1	3'	CCTCCCACCCCCACCCTGCCA 18807	A	TAAAGAA
			TGG AGG GTGGGAGG		
			ACC TCC CACCCTCC		
			G CACCCC _		
GAM1197	OBSCN	3'	CCTCCCGCTCACCTTCC 70651	AAA	A
			GGAAGGT GA GTGGGAGG		
			CCTTCCA CT CGCCCTCC		
			— —		
GAM1197	OSBPL7	3'	CTCCTCCTGCCTCCACCCCC 34807	AA	AAA A TG
			GG GGT GA G GGAGGAG		
			CC CCA CT C CCTCCTC		
			C_ C_ C GT		
GAM1197	PCDH10	5'	CTCCTCCTCGTTCTCCTCCCA 40424	A	TAA GT
			TGG AGG AGAA GGGAGGAG		
			ACC TCC TCTT TCCTCCTC		
			C _ GC		
GAM1197	PCDH10	5'	CTCCTCCTCGTTCTCCTCCCA 51988	A	TAA GT
			TGG AGG AGAA GGGAGGAG		
			ACC TCC TCTT TCCTCCTC		
			C _ GC		
GAM1197	PDEF	3'	TCCATCCCCCTGCCTCCCA 24752	A	AAAGA T _
			TGG AGGT AG GGGA GGA		
			ACC TCCG TC CCCT CCT		
			C _ C A		
GAM1197	PEPP3	3'	TCCTCCCACCTCATCCCT 30044	TAAA	A
			AGG GA GTGGGAGGA		
			TCC CT CACCCTCCT		
			CTA_ C		
GAM1197	PF1	3'	TCCATCCCATACCTTCCA 95123	AAAGAA	_
			TGGAAGGT GTGGGA GGA		

ACCTTCCA TACCCT CCT  
 \_\_\_\_\_ A  
 GAM1197 PGLYRP 3' CCCATTCTCCCTCCCA 17454 A TAA A  
 TGG AGG AG AGTGGG  
 ||| ||| || |||||  
 ACC TCC TC TTACCC  
 C CC\_ C  
 GAM1197 PHRET1 5' CTCCCCCTCCAGCTCCCA 41057 A AAA A T  
 TGG AGGT GA G GGGAG  
 ||| ||| || | |||||  
 ACC TCCG CT C CCCTC  
 C AC\_ \_ C  
 GAM1197 PHYHIP 3' CTCCTTCTCCACCTGCCA 28608 A\_ AA T  
 TGG AGGT AGAAG GGG  
 ||| ||| ||||| |||  
 ACC TCCA TCTTC CTC  
 CG CC \_  
 GAM1197 PI15 5' CTCTTCTTCTCCACCCCTCA 31893 AA AA T  
 TGG GGT AGAAG GGGAG  
 ||| ||| ||||| |||||  
 ACT CCA TCTTC TTCTC  
 CC CC \_  
 GAM1197 PKNOX2 3' CCTCCCACCCACCTTCCA 90876 AAAGAA  
 TGGAAGGT GTGGGAGG  
 ||||| |||||  
 ACCTTCCA CACCCTCC  
 CC\_\_\_\_  
 GAM1197 PPFIA4 3' TCCTTTCTCTGACCTCCCA 70333 A AA AGT GG  
 TGG AGGT AGA G AGGA  
 ||| ||| ||| | |||  
 ACC TCCA TCT C TCCT  
 C G\_ \_ TT  
 GAM1197 PPP4R1L 5' TCGGCCCTTCACTTCCA 79505 GTAAA T AG  
 TGGAAG GAAG GGG GA  
 ||||| ||| ||| ||  
 ACCTTC CTTC CCC CT  
 A\_ \_ GG  
 GAM1197 PPY2 3' CTCCCGCCCCCTACCACTCCA 40821 A\_ AAGAA  
 TGGA GGTA GTGGGAG  
 ||| ||| |||||  
 ACCT CCAT CGCCCTC  
 CA CCCC\_  
 GAM1197 PRKRI 5' CTCCCCCTGTAACCTCTTCCCT 20756 A TA A \_\_\_\_ A  
 CCA GGA GG AAGA GT GGG GGAG  
 ||| ||| ||| ||| ||| |||  
 CCT CC TTCT CA CCC CCTC  
 C \_ C ATGT \_  
 GAM1197 PRO2831 5' CTCCCACCTCAACCTCCCA 37601 A AAA A  
 TGG AGGT GA GTGGGAG  
 ||| ||| || |||||

		ACC TCCA CT CACCCTC		
		C A__ C		
GAM1197 PSMF1	3'	CCACTTCCCTCCTTCCA 22349	TAAA	
		TGGAAGG GAAGTGG		
		ACCTTCC CTTCACC		
		TCC_		
GAM1197 PTPNS1	3'	CCTCCCCACCACCTCTCA 54997	GA AAAGAA _	
		TG AGGT GTGGG AGG		
		AC TCCA CACCC TCC		
		TC C_____ C		
GAM1197 QSCN6	3'	CCCATTCCTCCCTCCCA 11036	A TAA A_	
		TGG AGG AG AGTGGG		
		ACC TCC TC TTACCC		
		C CC_ CC		
GAM1197 QSCN6	3'	CCTCCCACCCCTTGCTCCT 11038	TA_ AA	
		AGG AAG GTGGGAGG		
		TCC TTC CACCCTCC		
		TCG CC		
GAM1197 RABL4	5'	CTCCCCTCCCCACCTTCC 22474	AAA A T	
		GGAAGGT GA G GGGAG		
		CCTTCCA CT C CCCTC		
		CCC _ _		
GAM1197 RBPMS	5'	CCCCCGTCCCCTCCTTCCA 22490	TAAA AG A	
		TGGAAGG GA TGGG GG		
		ACCTTCC CT GCCC CC		
		TCCC _ _		
GAM1197 RIP60	3'	CCTCCCACCTGCCCCC 25455	AA AAGAA	
		GG GGTA GTGGGAGG		
		CC CCGT CACCCTCC		
		C_ C_____		
GAM1197 RNF8	3'	CTCCCACCTCAACCTCCA 14223	A AAA A	
		TGG AGGT GA GTGGGAG		
		ACC TCCA CT CACCCTC		
		C A__ C		
GAM1197 RNPC1	3'	CTCCTGCCTCTCCCACTCCA 33988	AG AA A TG	
		TGGA GT AGA G GGAG		
		ACCT CA TCT C CCTC		
		CA CC C GT		
GAM1197 RPH3A	3'	CTCCTCCCTCTTCTTCCCTTC 30242	T T	
CA		TGGAAGG AAAGAAG GGGAGGAG		

ACCTTCC TTTCTTC CCCTCCTC  
 C T  
 GAM1197 SCGF 5' CCTCCCACCCCAGACATCCA 11439 AG AAAGAA  
 TGGA GT GTGGGAGG  
 |||| || |||||  
 ACCT CA CACCCTCC  
 A\_ GACCC\_  
 GAM1197 SCYA13 3' CTCTAAGCCCCCTTCCCTTCCA 18255 TAAA T A\_  
 TGGAAGG GAAG GGG GGAG  
 ||||| ||| ||| |||  
 ACCTTCC CTTC CCC TCTC  
 \_\_\_\_ C GAA  
 GAM1197 SEMA4G 3' CTCCCACCTCCACCCCA 35435 AA AAA A  
 TGG GGT GA GTGGGAG  
 ||| ||| || |||||  
 ACC CCA CT CACCCTC  
 \_ C\_ C  
 GAM1197 SEMA4G 3' CTCCCACCTCCACCCCA 94678 AA AAA A  
 TGG GGT GA GTGGGAG  
 ||| ||| || |||||  
 ACC CCA CT CACCCTC  
 \_ C\_ C  
 GAM1197 SERPINA6 3' CTCCTCCAAGTTCTTCTCCCTC 8281 A TA GTG  
 CA TGGA GG AAGAA GGAGGAG  
 |||| || |||| |||||  
 ACCT CC TTCTT CCTCCTC  
 C TC GAA  
 GAM1197 SHANK3 3' CCTCCCTTCTACTTCCA 65491 GTAA GT  
 TGGAAG AGAA GGGAGG  
 ||||| ||| |||||  
 ACCTTC TCTT CCCTCC  
 A\_ \_  
 GAM1197 SIMRP7 3' TCTCCCCTTCTACCCTCCA 92372 A AA T  
 TGGA GGT AGAAG GGGAGG  
 |||| ||| |||| |||||  
 ACCT CCA TCTTC CCCTCT  
 C \_ \_  
 GAM1197 SLC26A1 3' CCCCCAGCCCTCCCCTCCCA 41863 A TAA AAG A  
 TGG AGG AG TGGG GG  
 ||| ||| || |||||  
 ACC TCC TC ACCC CC  
 C CC\_ CCG \_  
 GAM1197 SLC26A10 5' CTCCCTCTTATCTCCACCCCCC 56029 AA AA \_ T  
 A TGGA GGT AGA AG GGGAG  
 ||| ||| ||| || |||||  
 ACC CCA TCT TC CCCTC  
 CC CC AT T  
 GAM1197 SMARCF1 3' CTCCTGTTTCTCTCTCCTCCTT 57484 TAA\_ TG  
 CCA TGGAAGG AGAAG GGAG  
 ||||| |||| |||

		ACCTTCC	TCTTT	CCTC		
		TCCTCTC	GT			
GAM1197	SMARCF1	3'	CTCCTTCCACCTCCCCTCCCTC	57485	A TAAA	A
	CA		TGGA GG GA GTGGGAGGAG			
			ACCT CC CT CACCTTCCTC			
			C TCCC C			
GAM1197	SMARCF1	3'	CTCCTGTTTCTCTCTCCTCCTT	37434	TAA_____	TG
	CCA		TGGAAGG AGAAG GGAG			
			ACCTTCC TCTTT CCTC			
			TCCTCTC GT			
GAM1197	SMARCF1	3'	CTCCTTCCACCTCCCCTCCCTC	37435	A TAAA	A
	CA		TGGA GG GA GTGGGAGGAG			
			ACCT CC CT CACCTTCCTC			
			C TCCC C			
GAM1197	SMARCF1	3'	CTCCTGTTTCTCTCTCCTCCTT	20038	TAA_____	TG
	CCA		TGGAAGG AGAAG GGAG			
			ACCTTCC TCTTT CCTC			
			TCCTCTC GT			
GAM1197	SMARCF1	3'	CTCCTTCCACCTCCCCTCCCTC	20039	A TAAA	A
	CA		TGGA GG GA GTGGGAGGAG			
			ACCT CC CT CACCTTCCTC			
			C TCCC C			
GAM1197	SPR1	3'	CTCGGCCCCACCTACCTCCCA	25953	A AAGAA	AG_
			TGG AGGTA GTGGG GAG			
			ACC TCCAT CACCC CTC			
			C C_____ CGG			
GAM1197	SRF	3'	TTCTTCCCGCCCCACCTCCCA	11953	A AAAGAA	
			TGG AGGT GTGGGAGGAG			
			ACC TCCA CGCCCTTCTT			
			C CCC_____			
GAM1197	SSBP3	3'	CCTCCCACCCCATCCA	36061	A TAAAGAA	
			TGGA GG GTGGGAGG			
			ACCT CC CACCCTCC			
			A C_____			
GAM1197	STIM2	3'	CCCCACCCCTCCACTCCCA	40474	AA AA AA	A
			TGG GGT AG GTGGG GG			
			ACC TCA TC CACCC CC			
			CC CC C_ _			
GAM1197	THG-1	5'	CCTCCCGCCACCTCCC	48184	A AAAGAA	
			GG AGGT GTGGGAGG			

		CC TCCA CGCCCTCC		
		C C_____		
GAM1197	TRIP-Br2	3' CTCCCCCAATTCCCCCCCCA	28581	AA TAAA G A
		TGG GG GAA TGGG GGAG		
		ACC CC CTT ACCC CCTC		
		CC C___ A C		
GAM1197	TSC22	3' CTCCCTACCCCTCACTTCCA	20065	GTAA AA _
		TGGAAG AG GT GGGAG		
		ACCTTC TC CA CCCTC		
		AC__ CC T		
GAM1197	TUBB5	3' CTCACCTTTACCCCCCA	20299	AA _ AA
		TGG GGT AAAG GTGGG		
		ACC CCA TTTC CACTC		
		CC C _		
GAM1197	UPK1A	3' CTCACCTCTCACCTCCCA	22795	A AA A
		TGG AGGT AGA GTGGG		
		ACC TCCA TCT CACTC		
		C C_ C		
GAM1197	WBSCR23	3' CTCCTGCCTCCGCCTCCCA	46758	A AAA A TG
		TGG AGGT GA G GGAG		
		ACC TCCG CT C CCTC		
		C C_ C GT		
GAM1197	ZDHC5	5' TCTGTTGCTTCCCTCCTCCCA	91562	A TAAA TG G
		TGG AGG GAAG G AGG		
		ACC TCC CTTC T TCT		
		C TCC_ GT G		
GAM1197	ZIN	3' CTCCCCCATCCCCCATCCTCCC	25489	A TAAAGAA A
	A	TGG AGG GTGGG GGAG		
		ACC TCC TACCC CCTC		
		C TACCCCC _		
GAM1197	ZNF213	3' CCTCCCACTCCCGTTTCCA	65096	GTAAA A
		TGGAAG GA GTGGGAGG		
		ACCTTT CT CACCCTCC		
		GCC__ _		
GAM1197	ZNF238	3' CTCCCCTTCCTCCTTACCCTCC	20959	A A__ T
		GGA GGTA GAAG GGGAG		
		CCT CCATT CTTC CCCTC		
		C CCTC _		
GAM1197	ZNF304	3' CCCCCCACTTACCCCCTACCA	40313	A TAAA A
		TGG AGG GAAGTGGG GG		

ACC TCC CTTCACCC CC  
 A CCCA C  
 GAM1197 LOC112817 3' CTCCCATCCCTGCCCTCCA 56510 A AA AA  
 TGGA GGT AG GTGGGAG  
 |||| || || |||||  
 ACCT CCG TC TACCCTC  
 C \_ CC  
 GAM1197 LOC115129 3' CTCCTCCCCAGTTCCCCTCCA 73230 A TAAA G \_  
 TGGA GG GAA TGGG AGGAG  
 |||| || || |||| ||||  
 ACCT CC CTT ACCC TCCTC  
 C \_ \_ G C  
 GAM1197 LOC115207 3' CTCCCATTCTCCCCCTCCA 56601 A TAA G  
 TGGA GG AGAA TGGGAG  
 |||| || |||| |||||  
 ACCT CC TCTT ACCCTC  
 C CC\_ \_  
 GAM1197 LOC115219 5' CTCCTCTTCTCCCCACCCCCA 73305 AA AAA A TG  
 TGG GGT GA G GGAGGAG  
 || || || || |||||  
 ACC CCA CT C TCTCCTC  
 C\_ CCC \_ CT  
 GAM1197 LOC123242 5' CCCCCAACCTTCCA 75597 AAAGAAG A  
 TGGAAGGT TGGG GG  
 ||||| |||| ||  
 ACCTTCCA ACCC CC  
 \_\_\_\_\_  
 GAM1197 LOC123775 3' CTCATTTCCCACCCACCCCCA 75624 AA AAAGAA \_  
 TGG GGT GTGGGAG GAG  
 || || ||||| ||  
 ACC CCA CACCCTT CTC  
 CC CC\_ TA  
 GAM1197 LOC124446 5' CCCCTGTTTATCTCTTCGCCTT 74287 TA \_ TG A  
 CCA TGGAAGG AAGA AG GG GG  
 ||||| |||| || ||  
 ACCTTCC TTCT TT CC CC  
 GC CTAT GT \_  
 GAM1197 LOC126364 3' CTCCCAAATTGCTCCCCACCTC 75686 A AA\_ AAG\_  
 CCA TGG AGGT AG TGGGAG  
 || |||| || |||||  
 ACC TCCA TC ACCCTC  
 C CCCC GTTAA  
 GAM1197 LOC126669 3' CCCTTGTTTCTCCCTCCTTCCA 75401 TAA\_ TG A  
 TGGAAGG AGAAG GG GG  
 ||||| |||| || ||  
 ACCTTCC TCTTT TC CC  
 TCCC GT \_  
 GAM1197 LOC128387 3' TCCTCCCTCAGCCTCCA 74754 A AAA AGT  
 TGG AGGT GA GGGAGGA  
 || |||| || |||||



ACC TCCG CT CCCTCCT  
 C A\_\_ \_\_  
 GAM1197 LOC128954 5' CTCCTCTTACTCCCTAACCTCC 75797 A AAAGA  
 CA TGG AGGT AGTGGGAGGAG  
 ||| ||| |||||  
 ACC TCCA TCATTCTCCTC  
 C ATCCC  
 GAM1197 LOC130589 3' CTCCTCCTTCACCTCCA 57131 A AAA TG  
 TGGG GGT GAAG GGAG  
 ||| ||| ||| |||  
 ACCT CCA CTTC CCTC  
 \_ \_ CT  
 GAM1197 LOC138399 5' CTCCTCTTCATCTTGTTACCT 75327 A G \_ \_  
 TCCA TGGAGGT AA AAG TGG GAGGAG  
 ||||| || ||| ||| |||||  
 ACCTTCCA TT TTC ACT CTCCTC  
 C G T T  
 GAM1197 LOC139163 5' TCCCCCAGGCTCCCTCCA 75818 A TAA AAG A  
 TGG AGG AG TGGG GGA  
 ||| ||| || ||| |||  
 ACC TCC TC ACCC CCT  
 C C\_ GG\_ \_  
 GAM1197 LOC144473 3' CTCCCCCTCTTCTACCCTCC 83071 A AA T A  
 GGA GGT AGAAG GGG GGAG  
 ||| ||| ||||| ||| |||||  
 CCT CCA TCTTC CCC CCTC  
 C \_ T \_  
 GAM1197 LOC144501 3' CTCCCCCTTCACCTTCC 83106 AAA T  
 GGAAGGT GAAG GGGAG  
 ||||| ||| |||||  
 CCTTCCA CTTC CCCTC  
 \_ C  
 GAM1197 LOC144501 3' CTCCTCCCATGGGTCCCTCCA 83107 A TAAAGAA  
 TGG AGG GTGGGAGGAG  
 ||| ||| |||||  
 ACC TCC TACCCTCCTC  
 C CTGGG\_  
 GAM1197 LOC145216 3' CTCCTGCCTTTGACCTCCA 83264 A \_ AA TG  
 TGG AGGT AAAG G GGAG  
 ||| ||| ||| | |||  
 ACC TCCA TTTC C CCTC  
 C G \_ GT  
 GAM1197 LOC145371 3' CTCCATTCTCTACCTCCA 77151 A A GTG  
 TGG AGGTA AGAA GGAG  
 ||| ||||| ||| |||  
 ACC TCCAT TCTT CCTC  
 C C A\_  
 GAM1197 LOC146268 3' CTCCCCTCTCCACTTCC 77809 GTAA A  
 GGAAG AGA GTGGGAG  
 ||||| ||| |||||

CCTTC TCT CACCCTC  
 ACC\_ \_  
 GAM1197 LOC146438 3' CCCACCTTCCCCACCTTC 77890 AAA \_  
 GAAGGT GAAG TGGG  
 ||||| ||| |||  
 CTTCCA CTTC ACCC  
 CCC C  
 GAM1197 LOC147495 3' TCCTCTCCCTCCCTCCCA 84016 A TAAA A T  
 TGG AGG GA G GGGAGGA  
 ||| ||| ||| |||||  
 ACC TCC CT C CTCTCCT  
 C \_ \_ C  
 GAM1197 LOC147622 5' CTCTGCCCTCCTCACCTTCCA 84048 AAA AGT A  
 TGGAAGGT GA GGG GGAG  
 ||||| || ||| |||  
 ACCTTCCA CT CCC TCTC  
 \_ CCT G  
 GAM1197 LOC148195 5' CTCCTCTTTCTTCACTCCTCCA 84127 A TAAA TG  
 TGGA GG GAAG GGAGGAG  
 ||| || ||| |||||  
 ACCT CC CTTC TCTCCTC  
 \_ TCA\_ TT  
 GAM1197 LOC149448 3' CCTCCCACCACCCCA 84421 AA AAAGAA  
 TGG GGT GTGGGAGG  
 ||| ||| |||||  
 ACC CCA CACCCTCC  
 \_ C \_  
 GAM1197 LOC149773 5' CTCCTCCTGCCCCCTCCCTCC 79476 A TAAAGAA TG  
 CA TGG AGG G GGAGGAG  
 ||| ||| | |||||  
 ACC TCC C CCTCCTC  
 C CTCCCC GT  
 GAM1197 LOC150319 3' CTCCCTCCTCTCTCCCTCCCA 79652 A TAA A T GA  
 TGG AGG AGA G GG GGAG  
 ||| ||| ||| ||| |||  
 ACC TCC TCT C CC CCTC  
 C C \_ \_ T TC  
 GAM1197 LOC150407 3' TCCTCCCTCTGCCTCCCA 79834 A AAAGA T  
 TGG AGGT AG GGGAGGA  
 ||| ||| || |||||  
 ACC TCCG TC CCCTCCT  
 C \_ \_ T  
 GAM1197 LOC151361 3' TCCCCCACATTCTCCCA 85329 A TAAAGAA A  
 TGG AGG GTGGG GGA  
 ||| ||| ||||| |||  
 ACC TCC CACCC CCT  
 C TTA \_ C  
 GAM1197 LOC151534 3' CTCCTTTTTGTCCCCATCC 56684 A TAAA AGT  
 GGA GG GA GGGAGGAG  
 ||| || || |||||

	CCT CC CT TTTTCCTC		
	A C__ GT_		
GAM1197 LOC151614 3'	CTCCCACCTTGACCTTCCA 80303	A AA	
	TGGAAGGT AAG GTGGGAG		
	ACCTTCCA TTC CACCCTC		
	G _		
GAM1197 LOC152018 3'	CTCCCCGCTTCCACCCTCCA 85543	A AAA AG	
	TGGA GGT GAAGTGGG G		
	ACCT CCA CTTCGCCC C		
	C C__ CT		
GAM1197 LOC152245 5'	CTCCCCCTCTTCCCTCCCA 85602	A TAAA T A	
	TGG AGG GAAG GGG GGAG		
	ACC TCC CTTC CCC CCTC		
	C _ T _		
GAM1197 LOC153146 5'	TCCTCCCAGATACCTCTCA 85935	GA AAGAAG	
	TG AGGTA TGGGAGGA		
	AC TCCAT ACCCTCCT		
	TC AG__		
GAM1197 LOC153339 5'	CTCCTCCCACCCTCCACCCTC 86007	A AA AA	
	GA GGT AG GTGGGAGGAG		
	CT CCA TC CACCCTCCTC		
	C CC C_		
GAM1197 LOC153443 3'	CTCCCACCTCTGCCTCCCA 80823	A AA A	
	TGG AGGT AGA GTGGGAG		
	ACC TCCG TCT CACCCTC		
	C _ C		
GAM1197 LOC153770 3'	TCCTCCTCCTTACTCCCCA 80930	AA AAGA TG	
	TGG GGTA AG GGAGGA		
	ACC TCAT TC CCTCCT		
	CC _ CT		
GAM1197 LOC154007 3'	CTCCTGTCCTCAGCCTCCCA 81017	A AA AA TG	
	TGG AGGT AG G GGAG		
	ACC TCCG TC T CCTC		
	C AC C_ GT		
GAM1197 LOC157349 5'	CCCGCACCCCTGCACCTCCCA 81411	A AA AA__	
	TGG AGGT AG GTGGG		
	ACC TCCA TC CGCCC		
	C CG CCCA		
GAM1197 LOC157349 5'	CCCGCACCTCTGCACCTCCCA 81412	A AA A__	
	TGG AGGT AGA GTGGG		

ACC TCCA TCT CGCCC  
 C CG CCA  
 GAM1197 LOC157638 5' CTCCTCGCGCCCCACCTCCC 81512 A AAAGAA G  
 GG AGGT GTG GAGGAG  
 || ||| ||| |||||  
 CC TCCA CGC CTCCTC  
 C CCC\_\_ G  
 GAM1197 LOC157858 5' CTCCCTCTCCACCCCA 86588 AA AA AGT  
 TGG GGT AGA GGGAG  
 ||| ||| ||| |||||  
 ACC CCA TCT CCCTC  
 C\_ CC \_\_  
 GAM1197 LOC157931 3' CTCCCACCTCTCCTTCC 86661 TAA A  
 GGAAGG AGA GTGGGAG  
 ||||| ||| |||||  
 CCTTCC TCT CACCCTC  
 \_\_ C  
 GAM1197 LOC158263 3' CCCCCACCTTTGCCTTCCA 81843 AA A  
 TGGAAGGTAAAG GTGGG GG  
 ||||| ||||| ||||| ||  
 ACCTTCCGTTTC CACCC CC  
 \_\_ \_\_  
 GAM1197 LOC158402 5' CTCCCGTCTCCGCCTCCCA 86804 A AAA AG  
 TGG AGGT GA TGGGAG  
 ||| ||| ||| |||||  
 ACC TCCG CT GCCCTC  
 C C\_\_ CT  
 GAM1197 LOC159090 5' CTCCCTCTTCCCTCCTCCCTCC 82086 A TAAA\_\_ T  
 A  
 TGGA GG GAAG GGGAG  
 ||||| ||| |||||  
 ACCT CC CTTC CCCTC  
 C TCCTCC T  
 GAM1197 LOC161003 3' CCAACTCTCCACCTTCCA 59223 AA AG  
 TGGAAGGT AGA TGG  
 ||||| ||| |||  
 ACCTTCCA TCT ACC  
 CC CA  
 GAM1197 LOC161570 5' CTCCCCACCTTTCTTCCA 87093 T AA AG  
 TGGAAGG AAAG GTGGG G  
 ||||| ||||| ||||| |  
 ACCTTCC TTTC CACCC C  
 \_\_ \_\_ CT  
 GAM1197 LOC165552 3' CCCAAATCCTTCCTTCC 82485 T A AG  
 GGAAGG AA GA TGGG  
 ||||| ||| ||| |||||  
 CCTTCC TT CT ACCC  
 \_ C AA  
 GAM1197 LOC165721 5' TCCCCCACTCCTCTCA 82604 GA TAAAGA A  
 TG AGG AGTGGG GGA  
 || ||| ||||| |||

	AC TCC TCACCC CCT		
	TC _____ C		
GAM1197 LOC166793 5'	CTCCCGAGCACTTACCTTCCA 59228	AGAAG	
	TGGAAGGTAA TGGGAG		
	ACCTTCCATT GCCCTC		
	CACGA		
GAM1197 LOC170392 3'	TCCCCCACCGCCCTCTA 76366	A AAAGAA A	
	TGGA GGT GTGGG GGA		
	ATCT CCG CACCC CCT		
	C C_____ C		
GAM1197 LOC170393 3'	CCTCCCACCCTTGCCCCA 82844	AA AGAA	
	TGG GGTAAG GTGGGAGG		
	ACC CCGTT CACCCTCC		
	____ CC__		
GAM1197 LOC170393 3'	CCTCCCACCCTTGCCCCA 82845	AA AGAA	
	TGG GGTAAG GTGGGAGG		
	ACC CCGTT CACCCTCC		
	____ CC__		
GAM1197 LOC170393 3'	CCTCCCACCCTTGCCCCA 82846	AA AGAA	
	TGG GGTAAG GTGGGAGG		
	ACC CCGTT CACCCTCC		
	____ CC__		
GAM1197 LOC170393 3'	CCTCCCACCCTTGCCCCA 82847	AA AGAA	
	TGG GGTAAG GTGGGAGG		
	ACC CCGTT CACCCTCC		
	____ CC__		
GAM1197 LOC170393 3'	CCTCCCACCCTTGCCCCA 82848	AA AGAA	
	TGG GGTAAG GTGGGAGG		
	ACC CCGTT CACCCTCC		
	____ CC__		
GAM1197 LOC170393 3'	CCTCCCACCCTTGCCCCA 82849	AA AGAA	
	TGG GGTAAG GTGGGAGG		
	ACC CCGTT CACCCTCC		
	____ CC__		
GAM1197 LOC196500 3'	CTCCTCTCTTCCTTCCA 87740	TA AAGT	
	TGGAAGG AAG GGGAG		
	ACCTTCC TTC CCCTC		
	____ CT__		
GAM1197 LOC200169 5'	CTCCTCTCTTCCTTACCCTTCC 89948	A TG	
	GGAAGGTAA GAAG GGAGGAG		

CCTTCCATT CTTC TCTCCTC  
 C \_  
 GAM1197 LOC200269 3' CTCCTTGTCTCTACCTCC 88668 A A AGT  
 GGA GGTA AGA GGGAG  
 ||| ||| ||| |||||  
 CCT CCAT TCT TCCTC  
 \_ C GT\_  
 GAM1197 LOC200812 5' CTCCCACCTCCCCACCCCCA 88883 AA AAA A  
 TGG GGT GA GTGGGAG  
 ||| ||| || |||||  
 ACC CCA CT CACCCTC  
 C\_ CCC C  
 GAM1197 LOC202500 5' TCTCCCTACCTCCCA 89193 A AAGAAGT  
 TGG AGGTA GGGAGG  
 ||| ||||| |||||  
 ACC TCCAT CCCTCT  
 C \_  
 GAM1197 LOC202908 5' CTCCCATCTCAACCTCCCA 89233 A AAA AG  
 TGG AGGT GA TGGGAG  
 ||| ||| || |||||  
 ACC TCCA CT ACCCTC  
 C A\_ CT  
 GAM1197 LOC203248 3' CCTCCCCGACTCCCACTTCCA 89311 GTAA AAGT  
 TGGAAG AG GGGAGG  
 ||||| || |||||  
 ACCTTC TC CCCTCC  
 ACCC AGC\_  
 GAM1197 LOC219348 3' TCCTCTCACTCCCACTTCCA 91271 GTAAA A  
 TGGAAG GA GTGGGAGGA  
 ||||| || |||||  
 ACCTTC CT CACTCTCCT  
 AC\_ \_  
 GAM1197 LOC219654 3' CCTCCCACGACCCCCA 91301 AA AAAGAA  
 TGG GGT GTGGGAGG  
 ||| ||| |||||  
 ACC CCA CACCCTCC  
 C\_ G\_  
 GAM1197 LOC219818 3' CCTCCCATCCTTCACCTCC 90889 A A AA  
 GGA GGT AAG GTGGGAGG  
 ||| ||| ||| |||||  
 CCT CCA TTC TACCCTCC  
 \_ C C\_  
 GAM1197 LOC219972 3' CTACCCCTTCATCTTCCA 91638 AAA T A  
 TGGAAGGT GAAG GGG GG  
 ||||| ||| ||| ||  
 ACCTTCTA CTTC CCC TC  
 \_ \_ A  
 GAM1197 LOC220793 3' CTCCTCCCAGTACACCCCC 60362 AA AAAGAAG  
 GG GGT TGGGAGGAG  
 || ||| |||||

CC CCA ACCCTCCTC  
 C\_ CATG\_\_\_\_  
 GAM1197 LOC221399 5' TCCACTTCTTCACCTCTCA 93850 GA A  
 TG AGGT AAGAAGTGGG  
 || ||| |||||  
 AC TCCA TTCTTCACCT  
 TC C  
 GAM1197 LOC221466 3' CCTCCCGCCATCCTCCCA 93685 A TAAAGAA  
 TGG AGG GTGGGAGG  
 ||| ||| |||||  
 ACC TCC CGCCCTCC  
 C TAC\_\_\_\_  
 GAM1197 LOC221876 5' CTCTTCTTCCCCACCTTCC 93921 AAA T  
 GGAAGGT GAAG GGGAG  
 ||||| ||| |||||  
 CCTTCCA CTTC TTCTC  
 CCC \_  
 GAM1197 LOC222057 5' CTCCCACCTCAACCTCCCA 92773 A AAA A  
 TGG AGGT GA GTGGGAG  
 ||| ||| ||| |||||  
 ACC TCCA CT CACCCTC  
 C A\_ C  
 GAM1197 LOC253001 5' CCCCCAACCTTCCA 96255 AAAGAAG A  
 TGGAAGGT TGGG GG  
 ||||| ||| ||  
 ACCTTCCA ACCC CC  
 \_\_\_\_\_  
 GAM1197 LOC253148 5' CCCCCACACCTCCCA 96876 A AAAGAA A  
 TGG AGGT GTGGG GG  
 ||| ||| ||||| ||  
 ACC TCCA CACCC CC  
 C \_\_\_\_\_  
 GAM1197 LOC253150 3' CCTCCTGTCTCACCCCCC 95516 AA AAA AG  
 GG GGT GA TGGGAGG  
 || ||| ||| |||||  
 CC CCA CT GTCCTCC  
 CC \_ CT  
 GAM1197 LOC253609 5' TCCAGTCCTTCTCCCTCCA 96763 A TAA T GA  
 TGGA GG AGAAG GG GGA  
 |||| ||| ||||| |||  
 ACCT CC TCTTC CT CCT  
 C \_ \_ GA  
 GAM1197 LOC253891 3' CTCCTTTCCTCTCGCCACCTTC 94414 AAA \_ T GG  
 CA TGGAAGGT GA AG G AGGAG  
 ||||| || ||| |||||  
 ACCTTCCA CT TC C TCCTC  
 CCG C \_ TT  
 GAM1197 LOC253891 3' TCTCTTCCTTCCCCCA 94416 AA TAAA TG  
 TGG GG GAAG GGAGG  
 ||| || |||||

ACC CC CTTC TCTCT  
 C\_ \_\_\_\_ CT  
 GAM1197 LOC254268 3' TCCTCCCTCAGCCTCCCA 95414 A AAA AGT  
 TGG AGGT GA GGGAGGA  
 ||| ||| || |||||  
 ACC TCCG CT CCCTCCT  
 C A\_ \_\_\_\_  
 GAM1197 LOC254873 3' TTCCTCCCCACCTTCC 94573 AAAGAAGT  
 GGAAGGT GGGAGGAG  
 ||||| |||||  
 CCTTCCA CCCTCCTT  
 C\_\_\_\_\_  
 GAM1197 LOC255102 3' CTCCCACCTCCACACCCCA 96081 AA AAA A  
 TGG GGT GA GTGGGAG  
 ||| ||| || |||||  
 ACC CCA CT CACCCTC  
 C\_ CAC C  
 GAM1197 LOC255925 3' CTCCCACCTCCACACCCCA 96478 AA AAA A  
 TGG GGT GA GTGGGAG  
 ||| ||| || |||||  
 ACC CCA CT CACCCTC  
 C\_ CAC C  
 GAM1197 LOC255975 5' CTCCCATCTCAACCTCCCA 95892 A AAA AG  
 TGG AGGT GA TGGGAG  
 ||| ||| || |||||  
 ACC TCCA CT ACCCTC  
 C A\_ CT  
 GAM1197 LOC256094 3' CTCCTCTCTGCCCCCTGCCCCC 94892 AA AAGAAGT  
 CA TGG GGTA GGGAGGAG  
 ||| ||| |||||  
 ACC CCGT CTCTCCTC  
 CC CCCCCGT  
 GAM1197 LOC256454 3' CTCCCCAAAGGCCCCACCTTCC 96530 AAAGAAGTG A  
 A TGGAAGGT GG GGAG  
 ||||| || |||  
 ACCTTCCA CC CCTC  
 CCCCCGAAA \_  
 GAM1197 LOC256614 3' CTCCTGCACCTCCTCACCTCCC 96456 A AA\_\_ AA TG  
 A TGG AGGT AG G GGAG  
 ||| ||| || | |||  
 ACC TCCA TC C CCTC  
 C CTCC CA GT  
 GAM1197 LOC256878 5' CTCCCATCTCAACCTCCCA 96903 A AAA AG  
 TGG AGGT GA TGGGAG  
 ||| ||| || |||||  
 ACC TCCA CT ACCCTC  
 C A\_ CT  
 GAM1197 LOC256901 3' CCCCTTCTCCACCCTCTA 96621 A AA T  
 TGGA GGT AGAAG GGG  
 ||| ||| |||| |||



ATCT CCA TCTTC CCC  
 C CC \_  
 GAM1197 LOC257019 5' CCTCCCTCCTCCCCTCCCA 96162 A TAAA AGT  
 TGG AGG GA GGGAGG  
 ||| ||| || |||||  
 ACC TCC CT CCCTCC  
 C C\_\_ CCT  
 GAM1197 LOC257200 3' CCCCCACCTCCCACCCCCCA 95652 AA AAA A A  
 TGG GGT GA GTGGG GG  
 ||| ||| || ||||| ||  
 ACC CCA CT CACCC CC  
 CC CC\_ C \_  
 GAM1197 LOC257364 3' CTCCCTCTTCTCTCCCTTACTT 94965 \_\_\_\_\_ T  
 TCCA TGGAAGGTAA AGAAG GGGAG  
 ||||| |||| |||||  
 ACCTTTCATT TCTTC CCCTC  
 CCCTC T  
 GAM1197 LOC257468 3' CTCCTGTCCCCCCCACCTCC 95187 A AAAGAAGT \_  
 GGA GGT GGGA GGAG  
 ||| ||| |||| |||||  
 CCT CCA CCCT CCTC  
 \_ CCCC\_\_ GT  
 GAM1197 LOC51093 3' CCCCTTTCTCTCCTTCCA 32043 TAA T  
 TGGAAGG AGAAG GGG  
 ||||| |||| |||  
 ACCTTCC TCTTT CCC  
 TC\_ C  
 GAM1197 LOC51279 3' CTCCTCACCTCTACCTCCC 33313 A AA AT \_  
 GG AGGT AGA G GG GAGGAG  
 || |||| ||| || |||||  
 CC TCCA TCT C CC CTCCTC  
 C \_ \_ A  
 GAM1197 LOC51308 3' CTCCTCCCACCCTGAGCCCCA 33494 AA AA AA  
 TGG GGT AG GTGGGAGGAG  
 ||| ||| || |||||  
 ACC CCG TC CACCCTCCTC  
 \_ AG C\_  
 GAM1197 LOC51337 3' CTCCTCCTCCTCCTCTACCTCC 33586 A A A TG  
 A TGGA GGTA AG AG GGAGGAG  
 |||| |||| || || |||||  
 ACCT CCAT TC TC CCTCCTC  
 \_ C C CT  
 GAM1197 LOC56961 5' CTCCCAGCTGCTCCCCACCTCC 62907 A AA\_ A \_  
 C GG AGGT AG AG TGGGAG  
 || |||| || || |||||  
 CC TCCA TC TC ACCCTC  
 C CCCC G G  
 GAM1197 LOC90110 5' CCTCCTCACCTACTTCCA 61509 GTAAAGAA \_  
 TGGAAG GTG GGAGG  
 ||||| ||| |||||

ACCTTC CAC CCTCC  
 ATCC\_\_\_\_\_ T  
 GAM1197 LOC90378 3' CCTCCCCTACCACCCA 62523 AA AAAGA T  
 TGG GGT AG GGGAGG  
 ||| ||| || |||||  
 ACC CCA TC CCCTCC  
 CA \_\_\_\_\_  
 GAM1197 LOC90494 5' CTCCTTCCATGCTCCACCCTCC 63054 A AA AA  
 A TGGG GGT AG GTGGGAGGAG  
 |||| ||| || |||||  
 ACCT CCA TC TACCTTCCTC  
 C CC G\_  
 GAM1197 LOC90670 3' CTCCTTACCTTCCA 63740 AAGAAGT  
 TGGG AAGGTA GGGAG  
 ||||| ||||  
 ACCTTCCAT TCCTC  
 \_\_\_\_\_  
 GAM1197 LOC90785 3' TCACTTCTCTGACCTTCCA 64019 AA\_  
 TGGG AAGGT AGAAGTGG  
 ||||| |||||  
 ACCTTCCA TCTTCACT  
 GTC  
 GAM1197 LOC91445 3' CCTCCCACTCCCCCTCTTCTTC 60549 TAAAGA\_  
 C GGAAGG AGTGGGAGG  
 ||||| |||||  
 CCTTCT TCACCCTCC  
 TCTCCCCC  
 GAM1197 LOC91585 5' CCCTCTTCCTTGCCCTCCA 66572 A A T  
 TGGG GGTA GAAG GGG  
 ||| |||| ||| |||  
 ACCT CCGTT CTTC CCC  
 C C T  
 GAM1197 LOC91948 3' CTCCCCCACCCTTCCCCTCCA 67617 A TA AA A  
 TGGG GG AAG GTGGG GGAG  
 ||| || ||| |||| ||||  
 ACCT CC TTC CACCC CCTC  
 \_ CC C\_ \_  
 GAM1197 LOC92154 3' TCCTCCCCGCCCCCTCCA 68357 A TAAAGAA \_  
 TGGG GG GTGGG AGGA  
 ||| || |||| ||||  
 ACCT CC CGCCC TCCT  
 C C\_\_\_\_\_ C  
 GAM1197 LOC92303 3' TCCTCCCTCAGCCTCCCA 68828 A AAA AGT  
 TGG AGGT GA GGGAGGA  
 ||| ||| || |||||  
 ACC TCCG CT CCCTCCT  
 C A\_ \_  
 GAM1197 LOC92579 3' CTCCCTTTCCTTTCCTCCCA 69837 A T \_ T  
 TGG AGG AAAG AAG GGGAG  
 ||| ||| ||| ||| ||||

			ACC TCC TTTC TTT CCCTC		
			C C C _		
GAM1198	ABCC1	3'	TGATGTGGGGTAAATATTAAGG 17183	CA	AAA C
	A		TCC AATATTTAC GC ATCA		
			AGG TTATAAATG TG TAGT		
			AA GGG _		
GAM1198	ABCC1	3'	TGATGTGGGGTAAATATTAAGG 39136	CA	AAA C
	A		TCC AATATTTAC GC ATCA		
			AGG TTATAAATG TG TAGT		
			AA GGG _		
GAM1198	ABCC1	3'	TGATGTGGGGTAAATATTAAGG 39128	CA	AAA C
	A		TCC AATATTTAC GC ATCA		
			AGG TTATAAATG TG TAGT		
			AA GGG _		
GAM1198	ASIC4	3'	TTTGTAATATTTAGGG 37924 _		
			CCC AAATATTTACAAA		
			GGG TTTATAAATGTTT		
			A		
GAM1198	CREBBP	3'	GATAACTTTGTGATGTTTCGGG 15207	_	T CC
	A		TCCC AAATATT ACAAAG ATC		
			AGGG TTTGTAG TGTTTC TAG		
			C _ AA		
GAM1198	CTSS	3'	TGATGGCTTAAAAATA 14545 ACA		
			TATTT AAGCCATCA		
			ATAAA TTCGGTAGT		
			AA_		
GAM1198	EYA1	5'	GATGGCTCCGAGTTTGGGG 4954	ATTTACAA	
			TCCCAAAT AGCCATC		
			GGGGTTTG TCGGTAG		
			AGCC_		
GAM1198	FBXW1B	3'	TGACAGCTTTGTACTGTGG 53342	AATATT	CA
			CCA TACAAAGC TCA		
			GGT ATGTTTCG AGT		
			GTC_ AC		
GAM1198	FBXW1B	3'	TGACAGCTTTGTACTGTGG 24527	AATATT	CA
			CCA TACAAAGC TCA		
			GGT ATGTTTCG AGT		
			GTC_ AC		
GAM1198	FBXW1B	3'	TGACAGCTTTGTACTGTGG 53331	AATATT	CA
			CCA TACAAAGC TCA		

GGT ATGTTTCG AGT  
GTC\_\_\_ AC  
GAM1198 GCN5L2 3' TGATGGCTTCAGGGGTTGG 59841 ATA ACA  
CCAA TTT AAGCCATCA  
||||| ||| |||||  
GGTT GGA TTCGGTAGT  
GG\_ C\_  
GAM1198 GSPT1 3' GCTTTGTAAGTGATGTGG 9143 AA\_  
CCA TATTTACAAAGC  
||| |||||  
GGT GTGAATGTTTCG  
GTA  
GAM1198 PTPN11 3' TGATGAGAAGAAATGATTTGGG 11085 \_ ACAAAGC  
A TCCCAAAT ATTT CATCA  
||||| ||| |||||  
AGGGTTTA TAAA GTAGT  
G GAAGA\_  
GAM1198 RNMT 3' TGATAGCTTTGTAGGTACAGGA 13725 CAAA C  
TCC TATTTACAAAGC ATCA  
||| ||||| |||||  
AGG ATGGATGTTTCG TAGT  
AC\_ A  
GAM1198 ROR2 3' TGACAGCTTTGTATTTGGTGA 15855 \_ TATT CA  
TC CCAA TACAAAGC TCA  
|| ||||| ||||| |||  
AG GGTTT ATGTTTCG AGT  
T \_ AC  
GAM1198 STAM 3' TTGTAATTATTTGGGA 12964 T  
TCCCAAATA TTACAA  
||||| |||||  
AGGGTTTAT AATGTT  
T  
GAM1198 TGFB2 3' CTTTATAAATATTTGG 12267 C  
CCAAATATTTA AAAG  
||||| |||||  
GGTTTATAAAT TTTC  
A  
GAM1198 ZNF14 3' TGTAAGACATTTGGGA 40718 A\_  
TCCCAAAT TTTACA  
||||| |||||  
AGGGTTTA GAATGT  
CA  
GAM1198 DKFZP434L1123 5' TGGTTTGTAATATTTG 49585 G  
CAAATATTTACAAA CCA  
||||| ||||| |||  
GTTTATAAATGTTT GGT  
-  
GAM1198 DKFZP434O047 5' TGATGGCTCCACATCTTGGGG 31517 ATATTTACAA  
TCCCAA AGCCATCA  
||||| |||||

		GGGGTT	TCGGTAGT		
		CTACACC__			
GAM1198	DKFZP564G092 5'	TGGACAGTAAATATTTG	31539	AAAG	
		CAAAATATTTAC CCA			
		GTTTATAAATG GGT			
		ACA_			
GAM1198	DKFZP564O0823 3'	ATGGCTGTAAAATGTTT	59519	ACAA	
		AAATATTT AGCCAT			
		TTTGTAAG TCGGTA			
		ATG_			
GAM1198	FLJ10036 3'	GCTTTGTAAATATTTTCAGA	94950	CC	
		TC AAATATTTACAAAGC			
		AG TTTATAAATGTTTCG			
		AC			
GAM1198	FLJ11267 5'	TGATGGCTCTAGAATGTCTAGG	39007	CAA	ACAA
	A	TCC ATATTT AGCCATCA			
		AGG TGTAAG TCGGTAGT			
		ATC ATC_			
GAM1198	FLJ11730 3'	TGGAGGCTGTAAATATCTGG	42798	A	AA AT
		CCA ATATTTACA GCC CA			
		GGT TATAAATGT CGG GT			
		C _ AG			
GAM1198	FLJ13194 3'	TGATAACTTTGTAAAGATGGGA	47131	AATA	CC
		TCCCA TTTACAAAG ATCA			
		AGGGT GAATGTTTC TAGT			
		A__ AA			
GAM1198	FLJ14564 3'	ATGGGGAAAATATTTGGGA	76499	ACAAAG	
		TCCCAAATATTT CCAT			
		AGGGTTTATAAA GGTA			
		AGG__			
GAM1198	FLJ22596 5'	TGATGGCTTGATGGTATCTGG	46964	A	TACA
		CCA ATATT AAGCCATCA			
		GGT TATGG TTCGGTAGT			
		C TAG_			
GAM1198	FLJ25200 5'	TGATGGCTTCATTAAGTATCTG	58514	A T	CA_
	G	CCA ATA TTA AAGCCATCA			
		GGT TAT AAT TTCGGTAGT			
		C C TAC			
GAM1198	FRAT1 3'	TGAGGGCCAAAATATTTGG	18496	ACAAA	A
		CCAAATATTT GCC TCA			

GGTTTATAAA CGG AGT  
AC\_\_ G  
GAM1198 GLUC 3' ATGGCCTTTATTTGTATTTGG 40586 TTAC \_  
CCAAATAT AAAG CCAT  
||||| ||| |||  
GGTTTATG TTTC GGTA  
TTTA C  
GAM1198 GPR 3' GGATTGTAAATTCTTGG 23336 AT AG  
CCAA ATTTACAA CC  
||| ||||| ||  
GGTT TAAATGTT GG  
CT A\_  
GAM1198 GSPT2 3' GCTTTGTAAGTGATGTGG 36120 AA\_  
CCA TATTTACAAAGC  
||| |||||  
GGT GTGAATGTTTCG  
GTA  
GAM1198 KIAA0453 3' GTGTGTTTGTAATATATAGGA 69051 CAA GC  
TCC ATATTTACAAA CAT  
||| ||||| |||  
AGG TATAAATGTTT GTG  
ATA GT  
GAM1198 KIAA0746 3' GCTTTGTAAATTGG 69454 AAT  
CCA ATTTACAAAGC  
||| |||||  
GGT TAAATGTTTCG  
  
GAM1198 KIAA0884 3' TGATTATTGTAAATATTTTGGA 70207 C AGCC  
TCC AAATATTTACAA ATCA  
||| ||||| |||  
AGG TTTATAAATGTT TAGT  
T AT\_  
GAM1198 KIAA0930 3' TGATGGCTTTGCCCTGGGCTGG 70554 AATATTTA  
GA TCCA CAAAGCCATCA  
||||| |||||  
AGGGT GTTTCGGTAGT  
CGGGTCCC  
GAM1198 KIAA1052 3' TGATGGCTTTTATCCTCCTGGG 30252 AATATT C  
A TCCA TA AAAGCCATCA  
||||| || |||||  
AGGGT AT TTTTCGGTAGT  
CCTCCT \_  
GAM1198 KIAA1557 3' TTGTAAATATTTGTGA 61140 C  
TC CAAATATTTACAA  
|| |||||  
AG GTTTATAAATGTT  
T  
GAM1198 KIAA1587 3' TGATAGCTCTATAAAATGTTTT 40512 C ACAA\_ C  
GGA TCC AAATATTT AGC ATCA  
||| ||||| ||| |||

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AGG TTTGTAAA TCG TAGT
T ATATC A
GAM1198 LIPI 3' ATGACTTTGTAAATATTT 79564 C
AAATATTTACAAAG CAT
||||||||||| |||
TTTATAAATGTTTC GTA
A
GAM1198 MARCKS 3' GTTTTGTAAATACTGGAGA 9870 _ AA
TC CCA TATTTACAAAGC
|| ||| |||||||||
AG GGT ATAAATGTTTTG
A C_
GAM1198 MED6 3' TGATGGCTTTGTTGCAGCTGAG 18439 C AATATTT
A TC CA ACAAAGCCATCA
|| || |||||||||
AG GT TGTTTCGGTAGT
A CGACGT_
GAM1198 MGC17330 3' GTTTTTAAATATTTGGGA 53531 AC
TCCCAAATATTT AAAGC
||||||||||| ||||
AGGGTTTATAAA TTTTG
AT
GAM1198 OR51E2 3' ATGGCTTTGTACTTGTGATG 47790 A_ TT
CA ATA TACAAAGCCAT
|| ||| |||||||||
GT TGT ATGTTTCGGTA
AG TC
GAM1198 PSTPIP2 3' CTTTCACAAATATTTGGG 44389 AC_
CCCAAATATTT AAAG
||||||||||| ||||
GGGTTTATAAA TTTC
CAC
GAM1198 PURG 3' ATGGCTTTGCTATGG 25336 AATATT _
CCA TA CAAAGCCAT
||| || |||||||||
GGT AT GTTTCGGTA
_____ C
GAM1198 VDU1 3' TGATGGCTTTGTTTGGTTTGG 30431 ATTT
GG TCCCAAAT ACAAAGCCATCA
||||||| |||||||||
GGGGTTTG TGTTTCGGTAGT
GTTT
GAM1198 ZNF294 3' GCTTTGTAAATGTTTGG 70828
CCAAATATTTACAAAGC
|||||||||||
GGTTTGTAATGTTTCG
GAM1198 LOC127162 3' TGATGGCTACATATACTAGGGA 74638 AAA TTACAA
TCCC TAT AGCCATCA
||| ||| |||||||

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AGGG ATA TCGGTAGT  
 ATC TACA\_\_  
 GAM1198 LOC148936 5' TGATGGCTCTATAAGGGGGA 84303 AAA TTACAA  
 TCCC TAT AGCCATCA  
 |||| ||| |||||||  
 AGGG ATA TCGGTAGT  
 GGA TC\_\_\_\_  
 GAM1198 LOC148938 5' TGATGGCTCTATAAGGGGGA 84284 AAA TTACAA  
 TCCC TAT AGCCATCA  
 |||| ||| |||||||  
 AGGG ATA TCGGTAGT  
 GGA TC\_\_\_\_  
 GAM1198 LOC152084 5' GATGGCTTTCCTCAGCCTGGGA 85553 AATATTTAC  
 TCCCA AAAGCCATC  
 |||| |||||||  
 AGGGT TTTCGGTAG  
 CCGACTCC\_  
 GAM1198 LOC152573 3' GATGACTATATATTTGGG 80618 TTACAA C  
 CCCAAATAT AG CATC  
 ||||||| || ||||  
 GGGTTTATA TC GTAG  
 TA\_\_\_\_ A  
 GAM1198 LOC152627 5' ATGGCTTCTAAGTATTCAGG 80627 CA CA  
 CC AATATTTA AAGCCAT  
 || ||||||| |||||||  
 GG TTATGAAT TTCGGTA  
 AC C\_  
 GAM1198 LOC200301 3' GCTTGTTATTTGGGG 88748 TTT A  
 TCCCAAATA ACAA GC  
 ||||||| |||| ||  
 GGGGTTTAT TGTT CG  
 — —  
 GAM1199 ADH1B 3' CTTAGACATAAAGTAAAAT 72644 C CAC  
 ATTT ACTTT TGTCTGAG  
 |||| |||| |||||||  
 TAAA TGAAA ACAGATTC  
 A T\_  
 GAM1199 AHR 3' ATCTCAGATGTTAAATAAATG 7875 CAC C T  
 CATTT TTT AC GTCTGAGAT  
 |||| ||| || |||||||  
 GTAAA AAA TG TAGACTCTA  
 TA\_ T \_  
 GAM1199 FDFT1 3' TAGGAAAGTGAAATG 15518 A  
 CATTTCACTTTC CTG  
 ||||||||| |||  
 GTAAAGTGAAAG GAT  
 —  
 GAM1199 JTB 3' ATCTCAGACAGTGAAAGTGAAA 21959  
 TG CATTTCACTTTCACTGTCTGAGAT  
 |||||||||||||||||



GTAAAGTGAAAGTGACAGACTCTA

GAM1199	KLF4	3'	TCCCAGACAGTGGATATG	14891	CT	A
			CA TTCACTGTCTG GA			
			GT AGGTGACAGAC CT			
			AT C			
GAM1199	PHYH	3'	ACAGTAAAAGTGAAAT	20608		C
			ATTTCACTTT ACTGT			
			TAAAGTGAAA TGACA			
			A			
GAM1199	PKD2	3'	TCCAGGTTGAAAGTGAAA	60096	CTG	A
			TTTCACTTTCA TCTG GA			
			AAAGTGAAAGT GGAC CT			
			T_ _			
GAM1199	WRN	3'	GGGCAGTGAAAATGAAA	5098		C
			TTTCA TTTCACTGTCT			
			AAAGT AAAGTGACGGG			
			A			
GAM1199	ZNF216	3'	ATCTGCACAGCAAAGTGAAA	20017	CA	CTG
			TTTCACTTT CTGT AGAT			
			AAAGTGAAA GACA TCTA			
			C_ CG_			
GAM1199	CG012	5'	CTCACTCTGAAAGTGAA	83218	CT	CT
			TTCAC TTTCA GT GAG			
			AAGTGAAAGT CA CTC			
			CT _			
GAM1199	EIF2C2	3'	ATCTTCTGAGAGTGAAAG	71946	G	T_
			CTTTCACT TC GAGAT			
			GAAAGTGA AG TTCTA			
			G TC			
GAM1199	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT	45802	ACTTTCACT	
	G		CATTTT GTCTGAGAT			
			GTAAAG CAGACTCTA			
			AAACATTT_			
GAM1199	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG	45281	CTT	
			CATTTCA TCACTGTCTGAGAT			
			GTAAAGT AGTGACAGACTCTA			
			C_			
GAM1199	KIAA0984	3'	TTTGTCCAGTGAAAATGAA	65534	C	TC
			TTCA TTTCACTG TGAG			

			AAGT AAAGTGAC GTTT		
			A CT		
GAM1199	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A _	
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1199	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T	
			ATT CACTTTCACTGT		
			TAA GTGAAAGTGACG		
			C		
GAM1199	PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA 53598	CA G	
			TTCAC TTT CT TCTGAGAT		
			AAGTGAAA GG AGACTCTA		
			CC G		
GAM1199	PP35	3'	ATCTCAGACTGAAA 22814	CT	
			TTTCA GTCTGAGAT		
			AAAGT CAGACTCTA		
			—		
GAM1199	PRTD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148	TCAC C_	
			CATTTCACTT TGT TGAG		
			GTAAAGTGAA ACG ACTC		
			TA_ TT		
GAM1199	SEP15	3'	TCCTACAGTAAGAGTGAAA 14934	C CT	
			TTTCACTTT ACTGT GA		
			AAAGTGAGA TGACA CT		
			A TC		
GAM1199	SFXN2	3'	CTCAGGGGAAAAAAGTGAAA 73941	CACTG	
			TTTCACTTT TCTGAG		
			AAAGTGAAA GGA CTC		
			AAAGG		
GAM1199	LOC149703	3'	ATCTCAGACAGCCGTTTGAAA 84647	ACTTTCA	
			TTTC CTGTCTGAGAT		
			AAAG GACAGACTCTA		
			GTTTGCC		
GAM1199	LOC154007	3'	ATCTCAAACCCTTTAGTGAAA 81015	TTCAC T C	
			TTTCACT GT TGAGAT		
			AAAGTGA CA ACTCTA		
			TTTCC_ A		
GAM1199	LOC155004	3'	TCATTTAAGTGAAAAGGAAA 81226	A GTC_	
			TTTC CTTTCACT TGA		

			AAAG GAAAGTGA	ACT		
			—	ATTT		
GAM1199	LOC222134	5'	ACAGTGAAGTCAAATG	94136	T	
			CATTTCACTT CACTGT			
			GTAAAGTGAA GTGACA			
			—			
GAM1200	CHRM1	5'	AATTGGGTGCCCTGGTGAA	94784	TAA_	
			TTCACCAGGGC AGTT			
			AAGTGGTCCCG TTAA			
			TGGG			
GAM1200	EFNA1	3'	GAGCCCCCAGCCCTGGGAA	15390	A	AAA_
			TTC CCAGGGCT GTTC			
			AAG GGTCCCGA CGAG			
			—	CCCC		
GAM1200	F8	3'	CAAATGGTTTATAGCCCTGTGA	3724	C	A TT C
	A		TTCAC AGGGCTA AG CA TTG			
			AAGTG TCCCGAT TT GT AAC			
			—	A TG A		
GAM1200	IL21	3'	CAAGTGGAGGAGCCCT	41439	AAAG	
			AGGGCT TTCAC TTG			
			TCCCGA AGGTGAAC			
			GG_			
GAM1200	C9orf14	5'	CAAATGAACTTTAGCACTTG	86672	—	C
			CAGG GCTAAAGTTCA TTG			
			GTTC CGATTTCAAGT AAC			
			A A			
GAM1200	EBF2	5'	AGCCATTAGCCCGAGTGAA	42642	CA	A_
			TTCAC GGGCTAA GTT			
			AAGTG CCCGATT CGA			
			AG AC			
GAM1200	FLJ10716	3'	CAAGTGATTGAAGCCCAGTGAA	36482	CA	AA T
			TTCAC GGGCT AGT CACTTG			
			AAGTG CCCGA TTA GTGAAC			
			A_ AG _			
GAM1200	MPPE1	5'	AGTTCACTTGCACCCTGCCCTG	43560	TA_____	TTCA
			GTGAA ACCAGGGC AAG CT			
			TGGTCCCG TTC GA			
			TCCCAC   G ACTT			
GAM1200	RNF2	3'	ACTTTAGCCTTGATGAA	23296	C	
			TTCA CAGGGCTAAAGT			

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AAGT GTTCCGATTTC
A
GAM1200 SNRPB2 3' AGTGTTCCTTTAGCCTTGGTGA 11857 TT_
A TTCACCAGGGCTAAAG CACT
||||| |||
AAGTGGTTCCGATTTC GTGA
TTT
GAM1200 LOC128259 5' CAAGTGAAGTTCAGCAGGG 74725 AGG A
CC GCT AAGTTCAGTTG
|| ||| |||
GG CGA TTCAAGTGAAC
GA_ C
GAM1201 TNFAIP1 3' CATCAGCTGAGGACAGCAAAGT 40917 AG G
CC GGA TTGCTG CTTAGCTGATG
||| ||| |||
CCT AACGAC GGAGTCGACTAC
CA A
GAM1201 C1orf2 3' CAGCTGGTTGGGACCAGCAGCC 21681 AA _ _
CCC GG GTTGCTGG CT TCAGCTG
|| ||| |||
CC CGACGACC GG GGTCGAC
CC A GTT
GAM1201 C1orf2 3' CAGCTGGTTGGGACCAGCAGCC 94622 AA _ _
CCC GG GTTGCTGG CT TCAGCTG
|| ||| |||
CC CGACGACC GG GGTCGAC
CC A GTT
GAM1201 C20orf59 3' CATCCCTAGCCAGCAGCTCC 41992 A TC CT
GGA GTTGCTGGCT AG GATG
||| ||| |||
CCT CGACGACCGA TC CTAC
_ _ C_
GAM1201 FLJ20079 3' CATTCTGGTAAACCAGCAGCCT 34490 A CT_ CT
CC GGA GTTGCTGG TCAG GATG
||| ||| |||
CCT CGACGACC GGTC TTAC
C AAAT _
GAM1201 SSAT2 3' CATCAGCTGAAGCACTCTTC 56041 TTGCTG
GAAG GCTTCAGCTGATG
||| |||
CTTC CGAAGTCGACTAC
TCA_
GAM1201 SYNJ2 3' ATCAGCTTAAGCAATTCC 61763 GTTGCTG C
GGAA GCTT AGCTGAT
||| ||| |||
CCTT CGAA TCGACTA
AA_ T
GAM1201 LOC162333 5' CTGAAGCCAGCAATTCC 87131 G
GGAA TTGCTGGCTTCAG
||| |||

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CCTT AACGACCGAAGTC

GAM1201 LOC222060 5' CACCTCCCACCAGCAACCCCC 94104 AA CTTC C  
GG GTTGCTGG AG TG  
|| ||||| ||  
CC CAACGACC TC AC  
CC ACCC C

GAM1201 LOC255650 3' CATCAGCCCCAGGCAACTTCC 96711 \_ CTTCA  
GGAAGTTGC TGG GCTGATG  
||||| || |||||  
CCTTCAACG ACC CGACTAC  
G C \_

GAM1202 CDH6 3' ACACTTGAACCTAATACC 17026 TG T\_  
GGTATTAGGT TCA TGT  
||||| || ||  
CCATAATCCA AGT ACA  
\_ TC

GAM1202 SH3BP2 3' CATAAATGCACAACCTAACAC 11597 A \_ G  
GT TTAGGTTGT CATT TATG  
|| ||||| || ||||  
CA AATCCAACA GTAA ATAC  
C C \_

GAM1202 DKFZP434I116 5' CATACAATGATCCAACAACCT 31322 ATTA TT  
AGGT GG GTCATTGTATG  
||| || |||||  
TCCA CC TAGTAACATAC  
ACAA \_

GAM1202 LOC145844 3' ATAGGTACAACCTAACAC 77537 A CA  
GT TTAGGTTGT TTGT  
|| ||||| |||  
CA AATCCAACA GATA  
C TG

GAM1202 LOC146952 5' CATATGCCTCAACCTAACACTT 83863 A TCATT  
AGGT TTAGGTTG GTATG  
||| ||||| ||||  
TTCA AATCCAAC TATAC  
C TCCG\_

GAM1203 ADH1B 3' CTTAGACATAAAGTAAAAT 72644 C CAC  
ATTT ACTTT TGTCTGAG  
||| |||| |||||  
TAAA TGAAA ACAGATTC  
A T\_

GAM1203 AHR 3' ATCTCAGATGTTAAATAAATG 7875 CAC C T  
CATTT TTT AC GTCTGAGAT  
||| || |||||  
GTAAA AAA TG TAGACTCTA  
TA\_ T \_

GAM1203 FDFT1 3' TAGGAAAGTGAAATG 15518 A  
CATTTCACTTTC CTG  
||||||| |||

GTAAAGTGAAAG GAT

GAM1203 JTB 3' ATCTCAGACAGTGAAAGTGAAA 21959

TG

CATTTCACTTTCACTGTCTGAGAT

|||||

GTAAAGTGAAAGTGACAGACTCTA

GAM1203 KLF4 3' TCCCAGACAGTGGATATG 14891 CT A

CA TTCACTGTCTG GA

|| |||

GT AGGTGACAGAC CT

AT C

GAM1203 PHYH 3' ACAGTAAAAGTGAAAT 20608 C

ATTTCACTTT ACTGT

|||||

TAAAGTGAAA TGACA

A

GAM1203 PKD2 3' TCCAGGTTGAAAGTGAAA 60096 CTG A

TTTCACTTTCA TCTG GA

||||| |||

AAAGTGAAAGT GGAC CT

T \_ \_

GAM1203 WRN 3' GGGCAGTGAAAATGAAA 5098 C

TTTCA TTTCACTGTCT

|||||

AAAGT AAAGTGACGGG

A

GAM1203 ZNF216 3' ATCTGCACAGCAAAGTGAAA 20017 CA CTG

TTTCACTTT CTGT AGAT

||||| |||

AAAGTGAAA GACA TCTA

C\_ CG\_

GAM1203 CG012 5' CTCACTCTGAAAGTGAA 83218 CT CT

TTCACTTTCA GT GAG

||||| ||

AAGTGAAAGT CA CTC

CT \_

GAM1203 EIF2C2 3' ATCTTCTGAGAGTGAAAG 71946 G T\_

CTTTCACT TC GAGAT

||||| ||

GAAAGTGA AG TTCTA

G TC

GAM1203 FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802 ACTTTCACT

G

CATTTT GTCTGAGAT

|||||

GTAAAG CAGACTCTA

AAACATTT\_

GAM1203 FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281 CTT

CATTTCA TCACTGTCTGAGAT

|||||

			GTAAAGT AGTGACAGACTCTA		
			C__		
GAM1203	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C	TC
			TTCA TTTCAGTG TGAG		
			AAGT AAAGTGAC GTTT		
			A CT		
GAM1203	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A	_
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1203	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T	
			ATT CACTTTCACTGT		
			TAA GTGAAAGTGACG		
			C		
GAM1203	PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA 53598		CA G
			TTCACTTT CT TCTGAGAT		
			AAGTGAAA GG AGACTCTA		
			CC G		
GAM1203	PP35	3'	ATCTCAGACTGAAA 22814	CT	
			TTTCA GTCTGAGAT		
			AAAGT CAGACTCTA		
			—		
GAM1203	PRTD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148		TCAC C_
			CATTTCACTT TGT TGAG		
			GTAAAGTGAA ACG ACTC		
			TA__ TT		
GAM1203	SEP15	3'	TCCTACAGTAAGAGTGAAA 14934	C	CT
			TTTCACTTT ACTGT GA		
			AAAGTGAGA TGACA CT		
			A TC		
GAM1203	SFXN2	3'	CTCAGGGGAAAAAAGTGAAA 73941		CACTG
			TTTCACTTT TCTGAG		
			AAAGTGAAA GGA CTC		
			AAAGG		
GAM1203	LOC149703	3'	ATCTCAGACAGCCGTTTGAAA 84647		ACTTTCA
			TTTC CTGTCTGAGAT		
			AAAG GACAGACTCTA		
			GTTTGCC		
GAM1203	LOC154007	3'	ATCTCAAACCCTTTAGTGAAA 81015		TTCAC T C
			TTTCACT GT TGAGAT		

			AAAGTGA	CA	ACTCTA		
			TTTCC_	A			
GAM1203	LOC155004	3'	TCATTTAAGTGAAAGGAAA	81226	A	GTC_	
			TTTC	CTTTC	CACT	TGA	
			AAAG	GAAAGTGA	ACT		
			_	ATTT			
GAM1203	LOC222134	5'	ACAGTGAAGTGAAATG	94136	T		
			CATTTCACTT	CACTGT			
			GTAAAGTGAA	GTGACA			
GAM1204	ABCC1	3'	GCAGTTTTGTGGTTGAGG	39126	A	TA	AG
			TC	TAGCCACAAA	GCTG		
			GG	GTTGGTGT	TTT	TGAC	
			A	_	GT		
GAM1204	ABCC1	3'	GCAGTTTTGTGGTTGAGG	39134	A	TA	AG
			TC	TAGCCACAAA	GCTG		
			GG	GTTGGTGT	TTT	TGAC	
			A	_	GT		
GAM1204	ABCC1	3'	GCAGTTTTGTGGTTGAGG	17181	A	TA	AG
			TC	TAGCCACAAA	GCTG		
			GG	GTTGGTGT	TTT	TGAC	
			A	_	GT		
GAM1204	ADAM19	3'	TCAGGGTGGCTGTGA	52712		AAATAG	
			TCATAGCCAC	CTGA			
			AGTGT	CGGTG	GA	CT	
			G				
GAM1204	ADAMTS4	3'	CTCAGTGGGGAGGGGCTGTGG	17507		ACAAATA	
			TCATAGCC	GCTGAG			
			GGTGT	CGG	TG	ACTC	
			GGAGGGG				
GAM1204	AF5Q31	3'	CTTAGTTATTCTGCCTAT	27021	C	C	
			ATAG	CA	AAATAGCTGAG		
			TATC	GT	TTTATTGATTC		
			C	C			
GAM1204	AKAP1	3'	TTCAGCTGTGGAGTGTGGTTGG	57710	A	A	
	AG		TTC	TAGCCACA	ATAGCTGAG		
			GAG	GTTGGTGT	TGTCGACTT		
			_	GAGG			
GAM1204	ALDH3B2	3'	CTTGGCTGTGGCCCTCTGTG	5505		AATA	TG
			CATA	GCCACA	GC	AG	



			GTGT CGGTGT CG TC		
			CTCC ____ GT		
GAM1204	AMD1	5'	TTTAGTTGATTTTCTGTGGTTG 7903	____	—
	T		ATAGCCACA AAT AGCTGAG		
			TGTTGGTGT TTA TTGATTT		
			CTT G		
GAM1204	ANK1	3'	CTTTTTGTGGCTGGGGA 60389	A	T
			TTC TAGCCACAAA AG		
			AGG GTCGGTGTTT TC		
			G T		
GAM1204	ANK1	3'	CTTTTTGTGGCTGGGGA 40026	A	T
			TTC TAGCCACAAA AG		
			AGG GTCGGTGTTT TC		
			G T		
GAM1204	ANK1	3'	CTTTTTGTGGCTGGGGA 40032	A	T
			TTC TAGCCACAAA AG		
			AGG GTCGGTGTTT TC		
			G T		
GAM1204	ANK1	3'	CTTTTTGTGGCTGGGGA 40035	A	T
			TTC TAGCCACAAA AG		
			AGG GTCGGTGTTT TC		
			G T		
GAM1204	ANK1	3'	CTTTTTGTGGCTGGGGA 40038	A	T
			TTC TAGCCACAAA AG		
			AGG GTCGGTGTTT TC		
			G T		
GAM1204	ANK1	3'	CTTTTTGTGGCTGGGGA 3472	A	T
			TTC TAGCCACAAA AG		
			AGG GTCGGTGTTT TC		
			G T		
GAM1204	ANKRA2	5'	TTCAGCTGCATTGCTGCGGA 43528	A	CACAAA
			TTC TAGC TAGCTGAG		
			AGG GTCG GTCGACTT		
			C TTAC__		
GAM1204	APOBEC3B	5'	TGGCTGTGCTATGAA 16917	CACAA	TG
			TTCATAGC ATAGC A		
			AAGTATCG TGTCG T		
			____ GT		
GAM1204	APPBP2	3'	TTCACCTCTTGGCTGTGGA 21085	CAAAT	C
			TTCATAGCCA AG TGAG		

			AGGTGTCGGT	TC ACTT	
			TC___ C		
GAM1204	ARNT2	3'	AGTTTGGTTGTGAA	29453	CAAAT
			TTCATAGCCA	AGCT	
			AAGTGTTGGT	TTGA	
			_____		
GAM1204	ATP10C	3'	CTCGGCACCGGGGCTGTGAA	44411	ACAAATA
			TTCATAGCC	GCTGAG	
			AAGTGTCGG	CGGCTC	
			GGCCA__		
GAM1204	ATP11B	3'	TCAGGTGTGGCTGTGGA	80320	AATAG
			TTCATAGCCACA	CTGA	
			AGGTGTCGGTGT	GA CT	
			G_____		
GAM1204	ATP8A2	3'	ATTTGTTGGCTATGAG	93508	—
			TTCATAGCCA	CAAAT	
			GAGTATCGGT	GTTTA	
			T		
GAM1204	C21orf2	3'	CTCAGCTGTGAGGTTGTGGA	17009	ACAA
			TTCATAGCC	ATAGCTGAG	
			AGGTGTTGG	TGTCGACTC	
			AG__		
GAM1204	CALCR	3'	CTGTATTTGGCTATGGA	8218	CAA
			TTCATAGCCA	ATAG	
			AGGTATCGGT	TGTC	
			TTA		
GAM1204	CALM3	3'	TCAGTTCAAGCTGTGAA	17746	CACAAAT
			TTCATAGC	AGCTGA	
			AAGTGTCG	TTGACT	
			AAC_____		
GAM1204	CASP2	5'	TTGTTTGGGCTGTGG	52149	A
			TCATAGCC	CAAATAG	
			GGTGTCGG	GTTTGTT	
			—		
GAM1204	CASP2	5'	TTGTTTGGGCTGTGG	52163	A
			TCATAGCC	CAAATAG	
			GGTGTCGG	GTTTGTT	
			—		
GAM1204	CASP3	5'	CTCATACCTGTGGCTGTG	15101	AA GC
			CATAGCCACA	TA TGAG	

GTGTCGGTGT AT ACTC  
 CC \_  
 GAM1204 CD209L 3' TTTGGCTGTTTCTGAGTTGT 26521 \_ C TG  
 ATAGC CA AAATAGC AG  
 ||||| || ||||| ||  
 TGTTG GT TTTGTCG TT  
 A C GT  
 GAM1204 CEACAM1 3' CTTGGGAAATGGGGCTGTGAG 8149 A AATAG TG  
 TTCATAGCC CA C AG  
 ||||| || | ||  
 GAGTGTCCG GT G TC  
 G AAAG\_ GT  
 GAM1204 CERD4 3' CTCAGTTGTTTGTGTTG 23851 C  
 TAGC ACAAATAGCTGAG  
 ||| ||||| |||||  
 GTTG TGTTTGTGACTC  
 \_  
 GAM1204 CLTC 3' TCAGTTTTGTTTGTGG 16783 \_  
 CCACAAATA GCTGA  
 ||||| |||||  
 GGTGTTTGT TGA CT  
 TT  
 GAM1204 COL3A1 3' TTGTATGTGGTTGTTGA 3616 \_ A  
 TCA TAGCCACA ATAG  
 ||| ||||| |||||  
 AGT GTTGGTGT TGTT  
 T A  
 GAM1204 CPNE3 3' CTTGGGAACTGCTGGTTATGAG 14028 \_ AATAG TG  
 TTCATAGCCA CA C AG  
 ||||| || | ||  
 GAGTATTGGT GT G TC  
 C CAAG\_ GT  
 GAM1204 CRKL 5' TTTGTTGCTGTGGCTATTGG 17797 \_ AA TGAG  
 TCA TAGCCACA TAGC  
 ||| ||||| |||||  
 GGT ATCGGTGT GTTG  
 T C\_ TTT  
 GAM1204 CROT 3' TTTAGCTGCCAAAGGGTATGAA 40951 G ACAA  
 TTCATA CC TAGCTGAG  
 ||||| || |||||  
 AAGTAT GG GTCGATTT  
 G AAACC  
 GAM1204 CRY2 3' GTGTGTGTGGCTATGAG 72210 AATA  
 TTCATAGCCACA GC  
 ||||| ||||| ||  
 GAGTATCGGTGT TG  
 GTG\_  
 GAM1204 CSNK1D 3' CTCGGTTGTAACGGGGCTGGGA 8551 A ACAA\_  
 TTC TAGCC ATAGCTGAG  
 ||| ||||| |||||

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AGG GTCGG  TGTTGGCTC
_  GGCAA
GAM1204 CSNK1D  3' CTCGGTTGTAACGGGGCTGGGA 57407  A  ACAA_
TTC TAGCC  ATAGCTGAG
||| ||||  |||||
AGG GTCGG  TGTTGGCTC
_  GGCAA
GAM1204 CYP1B1  3' CTGTTTTGTGGTTTGA 3654  T  _
TTCA AGCCACAAA TAG
|||| ||||| |||
AGGT TTGGTGTTC GTC
_  T
GAM1204 CYP26A1 3' CTTAGCTGTTTTTTATG 54048  CCAC
CATAG AAATAGCTGAG
|||| |||||
GTATT TTTGTCGATTC
T__
GAM1204 CYP26A1 3' CTTAGCTGTTTTTTATG 5770  CCAC
CATAG AAATAGCTGAG
|||| |||||
GTATT TTTGTCGATTC
T__
GAM1204 CYP7A1  3' GAAGCTTTGGTTATGAA 5761  CAAAT  GAG
TTCATAGCCA AGCT
||||| |||
AAGTATTGGT TCGA
T__ AGG
GAM1204 DBN1 3' CTCAGCTGGCCGGGTTGGAG 55150  A  ACAAA
TTC TAGCC  TAGCTGAG
||| ||||  |||||
GAG GTTGG  GTCGACTC
_  GCCG_
GAM1204 DBN1 3' TTCAGGTCAGGGCTATGGA 55152  ACAAATAG
TTCATAGCC  CTGAG
||||| |||
AGGTATCGG  GACTT
GACTG__
GAM1204 DBN1 3' CTCAGCTGGCCGGGTTGGAG 15284  A  ACAAA
TTC TAGCC  TAGCTGAG
||| ||||  |||||
GAG GTTGG  GTCGACTC
_  GCCG_
GAM1204 DBN1 3' TTCAGGTCAGGGCTATGGA 15285  ACAAATAG
TTCATAGCC  CTGAG
||||| |||
AGGTATCGG  GACTT
GACTG__
GAM1204 DCLRE1C 5' TCAGCTGCGGTTTTGG 42530  T  A AATA
TCA AGCC CA  GCTGA
||| ||| ||  ||||

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			GGT TTGG GT CGACT		
			T C ____		
GAM1204 DES	3'	CTTGGCTGTTGGCAGTGAG	72126	A CAA TG	
		TTCAT GCCA ATAGC AG			
		GAGTG CGGT TGTCG TC			
		A ____ GT			
GAM1204 DGCR2	3'	TCACACTGTGGCTGGAG	17631	A AATAGC	
		TTC TAGCCACA TGA			
		GAG GTCGGTGT ACT			
		____ CAC ____			
GAM1204 DLEC1	3'	CTTGGCTGAGTTGGGTTGGAG	23698	A A A_ TG	
		TTC TAGCC CAA TAGC AG			
		GAG GTTGG GTT GTCG TC			
		____ _ GA GT			
GAM1204 DLST	3'	TTCAGTTAAGTTGCTGT	8649	C AAA	
		ATAGC AC TAGCTGAG			
		TGTCG TG ATTGACTT			
		T A ____			
GAM1204 DSC1	3'	CTTTTTGTGCTGTGGA	17060	C T	
		TTCATAGC ACAAA AG			
		AGGTGTCG TGTTT TC			
		____ T			
GAM1204 DSC1	3'	CTTTTTGTGCTGTGGA	44329	C T	
		TTCATAGC ACAAA AG			
		AGGTGTCG TGTTT TC			
		____ T			
GAM1204 DYRK2	3'	TCAGCTGTGATTATGA	21393	GC AATA	
		TCATA CACA GCTGA			
		AGTAT GTGT CGACT			
		TA ____			
GAM1204 DYRK2	3'	TCAGCTGTGATTATGA	13129	GC AATA	
		TCATA CACA GCTGA			
		AGTAT GTGT CGACT			
		TA ____			
GAM1204 E2F3	3'	TCAGTTTAAGCTATGAA	8702	CACAAAT	
		TTCATAGC AGCTGA			
		AAGTATCG TTGACT			
		AAT ____			
GAM1204 EFNA3	3'	CAGGATTGTGGTTTGGGA	17065	T ATAG	
		TTCA AGCCACAA CTG			

			AGGT TTGGTGTGTT GAC			
			AG__			
GAM1204	EIF2C1	3'	TCAGCTGGGGCTTGAA 24180	T	ACAAA	
			TTCA AGCC TAGCTGA			
			AAGT TCGG GTCGACT			
			G__			
GAM1204	ELMO1	5'	GAATCAGTATTTGTGGTTGGGA 55280	A	G G	
	A		TTC TAGCCACAAATA CTGA			
			AAG GTTGGTGTATTAT GACT			
			G _ AAGA			
GAM1204	ENC1	3'	TTTGCACATTTTGTGGCTGTTG 13286	_	TA__ TGAG	
	AG		TTCA TAGCCACAAA GC			
			GAGT GTCGGTGTTT CG			
			T TACA TTT			
GAM1204	EXTL3	3'	TTTGGCTGGGGGAGTGTGAG 7538	G_	ACAAA TG	
			TTCATA CC TAGC AG			
			GAGTGT GG GTCG TT			
			GA GG__ GT			
GAM1204	FECH	3'	CTTGGTATTTGTGCTGTGAA 3755	C	G TG	
			TTCATAGC ACAAATA C AG			
			AAGTGTCG TGTTTAT G TC			
			_ _GT			
GAM1204	FGFR4	3'	TTTGGCTGAGCCTGGCTGGAG 43354	A	CAAA TG	
			TTC TAGCCA TAGC AG			
			GAG GTCGGT GTCG TT			
			_ CCGA GT			
GAM1204	FGFR4	3'	TTTGGCTGAGCCTGGCTGGAG 8894	A	CAAA TG	
			TTC TAGCCA TAGC AG			
			GAG GTCGGT GTCG TT			
			_ CCGA GT			
GAM1204	FLOT2	3'	CTTGGCAGGGGTGCTGTGAA 15576	C	AAATA TG	
			TTCATAGC AC GC AG			
			AAGTGTCG TG CG TC			
			_ GGGA_ GT			
GAM1204	FZD4	3'	CTTGGCTGTGGGCTTTGGG 24139	T	A AA TG	
			TTCA AGCC CA TAGC AG			
			GGGT TCGG GT GTCG TC			
			T _ _ GT			
GAM1204	GABRE	5'	CTTGGCTGTGGTGCATGGCTGT 41807	_	A_ TG	
	GGA		TCATAGCCA CA ATAGC AG			

			GGTGTCTGGT GT TGTCTG TC		
			AC GG GT		
GAM1204	GFI1	3'	TCAGTAGGGCTGTGAA 17935	ACAAATA	
			TTCATAGCC GCTGA		
			AAGTGTCTGG TGA		
			GA_____		
GAM1204	GIPR	3'	TCAGCCTTGGCTGGAG 3898	A CAAATA	
			TTC TAGCCA GCTGA		
			GAG GTCGGT C		
			TC_____		
GAM1204	GJA1	3'	CTCATGGATTTTTGTGGTGTGG 3901	G TAG _	
			TCATA CCACAAA CT GAG		
			GGTGT GGTGTTT GG CTC		
			TTA TA		
GAM1204	GJB3	5'	CTCAGAGGGTCTGTTGTGAG 43766	C AAATAG	
			TTCATAGC AC CTGAG		
			GAGTGTTG TG GACTC		
			C GGA_____		
GAM1204	GLTSCR1	3'	TTCAGCTGGGTTGCTGG 31680	_ A_	
			CCA CAA TAGCTGAG		
			GGT GTT GTCGACTT		
			C GG		
GAM1204	GM2A	3'	CTCACCTGTGAGCTGTGG 67775	_ AATA C	
			TCATAGC CACA G TGAG		
			GGTGTCTG GTGT C ACTC		
			A _____ C		
GAM1204	GRB10	5'	CTTGAGGCATGTGCGTTATGGA 17978	_ AATAG TG	
			TTCATAGC CACA C AG		
			AGGTATTG GTGT G TC		
			C ACGA_ GT		
GAM1204	GRP58	3'	CTTAGCTGCACTGTTTATGGA 17998	C CAAA	
			TTCATAG CA TAGCTGAG		
			AGGTATT GT GTCGATTC		
			T CAC_		
GAM1204	GTF2H1	3'	TGTTTGTGGTTTGGA 18008	T	
			TTCA AGCCACAAATA		
			AGGT TTGGTGTTTGT		
			_____		
GAM1204	HD	3'	TCAGTTGTTTCTAAGAG 9192	A CCAC	
			TTC TAG AAATAGCTGA		

			GAG ATC TTTGTTGACT		
			A ____		
GAM1204 HGF	3'	GTTTGGCTGTTTGAATAATGGT 94236	_____	TG	
		TATG TAGCCA CAAATAGC AG T			
		ATTGGT GTTTGTCG TT G			
		AATAA GT			
GAM1204 HMGB3	3'	CTCGGCGTTGAGGCTGTGG 18071		A ATA	
		TCATAGCC CAA GCTGAG			
		GGTGTCCG GTT CGGCTC			
		A G__			
GAM1204 HMGN1	3'	GTTACTGTGCTGTGAA 17118		C AA	
		TTCATAGC ACA TAGC			
		AAGTGTCTG TGT ATTG			
		_ C_			
GAM1204 HOXC6	3'	TTAGCTGTATTTGTGGT 15702	_____		
		GCCACAA ATAGCTGA			
		TGGTGTT TGTCGATT			
		TA			
GAM1204 HPS3	3'	TTTAGCTAGAGTGTATGTGAA 50484		GC AAA	
		TTCATA CAC TAGCTGAG			
		AAGTGT GTG ATCGATTT			
		AT AG_			
GAM1204 HR	5'	TGTGCCCTTGGGCTATGGA 17644		A ATA TGAG	
		TTCATAGCC CAA GC			
		AGGTATCCG GTT CG			
		_ CC_ TGTT			
GAM1204 HYAL1	3'	CTCACAATGAGGCTATGAG 52536		A AATAGC	
		TTCATAGCC CA TGAG			
		GAGTATCCG GT ACTC			
		A AAC__			
GAM1204 HYAL1	3'	CTCACAATGAGGCTATGAG 23607		A AATAGC	
		TTCATAGCC CA TGAG			
		GAGTATCCG GT ACTC			
		A AAC__			
GAM1204 IHPK1	3'	GCAGTTCTTGTGCTATGG 95758		C AT AG	
		TCATAGC ACAA AGCTG			
		GGTATCG TGTT TTGAC			
		_ C_ GT			
GAM1204 IL10RA	3'	TTCAGCTGTGTGATTTTGA 59648		T GC AA	
		TTCA A CACA TAGCTGAG			



			AGGT T GTGT GTCGACTT		
			T TA _		
GAM1204	INHBB	3'	CTGTTGGGCTGTGGA 9340	A A	
			TTCATAGCC CAA TAG		
			AGGTGTCGG GTT GTC		
			- -		
GAM1204	INHBB	3'	TTTGA CTGTTTGTGGCTTGG 9346	T	CT
			TCA AGCCACAAATAG GAG		
			GGT TCGGTGTTTGTC TTT		
			- AG		
GAM1204	INPP5A	3'	TTCAGCTGTTGGTCGTTCTGAG 18660	T C A	
			TTCA AGC AC AATAGCTGAG		
			GAGT TTG TG TTGTCGACTT		
			C C G		
GAM1204	INPP5D	3'	CTCAGTTCTTTGGTTGGAA 82808	A	CA T
			TTC TAGCCA AA AGCTGAG		
			AAG GTTGGT TT TTGACTC		
			- - C		
GAM1204	INSRR	3'	TTCAGCTGCAGGAGCTGATGAG 68466	-	CACAAA
			TTCAT AGC TAGCTGAG		
			GAGTA TCG GTCGACTT		
			G AGGAC_		
GAM1204	KCNA7	3'	TGGTTGGGTTGTGAG 49062	ACAAA	TG
			TTCATAGCC TAGC A		
			GAGTGTTGG GTTG T		
			- - - GT		
GAM1204	KRT1	3'	CTCAGTCCCCTGGCTATGA 20388		CAAATA
			TCATAGCCA GCTGAG		
			AGTATCGGT TGA CTC		
			CCCC_		
GAM1204	LDB3	3'	CTTAGATTCTGTGGTTGGAA 76406	A	AATAG
			TTC TAGCCACA CTGAG		
			AAG GTTGGTGT GATTC		
			- CTTA_		
GAM1204	LIM2	3'	CTCAGTTCTGGACTGTGG 47666	-	CAAAT
			TCATAG CCA AGCTGAG		
			GGTGTC GGT TTGACTC		
			A C_		
GAM1204	LPIN1	3'	TTCACGTGCAGTTTGGGGCTGT 67396	A A	_
	GAA		TCATAGCC CAAAT GC TGAG		

			AGTGTCTGG GTTTG CG ACTT		
			G A TGC		
GAM1204	MAD2L2	3'	CTCAAATACTGTGCTGTGAG 20948	C	AA GC
			TTCATAGC ACA TA TGAG		
			GAGTGTCTG TGT AT ACTC		
			_ C_ AA		
GAM1204	MAN1A1	3'	TTTAGTTATTTTAGCTTTTGAA 91905	T_	CAC
			TTCA AGC AAATAGCTGAG		
			AAGT TCG TTTATTGATTT		
			TT AT_		
GAM1204	MAN2A2	3'	CTCTGCTTTGGGTTGTGAG 20395	A	AT T
			TTCATAGCC CAA AGC GAG		
			GAGTGTTGG GTT TCG CTC		
			_ _ T		
GAM1204	MAP2	3'	AGCTGTGGTTGAGGA 48992	A	AATA
			TTC TAGCCACA GCT		
			AGG GTTGGTGT CGA		
			A _ _ _		
GAM1204	MCL1	3'	CTCAGTAATTAGTTATGAA 41716	CACA	A
			TTCATAGC AAT GCTGAG		
			AAGTATTG TTA TGACTC		
			A _ _ A		
GAM1204	MDM4	3'	TCAGCTATTTTCATGGC 9981	C_	
			GCCA AAATAGCTGA		
			CGGT TTTATCGACT		
			AC		
GAM1204	MFAP3	5'	CTTGTTGGGGTCGCTGCGAG 19807	A	C AAA TG
			TTC TAGC AC TAGC AG		
			GAG GTCG TG GTTG TC		
			C C GG_ GT		
GAM1204	MFRP	3'	CTCAGCTGGGGCTCATGG 48705	_	ACAAA
			TCAT AGCC TAGCTGAG		
			GGTA TCGG GTCGACTC		
			C G _ _		
GAM1204	MPP5	3'	CTTAGTTGTATCTCTGTGAA 42486	CCACAA	
			TTCATAG ATAGCTGAG		
			AAGTGTC TGTTGATTC		
			TCTA _		
GAM1204	MPP6	5'	CTCGGCGGCGCCTGTGGCTGAG 33191	A	AATA _
	G		TC TAGCCACA GCTGAG		

			GG GTCGGTGT CGGCTC	
			A CCGCGG	
GAM1204	MSL3L1	3'	CTCAGCTGCTCGCAGGCTGTGA 54365	ACAAA_
	A		TTCATAGCC TAGCTGAG	
			AAGTGTCGG GTCGACTC	
			ACGCTC	
GAM1204	MYO1D	3'	GCAGCCTGTGGCTGTGG 71769	AATA AG
			TCATAGCCACA GCTG	
			GGTGTCGGTGT CGAC	
			C__ GC	
GAM1204	NDUFA5	3'	CTCAGCTGTGATCTTATG 17194	CCACAA
			CATAG ATAGCTGAG	
			GTATT TGTCGACTC	
			CTAG__	
GAM1204	NDUFV1	5'	CTCAGCCTCAGTGCTATGAA 23023	C AAATA
			TTCATAGC AC GCTGAG	
			AAGTATCG TG CGACTC	
			_ ACTC_	
GAM1204	NEB	5'	TTCAGCTGCCTAAGCTGTGGG 15811	CACAAA
			TTCATAGC TAGCTGAG	
			GGGTGTCTG GTCGACTT	
			AATCC_	
GAM1204	NOC4	3'	CTCAGTTGTATGTTGCTAT 20268	C A
			ATAGC ACA ATAGCTGAG	
			TATCG TGT TGTTGACTC	
			T A	
GAM1204	NOVA1	3'	TTTAGCTGTTTGCTCCCATGA 21412	AGCCA
			TCAT CAAATAGCTGAG	
			AGTA GTTTGTCGATTT	
			CCCTC	
GAM1204	NOVA1	3'	TTTAGCTGTTTGCTCCCATGA 10250	AGCCA
			TCAT CAAATAGCTGAG	
			AGTA GTTTGTCGATTT	
			CCCTC	
GAM1204	NUCB1	3'	CTCAGCTGCCTGGGTTGTGG 20527	A AA
			TCATAGCC CA TAGCTGAG	
			GGTGTTGG GT GTCGACTC	
			_ CC	
GAM1204	ONECUT1	3'	CTTGGCTGTTTAGTGGTTTGGA 62134	T _ TG
			TTCA AGCCAC AAATAGC AG	

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AGGT TTGGTG TTTGTCG TC
  _ A GT
GAM1204 OPA1 3' TCGGTTGAGGATATGAA 55534 G A AATA
TTCATA CC CA GCTGA
||||| ||| ||||
AAGTAT GG GT TGGCT
A A ____
GAM1204 OPA1 3' TCGGTTGAGGATATGAA 55543 G A AATA
TTCATA CC CA GCTGA
||||| ||| ||||
AAGTAT GG GT TGGCT
A A ____
GAM1204 OPA1 3' TCGGTTGAGGATATGAA 55552 G A AATA
TTCATA CC CA GCTGA
||||| ||| ||||
AAGTAT GG GT TGGCT
A A ____
GAM1204 OPA1 3' TCGGTTGAGGATATGAA 55561 G A AATA
TTCATA CC CA GCTGA
||||| ||| ||||
AAGTAT GG GT TGGCT
A A ____
GAM1204 OPA1 3' TCGGTTGAGGATATGAA 55570 G A AATA
TTCATA CC CA GCTGA
||||| ||| ||||
AAGTAT GG GT TGGCT
A A ____
GAM1204 OTP 3' CTTGGTTGTTTGTGGT 49498 _ TG
GCCACAAA TAGC AG
||||||| |||| ||
TGGTGTTT GTTG TC
T GT
GAM1204 PCBP1 3' TTCAGCTGTTAATGCTGGGA 20569 A CACA
TTC TAGC AATAGCTGAG
||| |||| |||||||
AGG GTCG TTGTCGACTT
_ TAA_
GAM1204 PCOLN3 3' TTCAGCTGGGCTGGGGTTG 10914 A AA_
TAGCC CA TAGCTGAG
||||| || |||||||
GTTGG GT GTCGACTT
G CGG
GAM1204 PDGFRA 3' TTAGCTGAGGCTGAGAA 20599 A ACAA
TTC TAGCC TAGCTGA
||| |||| |||||||
AAG GTCGG GTCGATT
A A ____
GAM1204 PFN2 3' CTTGGCTGTCTTGTGATGAA 10527 AGC _ TG
TTCAT CACAA ATAGC AG
||||| ||||| |||| ||

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		AAGTA GTGTT TGTCG TC	
		___ C GT	
GAM1204 PFN2	3'	CTTGGCTGTCTTGTGATGAA 53826	AGC _ TG
		TTCAT CACAA ATAGC AG	
		AAGTA GTGTT TGTCG TC	
		___ C GT	
GAM1204 PLAB	3'	CTCAGTTGTCCTGCCCTGTGGA 65854	CCA A_
		TTCATAG CA ATAGCTGAG	
		AGGTGTC GT TGTTGACTC	
		CC_ CC	
GAM1204 PLAU	3'	TTGTGTGTGGGCTGTGAG 68969	_ A
		TTCATAGCC ACA ATAG	
		GAGTGTCCG TGT TGTT	
		G G	
GAM1204 PPP3CA	3'	CTTGGTTGTGGCTTGCTGAA 6270	T__ AATA TG
		TTCA AGCCACA GC AG	
		AAGT TCGGTGT TG TC	
		CGT ___ GT	
GAM1204 PTPRF	3'	TGTTTGTAGGCTGTGG 55269	_
		TCATAGCC ACAAATA	
		GGTGTCCG TGTTTGT	
		A	
GAM1204 PTPRF	3'	TGTTTGTAGGCTGTGG 11107	_
		TCATAGCC ACAAATA	
		GGTGTCCG TGTTTGT	
		A	
GAM1204 RAB4A	3'	CTGTTTTTGGCTGTGAG 15923	C
		TTCATAGCCA AAATAG	
		GAGTGTCCGT TTTGTC	
		T	
GAM1204 RBBP5	3'	CTTAGTTATGTTGCTGGAG 17335	A C AA
		TTC TAGC ACA TAGCTGAG	
		GAG GTCG TGT ATTGATTC	
		_ T _	
GAM1204 RBM8A	3'	CTCAGCTGTTTATAATTGAA 17544	TAGCCAC
		TTCA AAATAGCTGAG	
		AAGT TTTGTCGACTC	
		TAATA_	
GAM1204 RNMT	3'	CAGTTTGGCTGTGGA 13715	CAAAT
		TTCATAGCCA AGCTG	

AGGTGTCGGT TTGAC

GAM1204 RRM2B 3' TTTAGTTGTTAGTTGCTTTGG 67831 T C A  
TCA AGC AC AATAGCTGAG  
||| ||| || |||||  
GGT TCG TG TTGTTGATTT  
T T A

GAM1204 RTN3 3' CTCAGTTATTGAGTTTTTGTGA 73900 CC A\_  
TCATAG AC AATAGCTGAG  
||||| || |||||  
AGTGTT TG TTATTGACTC  
TT AG

GAM1204 RUNX1 3' TTAGCAATGCTGTGAA 8269 CACAA A  
TTCATAGC AT GCTGA  
||||| || ||||  
AAGTGTCTG TA CGATT  
\_\_\_\_\_ A

GAM1204 S100A9 3' CTTGGCTGTGGGGCTAGGG 11430 A ACAA TG  
TC TAGCC ATAGC AG  
|| |||| |||| ||  
GG ATCGG TGTCG TC  
G GG\_\_ GT

GAM1204 SALL2 3' CTCAGCTGGTGGGTATGG 63860 G AAA  
TCATA CCAC TAGCTGAG  
||||| ||| |||||  
GGTAT GGTG GTCGACTC  
G \_\_\_\_\_

GAM1204 SLC1A4 3' GCTGTTTGTGGCTGTTGA 11718 \_  
TCA TAGCCACAAATAGC  
||| |||||  
AGT GTCGGTGTGTTGTCG  
T

GAM1204 SLC21A9 3' TTCAGCTATGACCATCTGTG 23424 CCACAA  
CATAG ATAGCTGAG  
||||| |||||  
GTGTC TATCGACTT  
TACCAG

GAM1204 SLC2A2 5' TCAGCTGCCGCTGAGAA 4422 A CACAAA  
TTC TAGC TAGCTGA  
||| ||| |||||  
AAG GTCG GTCGACT  
A CC\_\_\_\_\_

GAM1204 SLC7A6 3' CTCAGCTGTCAATGGCTTGGA 14303 T CAA  
TTCA AGCCA ATAGCTGAG  
||||| |||||  
AGGT TCGGT TGTCGACTC  
\_ AAC

GAM1204 SLC7A7 5' CTCAGCTAACTTGCTCTGG 14292 T CACAAA  
TCA AGC TAGCTGAG  
||| ||| |||||

GGT TCG ATCGACTC  
C TTCA\_\_  
GAM1204 SMARCC1 3' CTTGGTTAGGATGGCTGGGG 11799 A CAAA TG  
TC TAGCCA TAGC AG  
|| ||||| ||| ||  
GG GTCGGT ATTG TC  
G AGG\_ GT  
GAM1204 SMG1 3' TTCAGTTATTAGTCTGTGAA 30658 CC A  
TTCATAG AC AATAGCTGAG  
||||| || |||||  
AAGTGTC TG TTATTGACTT  
\_ A  
GAM1204 SNAP23 3' GCTTTTGTGGTTGAGG 13813 A T  
TC TAGCCACAAA AGC  
|| ||||| |||  
GG GTTGGTGTTC TCG  
A \_  
GAM1204 SNAP23 3' GCTTTTGTGGTTGAGG 55466 A T  
TC TAGCCACAAA AGC  
|| ||||| |||  
GG GTTGGTGTTC TCG  
A \_  
GAM1204 SPP1 3' CTTTTGTGGTGTGAA 5154 G T  
TTCATA CCACAAA AG  
||||| ||||| ||  
AAGTGT GGTGTTC TC  
\_ T  
GAM1204 SQSTM1 3' TTTAGAGGATGTGGCTGT 14017 AATAG  
ATAGCCACA CTGAG  
||||| |||||  
TGTCGGTGT GATTT  
AGGA\_  
GAM1204 STK11 3' AGCTGTGGCTGTGAG 4845 AATA  
TTCATAGCCACA GCT  
||||| |||  
GAGTGTCGGTGT CGA  
\_\_\_\_\_  
GAM1204 SULT1A3 3' TTCAGCCCAGGAGTTGTGGA 12056 ACAAATA  
TTCATAGCC GCTGAG  
||||| |||||  
AGGTGTTGG CGACTT  
AGGACC\_  
GAM1204 TAF6 5' TCGGCTGCCGCTAGAG 18906 A CACAAA  
TTC TAGC TAGCTGA  
||| ||| |||||  
GAG ATCG GTCGGCT  
\_ CC\_\_\_\_  
GAM1204 TCF4 5' CTTGGCTGTGTGTCTGCGGA 12150 A C AA TG  
TTC TAG CACA TAGC AG  
||| ||| ||| ||| ||

AGG GTC GTGT GTCG TC  
 C T \_ GT  
 GAM1204 TEK 3' TTTAGTTTTGATGAGTTGTGAG 4860 \_ \_ TA  
 TTCATAGC CA CAAA GCTGAG  
 ||||| || ||| |||||  
 GAGTGTG GT GTTT TGATTT  
 A A \_  
 GAM1204 TEM7 3' CTCAGTTACAGGCTGT 39882 ACAA  
 ATAGCC TAGCTGAG  
 |||| | |||||  
 TGTCGG ATTGACTC  
 AC\_  
 GAM1204 THBD 3' TCAGCTAAGCTAGGAA 4495 A CACAAA  
 TTC TAGC TAGCTGA  
 || ||| |||||  
 AAG ATCG ATCGACT  
 G A\_  
 GAM1204 TJP1 5' CTTGGCTGTTGAGCGGCTGGAG 12298 A ACA\_ TG  
 TTC TAGCC AATAGC AG  
 || ||| |||| |  
 GAG GTCGG TTGTG TC  
 \_ CGAC GT  
 GAM1204 TM6SF2 3' TTTAGTCTTGGCTATGG 72365 CAAATA  
 TCATAGCCA GCTGAG  
 ||||| |||||  
 GGTATCGGT TGATTT  
 TC\_  
 GAM1204 TMOD3 3' CTTAGTTATTTAGGGT 27243 AC  
 GCC AAATAGCTGAG  
 || |||||  
 TGG TTTATTGATTC  
 GA  
 GAM1204 TNFAIP1 3' CTTGGTTGGTGCTGGCTGGGA 40922 A CAAA TG  
 TTC TAGCCA TAGC AG  
 || |||| | ||| |  
 AGG GTCGGT GTTG TC  
 \_ CGTG GT  
 GAM1204 TNFAIP2 3' TTTAGTTCCCACTGGCTGTG 20837 CAAAT  
 CATAGCCA AGCTGAG  
 ||||| |||||  
 GTGTGGT TTGATTT  
 CACCC  
 GAM1204 TNFRSF1A 3' TTCAGCTGGAGCTGTGGA 6516 CACAAA  
 TTCATAGC TAGCTGAG  
 |||| | |||||  
 AGGTGTCG GTCGACTT  
 AG\_  
 GAM1204 TXNRD1 3' CTCAGTTATGTGTTTGT 12458 C AA  
 ATAG CACA TAGCTGAG  
 || | || |||||



			TGTT GTGT ATTGACTC		
			T _		
GAM1204	TXNRD1	3'	TTTAGCTGTTTTGTGGT 12462		_
			GCCACAAA TAGCTGAG		
			TGGTGTTT GTCGATTT		
			T		
GAM1204	VIPR2	3'	CTCGGCTGTTCTCCCTGT 12609	CCACA_	
			ATAG AATAGCTGAG		
			TGTC TTGTCGGCTC		
			CCCTCC		
GAM1204	WASF3	3'	GCTGTGTGTTTGTGAA 21827	C AA	
			TTCATAG CACA TAGC		
			AAGTGTT GTGT GTCG		
			T _		
GAM1204	YWHAG	3'	CTCGGCAGGTGGCTGTGG 25019	AAATA	
			TCATAGCCAC GCTGAG		
			GGTGTCGGTG CGGCTC		
			GA_		
GAM1204	ZIC1	5'	CTCAGTTCCTGGCTATGAA 12722	CAAAT	
			TTCATAGCCA AGCTGAG		
			AAGTATCGGT TTGACTC		
			CC_		
GAM1204	ZNF175	5'	CTCGGCTGAAGACGAGGCTGTG 23092	ACAAA_	
	AG		TTCATAGCC TAGCTGAG		
			GAGTGTCGG GTCGGCTC		
			AGCAGAA		
GAM1204	ZNF18	3'	CTCAGCTGTGAATCCTCTGAA 78140	T CCACAA	
			TTCA AG ATAGCTGAG		
			AAGT TC TGTCGACTC		
			C CTAAG_		
GAM1204	ZNF278	3'	CTCAGTTGTGTACATGTGAG 26728	GCCACAA	
			TTCATA ATAGCTGAG		
			GAGTGT TGTTGACTC		
			ACACTG_		
GAM1204	ZNF278	3'	CTCAGTTGTGTACATGTGAG 49435	GCCACAA	
			TTCATA ATAGCTGAG		
			GAGTGT TGTTGACTC		
			ACACTG_		
GAM1204	ZNF278	3'	CTCAGTTGTGTACATGTGAG 49443	GCCACAA	
			TTCATA ATAGCTGAG		

			GAGTGT	TGTTGACTC		
			ACACTG_			
GAM1204	ZNF42	5'	TCACAGTGTGGCTGGGA	12786	A	AATAGC
			TTC TAGCCACA	TGA		
			AGG GTCGGTGT	ACT		
			_ GAC__			
GAM1204	ZNF76	3'	CTCAGGGGCCTGTGGCTGGAG	12809	A	AATAG
			TTC TAGCCACA	CTGAG		
			GAG GTCGGTGT	GA CTC		
			_ CCGGG			
GAM1204	ABCC13	3'	TTTGGCTGGAATGGCTATGG	56996		CAAA TG
			TCATAGCCA	TAGC AG		
			GGTATCGGT	GTCG TT		
			AAG_ GT			
GAM1204	ABIN-2	3'	TTTGGTCCCTTTGGCTATGGA	44210		CAAATA TG
			TTCATAGCCA	GC AG		
			AGGTATCGGT	TG TT		
			TTCCC_ GT			
GAM1204	ACAS2	3'	CTCAAGCCCTGTGGTTGT	37933		AATA _
			ATAGCCACA	GCT GAG		
			TGTTGGTGT	CGA CTC		
			CC_ A			
GAM1204	ACAS2	3'	CTCAAGCCCTGTGGTTGT	57703		AATA _
			ATAGCCACA	GCT GAG		
			TGTTGGTGT	CGA CTC		
			CC_ A			
GAM1204	ACTR1A	3'	TCAGTTAGGGGCTGGAG	62969	A	ACAAA
			TTC TAGCC	TAGCTGA		
			GAG GTCGG	ATTGACT		
			_ GG__			
GAM1204	ADMP	3'	GCACCCTTGTGTTGTGTTATGAA	58868		C CTGAG
			TTCATAGC	ACAAATAG		
			AAGTATTG	TGTTTGT		
			_ CCCACGT			
GAM1204	ARFRP1	3'	TCAGTCTGGCTGTGG	12244		CAAATA
			TCATAGCCA	GCTGA		
			GGTGTCGGT	TGACT		
			C__			
GAM1204	B3GNT1	3'	TTCAAGTGTGTCAGTTGTGG	21662		__
			CCACAA	ATAGCTGAG		

		GGTGTT TGTTGACTT		
		GAC		
GAM1204	B3GNT1	3' TTCAGTTGTCAGTTGTGG 52686	_____	
		CCACAA ATAGCTGAG		
		GGTGTT TGTTGACTT		
		GAC		
GAM1204	BCE-1	5' GTCAGTTTTGTTGTTATGAG 22800	C TA G	
		TTCATAGC ACAA GCTGA		
		GAGTATTG TGTTT TGA		
		T _ GA		
GAM1204	BPESC1	3' TGGTGTGGCTATGAG 41479	AAATA TG	
		TTCATAGCCAC GC A		
		GAGTATCGGTG TG T		
		_____ GT		
GAM1204	C11orf16	5' CTGGGAGTTTGGGGCTGTGG 40218	A AG G	
		TCATAGCC CAAAT CT AG		
		GGTGTCGG GTTTG GG TC		
		G A_ G		
GAM1204	C15orf5	5' CTCAGAATAATGTGGTTGGGGA 48198	A AATAG	
		TTC TAGCCACA CTGAG		
		AGG GTTGGTGT GACTC		
		G AATAA		
GAM1204	C16orf7	3' CTTGGCTGTGGGCTGTGAA 16940	A AA TG	
		TTCATAGCC CA TAGC AG		
		AAGTGTCGG GT GTCG TC		
		_____ GT		
GAM1204	C16orf7	3' TCACCTTGCTGTGG 16943	CAAAT C	
		TCATAGCCA AG TGA		
		GGTGTCGGT TC ACT		
		_____ C		
GAM1204	C1QTNF6	3' CTCAGTTTGCAGTGTGAA 49142	CACAAAT	
		TTCATAGC AGCTGAG		
		AAGTGTCG TTGACTC		
		TCACGT_		
GAM1204	C20orf121	3' TTTGGCTGCTGAGGCTCTGG 44279	T A AA TG	
		TCA AGCC CA TAGC AG		
		GGT TCGG GT GTCG TT		
		C A C_ GT		
GAM1204	C20orf150	3' TCAGCTCGGCTGTGA 65403	ACAAAT	
		TCATAGCC AGCTGA		

			AGTGTCCG	TCGACT		
			C_____			
GAM1204	C20orf18	3'	CTCTGCCTTTGTGGTTGGAG	48342	A	TA T
			TTC TAGCCACAAA GC GAG			
			GAG GTTGGTGTTT CG CTC			
			— C_ T			
GAM1204	C20orf18	3'	CTCTGCCTTTGTGGTTGGAG	48347	A	TA T
			TTC TAGCCACAAA GC GAG			
			GAG GTTGGTGTTT CG CTC			
			— C_ T			
GAM1204	C21orf42	5'	TTCAGTTGTGAAGCTAT	54208	CACAA	
			ATAGC ATAGCTGAG			
			TATCG TGTTGACTT			
			AAG_			
GAM1204	CEBPG	3'	AGCTTGTGGCTTGAA	8406	T	AAT
			TTCA AGCCACA AGCT			
			AAGT TCGGTGT TCGA			
			— —			
GAM1204	CG012	5'	TTCAGCTGTCCAGGTTAT	83229	ACAA	
			ATAGCC ATAGCTGAG			
			TATTGG TGTCGACTT			
			ACC_			
GAM1204	CHERP	3'	TTCAGTTATTTTAGTTGT	21103	CAC	
			ATAGC AAATAGCTGAG			
			TGTTG TTTATTGACTT			
			AT_			
GAM1204	CLONE24945	3'	TTAGCTGAGGCTTTGGA	31626	T	ACAAA
			TTCA AGCC TAGCTGA			
			AGGT TCGG GTCGATT			
			T A_			
GAM1204	CNOT7	3'	TTTAGCTATTTGAGATCGTGGA	25334	AGCCA	
			TTCAT CAAATAGCTGAG			
			AGGTG GTTTATCGATTT			
			CTAGA			
GAM1204	CNOT8	3'	TCAGCTGAGCTGTGAG	16531	CACAAA	
			TTCATAGC TAGCTGA			
			GAGTGTCG GTCGACT			
			A_			
GAM1204	CNR2	3'	CTTGGCTCTGGAGCTATGAA	8454	CA AAT	TG
			TTCATAGC CA AGC AG			

AAGTATCG GT TCG TC  
 AG C\_\_ GT  
 GAM1204 CUGBP2 3' TTTGTTTTTTTGTGCTGTGAG 21631 C T\_ TGAG  
 TTCATAGC ACAA AGC  
 ||||| |||| ||  
 GAGTGTCG TGTTT TTG  
 \_ TT TTT  
 GAM1204 CXorf9 3' CTCAGCTGGAGTGGTTGGGGA 38624 A AAA  
 TTC TAGCCAC TAGCTGAG  
 || ||||| |||||  
 AGG GTTGGTG GTCGACTC  
 G AG\_  
 GAM1204 DEPC-1 3' CTCATGATGTGGCTGTTGG 57547 \_ AATAGC  
 TCA TAGCCACA TGAG  
 || ||||| ||||  
 GGT GTCGGTGT ACTC  
 T AGT\_\_  
 GAM1204 DKFZP434B1727 3' CCCAGTGTGTTGTGGTGGTGGGA 49564 A G AG  
 TTCAT GCCACAAATA CTG  
 |||| ||||| ||||  
 AGGTG TGGTGTGTTGT GAC  
 G \_ CCT  
 GAM1204 DKFZP434G156 3' CTTGGCTATTGCAGCTGTGG 69781 CACA TG  
 TCATAGC AATAGC AG  
 ||||| |||| ||  
 GGTGTCG TTATCG TC  
 ACG\_ GT  
 GAM1204 DKFZP434G156 3' TGTTTGGGTTGTGGA 69784 A  
 TTCATAGCC CAAATA  
 ||||| ||||  
 AGGTGTTGG GTTTGT  
 \_  
 GAM1204 DKFZp547M236 3' TTTAGTTAAACGTGTCTGTGAA 38040 C AAA  
 TTCATAG CAC TAGCTGAG  
 ||||| || |||||  
 AAGTGTC GTG ATTGATTT  
 T CAA  
 GAM1204 DKFZP564I052 5' TTCAGCTGTTATAAACTGTGA 66724 CCACA  
 TCATAG AATAGCTGAG  
 |||| |||||  
 AGTGTC TTGTCGACTT  
 AAATA  
 GAM1204 DKFZP564O0423 5' CTTGGCTGTGTGTGCTGATGG 91688 \_ C A TG  
 TCAT AGC ACA ATAGC AG  
 ||| ||| || |||| ||  
 GGTA TCG TGT TGTCG TC  
 G \_ G GT  
 GAM1204 DKFZP566I1024 3' CTCAGCCAGTTGCTGTGGA 70100 C AAATA  
 TTCATAGC AC GCTGAG  
 ||||| || ||||

AGGTGTCG TG CGACTC  
 T AC\_\_\_  
 GAM1204 DKFZP566J091 3' CTCAAGGTCATTGTGGCTCTGG 48121 T ATA \_\_\_  
 TCA AGCCACAA GCT GAG  
 ||| ||||| ||| |||  
 GGT TCGGTGTT TGG CTC  
 C AC\_ AA  
 GAM1204 DKFZP566K0524 3' CTTGGCTATTGTTG 69350 CA TG  
 TAGCCA AATAGC AG  
 ||||| ||||| ||  
 GTTGGT TTATCG TC  
 \_\_\_ GT  
 GAM1204 DKFZp761D112 3' CTTTCTATATTGTGGTTATGG 50189 \_ CT  
 TCATAGCCACAA ATAG GAG  
 ||||| ||||| ||| |||  
 GGTATTGGTGT TATC TTC  
 A T\_  
 GAM1204 DKFZp761K1824 3' TTTGGTTATGTCTAGCTGTGAA 34208 CACAA TG  
 TTCATAGC ATAGC AG  
 ||||| ||||| ||  
 AAGTGTG TATTG TT  
 ATCTG GT  
 GAM1204 DPCR1 3' TTTGGCTTGCTGGGTTGTGG 55126 A AAT TG  
 TCATAGCC CA AGC AG  
 ||||| || ||| ||  
 GGTGTTGG GT TCG TT  
 \_ CGT GT  
 GAM1204 ENPP4 3' ATCGTGATTGGTGGTTATGAG 30046 A A T G  
 TTCATAGCCAC AAT GC GA  
 ||||| ||| ||| ||  
 GAGTATTGGTG TTA TG CT  
 G G \_ AT  
 GAM1204 ENPP4 3' TATTTGTGGTTGTTGAG 30048 \_  
 TTCA TAGCCACAAATA  
 ||| ||||| |||||  
 GAGT GTTGGTGT TAT  
 T  
 GAM1204 ESPL1 5' TTCAGCTATGTCAGCTGGGG 24462 A CACAA  
 TC TAGC ATAGCTGAG  
 || ||| ||||| |||||  
 GG GTCG TATCGACTT  
 G ACTG\_  
 GAM1204 FLJ10055 3' TGGCTGTGGCTGGAA 35778 A AATA TG  
 TTC TAGCCACA GC A  
 ||| ||||| || |  
 AAG GTCGGTGT CG T  
 \_ \_ GT  
 GAM1204 FLJ10094 3' TTTAGTTATATCTGTGGC 35811 A\_  
 GCCACA ATAGCTGAG  
 ||||| ||||| |||||

		CGGTGT TATTGATTT		
		CTA		
GAM1204	FLJ10420	3' CTCAGCTGGCCTGTGTTTGG	36108	TAGC AA_
		TCA CACA TAGCTGAG		
		GGT GTGT GTCGACTC		
		TT__ CCG		
GAM1204	FLJ10450	3' TCAGCTGGTTGCTTGAA	36121	T C AAA
		TTCA AGC AC TAGCTGA		
		AAGT TCG TG GTCGACT		
		_ T _		
GAM1204	FLJ10483	5' TTTAGCTTGCAGTTATGAA	36177	CA AAT
		TTCATAGC CA AGCTGAG		
		AAGTATTG GT TCGATTT		
		AC _		
GAM1204	FLJ10607	3' CTCAGCCTCCCATGTGGCTGGG	77112	A AATA_
	A	TTC TAGCCACA GCTGAG		
		AGG GTCGGTGT CGACTC		
		_ ACCCTC		
GAM1204	FLJ10901	3' CTCAGCTACAGAGCTGGAA	36820	A CACAAA
		TTC TAGC TAGCTGAG		
		AAG GTCG ATCGACTC		
		_ AGAC_		
GAM1204	FLJ10971	3' TATTTGTTGTTGTGAG	36928	C
		TTCATAGC ACAAATA		
		GAGTGTTG TGTTTAT		
		T		
GAM1204	FLJ11274	5' TTTGTTGTCTAGTGGTTGTGG	37203	AA_ TGAG
		TCATAGCCAC ATAGC		
		GGTGTGGTG TGTTG		
		ATC TTT		
GAM1204	FLJ11275	3' AAAGAAATATTTATGGTTATGG	37204	C GCTGAG
	A	TTCATAGCCA AAATA		
		AGGTATTGGT TTTAT		
		A AAAGAAAT		
GAM1204	FLJ12056	3' CTCATCTTCTGGCTGTGGA	46254	CAAAT C
		TTCATAGCCA AG TGAG		
		AGGTGTCGGT TC ACTC		
		CT__ T		
GAM1204	FLJ12439	3' TTTGGTTAGGATGGCTTGAA	43573	T CAAA TG
		TTCA AGCCA TAGC AG		

		AAGT TCGGT ATTG TT	
		_ AGG_ GT	
GAM1204 FLJ12587	3'	TTCAGCTTTGCAGTGGTTTGTG 42501	_ AAAT_
	G	TCATAG CCAC AGCTGAG	
		GGTGTT GGTG TCGACTT	
		T ACGTT	
GAM1204 FLJ12666	3'	CTTGGGGATTCTGGCTGTGAA 44768	CA AG TG
		TTCATAGCCA AAT C AG	
		AAGTGTCGGT TTA G TC	
		C_ GG GT	
GAM1204 FLJ12747	5'	TTTGGTTGTCCTGGCTTTGGA 49732	T CAA TG
		TTCA AGCCA ATAGC AG	
		AGGT TCGGT TGTTG TT	
		T CC_ GT	
GAM1204 FLJ13231	3'	CTTAGCTGTTGTGAATAGAG 43549	A GC A
		TTC TA CACAA TAGCTGAG	
		GAG AT GTGTT GTCGATTC	
		_ AA _	
GAM1204 FLJ13330	3'	CTCGGCTATTTGCACTGATGA 46974	AGCCA
		TCAT CAAATAGCTGAG	
		AGTA GTTTATCGGCTC	
		GTCAC	
GAM1204 FLJ13725	5'	CAGGTTGTGGCTGTGGA 68287	ATAG
		TTCATAGCCACAA CTG	
		AGGTGTCGGTGTT GAC	
		G__	
GAM1204 FLJ13782	3'	CTCAGCTGTTTCTCCTTGAG 46166	T CCAC
		TTCA AG AAATAGCTGAG	
		GAGT TC TTTGTCGACTC	
		_ CTC_	
GAM1204 FLJ14146	3'	CTTGCTGCCTCGGTTCTGAG 45242	T ACAAA TG
		TTCA AGCC TAGC AG	
		GAGT TTGG GTCG TC	
		C CTCC_ GT	
GAM1204 FLJ14154	3'	TTCAGCTGACCTGCTGAGGA 45822	A CACAAA
		TTC TAGC TAGCTGAG	
		AGG GTCG GTCGACTT	
		A TCCA__	
GAM1204 FLJ14326	3'	CTTAGCTGCTGTGGCAATGG 49806	A AA
		TCAT GCCACA TAGCTGAG	



			GGTA CGGTGT GTCGATTC		
			A C_		
GAM1204	FLJ14327	3'	TCAGGCTGGTTGTGAA 46146	CAAATA _	
			TTCATAGCCA GC TGA		
			AAGTGTGGT CG ACT		
			_____ G		
GAM1204	FLJ14642	3'	TCAGTTTTGCTATGAG 51508	CACAAAT	
			TTCATAGC AGCTGA		
			GAGTATCG TTGACT		
			TT_____		
GAM1204	FLJ14810	3'	TCAGCCTGGCTGTGG 51631	CAAATA	
			TCATAGCCA GCTGA		
			GGTGTGGT CGACT		
			C_____		
GAM1204	FLJ14936	3'	TTTGGTTTGTGTGGTTGGAA 51709	A AT TG	
			TTC TAGCCACAA AGC AG		
			AAG GTTGGTGT TTG TT		
			_ GT GT		
GAM1204	FLJ20070	5'	CTCGGGAGGAGTGGTTGTGG 34475	AAATAG	
			TCATAGCCAC CTGAG		
			GGTGTGGTG GGCTC		
			AGGAG_		
GAM1204	FLJ20244	5'	TTCGGTTTTCTGTGGCTACGAG 34780	A AAT	
			TTC TAGCCACA AGCTGAG		
			GAG ATCGGTGT TTGGCTT		
			C CTT		
GAM1204	FLJ20275	3'	CTCGGTAGGTGGCTAT 34822	AAATA	
			ATAGCCAC GCTGAG		
			TATCGGTG TGGCTC		
			GA_____		
GAM1204	FLJ20371	3'	TGGGACTATTTGTGGCATGGA 35068	A _ GAG	
			TTCAT GCCACAAATAG CT		
			AGGTA CGGTGTTTATC GG		
			_ A GT		
GAM1204	FLJ20396	3'	CTTAGCTGTTTGTTTTGATG 35120	AGCC	
			CAT ACAAATAGCTGAG		
			GTA TGTTTGTGCGATTC		
			GTTT		
GAM1204	FLJ20436	5'	CTCCTGAGGTTTTGGTTATGAA 35168	C AGCT_	
			TTCATAGCCA AAAT GAG		

AAGTATTGGT TTTG CTC  
 \_ GAGTC  
 GAM1204 FLJ20628 3' TTAGCTATTACTATGA 35476 CCACA  
 TCATAG AATAGCTGA  
 ||||| |||||  
 AGTATC TTATCGATT  
 A\_\_\_\_  
 GAM1204 FLJ20637 3' CTCAGTCTCTAATTGGCTGTGA 35481 CAAAT \_  
 G TTCATAGCCA AG CTGAG  
 ||||| || |||||  
 GAGTGTGGT TC GACTC  
 TAATC T  
 GAM1204 FLJ20666 3' TTCAGTTATACTTGTG 35513 \_  
 CACAA ATAGCTGAG  
 ||||| |||||  
 GTGTT TATTGACTT  
 CA  
 GAM1204 FLJ20666 3' TTCAGTTATACTTGTG 37090 \_  
 CACAA ATAGCTGAG  
 ||||| |||||  
 GTGTT TATTGACTT  
 CA  
 GAM1204 FLJ20725 3' TGT TTGTGGCTGGAG 35614 A  
 TTC TAGCCACAAATA  
 ||| |||||  
 GAG GTCGGTGTTTGT  
 \_  
 GAM1204 FLJ20811 3' TTCAGCTGCCTGCTGTGGA 67127 CACAAA  
 TTCATAGC TAGCTGAG  
 ||||| |||||  
 AGGTGTCG GTCGACTT  
 TCC\_\_\_\_  
 GAM1204 FLJ22056 3' CTTGGGGTGTTGTGGCTGGGAA 42534 A ATAG TG  
 TTC TAGCCACAA C AG  
 ||| ||||| | ||  
 AAG GTCGGTGTT G TC  
 G GTGG GT  
 GAM1204 FLJ22104 3' CTCAGCTGTTTAACTTATG 43349 CCAC  
 CATAG AAATAGCTGAG  
 ||||| |||||  
 GTATT TTTGTCGACTC  
 CAA\_  
 GAM1204 FLJ22457 5' ACAGAGTTGTGGCTGGAG 46082 A ATAG AG  
 TTC TAGCCACAA CTG  
 ||| ||||| |||  
 GAG GTCGGTGTT GAC  
 \_ GA\_\_ AC  
 GAM1204 FLJ22555 3' TTAGCAGTTGCTGTGAA 44513 C AAATA  
 TTCATAGC AC GCTGA  
 ||||| || |||||

			AAGTGTCG TG CGATT	
			T A_____	
GAM1204	FLJ23018	3'	TTCAGCTGTTTTCTGT 45656	CCAC
			ATAG AAATAGCTGAG	
			TGTC TTTGTCGACTT	
			CT__	
GAM1204	FLJ23074	3'	CTGTTTTGGTTATGAA 46816	C
			TTCATAGCCA AAATAG	
			AAGTATTGGT TTTGTC	
			—	
GAM1204	FLJ23590	3'	TTCAGCTATTTTAAAATGTG 45024	GCCAC_
			CATA AAATAGCTGAG	
			GTGT TTTATCGACTT	
			AAAATT	
GAM1204	FLJ32356	3'	CTCAGCTGGTGGGCTG 58360	A AA
			TAGCC CA TAGCTGAG	
			GTCGG GT GTCGACTC	
			_ G_	
GAM1204	FLJ32919	3'	CTTAGCTGGGGCTGTG 58076	ACAAA
			CATAGCC TAGCTGAG	
			GTGTCGG GTCGATTC	
			G_____	
GAM1204	FOXP1	5'	CTTTTATGGCTGTGAG 51066	C T
			TTCATAGCCA AAA AG	
			GAGTGTCGGT TTT TC	
			A T	
GAM1204	G4	3'	TTAGGGTGTGTTGTGTTTATGGA 90996	C G GAG
			TTCATAG CACAAATA CT	
			AGGTATT GTGTTTGT GG	
			T G ATTT	
GAM1204	GBTS1	3'	CTCAGTTCCTCGCTGGCTGT 59054	CAAAT_
			ATAGCCA AGCTGAG	
			TGTCGGT TTGACTC	
			CGCTCC	
GAM1204	GL009	3'	TTCAGCTGTTTGAAGTTG 72637	CA
			TAGC CAAATAGCTGAG	
			GTTG GTTTGTCGACTT	
			AA	
GAM1204	GMPPB	5'	CTTAGTGGGGGGCTATGG 95736	ACAAATA
			TCATAGCC GCTGAG	

GGTATCGG TGATTC  
GGGG\_\_\_\_  
GAM1204 GOLGA1 3' TCAGGTGTAGCTGTGG 9093 CACAA G  
TCATAGC ATA CTGA  
||||| ||| |||  
GGTGTCTG TGT GACT  
A\_\_\_\_ G  
GAM1204 H2BFQ 3' TTCAGCTGTTTTTGGCTAAGG 59361 A C  
TC TAGCCA AAATAGCTGAG  
|| ||||| |||||  
GG ATCGGT TTTGTCTGACTT  
A T  
GAM1204 HCA4 3' GTCAGCATGGTGGTTGTGG 77590 AAATA G  
TCATAGCCAC GCTGA  
||||||| |||||  
GGTGTGGTG C GACT  
GTA\_\_ GT  
GAM1204 HNT 5' TTCGGGGAAGTTGTGGCTGTCTG 33263 \_ ATAG\_  
A TC ATAGCCACAA CTGAG  
|| ||||| |||||  
AG TGTCGGTGTT GGCTT  
C GAAGG  
GAM1204 HRIHFB2436 3' AGCAGCCATTTGTGTTGTGAA 26790 C A AG  
TTCATAGC ACAAAT GCTG  
||||||| ||||| |||||  
AAGTGTG TGT TTA CGAC  
\_ C GAT  
GAM1204 HSMPP8 3' TCAGTCTGGGTTATGGA 93484 A AATA  
TTCATAGCC CA GCTGA  
||||||| || |||||  
AGGTATTGG GT T GACT  
\_ C\_\_\_\_  
GAM1204 HSPC121 3' TTCAGCTATTGCTTGTGAA 59761 \_ CACA  
TTCATA GC AATAGCTGAG  
||||| || |||||  
AAGTGT CG TTATCGACTT  
T \_\_\_\_  
GAM1204 IMAGE:4907098 3' CTCAGCTATTTGGGAGGCTG 91657 A\_\_\_\_  
TAGCC CAAATAGCTGAG  
||||| |||||  
GTCGG GTTTATCGACTC  
AGG  
GAM1204 KIAA0090 3' TTAGCTGAGGCTTGAG 88452 T ACAA  
TTCA AGCC TAGCTGA  
||| ||| |||||  
GAGT TCGG GTCGATT  
\_ A\_\_\_\_  
GAM1204 KIAA0276 3' CTAGTTGTGGCTTGAA 70964 T A  
TTCA AGCCACAA TAG  
||||| ||||| |||

		AAGT TCGGTGTT ATC	
		— G	
GAM1204 KIAA0284	3'	TCGGCAGTGGCTGTG 63117	AAATA
		CATAGCCAC GCTGA	
		GTGTCGGTG CGGCT	
		A___	
GAM1204 KIAA0319	3'	CTTGATGGCGTGGTTATGA 29035	AAA G TG
		TCATAGCCAC TA C AG	
		AGTATTGGTG GT G TC	
		CG_ A GT	
GAM1204 KIAA0447	3'	CTCAGCCTCCCATGTGGCTGGA 71670	A AATA__
A		TTC TAGCCACA GCTGAG	
		AAG GTCGGTGT CGACTC	
		— ACCCTC	
GAM1204 KIAA0450	5'	CTCAGCTGTGGGAGGCATGG 27637	A ACAA
		TCAT GCC ATAGCTGAG	
		GGTA CGG TGTCGACTC	
		— AGGG	
GAM1204 KIAA0450	5'	TTCGTGCATGTGGCTGT 27655	AATA _
		ATAGCCACA GC TGAG	
		TGTCGGTGT CG GCTT	
		A___ T	
GAM1204 KIAA0513	3'	CTTGCTTTGGCTGTTGG 28357	_ CAAAT TG
		TCA TAGCCA AGC AG	
		GGT GTCGGT TCG TC	
		T T___ GT	
GAM1204 KIAA0523	3'	CTCACAAGTGAGGCTGTGGA 67736	A AATAGC
		TTCATAGCC CA TGAG	
		AGGTGTCGG GT ACTC	
		A GAAC__	
GAM1204 KIAA0630	3'	CTTAATATTGGGCTATGGA 89391	A A GC
		TTCATAGCC CAA TA TGAG	
		AGGTATCGG GTT AT ATTC	
		— _ A_	
GAM1204 KIAA0648	3'	TTCGGTTCCTGCTATGAA 82660	CACAAAT
		TTCATAGC AGCTGAG	
		AAGTATCG TTGGCTT	
		TCCC__	
GAM1204 KIAA0711	3'	AAGAGTCTGTGGTTATGAG 29512	AATA GAG
		TTCATAGCCACA GCT	

GAGTATTGGTGT TGA  
 C\_\_\_ GAAA  
 GAM1204 KIAA0759 3' TTCAGCTGCCTCAGCTGGGA 67331 A CACAAA  
 TTC TAGC TAGCTGAG  
 ||| ||| |||||  
 AGG GTCG GTCGACTT  
 \_ ACTCC\_  
 GAM1204 KIAA0773 3' TGGTGTGGCTGTGGA 28062 AAATA TG  
 TTCATAGCCAC GC A  
 ||||| || |  
 AGGTGTCGGTG TG T  
 \_\_\_\_\_ GT  
 GAM1204 KIAA0831 3' CTCAGCTGCCCAGGCTGGAG 29971 A ACAAA  
 TTC TAGCC TAGCTGAG  
 ||| ||| |||||  
 GAG GTCGG GTCGACTC  
 \_ ACCC\_  
 GAM1204 KIAA0893 3' TCAGTTGTTGGTGTGC 30361 \_ A  
 GC CAC AATAGCTGA  
 || ||| |||||  
 CG GTG TTGTTGACT  
 T G  
 GAM1204 KIAA0894 3' CTTGGTTAGTGTGAGTGTGTTG 29704 \_ AAA\_\_\_ TG  
 TGG CATAGC CAC TAGC AG  
 ||||| ||| ||| ||  
 GTGTTG GTG ATTG TC  
 T AGTGTG GT  
 GAM1204 KIAA0979 3' AAAGATTTGTTTGTGTTTATGA 30438 C CTGAG  
 A TTCATAG CACAAATAG  
 ||||| |||||  
 AAGTATT GTGTTTGT  
 T TAGAAAT  
 GAM1204 KIAA1045 3' CTCGGCTGTACTGAGTTGGGAA 71050 A \_ CAA  
 TTC TAGC CA ATAGCTGAG  
 ||| ||| || |||||  
 AAG GTTG GT TGTCGGCTC  
 G A CA\_  
 GAM1204 KIAA1055 3' TCAGTTGTCCTGTGAGC 66069 \_ A\_  
 GC CACA ATAGCTGA  
 || ||| |||||  
 CG GTGT TGTTGACT  
 A CC  
 GAM1204 KIAA1056 3' CTCAGGACTGTGGCTGGAG 29694 A AATAG  
 TTC TAGCCACA CTGAG  
 ||| ||||| |||  
 GAG GTCGGTGT GACTC  
 \_ CAG\_  
 GAM1204 KIAA1068 3' TGGTGTGGTTGTGGA 31042 AAATA TG  
 TTCATAGCCAC GC A  
 ||||| || |

		AGGTGTTGGTG	TG T	
		_____ GT		
GAM1204	KIAA1078	3' TTCAGCTATTTAATTATGG	65125	CCAC
		TCATAG AAATAGCTGAG		
		GGTATT TTTATCGACTT		
		AA__		
GAM1204	KIAA1089	3' CTTGGCTGCTGTGCTGGGA	68843	A C AA TG
		TTC TAGC ACA TAGC AG		
		AGG GTCG TGT GTCG TC		
		_ _ C_ GT		
GAM1204	KIAA1096	3' TTTAGCTGGTGTTTATGAA	68531	C AAA
		TTCATAG CAC TAGCTGAG		
		AAGTATT GTG GTCGATTT		
		T ____		
GAM1204	KIAA1136	3' TTAGTTTTGGCTGTGG	91323	CAAAT
		TCATAGCCA AGCTGA		
		GGTGTCGGT TTGATT		
		T____		
GAM1204	KIAA1155	3' TTCAGTATGTGGCTGTGG	62244	AATA
		TCATAGCCACA GCTGAG		
		GGTGTCGGTGT TGA CTT		
		A__		
GAM1204	KIAA1163	3' GCAGTTGTGGTTGTGAG	78902	ATA
		TTCATAGCCACAA GC		
		GAGTGTTGGTGTT CG		
		GA_		
GAM1204	KIAA1171	3' CTCAGTTTCCCCAGCTGTGAA	87980	CACAAAT
		TTCATAGC AGCTGAG		
		AAGTGTCG TTGACTC		
		ACCCCT_		
GAM1204	KIAA1209	3' TTTGGTTATATTTGTGGT	60763	__ TG
		GCCACAAATA GC AG		
		TGGTGTTTAT TG TT		
		AT GT		
GAM1204	KIAA1210	3' TTCAGTTATTGTCACTCTGAG	96337	T CC A
		TTCA AG ACAA TAGCTGAG		
		GAGT TC TGTT ATTGACTT		
		C AC _		
GAM1204	KIAA1266	3' TGTTTGTGGGTATGAG	66132	G
		TTCATA CCACAAATA		

GAGTAT GGTGTTTGT  
 G  
 GAM1204 KIAA1266 3' GTGTTTTGTGGTTGGAG 66127 A TA  
 TTC TAGCCACAAA GC  
 ||| ||||| ||  
 GAG GTTGGTGTTT TG  
 \_ TG  
 GAM1204 KIAA1277 3' CTTAGCTGGAGTTATGGA 64455 CACAAA  
 TTCATAGC TAGCTGAG  
 ||||| |||||  
 AGGTATTG GTCGATTC  
 AG\_\_\_\_  
 GAM1204 KIAA1297 5' TTCAGCTCAGACAGCTATGGA 72193 CACAAAT  
 TTCATAGC AGCTGAG  
 ||||| |||||  
 AGGTATCG TCGACTT  
 ACAGAC\_  
 GAM1204 KIAA1318 3' TTCAGGTGGTGGGGTTATGG 67310 ACAA G  
 TCATAGCC TA CTGAG  
 ||||| || |||||  
 GGTATTGG GT GACTT  
 GGTG\_ G  
 GAM1204 KIAA1323 3' TTTAGTTGTTTGTGTTTGC 63048 \_\_\_\_  
 GC CACAAATAGCTGAG  
 || |||||  
 CG GTGTTTGTGATT  
 TTT  
 GAM1204 KIAA1395 3' CTCAGCTGTCTGTGCTGCGAG 76085 A C A  
 TTC TAGC ACA ATAGCTGAG  
 ||| ||| ||| |||||  
 GAG GTCG TGT TGTCGACTC  
 C \_ C  
 GAM1204 KIAA1431 3' TTTAGCTATTGACTATGG 63001 CCACA  
 TCATAG AATAGCTGAG  
 ||||| |||||  
 GGTATC TTATCGATT  
 AG\_\_\_\_  
 GAM1204 KIAA1432 5' TTCAGCTATTGATAAGCTTGGA 66753 T CACA\_  
 TTCA AGC AATAGCTGAG  
 ||||| ||| |||||  
 AGGT TCG TTATCGACTT  
 \_ AATAG  
 GAM1204 KIAA1462 3' TTCGTTTTTTGTGGCTGGAA 91392 A T T  
 TTC TAGCCACAAA AGC GAG  
 ||| ||||| ||| |||  
 AAG GTCGGTGTTT TTG CTT  
 \_ T \_  
 GAM1204 KIAA1486 3' TTTGGGTACGTGGTTGTGGA 67389 AAA G TG  
 TTCATAGCCAC TA C AG  
 ||||| ||| ||



	AGGTGTTGGTG AT G TT	
	C__ G GT	
GAM1204 KIAA1500 3'	ATTTGTGTGTTATGAA 64117	_
	TTCATAGC CACAAAT	
	AAGTATTG GTGTTTA	
	T	
GAM1204 KIAA1500 3'	TTATATGCTGGCTGTGAA 64124	_ A
	TTCATAGCCA CA ATAG	
	AAGTGTCGGT GT TATT	
	C A	
GAM1204 KIAA1553 3'	TTTAGTTGTTTGT TTTTGGGA 91924	TAGCC
	TTCA ACAAATAGCTGAG	
	AGGT TGT TTTGTTGATTT	
	TTTT_	
GAM1204 KIAA1559 3'	CTCAGTTTCTAGCTGGCTGT 73062	CAAAT_
	ATAGCCA AGCTGAG	
	TGTCGGT TTGACTC	
	CGATCT	
GAM1204 KIAA1580 5'	TTTGGTGGTGGTGGCTGTTGG 69451	_ AAATA TG
	TCA TAGCCAC GC AG	
	GGT GTCGGTG TG TT	
	T GTGG_ GT	
GAM1204 KIAA1634 3'	TTCAGTTATTTAATTATGAA 63396	CCAC
	TTCATAG AAATAGCTGAG	
	AAGTATT TTTATTGACTT	
	AA_	
GAM1204 KIAA1656 3'	TTTGGCTGTTGTGACTAGAG 65809	A C A TG
	TTC TAG CACAA TAGC AG	
	GAG ATC GTGTT GTCG TT	
	_ A _ GT	
GAM1204 KIAA1674 3'	CTTAGTTATTTGAGTGTGG 68778	_____
	CCACA AATAGCTGAG	
	GGTGT TTATTGATTC	
	GAGT	
GAM1204 KIAA1679 3'	AGTCTGTGGTTGTGAG 70146	AATA
	TTCATAGCCACA GCT	
	GAGTGTGGTGT TGA	
	C__	
GAM1204 KIAA1701 3'	TTTGGCTACATCTGGCTGGAG 67821	A CAAA TG
	TTC TAGCCA TAGC AG	

		GAG GTCGGT ATCG TT	
		CTAC GT	
GAM1204 KIAA1805	3'	TTCAGCTGTTTGTGTAAGGCTG 79970	_____
		TGA CATAGCC ACAAATAGCTGAG	
		GTGTCGG TGTTTGTCTGACTT	
		AATG	
GAM1204 KIAA1814	3'	TTTAGCTGGACTCGGCTGTG 70365	ACAAA
		CATAGCC TAGCTGAG	
		GTGTCGG GTCGATTT	
		CTCAG	
GAM1204 KIAA1822	3'	CTCAGGGAGGATGGCTGTGAG 67565	CAAATAG
		TTCATAGCCA CTGAG	
		GAGTGTCTGGT GACTC	
		AGGAGG_	
GAM1204 KIAA1853	3'	TTTGGATATTTGGGTTATGG 69400	A TAG_TG
		TCATAGCC CAAA C AG	
		I	
		GGTATTGG GTTT G TT	
		TATA GT	
GAM1204 KIAA1939	3'	CTCAGCTGTCTGCTGTTTAT 45764	C CAA
		ATAG CA ATAGCTGAG	
		TATT GT TGTCGACTC	
		T AC_	
GAM1204 KIAA1950	3'	TTCAGTTATTTATAGCTGGAG 92600	A CAC
		TTC TAGC AAATAGCTGAG	
		GAG GTCG TTTATTGACTT	
		ATA	
GAM1204 KIAA1966	3'	TTCAGCTGTCTGCCTATGAA 55896	CCA A
		TTCATAG CA ATAGCTGAG	
		AAGTATC GT TGTCGACTT	
		C_ C	
GAM1204 KIAA1987	3'	GAAGCAGTGTGCTGTGAA 88016	C AATA GAG
		TTCATAGC ACA GCT	
		AAGTGTCTG TGT CGA	
		GA_ AGT	
GAM1204 KLHL6	3'	TTCAGCTCTCTGCTGTGGA 55309	CACAAAT
		TTCATAGC AGCTGAG	
		AGGTGTCTG TCGACTT	
		TCTC_	
GAM1204 KRTAP9-4	3'	CTTAGCTATATGTTTCTG 52599	CC A
		TAG ACA ATAGCTGAG	

		GTC TGT TATCGATTC		
		TT A		
GAM1204	LY75	3' GCACTAATGTGGTTATGGA	9839	AA C AG
		TTCATAGCCACA TAG TG		
		AGGTATTGGTGT ATC AC		
		A_ _ GT		
GAM1204	MGC12904	5' CTTGGGATCTTGTGCTGTGAA	48332	C ATAG TG
		TTCATAGC ACAA C AG		
		AAGTGTCG TGTT G TC		
		_ CTAG GT		
GAM1204	MGC15906	5' CTCGGACTGTGGCTGGGG	51817	A AATAG
		TC TAGCCACA CTGAG		
		GG GTCGGTGT GGCTC		
		G CA_		
GAM1204	MGC16025	3' TTCAGCTGTGTGCCTGTGAG	51926	C AA
		TTCATAG CACA TAGCTGAG		
		GAGTGTC GTGT GTCGACTT		
		C _		
GAM1204	MGC19556	5' TGGGTTGGGCTGTGAA	53233	A ATAG TG
		TTCATAGCC CAA C A		
		AAGTGTCGG GTT G T		
		_ G_ GT		
GAM1204	MGC3040	3' CTGATTGTGGCTGAGAG	66845	A A
		TTC TAGCCACAA TAG		
		GAG GTCGGTGTT GTC		
		A A		
GAM1204	MGC4643	3' CTTAGCTCCTGATTGGTTGTG	51154	CAAAT_
		CATAGCCA AGCTGAG		
		GTGTTGGT TCGATTC		
		TAGTCC		
GAM1204	MGC4796	3' CTCAGCTGTCCAGCGCTGAGG	61485	A CACAA
		TC TAGC ATAGCTGAG		
		GG GTCG TGTCGACTC		
		A CGACC		
GAM1204	MGC8721	3' TTCAGTTTTAGGTGGTTGT	60359	AAAT
		ATAGCCAC AGCTGAG		
		TGTTGGTG TTGACTT		
		GATT		
GAM1204	MGC8974	3' TTCTACTTTTGTGGTGTGG	53635	G T CT
		TCATA CCACAAA AG GAG		

			GGTGT GGTGTTT TC CTT		
			— — AT		
GAM1204 MIDORI	3'	CTCATCTGGTGTGGTTGGAG	73785	A	AA C
		TTC TAGCCACA TAG TGAG			
		GAG GTTGGTGT GTC ACTC			
		— G_ T			
GAM1204 MRPL35	3'	CTCAGTTATTGGATATG	33543	G	CAA
		CATA CCA ATAGCTGAG			
		GTAT GGT TATTGACTC			
		A —			
GAM1204 MTO1	3'	CTTGGTTATACTAGGCTAGGAA	56112	A	ACAA TG
		TTC TAGCC ATAGC AG			
		AAG ATCGG TATTG TC			
		G ATCA GT			
GAM1204 MYNN	3'	TTCAGTTGTGACCTGTGG	37853	A	—
		CCACA ATAGCTGAG			
		GGTGT TGTGACTT			
		CCAG			
GAM1204 NFAT5	3'	CTCAGTTATTATTGCTAT	21710	CACA	
		ATAGC AATAGCTGAG			
		TATCG TTATTGACTC			
		TTA_			
GAM1204 NMT1	3'	CTTGGCTTTTCTTTGGGCTGTG	40783	A	T_ TG
G		TCATAGCC CAAA AGC AG			
		GGTGTCGG GTTT TCG TC			
		_ CTTT GT			
GAM1204 NMT1	3'	TTCGGTTGACCCAGGTCATGGA	40792	AG	ACAAA
		TTCAT CC TAGCTGAG			
		AGGTA GG GTTGGCTT			
		CT ACCCA			
GAM1204 NR6A1	3'	CTCAGAGCAAAGTGGCTGTG	7645	AAATAG	
		CATAGCCAC CTGAG			
		GTGTCGGTG GACTC			
		AAACGA			
GAM1204 NR6A1	3'	CTCAGAGCAAAGTGGCTGTG	52870	AAATAG	
		CATAGCCAC CTGAG			
		GTGTCGGTG GACTC			
		AAACGA			
GAM1204 NR6A1	3'	CTCAGAGCAAAGTGGCTGTG	52882	AAATAG	
		CATAGCCAC CTGAG			

			GTGTCGGTG	GA	CTC	
			AAACGA			
GAM1204	NUP133	3'	TTCAGTTAGGGCTAATGG	36690	_	ACAAA
			TCATAGCC	TAGCTGAG		
			GGTATCGG	ATTGACTT		
			A	G		
GAM1204	OR7C1	5'	TCAGTTAAGGCTGAGAG	33996	A	ACAAA
			TTC	TAGCC	TAGCTGA	
			GAG	GTCGG	ATTGACT	
			A	A		
GAM1204	OSBPL2	3'	CAGACTGTGGTTGTGAA	29207		AATAG
			TTCATAGCCACA	CTG		
			AAGTGTG	TGGTGT	GAC	
			CA			
GAM1204	OSBPL2	3'	CAGACTGTGGTTGTGAA	57858		AATAG
			TTCATAGCCACA	CTG		
			AAGTGTG	TGGTGT	GAC	
			CA			
GAM1204	OSBPL8	3'	TTCAGTAGGAGGAGGCTGTGAA	40461		ACAAATA
			TTCATAGCC	GCTGAG		
			AAGTGTCGG	TGACTT		
			AGGAGGA			
GAM1204	PCDH19	3'	TTCAGCTGAGGAAGGCTAGGA	63712	A	ACAAA
			TTC	TAGCC	TAGCTGAG	
			AGG	ATCGG	GTCGACTT	
			-	AAGGA		
GAM1204	PLU-1	3'	TAAGAGCTATTTGTGGTTGTTG	21757	-	GAG
	AG		TTCA	TAGCCACAAATAGCT		
			GAGT	GTTGGTGT	TTTATCGA	
			T	GAATT		
GAM1204	PLU-1	3'	TAAGAGCTATTTGTGGTTGTTG	87416	-	GAG
	AG		TTCA	TAGCCACAAATAGCT		
			GAGT	GTTGGTGT	TTTATCGA	
			T	GAATT		
GAM1204	PNMA3	3'	CTTGGACCAGGGTGGCTGTGAA	25344		AAATAG TG
			TTCATAGCCAC	C	AG	
			AAGTGTCGGTG	G	TC	
			GGACCA	GT		
GAM1204	PPIL2	3'	CTCACCTGCTCTGGCTGTGAA	26765		CAAA C
			TTCATAGCCA	TAG	TGAG	

AAGTGTCGGT GTC ACTC  
 CTC\_ C  
 GAM1204 PPP1R16B 3' TCAGGCTGTGGCTGGAA 61389 A AATAG  
 TTC TAGCCACA CTGA  
 ||| ||||| |||  
 AAG GTCGGTGT GACT  
 \_ CG\_\_  
 GAM1204 PRO1483 3' CTCAGCTGTTTGCTAGCTG 37721 CA\_  
 TAGC CAAATAGCTGAG  
 ||| |||||  
 GTCG GTTTGTCTGACTC  
 ATC  
 GAM1204 PRO1880 3' TTTAGCAATTCTTGTGGTTCTG 26044 T \_ A  
 AG TTCA AGCCACAA AT GCTGAG  
 ||| ||||| || |||||  
 GAGT TTGGTGT TA CGATTT  
 C CT A  
 GAM1204 PRO1942 5' TAAGTATTGATGGCTATGG 37776 CA G GAG  
 TCATAGCCA AATA CT  
 ||||| ||| ||  
 GGTATCGGT TTAT GA  
 AG \_ ATT  
 GAM1204 PTP4A1 3' TTTGGTTACTTGGGTTTGGA 12947 T A A TG  
 TTCA AGCC CAA TAGC AG  
 ||| ||| ||| ||| ||  
 AGGT TTGG GTT ATTG TT  
 \_ \_ C GT  
 GAM1204 PTPN3 3' TCAGCTGAGGCTCTGAG 11060 T ACAA  
 TTCA AGCC TAGCTGA  
 ||| ||| |||||  
 GAGT TCGG GTCGACT  
 C A\_\_  
 GAM1204 RAB6C 3' GCTGTAGGCTGTGGA 49569 ACAA  
 TTCATAGCC ATAGC  
 ||||| ||||  
 AGGTGTCGG TGTCG  
 A\_\_  
 GAM1204 REC8 5' CTCAGTTATCCTGGTGTGGG 17617 TA CAA  
 TTCA GCCA ATAGCTGAG  
 ||| ||| |||||  
 GGGT TGGT TATTGACTC  
 TG CC\_  
 GAM1204 RILP 3' CTTAGGGGTCTGGCTGTGGA 48692 CAA AG  
 TTCATAGCCA AT CTGAG  
 ||||| || |||||  
 AGGTGTCGGT TG GATTC  
 C\_\_ GG  
 GAM1204 RODH-4 3' TTGGGGTGTGCTATGAG 13540 \_ AAA  
 TTCATAGC CAC TAG  
 ||||| ||| |||

		GAGTATCG GTG GTT	
		T GG_	
GAM1204	RRN3	3' CTTGGTCTGATGGCTGTG 37355	_ AATA TG
		CATAGCCA CA GC AG	
		GTGTCGGT GT TG TC	
		A C__ GT	
GAM1204	RYK	3' CTTATCTTTTTGTGTTTGTGAG 82620	C T C
		TTCATAG CACAAA AG TGAG	
		GAGTGTT GTGTTT TC ATT C	
		T T T	
GAM1204	SDFR1	3' TGGGCTTGATGTGCTGTGAA 33919	C AAT GAG
		TTCATAGC ACA AGCT	
		AAGTGTCG TGT TCGG	
		_ AGT GTT	
GAM1204	SDFR1	3' TGGGCTTGATGTGCTGTGAA 24869	C AAT GAG
		TTCATAGC ACA AGCT	
		AAGTGTCG TGT TCGG	
		_ AGT GTT	
GAM1204	SH3BGRL2	3' TTTAGTTGAGAGGCTGTGA 48891	ACAAA
		TCATAGCC TAGCTGAG	
		AGTGTCGG GTTGATTT	
		AGA__	
GAM1204	SIMRP7	3' CTCAGCTGAAGGCTGAGAA 92362	A ACAA
		TTC TAGCC TAGCTGAG	
		AAG GTCGG GTCGACTC	
		A AA__	
GAM1204	SLC2A10	3' TTTGGTTGCTTAACTGGCTGTG 47832	C__ A TG
	G	TCATAGCCA AA TAGC AG	
		GGTGTCGGT TT GTTG TT	
		CAA C GT	
GAM1204	SLC38A1	3' CTCAGCTGAAAAGTGGTTG 47722	AAA_
		TAGCCAC TAGCTGAG	
		GTTGGTG GTCGACTC	
		AAAA	
GAM1204	SPTLC2	3' CTTAGCCCAAAGGGTTGTGAA 16801	ACAAATA
		TTCATAGCC GCTGAG	
		AAGTGTTGG CGATTC	
		GGAAACC	
GAM1204	SRP54	5' TTCGGGAAGTTGGGTTGTGG 11963	A ATAG
		TCATAGCC CAA CTGAG	

			GGTGTGG GTT GGCTT		
			_ GAAG		
GAM1204	STK36	3'	CTCAGCTCTAGGCTGTGG 72103	ACAAAT	
			TCATAGCC AGCTGAG		
			GGTGTCGG TCGACTC		
			ATC__		
GAM1204	SUPT4H1	3'	CTCAGCTGACTGTTGAG 12061	TAGCC AA	
			TTCA ACA TAGCTGAG		
			GAGT TGT GTCGACTC		
			_____ CA		
GAM1204	TBLR1	3'	TTCAGTTGGTGCATGTTGTGGA 45108	CACAAA	
			TTCATAGC TAGCTGAG		
			AGGTGTTG GTTGACTT		
			TACGTG		
GAM1204	TNKS2	3'	TTCAGTTGTTAGTTGG 47455	_A	
			CCA C AATAGCTGAG		
			GGT G TTGTTGACTT		
			T A		
GAM1204	TRPM3	5'	CAGCTGGCTGTGGA 64908	CAAATA	
			TTCATAGCCA GCTG		
			AGGTGTCGGT CGAC		
			_____		
GAM1204	TU12B1-TY	3'	TTAGTTGTTTGGCTTAGAG 33411	AT CA	
			TTC AGCCA AATAGCTGAG		
			GAG TCGGT TTGTTGATTT		
			AT _		
GAM1204	UBN1	3'	TTATGCTTTATTTGTGTAAT 33735	A _ TGAG	
	GAA		TTCAT GCCACAAAT AGC		
			AAGTA TGGTGTTTA TCG		
			A TT TATTT		
GAM1204	UHRF1	3'	TCAGCTGTCTGTTGAA 25221	TAGCC A	
			TTCA ACA ATAGCTGA		
			AAGT TGT TGTCGACT		
			_____ C		
GAM1204	UNC5D	3'	CTTAGTTATTCACTGTGA 55135	CCACA	
			TCATAG AATAGCTGAG		
			AGTGTC TTATTGATTC		
			AC__		
GAM1204	USP22	3'	CTTAGCTGGCTGGGCTGGGGA 68012	A A AA	
			TTC TAGCC CA TAGCTGAG		



			AGG GTCGG GT GTCGATTC	
			G _ CG	
GAM1204	USP22	3'	TTTAGCTCCCCATCTGGCTGTG 68034	CAAAT__
	AA		TTCATAGCCA AGCTGAG	
			AAGTGTGGT TCGATTT	
			CTACCCC	
GAM1204	VI	3'	TTCAGGAGGAGGCTGTGAG 25561	ACAAATAG
			TTCATAGCC CTGAG	
			GAGTGTGGT GACTT	
			AGGAG__	
GAM1204	VPS39	3'	TTCAGCAATGGTGTGGTTGGAG 62853	A A_ A
			TTC TAGCCACA AT GCTGAG	
			GAG GTTGGTGT TA CGACTT	
			_ GG A	
GAM1204	ZAK	3'	CTCAGCTATTTTAAAGAGGAA 56124	ATAGCCAC
			TTC AAATAGCTGAG	
			AAG TTTATCGACTC	
			GAGAAAT_	
GAM1204	ZF	3'	GTTATTTGGTTATGAA 41090	CA
			TTCATAGCCA AATAGC	
			AAGTATTGGT TTATTG	
			_	
GAM1204	ZFP106	3'	TTTGGCTGCTTATGGCTGTG 42482	C A TG
			CATAGCCA AA TAGC AG	
			GTGTCGGT TT GTCG TT	
			A C GT	
GAM1204	ZNF262	3'	CTTAGCTATCTGAATTATGA 17486	CCA A
			TCATAG CA ATAGCTGAG	
			AGTATT GT TATCGATTC	
			AA_ C	
GAM1204	ZNF302	3'	TTTAGCTAGTGGGCATGTGAA 37421	_ A AA
			TTCATA GCC CA TAGCTGAG	
			AAGTGT CGG GT ATCGATTT	
			A _ G_	
GAM1204	ZNF302	3'	TTTAGCTAGTGGGCATGTGAA 37931	_ A AA
			TTCATA GCC CA TAGCTGAG	
			AAGTGT CGG GT ATCGATTT	
			A _ G_	
GAM1204	ZNF323	3'	CTCCCCATTTGTGAGCTGTGG 48079	_ AGCT
			TCATAGC CACAAAT GAG	

	GGTGTCG GTGTTTA CTC	
	A CCC_	
GAM1204 LOC116068 3'	TTTAGCACATGTGCTATGAA 73730	C AATA
	TTCATAGC ACA GCTGAG	
	AAGTATCG TGT CGATTT	
	_ ACA_	
GAM1204 LOC116236 3'	GCTCTGTGTTGTGG 73813	AAT
	TCATAGCCACA AGC	
	GGTGTTGGTGT TCG	
	C_	
GAM1204 LOC118487 3'	CTTGCCCTTTTGTGTGAA 73919	GCC TA TG
	TTCATA ACAA GC AG	
	AAGTGT TGTTT CG TC	
	___ TC GT	
GAM1204 LOC124976 3'	CTTAGTTACTGGCTGGCTGTGG 74380	CAAA_
	TCATAGCCA TAGCTGAG	
	GGTGTCGGT ATTGATTC	
	CGGTC	
GAM1204 LOC126661 3'	CTCAGTTGCCAGGCTGGAG 74549	A ACAA
	TTC TAGCC TAGCTGAG	
	GAG GTCGG GTTGA CTC	
	_ ACCC_	
GAM1204 LOC126917 3'	TTTGGCTCCCTGGTTGGTTGTG 74600	_ AAAT_ TG
AA	TTCATAGCCA C AGC AG	
	AAGTGTGGT G TCG TT	
	T GTCCC GT	
GAM1204 LOC127262 3'	CGGTCTGTGGCTGTGG 76108	AATA
	TCATAGCCACA GCTG	
	GGTGTCGGTGT TGGC	
	C_	
GAM1204 LOC127795 3'	CTTAGTTTCTGGCTATGA 74690	CAAAT
	TCATAGCCA AGCTGAG	
	AGTATCGGT TTGATTC	
	CT_	
GAM1204 LOC130074 3'	TTCAGCTGTATGTTATGAA 76142	CACAA
	TTCATAGC ATAGCTGAG	
	AAGTATTG TGTCGACTT	
	TA_	
GAM1204 LOC130497 3'	CTCAGCTGGCGCCGTGG 74946	TA ACAA
	TCA GCC TAGCTGAG	

GGT CGG GTCGACTC  
GC CG\_\_\_\_  
GAM1204 LOC132617 5' CTTGGTGCACGTGTGGCTGTGG 75892 AATA\_ TG  
TCATAGCCACA GC AG  
||||||| || ||  
GGTGTCGGTGT TG TC  
GCACG GT  
GAM1204 LOC138046 3' CTTAGCTGTTGTCTTGTGCTGT 75294 \_ CA\_\_\_\_  
GGA TCATAGC CA AATAGCTGAG  
||||| || |||||  
GGTGTCG GT TTGTCGATTC  
T TCTG  
GAM1204 LOC139231 3' CTTAGCTTGTGGTTAT 75374 \_ AAT  
ATAGCCA CA AGCTGAG  
||||| || |||||  
TATTGGT GT TCGATTC  
T \_\_\_\_  
GAM1204 LOC143497 5' CTTGGCTGTGGTCCTGAG 76589 TA AATA TG  
TTCA GCCACA GC AG  
||| ||||| || ||  
GAGT TGGTGT CG TC  
CC \_\_\_\_ GT  
GAM1204 LOC144289 5' CTTAGTTTCTCTAGCTGTGAA 83025 CACAAAT  
TTCATAGC AGCTGAG  
||||| |||||  
AAGTGTCG TTGATTC  
ATCTCT\_  
GAM1204 LOC144308 3' CTCAAGAGTTGAGGTTGTGGA 83045 A ATAG \_  
TTCATAGCC CAA CT GAG  
||||||| ||| || |||  
AGGTGTTGG GTT GA CTC  
A GA\_\_ A  
GAM1204 LOC144319 5' CTCAGTTGGCCTGGTTGGAA 83056 A CAAA  
TTC TAGCCA TAGCTGAG  
||| ||||| |||||  
AAG GTTGGT GTTGA CTC  
\_ CCG\_  
GAM1204 LOC144698 3' TTAGTTGTAGCTGTGGT 76913 A\_\_\_\_  
GCCACA ATAGCTGA  
||||| |||||  
TGGTGT TGTTGATT  
CGA  
GAM1204 LOC145310 3' CTTGGTTGTGCAGGCTGGAG 83318 A ACAA TG  
TTC TAGCC ATAGC AG  
||| ||||| ||||| ||  
GAG GTCGG TGTTG TC  
\_ ACG\_ GT  
GAM1204 LOC145609 5' TCTGCTTGTGGTTAGAA 83378 A AAT T  
TTC TAGCCACA AGC GA  
||| ||||| ||| ||

	AAG ATTGGTGT TCG CT	
	— — T	
GAM1204 LOC145988 5'	TCATCTGAGGCTGTGAG 77613	ACAAA C
	TTCATAGCC TAG TGA	
	GAGTGTCGG GTC ACT	
	A — T	
GAM1204 LOC146223 3'	CTCAGCGTTTGGGGCTGTGGA 77709	A A
	TTCATAGCC CAAAT GCTGAG	
	AGGTGTCGG GTTTG CGACTC	
	G —	
GAM1204 LOC146316 5'	CTCAGCTATGACCTATGG 60869	CCACAA
	TCATAG ATAGCTGAG	
	GGTATC TATCGACTC	
	CAG —	
GAM1204 LOC146520 5'	TTTGGCTAATGAGCTTTGAA 77960	T _ CAAA TG
	TTCA AGC CA TAGC AG	
	AAGT TCG GT ATCG TT	
	T A A — GT	
GAM1204 LOC146540 3'	CTCAGTCCCCACTGGCTGTG 77973	CAAATA
	CATAGCCA GCTGAG	
	GTGTCGGT TGA CTC	
	CACCCC	
GAM1204 LOC146783 5'	GCTGTGTGGCTGTGG 83790	AA
	TCATAGCCACA TAGC	
	GGTGTCGGTGT GTCG	
	—	
GAM1204 LOC146856 5'	TCAGTTTAAGCTATGAA 82804	CACAAAT
	TTCATAGC AGCTGA	
	AAGTATCG TTGACT	
	AAT —	
GAM1204 LOC147174 5'	TTTGGCTCTGGCGGTGGCTATG 64770	AAAT — TG
G	TCATAGCCAC AGC AG	
	GGTATCGGTG TCG TT	
	GCGGTC GT	
GAM1204 LOC147299 5'	CTCAGGAAGGTGGCTGTG 78345	AAATAG
	CATAGCCAC CTGAG	
	GTGTCGGTG GACTC	
	GAAG —	
GAM1204 LOC148089 3'	TTCAGGGGTGTGGCTGT 78641	AATAG
	ATAGCCACA CTGAG	

			TGTCGGTGT	GACTT	
			GGG__		
GAM1204	LOC148188	5'	TTCAGCTGGAAGCTAGGAA	78727	A CACAAA
			TTC TAGC	TAGCTGAG	
			AAG ATCG	GTCGACTT	
			G AAG__		
GAM1204	LOC148254	3'	CTCAGCTATCCTACATGAA	78758	AGCCACAA
			TTCAT	ATAGCTGAG	
			AAGTA	TATCGACTC	
			CATCC__		
GAM1204	LOC148529	5'	CTTGTTAAATGGCTCTGAG	84168	T CAAA TG
			TTCA AGCCA	TAGC AG	
			GAGT TCGGT	ATTG TC	
			C AA__	GT	
GAM1204	LOC149086	5'	TTTGGTTGAAGGCTGTGG	84341	ACAAA TG
			TCATAGCC	TAGC AG	
			GGTGTCGG	GTTG TT	
			AA__	GT	
GAM1204	LOC149332	5'	CTTGTTATATAGGCATATGAG	84396	_ ACAA TG
			TTCATA GCC	ATAGC AG	
			GAGTAT CGG	TATTG TC	
			A ATA_	GT	
GAM1204	LOC149401	5'	CTTAGCTGTATTATGTGAA	79335	GCCACAA
			TTCATA	ATAGCTGAG	
			AAGTGT	TGTCGATTC	
			ATTA__		
GAM1204	LOC149668	5'	TGGCTGGGCTGTGGA	84551	ACAAA TG
			TTCATAGCC	TAGC A	
			AGGTGTCGG	GTCG T	
			_____	GT	
GAM1204	LOC150343	5'	CTCGGCTGGTAGGTTTGG	79671	T ACAAA
			TCA AGCC	TAGCTGAG	
			GGT TTGG	GTCGGCTC	
			_ ATG__		
GAM1204	LOC150481	3'	TTTGTGTTGCTGTGAA	79903	__
			TTCATAGC	CACAAA	
			AAGTGTCG	GTGTTT	
			TT		
GAM1204	LOC150759	3'	TTCAGTGTAATGTTGGCTGTGG	80011	_ AATA
			TCATAGCCA CA	GCTGAG	

	GGTGTCTGGT GT TGA	CTT	
	T AATG		
GAM1204 LOC151201 3'	TTTAGCAATTGAGTTATGAG	85298	CACA A
	TTCATAGC AAT GCTGAG		
	GAGTATTG TTA CGATTT		
	AG__ A		
GAM1204 LOC151405 5'	TTTGCTAATTTTGTGGCGTGG	85341	A ____ TGAG
A	TTCAT GCCACAAA TAGC		
	AGGTG CGGTGTTT ATCG		
	_ TTA TTT		
GAM1204 LOC151429 3'	CTCAGTGGCTGGCTGTGG	85350	CAAATA
	TCATAGCCA GCTGAG		
	GGTGTCTGGT TGA	CTC	
	CGG__		
GAM1204 LOC151647 3'	TTTGTATATGTGAGCTGTGAG	80335	_ A GCTGAG
	TTCATAGC CACA ATA		
	GAGTGTCG GTGT TAT		
	A A GTTT		
GAM1204 LOC151742 3'	TGAGCATTTGTGGTTAT	57673	A GAG
	ATAGCCACAAAT GCT		
	TATTGGTGTTTA CGA		
	_ GTG		
GAM1204 LOC151760 5'	CTTGGTCCTTGTGTTGTGAG	85494	C ATA TG
	TTCATAGC ACAA GC AG		
	GAGTGTTG TGTT TG TC		
	_ CC_ GT		
GAM1204 LOC152317 3'	TTTAGTTGTTTGTGTATCTGT	85654	C__
	ATAG CACAAATAGCTGAG		
	TGTC GTGTTTGTTGATTT		
	TAT		
GAM1204 LOC152343 3'	CTTATATATTCTGGTTATGAA	80564	CA GC
	TTCATAGCCA AATA TGAG		
	AAGTATTGGT TTAT ATTC		
	C_ AT		
GAM1204 LOC152804 3'	CTCAGATATGTGTTGTGAA	85881	C AATAG
	TTCATAGC ACA CTGAG		
	AAGTGTTG TGT GACTC		
	_ ATA__		
GAM1204 LOC152905 3'	CTCAGTTATTGAGTTATTGTGA	60476	CC A_
	TCATAG AC AATAGCTGAG		

	AGTGTT TG TTATTGACTC		
	AT AG		
GAM1204 LOC153205 3'	TTCAGCTCCTCTGTGCTGTGGA 85949	C	AAT_
	TTCATAGC ACA AGCTGAG		
	AGGTGTCG TGT TCGACTT		
	_ CTCC		
GAM1204 LOC153339 3'	TCAGTTAGGGTGTGAA 86013	G	ACAAA
	TTCATA CC TAGCTGA		
	AAGTGT GG ATTGACT		
	G _____		
GAM1204 LOC153577 5'	CTGTGGTGGCTGTGG 86058	AA	
	TCATAGCCAC ATAG		
	GGTGTCTGGTG TGTC		
	G_		
GAM1204 LOC153914 5'	AGTGCTGGGTTATGAG 80988	A	AATA
	TTCATAGCC CA GCT		
	GAGTATTGG GT TGA		
	_ CG_		
GAM1204 LOC154007 3'	TTCCCTGTTTGTGGTTTGAG 81026	T	CT
	TTCA AGCCACAAATAG GAG		
	GAGT TTGGTGTTTGTC CTT		
	_ C_		
GAM1204 LOC154184 5'	CTCAGTAGAAGTTGTTATGAG 86179	C	AAATA
	TTCATAGC AC GCTGAG		
	GAGTATTG TG TGA CTC		
	T AAGA_		
GAM1204 LOC157858 3'	CTTAGCAGATTGGGGCTATGG 86591	A	ATA
	TCATAGCC CAA GCTGAG		
	GGTATCGG GTT CGATTC		
	G AGA		
GAM1204 LOC158191 3'	TTTGTGTTGCTGTGAA 81788	___	
	TTCATAGC CACAAA		
	AAGTGTCG GTGTTT		
	TT		
GAM1204 LOC158382 3'	AGCTGTGGCTGGAG 86783	A	AATA
	TTC TAGCCACA GCT		
	GAG GTCGGTGT CGA		
	_ _____		
GAM1204 LOC158677 5'	TTTAGCTGGGTGTTATGGT 86889	___	AA
	GCC ACA TAGCTGAG		

	TGG TGT GTCGATTT		
	TAT GG		
GAM1204 LOC158730 3'	ATTTGTGAGTTATGAA 86890	—	
	TTCATAGC CACAAAT		
	AAGTATTG GTGTTTA		
	A		
GAM1204 LOC158956 3'	CTTGTTACTGTGCTGTGAA 66643	C AA TG	
	TTCATAGC ACA TAGC AG		
	AAGTGTCG TGT ATTG TC		
	— C_ GT		
GAM1204 LOC158978 5'	TTCAAGTCTGTGGTTGTGG 82077	AATA _	
	TCATAGCCACA GCT GAG		
	GGTGTTGGTGT TGA CTT		
	C_ A		
GAM1204 LOC159184 5'	TCAGGCTGGCTATGAA 60052	CAAATA _	
	TTCATAGCCA GC TGA		
	AAGTATCGGT CG ACT		
	_____ G		
GAM1204 LOC159989 3'	CTCAGTTGTACTGGTTTTGAA 82204	T CAA	
	TTCA AGCCA ATAGCTGAG		
	AAGT TTGGT TGTGACTC		
	T CA_		
GAM1204 LOC161742 3'	TTTAGTTGTTTTTTGTGGT 82294	_____	
	GCCACAA ATAGCTGAG		
	TGGTGTT TGTTGATTT		
	TTT		
GAM1204 LOC163101 5'	TCAGCTGCTGGCTGGAA 82409	A CAAA	
	TTC TAGCCA TAGCTGA		
	AAG GTCGGT GTCGACT		
	— C_		
GAM1204 LOC163115 5'	TTCAGGGATGTGGCTAT 82414	AATAG	
	ATAGCCACA CTGAG		
	TATCGGTGT GACTT		
	AGG_		
GAM1204 LOC163255 5'	TTCAGGGATGTGGCTAT 82451	AATAG	
	ATAGCCACA CTGAG		
	TATCGGTGT GACTT		
	AGG_		
GAM1204 LOC164312 5'	CTCAGTGGATGGGGTTGTGG 82505	A_ AATA	
	TCATAGCC CA GCTGAG		



	GGTGTGG GT TGA		
	GG AGG_		
GAM1204 LOC164397 3'	TCGGCTGGGGCCATGGA 82530	A	ACAAA
	TTCAT GCC TAGCTGA		
	AGGTA CGG GTCGGCT		
	C G_		
GAM1204 LOC164832 3'	TTGCGTGTGCTGTGAA 82455	C	AA
	TTCATAGC ACA TAG		
	AAGTGTCG TGT GTT		
	T GC		
GAM1204 LOC164955 3'	CTCAGTAGTCTGGGCTGTGAA 82457	A	A A
	TTCATAGCC CA AT GCTGAG		
	AAGTGTCGG GT TG TGA		
	_ C A		
GAM1204 LOC168283 5'	TCAGTTATTAGTGGCTATGGA 82691	A	G
	TTCATAGCCAC AATAGCTGA		
	AGGTATCGGTG TTATTGACT		
	A		
GAM1204 LOC168391 5'	TTCAGCTGTGACTCTGCTTGGA 82694	T	CACAA_
	TTCA AGC ATAGCTGAG		
	AGGT TCG TGTCGACTT		
	_ TCTCAG		
GAM1204 LOC169026 3'	TTTGCAACTTTATGGTTATGAG 82732	C	TA_ TGAG
	TTCATAGCCA AAA GC		
	GAGTATTGGT TTT CG		
	A CAA TTT		
GAM1204 LOC169611 3'	CTCAGGGTAGGGCTGTGAA 82763	ACAA	AG
	TTCATAGCC AT CTGAG		
	AAGTGTCGG TG GACTC		
	GA_ G_		
GAM1204 LOC195977 3'	TGTGATTATTTGTTGCTGTGGA 87543	C	CTGAG
	TTCATAGC ACAAATAG		
	AGGTGTCG TGTTTATT		
	T AGTGTC		
GAM1204 LOC196264 3'	CTCGCAGGTGTGTTGTGAA 87604	_	AAATA T
	TTCATAGC CAC GC GAG		
	AAGTGTTG GTG CG CTC		
	T GA_ _		
GAM1204 LOC196411 3'	GCTGTGTTGTTATGAA 87675	C	AA
	TTCATAGC ACA TAGC		

	AAGTATTG TGT GTCG		
	T _		
GAM1204 LOC196955 5'	CTCAGTGTCAATGGCTAGAG 77374	A	CAAATA
	TTC TAGCCA GCTGAG		
	GAG ATCGGT TGA CTC		
	_ AACTG_		
GAM1204 LOC197201 3'	CTCAGCTGTTTTTAAATGAA 87935	AGCCAC	
	TTCAT AAATAGCTGAG		
	AAGTA TTTGTCGACTC		
	AATT_		
GAM1204 LOC199692 3'	TTCA GTTGT TTGATTATATG 59243	GCCA	
	CATA CAAATAGCTGAG		
	GTAT GTTTGTTGACTT		
	ATTA		
GAM1204 LOC199704 5'	TTCA GGGATGTGGCTATCGA 88334	_	AATAG
	TC ATAGCCACA CTGAG		
	AG TATCGGTGT GACTT		
	C AGG_		
GAM1204 LOC199991 5'	TTCGGCGACGTCGCTGTGG 89917	C	AAATA
	TCATAGC AC GCTGAG		
	GGTGTCG TG CGGCTT		
	C CAG_		
GAM1204 LOC200227 3'	CTCAAGGTCATGTGGCTAGAA 88643	A	AATAGC
	TTC TAGCCACA TGAG		
	AAG ATCGGTGT ACTC		
	_ ACTGGA		
GAM1204 LOC201292 3'	CTCAGCTGAAGAAGGCATGG 88186	A	ACAAA
	TCAT GCC TAGCTGAG		
	GGTA CGG GTCGACTC		
	_ AAGAA		
GAM1204 LOC202451 3'	CTTAGTGTTGTGTTGTGG 90352	C	ATA
	TCATAGC ACAA GCTGAG		
	GGTGTTG TGTT TGATTC		
	_ G_		
GAM1204 LOC202934 3'	TTCA GCTGTAATTGGCATGAG 90436	A	CAA
	TTCAT GCCA ATAGCTGAG		
	GAGTA CGGT TGTCGACTT		
	_ TAA		
GAM1204 LOC219920 5'	CTCAGCTGGAGTGATTGTGG 93308	GC	AAA
	TCATA CAC TAGCTGAG		

	GGTGT GTG GTCGACTC		
	TA AG_		
GAM1204 LOC221431 3'	TTAGCATGGGCTATGAG 92102	A	AATA
	TTCATAGCC CA GCTGA		
	GAGTATCGG GT CGATT		
	_ A__		
GAM1204 LOC221474 5'	CTCGGTTGTTCCAGCTGAGGA 92379	A	CACA
	TTC TAGC AATAGCTGAG		
	AGG GTCG TTGTTGGCTC		
	A ACC_		
GAM1204 LOC221601 5'	CTCAGTAGAAGTTGTTATGAG 93647	C	AAATA
	TTCATAGC AC GCTGAG		
	GAGTATTG TG TGA CTC		
	T AAGA_		
GAM1204 LOC221656 3'	TCAGTTGAGGCCATGGA 92233	A	A AATA
	TTCAT GCC CA GCTGA		
	AGGTA CGG GT TGA CT		
	C A ____		
GAM1204 LOC221773 3'	CTTACATTTTTGTGGTTTTGAG 91044	T	TAGC
	TTCA AGCCACAAA TGAG		
	GAGT TTGGTGTTT ATTC		
	T TTAC		
GAM1204 LOC222224 5'	CTTGCGCTATTTGTGAGT 94196	_	TG
	GC CACAAATAGC AG		
	TG GTGTTTATCG TC		
	A GT		
GAM1204 LOC245771 3'	CTCAGCTACAGAGCTGGAA 92886	A	CACAAA
	TTC TAGC TAGCTGAG		
	AAG GTCG ATCGACTC		
	_ AGAC_		
GAM1204 LOC245806 3'	CTCAGTCTCACTGGTTGTGA 91891		CAAATA
	TCATAGCCA GCTGAG		
	AGTGTTGGT TGA CTC		
	CACTC_		
GAM1204 LOC253069 3'	TCAGGTGTGGCTGTGA 95712		AATAG
	TCATAGCCACA CTGA		
	AGTGTCGGTGT GACT		
	G____		
GAM1204 LOC253196 3'	CTTGGTTTAGACTGGTTATGA 96883		CAAAT TG
	TCATAGCCA AGC AG		

	AGTATTGGT	TTG TC	
	CAGAT GT		
GAM1204 LOC254499 3'	TTCAGCAGATGGCTATTGAA	96395	_ CAAATA
	TTCA TAGCCA GCTGAG		
	AAGT ATCGGT CGACTT		
	T AGA__		
GAM1204 LOC255104 3'	TCAGTATGGCTGTGAA	95399	CAAATA
	TTCATAGCCA GCTGA		
	AAGTGTCGGT TGA CT		
	A__		
GAM1204 LOC255452 3'	CTCATCATTGTAGCTGTGGA	97533	C ATAGC
	TTCATAGC ACAA TGAG		
	AGGTGTCG TGTT ACTC		
	A ACT__		
GAM1204 LOC255465 3'	TTCAGCTGTAATTGGCATGG	97307	A CAA
	TCAT GCCA ATAGCTGAG		
	GGTA CGGT TGTCGACTT		
	_ TAA		
GAM1204 LOC256021 3'	TCAGCTAAAGTTCTGAA	96517	T CACAAA
	TTCA AGC TAGCTGA		
	AAGT TTG ATCGACT		
	C AA__		
GAM1204 LOC256112 5'	TGAAGTCATCGTGGCTGTGGA	96368	AA AG GAG
	TTCATAGCCAC AT CT		
	AGGTGTCGGTG TA GA		
	C_ CT AGTT		
GAM1204 LOC256306 3'	CTCAGCTGCAAGGCTGCGG	96684	A ACAAA
	TC TAGCC TAGCTGAG		
	GG GTCGG GTCGACTC		
	C AAC__		
GAM1204 LOC256980 3'	CTCAGATGGGTGCCTGTGG	95219	C AAATAG
	TCATAG CAC CTGAG		
	GGTGTC GTG GACTC		
	C GGTA__		
GAM1204 LOC257068 3'	CACAGGGTTTGTGGTTCTGGA	95815	T AG AG
	TTCA AGCCACAAAT CTG		
	AGGT TTGGTGTTTG GAC		
	C G_ ACT		
GAM1204 LOC257358 3'	CTTAGCTGTGTGTTTCTG	97100	CC A
	TAG ACA ATAGCTGAG		

	GTC TGT TGTCGATTC	
	TT G	
GAM1204 LOC257426 3'	GCTTGTGGCTATGAG 66645	AAT
	TTCATAGCCACA AGC	
	GAGTATCGGTGT TCG	
	—	
GAM1204 LOC257476 3'	GCAGTTCTTGTGCTATGG 61253	C AT AG
	TCATAGC ACAA AGCTG	
	GGTATCG TGTT TTGAC	
	_ C_ GT	
GAM1204 LOC257486 3'	TTCAGTTATTGTCACTCTGAG 69252	T CC A
	TTCA AG ACAA TAGCTGAG	
	GAGT TC TGTT ATTGACTT	
	C AC _	
GAM1204 LOC257554 3'	TTAGGGTGTTTGTGTTTATGGA 97697	C G GAG
	TTCATAG CACAAATA CT	
	AGGTATT GTGTTTGT GG	
	T G ATTT	
GAM1204 LOC51339 5'	TTCATGCTGTGGCTGTG 33597	AATA _
	CATAGCCACA GC TGAG	
	GTGTCGGTGT CG ACTT	
	— T	
GAM1204 LOC51580 3'	TTCAGCTGTTTTGTTGGTTG 31868	_ _
	TAGCCA CAAA TAGCTGAG	
	GTTGGT GTTT GTCGACTT	
	T T	
GAM1204 LOC51580 3'	TTTAGCTATTATGAGTTAT 31871	_ CA
	ATAGC CA AATAGCTGAG	
	TATTG GT TTATCGATTT	
	A A_	
GAM1204 LOC57115 3'	GCTACTTGTTGTGAG 39861	CAAA
	TTCATAGCCA TAGC	
	GAGTGTTGGT ATCG	
	TC_	
GAM1204 LOC90155 3'	CTTGGCTGTAGCCAGCTAGAG 61694	A CACAA TG
	TTC TAGC ATAGC AG	
	GAG ATCG TGTCG TC	
	_ ACCGA GT	
GAM1204 LOC90326 3'	AGCTCTGGCTGTGGA 62272	CAAAT
	TTCATAGCCA AGCT	

			AGGTGTCGGT	TCGA		
			C_____			
GAM1204	LOC90379	3'	CTCGGCTACAGCTGTGGA	62537		CACAAA
			TTCATAGC	TAGCTGAG		
			AGGTGTCG	ATCGGCTC		
			AC_____			
GAM1204	LOC90786	3'	ACCAGTTGTGGCTGTGGA	64026		AATA AG
			TTCATAGCCACA	GCTG		
			AGGTGTCGGTGT	TGAC		
			_____	CAA		
GAM1204	LOC91266	5'	TTGTATGTGGCTGGAG	65419	A	A
			TTC	TAGCCACA ATAG		
			GAG	GTCGGTGT TGTT		
			-	A		
GAM1204	LOC91272	3'	TTTAGGGTTTGTGCTGTGG	65430	C	AG
			TCATAGC	ACAAAT CTGAG		
			GGTGTCG	TGTTTG GATTT		
			-	G_		
GAM1204	LOC91628	3'	CTTGGTATTTGTGGTGATGG	66758	A	G TG
			TCAT	GCCACAAATA C AG		
			GGTA	TGGTGTTTAT G TC		
			G	_GT		
GAM1204	LOC91948	3'	CTCAGCTATGATAGCTGT	67616		CACAA
			ATAGC	ATAGCTGAG		
			TGTCG	TATCGACTC		
			ATAG_			
GAM1204	LOC92231	3'	TTCAGCTATTGAGTGTGG	68556		_____
			CCACA	AATAGCTGAG		
			GGTGT	TTATCGACTT		
			GAG			
GAM1204	LOC92235	5'	TCGGCCTTGGCTAAGAA	68557	A	CAAATA
			TTC	TAGCCA GCTGA		
			AAG	ATCGGT CGGCT		
			A	TC_____		
GAM1204	LOC93259	5'	CTTGGCTGACGGGTTGGAA	71819	A	ACAAA TG
			TTC	TAGCC TAGC AG		
			AAG	GTTGG GTCG TC		
			-	GCA_ GT		
GAM1205	ADH1B	3'	CTTAGACATAAAGTAAAAT	72644	C	CAC
			ATTT	ACTTT TGTCTGAG		

			TAAA TGAAA ACAGATTC		
			A T__		
GAM1205	AHR	3'	ATCTCAGATGTTAAATAAATG 7875	CAC C T	
			CATTT TTT AC GTCTGAGAT		
			GTAAA AAA TG TAGACTCTA		
			TA_ T _		
GAM1205	FDFT1	3'	TAGGAAAGTGAAATG 15518	A	
			CATTTCACTTTC CTG		
			GTAAAGTGAAAG GAT		
			—		
GAM1205	JTB	3'	ATCTCAGACAGTGAAAGTGAAA 21959		
	TG		CATTTCACTTTCACTGTCTGAGAT		
			GTAAAGTGAAAGTGACAGACTCTA		
GAM1205	KLF4	3'	TCCCAGACAGTGGATATG 14891	CT A	
			CA TTCACTGTCTG GA		
			GT AGGTGACAGAC CT		
			AT C		
GAM1205	PHYH	3'	ACAGTAAAAGTGAAAT 20608	C	
			ATTTCACTTT ACTGT		
			TAAAGTGAAA TGACA		
			A		
GAM1205	PKD2	3'	TCCAGGTTGAAAGTGAAA 60096	CTG A	
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T__ _		
GAM1205	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1205	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA CTG	
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1205	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT CT	
			TTCACTTTCA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1205	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G T_	
			CTTTCACT TC GAGAT		

			GAAAGTGA AG TTCTA		
			G TC		
GAM1205	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT 45802		ACTTTCACCT
		G	CATTTT GTCTGAGAT		
			GTAAAG CAGACTCTA		
			AAACATTT_		
GAM1205	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281		CTT
			CATTTCA TCACTGTCTGAGAT		
			GTAAAGT AGTGACAGACTCTA		
			C_		
GAM1205	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C	TC
			TTCA TTCTACTG TGAG		
			AAGT AAAGTGAC GTTT		
			A CT		
GAM1205	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A _	
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1205	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T	
			ATT CACTTTTCACTGT		
			TAA GTGAAAGTGACG		
			C		
GAM1205	PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA 53598		CA G
			TTCACTTT CT TCTGAGAT		
			AAGTGAAA GG AGACTCTA		
			CC G		
GAM1205	PP35	3'	ATCTCAGACTGAAA 22814	CT	
			TTTCA GTCTGAGAT		
			AAAGT CAGACTCTA		
			—		
GAM1205	PRTD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148		TCAC C_
			CATTTCACTT TGT TGAG		
			GTAAAGTGAA ACG ACTC		
			TA_ TT		
GAM1205	SEP15	3'	TCCTACAGTAAGAGTGAAA 14934	C	CT
			TTTCACTTT ACTGT GA		
			AAAGTGAGA TGACA CT		
			A TC		
GAM1205	SFXN2	3'	CTCAGGGGAAAAAAGTGAAA 73941		CACTG
			TTTCACTTT TCTGAG		



		AAAGTGAAA	GGACTC		
		AAAGG			
GAM1205	LOC149703	3'	ATCTCAGACAGCCGTTTGGAAA	84647	ACTTTCA
			TTTC CTGTCTGAGAT		
			AAAG GACAGACTCTA		
			GTTTGCC		
GAM1205	LOC154007	3'	ATCTCAAACCCTTTAGTGAAA	81015	TTCACT C
			TTTCACT GT TGAGAT		
			AAAGTGA CA ACTCTA		
			TTTCC_ A		
GAM1205	LOC155004	3'	TCATTTAAGTGAAAAGGAAA	81226	A GTC_
			TTTC CTTTCACT TGA		
			AAAG GAAAGTGA ACT		
			_ ATTT		
GAM1205	LOC222134	5'	ACAGTGAAGTGAAATG	94136	T
			CATTTCAC TT CACTGT		
			GTAAAGTGAA GTGACA		
			-		
GAM1206	ACP2	3'	CACTGGCTTTCTCCAAACAGGA	7852	_____
	T		ATCCT GGAGAAAGCCAGTG		
			TAGGA CCTCTTTCGGTCAC		
			CAAA		
GAM1206	AK1	5'	CACTGGCCCCGCGGCCCA	4880	ATC AGAAA
			TGG CTGG GCCAGTG		
			ACC GGCC CGGTCAC		
			CGC C_____		
GAM1206	ALPL	3'	ACGTATTTCTCCAGACCCA	4891	ATC GCCA
			TGG CTGGAGAAA GT		
			ACC GACCTCTTT CA		
			CA_ ATG_		
GAM1206	ALX3	3'	CACTGGCTCCTCAGCTCCA	21420	TC GA AA
			TGGA CTG GA GCCAGTG		
			ACCT GAC CT CGGTCAC		
			C_ TC _		
GAM1206	ASK	5'	CTTTCTCCGGACCCA	22016	A T
			TGG TCC GGAGAAAG		
			ACC AGG CCTCTTTC		
			C _		
GAM1206	AXL	3'	CTCCCTCTCAGGATCCA	8098	_ AA
			TGGATCCTG GAG AG		

			ACCTAGGAC CTC TC		
			T CC		
GAM1206	AXL	3'	CTCCCTCTCAGGATCCA 41595	_	AA
			TGGATCCTG GAG AG		
			ACCTAGGAC CTC TC		
			T CC		
GAM1206	BLAME	3'	CACTGGAAGTTCTCCAGGATCC 39241		AG_
	A		TGGATCCTGGAGAA CCAGTG		
			ACCTAGGACCTCTT GGTCAC		
			GAA		
GAM1206	COL4A3	3'	GCACTGGCCTCCCCTGGCTCC 48556	T T A	AA
			GGA CC GG GA GCCAGTGC		
			CCT GG CC CT CGGTCACG		
			C T C C_		
GAM1206	CSPG3	3'	CACCAGGGGCCAGGATCCA 15228		AGAAAG A_
			TGGATCCTGG CC GTG		
			ACCTAGGACC GG CAC		
			GG_ AC		
GAM1206	ESPN	3'	GCTCAGCCCCCTCCAGGATGCA 48920	G	AAA C_
			TG ATCCTGGAG GC AGT		
			AC TAGGACCTC CG TCG		
			G CCC AC		
GAM1206	FNTB	3'	GCATCTCTCCAGGGTCCA 8952		AA_
			TGGATCCTGGAGA GC		
			ACCTGGGACCTCT CG		
			CTA		
GAM1206	GDF5	3'	GCACTGGCCCTCTGTCTTCC 5106	TCC	AAA
			GGA TGGAG GCCAGTGC		
			CCT GTCTC CGGTCACG		
			TCT C_		
GAM1206	GPR84	3'	ACTGTCTCCTCCAGGACCA 39805	A	AA C
			TGG TCCTGGAG AG CAGT		
			ACC AGGACCTC TC GTCA		
			_ C_ T		
GAM1206	GSTP1	3'	GCCTTCCTTTCTCCAGGACCA 5958	A	CC T
			TGG TCCTGGAGAAAG AG GC		
			ACC AGGACCTCTTTC TC CG		
			CT _		
GAM1206	GYPA	5'	CACTAACTTCAGGAACCA 87449	A	AAAGCC
			TGG TCCTGGAG AGTG		

			ACC AGGACTTC	TCAC		
			A AA_____			
GAM1206	GYPB	5'	CACTAACTTCAGGAACCA	9158	A	AAAGCC
			TGG TCCTGGAG	AGTG		
			ACC AGGACTTC	TCAC		
			A AA_____			
GAM1206	GYPE	5'	CACTAACTTCAGGAGCCA	9166	A	AAAGCC
			TGG TCCTGGAG	AGTG		
			ACC AGGACTTC	TCAC		
			G AA_____			
GAM1206	HOXD10	3'	GCACCGCGTTCCAGGGCCCA	9268	AT	GAAA CA
			TGG CCTGGA GC GTGC			
			ACC GGACCT CG CACG			
			CG TG__ C_			
GAM1206	HRH1	3'	GCTTTCTCCAGAACCA	5985	ATC	
			TGG CTGGAGAAAGC			
			ACC GACCTCTTTCG			
			AA_			
GAM1206	KIP2	3'	GCAATCTTTTTCCAAAACCCA	21091	ATCC	CCAG
			TGG TGGAGAAAG TGC			
			ACC ACCTTTTTC ACG			
			CAAA TA__			
GAM1206	MAP1A	3'	GCCCTCCCTTCCCCAAGGATCC	9899	_ A	A CC T
	A		TGGATCCT GG GAA G AG GC			
			ACCTAGGA CC CTT C TC CG			
			A C _CC C			
GAM1206	MMP11	3'	CTGTTCTCCAGAATCCA	19872	C	AGC
			TGGAT CTGGAGAA CAG			
			ACCTA GACCTCTT GTC			
			A _____			
GAM1206	NESH	5'	ACCAGTTTCCTCTCCAGGACCA	33144	A	_ CA
			TGG TCCTGGAGA AAGC GT			
			ACC AGGACCTCT TTTG CA			
			_ CC AC			
GAM1206	RELA	3'	CGCACTGGCTCTCTCCAGGATC	41753	A	
	CA		TGGATCCTGGAGA AGCCAGTGC	G		
			ACCTAGGACCTCT TCGGTCACG	C		
			C			
GAM1206	RNPEPL1	3'	GCTCTCTCCAGGCCCA	36678	AT	A
			TGG CCTGGAGA AGC			

			ACC GGACCTCT TCG		
			C_ C		
GAM1206	SHOC2	3'	GCACTGGCTTCAAACAATTCA 23766	CC	GAGA
			TGGAT TG AAGCCAGTGC		
			ACTTA AC TTCGGTCACG		
			_ AAC		
GAM1206	SMAP	5'	GCACTGGCCCCACAGAGCCA 21968	ATC	GAGAAA
			TGG CTG GCCAGTGC		
			ACC GAC CGGTCACG		
			GA_ ACCC_		
GAM1206	SORCS3	3'	GCACTGGCCCTCAGAGCTGACC 30374	A _ G_	AAA
	A		TGG TC CT GAG GCCAGTGC		
			ACC AG GA CTC CGGTCACG		
			_ TC GA C_		
GAM1206	STAC	3'	GCTGTCCCCCAGGATCC 11993	A_ A	
			GGATCCTGG GA AGC		
			CCTAGGACC CT TCG		
			CC G		
GAM1206	TCF7	3'	ACTGGTTTCTCAGAATCCA 12154	C G G	
			TGGAT CTG AGAAA CCAGT		
			ACCTA GAC TCTTT GGTCA		
			A _ _		
GAM1206	TMEM4	3'	CACTGGCTTGATGGATC 26515	TGGAGA	
			GATCC AAGCCAGTG		
			CTAGG TTCGGTCAC		
			TAG_		
GAM1206	ATP6V1D	3'	CACTGGCTTCATTTTAATTCA 32039	CCT	GA
			TGGAT GGA AAGCCAGTG		
			ACTTA TTT TTCGGTCAC		
			AT_ AC		
GAM1206	BAG5	3'	CACCTGCTCCAGGACCA 16838	A	AAAGCCA
			TGG TCCTGGAG GTG		
			ACC AGGACCTC CAC		
			_ GTC_		
GAM1206	BOP	5'	GCACTAACTTTCTCCCAGGGAT 85052	_	CC
	CTA		TGGATCCT GGAGAAAG AGTGC		
			ATCTAGGG CCTCTTTC TCACG		
			AC AA		
GAM1206	C5orf7	3'	CACTGGTGACTCCAGGAACCA 63867	A	AAA
			TGG TCCTGGAG GCCAGTG		

ACC AGGACCTC TGGTCAC  
 A AG\_  
 GAM1206 CGI-96 3' CACCCTCCTCTCCAGGACCC 31660 A A\_ CCA  
 GG TCCTGGAGA AG GTG  
 || ||||| || ||  
 CC AGGACCTCT TC CAC  
 C CC C\_  
 GAM1206 CLDN15 5' GCACCAGCCCCCAGGGTCC 56561 AGAAA CA  
 GGATCCTGG GC GTGC  
 ||||| || ||||  
 CCTGGGACC CG CACG  
 CCC\_ AC  
 GAM1206 CLDN15 5' GCACCAGCCCCCAGGGTCC 26784 AGAAA CA  
 GGATCCTGG GC GTGC  
 ||||| || ||||  
 CCTGGGACC CG CACG  
 CCC\_ AC  
 GAM1206 DKFZp434F142 3' CACTGGCCTCTCTAGGCCCA 50017 AT AA  
 TGG CCTGGAGA GCCAGTG  
 || ||||| |||||  
 ACC GGATCTCT CGGTCAC  
 C\_ C\_  
 GAM1206 DKFZp434F142 3' GCTCCCTCTCCAGGCCCA 50027 AT A\_  
 TGG CCTGGAGA AGC  
 || ||||| ||  
 ACC GGACCTCT TCG  
 C\_ CCC  
 GAM1206 DKFZp434F142 3' GGCCTCTCCAGGCCCA 50028 AT AA  
 TGG CCTGGAGA GCC  
 || ||||| ||  
 ACC GGACCTCT CGG  
 C\_ C\_  
 GAM1206 EDR2 3' GCACTGGCTTCCTCCAAAGTCC 60494 CC A  
 GGAT TGGAG AAGCCAGTGC  
 ||| |||| |||||  
 CCTG ACCTC TTCGGTCACG  
 AA C  
 GAM1206 FLJ00001 3' CGCACCAGCCCCTCCGTCTCCA 81816 AA\_\_\_\_\_ CA |||  
 GGCCCCA CCTGGAGA GC GTGC G  
 ||||| || ||| |  
 GGACCTCT CG CACG C  
 GCCTCCC AC |||  
 GAM1206 FLJ10232 3' GCTCACTCCTCCAGGAACCA 35926 A AA CC  
 TGG TCCTGGAG AG AGT  
 || ||||| || ||  
 ACC AGGACCTC TC TCG  
 A C\_ AC  
 GAM1206 FLJ10415 3' CACGTTGCCTCCAGGATC 36095 AA CA  
 GATCCTGGAG AGC GTG  
 ||||| || |||

CTAGGACCTC TTG CAC  
 CG \_\_\_\_  
 GAM1206 FLJ10901 3' GCACTGGCCCTCCACACC 36825 ATCC AAA  
 GG TGGAG GCCAGTGC  
 || |||| |||||  
 CC ACCTC CGGTCACG  
 AC\_\_ C\_\_  
 GAM1206 FLJ13490 3' GGTTTTTTCCCCAGAATCC 46302 C \_\_\_\_  
 GGAT CT GGAGAAAGCC  
 |||| || |||||  
 CCTA GA CCTTTTTTGG  
 A CC  
 GAM1206 FLJ20400 3' CACCATTTTCCCTCCAGGACCA 66512 A AAAGCCA\_  
 TGG TCCTGGAG GTG  
 ||| ||||| |||  
 ACC AGGACCTC CAC  
 \_ CCTTTTAC  
 GAM1206 FLJ31300 3' GCCCTCTCCAGGACCA 58286 A AA  
 TGG TCCTGGAGA GC  
 ||| ||||| ||  
 ACC AGGACCTCT CG  
 \_ CC  
 GAM1206 GIPC3 3' GCCCTTCTCTAGAATCCA 55711 C A\_  
 TGGAT CTGGAGAA GC  
 |||| ||||| ||  
 ACCTA GATCTCTT CG  
 A CC  
 GAM1206 HSRNAFEV 5' GCGTTTCTCCAGGACCC 34023 A \_  
 GG TCCTGGAGAAA GC  
 || ||||| ||  
 CC AGGACCTCTT CG  
 C G  
 GAM1206 KCND1 5' GCACCAGCTCCCTTTCCAGATC 17142 C A\_\_ CA  
 CA TGGATC TGGAGA AGC GTGC  
 |||| |||| ||| |||  
 ACCTAG ACCTT TCG CACG  
 \_ CCC AC  
 GAM1206 KIAA0475 3' CACTGACTTTCTGAAGGATTCA 29485 GG C  
 TGGATCCT AGAAAG CAGTG  
 ||||| |||| ||||  
 ACTTAGGA TCTTTC GTCAC  
 AG A  
 GAM1206 KIAA0483 3' CACTGGCTAAGGCAGAACCCCA 30789 ATC\_ GAGAA  
 TGG CTG AGCCAGTG  
 ||| ||| |||||  
 ACC GAC TCGGTCAC  
 CCAA GGAA\_  
 GAM1206 KIAA0543 3' GCACCAGGATCTCCAGGGCCCA 68936 AT AAG A\_  
 TGG CCTGGAGA CC GTGC  
 ||| ||||| || |||

ACC GGACCTCT GG CACG  
 CG A\_\_ AC  
 GAM1206 KIAA0616 3' GCACTGGCTCCCTCGCCCCCA 46662 ATCCTG AA  
 TGG GAG AGCCAGTGC  
 ||| ||| |||||  
 ACC CTC TCGGTCACG  
 CCGG\_\_ CC  
 GAM1206 KIAA0673 5' GCACCCGCTTCTCCAGGACCC 62270 A A CA  
 GG TCCTGGAGAA GC GTGC  
 || ||||| || |||  
 CC AGGACCTCTT CG CACG  
 C \_ CC  
 GAM1206 KIAA0677 3' ACTGGCCCCAGTCCA 27824 TC AGAAA  
 TGGA CTGG GCCAGT  
 ||| ||| |||||  
 ACCT GACC CGGTCA  
 \_ C\_\_\_\_  
 GAM1206 KIAA1854 3' GCACCAGCTTCTCTTTTCTCC 71742 TCCT A CA  
 GGA GGAG AAGC GTGC  
 ||| ||| ||| |||  
 CCT TCTC TTCG CACG  
 CTTT C AC  
 GAM1206 KIAA1879 5' CACTGACTTTCTCCTCCCTCC 73562 TCCT C  
 GGA GGAGAAAG CAGTG  
 ||| ||||| |||||  
 CCT CCTCTTTC GTCAC  
 CCCT A  
 GAM1206 KIAA1908 5' GCTTCCCTCCAGGGCCCA 73400 AT A\_  
 TGG CCTGGAG AAGC  
 ||| ||||| |||  
 ACC GGACCTC TTCG  
 CG CC  
 GAM1206 KRT6IRS 3' GCACTGGCCTTGGCCACCCA 53088 ATCC AG A  
 TGG TGG AA GCCAGTGC  
 ||| ||| || |||||  
 ACC ACC TT CGGTCACG  
 C\_\_ GG C  
 GAM1206 LATS1 3' GCACTGGCTTCAGATGGACACA 60278 GA TGGA A  
 TG TCC GAA GCCAGTGC  
 || ||| ||| |||||  
 AC AGG CTT CGGTCACG  
 AC TAGA \_  
 GAM1206 MGC11115 3' GCTGGTTTCTCCCCAGGACC 50241 A A \_  
 GG TCCTGG GA AAGCCAGT  
 || ||||| || |||||  
 CC AGGACC CT TTTGGTCG  
 \_ C C  
 GAM1206 MGC4248 5' CTTTCCTCCAGGACCCA 50328 A \_  
 TGG TCCTGGAG AAAG  
 ||| ||||| |||

			ACC AGGACCTC TTTC		
			C C		
GAM1206 NME3	3'	CACTCCAGCCTCCTCCAGGGCC 64231	AT	AAA C__	
CA		TGG CCTGGAG GC AGTG			
		ACC GGACCTC CG TCAC			
		CG CTC ACC			
GAM1206 NPTXR	3'	GCACTGGCCTTCCCTCCTGCC 54180	ATCCT A A		
		GG GG GAA GCCAGTGC			
		CC CC CTT CGGTCACG			
		GTCCT _ C			
GAM1206 NPTXR	3'	GCACTGGCCTTCCCTCCTGCC 26644	ATCCT A A		
		GG GG GAA GCCAGTGC			
		CC CC CTT CGGTCACG			
		GTCCT _ C			
GAM1206 OPTC	5'	GCTCTCCATCCAGGATCCA 26842		_ A	
		TGGATCCTGGA GA AGC			
		ACCTAGGACCT CT TCG			
		AC C			
GAM1206 PDE4DIP	3'	GCCTCATTCTCCAAGTCCA 95438	CC	A GCC T	
		TGGAT TGGAG AA AG GC			
		ACCTG ACCTC TT TC CG			
		A_ C AC_ _			
GAM1206 PTK9	3'	ACTTTTTTCTCCAAAACCA 11024	ATCC	CC	
		TGG TGGAGAAAG AGT			
		ACC ACCTCTTTT TCA			
		AAA_ T_			
GAM1206 RPF-1	5'	GCTCTTCTTCAGGATCCA 23408		_	
		TGGATCCTGGAGAA AGC			
		ACCTAGGACTTCTT TCG			
		C			
GAM1206 RYK	3'	CACTGAAACATTTCTCCAGAAC 82617	ATC	GC__	
CA		TGG CTGGAGAAA CAGTG			
		ACC GACCTCTTT GTCAC			
		AA_ ACAA			
GAM1206 SDCCAG3	3'	GCTGTCTCCTCCGGGACCCA 21819	A	AAAGC	
		TGG TCCTGGAG CAGT			
		ACC AGGGCCTC GTCG			
		C CTCCT			
GAM1206 TP53TG3	3'	CTTTCTCCAAGACCA 31106	A C		
		TGG TC TGGAGAAAG			



ACC AG ACCTCTTTC  
 \_ A  
 GAM1206 LOC143173 5' CTTTCTCCGGACCCA 60375 A T  
 TGG TCC GGAGAAAG  
 ||| ||| |||||  
 ACC AGG CCTCTTTC  
 C \_  
 GAM1206 LOC144058 5' GCACCAGCTTCCTCCTGGAACC 76667 A T A CA  
 A  
 TGG TCC GGAG AAGC GTGC  
 ||| ||| ||| ||| |||  
 ACC AGG CCTC TTCG CACG  
 A T C AC  
 GAM1206 LOC145384 3' GCGATTCTCAAGGATCCA 77197 \_ GA A\_  
 TGGATCCT G GAA GC  
 ||||| | ||| ||  
 ACCTAGGA C CTT CG  
 A TC AG  
 GAM1206 LOC145820 3' CACTACCCTAATCTTCCAGGAC 77511 A \_ A\_ CC\_  
 CCA  
 TGG TCCTGGA GA AG AGTG  
 ||| ||||| || || |||  
 ACC AGGACCT CT TC TCAC  
 C T AA CCA  
 GAM1206 LOC148181 5' CAGCCTCTCCAGGCCCA 78700 AT AA CAG  
 TGG CCTGGAGA GC TG  
 ||| ||||| || ||  
 ACC GGACCTCT CG AC  
 C\_ C\_ \_  
 GAM1206 LOC149132 5' CAGCCTCTCCAGGCCCA 79173 AT AA CAG  
 TGG CCTGGAGA GC TG  
 ||| ||||| || ||  
 ACC GGACCTCT CG AC  
 C\_ C\_ \_  
 GAM1206 LOC149132 5' CAGCCTCTCCAGGCCCA 79174 AT AA CAG  
 TGG CCTGGAGA GC TG  
 ||| ||||| || ||  
 ACC GGACCTCT CG AC  
 C\_ C\_ \_  
 GAM1206 LOC149773 5' CACTGGGTGCAGGATCCA 79474 GAGAAAG  
 TGGATCCTG CCAGTG  
 ||||| |||||  
 ACCTAGGAC GGTCAC  
 GTG\_  
 GAM1206 LOC152274 3' CACCTCCCTCAGGATCCA 80501 G AA CCA  
 TGGATCCTG AG AG GTG  
 ||||| || || |||  
 ACCTAGGAC TC TC CAC  
 \_ CC \_  
 GAM1206 LOC154990 5' CAGCCTCTCCAGGCCCA 81220 AT AA CAG  
 TGG CCTGGAGA GC TG  
 ||| ||||| || ||

		ACC GGACCTCT CG AC			
		C_ C_ ____			
GAM1206	LOC157697 5'	CACTGGCTCTGAGACCC	81548	A CT	GAAA
		GG TC GGA GCCAGTG			
		CC AG TCT CGGTCAC			
		C AG ____			
GAM1206	LOC157931 5'	GCACTGGCTTCCCGTCATCCG	86663	CC A A	
		TGGAT TGG GAA GCCAGTGC			
		GCCTA GCC CTT CGGTCACG			
		CT _ _			
GAM1206	LOC158382 5'	CTGCCTCCAGGATCCA	86784	AA	
		TGGATCCTGGAG AG			
		ACCTAGGACCTC TC			
		CG			
GAM1206	LOC202018 3'	CATCATTTCCAGGACCCA	89141	A	AAGCCA
		TGG TCCTGGAGA GTG			
		ACC AGGACCTTT TAC			
		C AC ____			
GAM1206	LOC202047 5'	GCTTCTCCAGGACCC	90302	A	A
		GG TCCTGGAGAA GC			
		CC AGGACCTCTT CG			
		C _			
GAM1206	LOC202908 3'	CAGCCTCTCCAGGCCCA	89228	AT	AA CAG
		TGG CCTGGAGA GC TG			
		ACC GGACCTCT CG AC			
		C_ C_ ____			
GAM1206	LOC219690 5'	GCACTGTGACCTCCAGGAGCCA	93072	A	AAA C
		TGG TCCTGGAG GC AGTGC			
		ACC AGGACCTC TG TCACG			
		G CAG _			
GAM1206	LOC223009 5'	CAGCCTCTCCAGGCCCA	94372	AT	AA CAG
		TGG CCTGGAGA GC TG			
		ACC GGACCTCT CG AC			
		C_ C_ ____			
GAM1206	LOC223009 5'	CAGCCTCTCCAGGCCCA	94373	AT	AA CAG
		TGG CCTGGAGA GC TG			
		ACC GGACCTCT CG AC			
		C_ C_ ____			
GAM1206	LOC245771 3'	GCACTGGCCCTCCACACC	92892	ATCC	AAA
		GG TGGAG GCCAGTGC			

CC ACCTC CGGTCACG  
 AC\_\_ C\_\_  
 GAM1206 LOC253216 3' GCACTGGCCCTGCGGGGCCCA 94959 AT G AAA  
 TGG CCTG AG GCCAGTGC  
 ||| |||| || |||||  
 ACC GGGC TC CGGTCACG  
 CG G C\_\_  
 GAM1206 LOC255975 5' CAGCCTCTCCAGGCCCA 95884 AT AA CAG  
 TGG CCTGGAGA GC TG  
 ||| ||||| || ||  
 ACC GGACCTCT CG AC  
 C\_ C\_ \_\_\_\_  
 GAM1206 LOC255975 5' CAGCCTCTCCAGGCCCA 95883 AT AA CAG  
 TGG CCTGGAGA GC TG  
 ||| ||||| || ||  
 ACC GGACCTCT CG AC  
 C\_ C\_ \_\_\_\_  
 GAM1206 LOC256878 3' CAGCCTCTCCAGGCCCA 96899 AT AA CAG  
 TGG CCTGGAGA GC TG  
 ||| ||||| || ||  
 ACC GGACCTCT CG AC  
 C\_ C\_ \_\_\_\_  
 GAM1206 LOC90120 5' GCCTCTCTCCAGGACCA 61537 A AA\_  
 TGG TCCTGGAGA GC  
 ||| ||||| ||  
 ACC AGGACCTCT CG  
 \_ CTC  
 GAM1206 LOC90342 5' CACTGGCTCCTCTGCAGCCCCA 62354 ATC G A\_  
 TGG CTG AGA AGCCAGTG  
 ||| ||| || |||||  
 ACC GAC TCT TCGGTCAC  
 CC\_ G CC  
 GAM1206 LOC90906 5' GCACTGGCTGATTACCAAAACC 64302 ATCC A A\_  
 GG TGG GA AGCCAGTGC  
 || ||| || |||||  
 CC ACC TT TCGGTCACG  
 AAA\_ A AG  
 GAM1207 ADAM19 3' CAGGAAGAAGACTGGCCATTAT 52703 C CTGAG  
 G CATGA GGCT TTCTTCCTG  
 |||| ||| |||||  
 GTATT CCGG AAGAAGGAC  
 A TCAG\_  
 GAM1207 FACL5 5' CAGGAAGAACTCAGAGCCG 64186  
 CGGCTCTGAGTTCTTCCTG  
 |||||  
 GCCGAGACTCAAGAAGGAC  
 GAM1207 GNAL 5' CAGGAAAGAGAGGAGCCGTCG 9058 GAG TC  
 TGACGGCTCT T TTCCTG  
 ||||| | ||||

GCTGCCGAGG A AAGGAC  
 AG\_GA  
 GAM1207 KAL1 3' CAGGAAGAACTTCTGTCA 4013 CTCT  
 TGACGG GAGTTCTTCCTG  
 ||||| |||||  
 ACTGTC TTCAAGAAGGAC  
  
 GAM1207 MYO1E 3' CAGGAGGACAAAACCACCATG 17187 AC CTC AGT  
 CATG GG TG TCTTCCTG  
 ||| || || |||||  
 GTAC CC AC AGGAGGAC  
 CA AAA \_\_\_\_  
 GAM1207 PRKAR2B 3' CAGAAAGAACTCAGATGT 10804 \_ C  
 GC TCTGAGTTCTT CTG  
 || ||||| |||  
 TG AGACTCAAGAA GAC  
 T A  
 GAM1207 PUM2 3' AGGATCAAAGCTGTCATG 31014 C GTTCT  
 CATGACGGCT TGA TCCT  
 ||||| ||| |||  
 GTACTGTCGA ACT AGGA  
 A \_\_\_\_  
 GAM1207 SKI 3' CAGGAAGTGCAGAGCCGCA 11701 A AGTT  
 TG CGGCTCTG CTTCCTG  
 || ||||| |||||  
 AC GCCGAGAC GAAGGAC  
 \_ GT\_  
 GAM1207 TEM8 3' AGGAAGATGCAACCCCATG 36326 AC CTC AGT  
 CATG GG TG TCTTCCT  
 ||| || || |||||  
 GTAC CC AC AGAAGGA  
 C\_ A\_ GT\_  
 GAM1207 ARHGEF4 5' AGAAAAAACTCAGGGC 52207 C C  
 GCTCTGAGTT TT CT  
 ||||| || ||  
 CGGGACTCAA AA GA  
 A A  
 GAM1207 FLJ31978 3' CAGGAAGGAACAAGCGCC 58348 T GAG  
 GGC CT TTCTTCCTG  
 ||| || |||||  
 CCG GA AGGAAGGAC  
 C ACA  
 GAM1207 HSU24186 5' AGAACTCAAAGCCGTC 25324 C  
 GACGGCT TGAGTTCT  
 ||||| |||||  
 CTGCCGA ACTCAAGA  
 A  
 GAM1207 KCNT1 3' AGCTCCAGGGCCGCCA 61825 A \_  
 TG CGGCTCT GAGTT  
 || ||||| |||||

		AC GCCGGGA CTCGA		
		C CC		
GAM1207 KIAA1867	3'	CAGGAAGAACCCAAGAGCTCAT 94822	CG	GA_
		ATGA GCTCT GTTCTTCCTG		
		TACT CGAGA CAAGAAGGAC		
		_ ACC		
GAM1207 KIAA1878	3'	AATTCAGAGAATCGTCATG 91707	_	
		CATGACGG CTCTGAGTT		
		GTACTGCT GAGACTTAA		
		AA		
GAM1207 MFN1	3'	CAGGAAGAACTCATGA 35541	_	
		TC TGAGTTCTTCCTG		
		AG ACTCAAGAAGGAC		
		T		
GAM1207 MIDORI	3'	CAGGGCCCTTCCAGAGCCTGTC 73784	_	AGTTCT
	ATG	CATGAC GGCTCTG TCCTG		
		GTACTG CCGAGAC GGGAC		
		T CTTCCC		
GAM1207 MYH7B	3'	CAGGAAGAACCTGGCTCGCATG 70530	A _	CTGA
		CATG CG GCT GTTCTTCCTG		
		GTAC GC CGG CAAGAAGGAC		
		_ T TC__		
GAM1207 RNAHP	3'	AGAAAGCAGCAGCCGTCAT 23761	_	AG
		ATGACGGCT CTG TTCT		
		TACTGCCGA GAC AAGA		
		C GA		
GAM1207 SLC37A1	3'	AGACGGAGCTCAGACCC 38561	C	TC
		GG TCTGAGTTCT CT		
		CC AGACTCGAGG GA		
		C CA		
GAM1207 LOC116236	3'	CAGGAAAAGCACAAACCTCAT 73809	C CTC A C	
		ATGA GG TG GTT TTCCTG		
		TACT CC AC CGA AAGGAC		
		_ AA_ A A		
GAM1207 LOC124801	3'	CAGGAAGAACTCTCTTGCATG 74336	A	CTCT
		CATG CGG GAGTTCTTCCTG		
		GTAC GTT CTCAAGAAGGAC		
		_ CT__		
GAM1207 LOC222160	5'	AGGAAGAACTCACCCC 94117	CTC	
		GG TGAGTTCTTCCT		

CC ACTCAAGAAGGA  
 CC\_  
 GAM1207 LOC51094 3' CAGGAAGAATAAAGCC 32045 CTGA  
 GGCT GTTCTTCCTG  
 ||| |||||  
 CCGA TAAGAAGGAC  
 AA\_  
 GAM1207 LOC92078 3' CAGGAAGAAGAATCGACCGTC 67977 C T G\_  
 GACGG TC GA TTCTTCCTG  
 |||| || |||||  
 CTGCC AG CT AAGAAGGAC  
 \_ \_ AAG  
 GAM1208 BACH1 5' GGGCGCTCTCGCTTCAGTCA 6800 AG GA  
 TGA CTGAA GAGAGT GCCC  
 ||||| ||||| |||  
 ACTGACTT CTCTCG CGGG  
 CG \_  
 GAM1208 CDC5L 5' CACTTTTTCCCTTTCAGCCA 6980 A \_  
 TG CTGAAAGG AGAGTG  
 || ||||| |||||  
 AC GACTTTCC TTTCAC  
 C CTT  
 GAM1208 CERD4 3' GGGACTCACTCTTCATTCA 23853 A C  
 TGAA GGAGAGTGAG CCC  
 ||| ||||| |||  
 ACTT CTTCTCACTC GGG  
 A A  
 GAM1208 CSN10 3' CACTCTCCTTCAGCCA 17804 A A  
 TG CTGAA GGAGAGTG  
 || |||| |||||  
 AC GACTT CCTCTCAC  
 C \_  
 GAM1208 EPHA8 3' CGGGGCTCCGGCCTCCTGCCA 40057 AA A \_  
 TG AGGAG GT GAGCCCCG  
 || |||| || |||||  
 AC TCCTC CG CTCGGGGC  
 CG \_ GC  
 GAM1208 FGFRL1 3' CGGGACCCGCCTGGTCTTTCAG 41620 A \_ A AGC  
 CCA TG CTGAAAGG AG GTG CCCG  
 || ||||| || ||| |||  
 AC GACTTTCT TC CGC GGGC  
 C GG \_ CCA  
 GAM1208 HAS3 3' CATCTCACCTTCAGTCA 56821 A A \_  
 TGA CTGAA GG GAG TG  
 ||||| || ||| ||  
 ACTGACTT CC CTC AC  
 \_ A T  
 GAM1208 KRTHB6 3' TCACTCTCCACCCAGCCA 9657 A AAA  
 TG CTG GGAGAGTGA  
 || ||| |||||

			AC GAC CCTCTCACT			
			C CCA			
GAM1208 LNK	3'	CACTCTCCTTCCAGTC	18457	A		
		GA CTG AAGGAGAGTG				
		CTGAC TTCCTCTCAC				
		C				
GAM1208 MGEA5	3'	GGACTCATT TTTTCATCA	24215	AA		_
		TGA GGAGAGTGAG CC				
		ACT TTTT TACTC GG				
		AC A				
GAM1208 PKHD1	3'	GGGCCTTCCCCTTTCA	56916	A	TGA	
		TGAAAGG GAG GCCC				
		ACTTTCC CTT CGGG				
		C C__				
GAM1208 SH2D1A	3'	GGGCTCACAGAATTCA TTCA	9849	A	GA__	
		TGAA GGA GTGAGCCC				
		ACTT CTT CACTCGGG				
		A AAGA				
GAM1208 TAGLN2	3'	CTCAAGCTCCTTTCTGTCA	13094	T	AG	
		TGAC GAAAGGAG TGAG				
		ACTG CTTTCCTC ACTC				
		T GA				
GAM1208 ULBP2	5'	GCTCTCCTTCCATCA	47407	C	A	
		TGA TG AAGGAGAGT				
		ACT AC TTCCTCTCG				
		_ C				
GAM1208 C20orf100	3'	CGGAGCACTGCTCTCCTTTTAA	51811	C	GA_ C	
	TCA	TGA TGAAAGGAGAGT GC CCG				
		ACT ATTTTCCTCTCG CG GGC				
		A TCA A				
GAM1208 C6orf5	3'	CACTCTCCTATCAATCA	31341	C	A	
		TGA TGA AGGAGAGTG				
		ACT ACT TCCTCTCAC				
		A A				
GAM1208 CLLD8	5'	CGGAGCTCACTCCTCAGGTCA	49165	GAAA A	C	
		TGACT GG GAGTGAGC CCG				
		ACTGG TC CTCACTCG GGC				
		AC__ _ A				
GAM1208 DKFZP761F241	3'	GGGCCTCCCTATCCAGCCA	48798	A	AA_ A	TGA
		TG CTG AGG GAG GCCC				

AC GAC TCC CTC CGGG  
 C CTA \_ \_  
 GAM1208 DSCR1L1 3' GCTGACTCTTCTCAATCA 19499 C AA G  
 TGA TGA GGAGAGT AGC  
 ||| ||| ||||| |||  
 ACT ACT CTTCTCA TCG  
 A \_ G  
 GAM1208 FLJ00024 3' CTCACTCTTCAGTCA 63760 AAGG  
 TGA CTGA AGAGTGAG  
 ||||| |||||  
 ACTGACT TCTCACTC  
  
 GAM1208 FLJ13162 3' CGGGGCTCCCTGTCCTCTCAGC 46555 A A G T  
 A TG CTGA AGGA AG GAGCCCCG  
 || ||| ||| || |||||  
 AC GACT TCCT TC CTCGGGGC  
 \_ C G C  
 GAM1208 FLJ21302 3' ACCCATTCTTTTCAGTTA 43207 GA\_  
 TGA CTGA AGGA GT  
 ||||| |||  
 ATTGACTTTCTT CA  
 ACC  
 GAM1208 GP5 5' GCTCTAAGTCTTTTCAGTTA 15650 AGAGT  
 TGA CTGA AGGA GAGC  
 ||||| |||  
 ATTGACTTTCT CTCG  
 GAAT\_  
 GAM1208 GR6 3' GGCTTGCTCACCTCTCAGCCA 23732 A A A TG  
 TG CTGA AGG GAG AGCC  
 || ||| ||| ||| |||  
 AC GACT TCC CTC TCGG  
 C C A GT  
 GAM1208 HABP2 3' GCCCACTCTCCTTGGCA 14697 A\_ A  
 TG AAGGAGAGTG GC  
 || ||||| |||  
 AC TTCCTCTCAC CG  
 GG C  
 GAM1208 KIAA1674 3' GGGGCCCTCCTTTTCAG 68787 AGTGA  
 CTGAAAGGAG GCCC  
 ||||| |||  
 GACTTTCCTC CGGGG  
 C\_  
 GAM1208 MCAM 3' CTCACTCTTCTCTCAGCCA 21453 A A  
 TG CTGA AGGAGAGTGAG  
 || ||| |||||  
 AC GACT TCTTCTCACTC  
 C C  
 GAM1208 MGC3047 3' CGGGGCTCACCCCCCTTCCAGC 50360 A A AGA  
 G TG CTG AAGG GTGAGCCCCG  
 || ||| ||| |||||



GC GAC TTCC CACTCGGGGC  
 \_ C CCC  
 GAM1208 MIDORI 3' GGGTATCTTCTCCTTCCAG 73790 A T GC  
 CTG AAGGAGAG GA CCC  
 ||| ||||| || |||  
 GAC TTCCTCTT CT GGG  
 C \_ AT  
 GAM1208 MMEL2 3' CGGGGCTCAGTGCCCCCGTCA 53094 TGAAA AGAG  
 TGAC GG TGAGCCCCG  
 ||| || |||||  
 ACTG CC ACTCGGGGC  
 CCC\_ GTG\_  
 GAM1208 NFAT5 5' GGGGCTCAGATTCCTGTCA 56946 TGAA AG  
 TGAC AGGAG TGAGCCCC  
 ||| ||| |||||  
 ACTG TCCTT ACTCGGGG  
 \_ AG  
 GAM1208 PDE8A 3' GCTCCTTGGTCCTTTCAGT 62636 \_ T  
 ACTGAAAGGA GAG GAGC  
 ||||| ||| |||  
 TGACTTTCCT TTC CTCG  
 GG \_  
 GAM1208 POPX1 3' CACCATCCCTTCAGTCA 29798 A GA  
 TGACTGAA GGA GTG  
 ||||| ||| |||  
 ACTGACTT CCT CAC  
 C AC  
 GAM1208 RYK 5' CGGGGCTCACTTGAAGCCTGTC 82619 TGAAAGGA  
 A TGAC GAGTGAGCCCCG  
 ||| |||||  
 ACTG TCACTCGGGGC  
 TCCGAAG\_  
 GAM1208 SERPINB7 5' GCTCTCCTTCATCA 13686 C A  
 TGA TGAA GGAGAGT  
 ||| ||| |||||  
 ACT ACTT CCTCTCG  
 \_ \_  
 GAM1208 ZNF300 3' GCTCATTTTCAGTTA 53477 AAGGA  
 TGACTGA GAGTGAGC  
 ||||| |||||  
 ATTGACT TTTACTCG  
 \_  
 GAM1208 ZNF33A 3' GGCTCATTGTCCCCAG 91351 AAA G  
 CTG GGA AGTGAGCC  
 ||| ||| |||||  
 GAC CCT TTA CTGG  
 C\_ G  
 GAM1208 LOC146332 3' CTCTCCTTTTCAGCCA 77823 A \_  
 TG CTGAAA GGAGAG  
 || ||||| |||||

		AC GACTTT CCTCTC			
		C T			
GAM1208	LOC148014 3'	GGGCCTCGCTTCCCCTGAGTCA	78609	GAAA AG	C
		TGACT GG AGTGAG CCC			
		ACTGA CC TCGCTC GGG			
		GTC_ CT C			
GAM1208	LOC148171 3'	GCTCCTGCCTTTCGGCCA	78698 A	AG T	
		TG CTGAAAGG AG GAGC			
		AC GGCTTTCC TC CTCG			
		C G_ _			
GAM1208	LOC153338 5'	GGCCCAAGGACCCTTCAGTCA	85997	A AGAG A	
		TGACTGAA GG TG GCC			
		ACTGACTT CC AC CGG			
		C AGGA C			
GAM1208	LOC162137 3'	GGAGGGTCCCCTTTCAG	87113	AGAGT G _	
		CTGAAAGG GA CC CC			
		GACTTTCC CT GG GG			
		C_ G A			
GAM1208	LOC221540 3'	TGGTTTCCTTTCATTCA	93842 C	G	
		TGA TGAAAGGAGA TG			
		ACT ACTTTCCTTT GT			
		T G			
GAM1208	LOC221608 3'	GCCAGCCTTCCTTCAGTCA	92186	A A GA	
		TGACTGAA GGAG GT GC			
		ACTGACTT CCTT CG CG			
		_ C AC			
GAM1208	LOC222031 3'	ACTGTCTTTTCAGCCA	94016 A	G	
		TG CTGAAAGGA AGT			
		AC GACTTTTCT TCA			
		C G			
GAM1208	LOC222057 3'	GCTCCTGCCTTTCGGCCA	92780 A	AG T	
		TG CTGAAAGG AG GAGC			
		AC GGCTTTCC TC CTCG			
		C G_ _			
GAM1208	LOC222302 5'	GGAAGCCCCTCTCTTCAGTCA	94314	AA TGA C_	
		TGACTGA GGAGAG GC CC			
		ACTGACT TCTCTC CG GG			
		_ CC_ AA			
GAM1208	LOC256019 3'	GCTCCTGCCTTTCGGCCA	95902 A	AG T	
		TG CTGAAAGG AG GAGC			

			AC GGCTTTCC TC CTCG		
			C G_ _		
GAM1208	LOC257545	3'	TGGTTTCCTTTCATTCA 97810	C	G
			TGA TGAAAGGAGA TG		
			ACT ACTTTCCTTT GT		
			T G		
GAM1208	LOC257598	3'	TGGTTTCCTTTCATTCA 97925	C	G
			TGA TGAAAGGAGA TG		
			ACT ACTTTCCTTT GT		
			T G		
GAM1208	LOC54499	3'	GCTTCCTTTTAGTCA 70632		G
			TGACTGAAAGGA AGT		
			ACTGATTTTCCT TCG		
			-		
GAM1208	LOC64744	3'	GGGACAGCTTTCCTCTCAGTCA 61798	A	GAG
			TGACTGA AGGAGAGT CCC		
			ACTGACT TCCTTTCG GGG		
			C ACA		
GAM1208	LOC91464	3'	GGAAAGCTCCTTTCATTCA 66142	C	AGTGAG
			TGA TGAAAGGAG CC		
			ACT ACTTTCCTC GG		
			T GAAA_		
GAM1209	ABCC3	3'	TACCGGCCGGGCCTAGACCTGG 39142		AA_ _A_
	TG		CACCAGGTCTA CTG C GTA		
			GTGGTCCAGAT GGC G CAT		
			CCG C GC		
GAM1209	ABCC3	3'	TACCGGCCGGGCCTAGACCTGG 39161		AA_ _A_
	TG		CACCAGGTCTA CTG C GTA		
			GTGGTCCAGAT GGC G CAT		
			CCG C GC		
GAM1209	ANGPT1	3'	CAGTTTCAAACCTTGGTGA 6702		CT_
			TCACCAGGT AAACCTG		
			AGTGGTTCA TTTGAC		
			AAC		
GAM1209	BLNK	3'	TATTGCCTGACCTGATGA 25257	C	TAAACT
			TCA CAGGTC GCAGTA		
			AGT GTCCAG CGTTAT		
			A TC_		
GAM1209	CELSR1	3'	CTGTCAGACCTGGTGA 26483		AAACT
			TCACCAGGTCT GCAG		

AGTGGTCCAGA TGTC  
 C\_\_\_\_  
 GAM1209 DGCR2 3' TACTGCAGCTCAGTGCCCAGTG 17630 CA \_ AAA  
 CAC GGT CT CTGCAGTA  
 ||| ||| || |||||  
 GTG CCG GA GACGTCAT  
 AC T CTC  
 GAM1209 FGF2 3' ACTGCAGTCCAGCCTAGG 8865 \_ T AA  
 CC AGG CT ACTGCAGT  
 || ||| || |||||  
 GG TCC GA TGACGTCA  
 A \_ CC  
 GAM1209 GRIN2B 3' TACTGGGGGCAACCCTGGTGA 5906 TCTAAA G  
 TCACCAGG CT CAGTA  
 ||||| || ||||  
 AGTGGTCC GG GTCAT  
 CAACG\_ G  
 GAM1209 GTF2H1 3' TTACTGCAGTTGCTCAGG 18009 A\_ CTA  
 CC GGT AACTGCAGTAA  
 || ||| |||||  
 GG TCG TTGACGTCATT  
 AC \_\_\_\_  
 GAM1209 HOXD4 3' ACTGCAGTCCCTAGGCT 27518 A\_\_\_\_  
 GGTCTA ACTGCAGT  
 ||||| |||||  
 TCGGAT TGACGTCA  
 CCC  
 GAM1209 IFNAR1 3' ACTGCACTCCAGCCTGGTGA 5280 CTAAAC  
 TCACCAGGT TGCAGT  
 ||||| |||||  
 AGTGGTCCG ACGTCA  
 ACCTC\_  
 GAM1209 IFNGR2 5' ACTGCACTCCAGCCTGGTGA 18648 CTAAAC  
 TCACCAGGT TGCAGT  
 ||||| |||||  
 AGTGGTCCG ACGTCA  
 ACCTC\_  
 GAM1209 KPNB1 5' TACCCAGACAGAGCCGGTGA 9626 A \_ AAA CA  
 TCACC GG TCT CTG GTA  
 ||||| ||| ||| |||  
 AGTGG CC AGA GAC CAT  
 \_ G CA\_ C\_  
 GAM1209 LPHH1 3' TACTGCAGCAGTCTGTGA 24539 C T AAA  
 TCAC AGG CT CTGCAGTA  
 ||| ||| || |||||  
 AGTG TCT GA GACGTCAT  
 \_ \_ C\_  
 GAM1209 MAPT 3' TTGCAGACCTGGGA 33712 A AACT  
 TC CCAGGTCT GCAG  
 || ||||| |||

			AG GGTCCAGA	CGTT		
			—			
GAM1209	MAPT	3'	TTGCAGACCTGGGA	33693	A	AAACT
			TC CCAGGTCT	GCAG		
			AG GGTCCAGA	CGTT		
			—			
GAM1209	MAPT	3'	TTGCAGACCTGGGA	19782	A	AAACT
			TC CCAGGTCT	GCAG		
			AG GGTCCAGA	CGTT		
			—			
GAM1209	MAPT	3'	TTGCAGACCTGGGA	33702	A	AAACT
			TC CCAGGTCT	GCAG		
			AG GGTCCAGA	CGTT		
			—			
GAM1209	MSL3L1	3'	ACTGCAGTCGAGCCTGG	54360	T	AA
			CCAGG CT	ACTGCAGT		
			GGTCC GA	TGACGTCA		
			— GC			
GAM1209	MYO1E	3'	TTATTGTATTTAAACCTGGTGA	17192	C	C
			TCACCAGGT TAAA	TGCAGTAA		
			AGTGGTCCA ATTT	ATGTTATT		
			A —			
GAM1209	NR3C1	3'	TACTGCAGCTTTACAT	3925	C	—
			GT TAAA	CTGCAGTA		
			TA ATTT	GACGTCAT		
			C C			
GAM1209	PXN	3'	TGCCCTAGGCCTGGCGA	11164	A	AACT
			TC CCAGGTCTA	GCA		
			AG GGTCCGGAT	CGT		
			C CC—			
GAM1209	RGS6	3'	ACCGCAGTCCAGGGCCTGG	15026	AA_	A
			CCAGGTCT	ACTGC GT		
			GGTCCGGG	TGACG CA		
			ACC C			
GAM1209	UBE2G2	3'	TTACTGCAGTTTTAC	64865	CT	
			GT AA	ACTGCAGTAA		
			CA TTTGACGTCATT			
			T_			
GAM1209	UBE3A	3'	TTACTGTAGATCAACCTGATGA	55583	C	CTAAA
			TCA CAGGT	CTGCAGTAA		

			AGT GTCCA	GATGTCATT		
			A	ACTA_		
GAM1209	UBE3A	3'	TTACTGTAGATCAACCTGATGA	4871	C	CTAAA
			TCA CAGGT	CTGCAGTAA		
			AGT GTCCA	GATGTCATT		
			A	ACTA_		
GAM1209	UBE3A	3'	TTACTGTAGATCAACCTGATGA	55596	C	CTAAA
			TCA CAGGT	CTGCAGTAA		
			AGT GTCCA	GATGTCATT		
			A	ACTA_		
GAM1209	WNT5A	3'	ACTGCAGTCCAGTTGGGA	12660	A	GT AA
			TC CCAG CT	ACTGCAGT		
			AG GGTT GA	TGACGTCA		
			-	CC		
GAM1209	ZNF215	5'	TTACTGCAATCTAGTAAGGCGG	25120	A	AGGT AAC
			TC CC	CTA TGCAGTAA		
			GG GG	GAT ACGTCATT		
			C	AAT_ CTA		
GAM1209	AAMP	3'	TTGCCCAGACCTGGTGG	6561		AAACT
			TCACCAGGTCT	GCAG		
			GGTGGTCCAGA	CGTT		
			CC			
GAM1209	ADMP	5'	TACTGCAGCTTGAAGG	58869	AGG	T A
			CC TC AA	CTGCAGTA		
			GG	AG TT GACGTCAT		
			A			
GAM1209	AKR1D1	3'	ACTGCAGTCCGGCCTGGGTGA	19971		TAA
			TCACC AGGTC	ACTGCAGT		
			AGTGG TCCGG	TGACGTCA		
			G	CC_		
GAM1209	AP1GBP1	3'	ACTGCAGTGTGCAGTGA	23388	CAG	CTAA
			TCAC GT	ACTGCAGT		
			AGTG CG	TGACGTCA		
			A	TG_		
GAM1209	AP1GBP1	3'	ACTGCAGTGTGCAGTGA	54514	CAG	CTAA
			TCAC GT	ACTGCAGT		
			AGTG CG	TGACGTCA		
			A	TG_		
GAM1209	C20orf121	5'	ACTGACAGAAGACCTGGT	44275	AAA	
			ACCAGGTCT	CTG CAGT		

TGGTCCAGA GAC GTCA  
 A\_\_ A  
 GAM1209 CPR2 3' ACTGCAGTCCAGCCTGG 48087 T AA  
 CCAGG CT ACTGCAGT  
 ||||| || |||||  
 GGTCC GA TGACGTCA  
 \_ CC  
 GAM1209 DIS3 3' ACTGCAGTTTCAGCCTGGATGA 30225 \_ T A  
 TCA CCAGG CT AACTGCAGT  
 ||| ||||| || |||||  
 AGT GGTCC GA TTGACGTCA  
 A \_ C  
 GAM1209 DNAJB5 3' ACTGCAGTGGCTGGAGA 24352 A G TAA  
 TC CCAG TC ACTGCAGT  
 || ||||| || |||||  
 AG GGTC GG TGACGTCA  
 A \_ \_  
 GAM1209 ELF4 5' TTA CTGCAGCTCAGGGGGT 7440 AGG AAA  
 ACC TCT CTGCAGTAA  
 ||| ||| |||||  
 TGG GGA GACGTCATT  
 G\_\_ CTC  
 GAM1209 FIGN 5' TGGTCTCGACCTGGTGA 95646 TAA  
 TCACCAGGTC ACTG  
 ||||| |||||  
 AGTGGTCCAG TGGT  
 CTC  
 GAM1209 FLJ10597 3' ACTGCATCACACAGACTGGTGA 36313 G AAAC\_\_  
 TCACCAG TCT TGCAGT  
 ||||| ||| |||||  
 AGTGGTC AGA ACGTCA  
 \_ CAACT  
 GAM1209 FLJ12750 3' ACTGCAGCCCTGGTGA 45120 TCTAAA  
 TCACCAGG CTGCAGT  
 ||||| |||||  
 AGTGGTCC GACGTCA  
 C\_\_\_\_  
 GAM1209 FLJ14117 3' ACTGCACTCCAGCCTGGTGA 42897 CTAAAC  
 TCACCAGGT TGCAGT  
 ||||| |||||  
 AGTGGTCCG ACGTCA  
 ACCTC\_  
 GAM1209 FLJ14457 3' TACTAGCTGGAAACTCTGGTGA 51388 \_ AACT \_  
 TCACCAGG TCTA GC AGTA  
 ||||| ||| || |||||  
 AGTGGTCT AGGT CG TCAT  
 CAA \_ A  
 GAM1209 FLJ20340 3' ACTGTACTCCAGCCTGGTGA 34971 CTAAAC  
 TCACCAGGT TGCAGT  
 ||||| |||||

AGTGGTCCG ATGTCA  
 ACCTC\_  
 GAM1209 FLJ20825 3' ACTGCAGTCCAGCCTGG 35692 T AA  
 CCAGG CT ACTGCAGT  
 ||||| || |||||  
 GGTCC GA TGACGTCA  
 \_ CC  
 GAM1209 H-L(3)MBT 3' TTACTGCAAGGATCCT 31310 \_ AAAC  
 AGG TCT TGCAGTAA  
 ||| ||| |||||  
 TCC AGG ACGTCATT  
 T A\_\_  
 GAM1209 HEYL 3' ACCACAGCCAAGGCCTGGAGA 27388 A AAA CA  
 TC CCAGGTCT CTG GT  
 || ||||| ||| ||  
 AG GGTCCGGA GAC CA  
 A ACC AC  
 GAM1209 HNRPA3 3' TTACTGCAGCTTAAACAGG 19263 AG C A  
 CC GT TAA CTGCAGTAA  
 || || ||| |||||  
 GG CA ATT GACGTCATT  
 A\_ A C  
 GAM1209 HSA250303 3' TACTGCAGTCCAGCCTGG 37412 T AA  
 CCAGG CT ACTGCAGTA  
 ||||| || |||||  
 GGTCC GA TGACGTCAT  
 \_ CC  
 GAM1209 HSGP25L2G 3' CAGCCTAGACCTGCTGA 62166 C AA  
 TCA CAGGTCTA CTG  
 ||| ||||| |||  
 AGT GTCCAGAT GAC  
 C CC  
 GAM1209 HSH2 3' ACTGCAGTCCAGCCTGGATGA 51670 \_ T AA  
 TCA CCAGG CT ACTGCAGT  
 ||| ||||| || |||||  
 AGT GGTCC GA TGACGTCA  
 A \_ CC  
 GAM1209 KIAA1909 5' CTGCATTAGGCCTG 73839 C  
 CAGGTCTAAA TGCAG  
 ||||| |||||  
 GTCCGGATTT ACGTC  
 -  
 GAM1209 LIM 3' ACTGCACTCCAGCCTGGTGA 21300 CTAAAC  
 TCACCAGGT TGCAGT  
 ||||| |||||  
 AGTGGTCCG ACGTCA  
 ACCTC\_  
 GAM1209 LIMK2 3' TTGTACATAGACCTGATGA 33631 C AAC  
 TCA CAGGTCTA TGCAG  
 ||| ||||| |||||



			AGT GTCCAGAT ATGTT		
			A AC_		
GAM1209	LIMK2	3'	TTGTACATAGACCTGATGA 18731	C	AAC
			TCA CAGGTCTA TGCAG		
			AGT GTCCAGAT ATGTT		
			A AC_		
GAM1209	LSM5	3'	TACTGCAGTAGCCAGTGG 24639	CA T	AA
			TCAC GG CT ACTGCAGTA		
			GGTG CC GA TGACGTCAT		
			A_ _ _		
GAM1209	MACMARCKS	3'	ACTGCCTGGACCTGGTG 43447		AACT
			CACCAGGTCTA GCAGT		
			GTGGTCCAGGT CGTCA		
			C_		
GAM1209	MGC17998	3'	ACTCCAGCCTGGTGA 58740	TCTAAA	C
			TCACCAGG CTG AGT		
			AGTGGTCC GAC TCA		
			_ C		
GAM1209	MGC23280	5'	ACTACAACCTGGTGA 58391	CTAAAC	C
			TCACCAGGT TG AGT		
			AGTGGTCCA AC TCA		
			_ A		
GAM1209	MGC2474	3'	ACTGCAGCCTAGACCTGCTGG 43712	C	AA
			TCA CAGGTCTA CTGCAGT		
			GGT GTCCAGAT GACGTCA		
			C CC		
GAM1209	MGC4663	3'	ACTGCCAACTTGGTGA 44503	CTAAACT	
			TCACCAGGT GCAGT		
			AGTGGTTCA CGTCA		
			AC_		
GAM1209	NFAT5	5'	GCGCGGACCTAGACCTGG 56944	AA_	A
			CCAGGTCTA CTGC GT		
			GGTCCAGAT GGCG CG		
			CCA _		
GAM1209	PTK9L	3'	ACTGCAGTTTGGGATGGTTGA 23466	_	GG
			TCA CCA TCTAAACTGCAGT		
			AGT GGT GGGTTTGACGTCA		
			T A_		
GAM1209	PTR4	3'	TACTGCAGCGTGTCTCCTGG 74057	TC_	AA
			CCAGG TA CTGCAGTAA		

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GGTCC GT GACGTCATT
TCT GC
GAM1209 RAB35 3' GCGCCTGGACCTGGCGA 22480 A AAC
TC CCAGGTCTA TGC
|| ||||| ||
AG GGTCCAGGT GCG
C CC_
GAM1209 SCN12A 3' ACTGCACTCCAGCCTGGTGA 26221 CTAAAC
TCACCAGGT TGCAGT
||||| ||||
AGTGGTCCG ACGTCA
ACCTC_
GAM1209 SULT1C2 3' CAGCCTAGACCTGCTGA 21675 C AA
TCA CAGGTCTA CTG
||| ||||| ||
AGT GTCCAGAT GAC
C CC
GAM1209 TOMM34 3' ACTGCAGTTCATCTG 22332 CTA
CAGGT AACTGCAGT
|||| |||||
GTCTA TTGACGTCA
C_
GAM1209 VEZATIN 3' TTA CTG CAGCTTAGGGATGG 34229 GG A
CCA TCTAA CTGCAGTAA
||| |||| |||||
GGT GGATT GACGTCATT
AG C
GAM1209 ZFP106 3' ACTGCACTCCAGCCTGGTGA 42460 CTAAAC
TCACCAGGT TGCAGT
||||| ||||
AGTGGTCCG ACGTCA
ACCTC_
GAM1209 LOC120227 5' ACTGCCAACTTGGTGA 74006 CTAAACT
TCACCAGGT GCAGT
||||| ||||
AGTGGTTCA CGTCA
AC_____
GAM1209 LOC124411 3' ACTTCAGAAAAGCCTGGTGA 74282 T AAA C
TCACCAGG CT CTG AGT
||||| || |||
AGTGGTCC GA GAC TCA
_ AAA T
GAM1209 LOC126282 3' ACTGCACTTCAGCCTGGTGA 74468 T A C
TCACCAGG CT AA TGCAGT
||||| || |||||
AGTGGTCC GA TT ACGTCA
_ C C
GAM1209 LOC127281 3' TAGTCCAGACCTGGGGA 74650 A AA
TC CCAGGTCT ACTG
|| ||||| |||

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	AG GGTCCAGA TGAT	
	G CC	
GAM1209 LOC142779 3'	ACTGCATTGCAGCCTGGTGA 76390	CTA C
	TCACCAGGT AA TGCAGT	
	AGTGGTCCG TT ACGTCA	
	ACG _	
GAM1209 LOC145078 3'	T TACTGCAGCTTAAACAGG 60294	AG C A
	CC GT TAA CTGCAGTAA	
	GG CA ATT GACGTCATT	
	A_ A C	
GAM1209 LOC148137 3'	CTGTAACCTAGACCTGG 58427	AAC
	CCAGGTCTA TGCAG	
	GGTCCAGAT ATGTC	
	CCA	
GAM1209 LOC148981 3'	T TACTGCAGCTTAAACAGG 84319	AG C A
	CC GT TAA CTGCAGTAA	
	GG CA ATT GACGTCATT	
	A_ A C	
GAM1209 LOC149332 5'	T TACTGCATTTAACATGATGA 84399	C G C C
	TCA CA GT TAAA TGCAGTAA	
	AGT GT CA ATTT ACGTCATT	
	A A _ _	
GAM1209 LOC150481 3'	ACTGCATTCCAGCCTGGTGA 79880	CTAAAC
	TCACCAGGT TGCAGT	
	AGTGGTCCG ACGTCA	
	ACCTT_	
GAM1209 LOC150935 3'	GGTTCTAGTACCTGGTGA 80037	_ _
	TCACCAGGT CTA AACT	
	AGTGGTCCA GAT TTGG	
	T C	
GAM1209 LOC151248 3'	ACTGCACTCCAGCCTGGTGA 80182	CTAAAC
	TCACCAGGT TGCAGT	
	AGTGGTCCG ACGTCA	
	ACCTC_	
GAM1209 LOC151258 5'	T TACTGCAGAAATGATGACCTG 80197	TAAA__
GT	ACCAGGTC CTGCAGTAA	
	TGGTCCAG GACGTCATT	
	TAGTAAA	
GAM1209 LOC153883 5'	TACTGCAGTTTTTAGTG 80985	CAGGTCT
	CAC AAACCTGCAGTA	

		GTG	TTTGACGTCAT		
		ATT	_____		
GAM1209	LOC158450 3'	TACTGAACAGCCTGGTGA	81932		CTAAACTG
		TCACCAGGT	CAGTA		
		AGTGGTCCG	GTCAT		
		ACAA	_____		
GAM1209	LOC158504 3'	TACTGAACAGCCTGGTGA	81940		CTAAACTG
		TCACCAGGT	CAGTA		
		AGTGGTCCG	GTCAT		
		ACAA	_____		
GAM1209	LOC166979 5'	CTGACTTAGACCTGGGA	82669	A	ACTG
		TC CCAGGTCTAA	CAG		
		AG GGTCCAGATT	GTC		
		-	CA		
GAM1209	LOC202404 5'	TTGTGTTTCAGCCTGGTGA	89169		T A T
		TCACCAGG CT AAC GCAG			
		AGTGGTCC GA TTG TGTT			
		-	C		
GAM1209	LOC202934 3'	TACTGCAGCACCTAGTGG	90426	C	CTAAA
		TCAC AGGT	CTGCAGTA		
		GGTG TCCA	GACGTCAT		
		A	CCAC		
GAM1209	LOC220988 3'	TTACTGCAGCTTAAACAGG	90849	AG C A	
		CC GT TAA CTGCAGTAA			
		GG CA ATT GACGTCATT			
		A	A C		
GAM1209	LOC253981 3'	TTACTTTTCCCTTTAGGCCTGG	95835		CTGC
		CCAGGTCTAAA	AGTAA		
		GGTCCGGATTT	TCATT		
		CCCTTT			
GAM1209	LOC255190 3'	TTACTGCAGCTTAAACAGG	97690	AG C A	
		CC GT TAA CTGCAGTAA			
		GG CA ATT GACGTCATT			
		A	A C		
GAM1209	LOC255465 3'	TACTGCAGCGCCACCTAGTGG	97300	C	CTAAA
		TCAC AGGT	CTGCAGTA		
		GGTG TCCA	GACGTCAT		
		A	CCGC		
GAM1209	LOC256433 5'	ACTGTAGTAAAACCCAGTGA	97475	CA	CTAA
		TCAC GGT	ACTGCAGT		

AGTG CCA TGATGTCA  
 AC AAA\_  
 GAM1209 LOC57149 3' ACTGCAGTCACCTTTGG 39935 \_\_\_ CTAA  
 CCA GGT ACTGCAGT  
 ||| ||| |||||  
 GGT CCA TGACGTCA  
 TT C\_\_\_  
 GAM1209 LOC92521 3' TACTGCAGCTTTTCCTGG 69598 TCT A  
 CCAGG AA CTGCAGTA  
 ||||| || |||||  
 GGTCC TT GACGTCAT  
 TT\_ C  
 GAM1209 LOC92979 3' ACCACGGTGACTTGGTGA 56436 TAA CA  
 TCACCAGGTC ACTG GT  
 ||||| ||| ||  
 AGTGGTTCAG TGGC CA  
 \_\_\_ AC  
 GAM1210 B3GAT1 3' CCAGCCAAGCTGGTGCTC 37828 CTG  
 GAGCACT AGCTTGGCTGG  
 ||||| |||||  
 CTCGTGG TCGAACCGACC  
 \_\_\_\_\_  
 GAM1210 B3GAT1 3' CCAGCCAAGCTGGTGCTC 53973 CTG  
 GAGCACT AGCTTGGCTGG  
 ||||| |||||  
 CTCGTGG TCGAACCGACC  
 \_\_\_\_\_  
 GAM1210 COL4A2 3' GCCAGCCGTGGCCAGAGGCTCG 8468 A A \_  
 A TCGAGC CTCTG GCT TGGCTGGC  
 ||||| ||||| || |||||  
 AGCTCG GAGAC CGG GCCGACCG  
 \_ \_ T  
 GAM1210 EVPL 5' CCAGCCAAGCCCAGCCTG 8804 CT A  
 CA CTG GCTTGGCTGG  
 || ||| |||||  
 GT GAC CGAACCGACC  
 CC C  
 GAM1210 OCLN 5' GCCAGGTCCAGAGCGCCGA 10316 A A AG  
 TCG GC CTCTG CTTGGC  
 ||| || ||||| |||||  
 AGC CG GAGAC GGACCG  
 \_ C CT  
 GAM1210 TBX1 3' CCAGTGCCAAAGCGCCCGG 54671 A A C A TTG  
 TCG GC CT TG GC GCTGG  
 ||| || || || || |||||  
 GGC CG GA AC CG TGACC  
 C C A \_ \_  
 GAM1210 TRIM14 3' GCCAAGGAAACCCAGAGTGC 28856 AG\_\_\_\_  
 GCACTCTG CTTGGC  
 ||||| |||||

			CGTGAGAC	GAACCG		
			CCAAAG			
GAM1210	USH3A	3'	GCCAGCAGACATCAGAACACAC	53784	AGCAC_	GCTTG
			CGA			
			TCG	TCTGA	GCTGGC	
			AGC	AGACT	CGACCG	
			CACACA	ACAGA		
GAM1210	Apg4B	3'	GCCCAGCTCAGAGTGCCCG	25285	A	T
			CG	GCACTCTGAGCT	GGC	
			GC	CGTGAGACTCGA	CCG	
			C	C		
GAM1210	APPD	3'	CCAGCCAAGCCCTGCCGA	44213	A	CTCTGA
			TCG	GCA	GCTTGGCTGG	
			AGC	CGT	CGAACCGACC	
			_	CC_		
GAM1210	ARFGAP1	3'	GCCAGCCATGCATGCGCCCGA	36592	A	ACTCTGA T
			TCG	GC	GC TGGCTGGC	
			AGC	CG	CG ACCGACCG	
			C	CGTA_	T	
GAM1210	dJ383J4.3	3'	GCCATTCTCAAAATGCTGA	66944	G	CTC CT
			TC	AGCA	TGAG TGGC	
			AG	TCGT	ACTC ACCG	
			_	AAA	TT	
GAM1210	FLJ12387	3'	GCCAGTCACCAGAGCGC	43067	A	AGCT
			GC	CTCTG	TGGCTGGC	
			CG	GAGAC	ACTGACCG	
			C	C_		
GAM1210	KIAA1453	3'	CCAGCCCAGAGCACTCGG	46972	CA	AGCTT
			TCGAG	CTCTG	GGCTGG	
			GGCTC	GAGAC	CCGACC	
			AC	_		
GAM1210	KIAA1854	3'	CAAGCTCAAAGTGCTC	71738	C	
			GAGCACT	TGAGCTTG		
			CTCGTGA	ACTCGAAC		
			A			
GAM1210	KIAA1948	5'	GCCAGCCATGCAAAGAG	82402	GA	T
			CTCT	GC TGGCTGGC		
			GAGA	CG ACCGACCG		
			AA	T		
GAM1210	MGC13114	3'	GCCAGCCAACAACAAATGCCTG	50415	A	CTC AGC
			TCG	GCA	TG TTGGCTGGC	

AGT CGT AC AACCGACCG  
 C AA\_ AAC  
 GAM1210 MYO3B 3' GCCAAATCAAAGTACTTGA 57307 C C GC  
 TCGAG ACT TGA TTGGC  
 ||||| ||| ||| |||||  
 AGTTC TGA ACT AACCG  
 A A A\_  
 GAM1210 PGLYRPIalpha 3' CCAGCCAAGCTGGCTC 53579 ACTCTG  
 GAGC AGCTTGGCTGG  
 |||| |||||  
 CTCG TCGAACCGACC  
 G\_\_\_\_\_  
 GAM1210 THEA 3' GCCAGGAACCAAGAGTGCTT 66285 AG\_  
 GAGCACTCTG CTTGGC  
 ||||| |||||  
 TTCGTGAGAC GGACCG  
 CAA  
 GAM1210 LOC128259 5' CCAACCAGCGGGTGCTC 74726 TGA T C  
 GAGCACTC GCT GG TGG  
 ||||| ||| |||  
 CTCGTGGG CGA CC ACC  
 \_\_\_\_ \_ A  
 GAM1210 LOC144308 3' GCCAGCCAGAGTGC 83047 A T  
 GCACTCTG GCT GGC  
 ||||| ||| |||  
 CGTGAGAC CGA CCG  
 \_\_\_\_ \_  
 GAM1210 LOC148029 3' GCTCGAGCTCAGAAGCCCGA 78620 A AC \_  
 TCG GC TCTGAGCTTG GC  
 ||| || ||||| |||  
 AGC CG AGACTCGAGC CG  
 C A\_ T  
 GAM1210 LOC151568 5' GCCAACCTGCAGAGCACTCG 56695 CA \_ C  
 CGAG CTCTG AG TTGGC  
 |||| ||||| |||  
 GCTC GAGAC TC AACCG  
 AC G C  
 GAM1210 LOC155036 5' CCAACCAAGCCAGTCAGC 86338 ACT A C  
 GC CTG GCTTGG TGG  
 || ||| ||||| |||  
 CG GAC CGAACC ACC  
 ACT C A  
 GAM1210 LOC200933 5' CCCATTGCTCAGAGCACTGA 90194 G CA T\_ CT  
 TC AG CTCTGAGC TGG GG  
 || || ||||| ||| |||  
 AG TC GAGACTCG ACC CC  
 \_ AC TT \_  
 GAM1210 LOC203601 3' GCCGTGGTCACTCAAAGTGCTT 90645 C CT \_  
 GA TCGAGCACT TGAG TGGCT GGC  
 ||||| ||| ||||| |||

			AGTTCGTGA ACTC ACTGG CCG		
			A _ TG		
GAM1211	ADH1B	3'	CTTAGACATAAAAGTAAAAT 72644	C	CAC
			ATTT ACTTT TGTCTGAG		
			TAAA TGAAA ACAGATTC		
			A T_		
GAM1211	AHR	3'	ATCTCAGATGTTAAAATAAATG 7875	CAC	C T
			CATTT TTT AC GTCTGAGAT		
			GTAAA AAA TG TAGACTCTA		
			TA_ T _		
GAM1211	FDFT1	3'	TAGGAAAGTGAAATG 15518	A	
			CATTTCACTTTC CTG		
			GTAAAGTGAAAG GAT		
			-		
GAM1211	JTB	3'	ATCTCAGACAGTGAAAGTGAAA 21959		
	TG		CATTTCACTTTCACTGTCTGAGAT		
			GTAAAGTGAAAGTGACAGACTCTA		
GAM1211	KLF4	3'	TCCCAGACAGTGGATATG 14891	CT	A
			CA TTCACTGTCTG GA		
			GT AGGTGACAGAC CT		
			AT C		
GAM1211	PHYH	3'	ACAGTAAAAGTGAAAT 20608	C	
			ATTTCACTTT ACTGT		
			TAAAGTGAAA TGACA		
			A		
GAM1211	PKD2	3'	TCCAGGTTGAAAGTGAAA 60096	CTG	A
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T_ _		
GAM1211	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1211	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA	CTG
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1211	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT	CT
			TTCAC TTTCA GT GAG		



AAGTGAAAGT CA CTC  
 CT \_  
 GAM1211 EIF2C2 3' ATCTTCTGAGAGTGAAAAG 71946 G T\_  
 CTTTCACT TC GAGAT  
 ||||| || ||||  
 GAAAGTGA AG TTCTA  
 G TC  
 GAM1211 FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802 ACTTTCACT  
 G CATTTC GTCTGAGAT  
 |||| | |||||  
 GTAAAG CAGACTCTA  
 AAACATTT\_  
 GAM1211 FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281 CTT  
 CATTTCA TCACTGTCTGAGAT  
 |||| | |||||  
 GTAAAGT AGTGACAGACTCTA  
 C\_  
 GAM1211 KIAA0984 3' TTTGTCCAGTGAAAATGAA 65534 C TC  
 TTCA TTTCACTG TGAG  
 ||| ||||| |||  
 AAGT AAAGTGAC GTTT  
 A CT  
 GAM1211 KLHL6 3' ATCTCAGAGCAGGAAA 55299 A \_  
 TTTC CTG TCTGAGAT  
 ||| ||| |||||  
 AAAG GAC AGACTCTA  
 \_ G  
 GAM1211 NIR3 3' GCAGTGAAAGTGCAAT 66242 T  
 ATT CACTTTCACTGT  
 ||| |||||  
 TAA GTGAAAGTGACG  
 C  
 GAM1211 PORIMIN 3' ATCTCAGAGGGCCAAAGTGAA 53598 CA G  
 TTCACTTT CT TCTGAGAT  
 ||||| || |||||  
 AAGTGAAA GG AGACTCTA  
 CC G  
 GAM1211 PP35 3' ATCTCAGACTGAAA 22814 CT  
 TTTC GTCTGAGAT  
 |||| | |||||  
 AAAGT CAGACTCTA  
 \_  
 GAM1211 PRD-NY3 3' CTCATTGCAATAAGTGAAATG 48148 TCAC C\_  
 CATTTCACTT TGT TGAG  
 ||||| || |||  
 GTAAAGTGAA ACG ACTC  
 TA\_\_ TT  
 GAM1211 SEP15 3' TCCTACAGTAAGAGTGAAA 14934 C CT  
 TTTCATTT ACTGT GA  
 ||||| |||| ||

		AAAGTGAGA TGACA CT		
		A TC		
GAM1211	SFXN2	3' CTCAGGGGAAAAAAGTGAAA 73941	CACTG	
		TTTCACTTT TCTGAG		
		AAAGTGAAA GGA CTC		
		AAAGG		
GAM1211	LOC149703	3' ATCTCAGACAGCCGTTTGAAAA 84647	ACTTTCA	
		TTTC CTGTCTGAGAT		
		AAAG GACAGACTCTA		
		GTTTGCC		
GAM1211	LOC154007	3' ATCTCAAACCCTTTAGTGAAA 81015	TTCACT C	
		TTTCACT GT TGAGAT		
		AAAGTGA CA ACTCTA		
		TTTCC_ A		
GAM1211	LOC155004	3' TCATTTAAGTGAAAGGAAA 81226	A GTC_	
		TTTC CTTTCACT TGA		
		AAAG GAAAGTGA ACT		
		_ ATTT		
GAM1211	LOC222134	5' ACAGTGAAGTGAAATG 94136	T	
		CATTTCACTT CACTGT		
		GTAAAGTGAA GTGACA		
		_		
GAM1212	CLCN5	5' TGAAATACCTAAGCTGCTCCAA 3595	_____	
		TTGGAGCAG GTTTCA		
		AACCTCGTC TAAAGT		
		GAATCCA		
GAM1212	FLRT2	5' ATTGAAAAATGAGGTCTGC 25056	GT CTC	
		GCAG TTCATT CAAT		
		CGTC GAGTAA GTTA		
		TG AAA		
GAM1212	IL17	3' TGGGGAAAATGAAACCCTCC 9333	CA _	
		GGAG GGTTTCAT TCTCCA		
		CCTC CCAAAGTA AGGGGT		
		_ AA		
GAM1212	NLGN1	5' TGAAGATGCTGCTCCAA 30026	G_	
		TTGGAGCAG TTTCA		
		AACCTCGTC GAAGT		
		GTA		
GAM1212	POLG	3' GTGATAAACCTGCTCCAA 10682	_	
		TTGGAGCAGGTT TCAT		

			AACCTCGTCCAA	AGTG		
			AT			
GAM1212	TPK1	3'	GGAGAACCTGTCCAA	42384	G	TTCAT
			TTGGA CAGGT	TCTCC		
			AACCT GTCCA	AGAGG		
			— ———			
GAM1212	C1orf8	5'	GAGAATGAAACCCTC	16832	CA	
			GAG GGTTTCATTCTC			
			CTC CCAAAGTAAGAG			
			—			
GAM1212	CLIC6	3'	TGGAGAACATGTTCCAA	82536	G	TTCAT
			TTGGAGCA GT	TCTCCA		
			AACCTTGT CA	AGAGGT		
			A	———		
GAM1212	CLIPR-59	3'	TGGAGAATTTCAATGCCCGA	31374	A	GGTTTC
			TTGG GCA	ATTCTCCA		
			AGCC CGT	TAAGAGGT		
			C AACTT_			
GAM1212	DKFZP547L112	3'	TGGAGAACTCTTGCTCCA	66532		TTTCA
			TGGAGCAGG	TTCTCCA		
			ACCTCGTTC	AAGAGGT		
			TC_	———		
GAM1212	EPS8R3	5'	GGACCACCTGCTCCAA	55701		TTCATTC
			TTGGAGCAGGT	TCC		
			AACCTCGTCCA	AGG		
			CC_	———		
GAM1212	EPS8R3	5'	GGACCACCTGCTCCAA	57404		TTCATTC
			TTGGAGCAGGT	TCC		
			AACCTCGTCCA	AGG		
			CC_	———		
GAM1212	FLJ20552	3'	AGAACAAAACCTGCTCCAA	35389	G	CA
			TTGGAGCAG TTT	TTCT		
			AACCTCGTC AAA	AAGA		
			_ AC	———		
GAM1212	FLJ22865	5'	TGGAGAAAACCTGCTCTAA	47071		GTTTCA
			TTGGAGCAG	TTCTCCA		
			AATCTCGTC	AAGAGGT		
			AA_	———		
GAM1212	KIAA0372	5'	ATTGAAATTTGTTACCTACTCC	27663	C	TT TTCTC
	AA		TTGGAG AGGT CA	CAAT		

			AACCTC TCCA GT	GTTA	
			A TT TTA	AA	
GAM1212	PRO0132	5'	ATGAAACCACTCCAA	26101	CA
			TTGGAG GGTTCAT		
			AACCTC CCAAAGTA		
			A_		
GAM1212	TEX27	3'	AGAGTGGAACCCGCTGCAA	41658	G A
			TTG AGC GGTTCATTCT		
			AAC TCG CCAAGGTGAGA		
			G C		
GAM1212	LOC149373	3'	ATTGGGGTGATGATACCCACCC	79312	AGCA T
			CAA		
			TTGG GGT TCATT CTCCAAT		
			AACC CCA AGTAG GGGGTTA		
			CCAC T T		
GAM1212	LOC152687	3'	TTGGAGAATATTGCTCC	80643	GTTTC
			GGAGCAG ATTCTCCAA		
			CCTCGTT TAAGAGGTT		
			A_		
GAM1212	LOC51202	3'	ATTGGAGAATGAAACCTGCTCC	33017	
			AA		
			TTGGAGCAGGTTTCATTCTCCAAT		
			AACCTCGTCCAAAGTAAGAGGTTA		
GAM1213	RERE	3'	CACACTGACACACTCCGCCAC	23962	ATCA A T
			GTG GA TGT TCAGTGTG		
			CAC CT ACA AGTCACAC		
			CGC_ C C		
GAM1213	FLJ10738	3'	CACACACTTCCACCCTATCAC	36529	C AA TTTC
			GTGAT AG TG AGTGTGTG		
			CACTA TC AC TCACACAC		
			_ CC CT_		
GAM1213	PROZ	3'	CACACACTGAGAGGCCGTCAC	13979	CAGAATG
			GTGAT TTTCAGTGTGTG		
			CACTG AGAGTCACACAC		
			CCGG_		
GAM1213	SLAM	3'	CACACACTGACCACCAGTCAC	11710	CAGAA TT
			GTGAT TG TCAGTGTGTG		
			CACTG AC AGTCACACAC		
			ACC_ C_		
GAM1213	LOC222031	3'	CACACACTGCATCACTGACCAC	94017	A AA TTT
			GTG TCAG TG CAGTGTGTG		

CAC AGTC AC GTCACACAC  
C \_ TAC  
GAM1214 TNFAIP1 3' CATCAGCTGAGGACAGCAAAC 40917 AG G  
CC GGA TTGCTG CTTCAGCTGATG  
||| ||||| |||||  
CCT AACGAC GGAGTCGACTAC  
CA A  
GAM1214 C1orf2 3' CAGCTGGTTGGGACCAGCAGCC 21681 AA \_ \_  
CCC GG GTTGCTGG CT TCAGCTG  
|| ||||| || |||||  
CC CGACGACC GG GGTCGAC  
CC A GTT  
GAM1214 C1orf2 3' CAGCTGGTTGGGACCAGCAGCC 94622 AA \_ \_  
CCC GG GTTGCTGG CT TCAGCTG  
|| ||||| || |||||  
CC CGACGACC GG GGTCGAC  
CC A GTT  
GAM1214 C20orf59 3' CATCCCTAGCCAGCAGCTCC 41992 A TC CT  
GGA GTTGCTGGCT AG GATG  
||| ||||| || |||||  
CCT CGACGACCGA TC CTAC  
\_ \_ C\_  
GAM1214 FLJ20079 3' CATTCTGGTAAACCAGCAGCCT 34490 A CT\_ CT  
CC GGA GTTGCTGG TCAG GATG  
||| ||||| ||| |||||  
CCT CGACGACC GGTC TTAC  
C AAAT \_  
GAM1214 SSAT2 3' CATCAGCTGAAGCACTCTTC 56041 TTGCTG  
GAAG GCTTCAGCTGATG  
||| |||||  
CTTC CGAAGTCGACTAC  
TCA\_  
GAM1214 SYNJ2 3' ATCAGCTTAAGCAATTCC 61763 GTTGCTG C  
GGAA GCTT AGCTGAT  
||| ||| |||||  
CCTT CGAA TCGACTA  
AA\_ T  
GAM1214 LOC162333 5' CTGAAGCCAGCAATTCC 87131 G  
GGAA TTGCTGGCTTCAG  
||| |||||  
CCTT AACGACCGAAGTC  
\_  
GAM1214 LOC222060 5' CACCTCCCACCAGCAACCCCC 94104 AA CTTC C  
GG GTTGCTGG AG TG  
|| ||||| ||  
CC CAACGACC TC AC  
CC ACCC C  
GAM1214 LOC255650 3' CATCAGCCCCAGGCAACTTCC 96711 \_ CTTCA  
GGAAGTTGC TGG GCTGATG  
||||| || |||||

CCTTCAACG ACC CGACTAC  
 G C\_\_\_\_  
 GAM1215 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
 GTA GGAT GGGTTGTTT  
 ||| ||| |||||  
 CGT CCTA CCCAACAAA  
 C CGTG\_  
 GAM1215 LCT 3' AACCGTAAAAATCCTT 9697 G  
 AAGGATTTTTTA GGTT  
 ||||| |||  
 TTCCTAAAAAT CCAA  
 G  
 GAM1215 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
 GTAAGGATTTTTAGGGTTGTTT  
 |||||  
 CATTCCTAAAAATCCCAACAAA  
  
 GAM1215 FBXO30 3' AACTAAAAAATCCTGAC 49573 A AG  
 GT AGGATTTTTT GGTT  
 || ||||| |||  
 CA TCCTAAAAA TCAA  
 G AA  
 GAM1215 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTTT  
 GTAAG AGGGTTGTT  
 ||| |||||  
 CATTC TCCCAACAA  
 AT\_\_\_\_  
 GAM1215 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
 TAAG TTTT GGGTTGTTT  
 ||| ||| |||||  
 GTTC AAAA CCCAACAAA  
 \_\_\_\_ C  
 GAM1215 SMT3H2 3' AACCAACATAAAAAATCCTTGC 22670 GG  
 GTAAGGATTTTTTA GTTGTT  
 ||||| |||  
 CGTTCCTAAAAAT CAACAA  
 A\_  
 GAM1215 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
 GTAAGGATTTTTT GGGTT  
 ||||| |||  
 CGTTCCTAAAAA TCCAA  
 GTA  
 GAM1215 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
 GGAT TT GGGTTGTTT  
 ||| || |||||  
 CCTG AA CCCAACAAA  
 T\_ C  
 GAM1215 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
 C GTA GGATTTTT TTGTTT  
 || ||||| |||

		CGT CCTAAAAA AACAAA		
		C GATAA		
GAM1215	LOC148089 3'	GGCCCTAAAAATTCCTAC	78637	A
		GTA GGATTTTTAGGGTT		
		CAT CTTAAAAATCCCGG		
		C		
GAM1215	LOC154547 3'	AACAACATAAAAAATCCTTGC	76050	GG
		GTAAGGATTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1215	LOC158104 3'	ACAGCCAAAAATCCTTA	60313	AG
		TAAGGATTTTT GTTGT		
		ATTCCTAAAAA CCGACA		
		—		
GAM1215	LOC205880 5'	AAACAACCATCATCCTGAC	90709	A TTTAG
		GT AGGAT GGTGTTT		
		CA TCCTA CCAACAAA		
		G CTA_		
GAM1215	LOC221561 3'	AACAACATAAAAAATCCTTGC	92130	GG
		GTAAGGATTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1215	LOC257591 3'	AACAACATAAAAAATCCTTGC	97840	GG
		GTAAGGATTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1215	LOC51145 3'	AGCTAAAATCCTTAC	32393	TAG
		GTAAGGATTTT GTT		
		CATTCCTAAAA TCGA		
		—		
GAM1216	ABCC3 3'	GGACCTGCCCCCACTCTGC	39157	AGT_ _
		GTAGAG GGGCA TCC		
		CGTCTC CCGT AGG		
		ACCC CC		
GAM1216	ACVR1 5'	GCCTCTTCTACTCTC	6609	A G T
		GA AGTAGA AG GGGC		
		CT TCATCT TC TCCG		
		C _ _		
GAM1216	ASB2 3'	CCTTCTCTACCTTCA	32355	A T
		TGAA GTAGAGAG GG		

			ACTT CATCTCTT CC		
			C _		
GAM1216	ASTN	3'	GATTCCCCTACTTTCA 69333	AGAGT	C
			TGAAAGTAG GGG ATC		
			ACTTTCATC CCC TAG		
			_____ T		
GAM1216	C1orf1	3'	TCCTCTCTCTATTTTCA 6868	T	
			TGAAAGTAGAGAG GGG		
			ACTTTTATCTCTC CCT		
			T		
GAM1216	C5R1	3'	GGATGCCCACTTCCCTCCAC 8207	A	_____
			GT GAG AGTGGGCATCC		
			CA CTC TCACCCGTAGG		
			C CCT		
GAM1216	CASP10	3'	GATGCCCCAGCCTGCTTTCA 52103	AGAGT	
			TGAAAGTAG GGGCATC		
			ACTTTCGTC CCCGTAG		
			CGAC_		
GAM1216	CASP8	3'	GATGCCTCAGCCTACTTTCA 52946	AGAGT	
			TGAAAGTAG GGGCATC		
			ACTTTCATC TCCGTAG		
			CGAC_		
GAM1216	CCR2	3'	GGA CTATGGCTCTACTTTCA 5383	A_	GCA
			TGAAAGTAGAG GTGG TCC		
			ACTTTCATCTC TATC AGG		
			GG _____		
GAM1216	CELL	3'	GGATGCCCCCTGTGCCCTCA 8412	AA_	G AGT
			TGA GTA AG GGGCATCC		
			ACT CGT TC CCCGTAGG		
			CCC G _____		
GAM1216	CELL	3'	GGATGCCCGTCTAC 8413	GAG	
			GTAGA TGGGCATCC		
			CATCT GCCCGTAGG		
			_____		
GAM1216	CPA3	3'	ATGCAGCTTCTATTTCA 8520	G	G GG
			TGAAA TAGA AGT GCAT		
			ACTTT ATCT TCG CGTA		
			_ _ A_		
GAM1216	CTNNA1	3'	GGAGCCTACTTCTA 65919	G	A
			TAGA AGTGGGC TCC		



ATCT TCATCCG AGG

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      - -
GAM1216 CXorf6  3' ATGCCCACTGCGTTCA    18510  A AGAG
      TGAA GT  AGTGGGCAT
      ||| | |||||
      ACTT CG  TCACCCGTA
      G ____
GAM1216 DCLRE1C 3' ATGTGTCTCTACTTACA    42525  A   GTGG
      TG AAGTAGAGA  GCAT
      || ||||| |
      AC TTCATCTCT  TGTA
      A   G ____
GAM1216 FSTL3   3' GGATGCCCCAGCCCCTAC    19610  AGA ____
      GTAG  GT  GGGCATCC
      ||| | |||||
      CATC  CG  CCCGTAGG
      CC_ AC
GAM1216 GATM    3' GGTATTACTCTCTACT    7628      GC
      AGTAGAGAGTGG ATC
      ||||| ||
      TCATCTCTCATT TGG
      A_
GAM1216 GFRA2   3' ATGCCCTTCACTTTC    7659    A AGT
      GAAAGT GAG  GGGCAT
      |||| | ||||
      CTTTCA CTT  CCCGTA
      - -
GAM1216 GNAS    3' GTTCCCTCTCACTTTCA    4969    A  T
      TGAAAGT GAGAG GGGC
      |||| | ||||
      ACTTTCA CTCTC CTTG
      - C
GAM1216 GNAS    3' GTTCCCTCTCACTTTCA    54425  A  T
      TGAAAGT GAGAG GGGC
      |||| | ||||
      ACTTTCA CTCTC CTTG
      - C
GAM1216 GNAS    3' GTTCCCTCTCACTTTCA    54427  A  T
      TGAAAGT GAGAG GGGC
      |||| | ||||
      ACTTTCA CTCTC CTTG
      - C
GAM1216 GNAS    3' GTTCCCTCTCACTTTCA    33442  A  T
      TGAAAGT GAGAG GGGC
      |||| | ||||
      ACTTTCA CTCTC CTTG
      - C
GAM1216 HCN4    3' GGATGCCCAGGTCACCTTACA 18491  A TA GAG
      TG AAG GA  TGGGCATCC
      || || | |||||
```

AC TTC CT ACCCGTAGG  
 A CA GG\_  
 GAM1216 HNRPK 3' ATGCTTGCCCCTACTTTT 48358 AGA TG  
 GAAAGTAG G GGCAT  
 ||||| | ||||  
 TTTTCATC C TCGTA  
 CC\_ GT  
 GAM1216 HNRPK 3' ATGCTTGCCCCTACTTTT 9248 AGA TG  
 GAAAGTAG G GGCAT  
 ||||| | ||||  
 TTTTCATC C TCGTA  
 CC\_ GT  
 GAM1216 HPS4 5' GGATGCCTGGCTACTC 41987 \_ \_  
 GAG AGT GGGCATCC  
 ||| ||| |||||  
 CTC TCG TCCGTAGG  
 A G  
 GAM1216 HSPB1 3' GGATGCCACCCCTGCTGCCG 7741 AA AGA  
 TG AGTAG GTGGGCATCC  
 || |||| |||||  
 GC TCGTC CACCCGTAGG  
 CG CC\_  
 GAM1216 ICA1 3' ATGCCTTCCTTCTCTGC 42252 T\_  
 GTAGAGAG GGGCAT  
 ||||| ||||  
 CGTCTCTT TCCGTA  
 CCT  
 GAM1216 IL1F5 3' GATGCTGGTCTCTATTCCCA 24380 AA G G  
 TG AGTAGAGA T GGCATC  
 || ||||| | ||||  
 AC TTATCTCT G TCGTAG  
 CC \_ G  
 GAM1216 IL1F5 3' GGACAATCACTCTCTCTGCTCT 24381 A \_ GCA  
 CA TGA AGT AGAGAGTGG TCC  
 ||| ||| ||||| |||  
 ACT TCG TCTCTCACT AGG  
 C TC AAC  
 GAM1216 KIF3C 3' GGACACAGCCCCACTCTCCACT 9606 A \_ A\_  
 TTC GAAAGT GAGAGTGGG C TCC  
 ||||| ||||| | |||  
 CTTTCA CTCTCACCC G AGG  
 C C ACAC  
 GAM1216 KLHL3 3' GGACACCCTCCCTACTTT 87459 A T GCA  
 AAAGTAG GAG GG TCC  
 ||||| ||| || |||  
 TTTTCATC CTC CC AGG  
 C \_ AC\_  
 GAM1216 LIPA 3' GATGCCCAGTTCACTCTAGTTT 4082 G \_ G  
 CA TGAAA TAGAG A TGGGCATC  
 |||| |||| | |||||

			ACTTT ATCTC T ACCCGTAG		
			G ACT G		
GAM1216 MPV17	3'	ATGCCACTCATCCCCACTCTTC 70509	_ A _ _	G	
A		TGAA AGT GA GAGTGG CAT			
		ACTT TCA CT CTCACC GTA			
		C CCC A _			
GAM1216 NAT2	3'	GATATCCTCTCTACCCTCA 3402 AA T GC			
		TGA GTAGAGAG GG ATC			
		ACT CATCTCTC CT TAG			
		CC _ A _			
GAM1216 NCAM2	3'	ATGCTTCTTTACTTCCA 15799 A GTG			
		TG AAGTAGAGA GGCAT			
		AC TTCATTTCT TCGTA			
		C _ _			
GAM1216 PHTF1	3'	GATACCCACCTGCTTGTTCA 21730 _ AGA C			
		TGAA AGTAG GTGGG ATC			
		ACTT TCGTC CACCC TAG			
		GT _ A			
GAM1216 PIK3CD	3'	GGATGCTTGCTCTCCACTTTT 17249 A TG			
		GAAAGT GAGAG GGCATCC			
		TTTTCA CTCTC TCGTAGG			
		C GT			
GAM1216 PRX	3'	GGATGCCACCTGCCCTCA 40534 AA AGA			
		TGA GTAG GTGGGCATCC			
		ACT CGTC CACCCGTAGG			
		CC _			
GAM1216 PSME3	3'	GCCTTCTCTCCCTACTTTCA 19373 _ T			
		TGAAAGTA GAGAG GGGC			
		ACTTTCAT CTCTC TCCG			
		CC T			
GAM1216 PXF	3'	GATGCCCTAGTCCACTTT 11152 A GAGT			
		AAAGT GA GGGCATC			
		TTTCA CT CCCGTAG			
		C GAT _			
GAM1216 RALB	3'	GATGCCCTCCCACTTTTA 11244 AGA GT			
		TGAAAGT GA GGGCATC			
		ATTTTCA CT CCCGTAG			
		CC _			
GAM1216 RGS3	3'	GGACACCATTTCTCCAGCTTCA 40861 A A _ GCA			
		TGAA GT GAGAGTGG TCC			

			ACTT CG CTCTTACC AGG			
			_ AC AC_			
GAM1216	RGS3	3'	GGACACCATTTCTCCAGCTTCA 35056	A A_		GCA
			TGAA GT GAGAGTGG TCC			
			ACTT CG CTCTTACC AGG			
			_ AC AC_			
GAM1216	RGS3	3'	GGACACCATTTCTCCAGCTTCA 57822	A A_		GCA
			TGAA GT GAGAGTGG TCC			
			ACTT CG CTCTTACC AGG			
			_ AC AC_			
GAM1216	RGS3	3'	GGACACCATTTCTCCAGCTTCA 57825	A A_		GCA
			TGAA GT GAGAGTGG TCC			
			ACTT CG CTCTTACC AGG			
			_ AC AC_			
GAM1216	RGS3	3'	GGACACCATTTCTCCAGCTTCA 55444	A A_		GCA
			TGAA GT GAGAGTGG TCC			
			ACTT CG CTCTTACC AGG			
			_ AC AC_			
GAM1216	RGS3	3'	GGACACCATTTCTCCAGCTTCA 56222	A A_		GCA
			TGAA GT GAGAGTGG TCC			
			ACTT CG CTCTTACC AGG			
			_ AC AC_			
GAM1216	SH3BP5	3'	GATGTCCTCTCCACTTT 16742	A GT		
			AAAGT GAGA GGGCATC			
			TTTCA CTCT CCTGTAG			
			C _			
GAM1216	SLC21A2	3'	GATGCCCAGGCTCACTTCA 18859	A A AG		
			TGAA GT GAG TGGGCATC			
			ACTT CA CTC ACCCGTAG			
			_ _ GG			
GAM1216	SLC21A3	3'	CCCTCCTACTTTCA 56227	A T		
			TGAAAGTAG GAG GG			
			ACTTTCATC CTC CC			
			_ _			
GAM1216	SLC21A3	3'	CCCTCCTACTTTCA 40828	A T		
			TGAAAGTAG GAG GG			
			ACTTTCATC CTC CC			
			_ _			
GAM1216	TNFSF12	3'	GCCCACTCTCCACCTCA 13745	AA A		
			TGA GT GAGAGTGGGC			

		ACT CA CTCTCACCCG		
		C_ C		
GAM1216 UBE2L3	3'	GGAGCTTGCTCTCCACTT	12504	A TG A
		AAGT GAGAG GGC TCC		
		TTCA CTCTC TCG AGG		
		C GT _		
GAM1216 UBQLN2	3'	TCGTTCTTTACTTTCA	25570	
		TGAAAGTAGAGAGTGG		
		ACTTTCATTTCTTGCT		
GAM1216 USP9Y	5'	ATGGTTAGTCTCCACTTTTA	64036	A G G
		TGAAAGT GAGA TGG CAT		
		ATTTTCA CTCT ATT GTA		
		C G G		
GAM1216 WAS	3'	GCCCACCCTCCACTCTC	4582	A A A
		GA AGT GAG GTGGGC		
		CT TCA CTC CACCCG		
		C C C		
GAM1216 WAS	3'	TCCACTCTCCTCTTCCA	4583	A TA
		TG AAG GAGAGTGGG		
		AC TTC CTCTCACCT		
		C TC		
GAM1216 WISP1	3'	CACTCCTCTACTCTTA	13941	A _
		TGA AGTAGAG AGTG		
		ATT TCATCTC TCAC		
		C C		
GAM1216 ARAP3	5'	GATGGCTCTGCTTCCA	42503	A GAGTG G
		TG AAGTAGA G CATC		
		AC TTCGTCT C GTAG		
		C _ _ _ G		
GAM1216 ARHU	3'	GACACCCAGAAAGGCTATTTTC	41074	AGAG_ CA
A		TGAAAGTAG TGGG TC		
		ACTTTTATC ACCC AG		
		GGAAAG AC		
GAM1216 BRE	3'	ATGCCCACGCCTTTCTTCCA	16915	A T A_
		TG AAG AGAG GTGGGCAT		
		AC TTC TTTC CACCCGTA		
		C _ CG		
GAM1216 C1orf16	3'	CCCAGCCTCCACTTTCA	29230	A AG
		TGAAAGT GAG TGGG		

		ACTTTCA CTC ACCC		
		C CG		
GAM1216	C21orf93	5' GGACTGCTCTCTGCTTCCA	59087	A TG GCA
		TG AAGTAGAGAG G TCC		
		AC TTCGTCTCTC C AGG		
		C GT__		
GAM1216	CLPTM1	3' GGATGCCCACGGCCGTTCA	7102	AGTAGAGA
		TGAA GTGGGCATCC		
		ACTT CACCCGTAGG		
		GCCGG__		
GAM1216	DKFZp434H2215	3' GGACACCCCTCACCTACTTTCA	34110	A_ T CA
		TGAAAGTAG GAG GGG TCC		
		ACTTTCATC CTC CCC AGG		
		CA _ AC		
GAM1216	EFA6R	3' TACTTCATCTATTTTCA	30989	__
		TGAAAGTAGA GAGTG		
		ACTTTTATCT TTCAT		
		AC		
GAM1216	FADS1	3' GATGCCATTCTCCAGTTTCA	25478	GTA G
		TGAAA GAGAGTGG CATC		
		ACTTT CTCTTACC GTAG		
		GAC _		
GAM1216	FGF19	3' GATCTATATCTCTACTTCCA	17587	A GTG C
		TG AAGTAGAGA GG ATC		
		AC TTCATCTCT TC TAG		
		C ATA _		
GAM1216	FLJ11088	3' ATGCATCTACTTTTCA	37039	GAGTGG
		TGAAAGTAGA GCAT		
		ACTTTCATCT CGTA		
		A__		
GAM1216	FLJ12806	3' TCTAGTCTTTACTTTTCA	43088	G
		TGAAAGTAGAGA TGGG		
		ACTTTCATTTCT ATCT		
		G		
GAM1216	FLJ14431	5' GGCTCCCCTCTCTACCTTC	51355	A CAT
		GAA GTAGAGAGTGGG CC		
		CTT CATCTCTCACCC GG		
		C TC_		
GAM1216	FLJ14437	5' GGACGGCTACTCTCTATTTCCA	50828	A GCA
		TG AAGTAGAGAGTGG TCC		

AC TTTATCTCTCATC AGG  
 C GGC  
 GAM1216 FLJ21135 3' GGACACCCCTTTCTAC 45886 T CA  
 GTAGAGAG GGG TCC  
 ||||| ||| |||  
 CATCTTTC CCC AGG  
 \_ AC  
 GAM1216 FLJ21916 3' GGATAATTCTCTACCCTCA 43645 AA GGGC  
 TGA GTAGAGAGT ATCC  
 || ||||| |||  
 ACT CATCTCTTA TAGG  
 CC A\_\_  
 GAM1216 FLJ23022 3' ATGCCCGCCTTTCTGC 46810 \_  
 GTAGAGAG TGGGCAT  
 ||||| |||||  
 CGTCTTTC GCCCGTA  
 C  
 GAM1216 FLJ25449 5' ATGCCACCATCGCTATCA 58512 A A GA  
 TGA AGT GA GTGGGCAT  
 || || || |||||  
 ACT TCG CT CACCCGTA  
 A \_ AC  
 GAM1216 GCN2 5' ATGCCACCTACCTATC 62767 A TAG A  
 GA AG AG GTGGGCAT  
 || || || |||||  
 CT TC TC CACCCGTA  
 A CA\_ \_  
 GAM1216 GGA2 3' CCTTGTCTCCATTTTCA 56876 A GT  
 TGAAAGT GAGA GGG  
 ||||| ||| |||  
 ACTTTTA CTCT TCC  
 C GT  
 GAM1216 GGA2 3' CCTTGTCTCCATTTTCA 30462 A GT  
 TGAAAGT GAGA GGG  
 ||||| ||| |||  
 ACTTTTA CTCT TCC  
 C GT  
 GAM1216 GIOT-3 5' GGATCTGCCTCCGCTTTCA 32750 TA A TG GC  
 TGAAAG GAG G G ATCC  
 ||||| ||| | |||  
 ACTTTC CTC C C TAGG  
 GC \_ GT \_  
 GAM1216 GPR107 3' GGAGCAGTGCTCTTCTCTCA 40565 A T G\_ A  
 TGA AG AGAGAGTG GC TCC  
 || || ||||| || |||  
 ACT TC TCTCTCGT CG AGG  
 C T GA \_  
 GAM1216 HEL308 5' GTCCCACTCTCCCTTCCA 56100 A TA \_  
 TG AAG GAGAGTGGG C  
 || || ||||| |

			AC TTC CTCTCACCC G		
			C C_ T		
GAM1216	HSPC159	3'	CCACCTCTATTTC	26358	G A
			TGAAA TAGAG GTGG		
			ACTTT ATCTC CACC		
			- -		
GAM1216	ISL2	3'	GATGCAACCTGCTTTCA	70840	AGA GG
			TGAAAGTAG GT GCATC		
			ACTTTCGTC CA CGTAG		
			- A-		
GAM1216	KIAA0063	3'	GATGCTGCCTCCACTTTC	29627	A A TG G
			GAAAGT GAG G G CATC		
			CTTTCA CTC C C GTAG		
			C _ GT _		
GAM1216	KIAA0064	3'	GGATGTCTGCCCTCTAC	28543	A TG
			GTAGAG G GGCATCC		
			CATCTC C CTGTAGG		
			C GT		
GAM1216	KIAA0408	3'	TTTGCTCTCTACTGTCA	28143	A TG
			TGA AGTAGAGAG GG		
			ACT TCATCTCTC TT		
			G GT		
GAM1216	KIAA0433	3'	ATGTTACACTTACTTTCA	30834	GAG _
			TGAAAGTA AGTG GGCAT		
			ACTTTCAT TCAC TTGTA		
			- A		
GAM1216	KIAA0446	3'	CCACTTCTCTACCTTCA	68859	A _
			TGAA GTAGAGA GTGG		
			ACTT CATCTCT CACC		
			C T		
GAM1216	KIAA0773	3'	ATGCCTCCTTTCTCCATTTC	28047	GT_ TG
			TGAAA AGAGAG GGCAT		
			ACTTT TCTTTC CCGTA		
			ACC CT		
GAM1216	KIAA0828	3'	ATGTATCTACTCTACCTTC	81191	A _ TGG
			GAA GTAGAG AG GCAT		
			CTT CATCTC TC TGTA		
			C A TA_		
GAM1216	KIAA1036	3'	GGATGCCTAACCTAACT	29824	AG AG
			AGT AG TGGGCATCC		



TCA TC ATCCGTAGG  
 A\_ CA  
 GAM1216 KIAA1437 5' GATGCCATGTACTCTCTCCT 60587 T \_\_\_\_  
 AG AGAGAGTG GGCATC  
 || ||||| |||||  
 TC TCTCTCAT CCGTAG  
 C GTA  
 GAM1216 KIAA1467 3' GGATACCCTCTCTACTCTC 71613 A T GC  
 GA AGTAGAGAG GG ATCC  
 || ||||| || |||||  
 CT TCATCTCTC CC TAGG  
 C \_ A\_  
 GAM1216 KIAA1509 3' GCCCACTCCCTCTCCCA 61615 AA T A  
 TG AG AG GAGTGGGC  
 || || || |||||  
 AC TC TC CTCACCCG  
 CC \_ C  
 GAM1216 KIAA1691 3' GCTTCACTCTCTCCCTCA 92558 AAGT \_  
 TGA AGAGAGTGG GC  
 ||| ||||| ||  
 ACT TCTCTCACT CG  
 CCC\_ T  
 GAM1216 LEAP-2 5' ATGCCCATGTCATTTCA 53740 GTA GA  
 TGAAA GA GTGGGCAT  
 |||| || |||||  
 ACTTT CT TACCCGTA  
 A\_ G\_  
 GAM1216 MGC10731 5' CCCACTCCCTGCTCTCA 48107 A A  
 TGA AGTAG GAGTGGG  
 ||| |||| |||||  
 ACT TCGTC CTCACCC  
 C C  
 GAM1216 MGC11386 3' GGATGCCACATGCTCTCTCCCA 51955 AA T A \_  
 TG AG AGAG GTG GGCATCC  
 || || |||| || |||||  
 AC TC TCTC TAC CCGTAGG  
 CC \_ G A  
 GAM1216 MGC14844 3' GATGCTTGGACTCTTCTCCCA 50340 AA T AG  
 TG AG AGAG TGGGCATC  
 || || |||| |||||  
 AC TC TCTC GTTCGTAG  
 CC T AG  
 GAM1216 MGC17919 3' TTATCCTCTTACTTTCA 58224 \_ AG  
 TGAAAGTA GAG TGG  
 ||||| ||| |||  
 ACTTTCAT CTC ATT  
 T CT  
 GAM1216 MGC21854 3' GCTCACTCCCTTCTCCCA 53491 AA T A  
 TG AG AG GAGTGGGC  
 || || || |||||

AC TC TC CTCACTCG  
 CC T C  
 GAM1216 MGC2541 3' GGATCCTCACCCCTTCCACTTTC 54751 A\_ A C  
 A TGAAAGT GAG GTGGG ATCC  
 ||||| || ||||| ||||  
 ACTTTCA TTC CACTC TAGG  
 CC C C  
 GAM1216 MGC8407 3' GATGCCCACCTCCTAC 43889 \_ A  
 GTAG AG GTGGGCATC  
 ||| || ||||| ||||  
 CATC TC CACCCGTAG  
 C \_  
 GAM1216 NYD-SP25 3' GGATGACCATCTCCACTTTC 53188 A G G  
 GAAAGT GAGA TGG CATCC  
 ||||| |||| || |||||  
 CTTTCA CTCT ACC GTAGG  
 C \_ A  
 GAM1216 P4HA2 5' GATGCCCAGTTGACCTTC 14839 A AGA G  
 GAA GT GA TGGGCATC  
 ||| || || ||||| ||||  
 CTT CA TT ACCCGTAG  
 C G\_ G  
 GAM1216 PAT2 3' GTCTGTAGTCTCTACTTCCA 80775 A \_ TG  
 TG AAGTAGAGA G GGC  
 || ||||| || ||||  
 AC TTCATCTCT T CTG  
 C GA GT  
 GAM1216 POPX1 3' ATGCCCACTCTTCTATT 29794 \_  
 AGTAGA GAGTGGGCAT  
 ||||| ||||| |||||  
 TTATCT CTCACCCGTA  
 T  
 GAM1216 PPP1R10 3' GCTCACTCCCTGCTCCCA 10734 AA A  
 TG AGTAG GAGTGGGC  
 || ||||| ||||| |||||  
 AC TCGTC CTCACTCG  
 CC C  
 GAM1216 PRO0082 3' GCCTTACTTCTACTTCCA 37735 A G \_  
 TG AAGTAGA AGTG GGC  
 || ||||| |||| ||||  
 AC TTCATCT TCAT CCG  
 C \_ T  
 GAM1216 RA-GEF-2 3' GGATACCAGTCTCCACTTTGCA 32955 \_ A G GC  
 TG AAAGT GAGA TGG ATCC  
 || ||||| |||| ||||  
 AC TTTCA CTCT ACC TAGG  
 G C G A\_  
 GAM1216 SCAMP5 3' CTGTTTCTACTTTCA 57259 G  
 TGAAAGTAGAGA TGG  
 ||||| ||||| ||||

ACTTTCATCTTT GTC

GAM1216 SFXN5 3' GGATGCCCTTCTTCCATTC 58037 AGTA T  
GAA GAGAG GGGCATCC  
||| |||| |||||  
CTT TTCTT CCCGTAGG  
ACC\_ \_

GAM1216 SLC16A6 3' GGAGCTAACCCCTCTACT 16274 A\_ G A  
AGTAGAG GT GGC TCC  
||||| || ||| |||  
TCATCTC CA TCG AGG  
CC A \_

GAM1216 STK22D 3' GATGAGCCTCTATTTTCA 49323 A GGG  
TGAAAGTAGAG GT CATC  
||||||| || |||  
ACTTTTATCTC CG GTAG  
\_ A\_

GAM1216 STK25 3' GAGGCCCTGCCACTTTCA 21051 AGAG T A  
TGAAAGT AG GGGC TC  
||||| || ||| ||  
ACTTTCA TC CCG AG  
CCG\_ \_ G

GAM1216 TCL6 5' ATGCTCATCTGACTTCCA 40124 A AG G  
TG AAGT AGA TGGGCAT  
|| ||| || |||||  
AC TTCA TCT ACTCGTA  
C G\_ \_

GAM1216 UPLC1 3' GGATGCCCACTTCTCTTCT 34726 T \_  
AG AGAGA GTGGGCATCC  
|| |||| |||||  
TC TCTCT CACCCGTAGG  
T T

GAM1216 ZMPSTE24 3' TCTGGTCTTACTTTCA 19597 A G  
TGAAAGT GAGA TGGG  
||||| ||| |||  
ACTTTCA TTCT GTCT  
\_ G

GAM1216 LOC126353 3' CCCGCTCCTCCACTTTCA 74499 A \_  
TGAAAGT GAG AGTGGG  
||||| ||| |||||  
ACTTTCA CTC TCGCCC  
C C

GAM1216 LOC128553 3' ATGCCTTAGTTTCCACTTTC 74760 A G \_  
GAAAGT GAGA TG GGCAT  
||||| ||| || |||  
CTTTCA CTTT AT CCGTA  
C G T

GAM1216 LOC144558 3' GGGTCTCTCACTTTCA 83148 A TGGGC  
TGAAAGT GAGAG ATCC  
||||| |||| |||

ACTTTCA CTCTC TGGG

GAM1216 LOC145082 5' GATGCTTGTGCCTTCTTTCA 83238 T AGA TG  
TGAAAG AG G GGCATC  
||||| || | |||||  
ACTTTC TC T TCGTAG  
T CG GT

GAM1216 LOC145384 3' TGCCCCTACTTTCA 77198 AGAGT  
TGAAAGTAG GGGCA  
||||||| |||||  
ACTTTCATC CCCGT

GAM1216 LOC146062 5' GGATTTGGCTCTCTACTTCCG 77661 A G C  
TG AAGTAGAGAGT GG ATCC  
|| ||||| || |||||  
GC TTCATCTCTCG TT TAGG  
C G \_

GAM1216 LOC146243 3' TCTGTCTCTACTTCA 83642 A G  
TGAA GTAGAGA TGGG  
||| ||||| |||||  
ACTT CATCTCT GTCT

GAM1216 LOC146287 5' GATGCTTTCTCCTTCA 83652 AAGT A TG  
TGA AG GAG GGCATC  
||| || ||| |||||  
ACT TC CTC TCGTAG  
\_ \_ TT

GAM1216 LOC146669 3' GGACAGGCATCTCTATTTTCA 78059 G GGCA  
TGAAAGTAGAGA TG TCC  
||||||| || |||  
ACTTTTATCTCT AC AGG  
\_ GGAC

GAM1216 LOC148018 5' GGATGTCTGCCTCCAGTTC 82420 AGTA A TG  
GAA GAG G GGCATCC  
||| ||| | |||||  
CTT CTC C CTGTAGG  
GAC \_ \_ GT

GAM1216 LOC148894 5' TGTCTTCTCTGCCTTCA 84261 A GT  
TGAA GTAGAGA GGGCA  
||| ||||| |||||  
ACTT CGTCTCT TCTGT  
C \_

GAM1216 LOC149668 5' GAAGCTCTCTCTACTCACA 84541 AA TG A  
TG AGTAGAGAG GGC TC  
|| ||||| ||| |||  
AC TCATCTCTC TCG AG  
AC \_ A

GAM1216 LOC149910 3' ATGCCTCCACGTACTTTCA 79529 GAGAGT  
TGAAAGTA GGGCAT  
||||||| |||||

ACTTTCAT TCCGTA  
 GCACC\_  
 GAM1216 LOC152633 5' GGATGCCCCACACTGC 85815 AGA \_  
 GTAG GTGGG CATCC  
 ||| |||| ||||  
 CGTC CACCC GTAGG  
 A\_ C  
 GAM1216 LOC154791 3' GGACATTTTCATCTTTACTCTCA 81158 A G CA\_  
 TGA AGTAGAGA TGGG TCC  
 || ||||| ||| ||  
 ACT TCATTTCT ACTT AGG  
 C \_ TAC  
 GAM1216 LOC157278 3' GGGTCTCTCACTTTCA 86425 A TGGGC  
 TGAAAGT GAGAG ATCC  
 ||||| |||| |||  
 ACTTTCA CTCTC TGGG  
 \_ \_  
 GAM1216 LOC162333 5' TTCACTCTCTCCTTTCA 87145 T  
 TGAAAG AGAGAGTGGG  
 ||||| |||||  
 ACTTTC TCTCTCACTT  
 C  
 GAM1216 LOC164955 3' GATGCCTCCACTCTCTA 82458 \_  
 TAGAGAGTGG GCATC  
 ||||| ||||  
 ATCTCTCACC CGTAG  
 TC  
 GAM1216 LOC165476 5' TTACCTCTGCTCTCA 87200 A A  
 TGA AGTAGAG GTGG  
 || ||||| ||||  
 ACT TCGTCTC CATT  
 C \_  
 GAM1216 LOC196500 3' GCTCACTCTCTCCCTCA 87742 AAGT  
 TGA AGAGAGTGGGC  
 || |||||  
 ACT TCTCTCACTCG  
 CCC\_  
 GAM1216 LOC200169 5' ATGCTGCTTTCCTCTTCCA 89943 A TA TG G  
 TG AAG GAGAG G CAT  
 || ||| |||| | |||  
 AC TTC CTTTC C GTA  
 C TC GT\_  
 GAM1216 LOC200197 3' GACGCCCTTCTCTCCACTTT 88615 A T\_ A  
 AAAGT GAGAG GGGC TC  
 |||| |||| ||| ||  
 TTTCA CTCTC CCCG AG  
 C TT C  
 GAM1216 LOC200197 3' GATGCCCACATTGCCCTGC 88616 A\_ \_  
 GTAG GA GTGGGCATC  
 ||| || |||||

		CGTC TT CACCCGTAG			
		CCG A			
GAM1216	LOC221962	3' GGGTCTCTCACTTTCA	92683	A	TGGGC
		TGAAAGT GAGAG ATCC			
		ACTTTCA CTCTC TGGG			
		— ———			
GAM1216	LOC222060	5' CTCACTCTCTACTTCA	94107	A	
		TGAA GTAGAGAGTGGG			
		ACTT CATCTCTCACTC			
		—			
GAM1216	LOC222134	5' GCAGATTCCTCTACTTCA	94139	A	_ GG
		TGAA GTAGAG AGT GC			
		ACTT CATCTC TTA CG			
		_ C GA			
GAM1216	LOC253150	3' ATGCCGGTCTCCTACTCTTCA	95514	_ A _ G	
		TGAA AGTAG GAG T GGCAT			
		ACTT TCATC CTC G CCGTA			
		C _ T G			
GAM1216	LOC254191	3' CCCACCCTCACTTTCA	94767	A A	
		TGAAAGT GAG GTGGG			
		ACTTTCA CTC CACCC			
		_ C			
GAM1216	LOC254753	3' CCCAACTCTCCACTTTCA	96146	A _	
		TGAAAGT GAGAGT GGG			
		ACTTTCA CTCTCA CCC			
		C A			
GAM1216	LOC255463	3' GGTGTGCATCTCTACTTCCA	94883	A	G G
		TG AAGTAGAGA TG GCATC			
		AC TTCATCTCT AC TGTGG			
		C _ G			
GAM1216	LOC51200	3' GATGATTCTCTACCCTCA	32997	AA	GGG
		TGA GTAGAGAGT CATC			
		ACT CATCTCTTA GTAG			
		CC —			
GAM1216	LOC56906	3' CCTATTCTCTACTTTCA	39316		
		TGAAAGTAGAGAGTGGG			
		ACTTTCATCTCTTATCC			
GAM1216	LOC90768	5' GCTCCACTCCCCACTTTTA	63958	AGA	_
		TGAAAGT GAGTGG GC			

			ATTTTCA CTCACC CG		
			CCC T		
GAM1217 AICDA	5'	GCCTGAGACTTGCAGGGAGGCA 40329	C	ATTTGC__	
AGAA		TTC TGCCTCCCT CAGGC			
		AAG ACGGAGGGA GTCCG			
		A CGTTCAGA			
GAM1217 ANK1	3'	GCCTCCGGCCCAGGGAGGCCAG 40027	CT	ATTT __	
AA		TTC GCCTCCCT GCC AGGC			
		AAG CGGAGGGA CGG TCCG			
		AC CC__ CC			
GAM1217 ANK1	3'	GCCTCCGGCCCAGGGAGGCCAG 3473	CT	ATTT __	
AA		TTC GCCTCCCT GCC AGGC			
		AAG CGGAGGGA CGG TCCG			
		AC CC__ CC			
GAM1217 EIF2C1	3'	CCCAAATCCAGAGGAAGCAAGG 24170	_ C _ _	CCA	
A		TCCT GC TCC CT ATTTG GG			
		AGGA CG AGG GA TAAAC CC			
		A A A CC _			
GAM1217 IKBKG	3'	CCCGGCACTGGGGAAGTCAAGA 13311	C _ C	TT A	
A		TTC TG C TCCCTA TGCC GG			
		AAG AC G AGGGGT ACGG CC			
		A T A C_ C			
GAM1217 IKBKG	3'	CCCGGCACTGGGGAAGTCAAGA 94663	C _ C	TT A	
A		TTC TG C TCCCTA TGCC GG			
		AAG AC G AGGGGT ACGG CC			
		A T A C_ C			
GAM1217 LY9	3'	AAATAAAAGGCAGGAA 71680	CCC		
		TTCCTGCCT TATTT			
		AAGGACGGA ATAAA			
		AA_			
GAM1217 MAFF	3'	TGGCAAATAGGGAGACAAGGA 24655	GC_		
		TCCT CTCCCTATTTGCCA			
		AGGA GAGGGATAAACGGT			
		ACA			
GAM1217 MC1R	5'	GCCCAGATGGAAGGAGGCAGG 9954	_	CCA	
		CCTGCCTCC CTATTTG GGC			
		GGACGGAGG GGTAGAC CCG			
		AA _			
GAM1217 MYO15A	3'	GCCTGAGGGAGGAGGCAGGAG 32671	_	ATTTGC	
		TTCCTGCCTCC CT CAGGC			

GAGGACGGAGG GG GTCCG  
 A GA\_\_\_\_  
 GAM1217 NRG1 3' GCAAATAGAAAACAGGAA 25646 CCTCC  
 TTCCTG CTATTTGC  
 ||||| |||||  
 AAGGAC GATAAACG  
 AAAA\_  
 GAM1217 NRG1 3' GCAAATAGAAAACAGGAA 25659 CCTCC  
 TTCCTG CTATTTGC  
 ||||| |||||  
 AAGGAC GATAAACG  
 AAAA\_  
 GAM1217 SEPN1 3' GCCTGGCAGAGGAAGAAGGAA 66369 GC C AT  
 TTCCT CT CCT TTGCCAGGC  
 |||| ||||| |||||  
 AAGGA GA GGA GACGGTCCG  
 A\_ A \_  
 GAM1217 SMURF1 3' GCCTAACCCGCGGGAGGCGGAA 92453 T TATTTGCC  
 TTCC GCCTCCC AGGC  
 ||| ||||| |||  
 AAGG CGGAGGG TCCG  
 \_ CGCCCAA\_  
 GAM1217 STAT6 3' GCCTAGGACGGATAGGCAGGAA 12021 CCCT \_ \_  
 TTCCTGCCT ATTTG CC AGGC  
 ||||| |||| |||||  
 AAGGACGGA TAGGC GG TCCG  
 \_ A A  
 GAM1217 TFF3 3' GCCCAGGCCTCAAGGGCAGGAA 63566 CCCTATTT A\_  
 TTCCTGCCT GCC GGC  
 ||||| ||| |||  
 AAGGACGGG CGG CCG  
 AACTC\_ AC  
 GAM1217 TOP3B 5' GCCCGGCGGCTCAGAAAGGCGG 14129 CC AT\_ A  
 GAA TTCCTGCCT CT TTGCC GGC  
 ||||| || ||||| |||  
 AAGGGCGGA GA GGCGG CCG  
 AA CTC C  
 GAM1217 VAV1 3' GCCTTGGCAGAGAGACGAG 18305 C\_ A \_  
 CTC CT TTTGCCA GGC  
 ||| ||||| |||  
 GAG GA AGACGGT CCG  
 CA G T  
 GAM1217 YWHAB 5' GCTGTGGATAGAGAAGCAGGAA 12692 C C TG CA  
 TTCCTGC TC CTATT C GGC  
 ||||| || ||||| | |||  
 AAGGACG AG GATAG G TCG  
 A A GT\_  
 GAM1217 AF020591 3' GCCTGGCAAACATGGCA 27141 TCCCTA  
 TGCC TTTGCCAGGC  
 ||| |||||



ACGG AAACGGTCCG  
 TAC\_\_  
 GAM1217 BCL2L1 3' CCTCAGGCAGGAAGGGCAGGAA 56804 CC ATT \_\_  
 TTCCTGCCT CT TGCC AGG  
 ||||| || ||| ||  
 AAGGACGGG GG ACGG TCC  
 AA \_\_ AC  
 GAM1217 BNIP-S 5' TAAAGAAGGAGGCAGGAA 56263 CTA  
 TTCCTGCCTCC TTTG  
 ||||| |||  
 AAGGACGGAGG AAAT  
 AAG  
 GAM1217 BTBD3 5' GCAAATAAGAGAAACAGGAA 30311 C\_\_ CC  
 TTCCTG CTC TATTTGC  
 |||| ||| |||||  
 AAGGAC GAG ATAAACG  
 AAA A\_  
 GAM1217 C20orf28 3' GCCTGAGACGGGAGGCAGGAA 31224 TAT GC  
 TTCCTGCCTCCC TT CAGGC  
 ||||| || |||||  
 AAGGACGGAGGG AG GTCCG  
 C\_\_ A\_  
 GAM1217 CHODL 5' CCCGGCAGGGAGGCAGGGA 46310 ATTT A  
 TTCCTGCCTCCCT GCC GG  
 ||||| ||| ||  
 AGGGACGGAGGGA CGG CC  
 \_\_ C  
 GAM1217 D2S448 3' CCTGAAGGGAAGCAGG 73519 C ATTTGC  
 CCTGC TCCCT CAGG  
 |||| ||| |||  
 GGACG AGGGA GTCC  
 A A\_\_  
 GAM1217 DKFZP434K1772 3' GCCTTACTCAGGAAGGCAGGAG 67714 C ATTTGCC  
 TTCCTGCCT CCT AGGC  
 ||||| || |||  
 GAGGACGGA GGA TCCG  
 A CTCAT\_\_  
 GAM1217 DKFZp547I094 3' CCTGGCAACCTGAGGGAGG 49637 AT\_\_  
 CCTCCCT TTGCCAGG  
 |||| |||||  
 GGAGGGA AACGGTCC  
 GTCC  
 GAM1217 DKFZP547L112 3' CCTGGATATAGCAAGGCAGGAA 66529 CC TTG  
 TTCCTGCCT CTAT CCAGG  
 ||||| ||| |||||  
 AAGGACGGA GATA GGTCC  
 AC TA\_  
 GAM1217 FABP7 5' CAAATAAGAAGGCAGGAG 7542 CCC  
 TTCCTGCCT TATTTG  
 ||||| |||||

GAGGACGGA ATAAAC  
 AGA  
 GAM1217 FLJ14957 3' CCCAAAGTGGGAGGCAGGGA 51744 TA CCA  
 TTCCTGCCTCCC TTTG GG  
 ||||| ||| ||  
 AGGGACGGAGGG AAAC CC  
 TG \_\_\_\_  
 GAM1217 FLJ20343 3' CCTGGCAAAGTACCAG 34998 CC CCTA  
 CTG TC TTTGCCAGG  
 ||| || |||||  
 GAC AG AAACGGTCC  
 C\_ TC\_\_  
 GAM1217 FLJ23185 3' CCTGGCAGGATGAGGCAGAGA 46830 \_ CCTA  
 TC CTGCCTC TTTGCCAGG  
 || ||||| |||||  
 AG GACGGAG GGACGGTCC  
 A TA\_\_  
 GAM1217 GGA2 3' GCCTGATGGGTGGGAGAAGGAA 30468 GC T GC  
 TTCCT CTCCC ATTT CAGGC  
 |||| |||| ||| ||||  
 AAGGA GAGGG TGGG GTCCG  
 A\_ \_ TA  
 GAM1217 GGA2 3' GCCTGATGGGTGGGAGAAGGAA 56882 GC T GC  
 TTCCT CTCCC ATTT CAGGC  
 |||| |||| ||| ||||  
 AAGGA GAGGG TGGG GTCCG  
 A\_ \_ TA  
 GAM1217 HDAC11 3' GCCCATAGGTCCAGGGAGGCAG 45718 ATTT A\_\_\_\_  
 G CCTGCCTCCCT GCC GGC  
 ||||| ||| ||  
 GGACGGAGGGA TGG CCG  
 CC\_\_ ATAC  
 GAM1217 IKKE 5' CACAAGGAGGCAGGGA 25746 CTAT CCA  
 TTCCTGCCTCC TTG G  
 ||||| ||| |  
 AGGGACGGAGG AAC C  
 \_\_\_\_ A\_  
 GAM1217 IL1F10 3' CAAGAAGGAGGCAGGAA 50771 CTA  
 TTCCTGCCTCC TTTG  
 ||||| |||  
 AAGGACGGAGG GAAC  
 AA\_  
 GAM1217 KIAA0370 5' GCCCAGCAAATAGGAGCCTGGA 73209 T\_ CTC CA  
 G TTCC GC CCTATTTGC GGC  
 ||| || ||||| |||  
 GAGG CG GGATAAACG CCG  
 TC A\_\_ AC  
 GAM1217 KIAA0551 3' GCCTGGTTGAGAAGGAGAG 66839 \_ A\_ T  
 CTC CCT TT GCCAGGC  
 ||| ||| || |||||

GAG GGA AG TGGTCCG  
 A AG T  
 GAM1217 KIAA1183 3' CCCGGATGGGAGGAGGAA 62530 G TATTTG A  
 TTCCT CCTCCC CC GG  
 |||| |||| ||  
 AAGGA GGAGGG GG CC  
 \_ TA\_\_ C  
 GAM1217 KIAA1464 3' CCTGACCCATGGAGGCAGGAG 68264 CTATTTGC  
 TTCCTGCCTCC CAGG  
 ||||| ||||  
 GAGGACGGAGG GTCC  
 TACCCA\_\_  
 GAM1217 MAPK8IP3 3' GCCTGGTAGATGAAGCAG 52987 C CCT  
 CTGC TC ATTTGCCAGGC  
 ||| || |||||  
 GACG AG TAGATGGTCCG  
 A \_\_  
 GAM1217 MGC2306 3' GCCTGGCAGGGGGTGAAGGCAG 50963 \_\_ AT  
 GAG TTCCTGCCT CCCT TTGCCAGGC  
 ||||| ||| |||||  
 GAGGACGGA GGGG GACGGTCCG  
 AGT \_\_  
 GAM1217 MGC2865 5' GCCTGGCAAACCGAAGCAAGAA 50451 C C CCTA  
 TTC TGC TC TTTGCCAGGC  
 ||| ||| || |||||  
 AAG ACG AG AAACGGTCCG  
 A A CC\_\_  
 GAM1217 MGC9753 3' GCCTGATTTTGGGGAGGAGGAA 53049 G TTTGC  
 TTCCT CCTCCCTA CAGGC  
 |||| ||||| ||||  
 AAGGA GGAGGGGT GTCCG  
 \_ TTTA\_  
 GAM1217 PALM 3' GCCTGGTAGGAGAGAGACAGGA 10414 C C A  
 TCCTG CTC CT TTTGCCAGGC  
 |||| ||| || |||||  
 AGGAC GAG GA GGATGGTCCG  
 A A \_  
 GAM1217 PDZD2 5' CCTGGCACGGAAGGAGGAA 80866 G C TATT  
 TTCCT CCT CC TGCCAGG  
 |||| ||| || |||||  
 AAGGA GGA GG ACGGTCC  
 \_ A C\_\_  
 GAM1217 PLPL 3' CCTGGAGGGGGAGGCAGGAG 39431 ATTTG  
 TTCCTGCCTCCCT CCAGG  
 ||||| ||||  
 GAGGACGGAGGGG GGTCC  
 GA\_\_  
 GAM1217 RABEX5 3' GCCTGGAATGGAAGGCGGGAA 27186 C TATTTG  
 TTCCTGCCT CC CCAGG  
 ||||| || |||||

		AAGGGCGGA GG	GGTCCG		
		A TAA__			
GAM1217 SHANK3	5'	GCCTGCTCGCAGGGAGGCAGAG	65500	_	ATTT C
	A	TC CTGCCTCCCT	GC AGGC		
		AG GACGGAGGGA	CG TCCG		
		A	CGCT _		
GAM1217 SRF	5'	CCGGGCCACAGGGGCAGGAA	11944		CCTATTT A
		TTCCTGCCTC	GCC GG		
		AAGGACGGGG	CGG CC		
		ACAC__	G		
GAM1217 TREX1	5'	CCCAGCAGAGGGAGGCAG	53280	AT	CA
		CTGCCTCCCT	TTGC GG		
		GACGGAGGGA	GACG CC		
		_	AC		
GAM1217 TREX1	5'	CCCAGCAGAGGGAGGCAG	53290	AT	CA
		CTGCCTCCCT	TTGC GG		
		GACGGAGGGA	GACG CC		
		_	AC		
GAM1217 URG4	3'	GCCCCCAGGGTAGGGAGACA	35506	C	GCCA
		TG CTCCCTATTT	GGC		
		AC GAGGGATGGG	CCG		
		A	ACCC		
GAM1217 LOC124222	3'	CCTGACAAACAGGCAGGGA	74271		CCCTA C
		TTCCTGCCT	TTTG CAGG		
		AGGGACGGA	AAAC GTCC		
		C__	A		
GAM1217 LOC131873	5'	CCCGGAGGAGAGGCAGGGA	75877	_	ATTTG A
		TTCCTGCCTC	CCT CC GG		
		AGGGACGGAG	GGA GG CC		
		A	C		
GAM1217 LOC144348	5'	CCTTCCGTAGAAAGACAGGCA	76806	CC A	C__
		TGCCT CT	TTTGC AGG		
		ACGGA	GA AGATG TCC		
		CA A	CCT		
GAM1217 LOC146316	5'	CTTCGAGAGGCAGGAA	60872		CCTAT CC
		TTCCTGCCTC	TTG AG		
		AAGGACGGAG	AGC TC		
		_____	T_		
GAM1217 LOC148529	5'	CCTGGCAGACAGGAAGACA	84167	C C	A
		TG CT CCT	TTTGCCAGG		

AC GA GGA AGACGGTCC  
 A A C  
 GAM1217 LOC149606 3' GCCCGCGGAGCAGGGAG 79454 A\_ CA  
 CTCCCT TTTGC GGC  
 ||||| ||||| ||  
 GAGGGA AGGCG CCG  
 CG C\_  
 GAM1217 LOC151057 3' CCAGGAAAGAAGGCAGGAA 85209 CCCTA G A  
 TTCCTGCCT TTT CC GG  
 ||||| || || ||  
 AAGGACGGA AAA GG CC  
 AG\_\_ \_ A  
 GAM1217 LOC153346 5' CCCAGATGGAAGGCA 86022 CC CCA  
 TGCCT CTATTTG GG  
 ||||| ||||| ||  
 ACGGA GGTAGAC CC  
 A\_ \_  
 GAM1217 LOC196418 5' CCTTCCGTAGAAAGACAGGCA 87696 CC A C\_  
 TGCCT CT TTTGC AGG  
 ||||| ||||| ||  
 ACGGA GA AGATG TCC  
 CA A CCT  
 GAM1217 LOC199786 3' GCCTGGCAGCTGAGGCAGAGA 88386 \_ CCTAT  
 TC CTGCCTC TTGCCAGGC  
 || ||||| |||||  
 AG GACGGAG GACGGTCCG  
 A TC\_  
 GAM1217 LOC200058 3' CCTGAAGGATGGGAAGCCAGGA 88556 C C GC  
 A TTCCTG CT CCTATTT CAGG  
 ||||| || ||||| |||||  
 AAGGAC GA GGGTAGG GTCC  
 C A AA  
 GAM1217 LOC204579 5' CCCGGCTATGAGGCAGGAA 89465 CCTATTT A  
 TTCCTGCCTC GCC GG  
 ||||| || || ||  
 AAGGACGGAG CGG CC  
 TAT\_\_ C  
 GAM1217 LOC219700 5' GCCTGGCAGTCCAAAGACCAAG 93064 C CCTCCCTAT  
 AA TTC TG TTGCCAGGC  
 ||| || |||||  
 AAG AC GACGGTCCG  
 A CAGAAACCT  
 GAM1217 LOC253181 5' GCCTGGCAAACAGCACAGGA 97558 CCTCC A  
 TCCTG CT TTTGCCAGGC  
 ||||| || |||||  
 AGGAC GA AAACGGTCCG  
 AC\_\_ C  
 GAM1217 LOC253296 3' GCCTGGGGCCACAGGAAAGGCA 94490 C\_ ATTTG\_  
 GGAA TTCCTGCCT CCT CCAGGC  
 ||||| || |||||

AAGGACGGA GGA GGTCCG  
 AA CACCGG  
 GAM1217 LOC253298 5' GCCTGGGGCCACAGGAAAGGCA 97215 C\_ ATTTG\_  
 GGAA TTCCTGCCT CCT CCAGGC  
 ||||| ||| |||||  
 AAGGACGGA GGA GGTCCG  
 AA CACCGG  
 GAM1217 LOC254107 5' CCCAGAGGGCAGGAA 94384 CCCTA CCA  
 TTCCTGCCT TTTG G  
 ||||| ||| |  
 AAGGACGGG AGAC C  
 \_\_\_\_\_ C\_  
 GAM1217 LOC255189 5' CTGACCAAGGCAGGAA 96589 CCCTATT C\_  
 TTCCTGCCT TG CAG  
 ||||| || |||  
 AAGGACGGA AC GTC  
 \_\_\_\_\_ CA  
 GAM1217 LOC257160 3' CCTGACTGGGGAGGAAG 94846 G TTTGC  
 CT CCTCCCTA CAGG  
 || ||||| |||  
 GA GGAGGGGT GTCC  
 A CA\_  
 GAM1217 LOC257570 3' GCCTGGGGCCACAGGAAAGGCA 97833 C\_ ATTTG\_  
 GGAA TTCCTGCCT CCT CCAGGC  
 ||||| ||| |||||  
 AAGGACGGA GGA GGTCCG  
 AA CACCGG  
 GAM1217 LOC257571 5' GCCTGGGGCCACAGGAAAGGCA 97945 C\_ ATTTG\_  
 GGAA TTCCTGCCT CCT CCAGGC  
 ||||| ||| |||||  
 AAGGACGGA GGA GGTCCG  
 AA CACCGG  
 GAM1218 ABCD1 3' AGACAGCAGCACCCACCC 3460 AATA  
 GGGTGGG GCTGTCT  
 ||||| |||||  
 CCCACCC CGACAGA  
 ACGA  
 GAM1218 AQP6 5' GAGACAGCCCCACATCCCACC 7950 CC ATA\_\_\_\_  
 CCATCA GA GGGTGGGA GCTGTCTC  
 || ||||| |||||  
 CT CCCACCCT CGACAGAG  
 AC ACACCCC  
 GAM1218 AQP6 5' GAGACAGCCCCACATCCCACC 53925 CC ATA\_\_\_\_  
 CCATCA GA GGGTGGGA GCTGTCTC  
 || ||||| |||||  
 CT CCCACCCT CGACAGAG  
 AC ACACCCC  
 GAM1218 FY 5' GAGACCTTGTCTCCCACCCG 8972 AT T\_\_\_\_  
 CGGGTGGGA AGC GTCTC  
 ||||| ||| |||||

GCCCACCCT TTG CAGAG  
 C\_ TTC  
 GAM1218 GJA5 3' GAGTCCCTGTCCCCACCCGGTC 74675 A CTGT  
 A TGACCGGGTGGG ATAG CTC  
 ||||| ||| ||  
 ACTGGCCCACCC TGTC GAG  
 C CCT\_  
 GAM1218 PCDH9 5' GAGACAGCCATTACACA 82797 G A  
 TG GAAT GCTGTCTC  
 || ||| |||||  
 AC CTTA CGACAGAG  
 A C  
 GAM1218 PVR 3' ACAGCCACTGACCCTGGTCA 21469 \_ G AATA  
 TGACC GGGT GG GCTGT  
 |||| ||| || ||||  
 ACTGG CCCA TC CGACA  
 T G AC\_  
 GAM1218 SERPINA4 5' GAGACAGCCACCCAGGGGGGTC 20611 GGG AATA  
 GACC TGGG GCTGTCTC  
 ||| ||| |||||  
 CTGG ACCC CGACAGAG  
 GGG AC\_  
 GAM1218 ARHGEF9 3' AGACAGAGCCCACCTGATCA 30805 C AATAG  
 TGA CGGGTGGG CTGTCT  
 || ||||| |||||  
 ACT GTCCACCC GACAGA  
 A GA\_  
 GAM1218 CAPN13 3' GAGACGTGGCGCCCCACCCAGT 58012 C AATA \_  
 C GAC GGGTGGG GCT GTCTC  
 || ||||| || |||||  
 CTG CCCACCC CGG CAGAG  
 A CG\_ TG  
 GAM1218 CLSTN1 3' ACATGCTCACTCCCACCCGGT 30101 AT\_ \_  
 ACCGGGTGGGA AGC TGT  
 ||||| ||| |||  
 TGGCCCACCCT TCG ACA  
 CAC T  
 GAM1218 DKFZP564O0423 3' AGACAGCTACTCTTTTGTGGCC 91677 A GGT A  
 G TG CCG GGA TAGCTGTCT  
 || ||| ||| |||||  
 GC GGT TTCT ATCGACAGA  
 C GTT C  
 GAM1218 FLJ20154 3' ACAAACATTCCCCACCCGG 72922 \_ AGC  
 CCGGGTGGG AAT TGT  
 ||||| ||| |||  
 GGCCCACCC TTA ACA  
 C CAA  
 GAM1218 MGC16186 5' GAGACAGCTAGCCAGCCAGCC 50430 G GAA\_  
 GG TGG TAGCTGTCTC  
 || ||| |||||

			CC ACC ATCGACAGAG		
			G GACCG		
GAM1218	LOC112609	3'	GAGACAGCCATCCCCTGCCT	72839	_ A A
			GGGT GGG AT GCTGTCTC		
			TCCG CCC TA CGACAGAG		
			T C C		
GAM1218	LOC116411	5'	GATCAGTCCCCACCCGGCCA	73865	A AATA _
			TG CCGGGTGGG GCTG TC		
			AC GGCCACCC TGAC AG		
			C CC_ T		
GAM1218	LOC164537	5'	GCCTCTCCCCACCCGGTCA	87219	AATA_
			TGACCGGGTGGG GC		
			ACTGGCCACCC CG		
			CTCTC		
GAM1218	LOC169021	5'	AGCCCATTCCCGCCAGTCA	82721	C A_
			TGAC GGGTGGGAAT GCT		
			ACTG CCCGCCCTTA CGA		
			A CC		
GAM1218	LOC253148	5'	AGACAGCTACCCCGGCC	96871	G AA
			GGGT GG TAGCTGTCT		
			CCCG CC ATCGACAGA		
			G CC		
GAM1218	LOC254003	5'	GCCCATCCCCACCCGCTCA	96290	C A A_
			TGA CGGGTGGG AT GC		
			ACT GCCCACCC TA CG		
			C C CC		
GAM1218	LOC91759	5'	GAGAGCTTCCCACCC	67087	AT G
			GGGTGGGA AGCT TC		
			CCCACCCT TCGA AG		
			_ G		
GAM1219	ASPH	3'	CATCATTTTGAAAGG	50616	TA
			CCTT TCAGGATGATG		
			GGAA AGTTTTACTAC		
			_		
GAM1219	ASPH	3'	CATCATTTTGAAAGG	50629	TA
			CCTT TCAGGATGATG		
			GGAA AGTTTTACTAC		
			_		
GAM1219	DDX6	5'	CTGCATTGCAATAAAGG	15287	CAGGAT
			CCTTTAT GATGCAG		



		GGAAATA TTACGTC	
		ACG____	
GAM1219	TRIP15	3' CTGCAGTGTAGTAAAGGTTT 14893	CAGGATGA
		AAACCTTTAT TGCAG	
		TTTGGAATG ACGTC	
		ATGTG____	
GAM1219	FLJ13593	3' CAGACCTGGCAAAGGTTT 45503	AT A_
		AAACCTTT CAGG TG	
		TTTGGAAA GTCC AC	
		CG AG	
GAM1219	FLJ21988	3' CTGCATCATCCCCAGCCAGGT 42554	A TTATCA_
	CC	A ACCT GGATGATGCAG	
		C TGGA CCTACTACGTC	
		C CCGACCC	
GAM1219	HIRIP5	5' CTGCATCAGTTTGTACAAAG 31653	AT_ A
		CTTT CAGG TGATGCAG	
		GAAA GTTT ACTACGTC	
		CAT G	
GAM1219	KIAA0547	3' TGCATCATCCCAGGTTT 28917	TTATCA
		AAACCT GGATGATGCA	
		TTTGGA CCTACTACGT	
		C_____	
GAM1219	KIAA1223	3' CTGCAGTTCCCTGATAAA 71145	ATGA
		TTTATCAGG TGCAG	
		AAATAGTCC ACGTC	
		CTTG	
GAM1219	KIAA1951	3' CTGCATCACCCCTGGTG 73759	A
		TATCAGG TGATGCAG	
		GTGGTCC ACTACGTC	
		C	
GAM1219	PFDN1	3' CTGCATCACCCCTGAGCCCCATT 10511	CCTTTA A
	TG	CAAA TCAGG TGATGCAG	
		GTTT AGTCC ACTACGTC	
		ACCCCG C	
GAM1219	SLC22A6	3' CATCATTTAAAGGTTTG 16570	ATCAG
		CAAACCTTT GATGATG	
		GTTTGGAAA TTACTAC	
		A_____	
GAM1219	LOC90835	3' CATTTTCCCCAATAAAGGTCTG 64127	A CA_ T
		CA ACCTTTAT GGA GATG	

GT TGGAAATA CCT TTAC  
 C ACC T  
 GAM1219 LOC92218 3' CTGCACTTTCTTGATAAATATT 68505 CC TGA  
 TG CAAA TTTATCAGGA TGCAG  
 ||| ||||| |||  
 GTTT AAATAGTTCT ACGTC  
 AT TTC  
 GAM1220 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
 GTA GGAT GGGTTGTTT  
 ||| ||| |||||  
 CGT CCTA CCCAACAAA  
 C CGTG\_  
 GAM1220 LCT 3' AACCGTAAAAATCCTT 9697 G  
 AAGGATTTTTTA GGTT  
 ||||| |||  
 TTCCTAAAAAT CCAA  
 G  
 GAM1220 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
 GTAAGGATTTTTAGGGTTGTTT  
 |||||  
 CATTCTAAAAATCCCAACAAA  
  
 GAM1220 FBXO30 3' AACTAAAAAATCCTGAC 49573 A AG  
 GT AGGATTTTT GGTT  
 || ||||| |||  
 CA TCCTAAAAA TCAA  
 G AA  
 GAM1220 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTTT  
 GTAAG AGGGTTGTT  
 ||| |||||  
 CATTCTCCCAACAA  
 AT\_\_\_\_  
 GAM1220 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
 TAAG TTTT GGGTTGTTT  
 ||| ||| |||||  
 GTTC AAAA CCCAACAAA  
 \_\_\_\_ C  
 GAM1220 SMT3H2 3' AACCAACATAAAAAATCCTTGC 22670 GG  
 GTAAGGATTTTTTA GTTGTT  
 ||||| |||  
 CGTTCCTAAAAAT CAACAA  
 A\_  
 GAM1220 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
 GTAAGGATTTTT GGGTT  
 ||||| |||  
 CGTTCCTAAAAA TCCAA  
 GTA  
 GAM1220 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
 GGAT TT GGGTTGTTT  
 ||| || |||||

			CCTG AA CCCAACAAA		
			T_ C		
GAM1220	LOC133088	5'	AAACAAAATAGAAAAATCCCTG 75075	A	AGGG_
		C	GTA GGATTTTT TTGTTT		
			CGT CCTAAAAA AACAAA		
			C GATAA		
GAM1220	LOC148089	3'	GGCCCTAAAAATTCCTAC 78637	A	
			GTA GGATTTTTAGGGTT		
			CAT CTTAAAAATCCCGG		
			C		
GAM1220	LOC154547	3'	AACAACATAAAAAATCCTTGC 76050		GG
			GTAAGGATTTTTA GTTGTT		
			CGTTCCTAAAAAT CAACAA		
			A_		
GAM1220	LOC158104	3'	ACAGCCAAAAATCCTTA 60313	AG	
			TAAGGATTTTT GTTGT		
			ATTCCTAAAAA CCGACA		
			—		
GAM1220	LOC205880	5'	AAACAACCATCATCCTGAC 90709	A	TTTTAG
			GT AGGAT GGTTGTTT		
			CA TCCTA CCAACAAA		
			G CTA_		
GAM1220	LOC221561	3'	AACAACATAAAAAATCCTTGC 92130		GG
			GTAAGGATTTTTA GTTGTT		
			CGTTCCTAAAAAT CAACAA		
			A_		
GAM1220	LOC257591	3'	AACAACATAAAAAATCCTTGC 97840		GG
			GTAAGGATTTTTA GTTGTT		
			CGTTCCTAAAAAT CAACAA		
			A_		
GAM1220	LOC51145	3'	AGCTAAAATCCTTAC 32393		TAG
			GTAAGGATTTT GTT		
			CATTCCTAAAA TCGA		
			—		
GAM1221	ABCC5	3'	AGTGCATATTCCTTTCT 19094	ATGT	
			AGAAG GTGTGCACT		
			TCTTT TATACGTGA		
			CCT_		
GAM1221	ACT	5'	TGCAGGGACCCTTCTGTT 40043	AT	GTG
			AACAGAAG GT TGCA		

			TTGTCTTC CA ACGT		
			C_ GGG		
GAM1221	ATF6	3'	ACAGTCATCTTCTTTTA 63948	C	TG
			TAA AGAAGATG TGT		
			ATT TCTTCTAC ACA		
			T TG		
GAM1221	BAZ2A	5'	ACACGGTCTGCACCTTCTGTTG 25589	A	_____
			TAACAGAAG TGT GTGT		
			GTTGTCTTC ACG CACA		
			C TCTGG		
GAM1221	BCL3	3'	TGCCACCCACATCTTC 17735	T	_
			GAAGATGTG GTG CA		
			CTTCTACAC CAC GT		
			C C		
GAM1221	C7orf2	3'	GCGCATTCTTCTGT 42403	TGT	
			ACAGAAGA GTGTGC		
			TGTCTTCT TACGCG		
			_____		
GAM1221	CERD4	3'	TGTGCCACATCTTCTG 23858	T	TG
			CAGAAGATGTG G CA		
			GTCTTCTACAC C GT		
			_GT		
GAM1221	CTBP2	3'	ACGACCAACTTCTGTTA 7179	A	TG
			TAACAGAAG TG TGT		
			ATTGTCTTC AC GCA		
			A CA		
GAM1221	CTBP2	3'	ACGACCAACTTCTGTTA 42987	A	TG
			TAACAGAAG TG TGT		
			ATTGTCTTC AC GCA		
			A CA		
GAM1221	DACH	3'	TGCAAGAGTGATTTTCTGTTA 54975		GTGTG_
			TAACAGAAGAT TGCA		
			ATTGTCTTTTA ACGT		
			GTGAGA		
GAM1221	GJB3	3'	AGTACACACACAATCACTG 43763	AA	_ C
			CAG GAT GTGTGTG ACT		
			GTC CTA CACACAC TGA		
			A_ A A		
GAM1221	GPM6B	3'	TACTTACATTTTCTGTTA 67076		T
			TAACAGAAGATGTG GTG		

		ATTGTCTTTTACAT CAT	
		T	
GAM1221 HOXA3	3'	GCAGGGCGGTCTTCTG 47689	G G_
		CAGAAGAT TGT TGC	
		GTCTTCTG GCG ACG	
		_ GG	
GAM1221 JAM3	3'	GTGCACATACCTCTGCT 51427	A T
		AG AGA GTGTGTGCAC	
		TC TCT CATAACCGTG	
		G C	
GAM1221 MKKS	5'	AGTGGCTGCTACCTTCTGTTA 38138	AT_ T G
		TAACAGAAG GTG GT CACT	
		ATTGTCTTC CGT CG GTGA	
		CAT _ _	
GAM1221 NSF	3'	GCACACATTGTGTTA 63071	G AGAT
		TAACA A GTGTGTGC	
		ATTGT T TACACACG	
		G _	
GAM1221 OGN	3'	AGTGCACACTACCTTC 25920	A T
		GAAG TG GTGTGCACT	
		CTTC AT CACACGTGA	
		C _	
GAM1221 OGN	3'	AGTGCACACTACCTTC 44325	A T
		GAAG TG GTGTGCACT	
		CTTC AT CACACGTGA	
		C _	
GAM1221 OGN	3'	AGTGCACACTACCTTC 52243	A T
		GAAG TG GTGTGCACT	
		CTTC AT CACACGTGA	
		C _	
GAM1221 PATE	3'	ACACATGGCTCCATCTTCTG 56311	_____
		CAGAAGATG TGTGT	
		GTCTTCTAC ACACA	
		CTCGGT	
GAM1221 PCSK1	3'	TACCCGCATCTTCTGTTA 4774	T
		TAACAGAAGATGTG GTG	
		ATTGTCTTCTACGC CAT	
		C	
GAM1221 PPP2R5A	3'	GTATTTCTCACATCTTTTGTTA 20709	T__
		TAACAGAAGATGTG GTGC	

ATTGTTTTCTACAC TATG  
 TCTT  
 GAM1221 RAB13 3' ATACACTGATTTATTCTGTTA 11200 GAT\_\_\_\_  
 TAACAGAA GTGTGT  
 ||||| |||||  
 ATTGTCTT CACATA  
 ATTTAGT  
 GAM1221 RP1 3' GCACACTCATTCTTTGT 20772 AG T  
 ACAGA ATG GTGTGC  
 |||| |||||  
 TGTTT TAC CACACG  
 CT T  
 GAM1221 SLC7A8 3' AGTACACACACCCCTCTCT 24275 A \_\_\_\_ C  
 AGA GA TGTGTGTG ACT  
 ||| ||||| |||  
 TCT CT ACACACAC TGA  
 \_ CCCC A  
 GAM1221 TEAD3 3' GCACACACACTCCCTG 12209 A\_ A  
 CAG AG TGTGTGTGC  
 ||| |||||  
 GTC TC ACACACACG  
 CC \_  
 GAM1221 TIMP3 5' GCACAGAAAACAGTCTTCT 4511 \_ G\_\_\_\_  
 AGAAGA TGT TGTGC  
 ||||| ||| |||||  
 TCTTCT ACA ACACG  
 G AAAG  
 GAM1221 TJP1 3' CACCACTACATTCTGTTA 12296 GAT\_ T  
 TAACAGAA GTG GTG  
 ||||| ||| |||  
 ATTGTCTT CAC CAC  
 ACAT \_  
 GAM1221 TMOD2 3' TGCACATGCCCTGTTG 27254 AAGAT  
 TAACAG GTGTGTGCA  
 ||||| |||||  
 GTTGTC CGTACACGT  
 C\_\_\_\_  
 GAM1221 UCHL1 3' ACACAGCTGTTCTTCTGTT 14815 TG\_\_\_\_  
 AACAGAAGA TGTGT  
 ||||| |||||  
 TTGTCTTCT ACACA  
 TGTCG  
 GAM1221 VIPR2 3' GCTCACACATCCTGT 12613 AA T  
 ACAG GATGTGTG GC  
 ||| ||||| |||  
 TGTC CTACACAC CG  
 \_ T  
 GAM1221 WHSC1L1 3' AGTGCATACAGCCTTT 43518 ATG  
 GAAG TGTGTGCACT  
 ||| |||||

			TTTC ACATACGTGA		
			CG_		
GAM1221	BIRC3	5'	CACATCACTCTTCTGT	67196	T _
			ACAGAAGA GTG TGTG		
			TGTCTTCT CAC ACAC		
			_ T		
GAM1221	BRD4	3'	GCACACGCCTTGTTA	54276	AAGAT
			TAACAG GTGTGTGC		
			ATTGTT CGCACACG		
			C_		
GAM1221	BTN1A1	3'	ACACACACCTTCAGTTA	8191	A A
			TAAC GAAG TGTGTGT		
			ATTG CTTC ACACACA		
			A C		
GAM1221	C19orf7	3'	GCACGCACGTTCTGT	61128	AG
			ACAGA ATGTGTGTGC		
			TGTCT TGCACGCACG		
			_		
GAM1221	CDA02	3'	AGTGCAAACACATCTTCTGTTA	67848	G
			TAACAGAAGATGTGT TGC ACT		
			ATTGTCTTCTACACA ACGTGA		
			A		
GAM1221	CHST3	3'	AGTGCACACACATCTATG	14967	GA
			CA AGATGTGTGTGCACT		
			GT TCTACACACACGTGA		
			A_		
GAM1221	DKFZP564I0422	3'	ACACAGATCTTCTGTT	48712	G
			AACAGAAGAT TGTGT		
			TTGTCTTCTA ACACA		
			G		
GAM1221	FLJ10540	3'	ATACTGTATTTTCTGTTA	36257	GT_
			TAACAGAAGAT GTGT		
			ATTGTCTTTTA CATA		
			TGT		
GAM1221	FLJ11113	3'	TGCACACTTTATCTTTT	59395	T_
			AGAAGATG GTGTGCA		
			TTTTCTAT CACACGT		
			TT		
GAM1221	FLJ12707	3'	GCAGCATTCTGTGA	41948	A GTG
			TAACAGA GATGT TGC		

ATTGTCT TTACG ACG

GAM1221 FLJ20546 3' GCGCCACCTTCTGTTG 35368 AT T  
TAACAGAAG GTG GTGC  
||||||| ||| |||  
GTTGTCTTC CAC CGCG

GAM1221 FLJ31890 3' TGTCAAGACATTTTCTGT 91342 G\_ T  
ACAGAAGATGT TG GCA  
||||||| ||| |||  
TGTCTTTTACA AC TGT

GAM1221 GMFB 3' ATAGAACATCTTCTGTT 14663 G\_  
AACAGAAGATGT TGT  
||||||| |||  
TTGTCTTCTACA ATA  
AG

GAM1221 GTF2A2 3' ACACCATCTTCTGTTA 15675 T  
TAACAGAAGATG GTGT  
||||||| |||  
ATTGTCTTCTAC CACA

GAM1221 H2AFJ 3' GTACACACCTCTGTTA 36841 AGAT  
TAACAGA GTGTGTGC  
||||| |||||  
ATTGTCT CACACATG  
C\_\_

GAM1221 HCA4 3' AGTGCAAATACCTTCT 77580 AT G  
AGAAG GTGT TGC ACT  
|||| ||| |||||  
TCTTC CATA ACGTGA

GAM1221 K6HF 3' GCAGCACCCGTCTGTTA 16271 AGAT G  
TAACAGA GTGT TGC  
||||| ||| |||  
ATTGTCT CACG ACG  
GCC\_ \_

GAM1221 KCNH8 3' AGTGCACAGCTCCTGCTG 58252 A AT G  
CAG AG GT TGTGCACT  
||| || ||| |||||  
GTC TC CG ACACGTGA  
G CT \_

GAM1221 KIAA0144 3' TGCACACACCTGCTGTTG 29286 A AT  
TAACAG AG GTGTGTGCA  
||||| || |||||  
GTTGTC TC CACACACGT  
G \_

GAM1221 KIAA0193 3' AGTGCACAGTGTCTCT 28649 A TG G  
AGA GA T TGTGCACT  
||| || | |||||



			TCT CT G ACACGTGA		
			_ GT _		
GAM1221	KIAA0193	3'	ACACAATGGCTACTTCTGTGA 28648	ATG_____	
			TAACAGAAG TGTGT		
			ATTGTCTTC ACACA		
			ATCGGTA		
GAM1221	KIAA0342	3'	AGTGTAGCTTCTTCTGTGA 70616	T GTG	
			TAACAGAAGA GT TGC ACT		
			ATTGTCTTCT CG ATGTGA		
			T _____		
GAM1221	KIAA0372	3'	ATGCAATTTTCTGTGA 27662	G	
			TAACAGAAGAT TGTGT		
			ATTGTCTTTTA ACGTA		
			_____		
GAM1221	KIAA0372	3'	TGCACAATTTTCTTTTGTGA 27665	TGTG	
			TAACAGAAGA TGTGCA		
			ATTGTTTTCT ACACGT		
			TTTA		
GAM1221	KIAA0419	3'	GCATACATTCCTGT 28190	AA T	
			ACAG GA GTGTGTGC		
			TGTC CT TACATACG		
			_____		
GAM1221	KIAA0451	3'	ACACACTTAGTGATTTCTGTGA 29100	AT_____	
			TAACAGAAG GTGTGT		
			ATTGTCTTT CACACA		
			AGTGATT		
GAM1221	KIAA0534	3'	ACATCTCATCTTCTTTTA 71426	C T_	
			TAA AGAAGATG GTGT		
			ATT TCTTCTAC TACA		
			T TC		
GAM1221	KIAA0547	3'	AGTGGCAGCATTCTTCTGT 28908	T G _	
			ACAGAAGA GTGT TGC ACT		
			TGTCTTCT TACG ACG TGA		
			_____ G		
GAM1221	KIAA0552	3'	TGACACATGTCCTGT 28322	AA G	
			ACAG GATGTGTGT CA		
			TGTC CTGTACACA GT		
			_____		
GAM1221	KIAA0992	3'	CACATGTATCTTTCATTA 32204	CA TG	
			TAA GAAGATG TGTG		

		ATT TTTCTAT ACAC		
		AC GT		
GAM1221 KIAA1128	3'	AGTGGGCATACATGTTCT 68471	G G	
		AGAA ATGTGTGT CACT		
		TCTT TACATACG GTGA		
		G G		
GAM1221 KIAA1198	3'	AGTCACAGACACACTCTG 63288	AGA G C	
		CAGA TGT TGTG ACT		
		GTCT ACA ACAC TGA		
		CAC G _		
GAM1221 KIAA1260	3'	GTACACATTTCTGTTA 60027	GAT	
		TAACAGAA GTGTGTGC		
		ATTGTCTT TACACATG		
		—		
GAM1221 KIAA1301	3'	GTACACAGTGAGTTCTGTT 66343	GATG_	
		AACAGAA TGTGTGC		
		TTGTCTT ACACATG		
		GAGTG		
GAM1221 KIAA1365	3'	GCACACACAAGCTCTTT 40423	—	
		GAAGA TGTGTGTGC		
		TTTCT ACACACACG		
		CGA		
GAM1221 KIAA1492	3'	AGTGCATGTTTTCTTCTGTTA 64503	TGT TG	
		TAACAGAAGA G TGC ACT		
		ATTGTCTTCT T ACGTGA		
		TT_GT		
GAM1221 KIAA1822	3'	AGTGCATGTGTGTCCTCTG 67559	A TG	
		CAGA GATG TGTGCACT		
		GTCT CTGT GTACGTGA		
		C GT		
GAM1221 KIAA1826	3'	ATACAGCTCTTCTGTTG 67215	TG	
		TAACAGAAGA TGTGT		
		GTTGTCTTCT ACATA		
		CG		
GAM1221 KLHL4	3'	CACATGCTTTTCTGTTA 38920	T	
		TAACAGAAGA GTGTGTG		
		ATTGTCTTTT CGTACAC		
		—		
GAM1221 KLHL4	3'	CACATACAGCCCTGTTA 38919	AAGA	
		TAACAG TGTGTGTG		

			ATTGTC ACATACAC		
			CCG_		
GAM1221 LIM	5'	GCATATTT	CATTTTCTGT	21304	T_
			ACAGAAGATG GTGTGC		
			TGTCTTTTAC TATACG		
			TT		
GAM1221 MGC10871	3'	GCCTTTT	ACTCTTCTGTTA	94779	T TGT_
			TAACAGAAGA GTG GC		
			ATTGTCTTCT CAT CG		
			_ TTTC		
GAM1221 MGC2452	5'	AGTGCACACAC	CCTGAGCCTG	50977	AAGAT_
			CAG GTGTGTGCACT		
			GTC CACACACGTGA		
			CGAGTC		
GAM1221 MRPS27	3'	ACACACATTT	CTGTTA	30632	A
			TAACAGA GATGTGTGT		
			ATTGTCT TTACACACA		
			-		
GAM1221 My015	3'	GTGAAGCATCTTT	GTTA	66655	A GTGTG
			TAACAGA GATGT CAC		
			ATTGTTT CTACG GTG		
			- AA_		
GAM1221 PASK	5'	AGGGGATCACATTT	CTGTTA	30711	A TGTGCA
			TAACAGA GATGTG CT		
			ATTGTCT TTACAC GA		
			- TAGGG_		
GAM1221 PLAGL2	3'	TGCACAGGGGCATATCTTT	GTTA	70459	A ____
			TAACAGA GATGTGT GTGCA		
			ATTGTTT CTATACG CACGT		
			- GGA		
GAM1221 SEPT3	3'	AGTGCGGTTGTACATCCTC		38883	A TG__
			GA GATGTG TGC ACT		
			CT CTACAT GCGTGA		
			C GTTG		
GAM1221 TIAF1	3'	ACACCCTGACCTTCTTCTGT		54324	T_ ____
			ACAGAAGA GT GTGT		
			TGTCTTCT CA CACA		
			TC GTCC		
GAM1221 TIP-1	3'	TGGACACACATCCTG		27509	AA G
			CAG GATGTGTGT CA		

GTC CTACACACA GT  
 — G  
 GAM1221 LOC123242 5' AGTGGAGGACACCTTCTGTT 75592 AT GTG\_  
 AACAGAAG GTGT CACT  
 ||||| ||| |||  
 TTGTCTTC CACA GTGA  
 — GGAG  
 GAM1221 LOC134637 3' AGTGCATACCCTTCT 75200 ATGT  
 AGAAG GTGTGCACT  
 |||| |||||  
 TCTTC CATACGTGA  
 C—  
 GAM1221 LOC139046 5' GCACACATTCCTGT 75811 AA T  
 ACAG GA GTGTGTGC  
 ||| || |||||  
 TGTC CT TACACACG  
 — —  
 GAM1221 LOC145624 5' AGTGCTGGGTATCTTCTGT 83405 TG T  
 ACAGAAGATG TG GCACT  
 ||||| || |||  
 TGTCTTCTAT GT CGTGA  
 GG \_  
 GAM1221 LOC145748 3' GCACATCTGTCTTCTG 83466 GT  
 CAGAAGAT GTGTGC  
 ||||| |||||  
 GTCTTCTG TACACG  
 TC  
 GAM1221 LOC145990 3' GCGGCCATCTTCTGT 77602 T G  
 ACAGAAGATG GT TGC  
 ||||| || |||  
 TGTCTTCTAC CG GCG  
 — —  
 GAM1221 LOC148343 5' GCACATGCCTTTTG 78794 AT  
 CAGAAG GTGTGTGC  
 |||| |||||  
 GTTTTC CGTACACG  
 —  
 GAM1221 LOC148758 3' AGTGACACACAACAGGTC 78964 AGA—  
 GA TGTGTGTGCACT  
 || |||||  
 CT ACACACACGTGA  
 GGACA  
 GAM1221 LOC151623 5' AGTGCAATGTATCTCCTG 85455 A TG G  
 CAG AGATG T TGCACT  
 || |||| | |||||  
 GTC TCTAT A ACGTGA  
 C GT\_  
 GAM1221 LOC153711 5' TACACACATGAACCTGTTA 86136 AAG\_  
 TAACAG ATGTGTGTG  
 |||| | |||||

	ATTGTC TACACACAT	
	CAAG	
GAM1221 LOC153883 3'	GCTCACATTCTGTTA 80982	AGAT T
	TAACAGA GTGTG GC	
	ATTGTCT TACAC CG	
	_____ T	
GAM1221 LOC157556 5'	GCACCAGCAATTTTCTG 86486	_ GT
	CAGAAGAT GT GTGC	
	GTCTTTTA CG CACG	
	A AC	
GAM1221 LOC161829 5'	GCAAAAGCATCTTCTGTTA 82314	GTG
	TAACAGAAGATGT TGC	
	ATTGTCTTCTACG ACG	
	AAA	
GAM1221 LOC162333 5'	AGTGCACACGAATTTGCTGT 87120	A G
	ACAG AGAT TGTGTGCACT	
	TGTC TTTA GCACACGTGA	
	G A	
GAM1221 LOC199923 3'	CACACACATCTTCTGTTG 88496	
	TAACAGAAGATGTGTGTG	
	GTTGTCTTCTACACACAC	
GAM1221 LOC253001 5'	AGTGGAGGACACCTTCTGTT 96250	AT GTG_
	AACAGAAG GTGT CACT	
	TTGTCTTC CACA GTGA	
	_____ GGAG	
GAM1221 LOC255461 5'	AGTGCAATGTGTCTCCTG 97315	A TG G
	CAG AGATG T TGCACT	
	GTC TCTGT A ACGTGA	
	C GT_	
GAM1221 LOC255516 5'	AGTGCAATGTGTCTCCTG 97328	A TG G
	CAG AGATG T TGCACT	
	GTC TCTGT A ACGTGA	
	C GT_	
GAM1221 LOC256809 3'	GCACTGGCAATCTTCTG 96394	_ GT
	CAGAAGAT GT GTGC	
	GTCTTCTA CG CACG	
	A GT	
GAM1221 LOC256848 3'	AGTGCACGGTCCTTCTGT 97511	ATGTG
	ACAGAAG TGTGCACT	

TGTCTTC GCACGTGA  
 CTG\_\_  
 GAM1221 LOC90170 5' GCTGACAGATCTTCTGT 61708 G GT  
 ACAGAAGAT TGT GC  
 ||||| ||| ||  
 TGTCTTCTA ACA CG  
 G GT  
 GAM1221 LOC90321 3' GCACACACTTTTCCTG 62264 \_ T  
 CAG AAGA GTGTGTGC  
 ||| ||| |||||  
 GTC TTTT CACACACG  
 C \_  
 GAM1221 LOC90488 3' TGTTAACCATCTTTTGTTA 63035 T GT  
 TAACAGAAGATG GT GCA  
 ||||| ||| |||  
 ATTGTTTTCTAC CA TGT  
 \_ AT  
 GAM1222 AXIN1 3' GCACCTGCCTCCAGCCG 60855 A A TCT  
 TG CT GAGGCAGGT GC  
 || || ||||| ||  
 GC GA CTCCGTCCA CG  
 C C \_  
 GAM1222 CLASP1 5' TAGTGTCTCTGCCTCAGTCA 65311 A TTC  
 TGACT GAGGCAGG TGCTA  
 |||| ||||| ||||  
 ACTGA CTCCGTCT GTGAT  
 \_ CT\_  
 GAM1222 GP9 3' CAGAACCTGGCTCCAGCCA 3917 A A G  
 TG CT GAG CAGGTTCTG  
 || || || |||||  
 AC GA CTC GTCCAAGAC  
 C C G  
 GAM1222 MGAT4B 3' GCACCCGGCCTGCCCCAGTCA 26551 AGA C\_  
 TGACT GGCAGGTT TGC  
 |||| ||||| |||  
 ACTGA CCGTCCGG ACG  
 CC\_ CCC  
 GAM1222 MGAT4B 3' GCACCCGGCCTGCCCCAGTCA 53950 AGA C\_  
 TGACT GGCAGGTT TGC  
 |||| ||||| |||  
 ACTGA CCGTCCGG ACG  
 CC\_ CCC  
 GAM1222 PDE6D 3' CAGAACCTACCTGCAGCCA 10487 A AG C  
 TG CT AGG AGGTTCTG  
 || || || |||||  
 AC GA TCC TCCAAGAC  
 C CG A  
 GAM1222 RPH3AL 5' CAGCTGCCTCCAGCA 22742 A A GTT  
 TG CT GAGGCAG CTG  
 || || ||||| |||

AC GA CTCCGTC GAC  
 \_ C \_  
 GAM1222 FLJ12770 3' AGCAGCTGGAACCTCTGAGTCA 49733 \_ \_ GTT  
 TGACT AGAGG CAG CTGCT  
 ||||| ||||| ||| |||||  
 ACTGA TCTCC GTC GACGA  
 G AAG \_  
 GAM1222 FLJ32734 5' GCCCAACCTGTCTCCAGCCA 58381 A A CT  
 TG CT GAGGCAGGTT GC  
 || || ||||| ||  
 AC GA CTCTGTCCAA CG  
 C C CC  
 GAM1222 GREAT 3' AGCAGAATGGCTCCTGTCA 55478 T AG AG  
 TGAC AG GC GTTCTGCT  
 ||||| || || |||||  
 ACTG TC CG TAAGACGA  
 \_ CT G\_  
 GAM1222 KIAA0759 3' AGCCATGCCTGCCTCTG 67319 TCT  
 TAGAGGCAGGT GCT  
 ||||| ||||| ||  
 GTCTCCGTC CGA  
 TAC  
 GAM1222 KIAA1130 3' AGCACTCCTGCCTCTAATC 62410 C TTC  
 GA TAGAGGCAGG TGCT  
 || ||||| ||||| ||  
 CT ATCTCCGTCC ACGA  
 A TC\_  
 GAM1222 PCSK7 3' CAGGGTCTGCCTCCAGCCA 16333 A A TT  
 TG CT GAGGCAGG CTG  
 || || ||||| ||  
 AC GA CTCCGTCT GAC  
 C C GG  
 GAM1222 PELI1 5' AGCTAATGCCTCTAGTTA 40253 GGTTCT  
 TGACTAGAGGCA GCT  
 ||||| ||||| ||  
 ATTGATCTCCGT CGA  
 AAT\_  
 GAM1222 PPP4R1L 5' GGATAACCTGCCTCCACTCA 79503 CTA CTG  
 TGA GAGGCAGGTT CT  
 ||| ||||| ||  
 ACT CTCCGTCCAA GG  
 CAC TA\_  
 GAM1222 UBXD2 3' CACAGCCTGCCTCCATCA 68343 CTA C  
 TGA GAGGCAGGTT TG  
 ||| ||||| ||  
 ACT CTCCGTCCGA AC  
 AC\_ C  
 GAM1222 LOC196266 3' CAGGGTCTGCCTCCAGCCA 87304 A A TT  
 TG CT GAGGCAGG CTG  
 || || ||||| ||

			AC GA CTCCGTCT GAC		
			C C GG		
GAM1222	LOC201164	3'	CAGTCTGCCCCTGTCA	88113	T A TT
			TGAC AG GGCAGG CTG		
			ACTG TC CCGTCT GAC		
			_ C _		
GAM1223	ADH1B	3'	CTTAGACATAAAGTAAAAT	72644	C CAC
			ATTT ACTTT TGTCTGAG		
			TAAA TGAAA ACAGATTC		
			A T_		
GAM1223	AHR	3'	ATCTCAGATGTTAAAATAAATG	7875	CAC C T
			CATTT TTT AC GTCTGAGAT		
			GTAAA AAA TG TAGACTCTA		
			TA_ T _		
GAM1223	FDFT1	3'	TAGGAAAGTGAAATG	15518	A
			CATTTCACTTTC CTG		
			GTAAAGTGAAAG GAT		
			-		
GAM1223	JTB	3'	ATCTCAGACAGTGAAAGTGAAA	21959	
	TG		CATTTCACTTTCACTGTCTGAGAT		
			GTAAAGTGAAAGTGACAGACTCTA		
GAM1223	KLF4	3'	TCCCAGACAGTGGATATG	14891	CT A
			CA TTCACTGTCTG GA		
			GT AGGTGACAGAC CT		
			AT C		
GAM1223	PHYH	3'	ACAGTAAAAGTGAAAT	20608	C
			ATTTCACTTT ACTGT		
			TAAAGTGAAA TGACA		
			A		
GAM1223	PKD2	3'	TCCAGGTTGAAAGTGAAA	60096	CTG A
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T_ _		
GAM1223	WRN	3'	GGGCAGTGAAAATGAAA	5098	C
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1223	ZNF216	3'	ATCTGCACAGCAAAGTGAAA	20017	CA CTG
			TTTCACTTT CTGT AGAT		



			AAAGTGAAA GACA TCTA	
			C_ CG_	
GAM1223	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT CT
			TTCAC TTTCA GT GAG	
			AAGTGAAAGT CA CTC	
			CT _	
GAM1223	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G T_
			CTTTCACT TC GAGAT	
			GAAAGTGA AG TTCTA	
			G TC	
GAM1223	FLJ23462	3'	ATCTCAGACTTTTACAAAGAAAT 45802	ACTTTCACT
	G		CATTTC GTCTGAGAT	
			GTAAAG CAGACTCTA	
			AAACATTT_	
GAM1223	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281	CTT
			CATTTC TCACTGTCTGAGAT	
			GTAAAGT AGTGACAGACTCTA	
			C_	
GAM1223	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C TC
			TTCA TTTCACTG TGAG	
			AAGT AAAGTGAC GTTT	
			A CT	
GAM1223	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A _
			TTTC CTG TCTGAGAT	
			AAAG GAC AGACTCTA	
			_ G	
GAM1223	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T
			ATT CACTTTCACTGT	
			TAA GTGAAAGTGACG	
			C	
GAM1223	PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA 53598	CA G
			TTCACTTT CT TCTGAGAT	
			AAGTGAAA GG AGACTCTA	
			CC G	
GAM1223	PP35	3'	ATCTCAGACTGAAA 22814	CT
			TTTCA GTCTGAGAT	
			AAAGT CAGACTCTA	
			_	
GAM1223	PRTD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148	TCAC C_
			CATTTCAC TT TGT TGAG	

			GTAAAGTGAA ACG ACTC		
			TA__ TT		
GAM1223	SEP15	3'	TCCTACAGTAAGAGTGAAA 14934	C	CT
			TTTCACTTT ACTGT GA		
			AAAGTGAGA TGACA CT		
			A TC		
GAM1223	SFXN2	3'	CTCAGGGGAAAAAAGTGAAA 73941	CACTG	
			TTTCACTTT TCTGAG		
			AAAGTGAAA GGA CTC		
			AAAGG		
GAM1223	LOC149703	3'	ATCTCAGACAGCCGTTTGAAA 84647	ACTTTCA	
			TTTC CTGTCTGAGAT		
			AAAG GACAGACTCTA		
			GTTTGCC		
GAM1223	LOC154007	3'	ATCTCAAACCTTTAGTGAAA 81015	TTC ACT C	
			TTTCACT GT TGAGAT		
			AAAGTGA CA ACTCTA		
			TTTCC_ A		
GAM1223	LOC155004	3'	TCATTTAAGTGAAAGGAAA 81226	A	GTC_
			TTTC CTTTCACT TGA		
			AAAG GAAAGTGA ACT		
			_ ATTT		
GAM1223	LOC222134	5'	ACAGTGAAGTGAAATG 94136	T	
			CATTTCACTT CACTGT		
			GTAAAGTGAA GTGACA		
			-		
GAM1224	AKR1B1	3'	GTCCCCAAGTGACCTATACC 7891	C	AAA A
			GG ATAGGTCAC TGGG GAC		
			CC TATCCAGTG ACCC CTG		
			A A_ _		
GAM1224	CD28	3'	GTCTCCCACTCATGAAATGAGC 20441	A GG	CAAA
	CA		TGGC TA TCA TGGGAGAC		
			ACCG GT AGT ACCCTCTG		
			A AA ACTC		
GAM1224	DRD3	3'	CCCTGTGATCTATACCA 53355	C	AAT
			TGG ATAGGTCACA GGG		
			ACC TATCTAGTGT CCC		
			A _		
GAM1224	DRD3	3'	CCCTGTGATCTATACCA 53357	C	AAT
			TGG ATAGGTCACA GGG		

ACC TATCTAGTGT CCC  
 A \_\_\_\_  
 GAM1224 EXTL3 3' TCTCCCATCCTCCCCAGCGCCA 7537 ATA TCACAA  
 TGGC GG ATGGGAGA  
 |||| || |||||  
 ACCG CC TACCCTCT  
 CGA CCTCC\_  
 GAM1224 GUCY1B2 3' TCTCCCACTTCGGGCAGCCA 14687 ATAG ACAA  
 TGGC GTC TGGGAGA  
 |||| || |||||  
 ACCG CGG ACCCTCT  
 A\_\_ CTTC\_  
 GAM1224 RHO 3' TCTCCCATCCCCTACACC 5021 CA TCACAA  
 GG TAGG ATGGGAGA  
 || |||| |||||  
 CC ATCC TACCCTCT  
 AC CC\_\_\_\_  
 GAM1224 SOX10 3' CCCATGCCACCTATGCCA 22684 CACAA  
 TGGCATAGGT ATGGG  
 ||||| ||||  
 ACCGTATCCA TACCC  
 CCG\_  
 GAM1224 SOX10 3' TCTGACATGCCCATGCCA 22689 A CACAA GG  
 TGGCAT GGT ATG AGA  
 ||||| || ||||  
 ACCGTA CCG TAC TCT  
 C \_\_\_\_ AG  
 GAM1224 SSX3 3' TCTCCCATCTGCTTTTCCCATT 40670 TA\_ TCA\_\_ A  
 GCCA TGGCA GG CA ATGGGAGA  
 |||| || |||||  
 ACCGT CC GT TACCCTCT  
 TAC TTTTC C  
 GAM1224 WNT4 3' TCTCCCAACCACCTACCCCA 47762 CA CACAAA  
 TGG TAGGT TGGGAGA  
 || |||| |||||  
 ACC ATCCA ACCCTCT  
 CC CC\_\_\_\_  
 GAM1224 CORO1A 3' CTCCCATTCCCAGCCA 22988 ATA TCACA  
 TGGC GG AATGGGAG  
 |||| || |||||  
 ACCG CC TTACCCTC  
 AC\_ \_\_\_\_  
 GAM1224 DDR2 3' TCACCCATGCCTATGCCA 20524 CACAA A  
 TGGCATAGGT ATGGG GA  
 ||||| |||| ||  
 ACCGTATCCG TACCC CT  
 \_\_\_\_ A  
 GAM1224 DKFZP434G1411 3' CTTCTGTAACCTATGC 92104 C AATG  
 GCATAGGT ACA GGAG  
 ||||| || ||||

				CGTATCCA TGT	CTTC		
			A	_____			
GAM1224	FLJ10726	3'	TCCCCCATTTGCACTACTGGCC	36508	A	GTCA_	A
	A		TGGC TAG CAAATGGG GA				
			ACCG GTC GTTTACCC CT				
			_ ATCAC C				
GAM1224	ILF2	3'	GTCTCCCATTGTGACCTATGC	66941			
	CA		TGGCATAGGTCACAAATGGGAGAC				
			ACCGTATCCAGTGTTTACCCTCTG				
GAM1224	KIAA0222	3'	CTCCCACCTGTGACCTGGCC	27681	A	AA	
			GGC TAGGTCACA TGGGAG				
			CCG GTCCAGTGT ACCCTC				
			_ CC				
GAM1224	KIAA0556	3'	CTCTTGTGACCCAAACCA	69083	CATA	AATG	
			TGG GGTCACA GGAG				
			ACC CCAGTGT TCTC				
			AAAC _____				
GAM1224	KIAA0836	3'	TTTATCTGTGACCTATATCA	64566	GC	A	
			TG ATAGGTCACA ATGGG				
			AC TATCCAGTGT TATTT				
			TA C				
GAM1224	KIAA1396	3'	TCCCCCTTGGGTGCCTATGCCA	62995	T	AAAT	A
			TGGCATAGG CAC GGG GA				
			ACCGTATCC GTG CCC CT				
			_ GGTT C				
GAM1224	MRPL45	3'	GTCTCCCATTCCCCTCATGCTA	50375	_	TCACA	
			TGGCAT AGG AATGGGAGAC				
			ATCGTA TCC TTACCCTCTG				
			C CC____				
GAM1224	SIRPB1	3'	TCATTCTGTGACCTTTACCA	20264	CAT	_	
			TGG AGGTCACA AATGG				
			ACC TCCAGTGT TTA CT				
			ATT C				
GAM1224	SNAP29	3'	CCCATGTGACCTTTGCCA	16539	T	AA	
			TGGCA AGGTCACA TGGG				
			ACCGT TCCAGTGT ACCC				
			T _____				
GAM1224	TRIM29	3'	TCTCCCATTACATGGCCCACC	23961	CATA	CA__	
			GG GGTCA AATGGGAGA				

CC CCGGT TTACCCTCT  
 AC\_\_ ACAC  
 GAM1224 UPK1A 3' CTCCCATTACAGATACC 22796 C AG CACA  
 GG AT GT AATGGGAG  
 || || || |||||  
 CC TA CA TTACCCTC  
 A GA C\_\_  
 GAM1224 LOC115294 3' TTTGGGACCTATGCCA 73020 A  
 TGGCATAGGTC CAAA  
 ||||| ||||  
 ACCGTATCCAG GTTT  
 G  
 GAM1224 LOC143458 3' CCCAGCATCACCTATGCCA 76572 CACAAA  
 TGGCATAGGT TGGG  
 ||||| ||||  
 ACCGTATCCA ACCC  
 CTACG\_  
 GAM1224 LOC146138 3' GTCTCCCACTCGATCCCTTCGC 83616 AT TCACAAA  
 CA TGGC AGG TGGGAGAC  
 ||| || |||||  
 ACCG TCC ACCCTCTG  
 CT CTAGCTC  
 GAM1224 LOC146784 5' CTCCCATTATGTGATC 78111 \_  
 GGTCACA AATGGGAG  
 ||||| |||||  
 CTAGTGT TTACCCTC  
 AT  
 GAM1224 LOC201220 5' CCTATGCCTATGCCA 87346 CACAA  
 TGGCATAGGT ATGGG  
 ||||| ||||  
 ACCGTATCCG TATCC  
 \_  
 GAM1224 LOC202460 5' CTCCCATTATGACTTA 89182 C  
 TAGGTCA AAATGGGAG  
 ||||| |||||  
 ATTCAGT TTTACCCTC  
 A  
 GAM1224 LOC90408 3' TCTCTGTGACCCATACC 62670 C A AAT  
 GG AT GGTCACA GGGA  
 || ||||| ||||  
 CC TA CCAGTGT CTCT  
 A C \_  
 GAM1224 LOC90917 3' TCCTCTTGACGCTACGCCA 64340 A CA AT  
 TGGC TAGGT CAA GGGA  
 ||| |||| ||| ||||  
 ACCG ATCCG GTT TCCT  
 C AC C\_  
 GAM1225 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
 GTA GGAT GGGTTGTTT  
 ||| |||| |||||

CGT CCTA CCCAACAAA  
 C CGTG\_  
 GAM1225 LCT 3' AACCGTAAAAATCCTT 9697 G  
 AAGGATTTTTTA GGTT  
 |||||  
 TTCCTAAAAAT CCAA  
 G  
 GAM1225 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
 GTAAGGATTTTTAGGGTTGTTT  
 |||||  
 CATTCCTAAAAATCCCAACAAA  
  
 GAM1225 FBXO30 3' AACTAAAAAAATCCTGAC 49573 A AG  
 GT AGGATTTTT GGTT  
 || |||||  
 CA TCCTAAAAA TCAA  
 G AA  
 GAM1225 KIAA0494 3' AACAACCCTTACTTAC 28736 GATTTTT  
 GTAAG AGGGTTGTT  
 |||| |||||  
 CATTC TCCCAACAA  
 AT\_\_\_\_  
 GAM1225 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
 TAAG TTTT GGGTTGTTT  
 ||| ||| |||||  
 GTTC AAAA CCCAACAAA  
 \_\_\_\_ C  
 GAM1225 SMT3H2 3' AACAACATAAAAAATCCTTGC 22670 GG  
 GTAAGGATTTTTTA GTTGTT  
 |||||  
 CGTTCCTAAAAAT CAACAA  
 A\_  
 GAM1225 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
 GTAAGGATTTTT GGGTT  
 |||||  
 CGTTCCTAAAAA TCCAA  
 GTA  
 GAM1225 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
 GGAT TT GGGTTGTTT  
 ||| || |||||  
 CCTG AA CCCAACAAA  
 T\_ C  
 GAM1225 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
 C GTA GGATTTTT TTGTTT  
 || ||||| |||||  
 CGT CCTAAAAA AACAAA  
 C GATAA  
 GAM1225 LOC148089 3' GGCCCTAAAAATTCCTAC 78637 A  
 GTA GGATTTTTAGGGTT  
 || |||||

		CAT CTTAAAAATCCCGG		
		C		
GAM1225	LOC154547 3'	AACAACATAAAAAATCCTTGC	76050	GG
		GTAAGGATTTTGA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1225	LOC158104 3'	ACAGCCAAAAATCCTTA	60313	AG
		TAAGGATTTT GGTGT		
		ATTCCTAAAAA CCGACA		
		—		
GAM1225	LOC205880 5'	AAACAACCATCATCCTGAC	90709	A TTTAG
		GT AGGAT GGTGT		
		CA TCCTA CCAACAAA		
		G CTA_		
GAM1225	LOC221561 3'	AACAACATAAAAAATCCTTGC	92130	GG
		GTAAGGATTTTGA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1225	LOC257591 3'	AACAACATAAAAAATCCTTGC	97840	GG
		GTAAGGATTTTGA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1225	LOC51145 3'	AGCTAAAATCCTTAC	32393	TAG
		GTAAGGATTTT GGT		
		CATTCCTAAAA TCGA		
		—		
GAM1226	ADAMTS8 5'	TCGGGCCGCCAGCACCTG	22886	_ ATAAG
		CAG TGCTGGC CTGA		
		GTC ACGACCG GGCT		
		C CCG_		
GAM1226	BAP1 3'	TCAGGGACCCAGCACTGG	16219	CATAAG
		CCAGTGCTGG CTGA		
		GGTCACGACC GACT		
		CAGG_		
GAM1226	BF 5'	TTCAGCTTGGGACACTG	8140	CTGGCA
		CAGTG TAAGCTGAA		
		GTCAC GTTCGACTT		
		AG_		
GAM1226	C1QB 3'	TTCAACTCTGTGTCCCAGCACT	4923	A _ _ C
	GGC	G CCAGTGCTGG CATA AG TGAA		

C GGTACGACC GTGT TC ACTT  
 \_ CT C A  
 GAM1226 CHC1 3' CAGCCCTGAGCACTGTGTC 7020 \_ \_ CATAA  
 GAC CAGTGCT GG GCTG  
 ||| ||||| || ||||  
 CTG GTCACGA CC CGAC  
 T GT \_\_\_\_  
 GAM1226 CMRF35 5' CAGAGCTGTGTCAGCACCGG 21929 A TAAG  
 CC GTGCTGGCA CTG  
 || ||||| ||||  
 GG CACGACTGT GAC  
 C CGA\_  
 GAM1226 EPHB6 3' TCAGCCCTGGCACTGGTC 15466 \_ TG CATAA  
 GACCAGTG C G GCTGA  
 ||||| | | ||||  
 CTGGTCAC G C CGACT  
 A GT C\_\_\_\_  
 GAM1226 EVPL 5' CAGCCTGAGCCAGCACT 8803 A A  
 AGTGCTGGC TA GCTG  
 ||||| || ||||  
 TCACGACCG GT CGAC  
 A C  
 GAM1226 GARP 3' CAGCCCAGCACTGG 18594 CATAA  
 CCAGTGCTGG GCTG  
 ||||| ||||  
 GGTCACGACC CGAC  
 \_\_\_\_  
 GAM1226 GJB5 3' CAGCTCGACGGCACTGG 17945 GCATA  
 CCAGTGCTG AGCTG  
 ||||| ||||  
 GGTCACGGC TCGAC  
 AGC\_  
 GAM1226 GPR81 3' CTTACCAGCATTAGTC 50757 C CA  
 GAC AGTGCTGG TAAG  
 || ||||| ||||  
 CTG TTACGACC ATTC  
 A \_  
 GAM1226 IFI16 5' AGCAAGCCAGCACTAGTC 71221 C ATAA  
 GAC AGTGCTGGC GCT  
 || ||||| ||||  
 CTG TCACGACCG CGA  
 A AA\_  
 GAM1226 KRT4 3' CAGCTGGGCCAGCACTGGT 9635 \_ ATA  
 ACCAGTGCTGG C AGCTG  
 ||||| | ||||  
 TGGTCACGACC G TCGAC  
 C GG\_  
 GAM1226 MAP3K9 3' TTCAGCTTCCCAAACACCAGT 60709 CA C\_ CAT  
 AC GTG TGG AAGCTGAA  
 || ||| || |||||



			TG CAC ACC TTCGACTT		
			AC AA C__		
GAM1226	MGAT5	5'	TCAGCTTACAGTTCCTG	10028	T_ GCA
			CAG GCTG TAAGCTGA		
			GTC TGAC ATTCGACT		
			CT ____		
GAM1226	MOCS1	3'	TTCAGCTTAACAGTTGCCCGGT	92037	A_ _ GCA
	C		GACC GTG CTG TAAGCTGAA		
			CTGG CGT GAC ATTCGACTT		
			CC T A__		
GAM1226	P23	3'	TCAGCTTATACCCGGGCT	21719	G C_
			AGT CTGG ATAAGCTGA		
			TCG GGCC TATTCGACT		
			_ CA		
GAM1226	PFKFB4	3'	TCAGCCACATGCAACACTGTGT	15874	_ CTG AA_
	C		GAC CAGTG GCAT GCTGA		
			CTG GTCAC CGTA CGACT		
			T AA_ CAC		
GAM1226	PTPRK	3'	TTCAGCCTGTGGCCAGCACTG	11125	_ A
	GTC		GACCAAGTGG CATA GCTGAA		
			CTGGTCACGACC GTGT CGACTT		
			CG C		
GAM1226	RNPEPL1	3'	CGGATGCCAGCACCTG	36676	_ AAG
			CAG TGCTGGCAT CTG		
			GTC ACGACCGTA GGC		
			C ____		
GAM1226	UBE2L3	3'	TCAGCCCTGGCACTGGC	12507	A TG CATAA
			G CCAAGTGC G GCTGA		
			C GGTCACG C CGACT		
			_ GT C__		
GAM1226	APXL2	5'	CAGCCTCAGCACTCATC	75185	CC CATAA
			GA AGTGCTGG GCTG		
			CT TCACGACT CGAC		
			AC C__		
GAM1226	ARHGEF9	3'	TTCAGCTTACCAAGCA	30824	_ CA
			TGCT GG TAAGCTGAA		
			ACGA CC ATTCGACTT		
			A ____		
GAM1226	CEGP1	3'	TTCAGCTTCCTCTAGCCCGG	40589	AGT CAT
			CC GCTGG AAGCTGAA		

GG CGATC TTCGACTT  
CC\_ TCC  
GAM1226 DKFZp547D155 3' CAGCCCTGAGACCACTGGTC 70435 CTGG TAA  
GACCAGTG CA GCTG  
||||||| || |||  
CTGGTCAC GT CGAC  
CAGA CC\_  
GAM1226 DKFZP727G051 3' TTCAGCCCATCAACCAGCATTG 69483 CATAA\_  
GTC GACCAGTGCTGG GCTGAA  
||||||| |||||  
CTGGTTACGACC CGACTT  
AACTACC  
GAM1226 DUSP14 5' CACTGTCACCAGCACTGCTC 22834 C CATA C  
GA CAGTGCTGG AG TG  
|| ||||| || ||  
CT GTCACGACC TC AC  
C ACTG \_  
GAM1226 FLJ10206 5' CAGCTTATGCCAGGAGTC 35898 CAGTG  
GAC CTGGCATAAGCTG  
||| |||||  
CTG GACCGTATTCGAC  
AG\_  
GAM1226 FLJ20967 5' GGCGCCAGCACTGGTT 41962 CATAA  
GACCAGTGCTGG GCT  
||||||| |||  
TTGGTCACGACC CGG  
CG\_  
GAM1226 FLJ22569 3' TTCAGCTTACTAACTG 43679 GC CA  
CAGT TGG TAAGCTGAA  
||| ||| |||||  
GTCA ATC ATTCGACTT  
A\_ \_  
GAM1226 FOXN4 3' TTCAGCTTGACACACTGG 75574 C GCA  
CCAGTG TG TAAGCTGAA  
||||| || |||||  
GGTCAC AC GTTCGACTT  
\_ AG\_  
GAM1226 GW112 3' TTCAACTGAAGCCAGCACTGGT 21194 ATA C  
T GACCAGTGCTGGC AG TGAA  
||||||| || |||  
TTGGTCACGACCG TC ACTT  
AAG A  
GAM1226 HOOK2 3' CAGCTCACATGGCGCCCAGCAC 25256 \_ A\_  
TGG CCAGTGCTGG CAT AGCTG  
||||||| ||| |||||  
GGTCACGACC GTA TCGAC  
CGCG CAC  
GAM1226 jdp2 3' TTCAGCACAGCCAGCAT 55327 ATAA  
GTGCTGGC GCTGAA  
||||||| |||||

			TACGACCG	CGACTT		
			ACA_			
GAM1226	KIAA0767	3'	TCTGCTGCCAGCACAGG	60632	A	TAA T
			CC GTGCTGGCA	GC GA		
			GG CACGACCGT	CG CT		
			A	__ T		
GAM1226	KIAA0923	3'	TCAGCTTGATGCATGGTC	25838	G	TGGCA
			GACCA TGC	TAAGCTGA		
			CTGGT ACG	GTTCTGACT		
			_ TA__			
GAM1226	KIAA0982	3'	TTCAGTGTGGCCAGCAC	25852		TA_ C
			GTGCTGGCA	AG TGAA		
			CACGACCGT	TC ACTT		
			TTG _			
GAM1226	KIAA1000	3'	TTCAGCTTTGCAAAGTACTGG	65281		G_ T
			CCAGTGCT	GCA AAGCTGAA		
			GGTCATGA	CGT TTCGACTT		
			AA _			
GAM1226	MAP3K3	3'	TCAGCCTGGGCGCTGGTC	9999		GG TAA
			GACCAAGTGCT	CA GCTGA		
			CTGGTCGCGG	GT CGACT		
			_ C__			
GAM1226	MGC16037	5'	CTTGTCCAGCACTAGTC	51821	C	C
			GAC AGTGCTGG	ATAAG		
			CTG TCACGACC	TGTTC		
			A	_		
GAM1226	MIDORI	3'	TCAGCTTATCCTGCAACT	73792		_ T C
			AGT GC GG	ATAAGCTGA		
			TCA CG CC	TATTCGACT		
			A T _			
GAM1226	MtFMT	5'	CAGTGGCGAGCACTGG	57651		G ATAA
			CCAGTGCT GC	GCTG		
			GGTCACGA CG	TGAC		
			G G__			
GAM1226	PCDH16	5'	TCAGTTCCAACCACTGG	72826		C_ CATA
			CCAGTG TGG	AGCTGA		
			GGTCAC ACC	TTGACT		
			CA ____			
GAM1226	QKI	3'	CAGCTTATCAACTCGTC	65439	C	GCTGGC
			GAC AGT	ATAAGCTG		

			CTG TCA TATTCGAC		
			C AC_____		
GAM1226	TNRC6	3'	CAACTTTTAGCACTG 70506	CAT	C
			CAGTGCTGG AAG TG		
			GTCACGATT TTC AC		
			_____ A		
GAM1226	TOB2	3'	CAGCCCAGGCCAGCACTG 95618	ATAA	
			CAGTGCTGGC GCTG		
			GTCACGACCG CGAC		
			GACC		
GAM1226	TU12B1-TY	3'	TCAGCCCACAGCACTGTC 33406	C	GCATAA
			GAC AGTGCTG GCTGA		
			CTG TCACGAC CGACT		
			_____ ACC_____		
GAM1226	TUSP	3'	TCAGCCTAAGAGCGCAGCACTG 39641	_____ A_____ A	
			CAGTGCTG GC TA GCTGA		
			GTCACGAC CG AT CGACT		
			G AGA C		
GAM1226	USP19	3'	TCAGCTTATGCATCTGGT 88959	TGCTG	
			ACCAG GCATAAGCTGA		
			TGGTC CGTATTCGACT		
			TA_____		
GAM1226	ZD52F10	3'	CAGCCTGTGCCAGCCCTGG 52819	T	A
			CCAG GCTGGCATA GCTG		
			GGTC CGACCGTGT CGAC		
			C C		
GAM1226	LOC145268	3'	TCAGCTTACAAGAGCCACTG 77062	_____	GGCA
			CAGTG CT TAAGCTGA		
			GTCAC GA ATTCGACT		
			C GAAC		
GAM1226	LOC149296	5'	CAGCTTATGGGCAGCA 79256	G_	
			TGCTG CATAAGCTG		
			ACGAC GTATTCGAC		
			GG		
GAM1226	LOC161877	5'	TCAGGGCAGGCCAGCGCTGG 82326	ATAAG	
			CCAGTGCTGGC CTGA		
			GGTCGCGACCG GACT		
			GACGG		
GAM1226	LOC163115	5'	TCAGCCCCTGACAGCACTGG 82413	G	TAA
			CCAGTGCTG CA GCTGA		

GGTCACGAC GT CGACT  
A CCC  
GAM1226 LOC196500 3' TCAGCTCACTCAGTGGTC 87744 AGT CATA  
GACC GCTGG AGCTGA  
||||| ||||| |||||  
CTGG TGA CT TCGACT  
\_\_\_ CAC\_

GAM1226 LOC197287 3' TCAGCTCATGTGTTTTGCACTG 60865 T\_ \_  
CAGTGC GGCATA AGCTGA  
||||| ||||| |||||  
GTCACG TTGTGT TCGACT  
TT AC

GAM1226 LOC200470 5' TCAGCCTGCGGCGCTGG 90069 G TAA  
CCAGTGCTG CA GCTGA  
||||||| || |||||  
GGTCGCGGC GT CGACT  
\_ C\_

GAM1226 LOC221584 3' CAGCTTATGTGGCAC 93828 G  
GTGCTG CATAAGCTG  
||||| |||||  
CACGGT GTATTGAC

GAM1226 LOC51716 3' CAGCTCATGGCCCTAGCA 32787 \_ A  
TGCTGG CAT AGCTG  
||||| ||| |||||  
ACGATC GTA TCGAC  
CCG C

GAM1226 LOC92196 5' CAGAGCACCAGCACTGGC 68456 A CATAAG  
G CCAGTGCTGG CTG  
| ||||| |||  
C GGTACGACC GAC  
\_ ACGA\_

GAM1227 IL2RA 3' GTAAATACACAACACACA 4698 CTAC  
TGTGTGTTG TTTAT  
||||||| |||||  
ACACACAAC AAATG  
ACAT

GAM1227 TSLRP 5' AACCCAACTGTGAACAGCACA 25005 C\_ TTTA  
CA TGTGTGTTG TAC TTGGGTT  
||||||| ||| |||||  
ACACACGAC GTG AACCCAA  
AA TCA\_

GAM1228 ABCC3 3' AGTCCTGTACTCTGGGGTG 39139 A CAGC  
CACC CAGA TGCAGGACT  
||| ||| |||||  
GTGG GTCT ATGTCCTGA  
G C\_

GAM1228 ABCC3 3' AGTCCTGTACTCTGGGGTG 39151 A CAGC  
CACC CAGA TGCAGGACT  
||| ||| |||||

			GTGG GTCT ATGTCCTGA		
			G C__		
GAM1228	ABCC3	3'	AGTCCTGTACTCTGGGGTG 13692	A	CAGC
			CACC CAGA TGCAGGACT		
			GTGG GTCT ATGTCCTGA		
			G C__		
GAM1228	ARVCF	3'	AGCCCTGCAGTCACGTGAGG 8026	A	GACA A
			CC CA GCTGCAGG CT		
			GG GT TGACGTCC GA		
			A GCAC C		
GAM1228	CCS	3'	AGCTGCTGTGGTGTT 17609	A	
			AACACCACAG CAGCT		
			TTGTGGTGTGTC GTCGA		
			-		
GAM1228	CELSR1	3'	TTTGTACTTCTGCGGTG 26492	A	C C
			CACC CAGA AG TGCAGG		
			GTGG GTCT TC ATGTTT		
			C _ _		
GAM1228	CELSR3	3'	GCAAAAGTTGTCTGTGGTG 7401		_____
			CACCACAGACAGCT GC		
			GTGGTGTCTGTTGA CG		
			AAA		
GAM1228	COL19A1	3'	AGCCACCAAGCTGTCTTTGGT 8506	C	GCA_ A
			ACCA AGACAGCT GG CT		
			TGGT TCTGTCTGA CC GA		
			T ACCA _		
GAM1228	DDC	3'	CTCAGCTGTCTGTGG 5797	C	
			CCACAGACAGCTG AG		
			GGTGTCTGTCTGAC TC		
			-		
GAM1228	DLEC1	3'	AGTCCTGCACCCTGCGG 23685	A	ACAGC
			CC CAG TGCAGGACT		
			GG GTC ACGTCCTGA		
			C CC__		
GAM1228	DLEC1	3'	AGTCCTGCACCCTGCGG 23696	A	ACAGC
			CC CAG TGCAGGACT		
			GG GTC ACGTCCTGA		
			C CC__		
GAM1228	DUSP2	3'	GCCCTGTCTGTGGGT 15347	A	CT
			AAC CCACAGACAG GC		

			TTG GGTGTCTGTC CG		
			— C—		
GAM1228	ERN2	5'	AGCCGTGCAGCTGCCCAGG 52701	ACAGA	— A
			CC CAGCTGCA GG CT		
			GG GTCGACGT CC GA		
			ACCC— G —		
GAM1228	EZH1	3'	TCTGCTTTCCTGTCTGTAGTG 8830	C	CT—
			CAC ACAGACAG GCAGG		
			GTG TGTCTGTC CGTCT		
			A CTTT		
GAM1228	FUT4	3'	AGTCCTGCAGGAGTGCTG 8961	— AG	
			CAG AC CTGCAGGACT		
			GTC TG GACGTCCTGA		
			G AG		
GAM1228	GGA3	3'	AGCCCTGGGAATGTCTGTGG 56825	GCTG	A
			CCACAGACA CAGG CT		
			GGTGTCTGT GTCC GA		
			AAGG C		
GAM1228	GGA3	3'	AGCCCTGGGAATGTCTGTGG 25741	GCTG	A
			CCACAGACA CAGG CT		
			GGTGTCTGT GTCC GA		
			AAGG C		
GAM1228	GPC1	3'	AGCCCCGCACGGGCTGTCTGGG 9098	A	— A A
	TGT		ACACC CAGACAGCT GC GG CT		
			TGTGG GTCTGTCGG CG CC GA		
			— GCA C C		
GAM1228	HMG3	3'	AGTCCTGTGCATACTGTGGTGT 14902	ACA	T
	T		AACACCACAG GC GCAGGACT		
			TTGTGGTGTGTC CG TGTCTGA		
			ATA —		
GAM1228	HPS1	3'	AGCCTCCTGTCTGCAGTG 3964	CA	CTGC A
			CAC CAGACAG AGG CT		
			GTG GTCTGTC TCC GA		
			AC C— —		
GAM1228	IGFBP1	3'	TCAAAGCTACCTGTGGTG 5180	AC	GCAG
			CACCACAG AGCT GA		
			GTGGTGTGTC TCGA CT		
			CA AA—		
GAM1228	IGFBP3	3'	AGCTCACAGCCTTCTGTGGTGT 5185	CA	CA A
			ACACCACAGA GCTG GG CT		

			TGTGGTGTCT CGAC TC GA		
			TC AC _		
GAM1228	IGFBP4	3'	AGTCCTGTCTCTGCCTGCGG 7758	A A CT	
			CC CAG CAG GCAGGACT		
			GG GTC GTC TGTCCTGA		
			C C TC		
GAM1228	IL19	3'	GTCCATGTCTGTGATGT 25360	C GCTGCA	
			ACA CACAGACA GGAC		
			TGT GTGTCTGT CCTG		
			A A _		
GAM1228	INPP5B	5'	AGTCCCGTGCGCCCTGTGGTG 95521	ACA T A	
			CACCACAG GC GC GGA		
			GTGGTGTC CG TG CCTGA		
			CCG _ C		
GAM1228	ISLR	3'	CTCACTGTCTGCGGTG 18669	A C C	
			CACC CAGACAG TG AG		
			GTGG GTCTGTC AC TC		
			C _ _		
GAM1228	KAI1	3'	AGCCCTGGCTGTTCTGTGGT 9495	_ TG A	
			ACCACAGA CAGC CAGG CT		
			TGGTGTCT GTCG GTCC GA		
			T _ C		
GAM1228	KDR	3'	TGAAGCTGTGTGTGGTGT 9596	G G	
			ACACCACA ACAGCT CA		
			TGTGGTGT TGTCGA GT		
			G A		
GAM1228	MLLT4	3'	AGTTATGGGCTCTCTGCAGTGT 72482	CA C G G	
	T		AACAC CAGA AGCT CA GACT		
			TTGTG GTCT TCGG GT TTGA		
			AC C _ A		
GAM1228	MPO	3'	TCCTGGCTCTGTGG 4204	CA TG	
			CCACAGA GC CAGGA		
			GGTGTCT CG GTCCT		
			_ _		
GAM1228	PACSIN1	3'	AGTCCTGCAGCACCAGGTG 92253	ACAGACA	
			CACC GCTGCAGGACT		
			GTGG CGACGTCCTGA		
			ACCA _		
GAM1228	PCLO	3'	CAGTGTCTGTGATGTT 94224	C G	
			AACA CACAGACA CTG		



		TTGT GTGTCTGT GAC		
		A _		
GAM1228	PLOD3	5' TCCTCGCCTTGTCTGTGG 6558	CT _	
		CCACAGACAG GC AGGA		
		GGTGTCTGTT CG TCCT		
		C_ C		
GAM1228	PPP1R8	5' AGCCCCGCATCCCTCTGTGGT 10722	CAGC A A	
		ACCACAGA TGC GG CT		
		TGGTGTCT ACG CC GA		
		CCCT C C		
GAM1228	PPP2R2B	3' TGAGGTTGTCTGTAGT 15909	C G	
		AC ACAGACAGCT CA		
		TG TGTCTGTTGG GT		
		A A		
GAM1228	RAX	3' AGCCCTGCAGCTGGAGGG 25536	ACAGA A	
		CC CAGCTGCAGG CT		
		GG GTCGACGTCC GA		
		GAG_ C		
GAM1228	REGL	3' AGTCCTGCAGCCAGGAGGGT 21485	ACAGACA	
		ACC GCTGCAGGACT		
		TGG CGACGTCCTGA		
		GAGGAC_		
GAM1228	RFC1	3' GTCCTGTCCTGTGATGG 11302	CAG CT	
		CCA ACAG GCAGGAC		
		GGT TGTC TGTCCTG		
		AG_ C_		
GAM1228	RRM2	3' AGTCCTGTCTGTTTATAGTG 6407	CAC CT	
		CAC AGACAG GCAGGACT		
		GTG TTTGTC TGTCCTGA		
		ATA _		
GAM1228	RU2	5' AGTCCTGCAAGCTCCTAGTG 33020	_ AC _	
		CAC AG AGCT GCAGGACT		
		GTG TC TCGA CGTCCTGA		
		A C_ A		
GAM1228	RXRA	3' CCTGCAGCCATCTGTG 11407	CA	
		CACAGA GCTGCAGG		
		GTGTCT CGACGTCC		
		AC		
GAM1228	SH3BP2	3' AGCCCTGCAGCTACAGCTG 11589	AC_ A	
		CAG AGCTGCAGG CT		

			GTC TCGACGTCC GA		
			GACA C		
GAM1228	SLC1A4	3'	TTGTATGTCTGTGGT 11721	GC	
			ACCACAGACA TGCAG		
			TGGTGTCTGT ATGTT		
			—		
GAM1228	TBXA2R	5'	AGCCTGCCCTGTCTG 6478	CT A	
			CAGACAG GCAGG CT		
			GTCTGTC CGTCC GA		
			C_ _		
GAM1228	TEM7	3'	AGCCCCAGCTTCTGT 39880	C CA A	
			ACAGA AGCTG GG CT		
			TGTCT TCGAC CC GA		
			_ C_ _		
GAM1228	UNC13	3'	AGTCCTGCTCATCTGTGG 21055	CAGCT	
			CCACAGA GCAGGACT		
			GGTGTCT CGTCCTGA		
			ACT_		
GAM1228	WASF3	3'	AGCCCTGCAGCTGTAGTACAGT 21823	CACAG_ A	
	G		CAC ACAGCTGCAGG CT		
			GTG TGTCGACGTCC GA		
			ACATGA C		
GAM1228	ZNF138	5'	AGGCCCAGCCTCTGTGG 81184	CA CA A	
			CCACAGA GCTG GG CT		
			GGTGTCT CGAC CC GA		
			C_ _ G		
GAM1228	ABCA9	3'	AGTCCATGTTTTGTCTGTTGTG 54409	C CT _	
			CAC ACAGACAG GCA GGACT		
			GTG TGTCTGTT TGT CCTGA		
			T T_ A		
GAM1228	APCL	5'	G TTCAGCTGTCTGT 19684	CAG	
			ACAGACAGCTG GAC		
			TGTCTGTCGAC TTG		
			—		
GAM1228	BRD1	5'	AGTCCTGCAACTGTGG 27413	ACAGC	
			CCACAG TGCAGGACT		
			GGTGTC ACGTCCTGA		
			A_		
GAM1228	C16orf5	3'	AGTCCCCAGGCCTGTGG 25445	ACA GCA	
			CCACAG GCT GGACT		

GGTGTC CGG CCTGA  
 \_\_\_\_ ACC

GAM1228 C1orf24 3' AGTCTCTGCTTTCTGCAGTG 53707 CA CAGCT \_  
 CAC CAGA GCAG GACT  
 ||| ||| ||| |||  
 GTG GTCT CGTC CTGA  
 AC TT\_\_ T

GAM1228 C1orf34 3' AGTCCCGGTCTGCTGTGGTGTT 60661 A \_ CA  
 AACACCACAG CAG CTG GGACT  
 ||||| ||| ||| |||  
 TTGTGGTGTC GTC GGC CCTGA  
 \_ T \_

GAM1228 C20orf82 5' AGTCTCTGGTCTGTCTG 84711 CTG \_  
 CAGACAG CAG GACT  
 ||||| ||| |||  
 GTCTGTC GTC CTGA  
 TG\_ T

GAM1228 DKFZP434C171 3' AGTCCTGATAGTCTGTGG 31551 AGCTG  
 CCACAGAC CAGGACT  
 ||||| |||||  
 GGTGTCTG GTCCTGA  
 ATA\_\_

GAM1228 DKFZP434P211 3' AGTCCTGCGATGCTAAGTG 27260 CAC A GC  
 CAC AG CA TGCAGGACT  
 ||| ||| |||||  
 GTG TC GT GCGTCCTGA  
 AA\_ \_ A\_

GAM1228 DMWD 3' AGCCCCAGGTCTGCAGTGT 60876 CA AG CA A  
 ACAC CAGAC CTG GG CT  
 ||| ||| ||| |||  
 TGTG GTCTG GAC CC GA  
 AC \_ C\_ \_

GAM1228 DOCK3 3' AGTCCTGCATGTTTCAGG 66495 ACA GC  
 CC GACA TGCAGGACT  
 || ||| |||||  
 GG TTGT ACGTCCTGA  
 AC\_ \_

GAM1228 FLJ10094 3' AGTTATATCTGTGGCGTT 35807 A C\_\_  
 AAC CCACAGA AGCT  
 ||| ||||| |||  
 TTG GGTGTCT TTGA  
 C ATA

GAM1228 FLJ10178 3' AGCCCTATAGTTCTGTG 35869 CA C A  
 CACAGA GCTG AGG CT  
 ||||| ||| ||| |||  
 GTGTCT TGAT TCC GA  
 \_ A C

GAM1228 FLJ10637 5' AGTCCCCTGTCTGTGG 68586 CTGCA  
 CCACAGACAG GGACT  
 ||||| |||

GGTGTCTGTC CCTGA  
C\_\_\_\_

GAM1228 FLJ12891 5' AGTCCTGCAGCCTCGCTGG 46336 CA CA  
CCA GA GCTGCAGGACT  
||| || |||||  
GGT CT CGACGTCCTGA  
CG C\_

GAM1228 FLJ12903 3' GTGCTATTGTGGTGT 42778 AC T  
ACACCACAG AGC GC  
||||| ||| ||  
TGTGGTGT TCG TG  
A\_ \_

GAM1228 FLJ13902 3' AGCCCTGTAGCATCTGTG 45038 CA A  
CACAGA GCTGCAGG CT  
||||| ||||| ||  
GTGTCT CGATGTCC GA  
A\_ C

GAM1228 FLJ20033 3' TTTTGCTAGCTGTGGTGT 34351 ACAGCT  
AACACCACAG GCAGGA  
||||| |||||  
TTGTGGTGTG CGTTTT  
GAT\_\_\_\_

GAM1228 FLJ20315 3' CCAGCTGCTGCCTGTGGCGT 34933 A A T A  
AC CCACAG CAGC GC GG  
|| ||||| ||| ||  
TG GGTGTC GTCG CG CC  
C C T A

GAM1228 FLJ20374 3' AGCCCTGCAGCTGGCTGGAGT 35077 CA A A  
AC CAG CAGCTGCAGG CT  
|| ||| ||||| ||  
TG GTC GTCGACGTCC GA  
AG G C

GAM1228 FLJ22127 3' AGTCCTGTGGCTGGCCCGTGAT 42881 C AGA\_ TG  
G CA CAC CAGC CAGGACT  
|| ||| ||| |||||  
GT GTG GTCG GTCCTGA  
A CCCG GT

GAM1228 FLJ23185 5' GTCCTGCAGTATGGCGT 46833 A CAGACA  
AC CCA GCTGCAGGAC  
|| ||| |||||  
TG GGT TGACGTCCTG  
C A\_\_\_\_

GAM1228 FLJ31762 5' AGTCCTGCAGATGTGCGTG 58139 \_ GACAG  
CAC CACA CTGCAGGACT  
||| ||| |||||  
GTG GTGT GACGTCCTGA  
C A\_\_\_\_

GAM1228 GIOT-2 3' CCTTCAGTTATCTGCAGT 32749 CA C C  
AC CAGA AGCTG AGG  
|| ||| ||||| |||

		TG GTCT TTGAC TCC	
		AC A T	
GAM1228 HRH3	3'	AGCCCCGCCGTGTCTGTGG 23364	GT A A
		CCACAGACA C GC GG CT	
		GGTGTCTGT G CG CC GA	
		_ C C C	
GAM1228 HYA22	3'	TCCTACGTGTTGGTCTGTGGT 19429	_ _ C
		ACCACAGAC AGC TG AGGA	
		TGGTGTCTG TTG GC TCCT	
		G T A	
GAM1228 KCNB2	5'	TCCCACAGCCCTTTGTGGTG 96102	CA CA
		CACCACAGA GCTG GGA	
		GTGGTGTTT CGAC CCT	
		CC AC	
GAM1228 KCNT1	3'	AGTCCTGCAGATCCCTCTGTGG 61826	CAG__
T		ACCACAGA CTGCAGGACT	
		TGGTGTCT GACGTCCTGA	
		CCCTA	
GAM1228 KIAA0218	3'	GTCCCTCGTCTGTGGT 28623	_ CTGCA
		ACCACAGAC AG GGAC	
		TGGTGTCTG TC CCTG	
		C _ _ _ _	
GAM1228 KIAA0828	3'	TCCTGTGCCTGTAGTGTT 81199	C ACA T
		AACAC ACAG GC GCAGGA	
		TTGTG TGTC CG TGCCT	
		A _ _ _	
GAM1228 KIAA0953	3'	AGTCCTGCATGTAGTTGGTG 66780	CAG GC
		CACCA ACA TGCAGGACT	
		GTGGT TGT ACGTCCTGA	
		TGA _	
GAM1228 KIAA1157	3'	AGTCCGTCCATGCTCTGTGG 72239	_ GCT A
		CCACAGA CA GC GGA	
		GGTGTCT GT TG CCTGA	
		C ACC _	
GAM1228 KIAA1183	3'	GCAGCCTGTGGTGTT 62535	ACA
		AACACCACAG GCTGC	
		TTGTGGTGTC CGACG	
		_ _ _ _	
GAM1228 KIAA1280	5'	AGCCTGACTGTCCGTGGTG 69710	A CTG A
		CACCAC GACAG CAGG CT	

		GTGGTG CTGTC GTCC GA	
		C A__ _	
GAM1228 KIAA1336	3'	TCCTGGGTTTTGTAATGTT 72325	CC CA G
		AACA ACAGA GCT CAGGA	
		TTGT TGTTT TGG GTCCT	
		AA __ _	
GAM1228 KIAA1505	5'	AGTCCCACCCATCTGTGGT 94185	CAGC CA
		ACCACAGA TG GGA CT	
		TGGTGTCT AC CCTGA	
		ACCC __	
GAM1228 KIAA1786	3'	AGTCCTTCCTTATCTGTGGT 66022	CAGCTGC
		ACCACAGA AGGA CT	
		TGGTGTCT TCCTGA	
		ATTCCT_	
GAM1228 MAD4	3'	CCTGTACCGGTCTGTGG 21271	AGC
		CCACAGAC TGCAGG	
		GGTGTCTG ATGTCC	
		GCC	
GAM1228 MGC10940	3'	AGCCCCCAATCTGTGGT 50214	CAGC CA A
		ACCACAGA TG GG CT	
		TGGTGTCT AC CC GA	
		A__ CC C	
GAM1228 MGC2654	5'	AGCTTGACCTGTCTGCAGT 44103	CA CTG A
		AC CAGACAG CAGG CT	
		TG GTCTGTC GTTC GA	
		AC CAG _	
GAM1228 MVD	3'	AGTCCTGCGGCCGCCCAGGTGT 10138	ACAGACA
		ACACC GCTGCAGGACT	
		TGTGG CGGCGTCCTGA	
		ACCCGC_	
GAM1228 NIN283	3'	AGCCCTCTGCCGGCTGTGGTGT 50065	ACA TGC A
		ACACCACAG GC AGG CT	
		TGTGGTGTG CG TCC GA	
		GGC TC_ C	
GAM1228 NTT5	3'	AGTCCTGCTACTTCTGGGGTG 25880	A C CT
		CACC CAGA AG GCAGGACT	
		GTGG GTCT TC CGTCCTGA	
		G _ AT	
GAM1228 P2RX1	3'	TCCTGGGCTCCCTGCCTGTGG 67172	A ____ G
		CCACAG CA GCT CAGGA	

			GGTGTC GT CGG GTCCT		
			C CCCT _		
GAM1228	PMAIP1	5'	TGCAGCTGTCCGAGGTG 40892	ACA	
			CACC GACAGCTGCA		
			GTGG CTGTCGACGT		
			AGC		
GAM1228	PMVK	3'	AGTCCCCTCAGCCTGTGGTG 21610	ACA	CA_
			CACCACAG GCTG GGACT		
			GTGGTGTC CGAC CCTGA		
			_ TCC		
GAM1228	PMVK	3'	AGTCCCCTCAGCCTGTGGTG 94612	ACA	CA_
			CACCACAG GCTG GGACT		
			GTGGTGTC CGAC CCTGA		
			_ TCC		
GAM1228	POLD3	3'	TCTGAGCTGTCTGCAAGG 91646	A__	G
			CC CAGACAGCT CAGG		
			GG GTCTGTCTGA GTCT		
			AAC _		
GAM1228	PRO2958	3'	AGTCCTAAACTGGCATCTGT 37651	CA	C__
			ACAGA GCTG AGGACT		
			TGTCT CGGT TCCTGA		
			A_ CAAA		
GAM1228	RAN	3'	GCAGCTGTCCTGTGATGT 20907	C	_
			ACA CACAG ACAGCTGC		
			TGT GTGTC TGTCGACG		
			A C		
GAM1228	RMP	3'	AGTTTTGTGCCAGCTGTG 13707	ACA	T
			CACAG GC GCAGGACT		
			GTGTC CG TGTTTTGA		
			GAC _		
GAM1228	RMP	3'	AGTTTTGTGCCAGCTGTG 56242	ACA	T
			CACAG GC GCAGGACT		
			GTGTC CG TGTTTTGA		
			GAC _		
GAM1228	SCYD1	3'	AGTCACCCCGGCCACCTGCGGT 90924	A	ACA CAG_
	G		CACC CAG GCTG GACT		
			GTGG GTC CGGC CTGA		
			C CAC CCCA		
GAM1228	SHAPY	5'	AGTCCCGCCTGTCTGT 57108	CT	A
			ACAGACAG GC GGACT		

TGTCTGTC CG CCTGA  
 \_ C  
 GAM1228 SMOC1 3' AGTCCTGCAATTGTACTGCGG 42147 A \_ C  
 CC CAG ACAG TGCAGGACT  
 || ||| ||| |||||  
 GG GTC TGTT ACGTCCTGA  
 C A A  
 GAM1228 SRPUL 3' TCCTGCAGTGTTTCCAGG 27101 AC\_ G  
 CC AGACA CTGCAGGA  
 || ||||| |||||  
 GG TTTGT GACGTCCT  
 ACC \_  
 GAM1228 SSH-3 3' AGCCCTGCACACTCACCTGTGG 35339 AC\_ C\_ A  
 CCACAG AG TGCAGG CT  
 ||||| || ||||| ||  
 GGTGTC TC ACGTCC GA  
 CAC AC C  
 GAM1228 TOSO 3' CCCAGGCTCGGACTGTGGTG 18389 AC\_\_ GCA  
 CACCACAG AGCT GG  
 ||||| ||| ||  
 GTGGTGTC TCGG CC  
 AGGC AC\_  
 GAM1228 TPC2 3' CCTGCAGCTTCCGTGGTG 57446 A C  
 CACCAC GA AGCTGCAGG  
 ||||| || |||||  
 GTGGTG CT TCGACGTCC  
 C \_  
 GAM1228 TRIM11 3' CCATGCCTGTCTGTG 72831 CT \_  
 CACAGACAG GCA GG  
 ||||| ||| ||  
 GTGTCTGTC CGT CC  
 \_ A  
 GAM1228 UGT2B10 3' AGCCCCAGTAATGCTCTGTGG 6540 \_ \_ CA A  
 CCACAGA CA GCTG GG CT  
 ||||| || ||| |||  
 GGTGTCT GT TGAC CC GA  
 C AA C\_ \_  
 GAM1228 LOC113386 3' AGTCCTGCATGTGTTGATG 57077 CA GC  
 CA GACA TGCAGGACT  
 || ||| |||||  
 GT TTGT ACGTCCTGA  
 AG GT  
 GAM1228 LOC130814 3' AGTGCTCAGACATCTGCAGTGT 74984 CA CAG C G  
 T AACAC CAGA CTG AG ACT  
 |||| ||| ||| |||  
 TTGTG GTCT GAC TC TGA  
 AC ACA \_ G  
 GAM1228 LOC131870 3' AGTCCTGCAGCCTCATATGG 75013 CAGACA  
 CCA GCTGCAGGACT  
 || |||||



GGT CGACGTCCTGA  
ATACTC  
GAM1228 LOC133491 5' GTCTGGCGCCTGTGGCGT 75096 A ACA T A  
AC CCACAG GC GC GGAC  
|| ||||| || |||||  
TG GGTGTC CG CG TCTG  
C \_ \_ G  
GAM1228 LOC139065 3' TCCTTTTGATTTGTGG 75817 \_ CTGC  
CCACAGA CAG AGGA  
||||| ||| |||||  
GGTGTTT GTT TCCT  
A T \_  
GAM1228 LOC145622 5' AGTCCTGCAAAGGTGATGGTGG 77291 AGA G \_  
T ACCAC CA CT GCAGGACT  
|||| ||| |||||  
TGGTG GT GA CGTCCTGA  
GTA G AA  
GAM1228 LOC145676 5' AGTCCTGTCCAGGGTCT 77333 AG \_  
AGAC CTG CAGGACT  
||| ||| |||||  
TCTG GAC GTCCTGA  
G\_ CT  
GAM1228 LOC145955 5' AGCCCTGAGATGTCCATGGT 83586 CA G G A  
ACCA GACA CT CAGG CT  
|||| ||| ||| ||| |||  
TGGT CTGT GA GTCC GA  
AC A \_ C  
GAM1228 LOC145957 5' CTGCTGTTGTCTGCGGT 56794 A T  
ACC CAGACAGC GCAG  
||| ||||| |||  
TGG GTCTGTTG CGTC  
C T  
GAM1228 LOC146287 5' TTGCAGCTGCCTCGGT 83654 AC A  
ACC AG CAGCTGCAG  
||| ||| |||||  
TGG TC GTCGACGTT  
C\_ C  
GAM1228 LOC146669 3' AGCCCTGCAGCCTGGG 78049 A ACA A  
CC CAG GCTGCAGG CT  
|| ||| ||||| |||  
GG GTC CGACGTCC GA  
\_ \_ C  
GAM1228 LOC147040 3' CAGTGTCTGTGATGT 78230 C G  
ACA CACAGACA CTG  
||| ||||| |||  
TGT GTGTCTGT GAC  
A \_  
GAM1228 LOC147160 5' AGCCCTGCAGTGC GTGTACAGG 83956 ACAG \_ A  
CC ACA GCTGCAGG CT  
|| ||| ||||| |||

	GG TGT TGACGTCC GA	
	ACA_ GCG C	
GAM1228 LOC149111 3'	CCTGCGTGTCTGTG 79181	GC
	CACAGACA TGCAGG	
	GTGTCTGT GCGTCC	
	—	
GAM1228 LOC150174 3'	AGTCCTGCGATGCTAAGTG 79604	CAC A GC
	CAC AG CA TGCAGGACT	
	GTG TC GT GCGTCCTGA	
	AA_ _ A_	
GAM1228 LOC150213 3'	AGTCCTGCGATGCTAAGTG 74851	CAC A GC
	CAC AG CA TGCAGGACT	
	GTG TC GT GCGTCCTGA	
	AA_ _ A_	
GAM1228 LOC150236 3'	AGTCCTGCGATGCTAAGTG 79683	CAC A GC
	CAC AG CA TGCAGGACT	
	GTG TC GT GCGTCCTGA	
	AA_ _ A_	
GAM1228 LOC154559 3'	GCAGCTGTCCTGTGATGT 81096	C _
	ACA CACAG ACAGCTGC	
	TGT GTGTC TGTCGACG	
	A C	
GAM1228 LOC158117 3'	CCTGGTCTGTTCTGTATTGTT 81703	CC _ CTG
	AACA ACAGA CAG CAGG	
	TTGT TGTCT GTC GTCC	
	TA T TG_	
GAM1228 LOC160897 3'	CCAGCTATTGTCTGTTGTGTT 82245	C CT A
	AACAC ACAGACAG GC GG	
	TTGTG TGTCTGTT CG CC	
	T AT A	
GAM1228 LOC161482 3'	GCACTTACCTGTGGTGTT 87089	AC_ C
	AACACCACAG AG TGC	
	TTGTGGTGTC TC ACG	
	CAT _	
GAM1228 LOC164382 3'	AGTCTCCCTGTCTGTGGT 87203	CTGCA
	ACCACAGACAG GGA CT	
	TGGTGTCTGTC TCTGA	
	CC__	
GAM1228 LOC200301 5'	AGCCTGTCTGTGTGTT 88736	C _
	AACAC ACAGACAG CT	

	TTGTG TGTCTGTC GA	
	— C	
GAM1228 LOC203275 3'	CCTGGTCTGTTCTGTATTGTT 89319	CC _ CTG
	AACA ACAGA CAG CAGG	
	TTGT TGTCT GTC GTCC	
	TA T TG_	
GAM1228 LOC219920 5'	TTGGGCACTGCCTGTGG 93323	A C AG
	CCACAG CAG TGC GA	
	GGTGTC GTC ACG TT	
	C _ GG	
GAM1228 LOC220932 3'	AGTCCTGTTCTCTGTTAATGT 93135	_ CT_
	ACA GACAG GCAGGACT	
	TGT TTGTC TGTCCTGA	
	AA TCT	
GAM1228 LOC221466 5'	GTCCTGTGTCCAGGGTG 93693	ACA AGCT
	CACC GAC GCAGGAC	
	GTGG CTG TGTCCTG	
	GAC _	
GAM1228 LOC221547 3'	GCAGCTGTCCTGTGATGT 91007	C _
	ACA CACAG ACAGCTGC	
	TGT GTGTC TGTCGACG	
	A C	
GAM1228 LOC221935 3'	AGCCGTCACCTGTCTGTG 92615	CT A A
	CACAGACAG GC GG CT	
	GTGTCTGTC TG CC GA	
	AC _ _	
GAM1228 LOC253681 3'	CAGTGTCTGTGATGT 95127	C G
	ACA CACAGACA CTG	
	TGT GTGTCTGT GAC	
	A _	
GAM1228 LOC257115 3'	AGTCCTGCAAGGTGAAGGCGTT 96523	A ACAGA G _
	AAC CC CA CT GCAGGACT	
	TTG GG GT GA CGTCCTGA	
	C AA_ G A	
GAM1228 LOC257577 3'	GCAGCTGTCCTGTGATGT 97838	C _
	ACA CACAG ACAGCTGC	
	TGT GTGTC TGTCGACG	
	A C	
GAM1228 LOC51112 5'	AGTCCTGCGGGCCGTGG 32082	AGACAG
	CCAC CTGCAGGACT	

		GGTG GCGTCCTGA		
		CCG____		
GAM1228	LOC51236	3' TCCTGCAGCTGTCTGCAGG	33205	A_
		CC CAGACAGCTGCAGGA		
		GG GTCTGTCGACGTCCT		
		AC		
GAM1228	LOC51713	3' TTTGTAAGTGTCTGCGG	32762	A C
		CC CAGACAG TGCAGG		
		GG GTCTGTC ATGTTT		
		C _		
GAM1228	LOC56920	3' AGCCTTCCAGCCTGCGGTG	39379	A ACA C_ A
		CACC CAG GCTG AGG CT		
		GTGG GTC CGAC TCC GA		
		C _ CT _		
GAM1228	LOC90408	3' AGTCCTGTGGTCCTGTG	62655	ACA TG
		CACAG GC CAGGACT		
		GTGTC TG GTCCTGA		
		C_ GT		
GAM1228	LOC91397	5' GCAGTATCTGTGGTG	65910	CA
		CACCACAGA GCTGC		
		GTGGTGTCT TGACG		
		A_		
GAM1229	KCNJ15	3' CATCAGAACTCCCTTCAAACAC	9544	CA _
		GTGT GA AGTTCTGATG		
		CACA CT TCAAGACTAC		
		AA TCCC		
GAM1229	RUVBL2	3' CAGAGTTCTGACACTGTG	21892	G
		CACAGTGTGAGAA TTCTG		
		GTGTCACAGTCTT GAGAC		
		-		
GAM1229	BG1	5' CACAGCTTCCCTACACTGTGCA	87307	CA_ C
		TGCACAGTGT GAAGTT TG		
		ACGTGTCACA CTTCGA AC		
		TCC C		
GAM1229	C20orf173	5' GACCTCTGACACTGTGC	55060	A
		GCACAGTGTGAGA GTT		
		CGTGTACAGTCT CAG		
		C		
GAM1229	FLJ22794	5' ATCAAGGATGCACTGTGCA	91602	CAGAA _
		TGCACAGTGT GTTCT GAT		

ACGTGTACAG TAGGA CTA  
 \_\_\_\_\_ A  
 GAM1229 FLJ23468 5' CAGATACTTCTGACATTGTGCA 44907 \_  
 TGCACAGTGTGAGAAGT TCTG  
 |||||  
 ACGTGTTACAGTCTTCA AGAC  
 T  
 GAM1229 GREAT 5' CATCAGAACTCCTGCTGAGGTA 55482 A\_ TGT A  
 TGC CAG CAG AGTTCTGATG  
 ||| ||| ||| |||||  
 ATG GTC GTC TCAAGACTAC  
 GA \_ C  
 GAM1229 KIAA0379 3' CAGAACTTCTATCCTG 68147 TG C  
 CAG T AGAAGTTCTG  
 ||| | |||||  
 GTC A TCTTCAAGAC  
 CT \_  
 GAM1229 KIAA1257 3' CATCAGAACCTCTTGAGAGGC 62733 G \_ A  
 GT TC AGA GTTCTGATG  
 || || ||| |||||  
 CG AG TCT CAAGACTAC  
 G AGT C  
 GAM1229 KIR3DS1 3' CATCAGGAGGTGACATACGCA 27210 ACA GAAG  
 TGC GTGTCA TTCTGATG  
 ||| ||||| |||||  
 ACG TACAGT AGGACTAC  
 CA\_ GG\_  
 GAM1229 OS4 3' CATCAGAACCTGCTGCCCCA 19176 CA T T AA  
 TG CAG G CAG GTTCTGATG  
 || ||| ||| |||||  
 AC GTC C GTC CAAGACTAC  
 CC \_ \_ C\_  
 GAM1229 RAB14 3' CATCAGAGGATTAACACTAGCA 32870 AC CA AG  
 TGC AGTGT GA TTCTGATG  
 ||| ||||| ||| |||||  
 ACG TCACA TT GAGACTAC  
 A\_ A\_ AG  
 GAM1229 LOC124411 3' AGGCCTCTGACACTGTACA 74283 C A TT  
 TG ACAGTGTGAGA G CT  
 || ||||| ||| ||  
 AC TGTCACAGTCT C GA  
 A \_ CG  
 GAM1229 LOC147700 3' CAGAACTTCCACAGACGC 59194 A\_  
 GTGTC GAAGTTCTG  
 ||||| |||||  
 CGCAG CTTCAAGAC  
 ACAC  
 GAM1229 LOC149606 5' TTTCTGACCTATGCA 79458 C T  
 TGCA AG GTCAGAAG  
 |||| || |||||

ACGT TC CAGTCTTT  
 A \_  
 GAM1229 LOC151996 3' CATCAGAACCTCACTTGGTAC 85530 GT \_\_\_\_ A  
 GT CA GA GTTCTGATG  
 || || || |||||  
 CA GT CT CAAGACTAC  
 TG TCA C  
 GAM1229 LOC153856 3' CAGTATAACTTCTGACAC 80970 \_\_\_\_  
 GTGTCAGAAAGTT CTG  
 ||||| ||  
 CACAGTCTTCAA GAC  
 TAT  
 GAM1229 LOC155382 3' GGGGCTTCTGACCTGTGCA 86390 T  
 TGCACAG GTCAGAAAGTTCT  
 ||||| |||||  
 ACGTGTC CAGTCTTCGGGG  
 -  
 GAM1229 LOC158476 3' CATCAGAAATTTGACAC 86840 AG  
 GTGTCAGA TTCTGATG  
 ||||| |||||  
 CACAGTTT AAGACTAC  
 A\_  
 GAM1229 LOC163231 3' CATCAGAACCTGTTTACCGTCA 82438 C A T\_ AA  
 TG AC GTG CAG GTTCTGATG  
 || ||| || |||||  
 AC TG CAT GTC CAAGACTAC  
 \_ C TT \_  
 GAM1230 SUV39H2 3' ACATTGGCACCTCAATGA 45134 C TAC  
 TCGTT AG GCCAATGT  
 |||| || |||||  
 AGTAA TC CGGTTACA  
 C CA\_  
 GAM1230 DKFZp761G0313 3' AACATTGGCGTAGACACAGT 65810 C \_ AG  
 ACT GT TC TACGCCAATGTT  
 || || || |||||  
 TGA CA AG ATGCGGTTACAA  
 \_ C \_  
 GAM1230 FAM8A1 3' TGGCATACTGAATAAGT 32726 CG C  
 ACT TTCAGTA GCCA  
 || ||||| ||  
 TGA AAGTCAT CGGT  
 AT A  
 GAM1230 FLJ13031 5' AACATTGGCTCAAAAAACGA 45197 CAGTAC\_  
 TCGTT GCCAATGTT  
 |||| |||||  
 AGCAA CGGTTACAA  
 AAAA ACT  
 GAM1230 FLJ23277 3' AACATTCTGCTCTGAACGA 49934 TAC C\_  
 TCGTTCAG GC AATGTT  
 ||||| || |||||

AGCAAGTC CG TTACAA  
 T\_\_ TC  
 GAM1230 HSXIAPAF1 3' AACATCATACTGAATGAG 34029 CGCCA  
 CTCGTTTCAGTA ATGTT  
 ||||| ||||  
 GAGTAAGTCAT TACAA  
 AC\_\_  
 GAM1231 ACK1 5' TGCAGGAGGGACAGGTGGTG 19347 T GG  
 CATC GCCTGTCCC CCTGTG  
 ||| ||||| ||||  
 GTGG TGGACAGGG GGACGT  
 \_ A\_  
 GAM1231 ACTN4 3' TGCAGTCCTCCGGGGTGGGTGG 17002 TG TG CCTG\_  
 GTG CATC CC TCCCGG TGCG  
 ||| || ||||| ||||  
 GTGG GG GGGGCC ACGT  
 GT GT TCCTG  
 GAM1231 ACVR1B 3' TGTGCAGGTCCGGGGTGTGGT 15036 TG\_\_ TG  
 GCC TCCCGGCCTG CG  
 ||| ||||| ||  
 TGG GGGGCTGGAC GT  
 TGTG GT  
 GAM1231 ACVRL1 3' TGTGTGCTGGGGATGGGCAGCT 3422 T \_ CT TG  
 G CA CTGCCTGTCCC GGC G CG  
 || ||||| ||| | ||  
 GT GACGGGTAGGG TCG T GT  
 C G \_\_GT  
 GAM1231 ADCY8 5' GCCTGTGCGTGTGCGAGGCAGG 6655 C \_\_\_\_\_ CTGT  
 CAGG TGCCTGTC CG GC GC  
 ||||| || || ||  
 ACGGACGG GC CG CG  
 A GTGT G TGTC  
 GAM1231 AGPAT2 3' CTGGGGAGGGCAGGTG 65822 GT  
 CATCTGCCT CCCGG  
 ||||| ||||  
 GTGGACGGG GGGTC  
 AG  
 GAM1231 AGPAT2 3' CTGGGGAGGGCAGGTG 21155 GT  
 CATCTGCCT CCCGG  
 ||||| ||||  
 GTGGACGGG GGGTC  
 AG  
 GAM1231 ARF4L 3' TGTGTTTGGGGGCGGGGGGATG 69816 G GGCCT TG  
 CATCT CCTGTCCC G CG  
 |||| ||||| | ||  
 GTAGG GGGCGGGG T GT  
 G GTT\_\_GT  
 GAM1231 ASCL2 5' CGCGCCGGGACCTGGAGCGGGC 87585 TC \_ \_ \_  
 GGGTG CTGCCTG CC GG CCTG TGCG  
 ||||| || || || ||||

GGCGGGC GG CC GGGC GCGC  
GA T A C  
GAM1231 ASCL2 5' CGCGCCGGGACCTGGAGCGGGC 17716 TC \_ \_ \_  
GGGTG CTGCCTG CC GG CCTG TGCG  
||||| || || ||| ||||  
GGCGGGC GG CC GGGC GCGC  
GA T A C  
GAM1231 ATP2A3 3' TGTGCAGGGCCCGGGCCGGT 17726 T C \_ TG  
GCC GTCC GGCC TG CG  
||| ||| ||| || ||  
TGG CGGG CCGG AC GT  
C C G GT  
GAM1231 ATSV 3' TGTGTGGGAGAGTGGGGGGGTG 15060 G TG CCCGG TG  
CATCT CC T CCTG CG  
||||| || | ||| ||  
GTGGG GG G GGGT GT  
G GT AGA\_\_ GT  
GAM1231 AUP1 3' ACAGGCTGGATGGGTGGGTG 23971 TG C  
CATC CCTGTCC GGCCTGT  
||| ||||| |||||  
GTGG GGGTAGG TCGGACA  
GT \_  
GAM1231 AXIN1 5' CGTCCACGCGGAGCGGGCGGGT 60851 TC G C TG  
G CATCTGCCTG CCG C TG CG  
||||||| ||| || ||  
GTGGGCGGGC GGC G AC GC  
GA \_C CT G  
GAM1231 B4GALT2 3' GCATGGGAGGCAGGTGGG 13679 TG CCGG  
TC CCTGTC CCTGTGC  
|| ||||| |||||  
GG GGACGG GGGTACG  
GT A\_\_  
GAM1231 B4GALT2 3' GCATGGGAGGCAGGTGGG 47582 TG CCGG  
TC CCTGTC CCTGTGC  
|| ||||| |||||  
GG GGACGG GGGTACG  
GT A\_\_  
GAM1231 BTEB1 5' CGTGCCGGGCGGGCGGGT 6844 T C  
ATCTGCCTG CCCGGC TG  
||||||| ||||| ||  
TGGGCGGGC GGGCCG GC  
\_ T  
GAM1231 C21orf2 3' GGCCGGGCTGGGCAGGTG 17014 T  
CATCTGCCTG CCCGGCC  
||||||| |||||  
GTGGACGGGT GGGCCGG  
C  
GAM1231 CACNA2D2 3' TGCCAAATGCTGGGGCAGGGGG 20090 G C\_\_ T  
TG CATCT CCTGTCCCGGC TG GCG  
||||| ||||| || |||



			GTGGG GGACGGGGTCG AC CGT		
			— TAA —		
GAM1231	CAPN10	3'	GGTAGCAATAGGTAGCTG 43609 T	CCCG C TG	
			CA CTGCCTGT GC TG C		
			GT GATGGATA CG AT G		
			C A___ _ GT		
GAM1231	CAPN7	5'	CGCGAAGTGGGGCGGCCGGGTG 26661 C	GC G	
			CATCTG CTGTCCCG CT TGCG		
			GTGGGC GGCGGGGT GA GCGC		
			C _ A		
GAM1231	CCND1	3'	CGTGTGAGGGAGGACAGGCGGG 53886	CGG _ TG	
			TCTGCCTGTCC CCT G CG		
			GGCGGACAGG GGA T GC		
			AG_ G GT		
GAM1231	CCND3	5'	CGCGCGGGCGGCGGGCGGGC 8305 T _		
			GCCTG CCCG GCCTGTGCG		
			CGGGC GGGC CGGGCGCGC		
			_ GG		
GAM1231	CDK10	3'	GCATGGGTTGGCTGTGGG 13403 TG C_		
			CC T CCGGCCTGTGC		
			GG G GGTGGGTACG		
			GT TC		
GAM1231	CDK10	3'	GCATGGGTTGGCTGTGGG 53770 TG C_		
			CC T CCGGCCTGTGC		
			GG G GGTGGGTACG		
			GT TC		
GAM1231	CDK10	3'	GCATGGGTTGGCTGTGGG 53779 TG C_		
			CC T CCGGCCTGTGC		
			GG G GGTGGGTACG		
			GT TC		
GAM1231	CDKN2A	5'	CGCGCTCAGGGAAGGCGGGTG 54223 G	GGCCT	
			CATCTGCCT TCCC GTGCG		
			GTGGGCGGA AGGG CGCGC		
			_ ACT_		
GAM1231	CELSR3	3'	GGCAGGGCTGGGGGGT 7403 GT _ TG		
			GCCT CCCGGCC TG C		
			TGGG GGGTCGG AC G		
			_ G GT		
GAM1231	CENTD2	5'	TGTGTGGGTCGGGGCTGTGTGG 30877 TG CT_ TG		
			C C GTCCCGGCCTG CG		

G G CGGGGCTGGGT GT  
 GT TGT GT  
 GAM1231 CFTR 3' TGTATAGGTTGATGGTGGTATG 4930 \_TG TGTCC  
 CAT C CC CGGCCTGTGCG  
 ||| | || |||||  
 GTA G GG GTTGGATATGT  
 T GT TA\_\_  
 GAM1231 CGTHBA 3' GCTGGGGTGCGCAGGTG 23863 C GT  
 CATCTGC T CCCGGC  
 ||||| | |||||  
 GTGGACG G GGGTCG  
 C TG  
 GAM1231 CYLN2 3' TGCCACCTGGTACAGGTAGGTG 12640 C CC T  
 CATCTGCCTGT CCGG TG GCG  
 ||||| ||| || |||  
 GTGGATGGACA GGTC AC CGT  
 T C\_ \_  
 GAM1231 CYP26A1 5' TGCTTTGGGCCGGGGCAGCGGG 54049 C T\_  
 TG CATCTGC TGTCCCGGCCTG GCG  
 ||||| ||||| |||  
 GTGGGCG ACGGGGCCGGGT CGT  
 \_ TT  
 GAM1231 CYP8B1 3' GCCTGTGCGCGTGTGTGGCAGG 15264 TGTCC \_\_\_\_ CTGT  
 TG CATCTGCC CG GC GC  
 ||||| || || ||  
 GTGGACGG GC CG CG  
 TGTGT G TGTC  
 GAM1231 DDX15 5' CGTGTGGGCTGTAGTAGCGGG 7230 C CC TG  
 TCTGC TGT CGGCCTG CG  
 |||| || ||||| ||  
 GGGCG ATG GTCGGGT GC  
 \_ AT GT  
 GAM1231 DPYSL3 3' CGCAGGTTATTTGGGGTGAGTG 7315 TG C GT \_\_\_\_ CG  
 GGTG C C T CCCG GCCTGTG  
 | || ||| |||||  
 G G G GGGT TGGACGC  
 GT A TG TTAT  
 GAM1231 DSC3 3' CGCACAGGCTGGAGTGCAG 8675 \_ GTC  
 CTGC CT CCGGCCTGTGCG  
 ||| || |||||  
 GACG GA GGTCCGACACGC  
 T \_\_\_\_  
 GAM1231 DSC3 3' CGCACAGGCTGGAGTGCAG 44340 \_ GTC  
 CTGC CT CCGGCCTGTGCG  
 ||| || |||||  
 GACG GA GGTCCGACACGC  
 T \_\_\_\_  
 GAM1231 E2F3 3' TGTGTGGGTATGCGTGGGTGTA 8703 CT TG CCCG TG  
 TG CAT GCC T GCCTG CG  
 ||| ||| | |||| ||

			GTA TGG G TGGGT GT		
			TG GT CGTA GT		
GAM1231	ELL	3'	GTGGGGAATGGGCAGGTG 21524	_	G
			CATCTGCCTGT CCC GC		
			GTGGACGGGTA GGG TG		
			A G		
GAM1231	EMS1	3'	CGTGCAGTCAGGTGGGCGG 17851	T C	C TG
			CTGCCTG CC GGC TG CG		
			GGCGGGT GG CTG AC GC		
			_ A _ GT		
GAM1231	EMS1	3'	CGTGCAGTCAGGTGGGCGG 56751	T C	C TG
			CTGCCTG CC GGC TG CG		
			GGCGGGT GG CTG AC GC		
			_ A _ GT		
GAM1231	ERBB4	3'	GCATGGGTTGGTCAGG 17875	TC	
			CCTG CCGGCCTGTGC		
			GGAC GGTGGGTACG		
			T_		
GAM1231	ESRRG	3'	TGCACGGGCTTTAGGGTAAATG 66394	C	GTCCC
			CAT TGCCT GGCCTGTGCG		
			GTA ATGGG TCGGGCACGT		
			A ATT_		
GAM1231	FBXL7	5'	CGGAGGGGATCGGGGCGGGCGG 24548	_	GTGCG
	ATG		CATCTGCCTGTCCCGG CCT		
			GTAGGCGGGCGGGGCT GGG		
			A GAGGC		
GAM1231	FGF18	5'	GGCAGGCTGGGCTAGG 53347	T	TG
			CCTG CCCGGCCTG C		
			GGAT GGGTCGGAC G		
			C GT		
GAM1231	FGF18	5'	GGCAGGCTGGGCTAGG 13912	T	TG
			CCTG CCCGGCCTG C		
			GGAT GGGTCGGAC G		
			C GT		
GAM1231	FGFR4	3'	TGTGCAGGCACATAGGCTGGTG 8893	T	CCCG TG
			CATC GCCTGT GCCTG CG		
			GTGG CGGATA CGGAC GT		
			T CA_ GT		
GAM1231	FGFR4	3'	TGTGCAGGCACATAGGCTGGTG 43353	T	CCCG TG
			CATC GCCTGT GCCTG CG		

			GTGG CGGATA CGGAC GT		
			T CA__ GT		
GAM1231	FLRT2	3'	TGCATGGGACAATCGCAGGCAG 25069	CCCCGG_	
	AT		ATCTGCCTGT CCTGTGCG		
			TAGACGGACG GGGTACGT		
			CTAACA		
GAM1231	FOXD2	5'	GGCGGGCTCGGGTGGGC 15568	T _ TG	
			GCCTG CCCG GCCTG C		
			CGGGT GGGC CGGGC G		
			_ T GT		
GAM1231	FUT7	3'	CGCTGGCCGGGGGAGGTGGGTG 15581	TG G T	
			CATC CCT TCCCGGCC GTG		
			GTGG GGA GGGGCCGG CGC		
			GT G T		
GAM1231	FUT7	3'	TGTGTAGGCTGGGGCGGG 15588	TG	
			CCTGTCCCGGCCTG CG		
			GGGCGGGGTCGGAT GT		
			GT		
GAM1231	G6PD	5'	CGCGCGAGGCCCGCGGGGCAGG 4634	___ _	
	CGGG		TGCCTGTCCC GGCCT GTGCG		
			GCGGACGGGG CCGGA CGCGC		
			CCG G		
GAM1231	GALNT2	3'	TGTGAAGGCTGGGTGGGGTGGG 15601	TG GT G	
	TG		CATC CCT CCCGGCCT TGCG		
			GTGG GGG GGGTCGGA GTGT		
			GT GT A G		
GAM1231	GCNT3	3'	GCTGGGACAGTGTGGGTG 16458	TG _	
			CATC C CTGTCCCGGC		
			GTGG G GACAGGGTCG		
			GT T		
GAM1231	GJA1	3'	TGTATGGGGTAGATGGGTGGA 3908	TG CCGG	
			TC CCTGTC CCTGTGCG		
			AG GGGTAG GGGTATGT		
			GT ATG_		
GAM1231	GLTSCR1	3'	GCCGGGACAGTCGGGTG 31672	C	
			CATCTG CTGTCCCGGC		
			GTGGGC GACAGGGCCG		
			T		
GAM1231	GNA11	3'	CGTGTGGGGCCACGTGGGCATG 76096	C TG CCC _TG	
	TG		CAT TGCC T GGCCT G CG		

			GTG ACGG G CCGGG T GC		
			T GT CA_ G GT		
GAM1231	GPR56	3'	GCGTGGGCTGGGCTAGGT 19069	T	TG
			GCCTG CCCGGCC TGC		
			TGGAT GGGTCGG GCG		
			C GT		
GAM1231	GPX3	5'	GCCCCGGGACGGGGAGGTG 9121	G	CCTGT
			CATCT CCTGTCCCGG GC		
			GTGGA GGGCAGGGCC CG		
			G C____		
GAM1231	GTF2E2	5'	GCGTGCGGGCAGGCGGG 9148	T	G CTG
			TCTGCCTG CCCG C TGC		
			GGGCGGAC GGGC G GCG		
			- - T__		
GAM1231	GUCY2D	3'	TGGGTCCTGGGAGGGTGGGTG 3937	TG	G _ _
			CATC CCT TCCC GG CCTG		
			GTGG GGG AGGG CC GGGT		
			GT _ T T		
GAM1231	HDGF	5'	GGCGGCGCGCGGGCGGA 15682	CCCG	_ TG
			TCTGCCTGT GC CTG C		
			AGGCGGGCG CG GGC G		
			____ C GT		
GAM1231	HNRPD	5'	CGGTTCGCGGCAGGCGGGTG 9244	C	GC
			CATCTGCCTGTC CG CTG		
			GTGGGCGGACGG GC GGC		
			C TT		
GAM1231	HNRPD	5'	CGGTTCGCGGCAGGCGGGTG 48575	C	GC
			CATCTGCCTGTC CG CTG		
			GTGGGCGGACGG GC GGC		
			C TT		
GAM1231	HOXC9	3'	CGTGCAGGCCGGCGCCTTGGGC 61263	__ C	TG
			GCCT GT CCGGCCTG CG		
			CGGG CG GGCCGGAC GC		
			TTC C GT		
GAM1231	HPS4	5'	CGCGCAGGTACGGGGCAG 41985	_	
			CTGTCCCG GCCTGTGCG		
			GACGGGGC TGGACGCGC		
			A		
GAM1231	HRMT1L1	5'	GCGCGGGTTGAGGGCGGT 65202	T	_
			GCC GTCC CGGCCTGTGC		

			TGG CGGG GTTGGGCGCG		
			— A		
GAM1231	ICAM1	3'	TGTACAGGTTGTACACTGCAGG 71580	C_	CC
			TCTGC TGT CGGCCTGTGCG		
			GGACG ACA GTTGGACATGT		
			TC T_		
GAM1231	IDE	3'	TGCATGGGAAAGTGCAAGTGGG 17123	TG C	CCCGG
	TG		CATC C TGT CCTGTGCG		
			GTAG G ACG GGGTACGT		
			GT A TGAAA		
GAM1231	IGJ	5'	CGCACGGGCTGGGCGGTGGG 58313	TG T T	
			TC CC G CCCGGCCTGTGCG		
			AG GG C GGGTCGGGCACGC		
			GT _ _		
GAM1231	IL11	3'	TGGGTAAGTGGGGCAGGGCAGG 5340	_	_____ TGCG
	TG		TCTGCC TGTCCCGG CCTG		
			GGACGG ACGGGGTC GGGT		
			G AAT G		
GAM1231	ILF1	3'	CTGTGCGCGCGTGGACAGGTGG 15719	TG	_ _____ CTGT
	A		TC CCTGTCC CG GC G		
			AG GGACAGG GC CG C		
			GT T GC G TGTC		
GAM1231	INSR	3'	GGCGGGGGCGGGCAGG 70980	G	
			TCTGCCTGTCCC GCC		
			GGACGGGCGGGG CGG		
			G		
GAM1231	ISGF3G	5'	TGCGTGGGCCGCGGGTGGGC 20296	TG	TG
			GCC TCCCGGCC TGCG		
			CGG GGGGCCGG GCGT		
			GT GT		
GAM1231	ITGA1	5'	GCGAAGGGGCGGGCGATG 63532	T	GGCCTG
			CATC GCCTGTCCC TGC		
			GTAG CGGGCGGGG GCG		
			_ AA_		
GAM1231	ITGAV	3'	GTATATAAGACAGGTAG 9398	CCGGCC	
			CTGCCTGTC TGTGC		
			GATGGACAG ATATG		
			AAT_		
GAM1231	JAG2	5'	TGCATATGCAGGTGCGCGGGTG 9472	CT TC	G C
			CATCTGC G CC GC TGTGCG		

		GTGGGCG C GG CG ATACGT	
		__GT A T	
GAM1231	KCNAB2	3' TGGGTCCTTGGGGCGGGCAGG 13310	___
		TCTGCCTGTCCC GGCCTG	
		GGACGGGCGGGG CTGGGT	
		TTC	
GAM1231	KCNK3	5' TGC GCGGGCCGGGGCGCCGGG 9554	___
		CCTG TCCCGGCTGTGCG	
		GGGC GGGGCCGGGCGCGT	
		CGCG	
GAM1231	KIAA0857	3' TGTGTGGGGCGCAGGGGCGGGT 66682	___ G TG
		GCCTGTCCC G CCTG CG	
		TGGGCGGGG C GGGT GT	
		ACG G GT	
GAM1231	KIF5C	5' CGCGTGGTCGCGGGCAGGTGG 15733	TG _ TGT
		C CCTGTCC CGGCC GCG	
		G GGACGGG GCTGG CGC	
		GT C TG_	
GAM1231	LASS1	3' CGCTAACCCGGGGCGGGCAGG 41195	CCTGT
		TCTGCCTGTCCCGG GCG	
		GGACGGGCGGGGCC CGC	
		CAAT_	
GAM1231	LIF	3' CGCGTGGGCAGTGTGCAGGCAG 9735	CCCG_ TG
	GT	ATCTGCCTGT GCC TGCG	
		TGGACGGACG CGG GCGC	
		TGTGA GT	
GAM1231	MADH7	3' GGCAGGAGCGGCAGATG 19745	T CCCGG TG
		CATCTGCC GT CCTG C	
		GTAGACGG CG GGAC G	
		_ A _ GT	
GAM1231	MHC2TA	3' GGTAGGGCGGGAGGATG 4180	GCCTG G TG
		CATCT TCCCG CCTG C	
		GTAGG AGGGC GGAT G	
		_____ G GT	
GAM1231	MHC2TA	3' GTACGTCTGACAGGCA 4182	CC CT
		TGCCTGTC GGC GTGC	
		ACGGACAG CTG CATG	
		T_ _	
GAM1231	MLC1	3' CCGGGGCGGGCTGATG 57590	T
		CATC GCCTGTCCCGG	

			GTAG CGGGCGGGGCC			
			T			
GAM1231	MLC1	3'	CCGGGGCGGGCTGATG 30778	T		
			CATC GCCTGTCCCGG			
			GTAG CGGGCGGGGCC			
			T			
GAM1231	MYO1C	3'	TGTGTGGGCTGGGCTCTGGT 61212	TGT_	TG	
			GCC CCCGGCCTG CG			
			TGG GGGTCGGGT GT			
			TCTC GT			
GAM1231	NAPB	3'	GTACATGATGGGTTAGGT 70188	T	GCC	
			GCCTG CCCG TGTGC			
			TGGAT GGGT ACATG			
			T AGT			
GAM1231	NCOA6IP	5'	CGCACCTCGGATAGGCGGG 45737		C CCT	
			TCTGCCTGTCC GG GTGCG			
			GGGCGGATAGG TC CACGC			
			C _			
GAM1231	NCOR2	3'	TGTGCAGGCCGACAGTCGG 20881	C	CC TG	
			CTG CTGTC GGCCTG CG			
			GGC GACAG CCGGAC GT			
			T _ GT			
GAM1231	NMB	5'	CGTGCGGGCCAGAGTGTGGGTG 73782	TG CTG CC	TG	
			CATC C TC GGCCTG CG			
			GTGG G AG CCGGGC GC			
			GT TG_ A_ GT			
GAM1231	OCRL	5'	CGCAGCCGAGGTGGGTGGGTG 4260	TG TG C	C	
			CATC CC TC CGGC TGTG			
			GTGG GG GG GCCG ACGC			
			GT GT A _			
GAM1231	OCRL	5'	CGCAGCCGAGGTGGGTGGGTG 7826	TG TG C	C	
			CATC CC TC CGGC TGTG			
			GTGG GG GG GCCG ACGC			
			GT GT A _			
GAM1231	P2RY1	3'	AAGCAACTGGGGTGGGCAGA 10376	TG	CCTG G	
			TCTGCC TCCCGG TGC			
			AGACGG GGGGTC ACG			
			GT A__ AAG			
GAM1231	P3	5'	TGCGCGGTGGCTGTGGCAGGT 39067	C	_	
			GCCTGTC CGGCC TGTGCG			



			TGGACGG GTCGG GCGCGT		
			T TG		
GAM1231	PABPN1	5'	CGCGTGTTGATTGACAGGCAGA 16178	C__ C CG	
		T	ATCTGCCTGTC CGGC TGTC		
			TAGACGGACAG GTTG GCGC		
			TTA T		
GAM1231	PAX7	5'	TGCAGCCAGGGGTGGGGGGTG 10437	G TG _ CTG	
			CATCT CC TCCC GGC TGCG		
			GTGGG GG GGGG CCG ACGT		
			_ GT A _		
GAM1231	PAX7	5'	TGCAGCCAGGGGTGGGGGGTG 25641	G TG _ CTG	
			CATCT CC TCCC GGC TGCG		
			GTGGG GG GGGG CCG ACGT		
			_ GT A _		
GAM1231	PFKFB4	3'	GCATGGGCTGCGCGGA 15869	CTGTCC	
			TCTGC CGGCCTGTGC		
			AGGCG GTCGGGTACG		
			C__		
GAM1231	PITX2	5'	CGCGTGGGGGGGGGGCGGGCAGA 4379	GG TG	
			TCTGCCTGTCCC CC TGCG		
			AGACGGGCGGGG GG GCGC		
			GG GT		
GAM1231	PPP2R2B	5'	CGCCTCCGGGGCGGGCGGG 15907	CCTGT	
			TCTGCCTGTCCCGG GCG		
			GGGCGGGCGGGGCC CGC		
			TC__		
GAM1231	PPP2R4	3'	CCAGCTGTGGGCTGGGGTGGGG 60557	TG _ TG TG _ G	
		TGGGTG	TC C C TCCCGGCC T GC		
			GG G G GGGGTCGG G CG		
			GT G GT GT T ACCG		
GAM1231	PRX	3'	GGGCTGGGATGGGAGGGTG 40535	G	
			CATCT CCTGTCCCGGCCT		
			GTGGG GGGTAGGGTCGGG		
			A		
GAM1231	PSD	3'	GTACAGGGTGGGCGGG 10934	T G	
			CCTG CCCG CCTGTGC		
			GGGC GGGT GGACATG		
			_ G		
GAM1231	PTPN14	5'	GCGCAGGATAGGCAGGC 18253	CCGG	
			GCCTGTC CCTGTGC		

			CGGACGG GGACGCG		
			ATA_		
GAM1231	PUM2	3'	TGTATATTTGGGGGGTGGGGGA 31016	G TG	GG ____
	TG		ATCT CC TCCC CC TGTGCG		
			TAGG GG GGGG GG ATATGT		
			_ GT _ TTT		
GAM1231	RAD51L3	5'	GGATCCCGGGCGGGCGGATG 56069	T	____
			CATCTGCCTG CCCGG CC		
			GTAGGCGGGC GGGCC GG		
			_ CTA		
GAM1231	RAD51L3	5'	GGATCCCGGGCGGGCGGATG 56076	T	____
			CATCTGCCTG CCCGG CC		
			GTAGGCGGGC GGGCC GG		
			_ CTA		
GAM1231	RAD51L3	5'	GGATCCCGGGCGGGCGGATG 56082	T	____
			CATCTGCCTG CCCGG CC		
			GTAGGCGGGC GGGCC GG		
			_ CTA		
GAM1231	RAD51L3	5'	GGATCCCGGGCGGGCGGATG 11236	T	____
			CATCTGCCTG CCCGG CC		
			GTAGGCGGGC GGGCC GG		
			_ CTA		
GAM1231	RERE	3'	TGCACAGGGAGTGCAGGAGGTG 23969	G	CCCGG
			CATCT CCTGT CCTGTGCG		
			GTGGA GGACG GGACACGT		
			_ TGAG_		
GAM1231	RNASEH1	3'	GCAGTGATGGGCAGATG 11353	CCG	
			CATCTGCCTGTC GC		
			GTAGACGGGTAG CG		
			TGA		
GAM1231	RNH	5'	GCCGTGGGGCAGGGGATG 11366	G	____
			CATCT CCTGTCCC GGC		
			GTAGG GGACGGGG CCG		
			_ TG		
GAM1231	RNH	5'	GCCGTGGGGCAGGGGATG 59621	G	____
			CATCT CCTGTCCC GGC		
			GTAGG GGACGGGG CCG		
			_ TG		
GAM1231	SACM1L	5'	CGCGGGGCGGGGCGGGCGGA 25820	G	
			TCTGCCTGTCCCG CCTGTG		

AGGCGGGCGGGGC GGGCGC  
 G  
 GAM1231 SCAMP1 5' TGC GCCTGGGTCGGGTGGGTG 53407 TG T CCT  
 CATC CCTG CCCGG GTGCG  
 |||| |||| ||||  
 GTGG GGGC GGGTC CGCGT  
 GT T \_  
 GAM1231 SCAMP1 5' TGC GCCTGGGTCGGGTGGGTG 16817 TG T CCT  
 CATC CCTG CCCGG GTGCG  
 |||| |||| ||||  
 GTGG GGGC GGGTC CGCGT  
 GT T \_  
 GAM1231 SEDL 3' TGTGCAGGCTGGAGTGCAG 27368 \_ GTC TG  
 CTGC CT CCGGCCTG CG  
 |||| || |||| ||||  
 GACG GA GGTCCGAC GT  
 T \_ GT  
 GAM1231 SEDL 3' TGTGCAGGCTGTAGTGCAG 27369 \_ TCC TG  
 CTGC CTG CGGCCTG CG  
 |||| || |||| ||||  
 GACG GAT GTCGGAC GT  
 T \_ GT  
 GAM1231 SHB 5' GCGCGGGCTCCGGCGGGC 11642 CC  
 GCCTGTC GGCCTGTGC  
 |||| || |||| ||||  
 CGGGCGG TCGGGCGCG  
 CC  
 GAM1231 SHOX 5' CGCACAGGGTTTGCGGGAGGTG 4833 G CCCGG  
 CATCT CCTGT CCTGTGCG  
 |||| |||| |||| ||||  
 GTGGA GGGCG GGACACGC  
 \_ TTTG\_  
 GAM1231 SHOX 5' CGCACAGGGTTTGCGGGAGGTG 22533 G CCCGG  
 CATCT CCTGT CCTGTGCG  
 |||| |||| |||| ||||  
 GTGGA GGGCG GGACACGC  
 \_ TTTG\_  
 GAM1231 SIM1 3' TGTGTGGGCTCCTTTAGGCAGG 17381 TCCC TG  
 T ATCTGCCTG GGCCTG CG  
 |||| || |||| ||||  
 TGGACGGAT TCGGGT GT  
 TTCC GT  
 GAM1231 SLC12A4 5' CGGGCGGCTGGGACGGCGGGTG 17391 T T G  
 CATCTGCC GTCCCGGCC GT CG  
 |||| || |||| |||| ||||  
 GTGGGCGG CAGGGTCGG CG GC  
 \_ \_ G  
 GAM1231 SLC22A2 5' GCCGGGACGGCTGGGTG 59532 \_ T  
 CATCT GCC GTCCCGGC  
 |||| || |||| ||||

			GTGGG CGG CAGGGCCG		
			T _		
GAM1231	SLC25A19	5'	GGTGGGCCAGAGGCAGG 41378	GTCCC	TG
			TCTGCCT GGCCTG C		
			GGACGGA CCGGGT G		
			GA__ GT		
GAM1231	SLC9A6	3'	GGAGGGGCTGGGGTGGGCAGA 21008	TG	GTGCG
			TCTGCC TCCCGGCCT		
			AGACGG GGGGTCGGG		
			GT GAGGT		
GAM1231	SMARCB1	3'	TGTATAGGAGCCCCAGGCAGG 65587	TCCCGG	
			TCTGCCTG CCTGTGCG		
			GGACGGAC GGATATGT		
			CCCGA_		
GAM1231	SMT3H1	3'	TGTATGGGCTCGGGTGGG 59962	T _	
			CCTG CCCG GCCTGTGCG		
			GGGT GGGC CGGGTATGT		
			_ T		
GAM1231	SMTN	5'	GCGCCGGACGGGTGGGC 22669	T G T	
			GCCTG CCCG CC GTGC		
			CGGGT GGGC GG CGCG		
			_ A C		
GAM1231	SMTN	5'	GCGCCGGACGGGTGGGC 56155	T G T	
			GCCTG CCCG CC GTGC		
			CGGGT GGGC GG CGCG		
			_ A C		
GAM1231	SMTN	5'	GCGCCGGACGGGTGGGC 56158	T G T	
			GCCTG CCCG CC GTGC		
			CGGGT GGGC GG CGCG		
			_ A C		
GAM1231	SURF5	5'	TGTGCGGGCGCTGGGGCGGGT 22186	_ TG	
			GCCTGTCCCG GCCTG CG		
			TGGGCGGGGT CGGGC GT		
			CG GT		
GAM1231	SURF5	5'	TGTGCGGGCGCTGGGGCGGGT 56105	_ TG	
			GCCTGTCCCG GCCTG CG		
			TGGGCGGGGT CGGGC GT		
			CG GT		
GAM1231	TPI1	5'	TGCGCAGGTCGGGGCGGTACTT 4525	TC T	
	G		CA TGCC GTCCCGGCCTGTGCG		

GT ATGG CGGGGCTGGACGCGT  
 TC \_  
 GAM1231 UQCRC1 5' GCGTGGAATGGGGAGATG 12554 GCCTG GC TG  
 CATCT TCCCG C TGC  
 |||| |||| I |||  
 GTAGA GGGGT G GCG  
 \_ \_ \_ AA GT  
 GAM1231 VAV1 5' CGTGCGGGCGGGTGGGTGGTG 18304 T T G TG  
 CATC GCCTG CCCG CCTG CG  
 ||| |||| ||| ||| ||  
 GTGG TGGGT GGGC GGGC GC  
 \_ \_ \_ GT  
 GAM1231 WHSC1L1 5' GCACAGGTCGCCGCGGA 43519 CTGTCC  
 TCTGC CGGCCTGTGC  
 |||| |||||||  
 AGGCG GCTGGACACG  
 CC\_ \_  
 GAM1231 WHSC1L1 5' GCACAGGTCGCCGCGGA 35031 CTGTCC  
 TCTGC CGGCCTGTGC  
 |||| |||||||  
 AGGCG GCTGGACACG  
 CC\_ \_  
 GAM1231 ZIC1 3' GGTTGGAGCGGGTGGGTG 12724 TG TC  
 CATC CCTG CCGGCC  
 ||| ||| |||||  
 GTGG GGGC GGTTGG  
 GT GA  
 GAM1231 ZNF79 3' CGTGCCGACTCAGGACAGGTGG 81805 TG \_ CTGTGCG  
 GTG C CCTGTCC CGGC  
 | ||||| |||  
 G GGACAGG GCCG  
 GT ACTCA T GCG  
 GAM1231 ZNFN2A1 3' CGTGCAAGTCCCGAGTGGGT 60737 TG TC \_ TG  
 GGA C CCTG CCGG CCTG CG  
 | ||| ||| ||| ||  
 G GGGT GGCC GGAC GC  
 GT GA ACT GT  
 GAM1231 AHCYL1 5' CGCGCGGGCAGGCGGGCGGGC 21763 CG\_ \_  
 GCCTGTCC GCCTGTGCG  
 ||||| |||||||  
 CGGGCGGG CGGGCGCGC  
 CGGA  
 GAM1231 AMOT 3' TGGATAGCTGGGGTTGGCAGAT 55728 TG C G  
 G CATCTGCC TCCCGGC TGT CG  
 ||||| ||||| ||| ||  
 GTAGACGG GGGGTCG ATA GT  
 TT \_ G  
 GAM1231 AMOTL1 3' GGCAAGTTGGGTGGATG 73651 CCTGT C TG  
 CATCTG CCCGGC TG C  
 ||||| ||||| || |

			GTAGGT	GGGTTG AC G		
			_____	A GT		
GAM1231	Apg4B	3'	TGTGTAGGTCGGGGAGCCGGA	25290	C G	TG
			TCTG CT TCCCGGCCTG	CG		
			AGGC GA GGGGCTGGAT	GT		
			C _	GT		
GAM1231	ARHGAP11A	5'	TGTGCAGGCCGGGAGGTAGA	28803	TG	TG
			TCTGCC TCCCGGCCTG	CG		
			AGATGG AGGGCCGGAC	GT		
			_____	GT		
GAM1231	ARHGDIG	3'	GGTTGGGGCAGGCAGG	6781		
			TCTGCCTGTCCCGGCC			
			GGACGGACGGGGTTGG			
GAM1231	ARHGEF9	3'	GGGGTGGGCTGGGGTGGATGGA	30816	GC TG	TG GCG
			TG			
			CATCT C TCCCGGCC	T		
			GTAGG G GGGGTCGG	G		
			TA GT	GT GGGT		
GAM1231	ARHU	5'	CGCGCGGCGCGCAGGCGGG	41072	CCCG _	
			TCTGCCTGT	GC CTGTGCG		
			GGGCGGACG	CG GGC		
			_____	C		
GAM1231	ASB13	3'	GCATGGGCCCGGCCTAGG	45219	TC	
			CCTG CCGGCCTGTGC			
			GGAT GGCCGGGTACG			
			CC			
GAM1231	BAL	3'	TCTTGGGGTTGGGGTAGGTAGA	48804	GT	GTGCG
			T			
			ATCTGCCT CCCGGCCT			
			TAGATGGA GGGTTGGG			
			TG	GTTCTG		
GAM1231	BCKDK	3'	CGTGTGTGGGGAGGGCAGGTG	59794	G G CT TG	
			CATCTGCCT TCCC GC G CG			
			GTGGACGGG AGGG TG T GC			
			_ G _	GT		
GAM1231	BRD4	3'	TGCGTGGGCTGGAGGCGGGC	54278	_ TG	
			GCCTGTC CCGGCC TGCG			
			CGGGCGG GGTCGG GCGT			
			A	GT		
GAM1231	C1orf34	3'	TGGGTCTGGGGCAGGTGGG	60684	TG	_
			TC CCTGTCCCGG CCTG			

		GG GGACGGGGTC GGGT		
		GT T		
GAM1231	C20orf100 5'	CGCGTGGGCTCCGTGGCGATG 51809	T	TGTCCC TG
		CATC GCC GGCC TGCG		
		GTAG CGG TCGG GCGC		
		_ TGCC_ GT		
GAM1231	C20orf139 3'	TGTTGACCTTGGGGTAGGCTGG 84761	_	GT CCTGTGCG
	GTG	CATCT GCCT CCCGG		
		GTGGG CGGA GGGTT		
		T TG CCAGTTGT		
GAM1231	C20orf178 3'	CGTGTGTGGGGCAGGCAGG 74793		GCC TG
		TCTGCCTGTCCCG TG CG		
		GGACGGACGGGGT GT GC		
		_ GT		
GAM1231	C20orf183 3'	TGTGCCAAGAGGAGGTGGGTAG 47810	TG _	GGCCT TG
	ATG	CATCTGCC TC CC G CG		
		GTAGATGG GG GG C GT		
		GT A AGAAC GT		
GAM1231	C20orf28 3'	GGCAGGTCCTGCAGATG 31227	CTGTCCC	TG
		CATCTGC GGCCTG C		
		GTAGACG CTGGAC G		
		TC_ GT		
GAM1231	C20orf58 5'	GCGTGGGGAGCGGGCGGA 74756	_	G CTGT
		TCTGCCTG TCCC GC GC		
		AGGCGGGC AGGG TG CG		
		G G _		
GAM1231	C21orf58 3'	GCTGACATGGACGGGCAGGTG 54195	_	
		CATCTGCCTGTCC CGGC		
		GTGGACGGGCAGG GTCG		
		TACA		
GAM1231	C22orf19 3'	CGGAAGGCTGAGGTGGGCGGAT 13421	TG C	GTGCG
	G	CATCTGCC TC CGGCCT		
		GTAGGCGG GG GTCGGA		
		GT A AGGC		
GAM1231	CAMKK2 3'	CGCTGGCTGGCTGGACAGGCGG 21581	C T _	
	GTG	ATCTGCCTGTCC GGCC GT GCG		
		TGGGCGGACAGG TCGG CG CGC		
		_ T GT		
GAM1231	CAMTA1 3'	TGCAGAGGGGCAGGTGTGTG 67919	CT	GGC
		CAT GCCTGTCCC CTGTG		

GTG TGGACGGGG GACGT  
 TG A\_\_  
 GAM1231 CAMTA1 5' TCGTGCGGCCGCGGGGCGGG 67920 \_\_ TG  
 CCTGTCCC GGCC TGCG  
 ||||| ||| |||  
 GGGCGGGG CCGG GCGT  
 CG GT  
 GAM1231 CASKIN1 3' GGTGTGGGGCGGGTGA 40401 TG \_  
 TC CCTGTCCCG GCC  
 || ||||| |||  
 AG GGGCGGGGT TGG  
 GT G  
 GAM1231 CDC16 5' TGCACGGGGCCTGGGTGGGGGG 14020 G TG C \_  
 TG CATCT CC TCC GGCCT GTGCG  
 |||| || ||| |||| ||||  
 GTGGG GG GGG CCGGG CACGT  
 \_ GT T G  
 GAM1231 CECR2 3' TGTACATAAAGTGGGAAGGGTG 48610 TG G GCC\_\_  
 GGTG ATC CCT TCCCG TGTGCG  
 ||| ||| |||| ||||  
 TGG GGG AGGGT ACATGT  
 GT A GAAAT  
 GAM1231 CENTA1 3' CGTGCGTGGGGCATGTAGGTG 22493 C \_ CTGTGCG  
 CATCTGC TGTCCCG GC  
 ||||| ||||| ||  
 GTGGATG ACGGGGT CG  
 T G T GCG  
 GAM1231 CINP 5' CGTTTCCGGTGGGGTGGGCGGG 50937 TG G TGT\_  
 TCTGCC TCCCG CC GCG  
 ||||| |||| || |||  
 GGGCGG GGGGT GG TGC  
 GT \_ CCTT G  
 GAM1231 CSRP2BP 5' TGCGCCTCGGGCGGGCGGG 70116 T CCT  
 TCTGCCTG CCCGG GTGCG  
 ||||| |||| ||||  
 GGGCGGGC GGGCT CGCGT  
 \_ C\_  
 GAM1231 DDM36 3' GGTTTGGGGCAGGCAGGT 40576 \_  
 ATCTGCCTGTCCCGG CC  
 ||||| ||||| ||  
 TGGACGGACGGGGTT GG  
 T  
 GAM1231 DDX33 3' GGTGGGCGGGGGGGGT 39376 G G TG  
 GCCT TCCCG CCTG C  
 ||| |||| ||| |  
 TGGG GGGGC GGGT G  
 G \_ GT  
 GAM1231 DJ37E16.5 3' TGTGTGCCAGTGATGGTGGGTG 39733 TG T CC\_ CT TG  
 CATC CC GTC GGC G CG  
 ||| ||| ||| | ||



			GTGG GG TAG CCG T GT		
			GT _ TGA __ GT		
GAM1231	DJ971N18.2	5'	GTGGGGAAGGTAGATG 40961	G G	
			CATCTGCCT TCCC GC		
			GTAGATGGA AGGG TG		
			_ G		
GAM1231	DKFZP434B172	3'	TGTGTAGGTGTGGGTGGCA 70039	TGT _ TG	
			TGCC CCCG GCCTG CG		
			ACGG GGGT TGGAT GT		
			T__ G GT		
GAM1231	DKFZP434C128	3'	TGTGTAACCTGGAGAGGCAGGT 64848	G C CC TG	
	G		CATCTGCCT TCC GG TG CG		
			GTGGACGGA AGG CC AT GT		
			G T A_ GT		
GAM1231	DKFZP434K028	3'	GGGCAGAGGCTGGGGCAGGAAG 93237	G G G	
	GTG		CATCT CCTGTCCCGGCCT TGC		
			GTGGA GGACGGGGTCGGA ACG		
			A G GGG		
GAM1231	DKFZP586M1120	3'	TGTGTGTTGGGCAGGCAGGT 48471	T CT TG	
			ATCTGCCTG CCCGGC G CG		
			TGGACGGAC GGGTTG T GT		
			_ __ GT		
GAM1231	DKFZp761B0514	3'	TGCAGACCCCAGGGTGGGCAGA 50161	TG C CCTG	
	TG		CATCTGCC TCC GG TGCG		
			GTAGACGG GGG CC ACGT		
			GT A CCAG		
GAM1231	DKFZp762A227	5'	CGCGTGGGCGGACGCGTGGGCG 34286	___ CG TG	
	GA		CTGCCT GTCC GCC TGCG		
			GGCGGG CAGG CGG GCGC		
			TGCG _ GT		
GAM1231	DRIL2	3'	GTGGGGGCGGGGAGGTG 21328	G G	
			CATCT CCTGTCCC GC		
			GTGGA GGGCGGGG TG		
			G G		
GAM1231	EDG2	5'	TGTGGGCCGCGCGCGGGTGGG 7385	TG _ _ TG CG	
	TG		CATC CCTGT CC CGGCC TG		
			GTGG GGGCG GG GCCGG GT		
			GT C C GT		
GAM1231	EDG2	5'	TGTGGGCCGCGCGCGGGTGGG 54067	TG _ _ TG CG	
	TG		CATC CCTGT CC CGGCC TG		

GTGG GGGCG GG GCCGG GT  
 GT C C GT  
 GAM1231 FASTK 3' GCCGGGACGGCCGGGTG 46990 C  
 CATCTG CTGTCCCGGC  
 ||||| |||||  
 GTGGGC GGCAGGGCCG  
 C  
 GAM1231 FEM-2 3' TGCACTGGGTGGCGGGCAGATG 27584 CCG \_  
 CATCTGCCTGTC GCCT GTGCG  
 ||||| ||| ||||  
 GTAGACGGGCGG TGGG CACGT  
 \_ T  
 GAM1231 FEM1B 5' TGC GCGGGCTGGGTGCGGGA 31025 CT T  
 TCTGC G CCCGGCCTGTGCG  
 |||| | |||||  
 AGGCG C GGGTCGGGCGCGT  
 \_ T  
 GAM1231 FLJ00024 3' TGCATGTCTGAGGATGGGTGGG 63772 TG \_ CCT  
 TC CCTGTCC CGG GTGCG  
 || ||||| ||| ||||  
 GG GGGTAGG GTC TACGT  
 GT A TG\_  
 GAM1231 FLJ10111 5' TGCGTGGGCCGGGGTGGGC 35826 TG TG  
 GCC TCCCGGCC TGCG  
 ||| ||||| |||  
 CGG GGGGCCGG GCGT  
 GT GT  
 GAM1231 FLJ10290 3' CGTGTGGGGGACACGCAGATG 35972 C GGC TG  
 CATCTGC TGTCCC CTG CG  
 ||||| ||||| ||| ||  
 GTAGACG ACAGGG GGT GC  
 C \_ GT  
 GAM1231 FLJ10350 3' GCCTGTGCGTGCGTGGAGAGGG 95507 TG G\_ \_ \_ CTGT  
 TGGGTG CCT TCC CG GC GC  
 ||| ||| || || ||  
 GGG AGG GC CG CG  
 GT AG T GT G TGTC  
 GAM1231 FLJ10420 3' GTTGGGGCAGGAAGGTG 36110 G  
 CATCT CCTGTCCCGGC  
 ||||| |||||  
 GTGGA GGACGGGGTTG  
 A  
 GAM1231 FLJ10539 3' TGTGCAGGAGGATGTGGGTAGG 36256 TG C\_ GG TG  
 T ATCTGCC T CC CCTG CG  
 ||||| | || ||| ||  
 TGGATGG G GG GGAC GT  
 GT TA A\_ GT  
 GAM1231 FLJ10803 3' TGGGAGGCTGGGGCGGGTGGAT 36672 TG GTGCG  
 ATC CCTGTCCCGGCCT  
 ||| |||||

TAG GGGCGGGGTCGGA  
 GT GGGT  
 GAM1231 FLJ11539 3' TCGCTCCGGGCGGGTGA 45382 TG T CCT  
 TC CCTG CCCGG GTGCG  
 || ||| |||| ||||  
 AG GGGC GGGCC CGCGT  
 GT \_ T\_  
 GAM1231 FLJ12438 3' TCCTAGGTTGGGCAGGTGGGTG 41646 TG T TGCG  
 CATC CCTG CCCGGCCTG  
 ||| ||| |||||  
 GTGG GGAC GGGTTGGAT  
 GT \_ CCTG  
 GAM1231 FLJ13491 3' TGTGGGGGTGGCAGGCAGGTG 44889 CCG G  
 CATCTGCCTGTC GCCT TGCG  
 ||||| ||| |||  
 GTGGACGGACGG TGGG GTGT  
 \_ G  
 GAM1231 FLJ13909 5' GCGCGGCAGGAGGGGGTGGGAG 47068 G TG GG \_  
 GATG ATCT CC TCCC CCTGT GCG  
 ||| || ||| ||| |||  
 TAGG GG GGGG GGACG CGC  
 A GT GA G GT  
 GAM1231 FLJ14326 3' GCACGCAGGATGGTGGGTG 49808 TG T CG CT  
 CATC CC GTCC GC GTGC  
 ||| || ||| || |||  
 GTGG GG TAGG CG CACG  
 GT \_ A\_ \_  
 GAM1231 FLJ14326 3' GGCAATGGGGTGGGGGGT 49811 G TG \_  
 CATCT CC TCCCG GCC  
 |||| || |||| |||  
 GTGGG GG GGGGT CGG  
 \_ GT AA  
 GAM1231 FLJ14356 5' CTGGGACGGGAGGTG 48031 G  
 CATCT CCTGTCCCGG  
 |||| |||||  
 GTGGA GGGCAGGGTC  
 \_  
 GAM1231 FLJ14457 5' TGTGCAGGCCGAGCTAGGCAG 51390 \_ TC TG  
 G TCTGCCT G CCGGCCTG CG  
 ||||| | ||||| ||  
 GGACGGA C GGCCGGAC GT  
 T GA GT  
 GAM1231 FLJ14525 3' CGTATGGGTTTCCTTTTGGTGGG 51415 TG TGTCCC  
 TG CATC CC GGCTGTGCG  
 ||| || |||||  
 GTGG GG TTGGGTATGC  
 GT TTTTC  
 GAM1231 FLJ14547 5' CGCGCGCCCGACGGGCCGGTG 51433 T CC CT  
 CATC GCCTGTC GGC GTGCG  
 ||| ||||| || |||

GTGG CGGGCAG CCG CGCGC  
 C C\_ \_  
 GAM1231 FLJ14596 3' TGTGGAGAATTGGGACAGGCAG 51466 C\_ G  
 A TCTGCCTGTCCCGG CT TGCG  
 ||||| |||||  
 AGACGGACAGGGTT GA GTGT  
 AA G  
 GAM1231 FLJ14641 3' CGTGTATCCTGATAGGTGGAT 51484 TG CC CC TG  
 ATC CCTGTC GG TG CG  
 ||| ||||| || || ||  
 TAG GGATAG CC AT GC  
 GT T\_ T\_ GT  
 GAM1231 FLJ14681 3' GCTGGGGTGGGTGGTG 51526 T TG  
 CATC GCC TCCCGGC  
 |||| ||| |||||  
 GTGG TGG GGGGTCG  
 \_ GT  
 GAM1231 FLJ14871 3' GCGCGCCAGGCAGGCGGA 51668 T C CT  
 TCTGCCTG CC GGC GTGC  
 ||||| || ||| |||||  
 AGGCGGAC GG CCG CGCG  
 \_ A \_  
 GAM1231 FLJ14888 3' CAGAGGCTGGGGTGGGCAGAT 51680 TG G  
 ATCTGCC TCCCGGCCT TG  
 ||||| ||||| ||  
 TAGACGG GGGGTCGGA AC  
 GT G  
 GAM1231 FLJ20306 5' CACGGGCAGGGTGGG 34914 T G  
 CCTG CCC GCCTGTG  
 |||| ||| |||||  
 GGGT GGG CGGGCAC  
 \_ A  
 GAM1231 FLJ20477 5' CGCCGGGGAGGTCTGGGACGGGC 35239 GT\_\_  
 AGG CTGCCTGTCCCGGCCT GCG  
 ||||| ||||| |||  
 GACGGGCAGGGCTGGA CGC  
 GGGGC  
 GAM1231 FLJ20647 5' CGCGCGCCTGGGGCGGGAGGAT 35494 G \_ CT  
 G CATCT CCTGTCCC GGC GTGCG  
 |||| ||||| ||| |||||  
 GTAGG GGGCGGGG CCG CGCGC  
 A T \_  
 GAM1231 FLJ20695 3' GGTGGGATGGGAGGGTG 35559 G G  
 CATCT CCTGTCCCG CC  
 |||| ||||| ||  
 GTGGG GGGTAGGGT GG  
 A \_  
 GAM1231 FLJ21276 3' TGCATGTGAAGGGGTGGGCAGG 44919 TG GGCCT  
 TCTGCC TCCC GTGCG  
 ||||| ||| |||||

GGACGG GGGG TACGT  
GT AAGTG  
GAM1231 FLJ21324 3' CGCGTGGGCCCTTGGAGGGT 91196 G C\_\_ TG  
GCCT TCC GGCC TGCG  
||||| ||| ||| |||  
TGGG AGG CCGG GCGC  
\_ TTC GT  
GAM1231 FLJ22059 5' CGTACTCATGGGGTAGGGGGTG 42769 G GT GCCT  
CATCT CCT CCCG GTGCG  
||||| ||| ||| |||  
GTGGG GGA GGGT CATGC  
\_ TG ACT\_  
GAM1231 FLJ22173 5' GTATAAGGACAGGTGGTG 46749 T CGGCC  
CATC GCCTGTCC TGTGC  
||||| ||| ||| |||  
GTGG TGGACAGG ATATG  
\_ A\_\_\_\_  
GAM1231 FLJ22378 3' GGCAGGTCCTGGCCGATG 46902 T TGTCCC TG  
CATC GCC GGCCTG C  
||||| ||| ||| ||| |  
GTAG CGG CTGGAC G  
C TC\_\_\_\_ GT  
GAM1231 FLJ22393 3' GCTCGGGGTGGGACGGGT 47060 G T  
GCCTGTCCCG CCTG GC  
||||| ||| ||| |||  
TGGGCAGGGT GGGC CG  
G T  
GAM1231 FLJ22570 3' TGCTCCCCCTGGGACAGGAGGG 45891 G CCTGT  
TG CATCT CCTGTCCCGG GCG  
||||| ||| ||| ||| ||| ||| |||  
GTGGG GGACAGGGTC CGT  
A CCCCT  
GAM1231 FLJ23375 5' TGCGCGGCCAGAGAGGGGCAGG 46360 G CC\_ T  
TG CATCTGCCT TC GGCC GTGCG  
||||| ||| ||| ||| ||| ||| |||  
GTGGACGGG AG CCGG CGCGT  
G AGA \_  
GAM1231 FLJ23506 5' TGTGTGGGCCCGCAGGTGGA 45748 TG TCC TG  
TC CCTG CGGCCTG CG  
|| ||| ||| ||| ||| |||  
AG GGAC GCCGGGT GT  
GT \_\_\_\_ GT  
GAM1231 FLJ23519 5' GCCGTGGGGCAGGGGATG 69204 G \_  
CATCT CCTGTCCC GGC  
||||| ||| ||| ||| ||| ||| |||  
GTAGG GGACGGGG CCG  
\_ TG  
GAM1231 FLJ23537 3' TGGGAGGCCCGGACAGGTGGAT 46027 TG GTGCG  
ATC CCTGTCCCGGCCT  
||| ||| ||| ||| ||| ||| |||

			TAG	GGACAGGGCCGGA				
			GT	GGGT				
GAM1231	FLJ31168	3'	GGTGGGTCTGGGCAGG	58510	C	TG		
			CCTGTCC GGCCTG C					
			GGACGGG CTGGGT G					
			T GT					
GAM1231	FLJ31762	5'	AGAATGGGTTGGGGGAGGCCGGG	58136	G	GCG		
	TG		CATCTGCCT TCCCGGCCTGT					
			GTGGGCGGA GGGGTTGGGTA					
			G AGAG					
GAM1231	GABARAPL1	3'	CACAAGACAGGTAGG	48600	CCGGCC			
			TCTGCCTGTC TGTG					
			GGATGGACAG ACAC					
			A_____					
GAM1231	GABARAPL3	3'	CACAAGACAGGTAGG	50800	CCGGCC			
			TCTGCCTGTC TGTG					
			GGATGGACAG ACAC					
			A_____					
GAM1231	GABBR1	3'	ACTGTTGGGATAGACAGATG	41570	C	CT		
			CATCTG CTGTCCCGGC GT					
			GTAGAC GATAGGGTTG CA					
			A T_					
GAM1231	GABBR1	3'	GGTTTGGGTAGGCATGTG	41574	C	T	CCT TG	
			CAT TGCCTG CCCGG G C					
			GTG ACGGAT GGGTT T G					
			T _ __GT					
GAM1231	GABBR1	3'	ACTGTTGGGATAGACAGATG	7605	C	CT		
			CATCTG CTGTCCCGGC GT					
			GTAGAC GATAGGGTTG CA					
			A T_					
GAM1231	GABBR1	3'	GGTTTGGGTAGGCATGTG	7609	C	T	CCT TG	
			CAT TGCCTG CCCGG G C					
			GTG ACGGAT GGGTT T G					
			T _ __GT					
GAM1231	GBTS1	3'	TGTGCAACCTGGGGTGCGCGGA	59063	C GT	CC TG		
	TG		CATCTGC T CCCGG TG CG					
			GTAGGCG G GGGTC AC GT					
			C TG CA GT					
GAM1231	GIOT-3	5'	GGCGGGCCAGGCGGA	32751	GTCCC	TG		
			TCTGCCT GGCCTG C					

			AGGCGGA CCGGC G		
			_____ GT		
GAM1231	GPS2	5'	TGGGACCCGGGCGAGGCGG 15672	___	
			CTGCCTGTCCCGG CTG		
			GGCGGACGGGGCC GGGT		
			CA		
GAM1231	GR6	5'	CGTGCTGGGTGGCTGGGTG 23729	_ TGT C	
			CATCT GCC CCCGGC TG		
			GTGGG CGG GGGTCG GC		
			T T__ T		
GAM1231	GRIN3A	5'	TGCAGATGGGGCGGGCAGG 55974	GC	
			TCTGCCTGTCCCG CTGTG		
			GGACGGGCGGGGT GACGT		
			A_		
GAM1231	HARSL	3'	TGCATGGGTGCAGATGGCTGGA 24201	_ T CCG	
	TG		CATCT GCC GTC GCCTGTGCG		
			GTAGG CGG TAG TGGGTACGT		
			T _ ACG		
GAM1231	HCCA2	5'	GCGCGTGGACGGGCAGA 66865	--	
			TCTGCCTGTCC CG GC		
			AGACGGGCAGG GC CG		
			T G		
GAM1231	HCRTR2	5'	GCTCATGGGGCAGGCGGA 7731	GCC T	
			TCTGCCTGTCCCG TG GC		
			AGGCGGACGGGGT AC CG		
			_____ T		
GAM1231	HEMGN	3'	TGTATAGGTCGGGAGAGGATA 37381	_ G_	
	G		CTG CCT TCCCGGCCTGTGCG		
			GAT GGA GGGGCTGGATATGT		
			A GA		
GAM1231	HES6	3'	TGTGCGGGCTCTGGGGGCAGA 37837	TGT __ TG	
			TCTGCC CCC GGCCTG CG		
			AGACGG GGG TCGGGC GT		
			_____ TC GT		
GAM1231	HIC2	3'	TGTGTGCCGTATGCATGGGCAG 65271	CC__ CT TG	
	ATG		TCTGCCTGT CGGC G CG		
			AGACGGGTA GCCG T GT		
			CGTAT __ GT		
GAM1231	HSJ001348	5'	CGCGCGCCCCGGGGCGGGCGGG 62161	CC	
			TCTGCCTGTCCCGG TGTGCG		

GGGCGGGCGGGGCC GCGCGC  
CC  
GAM1231 HSPF2 5' GCAGGGGGCTGGCAGGTG 18641 T G\_  
CATCTGCC GTCCC GC  
||||||| ||||| ||  
GTGGACGG CGGGG CG  
T GA  
GAM1231 HYPC 3' TGCCATGTGGGGTGGGTGATG 64612 T TG G C T  
CATC GCC TCCCG C TG GCG  
||||| ||||| | |||||  
GTAG TGG GGGGT G AC CGT  
\_ GT \_ T \_  
GAM1231 IL-17RE 3' GGGGTGGGGTGGGTGGGTG 58295 TG TG G  
CATC CC TCCCG CCT  
||||| || ||||| |||||  
GTGG GG GGGGT GGG  
GT GT G  
GAM1231 IMAGE:4907098 3' GCTGGGGTGGGGGGTG 91661 G TG  
CATCT CC TCCCGGC  
||||| || |||||  
GTGGG GG GGGGTGCG  
\_ GT  
GAM1231 ITGA8 5' GCGCAGTGCAGGCAGAT 93225 CCCGGC  
ATCTGCCTGT CTGTGC  
||||||| |||||  
TAGACGGACG GACGCG  
T\_\_\_\_\_  
GAM1231 KCNH4 5' CGTGTGGGGCCACGTGGCGGGT 24406 \_ CCC \_ TG  
G CATCTGCC TGT GGCCT G CG  
||||||| ||||| | |||||  
GTGGGCGG GCA CCGGG T GC  
T \_ G GT  
GAM1231 KCNH4 3' TGCCCATTTGGGCTGGGCAGATG 24408 T CC T  
CATCTGCCTG CCCGG TG GCG  
||||||| ||||| |||||  
GTAGACGGGT GGGTT AC CGT  
C \_ C  
GAM1231 KIAA0014 3' GCGCGGGCTGCTGCGGC 27847 T CC  
GCC GT CGGCCTGTGC  
||| || |||||  
CGG CG GTCGGGCGCG  
\_ TC  
GAM1231 KIAA0153 3' TGTATCACACGGGGCAGGCGGG 30706 GCCT  
T ATCTGCCTGTCCCG GTGCG  
||||||| |||||  
TGGGCGGACGGGGC TATGT  
ACAC  
GAM1231 KIAA0161 5' GGCGGGCTGCGCGGGC 28511 CC TG  
GCCTGT CGGCCTG C  
||||| ||||| |



CGGGCG GTCGGGC G  
C\_ GT  
GAM1231 KIAA0193 3' TGTGCATTGGGATGGGTGGA 28666 TG CC TG  
TC CCTGTCCCGG TG CG  
|| ||||| || ||  
AG GGGTAGGGTT AC GT  
GT \_ GT  
GAM1231 KIAA0232 3' GTGGTGGGTTGGGGCGGGTAGA 72757 TG GCG  
TCTGCCTGTCCCGGCC T  
||||||| |  
AGATGGGCGGGGTTGG G  
GT GTGT  
GAM1231 KIAA0275 3' GGTGCTGGGGGAGGTGGATG 28685 TG G \_  
CATC CCT TCCCGGC CT  
||| || ||||| ||  
GTAG GGA GGGGTCG GG  
GT G T  
GAM1231 KIAA0350 3' CGTGCAGGCTGGGACCAGCGGA 61173 CT TG  
TCTGC GTCCCGGCCTG CG  
|||| ||||| ||  
AGGCG CAGGGTCGGAC GC  
AC GT  
GAM1231 KIAA0420 3' GGTGGGCGGGGCGTGGT 63362 \_ G TG  
GCC TGTCCCG CCTG C  
|| ||||| ||| |  
TGG GCGGGGC GGGT G  
T \_ GT  
GAM1231 KIAA0453 3' TGCACCTTAGGAGAGGCAGATG 69056 G CG CCT  
CATCTGCCT TCC G GTGCG  
|||||| ||| | ||||  
GTAGACGGA AGG T CACGT  
G AT C\_  
GAM1231 KIAA0476 5' CGGGAAGCGCGGGACAGGCAGA 29377 \_ CTGTGCG  
TG CATCTGCCTGTCCCG GC  
||||||| ||  
GTAGACGGACAGGGC CG  
G AAGGGC  
GAM1231 KIAA0478 3' GTATAGAGTGGGCAGGC 29555 T GC  
GCCTG CCCG CTGTGC  
|||| ||| |||||  
CGGAC GGGT GATATG  
\_ GA  
GAM1231 KIAA0544 3' CACAGGCACGCAGATG 70890 CTGTCCCG  
CATCTGC GCCTGTG  
||||| |||||  
GTAGACG CGGACAC  
CA\_\_\_\_\_  
GAM1231 KIAA0544 3' TGCGGAGCCCTGGGCCAGGCAG 70910 T \_ C G  
GTG CATCTGCCTG CCC GG CT TGCG  
||||||| ||| || || |||

GTGGACGGAC GGG CC GA GCGT  
 C T C G  
 GAM1231 KIAA0616 5' TGC GCGGTGGCACGGGCGAGTG 46664 TC C G T  
 CA TGCCTGT CCG CC GTGCG  
 || ||||| || |||||  
 GT GCGGGCA GGT GG CGCGT  
 GA C \_ \_  
 GAM1231 KIAA0618 5' GCGCGGGCCGGGTAGAGG 29168 GT\_  
 CCT CCCGGCCTGTGC  
 ||| |||||  
 GGA GGGCCGGGCGCG  
 GAT  
 GAM1231 KIAA0635 3' TGTATACCTGGGGGTGGGCAG 27700 TG \_ CC  
 CTGCC TCCC GG TGTGCG  
 |||| ||| || |||||  
 GACGG GGGG CC ATATGT  
 GT GT \_  
 GAM1231 KIAA0645 3' GCTGGGGGAAGGTGGGTG 27821 TG G\_  
 CATC CCT TCCCGGC  
 |||| || |||||  
 GTGG GGA GGGGTCG  
 GT AG  
 GAM1231 KIAA0794 3' CGTGGTGACTGGGATAGGAAGG 80410 G C\_\_TG CG  
 TG CATCT CCTGTCCCGG C TG  
 |||| ||||| | ||  
 GTGGA GGATAGGGTC G GC  
 A AGT GT  
 GAM1231 KIAA0819 3' GTCGGGACAGGAGATG 63580 G  
 CATCT CCTGTCCCGGC  
 |||| |||||  
 GTAGA GGACAGGGCTG  
 \_  
 GAM1231 KIAA0892 3' TGTGTGCCAGGGCAGGCAG 71016 C CT TG  
 CTGCCTGTCC GGC G CG  
 ||||| ||| | ||  
 GACGGACGGG CCG T GT  
 A \_ GT  
 GAM1231 KIAA0930 3' TGCATAGGTCTGGGTTGGATG 70555 GCCTGT  
 CATCT CCCGGCCTGTGCG  
 |||| |||||  
 GTAGG GGGCTGGATACGT  
 TT\_\_  
 GAM1231 KIAA1033 5' CACGGGCTGGTTGGG 64514 TC  
 CCTG CCGGCCTGTG  
 |||| |||||  
 GGGT GGTCGGGCAC  
 T\_  
 GAM1231 KIAA1100 5' CGCGTGGGCCTCGCGAGGCAGA 29752 \_ CCC TG  
 TCTGCCT GT GGCC TGCG  
 ||||| || ||| |||

			AGACGGA CG CCGG GCGC		
			G CT_ GT		
GAM1231	KIAA1130	3'	TGTGGAGATGGGACAGTGGGTG 62429	TG C	GC G
			CATC C TGTCCCG CT TGCG		
			GTGG G ACAGGGT GA GTGT		
			GT_ A_ G		
GAM1231	KIAA1184	3'	CGTGCAGGTTGAAATCAGA 42612	CCTGTC	TG
			TCTG CCGGCCTG CG		
			AGAC GGTGAC GC		
			TAAA_ GT		
GAM1231	KIAA1190	3'	GCACCGGTGGGTGGG 71100	T G T	
			CCTG CCCG CC GTGC		
			GGGT GGGT GG CACG		
			_ _ C		
GAM1231	KIAA1190	3'	TGTGTGGAGTGGGGCAGGCAGG 71106	GC TG	
			TCTGCCTGTCCCG CTG CG		
			GGACGGACGGGGT GGT GT		
			GA GT		
GAM1231	KIAA1193	3'	GGGCTGGGGCGGCAGGTG 67644	T	
			CATCTGCC GTCCCGGCCT		
			GTGGACGG CGGGGTCGGG		
			_		
GAM1231	KIAA1228	3'	TGGGAGGCCGAGGCGGGCGGAT 65051	C	GTGCG
	G		CATCTGCCTGTC CGGCCT		
			GTAGGCGGGCGG GCCGGA		
			A GGGT		
GAM1231	KIAA1247	5'	CGTGCGCCGGGGACAGGCAGG 61852	_ CT TG	
			TCTGCCTGTCCC GGC G CG		
			GGACGGACAGGG CCG C GC		
			G _ GT		
GAM1231	KIAA1305	5'	CGTGCGGGGAGCGGGCGGG 46929	_ G C	
			TCTGCCTG TCCC GC TG		
			GGGCGGGC AGGG CG GC		
			G G T		
GAM1231	KIAA1322	3'	TGCACAGTTGAACGATGGGCAG 72743	C_ C	
			CTGCCTGTC CGGC TGTGCG		
			GACGGGTAG GTTG ACACGT		
			CAA _		
GAM1231	KIAA1340	5'	GCGCCCCGGGCGGGCGGA 69184	T CCT	
			TCTGCCTG CCCGG GTGC		

		AGGCGGGC GGGCC CGCG		
		— C—		
GAM1231	KIAA1465	5' CGCTGGCGGGACAGGCGCGTG 60826	C	G T
		CAT TGCCTGTCCCG CC GTG		
		GTG GCGGACAGGGC GG CGC		
		C — T		
GAM1231	KIAA1465	3' TAGTGTAGGGGGCGGGCGGG 60835	GG	TG G
		TCTGCCTGTCCC CCTG C		
		GGGCGGGCGGGG GGAT G		
		— GT ATG		
GAM1231	KIAA1577	3' TGTATGAATGGGGTGGGGGGTG 64483	G TG	GCC
		CATCT CC TCCCG TGTGCG		
		GTGGG GG GGGGT GTATGT		
		— GT AA—		
GAM1231	KIAA1613	3' TCCCCGAGGTCAGGGTGGGTAG 64820	TG C	GTGCG
	ATG	CATCTGCC TCC GGCCT		
		GTAGATGG GGG CTGGA		
		GT A GCCCCTC		
GAM1231	KIAA1643	3' TGGGAATCGGGGCGGGTGATG 64555	T	—
		CATC GCCTGTCCCGG CCTG		
		GTAG TGGCGGGGCT GGGT		
		— AA		
GAM1231	KIAA1668	3' GCCATGCTGGGGCAGGTGAGTG 66473	CT	C T G
		CAT GCCTGTCCCGGC TG GC		
		GTG TGGACGGGGTCG AC CG		
		AG T — G		
GAM1231	KIAA1808	3' TGTGTCCATGGGGTGGGCGGG 85870	TG	GCCT TG
		TCTGCC TCCCG G CG		
		GGGCGG GGGGT T GT		
		GT ACC_ GT		
GAM1231	KIAA1867	3' TGTGTGCCAGAGGTGGGCGGGT 94826	TG CC_	CT TG
	G	CATCTGCC TC GGC G CG		
		GTGGGCGG GG CCG T GT		
		GT AGA — GT		
GAM1231	KIAA1910	3' GCAGGGATGGGCAGTTG 73328	T	G
		CA CTGCCTGTCCC GC		
		GT GACGGGTAGGG CG		
		T A		
GAM1231	KIAA1912	5' CGCACAGGGGTGTGGGCGGA 73365	TC	GG
		TCTGCCTG CC CCTGTGCG		

AGGCGGGT GG GGACACGC  
 GT \_  
 GAM1231 KIAA1924 3' GGCGGGCAGGGCAGTGT 73683 \_ T G TG  
 GC CTG CCC GCCTG C  
 || ||| ||| ||| |  
 TG GAC GGG CGGGC G  
 T \_ A GT  
 GAM1231 KRTAP3-1 3' TGCACAGGTTCCGTGAGGTGGC 49230 TG\_ C \_  
 GCC TC CGG CCTGTGCG  
 ||| ||| ||| ||| |||  
 CGG AG GCC GGACACGT  
 TGG T TT  
 GAM1231 L3MBTL 3' TGTGTGGGCTGGCTTGAGTGCA 69532 \_ GTC\_ TG  
 TGC CT CCGGCCTG CG  
 ||| || ||| ||| |||  
 ACG GA GGTCGGGT GT  
 T GTTC GT  
 GAM1231 MACMARCKS 3' TAGGTAGGGGCAGGTGGGTG 43450 TG G  
 CATC CCTGTCCC GCCTG  
 ||| ||| ||| ||| |||  
 GTGG GGACGGGG TGGAT  
 GT A  
 GAM1231 MAD4 3' GCACCTGGGGCAGGTGGGTG 21278 TG CCT G  
 CATC CCTGTCCCGG GTGC  
 ||| ||| ||| ||| |||  
 GTGG GGACGGGGTC CACG  
 GT \_ A  
 GAM1231 MAFB 3' GCGCGCGGGCCGCGGGCGACGG 18414 \_ \_  
 GCGGGTG GCCTGTC CC GGCCTGTGCG C  
 ||| ||| ||| ||| ||| |  
 CGGGCAG GG CCGGGCGCGC G  
 C GCG  
 GAM1231 MAPK11 3' GGTGGGCACGTGTGGATG 10849 TG C CCCG TG  
 CATC C TGT GCCTG C  
 ||| ||| ||| |  
 GTAG G GCA CGGGT G  
 GT T \_ GT  
 GAM1231 MAPK8IP3 3' TGGGCCGCTGGGACGCGGTGGG 52998 TG \_ CT G  
 TG CATC CC TGTCCCGG GT CG  
 ||| ||| ||| ||| ||| |||  
 GTGG GG GCAGGGTCG CG GT  
 GT C C\_ G  
 GAM1231 MESDC2 3' TGTGGGGGGACAGGTGGA 72505 TG GG TG  
 TC CCTGTCCC CC TG  
 || ||| ||| ||| |||  
 AG GGACAGGG GG GT  
 GT \_ GT  
 GAM1231 MFN2 3' TGTATGGGGAGCTGGCAGAGCA 29606 \_ CCGG\_  
 GGTG ATCTGC CTGTC CCTGTGCG  
 ||| ||| ||| ||| |||

			TGGACG GACGG GGGTATGT		
			A TCGAG		
GAM1231	MGC16025	5'	CGCATGGGATGCAGGCGGCGTG 51918	_	CCCGG
			CAT CTGCCTGT CCTGTGCG		
			GTG GGCGGACG GGGTACGC		
			C TA__		
GAM1231	MGC32043	3'	GCCCCGCTGGGGCAGGCAGG 58049		CTGT G
			TCTGCCTGTCCCCGGC GC		
			GGACGGACGGGGTCG CG		
			CCC_ G		
GAM1231	MGC4504	3'	GTTGGTGTGGTGGGCAGGTG 44112	TG	__
			CATCTGCC TC CCGGC		
			GTGGACGG GG GGTG		
			GT TGT		
GAM1231	MGC4771	3'	TGGGAGGCTGAGGTGGGTGGAT 51034	TG TG C	GTGCG
			G CATC CC TC CGGCCT		
			GTAG GG GG GTCGGA		
			GT GT A GGGT		
GAM1231	MGC5139	5'	TGTGTGGGCTTTAGGGCGAGTG 74112	TC	GTCCC TG
			CA TGCCT GGCCTG CG		
			GT GCGGG TCGGGT GT		
			GA ATT__ GT		
GAM1231	MGC5309	5'	GGTGGGTCGGGGACGGG 80815	_	TG
			CCTGTCCC GGCCTG C		
			GGGCAGGG CTGGGT G		
			G GT		
GAM1231	MGC5338	5'	TGTGACTCTGGGATTGGCAGGT 43944	T	CCTG
			G CATCTGCC GTCCCGG TGCG		
			GTGGACGG TAGGGTC GTGT		
			T TCA_		
GAM1231	MGC9753	3'	CGCGTGCTGGTGGGCATGTG 53048	C	GTC C
			CAT TGCCT CCGGC TGTG		
			GTG ACGGG GGTCG GCGC		
			T T__ T		
GAM1231	MVD	3'	CGGACTCCTGGGACATGTGGGT 10140	TG C	CCT G
			G CATC C TGTCCCGG GT CG		
			GTGG G ACAGGGTC CA GC		
			GT T CT_ G		
GAM1231	N4BP3	3'	AGCTTGGGGTGGGGTGGATG 66251	TG _TG	C
			CATC C C TCCCGG CT		

			GTAG G G GGGGTT GA		
			GT G GT C		
GAM1231	NAKAP95	3'	GCTCGGGGCGGGCGGA 26873	—	
			TCTGCCTGTCCCG GC		
			AGGCGGGCGGGGC CG		
			T		
GAM1231	NR5A1	3'	TGTGTGTTTGGGAAGGTGGGTG 17106	TG G	CCT TG
			CATC CCT TCCCGG G CG		
			GTGG GGA AGGGTT T GT		
			GT _ TG_ GT		
GAM1231	NXPH3	3'	GCACCTGGTGGGTGGGT 65762	T G T_	
			GCCTG CCCG CC GTGC		
			TGGGT GGGT GG CACG		
			_ _ TC		
GAM1231	PGRMC2	3'	TGCATGGGGCTGTGGAGTGGGT 20893	TG CTG _ _	
	G		CATC C TCC CGGCCT GTGCG		
			GTGG G AGG GTCGGG TACGT		
			GT_ _ T G		
GAM1231	PIB5PA	3'	GGGTGGGGTAGGCAGATG 66055	GT G	
			CATCTGCCT CCCG CC		
			GTAGACGGA GGGT GG		
			TG G		
GAM1231	PP1665	5'	GCCGTGGGGCAGCAGATG 47915	C _	
			CATCTGC TGTCCC GGC		
			GTAGACG ACGGGG CCG		
			_ TG		
GAM1231	PPFIA1	5'	CGCGGCGTGGGGCGGGCAGG 13264	_ T	
			TCTGCCTGTCCCG GCC GTG		
			GGACGGGCGGGGT CGG CGC		
			G _		
GAM1231	PPFIA4	3'	TGTATGGGTGTGTGTGGGTGGG 70337	TG TG CCCG	
	TG		CATC CC T GCCTGTGCG		
			GTGG GG G TGGGTATGT		
			GT GT TGTG		
GAM1231	PSIP2	5'	GCGTGGACGCGGGTAGA 52637	TCC GC TG	
			TCTGCCTG CG C TGC		
			AGATGGGC GC G GCG		
			_ _ A_ GT		
GAM1231	PSMD3	3'	TGTACAGCAGGCAGGAGGGTG 10976	G CCG C	
			CATCT CCTGTC GC TGTGCG		

GTGGG GGACGG CG ACATGT  
A A\_\_ \_  
GAM1231 PYY2 3' CGCAGGCGCGGGGCGGGCGGA 40825 \_ CG  
TCTGCCTGTCCCG GCCTGTG  
||||||| |||||  
AGGCGGGCGGGGCGGACGC  
G  
GAM1231 RAB33B 5' CGTGCGGCGGGGCGGGCGGGTG 48492 G T TG  
CATCTGCCTGTCCCG CC G CG  
||||||| || ||  
GTGGGCGGGCGGGGCGG C GC  
\_ \_GT  
GAM1231 RAB33B 5' GGTGGCCGCGGGCAGGC 48501 \_ T TG  
GCCTGTCC CGGCC G C  
||||| |||| |  
CGGACGGG GCCGG T G  
C \_GT  
GAM1231 RAB33B 5' GTGTGCGGGCAAGGGCGGGGCG 48503 \_\_\_\_\_ TG  
GGAAGGTG CCTGTCCCG GCCTG CG T  
||||| |||| || |  
GGGCGGGGCGGGC GT G  
GGGAA GT  
GAM1231 RAB3D 5' CGCGCGGGATCCGGGTGGC 15007 TGT \_  
GCC CCCGG CCTGTGCG  
||| |||| |||||  
CGG GGGCC GGGCGCGC  
T\_ TA  
GAM1231 Rabip4R 3' TGTGTGGGGTAGGAAGGCAGGT 35793 G CGG TG  
G CATCTGCCT TCC CCTG CG  
||||||| ||| |||| ||  
GTGGACGGA AGG GGGT GT  
\_ ATG GT  
GAM1231 RAD51 5' GCGGGGTGCGGGCGCGT 11225 C T TG  
GC TG CCCGGCCTG C  
|| || ||||| |  
TG GC GGGCTGGGC G  
C \_ GT  
GAM1231 RAD51 5' GCGGGGTGCGGGCGCGT 56019 C T TG  
GC TG CCCGGCCTG C  
|| || ||||| |  
TG GC GGGCTGGGC G  
C \_ GT  
GAM1231 RBAK 5' GCGCGGGCCGGGTGGAGG 40976 GT\_  
CCT CCCGGCCTGTGC  
||| |||||  
GGA GGGCCGGGCGCG  
GGT  
GAM1231 RER1 3' TGCCAGGTGGGCAGGCAGG 22866 CG T  
TCTGCCTGTCC GCCTG GCG  
||||||| |||| |||



GGACGGACGGG TGGAC CGT

GAM1231 SDF2L1 3' TGTGTGGATGGATGGGTGGATG 41869 TG CGG T TG  
CATC CCTGTCC CC G CG  
|||| ||||| || |  
GTAG GGGTAGG GG T GT  
GT TA\_\_GT

GAM1231 SEC61A1 3' GCATGGGCTGTGGTGGT 25309 TGT \_  
GCC CC CGGCCTGTGC  
||| || |||||  
TGG GG GTCGGGTACG  
T\_\_ T

GAM1231 SEMA4C 3' TGT TTGGGGGAAGGGTGGGTG 35054 TG G GG T  
CATC CCT TCCC CCTG GCG  
|||| ||| ||| ||| |||  
GTGG GGG AGGG GGGT TGT  
GT A \_\_ T G

GAM1231 SERP1 5' GGCCGGGGCAGGTGGTG 27061 T  
CATC GCCTGTCCCGGCC  
|||| |||||  
GTGG TGGACGGGGCCGG

GAM1231 SHANK3 3' AGGGAGGCTGGGGCGGGAGGTG 65489 G GTGCG  
CATCT CCTGTCCCGCCT  
|||| |||||  
GTGGA GGGCGGGGTCGGA  
GGGAC

GAM1231 SLC21A12 3' TGTACGGCCCTGCAGTGGGTG 33016 TG C CCC T  
CATC C TGT GGCC GTGCG  
|||| ||| ||| |||  
GTGG G ACG CCGG CATGT  
GT\_ TC\_ \_

GAM1231 SLC26A6 5' TGCGAGCCATGGGGCTGGCGGA 43295 T \_\_ CTG  
TG CATCTGCC GTCCC GGC TGCG  
||||| |||| ||| |||  
GTAGGCGG CGGGG CCG GCGT  
T TA A\_\_

GAM1231 SLC26A6 5' TGCGAGCCATGGGGCTGGCGGA 56137 T \_\_ CTG  
TG CATCTGCC GTCCC GGC TGCG  
||||| |||| ||| |||  
GTAGGCGG CGGGG CCG GCGT  
T TA A\_\_

GAM1231 SLC26A6 5' TGCGAGCCATGGGGCTGGCGGA 56219 T \_\_ CTG  
TG CATCTGCC GTCCC GGC TGCG  
||||| |||| ||| |||  
GTAGGCGG CGGGG CCG GCGT  
T TA A\_\_

GAM1231 SNAPC2 3' TGTACAGGGTTGGGTGGGG 11847 GT \_  
CCT CCCGGCCT GTGCG  
||| ||||| ||||

			GGG GGGTTGGG CATGT			
			GT GA			
GAM1231	SPC18	3'	TGTGGGCGGGCGCATG	26669	C	_
			CAT TGCCTGTCC CG			
			GTA GCGGGCGGG GT			
			C T			
GAM1231	SPTLC2	5'	GGTTTCGGGGAGGTGGGTG	16805	TG G	_
			CATC CCT TCCCG GCC			
			GTGG GGA GGGGC TGG			
			GT _ TT			
GAM1231	STATI2	5'	CGCGCAGGCGATCAGTGGGTG	13923	TG CT	CCG
			CATC C GTC GCCTGTGCG			
			GTGG G TAG CGGACGCGC			
			GT AC _			
GAM1231	STMN3	3'	GGCAGGTCAGGGCAGGT	31900	C TG	
			GCCTGTCC GGCCTG C			
			TGGACGGG CTGGAC G			
			A GT			
GAM1231	STRAIT11499	5'	GCACCTGGGATGGGTAGG	41142	CCT	G
			TCTGCCTGTCCCGG GTGC			
			GGATGGGTAGGGTC CACG			
			_ A			
GAM1231	TED	3'	TGTGTGGGTTGGGGAGTAGGGG	31647	G _	TG
	G		CT CCTG TCCCGGCCTG CG			
			GG GGAT GGGTTGGGT GT			
			G GA GT			
GAM1231	TRAF3	5'	GTCAGGGGTGGGCGGGTG	59742	TG _	
			CATCTGCC TCCC GGC			
			GTGGGCGG GGGG CTG			
			GT A			
GAM1231	TRAF3	3'	TCGGGGCTGGCAGGTG	59745	T	
			CATCTGCC GTCCCGG			
			GTGGACGG CGGGGCT			
			T			
GAM1231	TRIAD3	3'	TGGGAGGCCGAGGCGGGCGGAT	94509	C	GTGCG
	G		CATCTGCCTGTC CGGCCT			
			GTAGGCGGGCGG GCCGGA			
			A GGGT			
GAM1231	UBF-fl	3'	TGGGAGGCCGAGGTGGGTGGAT	51574	TG TG C	GTGCG
	G		CATC CC TC CGGCCT			

			GTAG GG GG GCCGGA		
			GT GT A GGGT		
GAM1231	USP20	3'	GGCAGGCTGGGATCGGG	21926	_ TG
			CCTG TCCCGGCCTG C		
			GGGC AGGGTCGGAC G		
			T GT		
GAM1231	USP24	3'	TGTGTGGGCATGTGGCCAGGCA	91155	T _ _ TG
			GATG ATCTGCCTG CC CG GCCTG CG		
			TAGACGGAC GG GT CGGGT GT		
			C T A GT		
GAM1231	VILL	5'	TGCACAGATTGGTGTGGTGGAT	68415	TG T TC GC
			G CATC CC G CCG CTGTGCG		
			GTAG GG T GGT GACACGT		
			GT _GT TA		
GAM1231	WBSCR23	3'	GGTTTGGGATAGGCTGGGTG	46769	_ _
			CATCT GCCTGTCCCGG CC		
			GTGGG CGGATAGGGTT GG		
			T T		
GAM1231	WNT8A	5'	GTCCACTGGGGTAGGCAGG	49191	GT CC TG
			TCTGCCT CCCGG TG C		
			GGACGGA GGGTC AC G		
			TG _ CT		
GAM1231	WNT8A	5'	GTCCACTGGGGTAGGCAGG	54282	GT CC TG
			TCTGCCT CCCGG TG C		
			GGACGGA GGGTC AC G		
			TG _ CT		
GAM1231	YAP1	5'	GCCGGGGCGGGGGATG	20352	G
			CATCT CCTGTCCCGGC		
			GTAGG GGGCGGGGCCG		
			-		
GAM1231	YKT6	3'	TGCTAGGGCTGGGGTGGGTGGA	21609	TG TG GT
			TC CC TCCCGGCCT GCG		
			AG GG GGGGTCGGG CGT		
			GT GT AT		
GAM1231	ZDHC2	5'	CGGAGCTGGGCAGGTGGATG	33008	TG T _
			CATC CCTG CCCGGC CTG		
			GTAG GGAC GGGTCG GGC		
			GT _ A		
GAM1231	ZNF84	5'	TGCGCGGGACACGGGGGACGGG	12818	GG_____
			CGG TGCCTGTCCC CCTGTGCG		

		GCGGGCAGGG GGGCGCGT	
		GGCACA	
GAM1231 ZBPB	5'	CGCGCGGACGGTGGGCAGGC 22806	___ GC
		GCCTGTCC CG CTGTGCG	
		CGGACGGG GC GGC GCGC	
		TG A_	
GAM1231 LOC112885	3'	GCATCCAGGGTGGGCAG 56525	TG C CCT
		CTGCC TCC GG GTGC	
		GACGG GGG CC TACG	
		GT A ____	
GAM1231 LOC113091	5'	TGTGCGGGAAGCTGGGGGTGGA 72938	TG TGT ____ TG
	TG	ATC CC CCCGGC CTG CG	
		TAG GG GGGTCG GGC GT	
		GT ____ AAG GT	
GAM1231 LOC115209	5'	CGCATAGGTCGGGTCGGCGG 59128	T T
		CTGCC G CCCGGCCTGTGCG	
		GGCGG C GGGCTGGATACGC	
		_ T	
GAM1231 LOC115286	3'	CGTGCAGGAGGGCACGGTGGGT 73372	TG _ T GG TG
	G	CATC CC TG CCC CCTG CG	
		GTGG GG AC GGG GGAC GC	
		GT C _ A_ GT	
GAM1231 LOC124470	3'	TGCACGGCTCCACAGCAGGTG 75644	C CCC T
		CATCTGC TGT GGCC GTGCG	
		GTGGACG ACA TCGG CACGT	
		_ CC_ _	
GAM1231 LOC125704	5'	CGCGTGACCGCGGGCTGGGT 74408	_ _ C TG
		GCCT GTCC CGG C TGCG	
		TGGG CGGG GCC G GCGC	
		T C A GT	
GAM1231 LOC125704	3'	TGTGTGAGTGTGGGCAGGTGAG 74414	CT CG CT TG
	TG	CAT GCCTGTCC GC G CG	
		GTG TGGACGGG TG T GT	
		AG TG AG GT	
GAM1231 LOC126695	3'	TGTATTGGGGGGTGGGCAGG 75430	TG GG T
		TCTGCC TCCC CC GTGCG	
		GGACGG GGGG GG TATGT	
		GT _ T	
GAM1231 LOC128977	3'	CACATGCAGGCAGGTG 74821	CCCGGCC
		CATCTGCCTGT TGTG	

GTGGACGGACG ACAC  
 T\_\_\_\_\_  
 GAM1231 LOC132671 5' GCGCGGGACGGCGGATG 59170 T \_  
 CATCTGCC GTCCCG GC  
 ||||| ||||| ||  
 GTAGGCGG CAGGGC CG  
 \_ G  
 GAM1231 LOC134553 5' TGCGCGGCGGCCGCGGCGGGT 75199 C \_  
 GCCTGTC CGGCC TGTGCG  
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 C CG  
 GAM1231 LOC136288 3' GCATAGAAGGGGCAGGT 75254 GGC  
 GCCTGTCCC CTGTGC  
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 AA\_  
 GAM1231 LOC137964 3' TGTGCGGGCTGAGTGGTTGGGG 75288 G T \_ TG  
 AGATG CT CCTG CC CGGCCTG CG  
 || ||||| || ||||| ||  
 GA GGGT GG GTCGGGC GT  
 G T TGA GT  
 GAM1231 LOC143384 5' GCCTGTGAGGCGGGCGGGTG 76554 C \_  
 CATCTGCCTGTC C GGC  
 ||||| ||||| ||  
 GTGGGCGGGCGG G CCG  
 A TGT  
 GAM1231 LOC144667 3' TGCATGGGGTGGGACAGGTAGG 83174 G  
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 GGATGGACAGGGT GGGTACGT  
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 GAM1231 LOC145310 3' TGTGCAGGCTGGAGTGCAG 83319 \_ GTC TG  
 CTGC CT CCGGCCTG CG  
 ||||| ||||| ||||| ||  
 GACG GA GGTGGGAC GT  
 T \_ GT  
 GAM1231 LOC145757 3' GTCGGGGCAGGGGGATG 77471 G  
 CATCT CCTGTCCCGGC  
 ||||| ||||| |||||  
 GTAGG GGACGGGGCTG  
 G  
 GAM1231 LOC145828 5' GCATAGGTGGGGTAG 83537 T G  
 CTG CCC GCCTGTGC  
 ||||| ||||| |||||  
 GAT GGG TGGATACG  
 \_ G  
 GAM1231 LOC145945 5' CGTACGGGCAACAGGGCACGTG 83573 C GTCCCG  
 CAT TGCCT GCCTGTGCG  
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	GTG ACGGG CGGGCATGC	
	C ACAA__	
GAM1231 LOC146050 3'	TGCATGTGGTGACAGGTAGA 77654	CCG _
	TCTGCCTGTC GCC TGTGCG	
	AGATGGACAG TGG GTACGT	
	__ T	
GAM1231 LOC146725 5'	GCCGTGGGGCAGGCGGG 83745	_
	TCTGCCTGTCCC GGC	
	GGGCGGACGGGG CCG	
	TG	
GAM1231 LOC146856 3'	TGTGTGGGTATGCGTGGGTGTA 82805	CT TG CCCG TG
	TG CAT GCC T GCCTG CG	
	GTA TGG G TGGGT GT	
	TG GT CGTA GT	
GAM1231 LOC146953 3'	TGCGTAGGAGAAGGGGTGGGAA 78216	G TG GG__
	GATG ATCT CC TCCC CCTGTGCG	
	TAGA GG GGGG GGATGCGT	
	A GT AAGA	
GAM1231 LOC146990 5'	CGCAGGCCGGCTGGG 83885	TC
	CCTG CCGGCCTGTG	
	GGGT GGCCGGACGC	
	C_	
GAM1231 LOC147054 5'	TGTGCGGGCTGCCCAGGCAG 83926	TCC TG
	CTGCCTG CGGCCTG CG	
	GACGGAC GTCGGGC GT	
	CC_ GT	
GAM1231 LOC147160 5'	CGTGTGTTAGGGGACAGGCGG 83965	GGCCT TG
	CTGCCTGTCCC G CG	
	GGCGGACAGGG T GC	
	GATTG GT	
GAM1231 LOC147229 5'	CGCACACGTGTGGGACAGATAG 78319	C _ C
	ATG CATCTG CTGTCCCG GC TGTGCG	
	GTAGAT GACAGGGT TG ACACGC	
	A G C	
GAM1231 LOC149182 5'	GCGGAGGCACAGGTGGGTG 84374	TG CCCG G
	CATC CCTGT GCCT TGC	
	GTGG GGACA CGGA GCG	
	GT _ G	
GAM1231 LOC149668 5'	TGTAGAGGGGATGGTGTGGGTG 84553	TG_ GGC G
	CATC C CTGTCCC CT TGCG	

GTGG G GGTAGGG GA ATGT  
 GT T \_\_\_\_ G  
 GAM1231 LOC150111 3' CGCGTGTGGGGCGGGTGGG 84859 TG G C  
 TC CCTGTCCCG C TGTG  
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 GG GGGCGGGGT G GCGC  
 GT \_\_\_\_T  
 GAM1231 LOC150372 3' GCATGGGGCAGGCGGG 79801 \_  
 TCTGCCTGTCCCG GC  
 ||||| ||||  
 GGGCGGACGGGGT CG  
 A  
 GAM1231 LOC150481 5' TGTGTGTTGAGGGGTGGGGGGT 79899 G TG GGCCT TG  
 G CATCT CC TCCC G CG  
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 GTGGG GG GGGG T GT  
 \_ GT AGTTG GT  
 GAM1231 LOC150596 3' TGCATAGGTTGCTGAGAGGTGG 79951 TG G C\_  
 A TC CCT TC CGGCCTGTGCG  
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 AG GGA AG GTTGGATACGT  
 GT G TC  
 GAM1231 LOC150685 5' GTATGGGGTTGGGTGGAGG 87182 GT\_ \_  
 CCT CCCGGCCT GTGC  
 ||| ||||| ||||  
 GGA GGGTTGGG TATG  
 GGT G  
 GAM1231 LOC150933 3' GCCTGGGATATGCAGATG 85163 C \_  
 CATCTGC TGTCCC GGC  
 ||||| ||||| |||  
 GTAGACG ATAGGG CCG  
 T T  
 GAM1231 LOC151162 5' GTATGTCTGTAGGTAGGTG 85246 TCCC CT  
 CATCTGCCTG GGC GTGC  
 ||||| ||| ||||  
 GTGGATGGAT CTG TATG  
 GT\_ \_  
 GAM1231 LOC151188 5' TGCGGACCCGGGGCGGGGCAGG 80162 \_ C\_ CG  
 TG CATCTGCCT GTCCCGG CTGTG  
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 GTGGACGGG CGGGGCC GGCCT  
 G CA  
 GAM1231 LOC151234 3' TGTGGATAGGCTGATG 80177 T \_  
 CATC GCCTGTCC CG  
 ||| ||||| ||  
 GTAG CGGATAGG GT  
 T T  
 GAM1231 LOC151614 3' GCATGGGCCGGCACGGT 80305 T C  
 GCC GT CCGGCCTGTGC  
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TGG CA GGCCGGGTACG  
 \_ C  
 GAM1231 LOC151904 3' GGCAGGCTGGGCGTGGT 80392 \_ T TG  
 GCC TG CCCGGCCTG C  
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 TGG GC GGGTCGGAC G  
 T \_ GT  
 GAM1231 LOC151904 3' TGTGTAAGCCGGGAGGTGGGTG 80396 TG TG C TG  
 CATC CC TCCCGGC TG CG  
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 GTGG GG AGGGCCG AT GT  
 GT \_ A GT  
 GAM1231 LOC152317 3' GCCTGGGACAGGGAGGTG 85644 G \_  
 CATCT CCTGTCCC GGC  
 |||| ||||| |||  
 GTGGA GGACAGGG CCG  
 G T  
 GAM1231 LOC152453 5' TGTGTAGCATTGGGGACAGGCA 80604 GGC\_ TG  
 GA TCTGCCTGTCCC CTG CG  
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 AGACGGACAGGG GAT GT  
 GTTAC GT  
 GAM1231 LOC153579 3' CGCACAGGGAGTCGGGCGGATG 80894 TCCCGG  
 CATCTGCCTG CCTGTGCG  
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 GTAGGCGGGC GGACACGC  
 TGAG\_  
 GAM1231 LOC153592 3' GCCGGGGTGGGGGATG 86067 G TG  
 CATCT CC TCCCGGC  
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 GTAGG GG GGGGCCG  
 \_ GT  
 GAM1231 LOC153684 5' CGCATGGGGAACGGGCTGGTG 86081 T CCCGG  
 CATC GCCTGT CCTGTGCG  
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 GTGG CGGGCA GGGTACGC  
 T AAG\_  
 GAM1231 LOC157562 5' GGTCGAGGTAGGCAGGTG 86478 T \_  
 CATCTGCCTG CC CGGCC  
 ||||| || ||||  
 GTGGACGGAT GG GCTGG  
 \_ A  
 GAM1231 LOC157848 3' GGGGGTGGGCTGGGGGAGGCGG 81622 G TG GCG  
 GTG CATCTGCCT TCCCGGCC T  
 ||||| ||||| |  
 GTGGGCGGA GGGGTCGG G  
 G GT GGGGA  
 GAM1231 LOC157918 3' TGGAGCAGGGGCAGGTAGGTG 86651 G \_  
 CATCTGCCTGTCCC GC CTG  
 ||||| || |||



GTGGATGGACGGGG CG GGT  
 A A  
 GAM1231 LOC158125 5' GGCTGGGACAAGCGGGTG 81716 C  
 CATCTGC TGTCCCGGCC  
 ||||| |||||  
 GTGGGCG ACAGGGTCGG  
 A  
 GAM1231 LOC158310 3' TGCGCAGGCGAAAAGTGTGGATG 86765 TG\_ G CCG  
 CATC C CT TC GCCTGTGCG  
 ||| ||| |||||  
 GTAG G GA AG CGGACGCGT  
 GT T A \_\_\_\_  
 GAM1231 LOC158801 5' TGCGCGGGCTGGGTTTTTGG 86895 TGT\_\_  
 CC CCCGGCCTGTGCG  
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 GG GGGTCGGGCGCGT  
 TTTT  
 GAM1231 LOC162333 5' TGCATGACGCAAGGGACAGGCA 87142 G\_ CT\_  
 GA TCTGCCTGTCCC GC GTGCG  
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 AGACGGACAGGG CG TACGT  
 AA CAG  
 GAM1231 LOC196027 3' GTATGGGTTGGGAGCAG 87551 CTG  
 CTGC TCCCGGCCTGTGC  
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 \_\_\_\_  
 GAM1231 LOC196477 3' TGTATGACTATGGGTGGGTGGT 87723 T T GCCT\_  
 G CATC GCCTG CCCG GTGCG  
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 GTGG TGGGT GGGT TATGT  
 \_ \_ ATCAG  
 GAM1231 LOC197135 5' GCTGGGAGGGTGGGTG 87894 TG G  
 CATC CCT TCCCGGC  
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 GTGG GGG AGGGTCG  
 GT \_  
 GAM1231 LOC197342 3' CGCGACTGCTGGGGTGGGCGGA 87999 TG CTG  
 TCTGCC TCCCGGC TGCG  
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 AGGCGG GGGGTCG GCGC  
 GT TCA  
 GAM1231 LOC197408 5' GCCCTTTGGGATAGGGGATG 89749 G \_\_\_\_  
 CATCT CCTGTCCC GGC  
 |||| |||| |||  
 GTAGG GGATAGGG CCG  
 \_ TTTC  
 GAM1231 LOC199699 3' GCAGGGAGGGTAGATG 88306 G G  
 CATCTGCCT TCCC GC  
 ||||| ||| ||

		GTAGATGGG AGGG CG		
		— A		
GAM1231	LOC199782 5'	TGTGTGGGCCCCAGGGCAGG 89855	C__	TG
		CCTGTCC GGCCTG CG		
		GGACGGG CCGGGT GT		
		ACC GT		
GAM1231	LOC200107 5'	GGTGGGCTTGGGCGTGT 88576	C C	TG
		GC TGTCC GGCCTG C		
		TG GCGGG TCGGGT G		
		T T GT		
GAM1231	LOC200225 5'	CGTGTGGGGGAACACTACGGGCGG 89965	C__	GG TG
	ATG	TCTGCCTGT CC CCTG CG		
		AGGCGGGCA GG GGGT GC		
		TCAA __ GT		
GAM1231	LOC200310 3'	CGTGTGGGTGAGATAGGCA 65734	C G	TG
		TGCCTGTC CG CCTG CG		
		ACGGATAG GT GGGT GC		
		A _ GT		
GAM1231	LOC200473 5'	CGTAAAGCATGGGGTGGGGGGG 90074	G TG	_ CTG
	TG	CATCT CC TCCCG GC TGCG		
		GTGGG GG GGGGT CG ATGC		
		G GT A AA_		
GAM1231	LOC201910 3'	TGTGTAGCCAATAGGTGGTTG 89103	T TG	CCC C TG
		CA C CCTGT GGC TG CG		
		GT G GGATA CCG AT GT		
		T GT A__ _ GT		
GAM1231	LOC203377 5'	GTATGTCTGTAGGTAGGTG 90584	TCCC	CT
		CATCTGCCTG GGC GTGC		
		GTGGATGGAT CTG TATG		
		GT__ _		
GAM1231	LOC203396 5'	GCCGTGGGGCAGGCGGG 90624	__	
		TCTGCCTGTCCC GGC		
		GGGCGGACGGGG CCG		
		TG		
GAM1231	LOC204084 5'	TGTGCGCTCCGGGCGGTGGATG 89448	TG T T	CC TG
		CATC CC G CCCGG TG CG		
		GTAG GG C GGGCC GC GT		
		GT __ TC GT		
GAM1231	LOC204161 3'	CGAGCCTTGGGACGGGCTGGGT 90659	_	__ CTGTGCG
	G	ATCT GCCTGTCCC GGC		

		TGGG CGGGCAGGG CCG		
		T TT AGC G		
GAM1231	LOC219376 3'	TGGGAGGCTGGGGCAGGCGGAT 93901		GTGCG
		ATCTGCCTGTCCCGGCT		
		TAGCGGACGGGGTCGGA		
		GGGT		
GAM1231	LOC219920 5'	TGCACGTGACGCTGGGCAGATG 93322		TCC GCC
		CATCTGCCTG CG TGTGCG		
		GTAGACGGGT GC GCACGT		
		C__ AGT		
GAM1231	LOC219942 5'	TTGGGGCAGCAGGTG 93352 C		
		CATCTGC TGTCCCGG		
		GTGGACG ACGGGGTT		
		-		
GAM1231	LOC221100 5'	TGTACAGGCACCACAGGTACAT 93243 C		CCCG
	G	CAT TGCCTGT GCCTGTGCG		
		GTA ATGGACA CGGACATGT		
		C CCA_		
GAM1231	LOC221399 5'	TGCATAGGTTGTGTGTATATG 93852 C		CTGTCC
		CAT TGC CGGCCTGTGCG		
		GTA ATG GTTGGATACGT		
		T TGT__		
GAM1231	LOC221431 3'	CCGGGACAGGAGGGTG 92099 G		
		CATCT CCTGTCCCGG		
		GTGGG GGACAGGGCC		
		A		
GAM1231	LOC221466 5'	TGTGTGCCAGCAGGTGGGTG 93698 TG		CCC CT TG
		CATC CCTGT GGC G CG		
		GTGG GGACG CCG T GT		
		GT A__ __GT		
GAM1231	LOC221501 3'	CGCGCGGGCCGGGCGGGGCGGG 93792		_____
	CGGG	TGCCTGT CCCGGCCTGTGCG		
		GCGGGCG GGGCCGGGCGCGC		
		GGGC		
GAM1231	LOC221876 5'	GTGGGGGCTGGCAGGTG 93924 T		G
		CATCTGCC GTCCC GC		
		GTGGACGG CGGGG TG		
		T G		
GAM1231	LOC221922 5'	TGTGTGCCCCGCAGGCAGGTG 92707		CCC CT TG
		CATCTGCCTGT GGC G CG		

		GTGGACGGACG CCG T GT	
		CC_ _ GT	
GAM1231	LOC221935 3'	TGCACGGCAAACGGGCAGGTG 92628	CCCG T
		CATCTGCCTGT GCC GTGCG	
		GTGGACGGGCA CGG CACGT	
		AA_ _	
GAM1231	LOC222963 5'	CGCACAGTACAAGGGTGGCAGG 92879	TGT GGC_
	TG	CATCTGCC CCC CTGTGCG	
		GTGGACGG GGG GACACGC	
		T_ AACAT	
GAM1231	LOC253070 3'	GCGTGGGCGTGGGCAGG 97009	T _ TG
		CCTG CCCG GCC TGC	
		GGAC GGGT CGG GCG	
		_ G GT	
GAM1231	LOC253070 3'	TGTGTTTATGGGAGAGGTGGGT 97015	TG G GCCT TG
	G	CATC CCT TCCCG G CG	
		GTGG GGA AGGGT T GT	
		GT G ATT_ GT G	
GAM1231	LOC253148 3'	TGTGCGGGTCGGTGTTTGGG 96880	TC_ TG
		CCTG CCGGCCTG CG	
		GGGT GGCTGGGC GT	
		TTGT GT	
GAM1231	LOC253172 5'	GCGCGGGGTGGGCGGG 97552	T G
		CCTG CCCG CCTGTGC	
		GGGC GGGT GGGCGCG	
		_ G	
GAM1231	LOC253893 3'	GGGGGTGGGCTGGGGGAGGCGG 96116	G TG GCG
	GTG	CATCTGCCT TCCCGGCC T	
		GTGGGCGGA GGGGTCGG G	
		G GT GGGGA	
GAM1231	LOC253897 3'	TGTGCGGGCTGAGTGGTTGGGG 96108	G T _ TG
	AGATG	CT CCTG CC CGGCCTG CG	
		GA GGGT GG GTCGGGC GT	
		G T TGA GT	
GAM1231	LOC254016 3'	TGCACTTGGGGGTGGGTGGGTG 96924	TG TG GGCCT
		CATC CC TCCC GTGCG	
		GTGG GG GGGG CACGT	
		GT GT GTT_	
GAM1231	LOC254100 3'	TGGGAGGCCGAGGCGGGCAGAT 96421	C GTGCG
	G	CATCTGCCTGTC CGGCCT	

		GTAGACGGGCGG GCCGGA		
		A GGGT		
GAM1231	LOC254120 3'	TGCACAGGTCGGGGAAGGGGGC 97397	_ G__	
		CGGGTG TG CCT TCCCGCCTGTGCG		
		GC GGG GGGGCTGGACACGT		
		C GGAA		
GAM1231	LOC254532 3'	CGCACAGGCTGGGACA 96633		
		TGTCCCGCCTGTGCG		
		ACAGGGTCGGACACGC		
GAM1231	LOC255042 3'	TGTGTGGGCTGAAAGGCGAGGT 95326	_ GTCC TG	
		G CATCT GCCT CGGCCTG CG		
		GTGGA CGGA GTCGGGT GT		
		G AA__ GT		
GAM1231	LOC256306 5'	CTGGGGCAGGGGATG 96687	G	
		CATCT CCTGTCCCGG		
		GTAGG GGACGGGGTC		
GAM1231	LOC256789 3'	GCGGGGGCGGGGGGTG 97446	G G	
		CATCT CCTGTCCC GC		
		GTGGG GGGCGGGG CG		
		G		
GAM1231	LOC256812 5'	GCGTGGGCGGGGCAGG 97548	G TG	
		CCTGTCCCG CC TGC		
		GGACGGGGC GG GCG		
		GT		
GAM1231	LOC257095 5'	CGGGTCGGGTTGGGTCGGGTGG 96937	TG T _G	
		GTG CATC CCTG CCCGGCCTG T CG		
		GTGG GGC GGGTTGGGC G GC		
		GT T T G		
GAM1231	LOC257095 5'	GCCCCGGGGAAGGCAGGTG 96939	GT CCTGT	
		CATCTGCCT CCCGG GC		
		GTGGACGGA GGGCC CG		
		AG C__		
GAM1231	LOC257354 3'	GGTGGGCGGGGCGTGGT 95095	_ G TG	
		GCC TGTCCCG CCTG C		
		TGG GCGGGGC GGGT G		
		T _ GT		
GAM1231	LOC257358 3'	TGTGTGGTTTATGGGGTAGATG 97106	GTCCC T TG	
		CATCTGCCT GGCC G CG		

GTAGATGGG TTGG T GT  
 GTAT\_ \_GT  
 GAM1231 LOC257455 5' TGCACAGGCTGGGCACCTGGC 78749 T\_ \_  
 GCC GT CCCGGCCTGTGCG  
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 CGG CA GGGTCGGACACGT  
 TC C  
 GAM1231 LOC56965 3' TGTATATGAGGATGGTCAGGTG 39530 C \_ GCC  
 CATCTG CTGTCC CG TGTGCG  
 ||||| ||||| || |||||  
 GTGGAC GG TAGG GT ATATGT  
 T A \_  
 GAM1231 LOC56965 3' TGTATATGAGGATGGTCAGGTG 39531 C \_ GCC  
 CATCTG CTGTCC CG TGTGCG  
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 GTGGAC GG TAGG GT ATATGT  
 T A \_  
 GAM1231 LOC90183 3' GCGCGCGGGCCGCGGGCGACGG 61733 \_ \_  
 GCGGGTG GCCTGTC CC GGCCTGTGCG C  
 ||||| || ||||| |  
 CGGGCAG GG CCGGGCGCGC G  
 C GCG  
 GAM1231 LOC90529 3' TGCACAGATTCGCGGTGGGT 63164 TG C C\_  
 GCC TC CGG CTGTGCG  
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 TGG GG GCT GACACGT  
 GT C TA  
 GAM1231 LOC90673 5' TGCCTGACGCGGGGCGGGCGG 63822 GCCT\_  
 G TCTGCCTGTCCCG GTGCG  
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 GGGCGGGCGGGGC CGCGT  
 GCAGT  
 GAM1231 LOC90835 5' TGCATGGGTTCGGCCGCGCGGA 64134 C TC  
 TCTGC TG CCGGCCTGTGCG  
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 AGGCG GC GGCTGGGTACGT  
 C C\_  
 GAM1231 LOC91547 5' GCGCAGGCGGCGCGGGT 66405 C G  
 GCCTGT CCG CCTGTGC  
 ||||| || |||||  
 TGGGCG GGC GGACGCG  
 C \_  
 GAM1231 LOC91768 3' TGCACTTTCCCTGGGGCGTGT 67118 TG C CCT\_\_\_\_  
 GGGTG C C TGTCCCG GTGCG  
 | | ||||| |||||  
 G G GCGGGGTC CACGT  
 GT T CCCTTT  
 GAM1231 LOC92080 3' TGCACTTGAAGCGGGAGGGCGG 68061 G GCCT\_  
 ATG ATCTGCCT TCCCG GTGCG  
 ||||| ||||| |||||

			TAGGCGGG AGGGC CACGT		
			GAAGTT		
GAM1231	LOC92162	5'	CGCTCCTCGGGATGGGGGGTG 68363	G	CCTGT
			CATCT CCTGTCCCGG GCG		
			GTGGG GGGTAGGGCT CGC		
			CCT__		
GAM1231	LOC92299	3'	TGGGAGGCCGAGGCAGGTGGAT 68816	TG	C GTGCG
	G		CATC CCTGTC CGGCCT		
			GTAG GGACGG GCCGGA		
			GT A GGGT		
GAM1231	LOC92340	3'	TGTGTGGCTGTGAGGGCAGATG 68999	G C	T TG
			CATCTGCCT TC CGGCC G CG		
			GTAGACGGG AG GTCGG T GT		
			_ T _ GT		
GAM1231	LOC93626	3'	CGTGTGGGGCCACGTGGGCATG 72768	C	TG CCC _ TG
	TG		CAT TGCC T GGCCT G CG		
			GTG ACGG G CCGGG T GC		
			T GT CA_ G GT		
GAM1232	BACE2	3'	GCCAGGCCTGACCTCAAGCAA 23982	TC	AAA GA
			TTGCTTGAG CAG GT GGC		
			AACGAACTC GTC CG CCG		
			CA _ GA		
GAM1232	BACE2	3'	GCCAGGCCTGACCTCAAGCAA 57296	TC	AAA GA
			TTGCTTGAG CAG GT GGC		
			AACGAACTC GTC CG CCG		
			CA _ GA		
GAM1232	BACE2	3'	GCCAGGCCTGACCTCAAGCAA 57298	TC	AAA GA
			TTGCTTGAG CAG GT GGC		
			AACGAACTC GTC CG CCG		
			CA _ GA		
GAM1232	CNP	3'	GCCTCGAACTCCTGGGCTCAAG 52444	AAAG_	
	CAA		TTGCTTGAGTCCAG TGAGGC		
			AACGAACTCGGGTC GCTCCG		
			CTCAA		
GAM1232	DIAPH2	3'	CTCCTAGCCTCAAGCAA 22066	TCCAGAA	T
			TTGCTTGAG AG GAG		
			AACGAACTC TC CTC		
			CGA____ _		
GAM1232	DTX1	5'	GCCTCACTCCCTACCTGAGC 15344	GA	CC AA
			GCTT GT AG AGTGAGGC		

			CGAG CA TC TCACTCCG		
			TC _ CC		
GAM1232	FABP2	3'	CCTCAAACCTCCTGGACTCATGC 3743	T	AAAG_
	AA		TTGC TGAGTCCAG TGAGG		
			AACG ACTCAGGTC ACTCC		
			T CTCAA		
GAM1232	FCRH1	3'	CCTCTCAGGCTCAAGCAA 53626	CA	AAGT
			TTGCTTGAGTC GA GAGG		
			AACGAACTCGG CT CTCC		
			A_ _		
GAM1232	HCS	3'	CTCCTGAGCTCAAGCAA 38467	TC	AAAGT
			TTGCTTGAG CAG GAG		
			AACGAACTC GTC CTC		
			GA _		
GAM1232	KMO	3'	GCCTCCTGGGCTCAAGCAA 13451		AAAGT
			TTGCTTGAGTCCAG GAGGC		
			AACGAACTCGGGTC CTCCG		
			_		
GAM1232	LZTS1	3'	GCCTCATACTCCTGGGCTCAAG 40691		AAA_
	CAA		TTGCTTGAGTCCAG GTGAGGC		
			AACGAACTCGGGTC TACTCCG		
			CTCA		
GAM1232	MEN1	5'	TTTTCTGGATCAAGCAA 55475	G	
			TTGCTTGA TCCAGAAAG		
			AACGAACT AGGTCTTTT		
			-		
GAM1232	NCOA6	5'	GCCTCAACCTCCTGGGCTCAAG 25968		AAAG_
	CAA		TTGCTTGAGTCCAG TGAGGC		
			AACGAACTCGGGTC ACTCCG		
			CTCCA		
GAM1232	RAD51L3	3'	GCCTCACTCTCTGTAAGCA 56068	AGTC	A
			TGCTTG CAGA AGTGAGGC		
			ACGAAT GTCT TCACTCCG		
			_ C		
GAM1232	RAD51L3	3'	GCCTCACTCTCTGTAAGCA 56075	AGTC	A
			TGCTTG CAGA AGTGAGGC		
			ACGAAT GTCT TCACTCCG		
			_ C		
GAM1232	RAD51L3	3'	GCCTCACTCTCTGTAAGCA 56081	AGTC	A
			TGCTTG CAGA AGTGAGGC		



		ACGAAT GTCT TCACTCCG	
		_____ C	
GAM1232	RAD51L3	3' GCCTCACTCTCTGTAAGCA 11235	AGTC A
		TGCTTG CAGA AGTGAGGC	
		ACGAAT GTCT TCACTCCG	
		_____ C	
GAM1232	SERPINB9	3' CCTCCTCCTGGATTCAAGCAA 14753	AA T
		TTGCTTGAGTCCAG AG GAGG	
		AACGAACTTAGGTC TC CTCC	
		C_ _	
GAM1232	SHOX	3' GCCTCAAACCTCCTGGGCTCAAG 22539	AAAG_
	CAA	TTGCTTGAGTCCAG TGAGGC	
		AACGAACTCGGGTC ACTCCG	
		CTCAA	
GAM1232	SLA2	3' CCTCCATCTCCTGGATTCAAAC 49896	C AAA _
	AA	TTG TTGAGTCCAG GTG AGG	
		AAC AACTTAGGTC TAC TCC	
		A CTC C	
GAM1232	SPOCK	3' CCACATAAACTCAAGCAA 62816	CCAGAAA A
		TTGCTTGAGT GTG GG	
		AACGAACTCA TAC CC	
		AA_____ A	
GAM1232	TAL1	3' GCCTTGAACCTCTGGGCTCAAGC 12107	AAG
	AA	TTGCTTGAGTCCAGA TGAGGC	
		AACGAACTCGGGTCT GTTCCG	
		CAA	
GAM1232	TNFRSF11A	3' GCCTCTAACTCCTGGGCTCAAG 13853	AA _
	CAA	TTGCTTGAGTCCAG AGT GAGGC	
		AACGAACTCGGGTC TCA CTCCG	
		C_ AT	
GAM1232	AP1S3	3' CCTCCTGGGCTCAAGCAA 74919	AAAGT
		TTGCTTGAGTCCAG GAGG	
		AACGAACTCGGGTC CTCC	
		_____	
GAM1232	ASB16	3' GCCTGGACCTCCCAAGCTCAAG 69938	CCA_ AAGTG
	CA	TGCTTGAGT GA AGGC	
		ACGAACTCG CT TCCG	
		AACC CCAGG	
GAM1232	BC022889	3' CCTCATAGAGGAATCAAGCAA 83646	G AGAAA
		TTGCTTGA TCC GTGAGG	

AACGAACT AGG TACTCC  
 A AGA\_\_  
 GAM1232 BCL2L1 3' GCCTCACTTCCTACAAGAGCAG 56806 GA CC A  
 TTGCTT GT AG AAGTGAGGC  
 ||||| || || |||||  
 GACGAG CA TC TTCACTCCG  
 AA \_\_ C  
 GAM1232 C6orf33 3' CCTCCCCAGCTCAAGCAA 55877 CCAGAAAGT  
 TTGCTTGAGT GAGG  
 ||||| ||||  
 AACGAACTCG CTCC  
 ACCC\_\_\_\_  
 GAM1232 DKFZp434C0923 3' GCCTCGCCTCCTGGGCTCAAG 34215 AAA \_  
 CAA TTGCTTGAGTCCAG GTG AGGC  
 ||||| ||||  
 AACGAACTCGGGTC CGC TCCG  
 CTC C  
 GAM1232 DORFIN 5' GCCTGGAATTCCTGGGCTCAAG 31259 A GTG\_  
 CAA TTGCTTGAGTCCAG AA AGGC  
 ||||| || ||||  
 AACGAACTCGGGTC TT TCCG  
 C AAGG  
 GAM1232 FLJ10159 3' CCTCTGTCTAAAACTCAAGCAA 35860 CC\_ AAGT  
 TTGCTTGAGT AGA GAGG  
 ||||| || ||||  
 AACGAACTCA TCT CTCC  
 AAA GT\_\_  
 GAM1232 FLJ11125 5' GCCTCCATCTCCTGGGCTCAAG 59581 AAA \_  
 CAA TTGCTTGAGTCCAG GTG AGGC  
 ||||| ||||  
 AACGAACTCGGGTC TAC TCCG  
 CTC C  
 GAM1232 FLJ12668 3' CCTCCATCTCCCTGGGCTCAAGC 46514 T AA T\_\_  
 AA TTGCTTGAG CCAG AG GAGG  
 ||||| |||| ||||  
 AACGAACTC GGTC TC CTCC  
 \_ CC TAC  
 GAM1232 FLJ13072 5' CCTCACAGGCTCAAGCAA 89806 CAGAAA  
 TTGCTTGAGTC GTGAGG  
 ||||| ||||  
 AACGAACTCGG CACTCC  
 A\_\_\_\_  
 GAM1232 FLJ13150 3' ACTTTCTGGA CTCAAGGAA 45667 G  
 TT CTTGAGTCCAGAAAGT  
 || |||||  
 AA GAACTCAGGTCTTTCA  
 G  
 GAM1232 FLJ14351 3' CTCCTGAGCTCAAGCAA 45324 TC AAAGT  
 TTGCTTGAG CAG GAG  
 ||||| || ||||

			AACGAACTC GTC CTC		
			GA _____		
GAM1232	FLJ14351	3'	ACCTGCTGGGCTCAAGCAA 45318	AAA	
			TTGCTTGAGTCCAG GT		
			AACGAACTCGGGTC CA		
			GTC		
GAM1232	FLJ14803	3'	CCTCCCAGGCTCAAGCAA 51615	CAGAAAGT	
			TTGCTTGAGTC GAGG		
			AACGAACTCGG CTCC		
			ACC_____		
GAM1232	FLJ20671	3'	CCTCCCAGGCTCAAGCAA 35521	CAGAAAGT	
			TTGCTTGAGTC GAGG		
			AACGAACTCGG CTCC		
			ACC_____		
GAM1232	FLJ22316	5'	TTCTAGACTCAAGCAA 46925	C	
			TTGCTTGAGTC AGAA		
			AACGAACTCAG TCTT		
			A		
GAM1232	FLJ22969	3'	GCCTCCTGGGCTCAAGCAA 68653	AAAGT	
			TTGCTTGAGTCCAG GAGGC		
			AACGAACTCGGGTC CTCCG		
			_____		
GAM1232	FLJ23040	3'	TTCTGGGCTCAAGCAA 47201		
			TTGCTTGAGTCCAGAA		
			AACGAACTCGGGTCTT		
GAM1232	FLJ23416	3'	GCCTTGAACCTCCTGAGCTCAAG 49950	TC AA ____	
			CAA TTGCTTGAG CAG AGT GAGGC		
			AACGAACTC GTC TCA TTCCG		
			GA C_ AG		
GAM1232	KIAA0418	5'	CCTCCCTGGGCTCAAGCAA 27553	AAAGT	
			TTGCTTGAGTCCAG GAGG		
			AACGAACTCGGGTC CTCC		
			C_____		
GAM1232	KIAA0441	3'	GCCTCGAATTCCTGGGCTCAAG 28955	_ AG	
			CAA TTGCTTGAGTCCAG AA TGAGGC		
			AACGAACTCGGGTC TT GCTCCG		
			C AA		
GAM1232	KIAA0748	3'	CCTCACTTTCTGGCTC 28938	T	
			GAG CCAGAAAGTGAGG		

CTC GGTCTTTCACTCC

GAM1232 KIAA1198 3' CCTCCCGGATTCAAGCAA 63301 AGAAAGT  
TTGCTTGAGTCC GAGG  
||||||| |||  
AACGAACTTAGG CTCC  
CC\_\_\_\_

GAM1232 KIAA1237 5' GCCCACTTTCTGTCTCA 80471 TC A  
TGAG CAGAAAGTG GGC  
||| ||||| |||  
ACTC GTCTTTCAC CCG  
T\_ C

GAM1232 KIAA1320 5' GCCTTGACTTCCGAGACTCAAG 69303 CAGA \_  
CAA TTGCTTGAGTC AAGT GAGGC  
||||||| ||| |||||  
AACGAACTCAG TTCA TTCCG  
AGCC G

GAM1232 KIAA1671 3' TTCTGGGCTCAAGCAA 65699  
TTGCTTGAGTCCAGAA  
|||||||  
AACGAACTCGGGTCTT

GAM1232 KIAA1671 3' GCCTCCAACCTCCTGGGCTCAAG 65676 AA \_  
CAA TTGCTTGAGTCCAG AGT GAGGC  
||||||| ||| |||||  
AACGAACTCGGGTC TCA CTCCG  
C\_ AC

GAM1232 KIAA1751 3' GCCTCGACCTCCCGGGCTCAAG 71694 A\_ AAG  
CAA TTGCTTGAGTCC GA TGAGGC  
||||||| || |||||  
AACGAACTCGGG CT GCTCCG  
CC CCA

GAM1232 LNIR 3' GCCTTGAACCTCCTGGGCTCAAG 48131 AA \_  
CAA TTGCTTGAGTCCAG AGT GAGGC  
||||||| ||| |||||  
AACGAACTCGGGTC TCA TTCCG  
C\_ AG

GAM1232 MGC15606 5' GCCTCGACCTCCCAGGCTCAAG 58877 CA\_ AAG  
CAA TTGCTTGAGTC GA TGAGGC  
||||||| || |||||  
AACGAACTCGG CT GCTCCG  
ACC CCA

GAM1232 MGC21675 3' CACCCAGATTCAAGCAA 53479 CAGAAA  
TTGCTTGAGTC GTG  
||||||| |||  
AACGAACTTAG CAC  
ACC\_\_\_\_

GAM1232 MGC3113 3' TTCTGGGCTCAAGCAA 43854  
TTGCTTGAGTCCAGAA  
|||||||

AACGAACTCGGGTCTT

GAM1232	PPIL2	3'	GCCTCGACCTCCTGGGCTCAAG 26766	AAAG_
	CAA		TTGCTTGAGTCCAG TGAGGC	
			AACGAACTCGGGTC GCTCCG	
			CTCCA	
GAM1232	PRO0902	3'	GCCTCAAACCTACTGGGCTCAAG 53897	AAAG_
	CAA		TTGCTTGAGTCCAG TGAGGC	
			AACGAACTCGGGTC ACTCCG	
			ATCAA	
GAM1232	RAB33B	3'	GCCTTGAGCTCCTGGGCTCAAG 48495	AA _
	CAA		TTGCTTGAGTCCAG AGT GAGGC	
			AACGAACTCGGGTC TCG TTCCG	
			C_ AG	
GAM1232	RNF8	3'	CCTCCACCTCCCAGACTCAAGC 14220	CAGAAA _
			GCTTGAGTC GTG AGG	
			CGAACTCAG CAC TCC	
			ACCCTC C	
GAM1232	SLC1A7	3'	GCCCCACTTTCTGGATGACAG 21908	A_ A
			TTG GTCCAGAAAGTG GGC	
			GAC TAGGTCTTTCAC CCG	
			AG C	
GAM1232	TRIM5	3'	CCTCTCAGATTCAAGCAA 52297	CA AAGT
			TTGCTTGAGTC GA GAGG	
			AACGAACTTAG CT CTCC	
			A_ _	
GAM1232	LOC120939	3'	CCTCCCGGATTCAAGCAA 76252	AGAAAGT
			TTGCTTGAGTCC GAGG	
			AACGAACTTAGG CTCC	
			CC_	
GAM1232	LOC130813	3'	GCCTTGAACCTCCCGGGCTCAAG 75771	A_ AAG
	CAA		TTGCTTGAGTCC GA TGAGGC	
			AACGAACTCGGG CT GTTCCG	
			CC CAA	
GAM1232	LOC135293	3'	GCCTCAAACCTCCTGGGCTCAAG 76182	AAAG_
	CAA		TTGCTTGAGTCCAG TGAGGC	
			AACGAACTCGGGTC ACTCCG	
			CTCAA	
GAM1232	LOC138199	3'	CCTCAAACCTCCTGGACTCAAGC 75303	AAAG_
	GA		TTGCTTGAGTCCAG TGAGG	

		AGCGAACTCAGGTC	ACTCC	
		CTCAA		
GAM1232	LOC139422 5'	GCCTAGAACTCCTGAGCTCAAG	75842	TC AA G__
	CAA	TTGCTTGAG CAG AGT AGGC		
		AACGAACTC GTC TCA TCCG		
		GA C_ AGA		
GAM1232	LOC144970 5'	CCTCACAGTGACTCAAGC	76982	CAGAAA
		GCTTGAGTC GTGAGG		
		CGAACTCAG CACTCC		
		TGA__		
GAM1232	LOC145873 5'	CTCCTGAACTCAAGTAA	77554	C AAAGT
		TTGCTTGAGT CAG GAG		
		AATGAACTCA GTC CTC		
		A _____		
GAM1232	LOC147895 5'	GCCTCAACTTCCTGGACTCAAG	84079	A _
	CGA	TTGCTTGAGTCCAG AAGT GAGGC		
		AGCGAACTCAGGTC TTCA CTCCG		
		C A		
GAM1232	LOC148709 5'	CTCCTGAACTCAAGCAA	78942	C AAAGT
		TTGCTTGAGT CAG GAG		
		AACGAACTCA GTC CTC		
		A _____		
GAM1232	LOC149132 5'	GCCTCAAACCTCCCAGGCTCAAG	79176	CA_ AAG
	CAA	TTGCTTGAGTC GA TGAGGC		
		AACGAACTCGG CT ACTCCG		
		ACC CAA		
GAM1232	LOC149194 3'	TTTCTGGACTCAAACGA	79233	C
		TTG TTGAGTCCAGAAA		
		AGC AACTCAGGTCTTT		
		A		
GAM1232	LOC150587 3'	GCCTCAAACCTCCTGGGCTCAAG	85063	AAAG_
	CAA	TTGCTTGAGTCCAG TGAGGC		
		AACGAACTCGGGTC ACTCCG		
		CTCAA		
GAM1232	LOC152282 5'	CACCTGGGCTCAAACAA	80551	C AAA
		TTG TTGAGTCCAG GTG		
		AAC AACTCGGGTC CAC		
		A _____		
GAM1232	LOC154822 3'	CCTCTGTCTCCTGGGCTCAAGC	86259	AAAGT_
	AA	TTGCTTGAGTCCAG GAGG		

	AACGAACTCGGGTC	CTCC	
	CTCTGT		
GAM1232 LOC154877 3'	ACTTCCTGGGCTCAAGCAA	86277	A
	TTGCTTGAGTCCAG	AAGT	
	AACGAACTCGGGTC	TTCA	
	C		
GAM1232 LOC196996 3'	CAATTTTGGACTCAAGCAA	87858	G
	TTGCTTGAGTCCAGAAA	TG	
	AACGAACTCAGGTTTTT	AC	
	A		
GAM1232 LOC200860 3'	CCTCTCAGGCTCAAGCAA	90162	CA AAGT
	TTGCTTGAGTC	GA GAGG	
	AACGAACTCGG	CT CTCC	
	A_		
GAM1232 LOC202908 5'	CTGCCAGGCTCAAGCAA	89235	
	TTGCTTGAGTC	CAG	
	AACGAACTCGG	GTC	
	ACC		
GAM1232 LOC204804 3'	TCCCGGGCTCAAGCAA	89487	A_
	TTGCTTGAGTCC	GA	
	AACGAACTCGGG	CT	
	CC		
GAM1232 LOC221755 3'	GTGTCACAACTCAAGCAA	92396	CCAGAAA G
	TTGCTTGAGT	GTGA GC	
	AACGAACTCA	CACT TG	
	AA_	G	
GAM1232 LOC221960 3'	GCCTCAACCTCCTGAGCTCAAG	91083	TC AAAG_
CAA	TTGCTTGAG	CAG TGAGGC	
	AACGAACTC	GTC ACTCCG	
	GA	CTCCA	
GAM1232 LOC222057 5'	GCCTCAAACCTCCAGGCTCAAG	92778	CA_ AAG
CAA	TTGCTTGAGTC	GA TGAGGC	
	AACGAACTCGG	CT ACTCCG	
	ACC	CAA	
GAM1232 LOC222224 5'	GCCTCCTGGGCTCAAGCAA	94198	AAAGT
	TTGCTTGAGTCCAG	GAGGC	
	AACGAACTCGGGTC	CTCCG	
GAM1232 LOC254082 5'	CCTCCGCTTCCTGGATTCAAGC	97203	A _
AA	TTGCTTGAGTCCAG	AAGTG AGG	

		AACGAACTTAGGTC TTCGC TCC	
		C C	
GAM1232	LOC255975 5'	GCCTCAAACCTCCCAGGCTCAAG 95894	CA_ AAG
	CAA	TTGCTTGAGTC GA TGAGGC	
		AACGAACTCGG CT ACTCCG	
		ACC CAA	
GAM1232	LOC256878 5'	GCCTCAAACCTCCCAGGCTCAAG 96904	CA_ AAG
	CAA	TTGCTTGAGTC GA TGAGGC	
		AACGAACTCGG CT ACTCCG	
		ACC CAA	
GAM1232	LOC257054 5'	GCCTCGACCTCCTGGGCTCAAG 95663	AAAG_
	CAA	TTGCTTGAGTCCAG TGAGGC	
		AACGAACTCGGGTC GCTCCG	
		CTCCA	
GAM1232	LOC51219 5'	CCTCCCGGATTCAAGCAA 33116	AGAAAGT
		TTGCTTGAGTCC GAGG	
		AACGAACTTAGG CTCC	
		CC_____	
GAM1232	LOC51622 3'	GCCTCAACCTCCTGAGCTCAAG 31568	TC AAAG_
	CAA	TTGCTTGAG CAG TGAGGC	
		AACGAACTC GTC ACTCCG	
		GA CTCCA	
GAM1232	LOC93276 5'	CCTCACAATGACTCAAGC 71889	CAGAAA
		GCTTGAGTC GTGAGG	
		CGAACTCAG CACTCC	
		TAA_____	
GAM1233	ACCN1 3'	CTGCCATCACATCTCACTG 6583	A CA AAAAA
		CA TG ATGT GTGGCAG	
		GT AC TACA TACCGTC	
		C TC C_____	
GAM1233	BMP1 3'	CCTGCCACCTTCCGGGGCATT 20414	AA TAAAAA
		AATGC TG GTGGCAGG	
		TTACG GC CACCGTCC	
		GG CTTC_____	
GAM1233	CHRN2 3'	CCTGCCACCCTCTGCTGCA 5622	AT AAAA
		TGCA GTA GTGGCAGG	
		ACGT CGT CACCGTCC	
		___ CTCC	
GAM1233	CLASP1 3'	CCTGCCACCCTTTATTTATCA 65300	CAAT AA
		TG GTAAA GTGGCAGG	



			AC TATTT CACCGTCC			
			TATT CC			
GAM1233	CRP	3'	CCGCTTTTTTACACTGCAT 71627	A		_
			ATGCA TGTA AAAA GTGG			
			TACGT ACATTTTT CGCC			
			C T			
GAM1233	CYP24	3'	CTGCTACCACATTCACTG 5768	A C		AAAAA
			CA TG AATGT GTGGCAG			
			GT AC TTACA CATCGTC			
			C _ C _			
GAM1233	DRIL1	5'	CCTGCCACCCTGCACTGC 17827	A		AAAA
			GCA TGTA GTGGCAGG			
			CGT ACGT CACCGTCC			
			C CC _			
GAM1233	EGLN2	5'	CCTGCCACCCATCCACGTGCAT 34099	A	A	AAAAA _
	CA		C ATGCA TGT GTGGCAGG			
			A TACGT GCA CACCGTCC			
			C _ CCTACC			
GAM1233	FBXL11	3'	CCCTTTTACTTTGCATTG 24569	T		AT
			CAATGCAA GTAAAA G GG			
			GTTACGTT CATTTT C CC			
			T _ _			
GAM1233	GLP1R	3'	CCTGCCACTTCCAGGAGC 9031	AA _		TAAA
			GC TG AAGTGGCAGG			
			CG AC TTCACCGTCC			
			AGG C _			
GAM1233	GPR63	3'	CTGCAGTTACATTGAATTG 47890	G		AAAGTG
			CAAT CAATGTAA GCAG			
			GTTA GTTACATT CGTC			
			A GA _			
GAM1233	GPR86	3'	ACTTATCACATTGCATTG 43649			AAA
			CAATGCAATGT AAGT			
			GTTACGTTACA TTCA			
			CTA			
GAM1233	INSM1	3'	CCTGCCACTCTTGACATTCCAC 9351	A C		A A
	TG		CA TG AATGT AA AGTGGCAGG			
			GT AC TTACA TT TCACCGTCC			
			C C G C			
GAM1233	LENG4	5'	CGCCGGCACCTGCATTG 44164	A _		AAAAAG A
			CAATGCA TGT TGGC G			

GTTACGT ACG    GCCG C  
                  CC        C  
 GAM1233 RDS    5' CCTGCCACCACTACTGCATT 4359    AT AAAA  
                  AATGCA GTA    GTGGCAGG  
                  ||||| ||    |||||  
                  TTACGT CAT    CACCGTCC  
                  \_ CAC\_  
 GAM1233 RNF26    3' CCTGTCACTCCCACATCACA 49311    CA AAAA  
                  TG ATGT    AGTGGCAGG  
                  || |||    |||||  
                  AC TACA    TCACTGTCC  
                  AC CCC\_  
 GAM1233 SLC9A5    3' CCTGCCACTTTCTGTTTCATT 59768    C TAA  
                  AATG AATG    AAAGTGGCAGG  
                  ||| |||    |||||  
                  TTAC TTGT    TTTCACCGTCC  
                  T C\_  
 GAM1233 SLC9A5    3' CCTGCCACTTTCTGTTTCATT 15981    C TAA  
                  AATG AATG    AAAGTGGCAGG  
                  ||| |||    |||||  
                  TTAC TTGT    TTTCACCGTCC  
                  T C\_  
 GAM1233 TNFRSF1B 3' CTGCCACTTTGGTACAT    6521    A\_  
                  ATGTA AAAGTGGCAG  
                  |||| |  
                  TACAT TTTCACCGTC  
                  GG  
 GAM1233 UBE2V1    3' CCTGCCACCCTCTGCTGTCATC 12516    A \_ AT AAAA  
                  A                    C ATG CA GTA    GTGGCAGG  
                  | ||| ||    |||||  
                  A TAC GT CGT    CACCGTCC  
                  C T \_ CTCC  
 GAM1233 UBE2V1    3' CCTGCCACCCTCTGCTGTCATC 41791    A \_ AT AAAA  
                  A                    C ATG CA GTA    GTGGCAGG  
                  | ||| ||    |||||  
                  A TAC GT CGT    CACCGTCC  
                  C T \_ CTCC  
 GAM1233 UBE2V1    3' CCTGCCACCCTCTGCTGTCATC 42368    A \_ AT AAAA  
                  A                    C ATG CA GTA    GTGGCAGG  
                  | ||| ||    |||||  
                  A TAC GT CGT    CACCGTCC  
                  C T \_ CTCC  
 GAM1233 UBTF    3' CCTGCCACCTGGACCCCTGCAT 26447    AT\_ AAAAA  
                  TG                    CAATGCA GT    GTGGCAGG  
                  ||||| ||    |||||  
                  GTTACGT CA    CACCGTCC  
                  CCC GGTC\_  
 GAM1233 AASDHPPT 3' CCTCTTTCTTTCCTAAATTGCA 31244    GTAA\_ T\_ C  
                  TTG                    CAATGCAAT    AAAG GG AGG  
                  ||||| ||| || |||

GTTACGTTA TTTC TC TCC  
 AATCC TT \_  
 GAM1233 FLJ11078 3' CCTGCCACTCCCTGGCCTGC 37031 AT AAAA\_  
 GCA GT AGTGGCAGG  
 ||| || |||||  
 CGT CG TCACCGTCC  
 C\_ GTCCC  
 GAM1233 FLJ11151 3' CCGTTCACTTTTCACTTGCA 67873 T A CA  
 TGCAA GT AAAAGTGG GG  
 ||||| || ||||| ||  
 ACGTT CA TTTTCACT CC  
 \_ C TG  
 GAM1233 FLJ20509 3' CCACAGTTTTTACATTG 35312 \_  
 CAATGTAAAAA GTGG  
 ||||| ||||| |||||  
 GTTACATTTTT CACC  
 GA  
 GAM1233 HE3-ALPHA 3' CCTGCCACTCCCCGCTTACATT 60185 C AA\_\_\_\_  
 TA G AATGTAA AGTGGCAGG  
 | ||||| |||||  
 A TTACATT TCACCGTCC  
 T CGCCCC  
 GAM1233 HSPC065 3' CCTGCCACCTGGCAACTGC 26291 A\_ AAAAA  
 GCA TGT GTGGCAGG  
 ||| ||| |||||  
 CGT ACG CACCGTCC  
 CA GTC\_  
 GAM1233 KIAA0202 3' CCATGAGATTTCCACATTGCAT 64369 AAA GG \_  
 ATGCAATGT AAGT CA GG  
 ||||| ||| |||  
 TACGTTACA TTTA GT CC  
 CC\_ GA A  
 GAM1233 KIAA0435 3' CCTCCCACCTGCATTG 28973 AAAA C  
 CAATGTA GTGG AGG  
 ||||| ||| |||  
 GTTACGT CACC TCC  
 C\_ C  
 GAM1233 KIAA0527 3' CTGCCACCTCTTTTCAGCA 95798 AA T A\_  
 TGC TG AAAA GTGGCAG  
 ||| ||||| |||||  
 ACG AC TTTT CACCGTC  
 \_ \_ CTC  
 GAM1233 KIAA0552 5' CTGCCACCTACTGCA 28313 AT AAAA  
 TGCA GTA GTGGCAG  
 ||||| ||| |||||  
 ACGT CAT CACCGTC  
 \_ C\_  
 GAM1233 KIAA1026 3' CCTACCAGTTTTTAAATTGCAT 71190 G G C  
 TG CAATGCAAT TAAAAA TGG AGG  
 ||||| ||||| ||| |||

			GTTACGTTA ATTTT ACC TCC		
			A G A		
GAM1233 KIAA1143	3'	CCTGCTTCTCACTTGACATTGC 68675	AAA	_____	
		ATT AATGCAATGT AAGTG GCAGG			
		TTACGTTACA TTCAC CGTCC			
		G_ TCTT			
GAM1233 KIAA1437	5'	CTGCCACTCCCATGCA 60584	A TAAAA		
		TGCA TG AGTGGCAG			
		ACGT AC TCACCGTC			
		_ CC_			
GAM1233 KIAA1715	3'	CTGTTACATTGCATT 68119	AAAAAGT		
		AATGCAATGT GGCAG			
		TTACGTTACA TTGTC			
		C_			
GAM1233 KIAA1750	3'	CTGTTATCTACATTGC 68248	AAAA		
		GCAATGTA GTGGCAG			
		CGTTACAT TATTGTC			
		C_			
GAM1233 KIAA1946	3'	CCTTATTATTTTACACTGCA 82470	A C_		
		TGCA TGTA AAAAGTGG AGG			
		ACGT ACATTTTATT TCC			
		C AT			
GAM1233 KIAA1966	3'	CCATATTCTACATTGC 55892	A A		
		GCAATGTA AA GTGG			
		CGTTACAT TT TACC			
		C A			
GAM1233 MADCAM1	3'	TACTTTTTACATACATTG 55359	CA		
		CAATG ATGTAAAAAGTG			
		GTTAC TACATTTTCAT			
		A_			
GAM1233 MADCAM1	3'	TACTTTTTACATACATTG 55362	CA		
		CAATG ATGTAAAAAGTG			
		GTTAC TACATTTTCAT			
		A_			
GAM1233 MADCAM1	3'	TACTTTTTACATACATTG 55365	CA		
		CAATG ATGTAAAAAGTG			
		GTTAC TACATTTTCAT			
		A_			
GAM1233 MGC5149	3'	CCTGCCACCAGAATTGCA 72289	GTAAAAA		
		TGCAAT GTGGCAGG			

ACGTTA CACCGTCC  
 AGAC\_\_\_\_  
 GAM1233 NAG14 3' CTAATGCTTTCACATTGCA 42165 AA GC  
 TGCAATGT AAAGTG AG  
 ||||| ||||| ||  
 ACGTTACA TTTCGT TC  
 C\_ AA  
 GAM1233 PELI1 5' CTACTTTTACATTGC 40262 A  
 GCAATGTAAAA GTGG  
 ||||| ||||| |||||  
 CGTTACATTTT CATC  
 -  
 GAM1233 PTD002 3' CCTGCCACCTCATTATTTTGCA 32346 T AAA\_  
 TTG CAATGCAA GTAA GTGGCAGG  
 ||||| ||||| |||||  
 GTTACGTT TATT CACCGTCC  
 T ACTC  
 GAM1233 RoXaN 3' CTGCCACCTTGTACATT 46643 A A  
 AATGTA AA GTGGCAG  
 ||||| || |||||  
 TTACAT TT CACCGTC  
 G C  
 GAM1233 TSGA14 3' CCTGCCACCTTTTCATTCACTG 38044 A C T A  
 CA TG AATG AAAA GTGGCAGG  
 || || |||| ||||| |||||  
 GT AC TTAC TTTT CACCGTCC  
 C \_ \_ C  
 GAM1233 LOC126964 3' ACTTTTACATTAATTG 74612 GC  
 CAAT AATGTAAAAAGT  
 |||| |||||  
 GTTA TTACATTTTCA  
 A\_  
 GAM1233 LOC145501 3' CCTGCCACGAGCCACTGCA 77254 A TAAAAA  
 TGCA TG GTGGCAGG  
 |||| || |||||  
 ACGT AC CACCGTCC  
 C CGAG\_  
 GAM1233 LOC152286 3' CCTGCCACTTTTCCAATGC 85628 A TA  
 GCA TG AAAAGTGGCAGG  
 |||| || |||||  
 CGT AC TTTTCACCGTCC  
 A C\_  
 GAM1233 LOC155434 3' CCTGCCACTCTGCTCCGC 86402 AAT AAA  
 GC GTA AGTGGCAGG  
 || ||||| |||||  
 CG CGT TCACCGTCC  
 CCT C\_  
 GAM1233 LOC199232 3' CCTGCCACTTTTGACTGTGGAT 88971 A G AT A  
 CA C AT CA GT AAAAGTGGCAGG  
 || || || |||||

		A TA GT CA TTTTCACCGTCC		
		C G GT G		
GAM1233	LOC200734 3'	CCTGCCGCCACACTGCA	88861	A AAAAA
		TGCA TGT GTGGCAGG		
		ACGT ACA CGCCGTCC		
		C CC__		
GAM1233	LOC219899 3'	CCTGCCACTTGGTTATCATT	91502	_ A_
		AATG TAA AAGTGGCAGG		
		TTAC ATT TTCACCGTCC		
		T GG		
GAM1233	LOC221490 5'	CCGCCTTCTGCATTGCACTG	93657	A A A
		CA TGCAATGTA AA GTGG		
		GT ACGTTACGT TT CGCC		
		C C C		
GAM1233	LOC221773 3'	CCTGTGTATCCCTACATTACA	91043	C AAAA_ TG
		TG AATGTA G GCAGG		
		AC TTACAT T CGTCC		
		A CCCTA GT		
GAM1233	LOC222128 5'	TACTTTTTTACACAGCATCA	92717	A AA
		C ATGC TGTA AAAAGTG		
		A TACG ACATTTTTCAT		
		C AC		
GAM1233	LOC255187 5'	CTGCCACCCCTTTACAGTG	97182	A AA_
		CA TGTA AA GTGGCAG		
		GT ACATT CACCGTC		
		G CCC		
GAM1233	LOC90786 5'	CCTGCCTAGGTCACCTTTGCATT	64032	T AAAAAGT
		AATGCAA GT GGCAGG		
		TTACGTT CA CCGTCC		
		T CTGGAT_		
GAM1233	LOC91266 5'	CCACCTTAGGCTTTAATTGCAT	65411	____ AA A
	TG	CAATGCAAT GT AA GTGG		
		GTTACGTTA CG TT CACC		
		ATTT GA C		
GAM1234	CNGA1 3'	CAACTGATAATGTGCAAA	59507	GC A
		TTTGACATTA TAG TTG		
		AAACGTGTAAT GTC AAC		
		A_ _		
GAM1234	ESRRG 3'	TGGCAGTCTTATGTGCAAA	66396	TAGCT
		TTTGACAT AGATTGCCA		

			AAACGTGTA	TCTGACGGT	
			T_____		
GAM1234	KCNJ3	3'	GCAATAATGTGCAAA	9525	GCTAGA
			TTTGCACATTA	TTGC	
			AAACGTGTAAT	AACG	
			_____		
GAM1234	SDC2	3'	GCAAATTAATGTGTAAA	67132	CTAGA
			TTTGCACATTAG	TTGC	
			AAATGTGTAATT	AACG	
			A_____		
GAM1234	USP9X	3'	ATGGCCTGATGCTAATGTGTAA	16206	TAGATT
	A		TTTGCACATTAGC	GCCAT	
			AAATGTGTAATCG	CGGTA	
			TAGTC_		
GAM1234	AMOTL1	3'	GGCAAGTAATGTGCAAA	73650	G AGAT
			TTTGCACATTA CT	TGCC	
			AAACGTGTAAT GA	ACGG	
			_____		
GAM1234	BCAR3	3'	AGTAATAATGTGCAAA	13098	_____
			TTTGCACATTA	GCT	
			AAACGTGTAAT	TGA	
			AA		
GAM1234	DKFZP434B044	3'	TGACAATTAAATGTGCAGA	48930	AGCTA C
			TTTGCACATT	GATTG CA	
			AGACGTGTAA	TTAAC GT	
			A_____ A		
GAM1234	MGC3184	3'	ATGACATTTTCTAATGTGCAGA	48235	CT T C
			TTTGCACATTAG	AGA TG CAT	
			AGACGTGTAATC	TTT AC GTA	
			_____ T A		
GAM1234	PTD012	3'	ATGGCAATCTAGCTAATGTGCA	25891	
	AA		TTTGCACATTAGCTAGATTGCCAT		
			AAACGTGTAATCGATCTAACGGTA		
			_____		
GAM1235	F8	3'	ATGACTACACAGAATCTCCTGA	3723	ATGG
			TCAGGAGG	TTGTGTAGTCAT	
			AGTCCTCT	GACACATCAGTA	
			AA_____		
GAM1235	HDGF	3'	ACTGCTCCACCTCCTGA	15679	A TTGT
			TCAGGAGG TGG	GTAGT	

			AGTCCTCC ACC CGTCA		
			— CT—		
GAM1235	SLC12A7	3'	ACGAAACCACCTCCTGA 21697	A	G
			TCAGGAGG TGGTT TGT		
			AGTCCTCC ACCAA GCA		
			— A		
GAM1235	FLJ11193	3'	ACTAAGACATCCTTCCTGA 37153	—	GTTGTG
			TCAGGA GGATG TAGT		
			AGTCCT CCTAC ATCA		
			T AGA—		
GAM1235	PRO1386	3'	ATGACCATCCCCTCCTGA 48379	—	TG
			TCAGGA GGATGGT T		
			AGTCCT CCTACCA A		
			CC GT		
GAM1235	SYT13	3'	ACTTCTAACCATCCTCTGA 93448	G	TGT
			TCAG AGGATGGTTG AGT		
			AGTC TCCTACCAAT TCA		
			— CT—		
GAM1235	LOC152765	5'	ACAACCACACATCCTCTGA 80657	G	—
			TCAG AGGA TGGTTGT		
			AGTC TCCT ACCAACA		
			— ACAC		
GAM1235	LOC90410	5'	ACACACCTCCTCCTGA 62675	T	T
			TCAGGAGGA GGT GTGT		
			AGTCCTCCT CCA CACA		
			— —		
GAM1236	SCDGF-B	3'	CCTTTTCCTACCAGCAACCAA 52448	ATG	CTTT
			TTGGTTGCTG AG GAGG		
			AACCAACGAC TC TTCC		
			CA_ CTT_		
GAM1236	SCDGF-B	3'	CCTTTTCCTACCAGCAACCAA 47376	ATG	CTTT
			TTGGTTGCTG AG GAGG		
			AACCAACGAC TC TTCC		
			CA_ CTT_		
GAM1236	LOC145693	5'	CCCCACCACCAGCAGCCAA 77349	A	AGCTT A
			TTGGTTGCTG TG TG GG		
			AACCGACGAC AC AC CC		
			C C_ C		
GAM1237	A1BG	3'	GCCTTTTAATGTCTGCAC 55421	TG	AAG
			GTGCAGG TTAAG GGGC		



CACGTCT AATTT TCCG  
GT \_\_\_\_  
GAM1237 ABCC3 3' TTTGATACCTGCACTG 39144  
CAGTGCAGGTGTTAAG  
|||||||  
GTCACGTCCATAGTTT

GAM1237 ABCC3 3' AGTCCTCCCTGGTGTCTGCCCT 39150 T TG A AA  
G CAG GCAGG TTA G GGGGCT  
||| |||| | | |||||  
GTC CGTCT GGT C TCCTGA  
C GT \_CC

GAM1237 ABCC3 3' TTTGATACCTGCACTG 39164  
CAGTGCAGGTGTTAAG  
|||||||  
GTCACGTCCATAGTTT

GAM1237 ABR 3' GCCTTTTATTTTGCCTG 6575 TGTTAAG  
CAGTGCAGG AAGGGGC  
||||||| |||||  
GTCGCGTTT TTTTCCG  
TA\_\_\_\_

GAM1237 ABR 3' GCCTTTTATTTTGCCTG 41727 TGTTAAG  
CAGTGCAGG AAGGGGC  
||||||| |||||  
GTCGCGTTT TTTTCCG  
TA\_\_\_\_

GAM1237 ADAM17 3' AGTTTTTTTTTATACACTGTA 41552 \_ T  
TGCAG GTGT AAGAAGGGGCT  
|||| ||| |||||  
ATGTC CATA TTTTTTTTTGA  
A \_

GAM1237 ADAM17 3' AGTTTTTTTTTATACACTGTA 12080 \_ T  
TGCAG GTGT AAGAAGGGGCT  
|||| ||| |||||  
ATGTC CATA TTTTTTTTTGA  
A \_

GAM1237 ADAMTS5 3' AGCCTTTAAAATGCGTTTGTGT 22890 TG GG TAAGA  
T AG CA TGT AGGGGCT  
|| || | |||||  
TT GT GCG TTTCCGA  
GT TT TAAAA

GAM1237 ADAMTS8 5' GGCTTCTTCCCTCTCCTGCGC 22885 TGTTAA  
GTGCAGG GAAGGGGCT  
||||| |||||  
CGCGTCC CTTCTTCGG  
TCTCC\_

GAM1237 ADCY7 3' GGCTTCTTTGGACCTGCACTG 6642 GTTAA  
CAGTGCAGGT GAAGGGGCT  
||||||| |||||

		GTCACGTCCA TTTCTTCGG	
		GG__	
GAM1237 ADK	5'	AGTTGCTGTGGTACCTGCGCTG 6660	TT AGA G
		CAGTGCAGGTG A AG GGCT	
		GTCGCGTCCAT T TC TTGA	
		GG G__ G	
GAM1237 ADK	5'	AGTTGCTGTGGTACCTGCGCTG 22044	TT AGA G
		CAGTGCAGGTG A AG GGCT	
		GTCGCGTCCAT T TC TTGA	
		GG G__ G	
GAM1237 ADORA1	3'	GCCTGGAGCCCCTGTGTTG 5426	TG T AAGAAG
		CAG CAGG GTT GGGC	
		GTT GTCC CGA TCCG	
		GT C GG__	
GAM1237 ADPRT	3'	GTCCCTTGTTTTGTGTTG 7864	TG GTGTT G
		CAG CAG AA AAGGGGC	
		GTT GTT TT TTCCCTG	
		GT ____ G	
GAM1237 ADRBK2	3'	GGTCCCAGCAGCATCTGCCCTG 17684	T AAGAA
		CAG GCAGGTGTT GGGGCT	
		GTC CGTCTACGA CCCTGG	
		C CGA__	
GAM1237 ADSS	5'	GGCTCCTTCTTCCTCTGCAT 71760	TGTT
		GTGCAGG AAGAAGGGGCT	
		TACGTCT TTCTTCCTCGG	
		CC__	
GAM1237 AF3P21	3'	GGCCCTAAGAATGTTTTGCACT 33196	TGTTAAGAA
G		CAGTGCAGG GGGGCT	
		GTCACGTTT TCCCGG	
		TGTAAGAA_	
GAM1237 AGA	3'	AGCTGCTAATATTTAGTATTG 3441	_ AAGA G
		CAGTGC AGGTGTT AG GGCT	
		GTTATG TTTATAA TC TCGA	
		A ____ G	
GAM1237 AKAP13	3'	TTTtagtatttgcattg 89693	
		CAGTGCAGGTGTTAAGA	
		GTTACGTTTATGATTTT	
GAM1237 AKAP2	3'	GTCCCAGATGCCTGGGCTG 23267	G AAGAA
		CAGT CAGGTGTT GGGGC	

GTCG GTCCGTAG CCCTG  
 G A\_\_\_\_  
 GAM1237 AKAP2 3' TGCCAATTTTGATTTGTGTTG 23270 TG T AGG T  
 CAG CAGG GTTAAGA GGC  
 ||| ||| ||||| |||  
 GTT GTTT TAGTTTT CCG  
 GT \_ AA\_ TC  
 GAM1237 AKR1B1 3' AGTCTCTTCCAGTTTGCTTTG 7890 T GG GTTAA  
 CAG GCA T GAAGGGGCT  
 ||| ||| | |||||  
 GTT CGT G CTTCTCTGA  
 T TT AC\_\_\_\_  
 GAM1237 ALMS1 3' AGTCCCTTTTTGTATGTGTT 30672 TG GGTGT  
 AG CA TAAGAAGGGGCT  
 || || |||||  
 TT GT GTTTTTCCCTGA  
 GT AT\_\_\_\_  
 GAM1237 AMELX 5' AGTTTCAAACAGAACTTGCAC 6692 GTTAAGAA GG  
 TG CAGTGCAGGT G GCT  
 ||||| | |||  
 GTCACGTTCA C TGA  
 AAGACAAA TT  
 GAM1237 ANK3 5' AGCTTCTCCAGCATCTTTGCAT 40628 \_ AAGA  
 TG CAGTGCA GGTGTT AGGGGCT  
 ||||| ||||| |||||  
 GTTACGT CTACGA TCTTCGA  
 TT CC\_\_\_\_  
 GAM1237 ANKRA2 5' GCTTGAGAGGCTGTACTG 43526 G AAGAAGG  
 CAGTGCAGGT TT GGC  
 ||||| || |||  
 GTCATGTCCG AG TCG  
 G GT\_\_\_\_  
 GAM1237 AP1G1 3' CCTTTTCTGTGCATTG 6673 GGTGTTA  
 CAGTGCA AGAAGGGG  
 ||||| |||||  
 GTTACGT TCTTTTCC  
 G\_\_\_\_\_  
 GAM1237 AP2B1 3' AGCCTGCTCTGTGTCTGTGTTG 7055 TG TG TA AG  
 CAG CAGG T AGA GGGCT  
 ||| ||| | ||| |||||  
 GTT GTCT G TCT TCCGA  
 GT GT\_ CG  
 GAM1237 APBA1 5' CTTGGCACCAGCGCTG 69917 A  
 CAGTGC GGTGTTAAG  
 ||||| |||||  
 GTCGCG CCACGGTTC  
 A  
 GAM1237 APBA2 5' CCTCTTCTTGTGTCTG 18558 TG T  
 CAGG T AAGAAGGGG  
 |||| | |||||

			GTCT G TTCTTCTCC		
			GT_		
GAM1237	APLP2	3'	AGTCTTTGTAATGCTTGTAC 90893	AGAA	
			GTGCAGGTGTTA GGGGCT		
			CATGTTCGTAAT TTCTGA		
			GT__		
GAM1237	APPBP2	3'	AGTTTTTTTTTCAATCTGTATT 21072	GTT	
			AGTGCAGGT AAGAAGGGGCT		
			TTATGTCTA TTTTTTTTGA		
			AC_		
GAM1237	APPL	3'	TTTTTCTTCTTAGTTCTGCAT 23936	TGT	GG CT
	T		AGTGCAGG TAAGAAG G		
			TTACGTCT ATTCTTC T		
			TG_ TT TTTG		
GAM1237	APPL	3'	AGTTTTTGCCACATCTGCA 23923	TAAGA	
			TGCAGGTGT AGGGGCT		
			ACGTCTACA TTTTGA		
			CCG__		
GAM1237	APPL	3'	TTTAATTCTTGCATTG 23935	T	
			CAGTGCAGG GTTAAGA		
			GTTACGTTT TAATTTT		
			T		
GAM1237	AQP3	3'	AGCCCCTTCAGGATTTCCACTG 59587	C G AA	
			CAGTG AGGT TT GAAGGGGCT		
			GTCAC TTTA GA CTTCCCCGA		
			C G _		
GAM1237	ARF3	3'	GCCTCTCTGTGTTTGCG 8003	TG TA A	
			TGCAGG T AGA GGGGC		
			GCGTTT G TCT CTCCG		
			GT__ _		
GAM1237	ARF4L	3'	TTTTTTAGCATTTGCCTG 69819	T	
			CAG GCAGGTGTTAAGAAG		
			GTC CGTTTACGATTTTTT		
			-		
GAM1237	ARHGEF12	3'	GGTTTGACTCTAATTTTTGCAC 31001	T A AG_	
	TG		CAGTGCAGG GTTA GA GGGCT		
			GTCACGTTT TAAT CT TTTGG		
			T _ CAG		
GAM1237	ARHGEF6	3'	AGCCCTTTTTATTTTTGGTACT 68194	AGGTGTTA	
	G		CAGTGC AGAAGGGGCT		

GTCATG TTTTCCCGA  
 GTTTTTA\_  
 GAM1237 ASPH 3' AGCCTTTTTCTTTCTACACTG 50613 C TGTT \_  
 CAGTG AGG AAGAAGG GGCT  
 ||||| ||| ||||| |||||  
 GTCAC TCT TTCTTTT CCGA  
 A \_\_\_\_ T  
 GAM1237 ATF7 3' TTTGACACCTGTGCTG 22469 TG  
 CAG CAGGTGTTAAG  
 ||| |||||  
 GTC GTCCACAGTTT  
 GT  
 GAM1237 ATP11B 3' GGTCCCTCAGTGACCTGTGTTG 80317 TG GTTAA A  
 CAG CAGGT GA GGGGCT  
 ||| ||||| || |||||  
 GTT GTCCA CT CCCTGG  
 GT GTGA\_ \_  
 GAM1237 ATP2B2 3' AGTTTTTGAAACGCTTGACAC 8065 AAGA  
 GTGCAGGTGTT AGGGGCT  
 ||||| |||||  
 CACGTTCGCAA TTTTGA  
 AG\_  
 GAM1237 ATP7B 3' GGTCTTTCTGATGACGCCTGTC 3542 T \_\_\_\_ GCT  
 TG CAG GCAGGTGTTA AGAAGGG  
 ||| ||||| |||||  
 GTC TGTCCGCAGT TCTTTCT  
 \_ AG GG  
 GAM1237 ATRN 3' AGCTTCTTTTTTACATTACTG 57794 CAG T  
 CAGTG GTGT AAGAAGGGGCT  
 ||||| ||| |||||  
 GTCAT TACA TTTTCTTCGA  
 \_\_\_\_ C  
 GAM1237 ATSV 3' AGCTCTTTGCTGCTGCATCTGC 15052 G TA\_ \_  
 GGTG A TGCAGGTGT AG AAGGGGCT  
 | ||||| || |||||  
 T GCGTCTACG TC TTTCTCGA  
 G TCG G  
 GAM1237 B4GALT1 3' GGTTCTTTTTCCAGAAGGCTTT 7675 \_ G AA\_\_\_\_  
 GTATTG GCAG GT TT GAAGGGGCT  
 ||||| ||| |||||  
 TGTT CG AA TTTTCTTGG  
 T G GACCT  
 GAM1237 BCL10 3' AGCCTCTTTTTGATACT 14056  
 GGTGTTAAGAAGGGGCT  
 |||||  
 TCATAGTTTTTCTCCGA  
 GAM1237 BCL11A 3' AGCCAACCTAATTACCTGTATT 56721 TTAAGA \_  
 G CAGTGCAGGTG AGG GGCT  
 ||||| ||| |||||

			GTTATGTCCAT	TCC	CCGA	
			TAA__	AA		
GAM1237	BCL11A	3'	AGCCAACCTAATTACCTGTATT	35864	TTAAGA	__
	G		CAGTGCAGGTG	AGG	GGCT	
			GTTATGTCCAT	TCC	CCGA	
			TAA__	AA		
GAM1237	BCL11A	3'	GGCCTTTTCTATTCTGTGTA	43166	TGTTA	
			TGCAGG	AGAAGGGGCT		
			ATGTCC	TCTTTTCCGG		
			TTA__			
GAM1237	BCL11B	3'	GTTGTTTGCATTTGTACTG	43194	TAAG	G
			CAGTGCAGGTGT	AAG	GGC	
			GTCATGTTTACG	TTT	TTG	
			__	G		
GAM1237	BCL2L2	5'	GGCTCCTTGCCACCAGTGCTG	14470	TG A	TTAAG
			CAG C	GGTG	AAGGGGCT	
			GTC G	CCAC	TTCCTCGG	
			GT A	CG__		
GAM1237	CALCA	3'	GCTCTTTGGGCTGGTATTG	8213	A	GTTAAG
			CAGTGC	GGT	AAGGGGC	
			GTTATG	TCG	TTTCTCG	
			G	GG__		
GAM1237	CALD1	5'	CTCAGACATCTGATTG	52528	G	AAGAAG
			CAGT	CAGGTGTT	GGG	
			GTTA	GTCTACAG	CTC	
			-	A__		
GAM1237	CALD1	5'	CTCAGACATCTGATTG	52464	G	AAGAAG
			CAGT	CAGGTGTT	GGG	
			GTTA	GTCTACAG	CTC	
			-	A__		
GAM1237	CALM1	3'	TTTAGCGTTGTCTGCATTG	22555	__	
			CAGTGCAGG	TGTTAAG		
			GTTACGTCT	GCGATTT		
			GTT			
GAM1237	CAPN10	3'	AGCCCCAGCTGACACCTGGATT	43606	G	A AA
	G		CAGT	CAGGTGTTA	G	GGGGCT
			GTTA	GTCCACAGT	C	CCCCGA
			G	_	GA	
GAM1237	CAPN10	3'	AGCCCCGGCTGACACCTGGATT	43607	G	A AA
	G		CAGT	CAGGTGTTA	G	GGGGCT

			GTTA GTCCACAGT C CCCCCGA		
			G _ GG		
GAM1237	CAPN10	3'	AGCCCCGGCTGACACCTGGATT 43608	G	A AA
	G		CAGT CAGGTGTTA G GGGGCT		
			GTTA GTCCACAGT C CCCCCGA		
			G _ GG		
GAM1237	CASP8	3'	GGTCTTTTTATGCATTTGCATT 52926		TAA
			AGTGCAGGTGT GAAGGGGCT		
			TTACGTTTACG TTTTCTGG		
			TA_		
GAM1237	CASP8	3'	GGTCTTTTTATGCATTTGCATT 52937		TAA
			AGTGCAGGTGT GAAGGGGCT		
			TTACGTTTACG TTTTCTGG		
			TA_		
GAM1237	CASP8	3'	GGTCTTTTTATGCATTTGCATT 52952		TAA
			AGTGCAGGTGT GAAGGGGCT		
			TTACGTTTACG TTTTCTGG		
			TA_		
GAM1237	CASP8	3'	GGTCTTTTTATGCATTTGCATT 6920		TAA
			AGTGCAGGTGT GAAGGGGCT		
			TTACGTTTACG TTTTCTGG		
			TA_		
GAM1237	CAV3	3'	AGTCTTTGCGTTCACTTGTACT 52889		TTAAGA
	G		CAGTGCAGGTG AGGGGCT		
			GTCATGTTTAC TTTCTGA		
			TTGCG_		
GAM1237	CBFA2T3	3'	GGCCCCGAGCCTGGCATCTGTG 17759	TG	AGAAG_
	C		G CAGGTGTTA GGGCT		
			C GTCTACGGT CCCGG		
			GT CCGACG		
GAM1237	CBFA2T3	3'	GGCCCGTGGCTTGGCATCTGTG 17760	TG	AAG_
	T		G CAGGTGTTAAG GGGCT		
			T GTCTACGGTTC CCCGG		
			GT GGTG		
GAM1237	CBFA2T3	3'	GGTCTTTTCTCTTCTGTTCTG 17761	T	TGTTAA
			CAG GCAGG GAAGGGGCT		
			GTC TGTCT TTTTCTGG		
			T TCTC_		
GAM1237	CD53	5'	GCCCCGGATATCTGTGTT 5111	TG	AAGAA
			AG CAGGTGTT GGGGC		

TT GTCTATAG CCCCCG  
 GT G\_\_\_\_  
 GAM1237 CD69 3' AGCCCTTCATGCATTTGCACT 8354 TAA G  
 AGTGCAGGTGT GAAGGG CT  
 ||||| |||||  
 TCACGTTTACG CTTCCC GA  
 TA\_ \_  
 GAM1237 CD86 5' GGTCTCTTTTTGGAGCT 22556 G  
 GGT TTAAGAAGGGGCT  
 ||| |||||  
 TCG GGTTTTTCTCTGG  
 A  
 GAM1237 CDH2 3' CTTTGCCTCTGTATTG 8376 T TAAGAA  
 CAGTGCAGG GT GGGG  
 ||||| || ||||  
 GTTATGTCT CG TTTC  
 C \_\_\_\_\_  
 GAM1237 CDKN1A 3' GCCCCTCTGACCTGCACTG 54300 GTTA A  
 CAGTGCAGGT AGA GGGGC  
 ||||| || |||||  
 GTCACGTCCA TCT CCCCCG  
 G\_ \_  
 GAM1237 CDS2 3' AGTCTATGTGTTTAGAATTTGT 13774 TG G AAG\_  
 GTTG AG CAGGT TTAAG GGGCT  
 || ||||| |||||  
 TT GTTTA GATTT TCTGA  
 GT A GTGTA  
 GAM1237 CEACAM6 3' GCTTTAAATGTCTGCAT 10188 TG AAGAA  
 GTGCAGG TT GGGGC  
 ||||| || |||||  
 TACGTCT AA TTTCG  
 GT A\_\_\_\_  
 GAM1237 CELSR3 3' GCCCTAGGCACCTGGGCTG 7402 G AAGAA  
 CAGT CAGGTGTT GGGGC  
 ||| ||||| |||||  
 GTCG GTCCACGG TCCCG  
 G A\_\_\_\_  
 GAM1237 CHRNA3 5' GGCTCCAGGTCTGGGGTCTGCG 5608 TG A A\_  
 CTG AGTGCAGG TTA GA GGGGCT  
 ||||| ||| || |||||  
 TCGCGTCT GGT CT CCTCGG  
 GG \_ GGA  
 GAM1237 CHRNA4 3' AGCCCTGGGGTACTTCTGTGT 5612 TG T TAAGA  
 TG CAG CAGG GT AGGGGCT  
 ||| ||||| || |||||  
 GTT GTCT CA TCCCCGA  
 GT T TGGGG  
 GAM1237 CISH 3' GGCCCCGGGGGAGTGCCTGTG 25281 TG TG AAGAA\_  
 CTG CAG CAGG TT GGGGCT  
 ||| ||||| || |||||



GTC GTCC GA CCCC GG  
 GT GT GGGGGG  
 GAM1237 CISH 3' GTCTTTTCTCTTCCACTG 25282 C TGTTA  
 CAGTG AGG AGAAGGGGC  
 ||||| ||| |||||  
 GTCAC TTC TCTTTTCTG  
 C \_\_\_\_  
 GAM1237 CISH 3' GGCCCCGGGGGAGTGCCTGTG 59018 TG TG AAGAA\_  
 CTG CAG CAGG TT GGGGCT  
 ||| ||||| || |||||  
 GTC GTCC GA CCCC GG  
 GT GT GGGGGG  
 GAM1237 CISH 3' GTCTTTTCTCTTCCACTG 59019 C TGTTA  
 CAGTG AGG AGAAGGGGC  
 ||||| ||| |||||  
 GTCAC TTC TCTTTTCTG  
 C \_\_\_\_  
 GAM1237 CKTSF1B1 3' AGTCCTTTTAACTGTGCT 25362 TG GTTAA  
 AG CAGGT GAAGGGGCT  
 || ||||| |||||  
 TC GTCCA TTTTCCTGA  
 GT A\_\_\_\_  
 GAM1237 CLCN6 3' GCTTTGGGACCTTGTGCTG 41388 TG T AAGAA  
 CAG CAGG GTT GGGGC  
 ||| ||||| ||| |||||  
 GTC GTTC CAG TTTCG  
 GT \_ GG\_\_\_\_  
 GAM1237 CLCN6 3' GTCTTTTCTAGCTGATTG 41391 G G GTTA  
 CAGT CAG T AGAAGGGGC  
 ||||| ||| | |||||  
 GTTA GTC A TCTTTTCTG  
 \_ G\_\_\_\_  
 GAM1237 CLCN6 3' GCTTTGGGACCTTGTGCTG 41403 TG T AAGAA  
 CAG CAGG GTT GGGGC  
 ||| ||||| ||| |||||  
 GTC GTTC CAG TTTCG  
 GT \_ GG\_\_\_\_  
 GAM1237 CLCN6 3' GTCTTTTCTAGCTGATTG 41406 G G GTTA  
 CAGT CAG T AGAAGGGGC  
 ||||| ||| | |||||  
 GTTA GTC A TCTTTTCTG  
 \_ G\_\_\_\_  
 GAM1237 CLCN6 3' GCTTTGGGACCTTGTGCTG 7081 TG T AAGAA  
 CAG CAGG GTT GGGGC  
 ||| ||||| ||| |||||  
 GTC GTTC CAG TTTCG  
 GT \_ GG\_\_\_\_  
 GAM1237 CLCN6 3' GTCTTTTCTAGCTGATTG 7084 G G GTTA  
 CAGT CAG T AGAAGGGGC  
 ||||| ||| | |||||

GTTA GTC A TCTTTTCTG  
 \_ G \_  
 GAM1237 CLDN14 5' TCTTGAATGTCTGCTCTG 57842 T TG \_  
 CAG GCAGG T TAAGA  
 ||| |||| | ||||  
 GTC CGTCT A GTTCT  
 T GT A  
 GAM1237 CLECSF5 3' AGCTTCTTTCTTCTGCACTG 25125 TGTAA  
 CAGTGCAGG GAAGGGGCT  
 ||||| |||||  
 GTCACGTCT TTTCTTCGA  
 TC \_  
 GAM1237 CLECSF5 3' TTTTGAGTACCTGGCTG 25129 G \_  
 CAGT CAGGTG TTAAGA  
 ||| |||| |||||  
 GTCG GTCCAT AGTTTT  
 \_ G  
 GAM1237 CLN6 3' GCTTTGAGCGCCTGCATT 35408 AAGAAG  
 AGTGCAGGTGTT GGGC  
 ||||| ||||  
 TTACGTCCGCGA TTCG  
 GT \_  
 GAM1237 COIL 3' TTTTTTAGCATTTGAGTTG 67854 TG  
 CAG CAGGTGTTAAGAAG  
 || ||||| |||||  
 GTT GTTACGATTTTTT  
 GA  
 GAM1237 COL4A3 3' AGTTTTTTCTTCCTTGTCCTG 48550 \_ TGTT  
 CAGTG CAGG AAGAAGGGGCT  
 |||| ||| |||||  
 GTCAC GTTC TTCTTTTTTGA  
 T C \_  
 GAM1237 COL4A3 3' AGTTTTTTCTTCCTTGTCCTG 48562 \_ TGTT  
 CAGTG CAGG AAGAAGGGGCT  
 |||| ||| |||||  
 GTCAC GTTC TTCTTTTTTGA  
 T C \_  
 GAM1237 COL4A3 3' AGTTTTTTCTTCCTTGTCCTG 3617 \_ TGTT  
 CAGTG CAGG AAGAAGGGGCT  
 |||| ||| |||||  
 GTCAC GTTC TTCTTTTTTGA  
 T C \_  
 GAM1237 COX10 3' GGCTTTTTCAAGGCTGTATTG 7123 G G AA  
 CAGTGCAG T TT GAAGGGGCT  
 ||||| || |||||  
 GTTATGTC G AA CTTTTTCGG  
 \_ G \_  
 GAM1237 CPD 3' GGTCTCTTTTGTATCAACC 7130 \_  
 GGT GTTAAGAAGGGGCT  
 || ||||| |||||

		CCA TAGTTTTTCTCTGG		
		AC		
GAM1237 CPE	3'	GGTCTTTTTTTTAGATTTTGTG 8527	TG	TGTT_
C		G CAGG AAGAAGGGGCT		
		C GTTT TTTTTTCTGG		
		GT TAGAT		
GAM1237 CPNE6	3'	AGCCTCTCAGTGCCTGTCCTG 20093	TG	TG AA A
		CAG CAGG TT GA GGGGCT		
		GTC GTCC GA CT CTCCGA		
		CT GT _ _		
GAM1237 CRACC	3'	GGCTTCATTTATGCACTTGTGC 41010	TG	TA A
TG		CAG CAGGTGT AGA GGGGCT		
		GTC GTTCACG TTT CTTCGG		
		GT TA A		
GAM1237 CRP	3'	GGTTTTTGTTTGCTTGCACTG 71630	G	TTAAGA
		CA TGCAGGTG AGGGGCT		
		GT ACGTTCGT TTTTGG		
		G TTG_		
GAM1237 CSF3	3'	GGCCTCGGGACACCTGCCCTG 5666	T	AAGAA
		CAG GCAGGTGTT GGGGCT		
		GTC CGTCCACAG CTCCGG		
		C GG_		
GAM1237 CSNK1G3	3'	AGTTCATATTTTGTGACATCTG 15221	A	_
CATTG		TGCAGGTGTTA GAAG GGGCT		
		ACGTCTACAGT TTTT CTTGA		
		G ATA		
GAM1237 CTNS	3'	AGCCTCAGATAAGTATTTGTAC 17036	_	AGAA
T		AGTGCAGGTG TTA GGGGCT		
		TCATGTTTAT AAT CTCCGA		
		G AGA_		
GAM1237 CTPS	3'	GGCTCCTCTGTGGTGTCTGCCT 88593	T	TG _ A
G		CAG GCAGG TTA AGA GGGGCT		
		GTC CGTCT GGT TCT CCTCGG		
		_ GT G _		
GAM1237 CXCL6	3'	TTTTTGTTACTTGTATTG 11467	TT	
		CAGTGCAGGTG AAGAA		
		GTTATGTTTCAT TTTT		
		GG		
GAM1237 CYLN2	3'	GGTCTTGCCAGGCACCTGCAC 12636	AAGAA	
		GTGCAGGTGTT GGGGCT		

CACGTCCACGG TTCTGG  
ACCG\_  
GAM1237 CYP27A1 5' GGCTTTGAACCCGCCCTGCACT 5773 T TAAGAA  
G CAGTGCAGG GT GGGGCT  
||||||| || |||||  
GTCACGTCC CG TTTCGG  
\_ CCCAAG  
GAM1237 CYP8B1 3' GGTTTGGGAGATGATGCCTGCC 15268 T AGAAG\_  
TTG CAG GCAGGTGTTA GGGCT  
||| ||||| |||||  
GTT CGTCCGTAGT TTTGG  
C AGAGGG  
GAM1237 DBCCR1 3' GCCTCAGGTGCTGTATTG 27514 G TG AAGAA  
CAGTGCA G TT GGGGC  
||||||| | || |||||  
GTTATGT C GG CTCCG  
\_ GT A\_\_\_\_  
GAM1237 DDEF2 3' AGTTTTTTTTTTTTTTGGCATT 13950 AGGTGTT  
G CAGTGC AAGAAGGGGCT  
||||| |||||  
GTTACG TTTTTTTTGA  
GTTTTT\_  
GAM1237 DDX38 5' GCTCCTTGAGCCTGTCTG 25751 T GTTAAG  
CAG GCAGGT AAGGGGC  
||| ||||| |||||  
GTC TGTCCG TTCCTCG  
\_ AG\_\_\_\_  
GAM1237 DGCR2 3' GTCTGGGAGCACCTGTCTG 17629 T AAGAAG  
CAG GCAGGTGTT GGGC  
||| ||||| |||||  
GTC TGTCCACGA TCTG  
\_ GGG\_\_\_\_  
GAM1237 DLEU1 3' GCTCTTTCTCTTTGTATT 19697 TGTTA  
AGTGCAGG AGAAGGGGC  
||||||| |||||  
TTATGTTT TCTTTCTCG  
C\_\_\_\_  
GAM1237 DLG4 5' AGCTTCTTTTTGAGCTGC 7249 GTG  
GCAG TTAAGAAGGGGCT  
||| |||||  
CGTC AGTTTTTCTTCGA  
G\_\_\_\_  
GAM1237 DLG5 3' GGCTTTTTTTTTTTTGCCT 82919 TGTT  
AGTGCAGG AAGAAGGGGCT  
||||||| |||||  
TCACGTTT TTTTTTTTCGG  
TT\_\_\_\_  
GAM1237 DLST 3' GGTCTTTTCTTGCGTTCCTGC 8646 \_\_\_\_  
GCAGG TGTTAAGAAGGGGCT  
||||| |||||

			CGTCC GCGGTTCTTTTCTGG		
			TT		
GAM1237 DMRT1	3'	TTTGTTAATATTTTGCATTG	41702	—	G
		CAGTGCAGG TGTTAA AAG			
		GTTACGTTT ATAATT TTT			
		T G			
GAM1237 DPH2L2	3'	GGTCTAGCTAGACCTGCACTG	7281	G A	AAG
		CAGTGCAGGT TTA G GGGCT			
		GTCACGTCCA GAT C TCTGG			
		— _GA_			
GAM1237 DPYSL3	3'	GCCTCTTTCTTAGTGTT	7317	TG	—
		GG TTAAGAAGG GGC			
		TT GATTCTTTC CCG			
		GT T			
GAM1237 DSCR5	5'	GGCTCCCCAGTCGCGCTTGCG	33152	AAGAA_	
C		GTGCAGGTGTT GGGGCT			
		CGCGTTCGCGG CCTCGG			
		CTGACC			
GAM1237 DVL1	3'	GGCCCCACGTGTCTGTGCTG	59336	TG TG	TAAGAA
		CAG CAGG T GGGGCT			
		GTC GTCT G CCCC GG			
		GT GT CAC_			
GAM1237 DVL3	3'	TTTTGGCACCTGCCTG	15378	T	
		CAG GCAGGTGTTAAGA			
		GTC CGTCCACGGTTTT			
		—			
GAM1237 EIF1A	3'	GGTTTTTTTGATGTTACCTGAC	88603	G	TTAA_
TG		CAGT CAGGTG GAAGGGGCT			
		GTCA GTCCAT TTTTTTTGG			
		— TGTAG			
GAM1237 EIF2AK3	3'	TCCCCCTGTGTGGTAACTGTAT	16712	G TT	AGA CT
TG		CAGTGCAG TG A AGGGG			
		GTTATGTC AT T TCCCC			
		A GG GTG CTG			
GAM1237 EIF2B2	3'	AGCCTCTTAGTGACCTG	26452	GT	AG
		CAGGT TA AAGGGGCT			
		GTCCA GT TTCTCCGA			
		— GA			
GAM1237 EIF2B5	3'	GGCTCTTTCTGCTGCTTGTAT	61530	TTA	
		GTGCAGGTG AGAAGGGGCT			

TATGTTTCGT TCTTTCTCGG  
 CG\_  
 GAM1237 ELMO3 5' GCCCCTGGCCGCTGTGCTG 45252 TG GT AAGA  
 CAG CAG GTT AGGGGC  
 ||| ||| ||| |||||  
 GTC GTC CGG TCCCCG  
 GT GC \_\_\_\_  
 GAM1237 EN1 3' GGTCCCTTCTGTCGGTCTGTCT 7453 T TGTTA  
 G CAG GCAGG AGAAGGGGCT  
 ||| ||||| |||||  
 GTC TGTCT TCTTCCCTGG  
 \_ GGCTG  
 GAM1237 ENC1 3' CTTGACACCTGTCTTG 13281 T  
 CAG GCAGGTGTTAAG  
 ||| |||||  
 GTT TGTCCACAGTTC  
 C  
 GAM1237 ENPP2 3' TGCCACATTTAGTCCTGTACTG 20602 TGT AAGG T  
 CAGTGCAGG TAAG GGC  
 ||||| ||| |||  
 GTCATGTCC ATTT CCG  
 TG\_ ACA\_ TT  
 GAM1237 ENPP2 3' TTTGATATTTGCATTG 20603  
 CAGTGCAGGTGTTAAG  
 |||||  
 GTTACGTTTATAGTTT  
  
 GAM1237 EPB41L2 3' AGTTCTTTCTTTTTGTTGTTG 7480 T GTGTT  
 G GCAG AAGAAGGGGCT  
 ||||| |||||  
 G TGTT TTCTTTCTTGA  
 T GTTT\_  
 GAM1237 EPHA1 5' AGTCCCTTGCAACCTGGCGCTG 17859 \_ \_ TAAG  
 CAGTGC AGGT GT AAGGGGCT  
 ||||| ||||| ||| |||||  
 GTCGCG TCCA CG TTCCCTGA  
 G A \_\_\_\_  
 GAM1237 EPHA2 3' GGCCTTTGCAAGATGCTTG 15407 AAGA  
 CAGGTGTT AGGGGCT  
 ||||| |||||  
 GTTCGTAG TTTCCGG  
 AACG  
 GAM1237 EPS15 3' AGCTTTTGCCCTGCCTGTGCT 8793 TG GTTA A\_  
 AG CAGGT AG AGGGGCT  
 || ||||| || |||||  
 TC GTCCG TC TTTTCGA  
 GT \_\_\_\_ CG  
 GAM1237 ERBB2IP 3' AGCCTCTTTGATTTTGT 37982 T AA  
 GCAGG GTT GAAGGGGCT  
 ||||| ||| |||||

			TGTTT TAG TTTCTCCGA		
			T _		
GAM1237 EVC	3'	CCTGAATGCCTGGCTG	27294	G	AAGAAG
		CAGT CAGGTGTT	GGG		
		GTCG GTCCGTAA	TCC		
		_ G _			
GAM1237 EXTL1	5'	GCCCTGGCCTCTGCACTG	15494	T	AAGAA
		CAGTGCAGG GTT	GGGGC		
		GTCACGTCT CGG	TCCCG		
		C _			
GAM1237 EXTL3	3'	GCTCCTTTGTTCTGTATT	7533		TGTTAA
		AGTGCAGG GAAGGGGC			
		TTATGTCT TTTCTCG			
		TG _			
GAM1237 FDX1	5'	GGCCCTCGGGCGTCTGCGC	60343	GT	AAGAA
		GTGCAG GTT	GGGGCT		
		CGCGTC CGG	TCCCGG		
		TG GC _			
GAM1237 FECH	3'	GGTCATCTTGGTATTTGTGCTG	3757	TG	TT AGG
		CAG CAGGTG AAGA	GGCT		
		GTC GTTTAT TTCT	CTGG		
		GT GG A _			
GAM1237 FEZ1	5'	GGCTCTCCGCTGCGCTGCGCTG	42577	G	TA AA _
		CAGTGCAG TGT AG	GGGGCT		
		GTCGCGTC GCG TC	TCTCGG		
		_ _ GCC			
GAM1237 FEZ1	5'	GGCTCTCCGCTGCGCTGCGCTG	17531	G	TA AA _
		CAGTGCAG TGT AG	GGGGCT		
		GTCGCGTC GCG TC	TCTCGG		
		_ _ GCC			
GAM1237 FGF5	3'	AGCTTCAGCTATACTTACACTG	15530	C	TA AA
		CAGTG AGGTGT AG	GGGGCT		
		GTCAC TTCATA TC	CTTCGA		
		A _ GA			
GAM1237 FGF5	3'	AGCTTCAGCTATACTTACACTG	52476	C	TA AA
		CAGTG AGGTGT AG	GGGGCT		
		GTCAC TTCATA TC	CTTCGA		
		A _ GA			
GAM1237 FGFR3	3'	GGTCTCTTCTTGGGGCCCACTG	3775	G CA	G
		CA TG GGT TTAAGAAGGGGCT			

			GT AC CCG GGTTCTTCTCTGG		
			G _ G		
GAM1237 FKBP1A	3'	AGCCCCCTTCTCACCCCTTTGCT 5857		C T TA	
G		CAGTG AGG GT AGAAGGGGCT			
		GTCGT TCC CA TCTTCCCCGA			
		T C C_			
GAM1237 FLRT3	3'	AGTATTTTTTTAGTAATTTGTAC 25215		GT_ GG	
TG		CAGTGCAGGT TAAGAAG GCT			
		GTCATGTTTA ATTTTTT TGA			
		ATG A_			
GAM1237 FMOD	3'	GGCTCTTCAGAAAGCATCTGCA 8931		AAGA_	
T		GTGCAGGTGTT AGGGGCT			
		TACGTCTACGA TTCTCGG			
		AAGAC			
GAM1237 FMR1	3'	AGCTTTTTTTTTTAATTTTGTG 8936		T TGTT_	
TG		CAG GCAGG AAGAAGGGGCT			
		GTC TGTT TTTTTTTCGA			
		_ TAATT			
GAM1237 FMR1	3'	AGTCTCTTTTTACAAGGCTGTA 8937		G_ T	
TT		AGTGCAG TGT AAGAAGGGGCT			
		TTATGTC ACA TTTTCTCTGA			
		GGA _			
GAM1237 FNTA	3'	GGTCCTTCCCTTTGCCTGTGGT 8950		G TT A_	
G		CA TGCAGGTG AAG AGGGGCT			
		GT GTGTCCGT TTC TTCCTGG			
		G _ CC			
GAM1237 FNTB	3'	GGTCCTGGCAGTGCCTCTGCTG 8956		C TG AAGAA	
		CAGTG AGG TT GGGGCT			
		GTCGT TCC GA TCCTGG			
		C GT CGG_			
GAM1237 FPGS	3'	GCTTCCCACACCTGCCTG 17087		T TAAGAA	
		CAG GCAGGTGT GGGGC			
		GTC CGTCCACA CTTCG			
		_ CC_			
GAM1237 FUT3	3'	GGCCGGCATGGTGCCTGGGCTG 3803		G TG AGAAGG	
		CAGT CAGG TTA GGCT			
		GTCG GTCC GGT CCGG			
		G GT ACGG_			
GAM1237 FUT6	5'	AGTTCCTCAACATGCCTGCATT 3807		TAA A	
		AGTGCAGGTGT GA GGGGCT			



			TTACGTCCGTA CT CCTTGA		
			CAA _		
GAM1237 FZD8	3'	GCCCCCTTTTCCTCCATTG	49037	C	TGTTA
		CAGTG AGG	AGAAGGGGC		
		GTTAC TCC	TTTTCCCCG		
		C _			
GAM1237 GAB2	3'	AGTCCTTGATCTGCCTGTCTG	54442	T	GTTA _
		CAG GCAGGT	AGA AGGGGCT		
		GTC TGTCCG	TCT TTCCTGA		
		_ _	AG		
GAM1237 GAB2	3'	AGTCCTTGATCTGCCTGTCTG	24485	T	GTTA _
		CAG GCAGGT	AGA AGGGGCT		
		GTC TGTCCG	TCT TTCCTGA		
		_ _	AG		
GAM1237 GAK	3'	GCCCTGGTGTGTTGCAC	17911	TG	AAGAA
		GTGCAGG TT	GGGGC		
		CACGTTT GG	TCCCG		
		GT _			
GAM1237 GARP	3'	GGTCTGGAAGCATCCTGTGCTG	18599	TG	_ AAGAAG
		CAG CAGG TGTT	GGGCT		
		GTC GTCC ACGA	TCTGG		
		GT T AGG_			
GAM1237 GATA3	3'	AGCTCACTGTGGTGTCTGTGTT	9002	TG	TG AGAAG
		AG CAGG TTA	GGGCT		
		TT GTCT GGT	CTCGA		
		GT GT GTCA_			
GAM1237 GATA3	3'	AGTCCCTTTCGACTTGCA	9003		GTAA
		AGTGCAGGT	GAAGGGGCT		
		TTACGTTCA	TTCCCTGA		
		GC_			
GAM1237 GATA6	3'	GGTCCAGACAGTGGCGACTGCG	17918	G	AGAAG_
CTG		CAGTGCAG TGTTA	GGGCT		
		GTCGCGTC GCGGT	CCTGG		
		A GACAGA			
GAM1237 GBAS	3'	GTTTCACATCATGTATTG	7633	_	TAAGAA GG
		CAGTGCA GGTGT	G GC		
		GTTATGT CTACA	C TG		
		A _	TT		
GAM1237 GDI2	3'	GGCTCCAAATGATTTCTGTACT	7655	T	AGAA
G		CAGTGCAGG GTTA	GGGGCT		

			GTCATGTCT TAGT CCTCGG		
			T AAA_		
GAM1237	GJA1	3'	AGCAACTTTGATGTTTGC	3899	TG AA GG
			AGTGCAGG TT GAAG GCT		
			TCACGTTT AG TTTC CGA		
			GT _ AA		
GAM1237	GJB1	3'	TCTTAACCCTGTGCTG	59974	TG T
			CAG CAGG GTTAAGA		
			GTC GTCC CAATTCT		
			GT _		
GAM1237	GLDC	3'	GGTTTTTTTTTTTAAATCTGC	64239	GTT_
	ATT		AGTGCAGGT AAGAAGGGGCT		
			TTACGTCTA TTTTTTTTGG		
			ATTTT		
GAM1237	GLP1R	3'	AGTTTCTTTTTGAGGGGCTTTG	9027	T AGGTG GG
			CAG GC TTAAGAAG GCT		
			GTT CG AGTTTTTC TGA		
			T GGG_ TT		
GAM1237	GM2A	3'	GGTCCCTTTTCCTCTGTTTTG	67781	T TGTTA
			CAG GCAGG AGAAGGGGCT		
			GTT TGTCT TTTCCCTGG		
			T CC_		
GAM1237	GNAI1	3'	TTTAAATATTGGCTG	9057	G
			CAGT CAGGTGTTAAGA		
			GTCG GTTTATAATTTT		
			-		
GAM1237	GPC4	3'	GGTCCCTTCTTGGCACGTAAC	7555	GCAG
			GT GTGTTAAGAAGGGGCT		
			CA CACGGTTCTTCCCTGG		
			ATG_		
GAM1237	GPRK6	3'	CCTTCAGCACTGTGCTG	9109	TG G AA
			CAG CAG TGTT GAAGG		
			GTC GTC ACGA CTTCC		
			GT _ _		
GAM1237	GRIK5	3'	GGCTCTTAAGACCCACTATGTG	9136	TG _ TTAAGA
	CTG		CAG CA GGTG AGGGGCT		
			GTC GT TCAC TTCTCGG		
			GT A CCAGAA		
GAM1237	GRIN2A	3'	AGTTAAGAATGCATCTGCACTG	5893	TAAGAAGG
			CAGTGCAGGTGT GGCT		

			GTCACGTCTACG	TTGA		
			TAAGAA__			
GAM1237	GRLF1	3'	GGCTGGAAGGTGACATCTGTGT	78558	TG	AGAAGG
		T	AG CAGGTGTTA	GGCT		
			TT GTCTACAGT	TCGG		
			GT	GGAAGG		
GAM1237	GSBS	3'	GGCTCCTTCTTGTTTTTGC	91095	TG	
			GCAGG TTAAGAAGGGGCT			
			CGTTT GGTTCTTCCTCGG			
			TT			
GAM1237	GUCY1A3	5'	TCTCCGCGCCTGTCTG	63494	T	TAAGAA
			CAG GCAGGTGT	GGGG		
			GTC TGTCCGCG	CTCT		
			- C__			
GAM1237	GYPB	3'	GGCCTGCATGCTGCCTGTATTG	9159		_ TAAGAAG
			CAGTGCAGGT GT	GGGCT		
			GTTATGTCCG CG	TCCGG		
			T TACG__			
GAM1237	H3F3B	3'	AGTTCTTTTTCTTGTGGCATT	18020		
		GTATT	GCAGGTGTTA	AGAAGGGGCT		
			TGTTTACGGT	TTTTTCTTGA		
			GTTC			
GAM1237	HCFC1	3'	GGCCTGGGCAGCGCCTGTGC	70997	TG	AAGAAG
			G CAGGTGTT	GGGCT		
			C GTCCGCGA	TCCGG		
			GT	CGGG__		
GAM1237	HDAC1	3'	GCTCAGGGCAGCTGTGCTG	17115	TG G	AAGAAG
			CAG CAG TGTT	GGGC		
			GTC GTC ACGG	CTCG		
			GT G	GA__		
GAM1237	HLF	3'	AGTTCTTTTTGTACAGTATT	9216	AGG	_
			AGTGC TGT TAAGAAGGGGCT			
			TTATG ACA GTTTTTTCTTGA			
			__ T			
GAM1237	HMGA2	3'	GGCCTTTTAGAAACCTCATTG	13002	C	GTTAAG
			CAGTG AGGT	AAGGGGCT		
			GTTAC TCCA	TTTTCCGG		
			_ AAGA__			
GAM1237	HMGB2	3'	TTTTTTTAATTTCTGTGT	9230	TG T	
			G CAGG GTTAAGAAGG			

T GTCT TAATTTTTTT  
 GT T  
 GAM1237 HMGCR 3' AGCCTCTTAGTGATTGTGTCTG 5970 T\_\_\_ AG  
 CATTG TGCAGG GTTA AAGGGGCT  
 ||||| ||| |||||  
 ACGTCT TAGT TTCTCCGA  
 GTGT GA  
 GAM1237 HNF4G 3' GCTTCTTCATTGGTGCT 14701 TG \_  
 GG TTAA GAAGGGGC  
 || ||| |||||  
 TC GGTT CTTCTTCG  
 GT A  
 GAM1237 HNF4G 5' GGCCTCGCCAGCCTGCGCTG 14702 GTTAAGAA  
 CAGTGCAGGT GGGGCT  
 ||||| |||||  
 GTCGCGTCCG CTCCGG  
 ACCCG\_\_\_  
 GAM1237 HNRPD 3' GGCCTCTTTTTTGCTGCTGTTT 18428 T GT T  
 TG CAG GCAG GT AAGAAGGGGCT  
 ||| ||| || |||||  
 GTT TGTC CG TTTTCTCCGG  
 T GT T  
 GAM1237 HNRPK 3' TCTTGGCATTGTATTG 48359  
 CAGTGCAGGTGTTAAGA  
 |||||  
 GTTATGTTTACGGTTCT  
 GAM1237 HNRPK 3' TCTTGGCATTGTATTG 9249  
 CAGTGCAGGTGTTAAGA  
 |||||  
 GTTATGTTTACGGTTCT  
 GAM1237 HNRPM 3' GGTTCATTGACTGTTTGCAT 19917 GG\_ AA  
 TG CAGTGCA T GTTAAG GGGGCT  
 ||||| | ||||| |||||  
 GTTACGT G CAGTTT CCTTGG  
 TTT A\_  
 GAM1237 HOXA4 3' TTTTCTTACTTGCACT 9252 TTA  
 AGTGCAGGTG AGAAGGG  
 ||||| |||||  
 TTACGTTTCT TCTTTT  
 \_\_\_\_\_  
 GAM1237 HOXB3 5' GGCTTTTTTTTCTCAGCATCTG 9261 T \_\_\_\_  
 CTTTG GCAGGTGTT AAGAAGGGGCT  
 ||||| |||||  
 CGTCTACGA TTTTTTTCGG  
 T CTC  
 GAM1237 HOXC10 3' TCTCGTATTTGTACTG 61271 TTAAGAA  
 CAGTGCAGGTG GGGG  
 ||||| |||

GTCATGTTTAT CTCT  
 G\_\_\_\_\_  
 GAM1237 HOXC6 5' AGTTTTTTTTGTCTGTCCTG 15699 TG TGT  
 CAG CAGG TAAGAAGGGGCT  
 ||| ||| |||||  
 GTC GTCT GTTTTTTTTGA  
 CT \_\_\_\_  
 GAM1237 HRB 3' AGTCTTTAAAAAGCCTGCATTG 15704 GTTAAGA  
 CAGTGCAGGT AGGGGCT  
 ||||| |||||  
 GTTACGTCCG TTTCTGA  
 AAAAA\_  
 GAM1237 HS3ST3A1 3' TTTAATATTTGTGCTG 20153 TG  
 CAG CAGGTGTTAAG  
 ||| |||||  
 GTC GTTTATAATTT  
 GT  
 GAM1237 HSPA8 5' AGTTTTTTTTTTTTTTTGTG 21695 TG TGTT\_  
 C G CAGG AAGAAGGGGCT  
 | ||| |||||  
 C GTTT TTTTTTTTGA  
 GT TTTT  
 GAM1237 HSPA8 5' GTCTCTTTTGGTTTC 21696 TG  
 GG TTAAGAAGGGGC  
 || |||||  
 CT GGTCTTCTCTG  
 TT  
 GAM1237 HUNK 3' AGCTCTTGACCTAGCATCTGAC 27440 G AGA\_  
 TG CAGT CAGGTGTTA AGGGGCT  
 ||| ||||| |||||  
 GTCA GTCTACGAT TTCTCGA  
 \_ CCAG  
 GAM1237 IDH3A 3' GGCCTTTTCTTAACAAAATCTG 18645 \_\_\_\_  
 T GCAGG TGTTAAGAAGGGGCT  
 |||| |||||  
 TGTCT ACAATTCTTTCCGG  
 AAA  
 GAM1237 IDS 5' GGCCCGGGCGGCGGCTGTGTTG 3977 TG G AAGAAG  
 CAG CAG TGTT GGGCT  
 ||| ||| ||| |||||  
 GTT GTC GCGG CCGG  
 GT G CGGG\_  
 GAM1237 IGFBP5 5' GGCCCTTTATCCCTGCACT 5193 TG TAA  
 AGTGCAGG T GAAGGGGCT  
 ||||| | |||||  
 TCACGTCC A TTTCCCGG  
 CT \_\_\_\_  
 GAM1237 IL17E 3' GGTCCCTTTTGGGAAACCTG 42965 GT\_  
 CAGGT TAAGAAGGGGCT  
 |||| |||||

			GTCCA	GTTTTTCCCTGG		
			AAGG			
GAM1237	IL1RN	3'	GTTCTTTCTTCCTCTGCTG	5144	C	TGTT
			CAGTG AGG	AAGAAGGGGC		
			GTCGT TCC	TTCTTTCTTG		
			C	_____		
GAM1237	IL2RB	3'	AGCCCTCAGGCACCTGCACT	6068		AAGAA
			AGTGCAGGTGTT	GGGGCT		
			TCACGTCCACGG	TCCCGA		
			AC	_____		
GAM1237	IL2RB	3'	GCCTCAGAGTGCTTGGCTG	6072	G	TG AAGAA
			CAGT CAGG TT	GGGGC		
			GTCG GTTC GA	CTCCG		
			-	GT GA_____		
GAM1237	IMPDH1	3'	GCTCTCAGGACCTGCGCTG	6083		G AAGAA
			CAGTGCAGGT TT	GGGGC		
			GTCGCGTCCA GA	TCTCG		
			G	C_____		
GAM1237	INHBB	3'	TTTTAATGTTTGCACTG	9347		TG
			CAGTGCAGG TTAAGA			
			GTCACGTTT	AATTTT		
			GT			
GAM1237	INHBC	5'	CCCTGAGTCTGTATTG	18654		GTTAAGAA
			CAGTGCAGGT	GGGG		
			GTTATGTCTG	TCCC		
			AG	_____		
GAM1237	IRF2	3'	GGCTTCTTGGCTTTGTTTGTG	9356	T	T GGGCT
			CAG GCAGG GTTAAGAAG			
			GTT TGTTT CGGTTCTTC			
			T	-	GG	
GAM1237	IRTA1	3'	AGCCCCTTCACTTCTGCCTGCA	48416		GTAA_
	C		GTGCAGGT	GAAGGGGCT		
			CACGTCCG	CTTCCCCGA		
			TCTTCA			
GAM1237	ISL1	3'	GTCTCTTGGCCTGTCCTG	9367	TG	GTTAAG
			CAG CAGGT	AAGGGGC		
			GTC GTCCG	TTCTCTG		
			CT	G_____		
GAM1237	ITGA6	3'	TTTTTTAGACCTGTGTT	3990	TG	G
			AG CAGGT TTAAGAAG			

			TT GTCCA GATTTTTT		
			GT _		
GAM1237	ITPKB	3'	GGCCTCTTATTGGCAACTTG 9434	G _ _	G
	GCTG		GT CAGGT GTTAA AAGGGGCT		
			CG GTTCA CGGTT TTCTCCGG		
			_ TAA A		
GAM1237	ITPKB	3'	GGCTTGGAGGTGGTGGTTTGCAC 9435	TG	AGAAG
	TG		CAGTGCAGG TTA GGGCT		
			GTCACGTTT GGT TTCGG		
			GT GGAGG		
GAM1237	ITPR2	5'	GGCTTCTCTGGGCGCCTGGGCT 9450	G	TA A
	G		CAGT CAGGTGT AGA GGGGCT		
			GTCG GTCCGCG TCT CTTCGG		
			G GG _		
GAM1237	JAM3	3'	AGTTTCTTCTTAAAGGCTCTGC 51420	_ G_	GG
			GCAG GT TTAAGAAG GCT		
			CGTC CG AATTCTTC TGA		
			T GA TT		
GAM1237	JPH2	5'	GCTCTTTCAGCCTCTGC 94448	T	AA
			GCAGG GTT GAAGGGGC		
			CGTCT CGA CTTTCTCG		
			C _		
GAM1237	JPH3	3'	GGCCTTTTTCTGTGTGAGATCT 40308	G G _ _	
	GTGCTG		CAGGT TTA AGAAGG GGCT		
			GTCTA AGT TCTTTT CCGG		
			T G GTG T		
GAM1237	JPH3	3'	TTTTCACATCTCTGTACTG 40310	_	T
			CAGTGCAG GTGT AAGA		
			GTCATGTC TACA TTTT		
			TC C		
GAM1237	JRK	3'	AGCCTTTTTTCTATTTTCATTG 86521	C	TTA
			CAGTG AGGTG AGAAGGGGCT		
			GTTAC TTTAT TTTTTTCCGA		
			_ C_		
GAM1237	JRKL	3'	TTTTTTTTTTAGTGTTTTACT 13664	C TG	CT
	G		CAGTG AGG TTAAGAAGGGG		
			GTCAT TTT GATTTTTTTTT		
			T GT TT		
GAM1237	KCNN3	5'	GGCTTTGGGGTGGGGGCTTGTG 9561	TG	G AAGAA_
	CTG		CAG CAGGT TT GGGGCT		

		GTC GTTCG GG TTTCCG	
		GT G GTGGGG	
GAM1237 KCNS2	3'	GCTTCCAACTTGATTG 68310	GTTAAGAA
		CAGTGCAGGT GGGGC	
		GTTATGTTCA CTTCG	
		AAC_____	
GAM1237 KCNS2	3'	GGCCAGGCTTTGATATCTGT 68311	AAGG
		GCAGGTGTTAAG GGCT	
		TGTCTATAGTTT CCGG	
		CGGA	
GAM1237 KHK	3'	AGCTCTTCGGGGCCCTGCGTTG 4029	T AA G
		CAGTGCAGG GTT GAAGGG CT	
		GTTGCGTCC CGG CTTCTC GA	
		GG	
GAM1237 KHK	3'	AGCTCTTCGGGGCCCTGCGTTG 21399	T AA G
		CAGTGCAGG GTT GAAGGG CT	
		GTTGCGTCC CGG CTTCTC GA	
		GG	
GAM1237 KIF1B	3'	CCTCTGATGTCTGTGCTG 30588	TG TG AAGA
		CAG CAGG TT AGGGG	
		GTC GTCT AG TCTCC	
		GT GT _____	
GAM1237 KIF5C	3'	GCTTTATGTATCTGTAC 15737	TTAAGAA
		GTGCAGGTG GGGGC	
		CATGTCTAT TTTCG	
		GTA_____	
GAM1237 KLHL1	5'	GCTCTTTCTCTCTGCGCT 40489	TGTTA
		AGTGCAGG AGAAGGGGC	
		TCGCGTCT TCTTTCTCG	
		C_____	
GAM1237 KPNA1	3'	GGCTTTTCTAGCCAGATTTGC 80321	_____ A
ATT		GTGCAGGT GTTA GAAGGGGCT	
		TACGTTTA CGAT CTTTTTCGG	
		GAC _	
GAM1237 KRT1	3'	GCTCTTTCTTTTCTGC 20389	TGTT
		GCAGG AAGAAGGGGC	
		CGTCT TTCTTTCTCG	
		T_____	
GAM1237 KRTHA8	3'	GCTCAGAATATCTGGATTG 22259	G AAGAAG
		CAGT CAGGTGTT GGGC	



			GTTA GTCTATAA	CTCG	
			G GA_____		
GAM1237	LAIR1	5'	TTCTGTCCTTGCATTG	9663	TGTTAA A
			CAGTGCAGG	GA GGGG	
			GTTACGTTC	CT TCTT	
			_____ G		
GAM1237	LAIR1	5'	TTCTGTCCTTGCATTG	41358	TGTTAA A
			CAGTGCAGG	GA GGGG	
			GTTACGTTC	CT TCTT	
			_____ G		
GAM1237	LAIR1	5'	TTCTGTCCTTGCATTG	41360	TGTTAA A
			CAGTGCAGG	GA GGGG	
			GTTACGTTC	CT TCTT	
			_____ G		
GAM1237	LAMP1	3'	GTTTCTTCATTCTTTACTG	18706	C TGTTAA GG
			CAGTG AGG	GAAG GC	
			GTCAT TCT	CTTC TG	
			T TA_____ TT		
GAM1237	LANCL1	3'	AGTCCTTTATTATTTACACTG	20208	C TTAAG
			CAGTG AGGTG	AAGGGGCT	
			GTCAC TTTAT	TTTCCTGA	
			A TA_____		
GAM1237	LASS1	3'	GCCCCTGCCGCGCTGCGC	41198	TTAAGA
			GTGCAGGTG	AGGGGC	
			CGCGTCCGC	TCCCCG	
			CG_____		
GAM1237	LDB3	3'	AGCTCCTTTTTGAATTGT	76404	GGTG
			GCA TTAAGAAGGGGCT		
			TGT AGTTTTTCCTCGA		
			TA_____		
GAM1237	LEF1	5'	GGCCTCGGGGCGGGCGCCTGCG	32758	AAGAA_
			TGCAGGTGTT	GGGGCT	
			GCGTCCGCGG	CTCCGG	
			GCGGGG		
GAM1237	LENG4	3'	GGTTGGACCTTAACATCTGCAT	44169	AAGG
	TG		CAGTGCAGGTGTTAAG	GGCT	
			GTTACGTCTACAATTC	TTGG	
			CAGG		
GAM1237	LLGL1	3'	AGCCCTCCTGCAGGCATTTGGC	66876	G AAGAA_
	TG		CAGT CAGGTGTT	GGGGCT	

GTCG GTTTACGG TCCCGA  
 \_ ACGTCC  
 GAM1237 LMCD1 3' AGTTCCTTTTCTTTCTGT 27426 TGTTA  
 GCAGG AGAAGGGGCT  
 |||| |||||  
 TGTCT TTTTCCTTGA  
 TTC\_\_  
 GAM1237 LPIN2 3' GGCTCTCCTGGCCCTGTGTTG 27710 TG T A AG  
 CAG CAGG GTTA GA GGGCT  
 || |||| || ||||  
 GTT GTCC CGGT CT CTCGG  
 GT \_ C \_\_  
 GAM1237 LU 3' GGTCCCCCACCCTGACGTCTTG 18753 \_ AGAA\_\_  
 C GCAGG TGTTA GGGGCT  
 |||| |||| ||||  
 CGTTC GCAGT CCCTGG  
 T CCACCC  
 GAM1237 LUZP1 3' AGTCCCTTGAATATCTGCCTG 53295 T AAG  
 CAG GCAGGTGTT AAGGGGCT  
 || ||||| |||||  
 GTC CGTCTATAA TTCCCTGA  
 \_ G\_\_  
 GAM1237 LY9 3' GGCTCCTTCTTGAGCCT 71685 G  
 AGGT TTAAGAAGGGGCT  
 |||| |||||  
 TCCG GGTTCCTCCTCGG  
 A  
 GAM1237 LZTFL1 3' GGTTCCTTCTGTTTGACATTT 39754 G \_ GG\_  
 GTGTT CAGGTGTTA AGAAG G CT  
 ||||| |||| ||  
 GTTTACAGT TCTTC T GG  
 T TTG TT T  
 GAM1237 LZTFL1 3' TTTTCACTATATTTGTATTG 39763 TAA  
 CAGTGCAGGTGT GAAGG  
 ||||| ||||  
 GTTATGTTTATA CTTTT  
 TCA  
 GAM1237 LZTR1 3' CTTAGCAGACTTGCGCTG 22237 \_  
 CAGTGCAGGT GTTAAG  
 ||||| ||||  
 GTCGCGTTCA CGATTC  
 GA  
 GAM1237 MAD2L1 3' GCAATGGATATTTGTACTG 9875 AAGAAGGG  
 CAGTGCAGGTGTT GC  
 ||||| ||  
 GTCATGTTTATAG CG  
 GTAA\_\_  
 GAM1237 MADH9 3' AGCAGGACTTTGGTGCCTGTGC 19750 TG TG AAGGG  
 T AG CAGG TTAAG GCT  
 || |||| |||| ||

			TC GTCC GGTTT CGA		
			GT GT CAGGA		
GAM1237	MAGEL2	3'	TTTTGGCATCTGTGTT 38820 TG		
			AG CAGGTGTTAAGA		
			TT GTCTACGGTTTT		
			GT		
GAM1237	MAP3K13	3'	TTTAAACACTTTGTACTG 16358 _		
			CAGTGCAG GTGTTAAGA		
			GTCATGTT CACAATTTT		
			T		
GAM1237	MAP3K14	3'	AGCCCCTTCAGGCCAGCACTG 14206 A T AA		
			CAGTGC GG GTT GAAGGGGCT		
			GTCACG CC CGG CTTCCCCGA		
			A _ A_		
GAM1237	MAP3K7IP1	3'	AGCCTTTTCCTAACATCTGCCT 20375 T A		
	G		CAG GCAGGTGTTA GAAGGGGCT		
			GTC CGTCTACAAT CTTTCCGA		
			_ C		
GAM1237	MAPK14	3'	AGCCCCTAGTGCTATTCTGTGT 7156 TG TGTTAAGA		
	TG		CAG CAGG AGGGGCT		
			GTT GTCT TCCCCGA		
			GT TATCGTGA		
GAM1237	MAPK14	3'	AGCCCCTAGTGCTATTCTGTGT 57330 TG TGTTAAGA		
	TG		CAG CAGG AGGGGCT		
			GTT GTCT TCCCCGA		
			GT TATCGTGA		
GAM1237	MAPK14	3'	AGCCCCTAGTGCTATTCTGTGT 57341 TG TGTTAAGA		
	TG		CAG CAGG AGGGGCT		
			GTT GTCT TCCCCGA		
			GT TATCGTGA		
GAM1237	MAPRE1	3'	AGCCCCTGATGTATTTGTATTG 24660 TTAAGA		
			CAGTGCAGGTG AGGGGCT		
			GTTATGTTTAT TCCCCGA		
			GTAG__		
GAM1237	MAPRE2	3'	GGCTGCTCTTGACACTTCCATT 26541 C A G		
	G		CAGTG AGGTGTTAAGA G GGCT		
			GTTAC TTCACAGTTCT C TCGG		
			C _ G		
GAM1237	MASP1	3'	TCTCTTTCCTGTCTG 57475 T TGTTAA		
			CAG GCAGG GAAGGGG		

GTC TGTCC TTTCTCT  
 \_ C\_\_\_\_  
 GAM1237 MASP2 3' AGTCTCTTTTCATACTGGC 21736 A TA  
 GC GGTGT AGAAGGGGCT  
 || |||| |||||  
 CG TCATA TTTTCTCTGA  
 G C\_  
 GAM1237 MATN3 3' AGTCCTTTAAATTTTGC ACTG 9934 TGTTAAG  
 CAGTGCAGG AAGGGGCT  
 ||||| |||||  
 GTCACGTTT TTTCTCTGA  
 TAAA\_\_\_\_  
 GAM1237 MCC 3' TAGCTGGGAATCTTTTGTATAC 9962 \_\_\_\_\_  
 CTGTAGTG AGGTGTTAAGAAGG GGCT A  
 ||||| |||| I  
 TCCATAGTTTTTCT TCGA T  
 AAGGG  
 GAM1237 MCL1 3' AGCCCTTTTAGATTTTGGCACT 41713 AGGT AA  
 G CAGTGC GTT GAAGGGGCT  
 |||| || |||||  
 GTCACG TAG TTTTCCCGA  
 GTTT A\_  
 GAM1237 MCL1 3' GTCCCTTTTCCTTGGACTG 41718 G TGTTA  
 CAGT CAGG AGAAGGGGC  
 |||| || |||||  
 GTCA GTTC TTTTCCCTG  
 G C\_\_\_\_  
 GAM1237 MCM2 3' GTTCAGGATGCCTGCG 67929 AAGAAG  
 TGCAGGTGTT GGGC  
 ||||| ||||  
 GCGTCCGTAG CTTG  
 GA\_\_\_\_  
 GAM1237 MDM4 3' AGTTTTTTTTTTTTTTTGC ACT 9977 TGTT  
 AGTGCAGG AAGAAGGGGCT  
 ||||| |||||  
 TCACGTTT TTTTTTTTGA  
 TTT\_  
 GAM1237 MEF2A 3' GGCTTCCAAGCTGATGTTTGTA 18783 TG A AA\_\_\_\_  
 CT AGTGCAGG TTA G GGGGCT  
 ||||| |||| |||||  
 TCATGTTT AGT C CTTCCG  
 GT \_ GAAC  
 GAM1237 MEF2C 3' AGTTTTTTTTTTTTTCTTGCAG 9987 G TGTT  
 TG CA TGCAGG AAGAAGGGGCT  
 || |||| |||||  
 GT ACGTTC TTTTTTTTGA  
 G TTTT  
 GAM1237 MEF2C 3' CTTAGCACTTGAGTTG 9989 TG  
 CAG CAGGTGTTAAG  
 || |||||

			GTT GTTCACGATTC		
			GA		
GAM1237	MIPOL1	5'	AGCTCCTTCTATCTTGT 77065	TGTTA	
			GCAGG AGAAGGGGCT		
			TGTTT TCTTCCTCGA		
			TA__		
GAM1237	MLLT4	5'	GGTCCGATGGGTGGTGCTGTGT 72487	TG G TG AGAAG_	
	TG		CAG CA G TTA GGGCT		
			GTT GT C GGT CCTGG		
			GT _GT GGGTAG		
GAM1237	MMP10	3'	AGCCTTGCGAGATATCTGCAT 10069	AAGAA	
			GTGCAGGTGTT GGGGCT		
			TACGTCTATAG TTCCGA		
			ACG__		
GAM1237	MMP11	3'	GGTCTTGGTAGGTGCCTGCATC 19873	_ TG AAGAA	
	TG		CAG TGCAGG TT GGGGCT		
			GTC ACGTCC GG TTCTGG		
			T GT ATGG_		
GAM1237	MOX2	3'	GGCTTCTTTTCCATGCG 66930	_ TGTT	
			TGCA GG AAGAAGGGGCT		
			GCGT CC TTTTCTTCGG		
			A ____		
GAM1237	MPL	3'	GTTCCCTTTGATCTCGCTG 18151	C GTTAA	
			CAGTG AGGT GAAGGGGC		
			GTCGC TCTA TTTCCTTG		
			_ G__		
GAM1237	MPP2	3'	CCTTCATGGCACCTTCACTG 59819	C A	
			CAGTG AGGTGTTA GAAGG		
			GTCAC TCCACGGT CTTCC		
			T A		
GAM1237	MPP2	3'	GGTCTTTGGCTCACTCTGTGTT 59826	TG _ TTAAGA	
	G		CAG CAG GTG AGGGGCT		
			GTT GTC CAC TTTCTGG		
			GT T TCGG__		
GAM1237	MS4A2	3'	AGCTCCTTCTCTCTTACATTG 41695	C TGTTA	
			CAGTG AGG AGAAGGGGCT		
			GTTAC TTC TCTTCCTCGA		
			A TC__		
GAM1237	MSR1	3'	TTGTTAATACTGTATTG 56956	G G	
			CAGTGCGAG TGTTAA AA		

			GTTATGTC ATAATT TT		
			— G		
GAM1237	MSR1	3'	TTGTTAATACTGTATTG 56964	G	G
			CAGTGCAG TGTTAA AA		
			GTTATGTC ATAATT TT		
			— G		
GAM1237	MTF1	3'	GGTTCTTTCTCTCGGTTG 19885	G	TTA
			CAG TG AGAAGGGGCT		
			GTT GC TCTTTCTTGG		
			G TC_		
GAM1237	MTMR3	3'	GCTCTTTTTTGATCGATG 40814	GGT	
			CA GTTAAGAAGGGGC		
			GT TAGTTTTTCTCG		
			AGC		
GAM1237	MYBBP1A	3'	CTCTGGTGTTTGCCTG 27229	T	TG AAGAA
			CAG GCAGG TT GGGG		
			GTC CGTTT GG TCTC		
			— GT _____		
GAM1237	MYCL1	3'	AGTCCCCAACCGTGTCTGTCTG 18160	T	TG TAAGAA
			CAG GCAGG T GGGGCT		
			GTC TGTCT G CCCTGA		
			— GT CCAAC_		
GAM1237	MYL4	5'	GTTTCTTCTTAGATCACT 10177	—	GG
			GGTG TTAAGAAG GC		
			TCAC GATTCTTC TG		
			TA TT		
GAM1237	NACA	3'	AGCTTGTTTTGAAATTTGTACT 18791	G	AAG
	G		CAGTGCAGGT TTAAG GGGCT		
			GTCATGTTTA AGTTT TTCGA		
			A GG_		
GAM1237	NAPB	3'	AGTTTCTTTGCTTTTGTGTTG 70178	TG	TGTTAA GG
			CAG CAGG GAAG GCT		
			GTT GTTT TTTC TGA		
			GT TTCG_ TT		
GAM1237	NCALD	3'	TCATGACATCTCGCTG 49379	C	A
			CAGTG AGGTGTTA GA		
			GTCGC TCTACAGT CT		
			— A		
GAM1237	NDRG1	3'	AGTTTCTTAATGAGATATTTGT 59566	AAG_	GG
	ATT		AGTGCAGGTGTT AAG GCT		

		TTATGTTTATAG	TTC TGA	
		AGTAA TT		
GAM1237 NDRG1	3'	GGCCCCTTTTCGCCCTGCCT	59569	T TGTTA
G		CAG GCAGG AGAAGGGGCT		
		GTC CGTCC TTTTCCCCGG		
		_ CCCGC		
GAM1237 NEBL	3'	AGCTTCACGTAATAATGTTTGC	21117	TG AGAA__
AT		GTGCAGG TTA GGGGCT		
		TACGTTT AAT CTTCA		
		GT AATGCA		
GAM1237 NEDD4L	3'	GGTTCCTTTTCTTATTGGTTG	30951	T AG TT
		G GC GTG AAGAAGGGGCT		
		G TG TAT TTTTCCTTGG		
		T GT TC		
GAM1237 NELL1	3'	AGCTCCTTTTATTTATTTTGTT	20475	T TGTTA_
G		G GCAGG AGAAGGGGCT		
		G TGTTT TTTTCCTCGA		
		T TATTTA		
GAM1237 NESH	3'	GCAGCTGATGTCTGCACTG	33147	TG A AAGGG
		CAGTGCAGG TTA G GC		
		GTCACGTCT AGT C CG		
		GT _ GA__		
GAM1237 NEU1	5'	GGCTTAAGGGTGACATCTGCGC	4741	AGAAG
T		AGTGCAGGTGTTA GGGCT		
		TCGCGTCTACAGT TTCGG		
		GGGAA		
GAM1237 NEU3	5'	GTCCTTTCCTCTTTGGCTG	21852	GC TGTTAA
		CAGT AGG GAAGGGGC		
		GTCG TTC CTTTCCTG		
		GT TC__		
GAM1237 NFATC3	3'	AGCTAGGATTGGTGATTTGTAC	15850	_ TT GAAGG
TG		CAGTGCAGGT G AA GGCT		
		GTCATGTTTA T TT TCGA		
		G GG AGGA_		
GAM1237 NFE2L1	3'	GTCTAGAATGCTTGTGTTG	12175	TG AAGAAG
		CAG CAGGTGTT GGGC		
		GTT GTTCGTAA TCTG		
		GT GA__		
GAM1237 NFRKB	5'	AGTCTATCTGAAGCTTGCACTG	20494	GTTA AG
		CAGTGCAGGT AGA GGGCT		

GTCACGTTTCG TCT TCTGA  
 AAG\_ A\_  
 GAM1237 NID 3' GTCTCTGTTGCTGTGCTG 10232 TG GTGT GA  
 CAG CAG TAA AGGGGC  
 ||| ||| ||| |||||  
 GTC GTC GTT TCTCTG  
 GT \_\_\_\_ G\_  
 GAM1237 NKTR 3' AGCCTTAACTATAAATACCTGC 18198 A\_\_ AA  
 ACTG AGTGCAGGTGTT AG GGGGCT  
 ||||| || |||||  
 TCACGTCCATAA TC TTCCGA  
 ATA AA  
 GAM1237 NPR3 5' GCTCTTTCTTGCGGCAC 6175 AG GTT  
 GTGC GT AAGAAGGGGC  
 ||| || |||||  
 CACG CG TTCTTTCTCG  
 G\_ \_\_\_\_  
 GAM1237 NPY2R 5' GCCAAGTGGACCTGTACTG 6188 G AGAAGG  
 CAGTGCAGGT TTA GGC  
 ||||| ||| |||  
 GTCATGTCCA GGT CCG  
 \_ GAA\_\_\_\_  
 GAM1237 NR1D1 5' GCTGCTGGCGCCTGCGC 41364 AAGA G  
 GTGCAGGTGTT AG GGC  
 ||||| || |||  
 CGCGTCCGCGG TC TCG  
 \_\_\_\_ G  
 GAM1237 NRBP 3' CCCTGATCTGCGCTG 25431 GTTAAGAA  
 CAGTGCAGGT GGGG  
 ||||| ||| |||  
 GTCGCGTCTA TCCC  
 G\_\_\_\_\_  
 GAM1237 NRGNG 3' AGTCCCTATCCCACACCTGCCT 20511 T TAA \_  
 CAG GCAGGTGT GA AGGGGCT  
 ||| ||||| || |||||  
 GTC CGTCCACA CT TCCCTGA  
 \_ CC\_ A  
 GAM1237 NRIP1 5' GGCCTGGGGAAGTGTGTTGGATT 59953 G TG AAGAAG  
 G CAGT CAGG TT GGGCT  
 ||| ||| || |||||  
 GTTA GTTT GA TCCGG  
 G GT AGGGG\_  
 GAM1237 NRXN1 3' GGCTTTTTTGAAGACTTGTGT 16633 TG G AA  
 G CAGGT TT GAAGGGGCT  
 | |||| || |||||  
 T GTTCAAA TTTTTCGG  
 GT G G\_  
 GAM1237 NRXN1 3' GGCTTTTTTGAAGACTTGTGT 57030 TG G AA  
 G CAGGT TT GAAGGGGCT  
 | |||| || |||||



			T GTTCA AA TTTTTTCGG		
			GT G G_		
GAM1237 NRXN3	5'	GCTCAGAGTATCTGTGCT	16582	TG	AAGAAG
		AG CAGGTGTT	GGGC		
		TC GTCTATGA	CTCG		
		GT GA_			
GAM1237 NUMB	3'	GTTATATATATTTGTA	13625		TAAGAAGG
		CAGTGCAGGTGT	GGC		
		GTCATGTTTATA	TTG		
		TATA_			
GAM1237 ODC1	5'	GCTCCGGCGTCTGCGCT	10321	GT	AAGAA
		AGTGCAG GTT	GGGGC		
		TCGCGTC CGG	CCTCG		
		TG _			
GAM1237 OPA1	3'	GCCTCTTTTCTTCTGC	55567	TGTT	
		GCAGG AAGAAGGGGC			
		CGTCT TTTTCTCCG			
		TC_			
GAM1237 OPA1	3'	GCCTCTTTTCTTCTGC	55531	TGTT	
		GCAGG AAGAAGGGGC			
		CGTCT TTTTCTCCG			
		TC_			
GAM1237 OPA1	3'	GCCTCTTTTCTTCTGC	55540	TGTT	
		GCAGG AAGAAGGGGC			
		CGTCT TTTTCTCCG			
		TC_			
GAM1237 OPA1	3'	GCCTCTTTTCTTCTGC	55549	TGTT	
		GCAGG AAGAAGGGGC			
		CGTCT TTTTCTCCG			
		TC_			
GAM1237 OPA1	3'	GCCTCTTTTCTTCTGC	55558	TGTT	
		GCAGG AAGAAGGGGC			
		CGTCT TTTTCTCCG			
		TC_			
GAM1237 OTP	3'	GCTCTTCTGCATGTGC	49501	G TA	
		GCA GTGT AGAAGGGGC			
		CGT TACG TCTTTCTCG			
		G _			
GAM1237 P23	3'	AGTCCAGATTTGTATTTGCACT	21715	TT	GAAG
G		CAGTGCAGGTG AA	GGGCT		

			GTCACGTTTAT TT CCTGA		
			GT AGA_		
GAM1237	PACE	3'	AGCTCTGGCTGAACCCTGTGCT 10388	TG	T A AA
	G		CAG CAGG GTT AG GGGGCT		
			GTC GTCC CAA TC TCTCGA		
			GT _ G GG		
GAM1237	PAX2	3'	GGTTCTGAGCTGGCGTCTGAGC 14326	G	GT A AA_
	TG		CAGT CAG GTTA G GGGGCT		
			GTCG GTC CGGT C TCTTGG		
			A TG _ GAG		
GAM1237	PAX2	3'	GGTTCTGAGCTGGCGTCTGAGC 14335	G	GT A AA_
	TG		CAGT CAG GTTA G GGGGCT		
			GTCG GTC CGGT C TCTTGG		
			A TG _ GAG		
GAM1237	PCDH11X	3'	AGTTCCTTAAGTCATATTTGAC 52017	G	TAAG_
	TG		CAGT CAGGTGT AAGGGGCT		
			GTCA GTTTATA TTCCTTGA		
			_ CTGAA		
GAM1237	PCDH11X	3'	AGTTCCTTAAGTCATATTTGAC 52039	G	TAAG_
	TG		CAGT CAGGTGT AAGGGGCT		
			GTCA GTTTATA TTCCTTGA		
			_ CTGAA		
GAM1237	PCDH11Y	3'	AGTTCCTTAAGTCATATTTGAC 52074	G	TAAG_
	TG		CAGT CAGGTGT AAGGGGCT		
			GTCA GTTTATA TTCCTTGA		
			_ CTGAA		
GAM1237	PCDH9	5'	AGTCTTTGCACACGCTTGTGCT 82791	TG	TAAGA
			AG CAGGTGT AGGGGCT		
			TC GTTCGCA TTTCTGA		
			GT CACG_		
GAM1237	PCDHB2	3'	GTCCTTTTTTACTGCTTTG 38430	T	GTGT
			CAG GCAG TAAGAAGGGGC		
			GTT CGTC ATTTTTCCTG		
			T _		
GAM1237	PCDHB3	3'	GTCCTTTTTTACTGCTTTG 38431	T	GTGT
			CAG GCAG TAAGAAGGGGC		
			GTT CGTC ATTTTTCCTG		
			T _		
GAM1237	PCDHB7	3'	AGTCTTTTATCATATTTATACT 38442	C	TAAG
	G		CAGTG AGGTGT AAGGGGCT		

GTCAT TTTATA TTTTCTGA  
 A CTA\_  
 GAM1237 PCSK1 3' AGTCTTTCTTAGTGCCTGTGT 4769 TG TG GCT  
 G CAGG TTAAGAAGGG  
 | ||| |||||  
 T GTCC GATTCTTTCT  
 GT GT GA  
 GAM1237 PDCL 3' AGCCTTTTTTCTATGTATT 18208 GGTGTT  
 AGTGCA AAGAAGGGGCT  
 ||||| |||||  
 TTATGT TTTTTTCCGA  
 ATC\_  
 GAM1237 PDE1A 5' GCTTTGTACATCAGCACTG 17216 A TAAGAA  
 CAGTGC GGTGT GGGGC  
 ||||| ||||| |||||  
 GTCACG CTACA TTTCG  
 A TG\_  
 GAM1237 PDGFB 3' GTTCCTTCCCCTGCACCTG 10502 TAA\_  
 CAGGTGT GAAGGGGC  
 ||||| |||||  
 GTCCACG CTCCTTG  
 TCCC  
 GAM1237 PI3 3' GGTCTTGCTGCACCTGTGC 10547 TG TA A  
 G CAGGTGT AG AGGGGCT  
 | ||||| || |||||  
 C GTCCACG TC TTCCTGG  
 GT \_ G  
 GAM1237 PIAS1 5' GTTCACTGCGCTTGCGCTG 32403 TAAGA \_  
 CAGTGCAGGTGT AG GGGC  
 ||||| ||||| || |||||  
 GTCGCGTTCGCG TC CTTG  
 \_ A  
 GAM1237 PIK3R2 3' AGCCCCTTCTGGCTGCACCTG 17255 TA\_  
 CAGGTGT AGAAGGGGCT  
 ||||| |||||  
 GTCCACG TCTTCCCCGA  
 TCGG  
 GAM1237 PIK3R3 3' GGCTTTTCTTGGTTACACTGC 61062 \_ \_ TT  
 A TGCAG GT G AAGAAGGGGCT  
 ||||| || |||||  
 ACGTC CA T TTCTTTTTCGG  
 A T GG  
 GAM1237 PLA2G1B 5' AGTTTCTTTTCTCACCTTGACT 6248 GC TTA GG  
 G CAGT AGGTG AGAAG GCT  
 ||||| ||||| ||||| |||||  
 GTCA TCCAC TTTTC TGA  
 GT TC\_ TT  
 GAM1237 PLOD2 3' TTTCTTAATGTCTGCTCTG 6262 T TG  
 CAG GCAGG TTAAGAAG  
 ||||| ||||| |||||

GTC CGTCT AATTCTTT  
 T GT  
 GAM1237 PMCHL1 3' CTTTTTCTGTGCATTG 49072 GGTGTTA  
 CAGTGCA AGAAGGGG  
 ||||| |||||  
 GTTACGT TCTTTTTC  
 G\_\_\_\_\_  
 GAM1237 PML 3' GGCCCTTGGCTCTTCCTGCACT 52657 TGTTA A\_  
 G CAGTGCAGG AG AGGGGGCT  
 ||||| || |||||  
 GTCACGTCC TC TTCCCGG  
 TTC\_\_ GG  
 GAM1237 PMX1 3' AGTCTTTCTGAAGAATCTGTGC 42655 TG GTTA\_ GCT  
 TG CAG CAGGT AGAAGGG  
 || |||| |||||  
 GTC GTCTA TCTTTCT  
 GT AGAAG GA  
 GAM1237 PMX1 3' AGTCTTTCTGAAGAATCTGTGC 22587 TG GTTA\_ GCT  
 TG CAG CAGGT AGAAGGG  
 || |||| |||||  
 GTC GTCTA TCTTTCT  
 GT AGAAG GA  
 GAM1237 PNN 3' TCTTAAC TTTGTGTTG 71114 TG T  
 CAG CAGG GTTAAGA  
 || |||| |||||  
 GTT GTTT CAATTCT  
 GT \_  
 GAM1237 POLR2E 3' GGCCCTTCTTCTAAGCTTGCA 59920 \_ GTT\_  
 GCTG AG TGCAGGT AAGAAGGGGGCT  
 || ||||| |||||  
 TC ACGTTCG TTCTTCCCCGG  
 G AATC  
 GAM1237 POR 3' GGCTCTTTTCTCTCTGCTGAGCT 94175 \_\_\_\_ TGTTA  
 G AGT GCAGG AGAAGGGGGCT  
 || |||| |||||  
 TCG CGTCT TCTTTCTCGG  
 AGT C\_\_\_\_  
 GAM1237 PPP1R8 5' GGCTCTTTTTTTACTTTTCTGC 10726 T\_\_ T  
 GCAGG GT AAGAAGGGGGCT  
 |||| || |||||  
 CGTCT CA TTTTTTCTCGG  
 TTT T  
 GAM1237 PPP1R8 5' GGCTCTTTTTTTACTTTTCTGC 56742 T\_\_ T  
 GCAGG GT AAGAAGGGGGCT  
 |||| || |||||  
 CGTCT CA TTTTTTCTCGG  
 TTT T  
 GAM1237 PRKCM 3' GGTCAGGTTTAACATTTGCCTT 10814 T AAGG  
 G CAG GCAGGTGTTAAG GGCT  
 || ||||| |||||

			GTT CGTTTACAATTT CTGG		
			C GGA_		
GAM1237	PRKCN	3'	TCTTGATGCCAGTACTG 19449	A	
			CAGTGC GGTGTTAAGA		
			GTCATG CCGTAGTTCT		
			A		
GAM1237	PRODH	3'	GGCCGAACCTGATACCTGCCTG 32927	T	AAGA _
			CAG GCAGGTGTT AGG GGCT		
			GTC CGTCCATAG TCC CCGG		
			_ _ _ AAG		
GAM1237	PROX1	5'	GGCCCTTTTCCAGAATCACTT 10895	TTA_	
			GCACTG GCAGGTG AGAAGGGGCT		
			CGTTCAC TTTTCCCCGG		
			TAAGACC		
GAM1237	PSD	3'	AGCCCCTTTTGTGATAATGTT 10926	T	GGTGT_
			TTG CAG GCA TAAGAAGGGGCT		
			GTT TGT GTTTTCCCCGA		
			T AATAGT		
GAM1237	PTP4A2	5'	GGTCTTTTAAATGTTTCTGC 12985	TGTTAA_	
			GCAGG GAAGGGGCT		
			CGTCT TTTTCTGG		
			TTTGTA		
GAM1237	PTP4A2	5'	GGTCTTTTAAATGTTTCTGC 54415	TGTTAA_	
			GCAGG GAAGGGGCT		
			CGTCT TTTTCTGG		
			TTTGTA		
GAM1237	PTPN23	3'	AGTCTCTTACTCCATTTCTGC 63727	C	TTAAG
			TG CAGTG AGGTG AAGGGGCT		
			GTCGT TTTAC TTCTCTGA		
			C CCTCA		
GAM1237	PTPRA	3'	AGTCCTTTTCCAATGTTTTAT 55080	C	TG A_
			TG CAGTG AGG TT AGAAGGGGCT		
			GTTAT TTT AA TTTTCCTGA		
			_ GT CC		
GAM1237	PTPRA	3'	AGTCCTTTTCCAATGTTTTAT 55088	C	TG A_
			TG CAGTG AGG TT AGAAGGGGCT		
			GTTAT TTT AA TTTTCCTGA		
			_ GT CC		
GAM1237	PTPRA	3'	AGTCCTTTTCCAATGTTTTAT 11089	C	TG A_
			TG CAGTG AGG TT AGAAGGGGCT		

GTTAT TTT AA TTTTCCTGA  
 \_ GT CC  
 GAM1237 PTPRF 3' AGCCTTTTTTTAGGCCACATTG 11104 CA G  
 CAGTG GGT TTAAGAAGGGGCT  
 ||||| ||| |||||  
 GTTAC CCG GATTTTTTTCCGA  
 A\_ \_  
 GAM1237 PTPRF 3' AGCCTTTTTTTAGGCCACATTG 55266 CA G  
 CAGTG GGT TTAAGAAGGGGCT  
 ||||| ||| |||||  
 GTTAC CCG GATTTTTTTCCGA  
 A\_ \_  
 GAM1237 PTPRG 5' GGCTCTCGGGCTGTGCTGCGCT 11111 GT\_\_ AAGAA  
 G CAGTGCAG GTT GGGGCT  
 ||||| ||| |||||  
 GTCGCGTC CCG TCTCGG  
 GTGT GC\_\_  
 GAM1237 PTPRN 3' AGTTCCTGAACATCTGTGT 11128 TG A AA  
 G CAGGTGTT AG GGGGCT  
 | ||||| || |||||  
 T GTCTACAA TC CCTTGA  
 GT G \_  
 GAM1237 PTPRZ1 3' TTTTCTGACATTGTATTG 11142 G A  
 CAGTGCAG TGTTA GAAGG  
 ||||| ||||| |||||  
 GTTATGTT ACAGT CTTTT  
 \_ \_  
 GAM1237 PVT1 3' GTCCAAAGGCACCTGCCTG 65573 T AAGAAG  
 CAG GCAGGTGTT GGGC  
 ||| ||||| |||||  
 GTC CGTCCACGG CCTG  
 \_ AAA\_\_  
 GAM1237 RAB5A 3' GTCTCCATATCTGTATT 14781 TAAGAA  
 AGTGCAGGTGT GGGGC  
 ||||| ||||| |||||  
 TTATGTCTATA CTCTG  
 C\_\_\_\_  
 GAM1237 RAD21 3' GTTCTTCATTACTGCATTG 20760 GTGT GA  
 CAGTGCAG TAA AGGGGC  
 ||||| ||| |||||  
 GTTACGTC ATT TTCTTG  
 \_ AC  
 GAM1237 RAG1 3' AGCCTTTTTTTTTTTGTATT 4810 TGTT  
 AGTGCAGG AAGAAGGGGCT  
 ||||| |||||  
 TTATGTTT TTTTTTCCGA  
 T\_\_\_\_  
 GAM1237 RAI14 3' GGCCTCAGTGGGTGCTTGGCTG 31481 G TG AAGAA  
 CAGT CAGG TT GGGGCT  
 ||| |||| || |||||

GTCG GTTC GG CTCCGG  
 \_ GT GTGA\_  
 GAM1237 RAI2 3' CTTTTTAAAATTTGTAT 41415 G  
 GTGCAGGT TTAAGAAG  
 ||||| |||||  
 TATGTTTA AATTTTTC  
 A  
 GAM1237 RANBP3 3' GGCCTGGAGAGTGCCTGTCTG 13258 T TG AAGAAG  
 CAG GCAGG TT GGGCT  
 ||| ||| || ||||  
 GTC TGTCC GA TCCGG  
 \_ GT GAGG\_  
 GAM1237 RAP1GA1 3' GCCTGGGGGTCTGCGCTG 11253 TG AAGAAG  
 CAGTGCAGG TT GGGC  
 ||||| || |||  
 GTCGCGTCT GG TCCG  
 GG G\_\_\_\_  
 GAM1237 RARA 3' GGCTCCTGGCCTTGGCACTTGC 6369 T A\_\_\_\_  
 CTG AG GCAGGTGTTAAG AGGGGCT  
 || ||||| |||||  
 TC CGTTCACGGTTC TCCTCGG  
 \_ CGG  
 GAM1237 RBBP5 3' AGCTTTTTTTTTGACATTTGTT 17328 T \_  
 G GCAGGTGTTAAGAAGGG GCT  
 | ||||| ||||| |||  
 G TGTTTACAGTTTTTTT CGA  
 T T  
 GAM1237 RBP5 3' AGTCCTTTCTCACACTCCACTG 48983 CA TA  
 CAGTG GGTGT AGAAGGGGCT  
 |||| |||| |||||  
 GTCAC TCACA TCTTTCCTGA  
 C\_ C\_  
 GAM1237 RERE 3' GGTCTCTTCTGCCATTGTGCTG 23968 TG G TTA  
 CAG CAG TG AGAAGGGGCT  
 ||| ||| || |||||  
 GTC GTT AC TCTTCTCTGG  
 GT \_ CG\_  
 GAM1237 RGR 3' GGTTTCTTTTGTATATACTG 11323 \_ GG  
 CAG GTGTTAAGAAG GCT  
 ||| ||||| |||  
 GTC TATAGTTTTTC TGG  
 A TT  
 GAM1237 RLN1 3' AGTCTTGATGACATTTCACTG 22604 C AGAA  
 CAGTG AGGTGTTA GGGGCT  
 |||| ||||| |||||  
 GTCAC TTTACAGT TTCTGA  
 \_ AG\_  
 GAM1237 RNH 5' GGCCCCTGGCGGGTACCTGAGC 11367 G AAGA  
 TG CAGT CAGGTGTT AGGGGCT  
 |||| ||||| |||||

			GTCG GTCCATGG TCCCCGG		
			A GCGG		
GAM1237 RNH	5'	GGCCCCTGGCGGGTACCTGAGC 59622	G	AAGA	
	TG	CAGT CAGGTGTT AGGGGCT			
		GTCG GTCCATGG TCCCCGG			
		A GCGG			
GAM1237 RPH3AL	3'	AGTTTCTTTGGTTTTGTAT 22740	TGTTAA	GG	
		GTGCAGG GAAG GCT			
		TATGTTT TTTC TGA			
		TTGG__ TT			
GAM1237 RPN1	3'	GCCCAGGGTGCCTGCACT 11391	TG	AAGAAG	
		AGTGCAGG TT GGGC			
		TCACGTCC GG CCCG			
		GT GA__			
GAM1237 RPN2	3'	GTCTCTTTCTCTGACACT 11394	-	-	
		GGTGTTA AGAAGG GGC			
		TCACAGT TCTTTC CTG			
		C T			
GAM1237 RPP20	3'	AGCCCAAAGGACTCTGCATTG 19549	T	AAGAAG	
		CAGTGCAGG GTT GGGCT			
		GTTACGTCT CAG CCCGA			
		_ GAAA__			
GAM1237 RPS6KA5	3'	TTTTTAATTTTGCCTG 16468	T		
		CAGTGCAGG GTTAAGAA			
		GTCACGTTT TAATTTT			
		-			
GAM1237 RRM2B	3'	AGTCCTTTACCATCTATGTTG 67824	GT C	TTAAG	
		CA G AGGTG AAGGGGCT			
		GT T TCTAC TTTCTGA			
		TG A CA__			
GAM1237 RUNX3	3'	AGCCTCTGGCTGCATCTGTGC 15109	TG	TAAGA	
		G CAGGTGT AGGGGCT			
		C GTCTACG TCTCCGA			
		GT TCGG__			
GAM1237 RXRA	3'	AGCCTCACTGAACGCCTGCTCT 11400	T	A AA	
	G	CAG GCAGGTGTT AG GGGGCT			
		GTC CGTCCGCAA TC CTCCGA			
		T G A_			
GAM1237 S100A4	3'	GGCTCCTTCAGACACGTGCTTG 11422	___	G AA	
	ATGCTG	GCA GTGTT GAAGGGGCT			



CGT CACAG CTCCTCGG  
 AGTT G A\_  
 GAM1237 S100A4 3' GGCTCCTTCAGACACGTGCTTG 38952 \_\_\_\_ G AA  
 ATGCTG GCA GTGTT GAAGGGGCT  
 ||| |||| |||||  
 CGT CACAG CTCCTCGG  
 AGTT G A\_  
 GAM1237 SBF1 3' GCCCCCAGCACTTGTGT 65457 TG AAGAA  
 G CAGGTGTT GGGGC  
 | ||||| ||||  
 T GTTCACGA CCCC  
 GT C\_\_\_\_  
 GAM1237 SCAMP1 3' TTTTGGCTTCTGTACTG 16818 T  
 CAGTGCAGG GTTAAGA  
 ||||| |||||  
 GTCATGTCT CGGTTTT  
 T  
 GAM1237 SCN4A 3' GCCCGAGCGCCTGCG 4415 AAGAAG  
 TGCAGGTGTT GGGC  
 ||||| ||||  
 GCGTCCGCGA CCCG  
 G\_\_\_\_  
 GAM1237 SDS 3' GGACCTTTTGGTATCTGTGT 22425 TG TT GG  
 G CAGGTG AAGAAGG CT  
 | |||| ||||| ||  
 T GTCTAT TTTTCC GG  
 GT GG A\_  
 GAM1237 SERPINE2 3' AGCCTCTTTGTGTTTTTGTG 74921 T TGTTAA  
 G GCAGG GAAGGGGCT  
 | |||| |||||  
 G TGT TTCTCCGA  
 T TTGTG\_  
 GAM1237 SET 3' GTTCTTTTTGTTTCACTG 11558 C TGT GG  
 CAGTG AGG TAAGAAG GC  
 |||| || ||||| ||  
 GTCAC TTT GTTTTC TG  
 - \_\_\_\_ TT  
 GAM1237 SFPQ 3' AGCCCTATAAATGGCTTGTATT 17370 GTTAAGAA  
 G CAGTGCAGGT GGGGCT  
 ||||| |||||  
 GTTATGTTG TCCCGA  
 GTAAATA\_  
 GAM1237 SGCB 3' GTTCCTTAGTTTTGCACTG 4067 TGTTAAG  
 CAGTGCAGG AAGGGGC  
 ||||| |||||  
 GTCACGTTT TTCCTTG  
 TGA\_\_\_\_  
 GAM1237 SH3GL3 3' GGTCTTTTCTTTTCATTGTATT 11635 G TT  
 AGTGCAG TG AAGAAGGGGCT  
 ||||| || |||||

TTATGTT AC TTCTTTTCTGG  
 \_ TT  
 GAM1237 SIRT6 3' AGCCTCTGACTTGCTGTGTTG 33295 TG GTGT A\_  
 CAG CAG TAAG AGGGGCT  
 ||| ||| |||| |||||  
 GTT GTC GTTC TCTCCGA  
 GT \_\_\_\_ AG  
 GAM1237 SLC20A2 3' TTTTCTTGGTACTTCATTG 22178 C TT  
 CAGTG AGGTG AAGAAGG  
 ||||| ||||| |||||  
 GTTAC TTCAT TTCTTTT  
 \_ GG  
 GAM1237 SLC21A9 3' CTTCTGCGCCCTGTGCTG 23419 TG T A  
 CAG CAGG GTTA GAAG  
 ||| ||||| ||||| |||||  
 GTC GTCC CGGT CTC  
 GT \_ C  
 GAM1237 SLC21A9 3' GGTTCTCCGATGCCTGGGCTG 23423 G AAGAA  
 CAGT CAGGTGTT GGGGCT  
 ||||| ||||| |||||  
 GTCG GTCCGTAG TCTTGG  
 G CC\_\_\_\_  
 GAM1237 SLC22A2 5' GGCCGAGCTGAGTCTGCGCTG 59536 GTTA AAGG  
 CAGTGCAGGT AG GGCT  
 ||||| ||| |||||  
 GTCGCGTCTG TC CCGG  
 AG\_\_ GAG\_  
 GAM1237 SLC25A13 3' AGTACTTTTGGCATTTTACTG 26501 C A GG  
 CAGTG AGGTGTTAAGA G GCT  
 ||||| ||||| ||||| | |||  
 GTCAT TTTACGGTTTT C TGA  
 \_ \_A\_  
 GAM1237 SLC2A3 3' GCCCCTTTTTTCATATGTTG 22662 T G TT  
 G GCA GTG AAGAAGGGGC  
 | ||| ||| ||||| |||||  
 G TGT TAC TTTTCCCG  
 T A \_  
 GAM1237 SLC2A6 3' GTCCCTTTCCCTTGCG 34160 TGTTAA  
 TGCAGG GAAGGGGC  
 ||||| ||||| |||||  
 GCGTTC TTTCCCTG  
 CC\_\_\_\_  
 GAM1237 SLC38A2 3' AGCCCTTTTTTGACATTGC 38586 G  
 GCAG TGTTAAGAAGGGGCT  
 ||||| ||||| ||||| |||||  
 CGTT ACAGTTTTTTCCCGA  
 \_  
 GAM1237 SLC4A4 3' GGTTCCTTTTTAACTGTGTT 13641 TG GTGTT  
 AG CAG AAGAAGGGGCT  
 || ||| ||||| |||||

TT GTC TTTTCCTTGG  
 GT AAT\_\_  
 GAM1237 SLC6A12 3' GCTCCTTCCCCTTTGCTG 11736 C TGTAA  
 CAGTG AGG GAAGGGGC  
 ||||| ||| |||||  
 GTCGT TCC CTTCTCTG  
 T C\_\_\_\_  
 GAM1237 SLC7A5 3' AGCCCCTTCTGGCCGGTGCTG 13008 TG A GTTA  
 CAG C GGT AGAAGGGGCT  
 ||| | ||| |||||  
 GTC G CCG TCTTCCCCGA  
 GT G G\_\_\_\_  
 GAM1237 SLC7A5 3' GGTCTCTTCTGGGCGTCTGAGC 13013 G GT TA  
 TG CAGT CAG GT AGAAGGGGCT  
 ||||| ||| |||||  
 GTCG GTC CG TCTTCTCTGG  
 A TG GG  
 GAM1237 SLC9A3R1 5' GGTTCCTGGGACACCTGC 70423 AAGA  
 GCAGGTGTT AGGGGCT  
 ||||| |||||  
 CGTCCACAG TCCTTGG  
 GG\_\_\_\_  
 GAM1237 SMAC 3' TCTCAGGCTTGCGCTG 39113 GTTAAGAA  
 CAGTGCAGGT GGGG  
 ||||| |||||  
 GTCGCGTTTCG CTCT  
 GA\_\_\_\_\_  
 GAM1237 SMAC 3' TCTCAGGCTTGCGCTG 57197 GTTAAGAA  
 CAGTGCAGGT GGGG  
 ||||| |||||  
 GTCGCGTTTCG CTCT  
 GA\_\_\_\_\_  
 GAM1237 SMAC 3' TCTCAGGCTTGCGCTG 57219 GTTAAGAA  
 CAGTGCAGGT GGGG  
 ||||| |||||  
 GTCGCGTTTCG CTCT  
 GA\_\_\_\_\_  
 GAM1237 SMARCA1 3' AGTCCTTGTTCTTTTGAAGCTT 57388 G GTT\_\_ \_\_  
 GTGCTG CAGGT AAGAA GGGGCT  
 ||||| ||||| |||||  
 GTTCG TTCTT TCCTGA  
 T AAGTT GT  
 GAM1237 SMARCA1 3' AGTCCTTGTTCTTTTGAAGCTT 11778 G GTT\_\_ \_\_  
 GTGCTG CAGGT AAGAA GGGGCT  
 ||||| ||||| |||||  
 GTTCG TTCTT TCCTGA  
 T AAGTT GT  
 GAM1237 SMARCA3 3' AGCTTTTCATAATATCTATGCT 11785 GC A G  
 G CAGT AGGTGTTA GAAGGG CT  
 ||||| ||||| ||||| ||

GTCG TCTATAAT CTTTTC GA  
 TA A \_  
 GAM1237 SMARCA3 3' AGTCCTTTTCTCCCTGTGC 11787 TG TGTAA  
 G CAGG GAAGGGGCT  
 | ||| |||||  
 C GTCC TTTTCCTGA  
 GT CTC\_\_  
 GAM1237 SMARCA3 3' AGTCCTTTTCTCCCTGTGC 57396 TG TGTAA  
 G CAGG GAAGGGGCT  
 | ||| |||||  
 C GTCC TTTTCCTGA  
 GT CTC\_\_  
 GAM1237 SMARCC1 3' GGTCCCTTTTGTTTTGTTCTG 11801 T TGTAA  
 CAG GCAGG GAAGGGGCT  
 ||| ||| |||||  
 GTC TGTT TTTTCCTGG  
 T TTG\_\_  
 GAM1237 SMURF1 3' GTCCCTTTTGCTGCATT 92458 GTGTTA  
 AGTGCAG AGAAGGGGC  
 ||||| |||||  
 TTACGTC TTTTCCTG  
 G\_\_  
 GAM1237 SNAI2 3' AGCCTTTTTTTGATTACCTGTA 11773 G \_  
 GTG CA TGCAGGTG TTAAGAAGGGGCT  
 || ||||| |||||  
 GT ATGTCCAT AGTTTTTTTCCGA  
 G T  
 GAM1237 SNRPN 5' AGCTTCTGCCCAGCTTGCATTG 42990 GTTAAGA  
 CAGTGCAGGT AGGGGCT  
 ||||| |||||  
 GTTACGTTTCG TCTTCGA  
 ACCCG\_\_  
 GAM1237 SNRPN 5' AGCTTCTGCCCAGCTTGCATTG 42997 GTTAAGA  
 CAGTGCAGGT AGGGGCT  
 ||||| |||||  
 GTTACGTTTCG TCTTCGA  
 ACCCG\_\_  
 GAM1237 SNRPN 5' AGCTTCTGCCCAGCTTGCATTG 43004 GTTAAGA  
 CAGTGCAGGT AGGGGCT  
 ||||| |||||  
 GTTACGTTTCG TCTTCGA  
 ACCCG\_\_  
 GAM1237 SNRPN 5' AGCTTCTGCCCAGCTTGCATTG 43012 GTTAAGA  
 CAGTGCAGGT AGGGGCT  
 ||||| |||||  
 GTTACGTTTCG TCTTCGA  
 ACCCG\_\_  
 GAM1237 SQSTM1 3' GGTCCCTTGCTTAGCCTGTGCT 14016 TG GT \_  
 G CAG CAGGT TAAG AAGGGGCT  
 || ||| ||| |||||

GTC GTCCG ATTC TTCCCTGG  
 GT \_ G  
 GAM1237 SRGAP1 3' GTCTGTGGCACTTGGGCTG 72266 G AGAAG  
 CAGT CAGGTGTTA GGGC  
 ||| ||||| |||  
 GTCG GTTCACGGT TCTG  
 G G\_\_\_\_  
 GAM1237 SRGAP2 3' AGTCTCCAAACCTGGTGCCTGT 74603 TG TG AGAA\_  
 GCT AG CAGG TTA GGGGCT  
 || ||| || |||||  
 TC GTCC GGT CTCTGA  
 GT GT CCAAAC  
 GAM1237 SRRM2 3' TTTTAAATCTGTAC 32919 G  
 GTGCAGGT TTAAGAAG  
 ||||| |||||  
 CATGTCTA AATTTTTT  
 A  
 GAM1237 SSPN 3' AGCTCTGACTGTACTTACGCTG 17440 C TTA AA  
 CAGTG AGGTG AG GGGGCT  
 |||| ||| || |||||  
 GTCGC TTCAT TC TCTCGA  
 A G\_ AG  
 GAM1237 SSX4 3' AGTTCGATGTTGGCGTTTCCGC 94661 C GG GAAG  
 TG CAGTG A TGTTAA GGGCT  
 |||| | ||||| |||||  
 GTCGC T GCGGTT CTTGA  
 C TT GTAG  
 GAM1237 SSX4 3' AGTTCGATGTTGGCGTTTCCGC 18877 C GG GAAG  
 TG CAGTG A TGTTAA GGGCT  
 |||| | ||||| |||||  
 GTCGC T GCGGTT CTTGA  
 C TT GTAG  
 GAM1237 ST3GALVI 5' GGCTTCGCTGCGGGTTTGCCT 20344 GG GTTA AA  
 G CAGTGCA T AG GGGGCT  
 ||||| | || |||||  
 GTCACGT G TC CTTCCG  
 TT GGCG G\_  
 GAM1237 STARD4 3' GGTTTCTTCTTTTTTTTGTTC 57515 T TGTT GG  
 TG CAG GCAGG AAGAAG GCT  
 || |||| ||||| |||  
 GTC TGTT TTCTTC TGG  
 T TTTT TT  
 GAM1237 STAU 3' GGTCTTTTTTTTCCCTGTGT 33896 TG TGTT  
 G CAGG AAGAAGGGGCT  
 | ||| |||||  
 T GTCC TTTTTTCTGG  
 GT CCT\_  
 GAM1237 STAU 3' GGTCTTTTTTTTCCCTGTGT 33902 TG TGTT  
 G CAGG AAGAAGGGGCT  
 | ||| |||||

T GTCC TTTTTTCTGG  
 GT CCT\_  
 GAM1237 STAU 3' GGTCTTTTTTTTCCCCTGTGT 33909 TG TGTT  
 G CAGG AAGAAGGGGCT  
 I IIII IIIIIIIII  
 T GTCC TTTTTTCTGG  
 GT CCT\_  
 GAM1237 STAU 3' GGTCTTTTTTTTCCCCTGTGT 16008 TG TGTT  
 G CAGG AAGAAGGGGCT  
 I IIII IIIIIIIII  
 T GTCC TTTTTTCTGG  
 GT CCT\_  
 GAM1237 SYNGR1 3' GGCTCCACAAATATATCTGTGT 16320 TG TAAGAA  
 G CAGGTGT GGGGCT  
 I IIIII IIIII  
 T GTCTATA CCTCGG  
 GT TAAACA  
 GAM1237 TAF11 3' AGCCTGATTGATACTTGCCTTG 18914 T GAAG  
 CAG GCAGGTGTAA GGGCT  
 III IIIIIIIII IIII  
 GTT CGTTCATAGTT TCCGA  
 C AG\_  
 GAM1237 TAF15 3' GCCTCTTCTTGGGTAGTG 13016 G AGGTG  
 CA TGC TTAAGAAGGGGC  
 II IIII IIIIIIIII  
 GT ATG GGTTCTTCTCCG  
 G \_\_\_\_\_  
 GAM1237 TAF15 3' GCCTCTTCTTGGGTAGTG 57632 G AGGTG  
 CA TGC TTAAGAAGGGGC  
 II IIII IIIIIIIII  
 GT ATG GGTTCTTCTCCG  
 G \_\_\_\_\_  
 GAM1237 TBX3 3' AGTTCTTTCTCTTTCCTGTAT 33350 TGTTA  
 GTGCAGG AGAAGGGGCT  
 IIIII IIIIIIIII  
 TATGTCC TCTTTCTTGA  
 TTTC\_  
 GAM1237 TCEB1L 3' AGTTTCTTTTTTCTTTGCTCTG 12145 T TGTT GG  
 CAG GCAGG AAGAAG GCT  
 III IIII IIIII IIII  
 GTC CGTTT TTTTTC TGA  
 T CT\_\_ TT  
 GAM1237 TCF1 3' GCCCTGGGGCCTGTACTG 5034 G AAGAA  
 CAGTGCAGGT TT GGGGC  
 IIIIIII II IIII  
 GTCATGTCCG GG TCCCG  
 G \_\_\_\_\_  
 GAM1237 TCF19 5' CTTAACCAATTTTGCATTG 97735 T\_\_\_\_  
 CAGTGCAGG GTTAAG  
 IIIIIII IIIII

			GTTACGTTT CAATTC		
			TAAC		
GAM1237	TCF19	5'	CTTAACCAATTTTGCATTG 97865	T___	
			CAGTGCAGG GTTAAG		
			GTTACGTTT CAATTC		
			TAAC		
GAM1237	TCF8	3'	GGCTCAGGGCGGTGCCCT 47727	T	TG AAGAAG
	G		CAG GCAGG TT GGGCT		
			GTC CGTCC GG CTCGG		
			C GT CGGGA_		
GAM1237	TCFL4	3'	AGTCCTTGGGATGGGCGTCTGC 63456	T	GT AAGA__
	TCTG		AG GCAG GTT AGGGGCT		
			TC CGTC CGG TTCCTGA		
			T TG GTAGGG		
GAM1237	TCOF1	3'	AGCTTCAGGGGTCCCTGTGCTG 4485	TG	TG AAGAA
			CAG CAGG TT GGGGCT		
			GTC GTCC GG CTCGA		
			GT CT GGA__		
GAM1237	TDRD1	3'	GGTTTGGTCATAATGCTTCTGC 48396	C	A AG
	TG		CAGTG AGGTGTGA GA GGGCT		
			GTCGT TTCGTAAT CT TTTGG		
			C A GG		
GAM1237	TFDP2	3'	AGTCTTTGCCTTTGTTTGCCT 20807	TGTT	A_
	G		CAGTGCAGG AAG AGGGGCT		
			GTCACGTTT TTC TTTCTGA		
			GT__ CG		
GAM1237	TGFBR2	3'	GCCAATAACATTTGCACT 12268		AGAAGG
			AGTGCAGGTGTTA GGC		
			TCACGTTTACAAT CCG		
			AA__		
GAM1237	THY1	3'	GCTTATGGCATCTCATTG 20812	C	AGAAG
			CAGTG AGGTGTTA GGGC		
			GTTAC TCTACGGT TTCG		
			_ A__		
GAM1237	TIMP3	3'	AGCCCAGTGATGCTTGTGTTG 4501	TG	AGAAG
			CAG CAGGTGTTA GGGCT		
			GTT GTTCGTAGT CCCGA		
			GT GA__		
GAM1237	TK2	3'	AGTCGCTTTTGGTGCCTGGCTG 16059	G	TG A G
			CAGT CAGG TTAAGA G GGCT		

GTCG GTCC GGT TTT C CTGA  
 \_ GT \_ G  
 GAM1237 TM4SF2 3' GGCCCTTTGGGCCCTGCAT 16065 T TAA  
 GTGCAGG GT GAAGGGGCT  
 ||||| || |||||  
 TACGTCC CG TTTCCCCGG  
 \_ GG\_  
 GAM1237 TME2 3' AGCCTCTTTGACTGTATATT 25418 G TA\_\_\_\_  
 GTGTT CAGGTGT AGAAGGGGCT  
 ||||| |||||  
 GTTTATA TTTTCTCCGA  
 T TGT CAG  
 GAM1237 TNFRSF10D 3' AGTCTTTTTTCTGCTTCTTAT 13859 C T\_ T\_  
 ATTG AGTG AGG GT AAGAAGGGGCT  
 ||| ||| || |||||  
 TTAT TTC CG TTTTTTCTGA  
 A TT TC  
 GAM1237 TNFRSF1B 3' AGTCTTGTGTCTGCGTCTGTGT 6517 TG GT TAAGAA  
 TG CAG CAG GT GGGGCT  
 ||| ||| || |||||  
 GTT GTC CG TTCTGA  
 GT TG TCTGTG  
 GAM1237 TNFRSF7 3' GCCAGCTGCGCCTGCGCTG 6956 TA AAGG  
 CAGTGCAGGTGT AG GGC  
 ||||| || |||  
 GTCGCGTCCGCG TC CCG  
 \_ GA\_  
 GAM1237 TNS 3' GGCTCTCTCCTGGTGCCTGCAC 42630 TG A AG  
 GTGCAGG TTA GA GGGCT  
 ||||| ||| || |||||  
 CACGTCC GGT CT CTCGG  
 GT C CT  
 GAM1237 TP63 3' GGCCTTGGAATTCCTGTACTG 13568 T AAGAA  
 CAGTGCAGG GTT GGGGCT  
 ||||| || |||||  
 GTCATGTCC TAA TTCCGG  
 T AGG\_  
 GAM1237 TPS1 3' GCCCCTTCCCCTGTCCTG 60490 TG TGTTAA  
 CAG CAGG GAAGGGGC  
 ||| ||| |||||  
 GTC GTCC CTTCCCCG  
 CT C\_\_\_\_  
 GAM1237 TPSB1 3' GCCCCTTCCCCTGTCCTG 12375 TG TGTTAA  
 CAG CAGG GAAGGGGC  
 ||| ||| |||||  
 GTC GTCC CTTCCCCG  
 CT C\_\_\_\_  
 GAM1237 TRPC5 5' GCTCAGGATTTCTGCATTG 24999 T AAGAAG  
 CAGTGCAGG GTT GGGC  
 ||||| || |||



		GTTACGTCT TAG CTCG	
		T GA_____	
GAM1237 TXNRD1	3'	GGTTCTTGGGCTCTTGGCACCT 12461	_____
		GCG GCAGGTGTTAAGA AGGGGCT	
		CGTCCACGGTTCT TTCTTGG	
		CGGG	
GAM1237 UBE4A	3'	AGCTTCTGCCTATTTGCATT 16556	TTAAGA
		AGTGCAGGTG AGGGGCT	
		TTACGTTTAT TCTTCGA	
		CCG_____	
GAM1237 UBL3	3'	GCCGTGGTGGCTGCACTG 23033	G GT AGAAGG
		CAGTGCAG T TA GGC	
		GTCACGTC G GT CCG	
		G TG G_____	
GAM1237 UCP3	5'	AGCCCTAGGGAGCCCCTGTGCT 12534	TG T AAGAA
		G CAG CAGG GTT GGGGCT	
		GTC GTCC CGA TCCCGA	
		GT C GGGA_	
GAM1237 UCP3	5'	AGCCCTAGGGAGCCCCTGTGCT 42989	TG T AAGAA
		G CAG CAGG GTT GGGGCT	
		GTC GTCC CGA TCCCGA	
		GT C GGGA_	
GAM1237 VCL	3'	GGCCCTCAGCATATTTGTAT 12580	TAAGAA
		GTGCAGGTGT GGGGCT	
		TATGTTTATA TCCCGG	
		CGAC_____	
GAM1237 VCL	3'	GGCCCTCAGCATATTTGTAT 25739	TAAGAA
		GTGCAGGTGT GGGGCT	
		TATGTTTATA TCCCGG	
		CGAC_____	
GAM1237 WHSC1L1	3'	GGTCTTTTCTTGCCTTTTATTG 43521	C T T
		CAGTG AGG GT AAGAAGGGGCT	
		GTTAT TTC CG TTCTTTTCTGG	
		T _ _	
GAM1237 WRB	3'	AGTTCTTTGAAGACTTAGTGCT 16124	TG _ G AAG
		G CAG C AGGT TT AAGGGGCT	
		GTC G TTCA AA TTTCTTGA	
		GT A G G_____	
GAM1237 WRN	5'	GCCTGGATGCCTGGGTTG 5097	G AAGAAG
		CAGT CAGGTGTT GGGC	

GTTG GTCCGTAG TCCG  
 G G\_\_\_\_  
 GAM1237 XPNPEP2 3' AGCCTAACAAAGACACTTGCCT 12681 T AAGAAG  
 G CAG GCAGGTGTT GGGCT  
 ||| ||||| ||||  
 GTC CGTTCACAG TCCGA  
 \_ AAACAA  
 GAM1237 XRCC3 3' GGCCTTTAAAACGCGTCTGCCT 18341 T GT TAAGA  
 G CAG GCAG GT AGGGGCT  
 ||| ||| || |||||  
 GTC CGTC CG TTTCCGG  
 \_ TG CAAAA  
 GAM1237 XT3 3' AGTTTCTGTGGATATATTTGCA 39519 TAAGA\_ GG  
 C GTGCAGGTGT AG GCT  
 ||||| || |||  
 CACGTTTATA TC TGA  
 TAGGTG TT  
 GAM1237 YWHAG 3' AGCCTCACACTGGCGTCTGGAC 25014 G GT AGAA  
 TG CAGT CAG GTTA GGGGCT  
 ||| ||| ||| |||||  
 GTCA GTC CGGT CTCCGA  
 G TG CACA  
 GAM1237 ZFP37 3' CAGCTCTTTCTTAATGTCTGTG 12714 TG TG  
 TTG CAG CAGG TTAAGAAGGGGCT  
 ||| ||| |||||  
 GTT GTCT AATTCTTTCTCGA  
 GT GT CC  
 GAM1237 ZIC3 3' TTTTAACACTTGTCTG 12733 TG  
 CAG CAGGTGTTAAGA  
 ||| |||||  
 GTC GTTCACAATTTT  
 CT  
 GAM1237 ZNF136 5' GTTTCCTGTACCTGCCTTG 59891 T TTA AA GG  
 CAG GCAGGTG AG G GC  
 ||| ||||| || | ||  
 GTT CGTCCAT TC C TG  
 C G\_\_ \_\_TT  
 GAM1237 ZNF157 3' GGTTTTTCTTCTGTGCATTG 12880 \_ TGTT  
 CAGTGCA GG AAGAAGGGGCT  
 ||||| || |||||  
 GTTACGT TC TTCTTTTTTG  
 G \_\_\_\_  
 GAM1237 ZNF189 3' AGCTGAGATATTTTGGTATTGC 12903 G TT AGG\_\_\_\_  
 ATTG GTGCAG TG AAGA GGCT  
 ||||| || ||| |||  
 TACGTT AT TTTT TCGA  
 \_ GG ATAGAG  
 GAM1237 ZNF215 3' TTTTAATGTCTGATATTG 25122 \_ TG  
 CAGTG CAGG TTAAGA  
 ||||| ||| |||||

GTTAT GTCT AATTTT  
 A GT  
 GAM1237 ZNF24 3' GCCTCTTCCCCTTGTCTG 22727 T TGTAA  
 CAG GCAGG GAAGGGGC  
 ||| |||| |||||  
 GTC TGTC CTTCTCCG  
 \_ CC\_\_\_\_  
 GAM1237 ZNF274 3' AGCCAGGTAATTAATAATCTGC 56055 \_ GAAGG\_  
 ACTG AGTGCAGGT GTTAA GGCT  
 ||||| |||| |||  
 TCACGTCTA TAATT CCGA  
 A AATGGA  
 GAM1237 ZNF274 3' AGCCAGGTAATTAATAATCTGC 32880 \_ GAAGG\_  
 ACTG AGTGCAGGT GTTAA GGCT  
 ||||| |||| |||  
 TCACGTCTA TAATT CCGA  
 A AATGGA  
 GAM1237 7h3 3' GCTTTGAGCACTGCACTG 52275 G AAGAAG  
 CAGTGCAG TGTT GGGC  
 ||||| ||| |||  
 GTCACGTC ACGA TTCG  
 \_ GT\_\_\_\_  
 GAM1237 ACTR3 3' AGCTCTATAATGCTTGAATTG 19144 G AGAA  
 CAGT CAGGTGTTA GGGGCT  
 ||| ||||| |||||  
 GTTA GTTCGTAAT TCTCGA  
 A A\_\_\_\_  
 GAM1237 AF311304 3' TTTTAGCACTTGCACT 48330  
 AGTGCAGGTGTTAAGA  
 ||||| |||||  
 TCACGTTACGATTTT  
 GAM1237 AF9Q34 3' TTCTTGGTGTTTGA CTG 50742 G TG  
 CAGT CAGG TTAAGAA  
 ||| ||| |||||  
 GTCA GTTT GGTTCTT  
 \_ GT  
 GAM1237 AK000009 3' TTAAAACTTGTACTG 77000 G\_  
 CAGTGCAGGT TTAAG  
 ||||| |||||  
 GTCATGTTCA AATTT  
 AA  
 GAM1237 AKAP11 3' GGTTTTTTTTTAACCATCTGT 32712 \_  
 GCAGGTG TTAAGAAGGGGCT  
 ||||| ||||| |||||  
 TGTCTAC AATTTTTTTTTTGG  
 C  
 GAM1237 AKAP6 3' GTTCTTTCTTAGGTTGC 14994 GTG  
 GCAG TTAAGAAGGGGC  
 ||| ||||| |||||

CGTT GATTCTTTCTTG  
G\_\_

GAM1237 AKAP9 3' GGTTCCTTTTGCTTTTGTATT 19240 T TAA  
G CAGTGCAGG GT GAAGGGGCT  
||||||| || |||||||  
GTTATGTTT CG TTTTCTTGG  
T TG\_

GAM1237 AMOTL1 3' GGCCTCCATTCTGACATCTGGG 73653 G A \_ \_  
CTG AGT CAGGTGTTA GAA GG GGCT  
||| ||||||| ||| || |||||  
TCG GTCTACAGT CTT CC CCGG  
G \_ A T

GAM1237 ANGPTL1 5' GTTCCTTCTTACAGCTTG 16247 GT  
CAGGT TAAGAAGGGGC  
||||| |||||||||  
GTTTCG ATTCTTCCTTG  
AC

GAM1237 APCL 5' CCTTCGTGGTGTTCATTG 19669 C TG A  
CAGTG AGG TTA GAAGG  
||||| ||| ||| |||||  
GTTAC TTT GGT CTTCC  
T GT G

GAM1237 APEG1 3' GCCCCAGGCTCTGTGCTG 72133 TG T AAGAA  
CAG CAGG GTT GGGGC  
||| ||||| ||| |||||  
GTC GTCT CGG CCCCCG  
GT \_ A\_\_\_\_

GAM1237 APOL2 3' AGTGACTTTGGCATTGTGT 48044 TG AA GG  
G CAGGTGTT GAAG GCT  
| ||||||| ||||| |||  
T GTTTACGG TTTC TGA  
GT \_ AG

GAM1237 APOL6 3' GCCCTAAACACTGTGTTG 47620 TG G AAGAA  
CAG CAG TGTT GGGGC  
||| ||| ||||| |||||  
GTT GTC ACAA TCCCG  
GT \_ A\_\_\_\_

GAM1237 AQP9 3' TTCCCAACTGCTTTGTGCTG 40610 TG T TA AA CT  
CAG CAGG GT AG GGGG  
||| ||||| || ||| |||||  
GTC GTTT CG TC CCCT  
GT \_ \_ AA TT

GAM1237 ARNTL2 3' AGCTCTTTTCCAGTTCACTTGT 39453 TG TTAA\_\_  
GCT G CAGGTG GAAGGGGCT  
| ||||| |||||||  
C GTTCAC TTTTCTCGA  
GT TTGACC

GAM1237 ARPC5 3' AGCTTGCTTAGTATTTACAT 19138 C AAG  
TG CAGTG AGGTGTAAAG GGGCT  
||||| ||||||||| |||||

			GTTAC TTTATGATTC TTCGA		
			A GTG		
GAM1237	BAIAP1	5'	AGCTCGCGGGCGCCTGTGC 16448	TG	AAGAAG
			G CAGGTGTT GGGCT		
			C GTCCGCGG CTCGA		
			GT GCG__		
GAM1237	BART1	3'	GCTCTGTGTTTCTGTACTG 23986		TGTTAAGAA
			CAGTGCAGG GGGGC		
			GTCATGTCT TCTCG		
			TTGTG__		
GAM1237	BIRC1	3'	AGTCTCTCCCATTCTGTACTG 15785		TGTTAA A
			CAGTGCAGG GA GGGGCT		
			GTCATGTCT CT CTCTGA		
			TACC__ _		
GAM1237	BMF	3'	GGCCCCTTCCTCCTCTGCCTG 53160	T	TGTTAA
			CAG GCAGG GAAGGGGCT		
			GTC CGTCT CTTCCCCGG		
			_ CCTC__		
GAM1237	BRD1	3'	AGCTTTTCTTAAAGACTT 27412	G_	
			AGGT TTAAGAAGGGGCT		
			TTCA AATTCTTTTCGA		
			GA		
GAM1237	BRD4	3'	AGTTCCTTCCACCTGTGTT 54272	TG	TTAA
			AG CAGGTG GAAGGGGCT		
			TT GTCCAC CTCCTTGA		
			GT C__		
GAM1237	BRPF3	3'	GGCTCCTTCTTGAGGGGCTGCC 92320	T	GTG_
	TG		CAG GCAG TTAAGAAGGGGCT		
			GTC CGTC AGTTCTTCCTCGG		
			_ GGGG		
GAM1237	C11orf15	3'	GGTTTCATTTTAATACCTTGTT 40223	T _	A GG
	G		G GCA GGTGTTAAGA G GCT		
			G TGT CCATAATTTT C TGG		
			T T A TT		
GAM1237	C11orf25	3'	GTTTCTTTTTCATGACTG 48645	G	GGTGTT GG
			CAGT CA AAGAAG GC		
			GTCA GT TTTTTC TG		
			_ ACT__ TT		
GAM1237	C16orf5	3'	AGCCCCTTCCCGTCTGCCCTG 25444	T	GT TTAA
			CAG GCAG G GAAGGGGCT		

GTC CGTC C CTTCCCCGA  
 C TG C\_\_\_\_  
 GAM1237 C1orf25 3' GGTTCTCAGGTGTCTGTAT 72538 TG AAGAA  
 GTGCAGG TT GGGGCT  
 ||||| || |||||  
 TATGTCT GG TCTTGG  
 GT AC\_\_\_\_  
 GAM1237 C20orf100 3' GGCCCTGGCGAGTGTCTGTCTT 51813 T TG AAGAA  
 G CAG GCAGG TT GGGGCT  
 || |||| || |||||  
 GTT TGTCT GA TCCCGG  
 C GT GCGG\_  
 GAM1237 C20orf110 3' AGCCCTTGTCTACTGTATTG 79541 \_ TTAAGA  
 CAGTGCAG GTG AGGGGCT  
 ||||| || |||||  
 GTTATGTC TAC TTCCCGA  
 A TG\_\_\_\_  
 GAM1237 C20orf124 3' GGCTCCGCGTGC GCCTGTAC 45488 TAAGAA  
 GTGCAGGTGT GGGGCT  
 ||||| |||||  
 CATGTCCGCG CCTCGG  
 TGCG\_\_\_\_  
 GAM1237 C20orf142 3' GGCCCAGGGCATCTGTAC 74781 AAGAAG  
 GTGCAGGTGTT GGGCT  
 ||||| |||||  
 CATGTCTACGG CCCGG  
 GA\_\_\_\_  
 GAM1237 C20orf177 3' AGTTCCTGAGTGATGTCTGTGT 62142 TG TG AGA  
 G CAGG TTA AGGGGCT  
 | ||| || |||||  
 T GTCT AGT TCCTTGA  
 GT GT GAG  
 GAM1237 C20orf183 3' GCTCGGGGCATCTGCCTG 47805 T AAGAAG  
 CAG GCAGGTGTT GGGC  
 || ||||| |||||  
 GTC CGTCTACGG CTCG  
 \_ GG\_\_\_\_  
 GAM1237 C22orf2 3' AGTTCTACAGAGCTCTGTGTTG 94453 TG T AAGAA  
 CAG CAGG GTT GGGGCT  
 || |||| || |||||  
 GTT GTCT CGA TCTTGA  
 GT \_ GACA\_  
 GAM1237 C3orf4 3' GCTGTTTGTATCTGCACTG 39121 TTAAG G  
 CAGTGCAGGTG AAG GGC  
 ||||| |||||  
 GTCACGTCTAT TTT TCG  
 G\_\_\_\_ G  
 GAM1237 C5orf6 3' GCCTTTTTGACCTGC 33483 GTTAA  
 GCAGGT GAAGGGGC  
 ||||| |||||

			CGTCCA	TTTTTCCG		
			G			
GAM1237	C6orf33	3'	GGTTCTTTGGTTACTGCACTG	55885	GTGTTAAG	
			CAGTGCAG	AAGGGGCT		
			GTCACGTC	TTTCTTGG		
			ATTGG			
GAM1237	CACNG4	3'	GGTGCTTTGGCCTTTGCGCTG	26955	T	GAA G
			CAGTGCAGG GTTAA	GG GCT		
			GTCGCGTTT CGGTT	TC TGG		
			C			
GAM1237	CALN1	3'	GCTTTGCCGCGCTGTGCTG	48871	TG	TTAAGAA
			CAG CAGGTG	GGGGC		
			GTC GTCCGC	TTTCG		
			GT	CG		
GAM1237	CAP350	3'	AGCCTTTTCTTTTCAGTTTGTG	29043	TG	_ TT
	TT		AG CAGG TG	AAGAAGGGGCT		
			TT GTTT AC	TTCTTTTCCGA		
			GT	G TT		
GAM1237	CARD9	5'	GGCTCCTGGTGTGTCTGCAGTG	42289	G	TG TAAGA
			CA TGCAGG T	AGGGGCT		
			GT ACGTCT G	TCCTCGG		
			G	GT TGG		
GAM1237	CARD9	5'	GGCTCCTGGTGTGTCTGCAGTG	53376	G	TG TAAGA
			CA TGCAGG T	AGGGGCT		
			GT ACGTCT G	TCCTCGG		
			G	GT TGG		
GAM1237	CARD9	5'	GGCTCCTGGTGTGTCTGCAGTG	53382	G	TG TAAGA
			CA TGCAGG T	AGGGGCT		
			GT ACGTCT G	TCCTCGG		
			G	GT TGG		
GAM1237	CASPR3	5'	GTCTCAGGGCGCCTGGCTG	53350	G	AAGAA
			CAGT CAGGTGTT	GGGGC		
			GTCG GTCCGCGG	CTCTG		
				GA		
GAM1237	CBX6	3'	AGTTTCTTCCCTATCTGCAT	26609	TTAA	GG
			GTGCAGGTG	GAAG GCT		
			TACGTCTAT	CTTC TGA		
			CC	TT		
GAM1237	CCT4	3'	GGTCTTCCAGTTGGCATTG	21220	T	GAA
	TG		CAG GCAGGTGTAA	GGGGCT		

GTC CGTTTACGGTT TTCTGG  
 \_ GACC  
 GAM1237 CCT5 5' AGTCCCGCGCGTCTTGTGCTG 72638 TG \_ TAAGAA  
 CAG CAGG TGT GGGGCT  
 ||| ||||| ||| |||||  
 GTC GTTC GCG CCCTGA  
 GT T CG\_\_\_\_  
 GAM1237 CDC10 3' TTTTGTGACACTTCCATTG 91113 C  
 CAGTG AGGTGTTAAGAAG  
 ||||| ||||| ||||| |||||  
 GTTAC TTCACAGTTTTTT  
 C  
 GAM1237 cerk 3' AGCATGACCTTGGCGTCTGTTC 42842 T GT AAGGG  
 TG CAG GCAG GTTAAG GCT  
 ||| ||||| ||||| |||  
 GTC TGTC CGGTTC CGA  
 T TG CAGTA  
 GAM1237 cerk 3' GCCCTTTGCTATCTGCGC 42849 \_ TAAG  
 GTGCAGGT GT AAGGGGC  
 ||||| || |||||  
 CGCGTCTA CG TTTCCCG  
 T \_\_\_\_  
 GAM1237 CFDP1 3' GGTCTTTTTTTTTTCTACATTG 20902 C TGTT  
 CAGTG AGG AAGAAGGGGCT  
 ||||| ||| ||||| |||||  
 GTTAC TCT TTTTTTCTGG  
 A TT\_\_\_\_  
 GAM1237 CG012 5' GCCATAATTTTGTAT 83222 AGAAGG  
 GTGCAGGTGTTA GGC  
 ||||| ||||| |||  
 TATGTTTATAAT CCG  
 A\_\_\_\_  
 GAM1237 CG018 5' GGCAATTTTAGCATCTGCTCTG 53394 T AGGG  
 CAG GCAGGTGTTAAGA GCT  
 ||| ||||| ||||| |||  
 GTC CGTCTACGATTTT CGG  
 T AA\_\_\_\_  
 GAM1237 CHST4 3' AGTTCACAGGGTGCCTGGGCTG 19303 G TG AAGAAG  
 CAGT CAGG TT GGGCT  
 ||||| ||||| ||| |||||  
 GTCG GTCC GG CTTGA  
 G GT GACA\_\_\_\_  
 GAM1237 CLIPR-59 3' GCCCACAGCTCCTGTGCTG 31373 TG T AAGAAG  
 CAG CAGG GTT GGGC  
 ||| ||||| ||| |||||  
 GTC GTCC CGA CCCG  
 GT T CA\_\_\_\_  
 GAM1237 CNNM1 3' GCCCCGGGGTGCCTGCCTG 39773 T TG AAGAA  
 CAG GCAGG TT GGGGC  
 ||| ||||| ||| |||||



			GTC CGTCC GG CCCCCG		
			_ GT GG__		
GAM1237	CNNM4	3'	AGCTGCCTGAGCACCTGCGCTG 39472	TAAGA	_
			CAGTGCAGGTGT AGG GGCT		
			GTCGCGTCCACG TCC TCGA		
			AG__ G		
GAM1237	CNNM4	3'	GTCATCAGCATCTGCGTTG 39483	AAGAAGG	
			CAGTGCAGGTGTT GGC		
			GTTGCGTCTACGA CTG		
			CTA__		
GAM1237	CNOT7	3'	CTCTTTTACTGCATTG 53985	GTGTTAA	
			CAGTGCAG GAAGGGG		
			GTTACGTC TTTTCTC		
			A__		
GAM1237	CNTNAP1	3'	AGCACCTTAGTACCTCCGCTG 13275	C TTAAG	G
			CAGTG AGGTG AAGG GCT		
			GTCGC TCCAT TTCC CGA		
			C GA__ A T		
GAM1237	COASTER	3'	AGTTCTTTAATTTTATTTGTAC 31445	TTAAG	
	TG		CAGTGCAGGTG AAGGGGCT		
			GTCATGTTTAT TTTCTTGA		
			TTTAA		
GAM1237	COASTER	3'	GTCCTTTTTTATATATT 31447	_	
			GGTGT TAAGAAGGGGC		
			TTATA ATTTTTCCTG		
			T		
GAM1237	COVA1	3'	GTCCCTTTGCTTCTGTTG 73261	T T TAA	
			G GCAGG GT GAAGGGGC		
			G TGTCT CG TTTCCCTG		
			T T _		
GAM1237	CPEB1	5'	AGTTTCTTTCATGATTCCTGT 47595	T_ A_ GG	
	ATTG		AGTGCAGG GTTA GAAG GCT		
			TTATGTCC TAGT TTTC TGA		
			TT AC TT		
GAM1237	CRK7	3'	AGTCTCTTTCCTTTTTTGC 33251	TGTTAA	
			GCAGG GAAGGGGCT		
			CGTTT TTTCTCTGA		
			TTTCC_		
GAM1237	CSE-C	3'	AGCCCAGCGAAGGCACTTGGGC 91480	G AAGAAG	
	TG		CAGT CAGGTGTT GGGCT		

			GTCG GTTCACGG	CCCGA		
			G	AAGCGA		
GAM1237	CSMD1	3'	TTCTAAATGCCTGGCTG	52643	G	A
			CAGT CAGGTGTT AGAA			
			GTCG GTCCGTAA TCTT			
			—	A		
GAM1237	CTAGE-1	3'	AGTTCCTTGTGTCTGACATTG	42649	—	TG TAAG
			CAGTG CAGG T AAGGGGCT			
			GTTAC GTCT G TTCCTTGA			
			A GT	—		
GAM1237	CUL4A	3'	AGTCCCTGTTTTTTTGCATTG	13151		TGTTAAGA
			CAGTGCAGG AGGGGCT			
			GTTACGTTT TCCCTGA			
			TTTTG	—		
GAM1237	CUL4A	3'	AGTCTCTTTTTGAAACATGCG	13152	G	G
			TGCA GT TTAAGAAGGGGCT			
			GCGT CA AGTTTTTCTCTGA			
			A A			
GAM1237	CYorf15B	3'	AGTTTTTTGACAATATTTGTAT	50817		AAG
			GTGCAGGTGTT AAGGGGCT			
			TATGTTTATAA TTTTTTGA			
			CAG			
GAM1237	DATF1	5'	GCTTCCGTACTTGCGC	42070		TTAAGAA
			GTGCAGGTG GGGGC			
			CGCGTTCAT CTTCG			
			GC	—		
GAM1237	DDX17	5'	AGCTCCTTTTTTTTACTTTGCTC	48037	T	— TT
	TG		CAG GCAG GTG AAGAAGGGGCT			
			GTC CGTT CAT TTTTCCTCGA			
			T T T	—		
GAM1237	DDX21	5'	GCCTGGGCAACCTGCGCTG	16385	—	AAGAAG
			CAGTGCAGGT GTT GGGC			
			GTCGCGTCCA CGG TCCG			
			A G	—		
GAM1237	DDX32	5'	GGCTTTTAAGCCCTGTTTGC	36418	—	T A GGGCT
			GT GCAGG GTT AGAAG			
			CG TGTCC CGA TTTTC			
			TT — A GG			
GAM1237	DGCR6L	3'	GGCCCACCCGAGCGCTTGTCT	52689	T	AAGAAG
	G		CAG GCAGGTGTT GGGCT			

GTC TGTTCGCGA CCCGG  
 T GCCCA\_  
 GAM1237 DGKD 3' CTTCTTGTGCGCCTGCTGCTG 59406 \_ T  
 CAGT GCAGGTG TAAGAAG  
 |||| ||||| |||||  
 GTCG CGTCCGC GTTCTTC  
 T T  
 GAM1237 DJ667H12.2 3' AGTTTCTGGCTTGCCTGT 38983 GTT A\_ GG  
 GCAGGT AAG AG GCT  
 ||||| ||| || |||  
 TGTCCG TTC TC TGA  
 \_ GG TT  
 GAM1237 DKFZP434A1315 3' GGCTCTTTTGTCAATTGTGCTG 67706 TG G TTAA  
 CAG CAG TG GAAGGGGCT  
 ||| ||| || |||||  
 GTC GTT AC TTTTCTCGG  
 GT \_ TG\_  
 GAM1237 DKFZp434A2417 3' TTCTTTGTTTGCCTG 66112 TT G  
 CAGGTG AA AAGGGG  
 ||||| || |||||  
 GTCCGT TT TTTCTT  
 \_ G  
 GAM1237 DKFZP434C0826 5' AGCCTCTTCATTAGGCTTGC 84033 G \_  
 GCAGGT TTAA GAAGGGGCT  
 ||||| ||| |||||  
 CGTTCG GATT CTTCTCCGA  
 \_ A  
 GAM1237 DKFZP434C1715 3' AGTCTAAGAAATAGTTATTTGC 86143 TTAAGAAG\_  
 ATTG AGTGCAGGTG GGGCT  
 ||||| ||| |||||  
 TTACGTTTAT TCTGA  
 TGATAAAGAA  
 GAM1237 DKFZP434C212 3' GGCTCTTTCCTTTCTGAGTTG 68915 TG TGTTAA  
 CAG CAGG GAAGGGGCT  
 ||| ||| |||||  
 GTT GTCT CTTTCTCGG  
 GA TTC\_  
 GAM1237 DKFZP434E2135 3' AGCCAGGATAGTGTCTGTCTG 47949 T TG AGAAGG  
 CAG GCAGG TTA GGCT  
 ||| |||| ||| |||||  
 GTC TGTCT GAT CCGA  
 \_ GT AGGA\_  
 GAM1237 DKFZP434E2135 3' ATAATTTTCTTGGTGCCTTAT 47950 C TG GCT  
 TG CAGTG AGG TTAAGAAGGG  
 ||||| ||| |||||  
 GTTAT TCC GGTTCTTTT  
 \_ GT AATAA  
 GAM1237 DKFZp434G179 3' GAAGCTTTTCTAGACATTTGTG 80090 TG A G  
 TTG CAG CAGGTGTT AGAAGGG CT  
 ||| ||||| ||||| |||

GTT GTTTACAG TCTTTTC GA  
 GT A \_ AGA  
 GAM1237 DKFZP434I0714 5' GTTCTTTCTTACGGTTTG 85801 GG GT  
 CA T TAAGAAGGGGC  
 || | |||||  
 GT G ATTCTTTCTTG  
 TT GC  
 GAM1237 DKFZp434I1930 3' AGTCTTGCGATGAATTCTGCAT 50031 TG AGAA  
 TG CAGTGCAGG TTA GGGGCT  
 ||||| || |||||  
 GTTACGTCT AGT TTCTGA  
 TA AGCG  
 GAM1237 DKFZP434N014 3' GGTCAGGAAGCTGGTGCTGTACT 60601 G TG AGAAGG  
 G CAGTGCA G TTA GGCT  
 ||||| | || |||||  
 GTCATGT C GGT CTGG  
 \_GT CAAGGA  
 GAM1237 DKFZp434O0320 3' AGCCAGTGAGGCCTGTGCTG 83690 TG G AGAAG  
 CAG CAGGT TTA GGGCT  
 || |||| || |||||  
 GTC GTCCG AGT CCCGA  
 GT G GA\_\_  
 GAM1237 DKFZP434P1750 3' GGCTCTCATTCTGGACCTGTGT 31378 TG GTTA \_\_  
 TG CAG CAGGT AGAA GGGGCT  
 || |||| || |||||  
 GTT GTCCA TCTT TCTCGG  
 GT GG\_\_ AC  
 GAM1237 DKFZp547I094 3' CCCGGGCACCTGCCTG 49635 T AAGAAG  
 CAG GCAGGTGTT GGG  
 || ||||| ||  
 GTC CGTCCACGG CCC  
 \_ G\_\_\_\_  
 GAM1237 DKFZp547M236 5' GGCTTCCAGATTTGCATCTGTG 38038 TG T GAA\_  
 CTG CAG CAGGTGT AA GGGGCT  
 || ||||| || |||||  
 GTC GTCTACG TT CTTCGG  
 GT T AGAC  
 GAM1237 DKFZP564A2416 3' GGCTCAGTTAGCAACCTGTGTT 31388 TG \_ GAAG  
 G CAG CAGGT GTTAA GGGCT  
 || |||| |||| |||||  
 GTT GTCCA CGATT CTCGG  
 GT A GA\_\_  
 GAM1237 DKFZP564D0478 3' AGCCCTTTTGTCTTCTGTTG 49531 T TGTTAA  
 G GCAGG GAAGGGGCT  
 | |||| |||||  
 G TGTCT TTTCCCCGA  
 T TCTTG\_  
 GAM1237 DKFZP564D166 3' AGCCTTTTTTTAAAGAGGTGT 47669 TG AGGTG  
 T AG C TTAAGAAGGGGCT  
 || | |||||

TT G AATTTTTTCCGA  
 GT GAGAA  
 GAM1237 DKFZP564D172 3' GCTGTTAATATCTCATTG 49389 C AGAA G  
 CAGTG AGGTGTTA G GGC  
 ||||| ||||| I |||  
 GTTAC TCTATAAT T TCG  
 \_ \_ \_ G  
 GAM1237 DKFZP564I122 3' GGCCCTGGGAATTCTGTACTG 63176 T AAGAA  
 CAGTGCAGG GTT GGGGCT  
 ||||| ||| |||||  
 GTCATGTCT TAA TCCCGG  
 \_ GGG \_  
 GAM1237 DKFZp564K142 3' AGCTTCTTCATCTTTGTGT 49523 TG T TAA  
 G CAGG GT GAAGGGGCT  
 I ||||| || |||||  
 T GTTT TA CTTCTTCGA  
 GT C \_  
 GAM1237 DKFZP564K2062 3' AGTTCTTACAGCACTTGT 31236 AAGA  
 GCAGGTGTT AGGGGCT  
 ||||| |||||  
 TGTTCACGA TTCTTGA  
 CA \_  
 GAM1237 DKFZP564L0862 3' AGTTTTTTCGATTAGATTTGTA 44022 GTTAA \_  
 TT AGTGCAGGT GAAGGGGCT  
 ||||| |||||  
 TTATGTTTA CTTTTTGA  
 GATTAG  
 GAM1237 DKFZP564M182 3' TTAGCATTTGCTCTG 78048 T  
 CAG GCAGGTGTTAAG  
 ||| |||||  
 GTC CGTTTACGATTT  
 T  
 GAM1237 DKFZp566H0824 5' GCCTCTTGCTATCTGCCTG 34052 T \_ TAAG  
 CAG GCAGGT GT AAGGGGC  
 ||| ||||| || |||||  
 GTC CGTCTA CG TTCTCCG  
 \_ T \_  
 GAM1237 DKFZp566H0824 5' GGCTCCTTTTGGCACTTCCAT 34057 A C  
 CC C GTG AGGTGTTAAGAAGGGGCT  
 I ||| |||||  
 C TAC TTCACGGTTTTTCCTCGG  
 C C  
 GAM1237 DKFZp566H0824 5' AGCCTTTTCTCCACTGATTTGT 34045 TG \_ TA  
 GTTG AG CAGGT GT AGAAGGGGCT  
 || ||||| || |||||  
 TT GTTTA CA TCTTTTCCGA  
 GT GT CC  
 GAM1237 DKFZP566M1046 3' CTCCTTTTATGTTTG 49536 TG T  
 CAGG T AAGAAGGGG  
 |||| I |||||

GTTT A TTTTCCTC  
 GT\_  
 GAM1237 DKFZP586J1624 3' GTCTGAGGGCACCTGGCTG 31398 G AAGAAG  
 CAGT CAGGTGTT GGGC  
 ||| ||||| |||  
 GTCG GTCCACGG TCTG  
 \_ GAG\_  
 GAM1237 DKFZP586M0622 5' GCTTAAACACTTGTGGTG 31484 G AAGAAG  
 CA TGCAGGTGTT GGGC  
 || ||||| |||  
 GT GTGTTCAAA TTCG  
 G AA\_  
 GAM1237 DKFZP727M111 3' CTTCTGAAGGTCTGTGCTG 31409 TG TG A  
 CAG CAGG TT AGAAG  
 ||| ||| || |||||  
 GTC GTCT AA TCTTC  
 GT GG G  
 GAM1237 DKFZP761D0211 3' GCCATGGTGCTCTGTACTG 49355 T TAAGAAGG  
 CAGTGCAGG GT GGC  
 ||||| || |||  
 GTCATGTCT CG CCG  
 \_ TGGTA\_  
 GAM1237 DKFZP761D0211 3' GGCCCTCCCTGGGTCTCTGCA 49356 TG TA A\_  
 CTG CAGTGCAGG T AG AGGGGCT  
 ||||| | || |||||  
 GTCACGTCT G TC TTCCCGG  
 CT GG CC  
 GAM1237 DKFZP761E2110 3' AGCTCTTTTTCCTTTCTGC 48223 TGTT  
 GCAGG AAGAAGGGGCT  
 |||| |||||  
 CGTCT TTTTTCTCGA  
 TTCC  
 GAM1237 DKFZp761G0313 3' GCTTTTCTTAGCTGATG 65816 GGT  
 CA GTTAAGAAGGGGC  
 || |||||  
 GT CGATTCTTTTCG  
 AGT  
 GAM1237 DKFZP761G1913 3' GGCCTCTTGAGCTTAAGCTTGT 48915 G \_  
 ATTG GTGCAGGT TTAAG AAGGGGCT  
 ||||| |||| |||||  
 TATGTTCA AATTC TTCTCCGG  
 \_ GAG  
 GAM1237 DKFZp761H079 3' GGTGCTTTTGGTAACTTGTACT 58735 GTTAA G  
 G CAGTGCAGGT GAAGG GCT  
 ||||| |||| |||  
 GTCATGTTCA TTTTC TGG  
 ATGG\_ G  
 GAM1237 DMRTB1 3' TTCAATCCTGCGCTG 66246 T AAGAA GG  
 CAGTGCAGG GTT G G  
 ||||| || | |

			GTCGCGTCC TAA C T		
			— TT		
GAM1237	DNAJA2	3'	AGTTTCAATCCTGGTATCTGTG 59779	TG	TT A A_ GG
	CT		AG CAGGTG A GA G GCT		
			TC GTCTAT T CT C TGA		
			GT GG C AA TT		
GAM1237	DNAJA4	5'	AGTCCCTTAATATGTTTGCCCT 37753	T	TG TAAG
	G		CAG GCAGG T AAGGGGCT		
			GTC CGTTT A TTCCCTGA		
			C GT TAA_		
GAM1237	DORFIN	3'	GGCCAAAATACTGCCTGTACTG 31260		_ TAAGAAGG
			CAGTGCAGGT GT GGCT		
			GTCATGTCCG CA CCGG		
			T TAAAA_		
GAM1237	EHM2	3'	AGTCTTTAACATTCATTTGTAT 38912		TTAAGA
	T		AGTGCAGGTG AGGGGCT		
			TTATGTTTAC TTTCTGA		
			TTACAA		
GAM1237	EIF5	5'	GCCATTGGTACCTGTATTG 8760		TT GAAGG
			CAGTGCAGGTG AA GGC		
			GTTATGTCCAT TT CCG		
			GG A_		
GAM1237	ELAC1	3'	TTTTGGCAGTTTGTATTG 90974		_
			CAGTGCAGG TGTTAAGA		
			GTTATGTTT ACGGTTTT		
			G		
GAM1237	EPN2	3'	GGCTGGTTTTGAAC TTGTGTTG 30327	TG	G AGG
			CAG CAGGT TTAAGA GGCT		
			GTT GTTCA AGTTTT TCGG		
			GT _ GG_		
GAM1237	ESPL1	5'	GCCCCTCCATGCCTGC 24459		TAA A
			GCAGGTGT GA GGGGC		
			CGTCCGTA CT CCCC		
			C_ _		
GAM1237	ETR101	3'	TTTTTCTCATCTGCATT 72368		TTA
			AGTGCAGGTG AGAAGGG		
			TTACGTCTAC TCTTTT		
			—		
GAM1237	FARP1	3'	GGTAAAATTAACACCTGTCTG 19281	T	GAAGGG
			CAG GCAGGTGTAA GCT		

GTC TGTCCACAATT TGG  
 \_ AAAA\_  
 GAM1237 FARSL 3' GGTTCCTTCTGTTGTCCTGTGT 15515 TG TGTTA  
 G CAGG AGAAGGGGCT  
 | ||| |||||  
 T GTCC TCTTCCTTGG  
 GT TGTTG  
 GAM1237 FASTK 3' GGCCCTGGGCCTGCGCTG 52247 GTTAAGAA  
 CAGTGCAGGT GGGGCT  
 ||||| ||||  
 GTCGCGTCCG TCCCGG  
 GG\_\_\_\_\_ A  
 GAM1237 FASTK 3' GGCCCTGGGCCTGCGCTG 46992 GTTAAGAA  
 CAGTGCAGGT GGGGCT  
 ||||| ||||  
 GTCGCGTCCG TCCCGG  
 GG\_\_\_\_\_ A  
 GAM1237 FBP17 3' AGCTTCCACTGGAGGCTTGTAT 72778 G A AA  
 TG CAGTGCAGGT TT AG GGGGCT  
 ||||| || || ||||  
 GTTATGTTTCG AG TC CTTCGA  
 G G AC  
 GAM1237 FBXL9 5' AGTTGGGCTTGGTACCGTGCTG 24079 TG A TT AAGG  
 CAG C GGTG AAG GGCT  
 || | ||| || ||||  
 GTC G CCAT TTC TTGA  
 GT\_ GG GGG\_  
 GAM1237 FKSG17 3' AGCTTGGTTTGAAATTTGTACT 49327 G AAG  
 G CAGTGCAGGT TTAAG GGGCT  
 ||||| |||| ||||  
 GTCATGTTTA AGTTT TTCGA  
 A GG\_  
 GAM1237 FLJ00007 3' GTCCTCCATTCTGTACTG 71278 TGTTAAGAA  
 CAGTGCAGG GGGGC  
 ||||| ||||  
 GTCATGTCT TCCTG  
 TACC\_\_\_\_\_  
 GAM1237 FLJ10035 3' AGTTTCAAAATATTTGCA 35745 AAGAA GG  
 TGCAGGTGTT G GCT  
 ||||| | |||  
 ACGTTTATAA C TGA  
 AA\_\_ TT  
 GAM1237 FLJ10043 3' TCCCTTTGTCTGTCTG 35763 T GT TTAAG  
 CAG GCAG G AAGGGG  
 || ||| | ||||  
 GTC TGTC T TTCCCT  
 \_ TG\_\_\_\_\_  
 GAM1237 FLJ10052 3' AGCCTCTGCAGAAAGTTTGTGT 35770 TG TG AAGA  
 TG CAG CAGG TT AGGGGCT  
 || ||| || |||||



GTT GTTT AA TCTCCGA  
 GT GA GACG  
 GAM1237 FLJ10055 3' AGTCTTTTTTGGCTGTGGCTG 35775 \_ G GTTA  
 CAGT GCAG T AGAAGGGGCT  
 |||| ||| | |||||  
 GTCG TGTC G TTTTTTCTGA  
 G G \_\_\_\_  
 GAM1237 FLJ10058 3' CTTTTTGTGTCTGTGTTG 35784 TG GT T  
 CAG CAG G TAAGAAG  
 ||| ||| | |||||  
 GTT GTC T GTTTTTT  
 GT TG T  
 GAM1237 FLJ10178 3' GGCCCGGTGGTTGACATCTGTG 35870 TG GAAG\_  
 T G CAGGTGTAA GGGCT  
 | ||||| ||||  
 T GTCTACAGTT CCCGG  
 GT GGTGG  
 GAM1237 FLJ10193 3' AGCTTCTTGAAACATTTGCAT 35880 AAG  
 GTGCAGGTGTT AAGGGGCT  
 ||||| |||||  
 TACGTTTACAA TTCTTCGA  
 AG\_  
 GAM1237 FLJ10204 3' GCCCCTCATGTCTGTTTTG 35895 T TG TAA A  
 CAG GCAGG T GA GGGGC  
 ||| ||| | || ||||  
 GTT TGTCT A CT CCCCCG  
 T GT \_\_\_\_  
 GAM1237 FLJ10210 5' GGCTCCTTCTCTCCCTTTGCTG 35901 C TGTTA  
 CAGTG AGG AGAAGGGGCT  
 |||| ||| |||||  
 GTCGT TCC TCTTCCTCGG  
 T CTC\_  
 GAM1237 FLJ10352 3' TTCTGTGTTTGCATTG 49563 TG TAAGAA  
 CAGTGCAGG T GGGG  
 ||||| | ||||  
 GTTACGTTT G TCTT  
 GT \_\_\_\_  
 GAM1237 FLJ10385 5' GGTTTCTTTAGCTCTGCG 36084 T GA GG  
 TGCAGG GTTAA AG GCT  
 |||| |||| || |||  
 GCGTCT CGATT TC TGG  
 \_ \_ TT  
 GAM1237 FLJ10458 3' GCCCCCGCCCTTGCACTG 36124 T TAAGAA  
 CAGTGCAGG GT GGGGC  
 ||||| || ||||  
 GTCACGTTC CG CCCCCG  
 C C \_\_\_\_  
 GAM1237 FLJ10498 3' GTCCAGACACACTGTATTG 36194 \_ AAGAAG  
 CAGTGCAG GTGTT GGGC  
 ||||| |||| ||||

GTTATGTC CACAG CCTG  
 A A\_\_\_\_  
 GAM1237 FLJ10546 3' AGTTTTTTTTTAGGGTGCTG 59474 TG AGGTGT  
 CAG C TAAGAAGGGGCT  
 ||| | |||||  
 GTC G ATTTTTTTTGA  
 GT GG\_\_\_\_  
 GAM1237 FLJ10579 3' GGCTTTTTTCCTTAGACCTTGC 36302 C G \_\_\_\_  
 TG CAGTG AGGT TTAAG AAGGGGCT  
 |||| ||| |||| |||||  
 GTCGT TCCA GATTC TTTTTCGG  
 \_ \_ CT  
 GAM1237 FLJ10661 3' GGCTCCAAAAATAGCATTTTCA 36391 C AGAA\_  
 TTG CAGTG AGGTGTTA GGGGCT  
 |||| ||||| |||||  
 GTTAC TTTACGAT CCTCGG  
 T AAAAA  
 GAM1237 FLJ10702 3' AGTCTTTGTTCAAACATCTGT 36437 AAGA\_  
 GCAGGTGTT AGGGGCT  
 ||||| |||||  
 TGTCTACAA TTTCTGA  
 ACTTG  
 GAM1237 FLJ10704 3' TCTTCTTAGCATTTTACTG 36459 C  
 CAGTG AGGTGTTAAGAAGG  
 |||| |||||  
 GTCAT TTTACGATTCTTCT  
 \_  
 GAM1237 FLJ10743 3' GCTCTGAGTTCTGTACTG 36550 TGTTAAGAA  
 CAGTGCAGG GGGGC  
 ||||| |||||  
 GTCATGTCT TCTCG  
 TGAG\_\_\_\_  
 GAM1237 FLJ10769 3' GCTTGGTGGTATCTGGCTG 36598 G TT AGAAG  
 CAGT CAGGTG A GGGC  
 ||| ||||| | |||  
 GTCG GTCTAT T TTCG  
 \_ GG GG\_\_\_\_  
 GAM1237 FLJ10983 3' AGCCTTGGGTATACTTGCACTT 36939 TAAGAA  
 AGTGCAGGTGT GGGGCT  
 ||||| |||||  
 TTACGTTTATA TTCCGA  
 TGGG\_\_\_\_  
 GAM1237 FLJ10986 5' AGTCCTCCGAGGACATCTGGGC 36942 G AAGAA  
 TG CAGT CAGGTGTT GGGGCT  
 ||| ||||| |||||  
 GTCG GTCTACAG TCCTGA  
 G GAGCC  
 GAM1237 FLJ11053 3' GGTTTCTTTCTACTCTGC 88731 T TAA GG  
 GCAGG GT GAAG GCT  
 |||| || ||| |||

CGTCT CA TTTC TGG  
\_ TC\_ TT

GAM1237 FLJ11088 3' GGTTTCTTCTTTACATTTACTG 37041 CA T GG  
CAGTG GGTGT AAGAAG GCT  
||||| ||||| ||||| |||  
GTCAT TTACA TTCTTC TGG  
\_ T TT

GAM1237 FLJ11210 3' AGCTTCTCCTTAACCTGTATTG 59574 GT A  
CAGTGCAGGT TAAG AGGGGCT  
||||||| ||| |||||  
GTTATGTCCA ATTC TCTTCGA  
\_ C

GAM1237 FLJ11259 5' GGTGTCTTTAGTGCTTGGATTG 37191 G TG GA G  
CAGT CAGG TTAA AGG GCT  
||||| ||| ||| |||  
GTTA GTTC GATT TCT TGG  
G GT \_ G

GAM1237 FLJ11506 3' AGCTCTGAGCTATGATGCTTTT 45109 C \_ AA\_  
ATTG AGTG AGGTGTTA AG GGGGCT  
||||| ||| |||||  
TTAT TTCGTAGT TC TCTCGA  
T A GAG

GAM1237 FLJ11608 3' GGCCTTTTCTCCTTACTGCATC 44651 \_ GTGTTA  
TG CAG TGCAG AGAAGGGGCT  
||| ||||| |||||  
GTC ACGTC TCTTTTCCGG  
T ATTCC\_

GAM1237 FLJ11827 3' AGTTCTGGGCTGTAGTGCACCTG 46983 TG \_TG \_ AA\_  
TGCTG CAG G TTA AG GGGGCT  
||| ||| ||| |||||  
GTC C GAT TC TCTTGA  
GT A GT G GGG

GAM1237 FLJ12132 3' AGCCCCTTGTGACCTGCTTCAC 46465 C \_ AG  
TG CAGTG AGGT GTTA AAGGGGCT  
||||| ||| |||||  
GTCAC TTCG CAGT TTCCCCGA  
\_ TC G\_

GAM1237 FLJ12568 3' TTCTTGGTGTGTTGACTG 46503 G TG  
CAGT CAGG TTAAGAA  
||||| |||||  
GTCA GTTT GGTTCTT  
\_ GT

GAM1237 FLJ12587 3' GGCTTCCCAGGCACCTGCAGTG 42498 G AAGAA  
CA TGCAGGTGTT GGGGCT  
|| ||||| |||||  
GT ACGTCCACGG CTTCGG  
G ACC\_

GAM1237 FLJ12770 3' AGCTACTACTTTGCATCTGTAC 49734 T A GG  
TG CAGTGCAGGTGT AAG AG GCT  
||||||| ||| ||| |||

GTCATGTCTACG TTC TC CGA  
 T A AT  
 GAM1237 FLJ12891 3' GCCCCTTGGA CTGGTGCTG 46342 TG AGGT AAG  
 CAG C GTT AAGGGGC  
 ||| | ||| |||||  
 GTC G CAG TTCCCCG  
 GT GT\_ G\_  
 GAM1237 FLJ13187 3' AGTCTCTTTTTTACAAAGCCTG 44841 TG \_ T  
 TGTT CAGGT GT AAGAAGGGGCT  
 |||| || |||||  
 GTCCG CA TTTTCTCTGA  
 GT AAA T  
 GAM1237 FLJ13213 3' GGTTTTGTAAATACTTGTAT 45399 AAGAA  
 GTGCAGGTGTT GGGGCT  
 ||||| |||||  
 TATGTTCATAA TTTTGG  
 ATG\_  
 GAM1237 FLJ13340 3' GTCTCTTGACCTGTATT 54108 GTTAAG  
 AGTGCAGGT AAGGGGC  
 ||||| |||||  
 TTATGTCCA TTCTCTG  
 G\_  
 GAM1237 FLJ13441 3' GGTTCTCCTTGGCACCTGTGC 43671 TG AA  
 G CAGGTGTTAAG GGGGCT  
 | ||||| |||||  
 C GTCCACGGTTC TCTTGG  
 GT C\_  
 GAM1237 FLJ13449 3' AGTTCTTGATCCACTTGCATT 44616 TTAAGA  
 AGTGCAGGTG AGGGGCT  
 ||||| |||||  
 TTACGTTAC TTCTTGA  
 CTAG\_  
 GAM1237 FLJ13593 3' TTTTAAATACCTGGATTG 45504 G  
 CAGT CAGGTGTTAAGAA  
 ||| |||||  
 GTTA GTCCATAATTTT  
 G  
 GAM1237 FLJ13769 3' AGCTGACCCTAGTGCTTGTAGT 46596 G TG AAGA \_  
 G A TGCAGG TT AGGG GCT  
 | |||| || ||| |||  
 T ATGTTT GA TCCC CGA  
 G GT \_ AGT  
 GAM1237 FLJ13782 3' AGCTCCTTCTCCAGCTTTGGCT 46160 GC GTTA  
 G CAGT AGGT AGAAGGGGCT  
 ||| ||| |||||  
 GTCG TTCG TCTTCCTCGA  
 GT ACC\_  
 GAM1237 FLJ13848 3' GGCCCTCTGCTGAGCACTTTG 45469 \_ A A\_  
 CGCTG TGCAG GTGTT AG AGGGGCT  
 |||| |||| || |||||

GCGTT CACGA TC TCCCCGG  
 T G GTC  
 GAM1237 FLJ13993 3' GGCTCTTTCTGGCTTGAAGT 60463 G GTTA  
 CAGT CAGGT AGAAGGGGCT  
 |||| |||| ||||  
 GTCA GTTCG TCTTTCTCGG  
 A G\_\_  
 GAM1237 FLJ13993 3' GTTTCTTCCTCTCCGCTG 60464 C TGTTAA GG  
 CAGTG AGG GAAG GC  
 |||| || |||| ||  
 GTCGC TCT CTTC TG  
 C C\_\_ TT  
 GAM1237 FLJ14082 5' AGCTCCATAGGTGACTGCACTG 46666 GTGTAAAGAA  
 CAGTG CAG GGGGCT  
 |||| || ||||  
 GTCACGTC CCTCGA  
 AGTGGATA\_\_  
 GAM1237 FLJ14082 3' AGTCCCTTTTGCCGGCACCTG 46667 T TA\_\_  
 CCTG G GCAGGTGT AGAAGGGGCT  
 | |||| ||||  
 C CGTCCACG TTTTCCTGA  
 \_ GCCGG  
 GAM1237 FLJ14251 3' AGCTCAGAGCACTTGTGTCTG 45965 \_ AAGAAG  
 CAG TGCAGGTGTT GGGCT  
 || |||| ||||  
 GTC GTGTTACGA CTCGA  
 T GA\_\_  
 GAM1237 FLJ14251 3' TTCCCACTGGTGATGCCTGTCT 45980 T AGA \_ CT  
 G CAG GCAGGTGTTA AG GGG  
 || |||| || ||||  
 GTC TGTCCGTAGT TC CCC  
 \_ GG\_ A TTG  
 GAM1237 FLJ14326 3' AGCTTCTCTGGTGCCTTTGCTG 49798 C TG A A  
 CAGTG AGG TTA GA GGGGCT  
 |||| || || ||||  
 GTCGT TCC GGT CT CTTCGA  
 T GT \_ \_  
 GAM1237 FLJ14326 3' GGTCTTTGGACCACTCTGTGTT 49816 TG \_ TTAAGA  
 G CAG CAG GTG AGGGGCT  
 || || || ||||  
 GTT GTC CAC TTTCTGG  
 GT T CAGG\_\_  
 GAM1237 FLJ14327 3' GCCCTCCAGCATCTGTCTG 46140 T AAGAA  
 CAG GCAGGTGTT GGGGC  
 || |||| ||||  
 GTC TGTCTACGA TCCCG  
 \_ CC\_\_  
 GAM1237 FLJ14327 3' TCTAGCGCCTGTACTG 46149 A  
 CAGTGCAGGTGTTA GA  
 |||| |||| ||

GTCATGTCCGCGAT CT

GAM1237 FLJ14437 5' AGCTTCTTACAGCCATCTTCAC 50824 C TTAAG  
TG CAGTG AGGTG AAGGGGCT

||||| ||||| |||||  
GTCAC TCTAC TTCTTCGA  
T CGACA

GAM1237 FLJ14641 3' GTTCCTACTGCCTGTGCTG 51491 TG GTTA A  
CAG CAGGT AG AGGGGC

||| ||||| || |||||  
GTC GTCCG TC TCCTTG  
GT \_\_\_\_ A

GAM1237 FLJ14681 3' ACTTCTCTTTGACATTTGTA 51521 GA CT  
G CAGTGCAGGTGTAA AGGGG

||||||| |||||  
GTCATGTTTACAGTT TCTTC  
TC A

GAM1237 FLJ14775 3' GGCTTAACAGTTGGCATCGTAC 51604 A GAAG\_  
TG CAGTGC GGTGTAA GGGCT

||||| ||||| |||||  
GTCATG CTACGGTT TTCGG  
GACAA

GAM1237 FLJ14824 3' AGCCTCTTTTAAAGTGTG 51639 G TG  
CA G TTAAGAAGGGGCT

||| |||||  
GT T AATTTTCTCCGA  
G GA

GAM1237 FLJ14904 3' AGCATCTTGGCATTGTGCT 51692 TG AGGG  
AG CAGGTGTAAAGA GCT

|| ||||| |||||  
TC GTTACGGTTCT CGA  
GT A\_\_

GAM1237 FLJ20033 3' GCTCGGAATAGTTGCACTG 34346 G AAGAAG  
CAGTGCAG TGTT GGGC

||||| ||||| |||||  
GTCACGTT ATAA CTCG  
G GG\_\_

GAM1237 FLJ20034 3' AGCCTCTTTGATCTTGATT 34355 TGTTAA  
AGTGCAGG GAAGGGGCT

||||| |||||  
TTATGTTT TTTCTCCGA  
TAG\_\_

GAM1237 FLJ20034 3' GGTCCTGCGTTAGTGTCTGCAC 34380 TG GAA  
GTGCAGG TAA GGGGCT

||||| ||||| |||||  
CACGTCT GATT TCCTGG  
GT GCG

GAM1237 FLJ20128 3' AGCCCCTTTACCCTGGTCCTGT 34596 TGTTAA\_  
ACTG AGTGCAGG GAAGGGGCT

||||| |||||

TCATGTCC    TTTCCCCGA  
           TGGTCCCA  
 GAM1237 FLJ20128 3' GGTCCCTGTGTATGTTTGCAT 34597    TG TAAGA  
                   GTGCAGG T   AGGGGCT  
                   ||||| |    |||||  
                   TACGTTT A   TCCCTGG  
                   GT TGTG\_  
 GAM1237 FLJ20139 3' AGCTGACCCTTTAATGGTTGTA 34621    G   GA   \_  
                   TTG                    GTGCAG TGTAA AGGG GCT  
                   ||||| ||||| ||| ||  
                   TATGTT GTAATT TCCC CGA  
                   G   \_   AGT  
 GAM1237 FLJ20156 5' GGTCTCTTTGAATCTCCGCTG 34652    C GTTAA  
                   CAGTG AGGT   GAAGGGGCT  
                   |||| |||    |||||  
                   GTCGC TCTA   TTTCTCTGG  
                   C AG\_  
 GAM1237 FLJ20184 3' AGCCTCTTCTTAAAGCTATTG 34693    GCA G  
                   CAGT GGT TTAAGAAGGGGCT  
                   ||| || |||||  
                   GTTA TCG AATTCTTCTCCGA  
                   \_ A  
 GAM1237 FLJ20208 3' AGTTCTTTCTTAAACAGCTG 34740    G \_  
                   CAG TGT TAAGAAGGGGCT  
                   ||| || |||||  
                   GTC ACA ATTCTTTCTTGA  
                   G AA  
 GAM1237 FLJ20232 3' GGTCCTGCTGCCTGGTGTCTT 38671    C TG   \_ A  
                   GCTG                    GTG AGG TTA AG AGGGGCT  
                   ||| ||| ||| || |||||  
                   CGT TCT GGT TC TCCTTGG  
                   \_ GT CCG G  
 GAM1237 FLJ20254 5' AGCTCTTTTTTGACCACTGTCT 34784    T GT  
                   G                    CAG GCAG GTTAAGAAGGGGCT  
                   ||| ||| |||||  
                   GTC TGTC CAGTTTTTCTCGA  
                   \_ AC  
 GAM1237 FLJ20254 3' GCCTCCATCCTTGTGCTG 34793    TG TGTTAA A \_  
                   CAG CAGG    GA GG GGC  
                   ||| |||    || |||  
                   GTC GTTC    CT CC CCG  
                   GT   \_   A T  
 GAM1237 FLJ20274 3' TTTTTTTTTTAACATTTGTGT 62647    TG            CT  
                   G CAGGTGTTAAGAAGGGG  
                   | |||||  
                   T GTTTACAATTTTTTTT  
                   GT            TT  
 GAM1237 FLJ20303 3' GGTCTTTTGTTAAGCCTGTATT 34911    G G  
                   G                    CAGTGCAGGT TTAA AAGGGGCT  
                   ||||||| ||| |||||

GTTATGTCCG AATT TTTTCTGG  
 \_ G  
 GAM1237 FLJ20371 3' GGTTCTTTTTTACAGAAGTACT 35065 AGG T  
 AGTGC TGT AAGAAGGGGCT  
 ||||| ||| |||||  
 TCATG ACA TTTTCTTGG  
 AAG \_  
 GAM1237 FLJ20371 3' TCTTGATGTTGCATTG 35067 G TG  
 CAGTGCA G TTAAGA  
 ||||| | |||||  
 GTTACGT T AGTTCT  
 \_GT  
 GAM1237 FLJ20392 3' AGTCTTTCACCAGATGACTGCA 35119 GT AAGA\_  
 CTG CAGTGCAG GTT AGGGGCT  
 ||||| || |||||  
 GTCACGTC TAG TTTCTGA  
 AG ACCAC  
 GAM1237 FLJ20450 3' AGCCCGTCCTGACATCTGTGTT 35191 TG A AG  
 AG CAGGTGTTA GA GGGCT  
 || ||||| || |||||  
 TT GTCTACAGT CT CCCGA  
 GT C G\_  
 GAM1237 FLJ20509 3' AGCCTCTTTTCTGGCTGTGTT 35310 TG G TTA  
 AG CAG TG AGAAGGGGCT  
 || ||| || |||||  
 TT GTC GT TTTTCTCCGA  
 GT G C\_  
 GAM1237 FLJ20511 5' AGTTTCTTTTCTGCGCTTGTGC 35319 TG TA GG  
 G CAGGTGT AGAAG GCT  
 | ||||| ||||| |||  
 C GTTCGCG TTTTC TGA  
 GT TC TT  
 GAM1237 FLJ20548 3' AGTCCCTTCCAAGCTGCACTG 35374 G\_ TTAA  
 CAGTGCAG TG GAAGGGGCT  
 ||||| || |||||  
 GTCACGTC AC CTTCCCTGA  
 GA \_\_\_\_  
 GAM1237 FLJ20551 3' TCTTGGCCCCTGTACTG 35388 T  
 CAGTGCAGG GTTAAGA  
 ||||| |||||  
 GTCATGTCC CGGTTCT  
 C  
 GAM1237 FLJ20580 3' AGCCCCTGTTACAGCTGCACTG 35423 \_ TTAAGA  
 CAGTGCAG GTG AGGGGCT  
 ||||| || |||||  
 GTCACGTC CAC TCCCCGA  
 G TTG\_\_\_\_  
 GAM1237 FLJ20618 3' GGTTTTGAAGCTGGTGCCTCAT 35459 C TG A AA\_  
 TG CAGTG AGG TTA G GGGGCT  
 ||||| ||| ||| | |||||



GTTAC TCC GGT C TTTTGG  
 \_ GT \_ GAAG  
 GAM1237 FLJ20628 3' TTTTGACACTTGTCTTG 35477 T  
 CAG GCAGGTGTTAAGA  
 ||| |||||  
 GTT TGTTACAGTTTT  
 C  
 GAM1237 FLJ20979 5' AGTTTCTCATCTACACCTGCCT 44145 T TA \_ GG  
 G CAG GCAGGTGT AGA AG GCT  
 ||| ||||| ||| || |||  
 GTC CGTCCACA TCT TC TGA  
 \_ \_ AC TT  
 GAM1237 FLJ21174 3' AGCCTTTTGACCTATCTGCA 45872 TTAAG  
 TGCAGGTG AAGGGGCT  
 ||||| |||||  
 ACGTCTAT TTTTCCGA  
 CCAG\_  
 GAM1237 FLJ21432 3' GGTTCAGAAAGGCATCTGTGT 44638 TG AAGAA  
 G CAGGTGTT GGGGCT  
 | ||||| |||||  
 T GTCTACGG CCTTGG  
 GT AAAGA  
 GAM1237 FLJ21478 3' GCCTCCTGGCTTGCACTG 44870 GTTA AA  
 CAGTGCAGGT AG GGGGC  
 ||||| || |||||  
 GTCACGTTCTG TC CTCCG  
 G\_ \_  
 GAM1237 FLJ21657 3' GGCTACAGTAGCACTTTACTG 42512 C AGAAGG  
 CAGTG AGGTGTTA GGCT  
 |||| ||||| |||||  
 GTCAT TTCACGAT TCGG  
 \_ GACA\_  
 GAM1237 FLJ22167 5' TTTTATACCTGCCTG 44586 T T  
 CAG GCAGGTGT AAGA  
 ||| ||||| |||||  
 GTC CGTCCATA TTTT  
 \_ \_  
 GAM1237 FLJ22318 3' GTTTCAGAGCGCCTGGCTG 42832 G AAGAA GG  
 CAGT CAGGTGTT G GC  
 |||| ||||| | |||  
 GTCG GTCCGCGA C TG  
 \_ GA\_ TT  
 GAM1237 FLJ22479 3' GGCCTGAAGCAGTCTGCACTG 46077 \_ AAGAAG  
 CAGTGCAGG TGTT GGGCT  
 ||||| ||||| |||||  
 GTCACGTCT ACGA TCCGG  
 G AG\_  
 GAM1237 FLJ22578 5' GGTCCACCAGGGTGTCTGCAT 45874 TG AAGAAG  
 GTGCAGG TT GGGCT  
 ||||| || |||||

TACGTCT GG CCTGG  
 GT GACCA\_  
 GAM1237 FLJ22671 3' GGCTCCCCAACAGACTCTGCAC 45866 T AAGAA\_  
 TG CAGTGCAGG GTT GGGGCT  
 ||||| || |||||  
 GTCACGTCT CAG CCTCGG  
 \_ ACAACC  
 GAM1237 FLJ23153 3' GTTTTTCTGTTTGTACT 44927 GG GTTA  
 AGTGCA T AGAAGGGGC  
 ||||| | |||||  
 TCATGT G TCTTTTGT  
 TT \_\_\_\_  
 GAM1237 FLJ23186 3' GGCTGTTTAATATCTGCTCTG 60405 T GAA G  
 CAG GCAGGTGTAA G GGCT  
 || ||||| || |||||  
 GTC CGTCTATAATT T TCGG  
 T \_\_\_\_ G  
 GAM1237 FLJ23251 5' AGTCTCGGAGACGTGTCTGTCT 45686 T TG TAAGAA  
 G CAG GCAGG T GGGGCT  
 || |||| | |||||  
 GTC TGTCT G CTCTGA  
 \_ GT CAGAGG  
 GAM1237 FLJ23462 3' GGCCTACCTTGACACTTGT 45806 AAG  
 GCAGGTGTAAAG GGGCT  
 ||||| |||||  
 TGTTACAGTTC TCCGG  
 CA\_  
 GAM1237 FLJ23462 3' GGTTTCTTGAAATAATTTGTAT 45807 GTTAAG GG  
 TG CAGTGCAGGT AAG GCT  
 ||||| || |||||  
 GTTATGTTTA TTC TGG  
 ATAAAG TT  
 GAM1237 FLJ23476 3' GTTTCTTCTGTCTGTTTTG 44963 T TGTTA GG  
 CAG GCAGG AGAAG GC  
 || |||| |||| ||  
 GTT TGTCT TCTTC TG  
 T G\_\_\_\_ TT  
 GAM1237 FLJ23506 5' GGTTCTGTAACGCTTGTGT 45747 TG AGAA  
 G CAGGTGTAA GGGGCT  
 | ||||| |||||  
 T GTTCGCAAT TCTTGG  
 GT G\_\_\_\_  
 GAM1237 FLJ23511 3' AGTAATTTAAACCTGCATTG 49957 G AAGGG  
 CAGTGCAGGT TTAAG GCT  
 ||||| |||| |||||  
 GTTACGTCCA AATTT TGA  
 A AA\_\_\_\_  
 GAM1237 FLJ23518 3' AGCATATTTTGGTATCTGCATT 45305 TT AGGG  
 G CAGTGCAGGTG AAGA GCT  
 ||||| |||| |||||

GTTACGTCTAT TTTT CGA  
 GG ATA\_  
 GAM1237 FLJ23519 5' GGCCCCTGGCGGGTACCTGAGC 69205 G AAGA  
 TG CAGT CAGGTGTT AGGGGCT  
 |||| ||||| |||||  
 GTCG GTCCATGG TCCCCGG  
 A GCGG  
 GAM1237 FLJ23519 5' GGCCCCTGGCGGGTACCTGAGC 49970 G AAGA  
 TG CAGT CAGGTGTT AGGGGCT  
 |||| ||||| |||||  
 GTCG GTCCATGG TCCCCGG  
 A GCGG  
 GAM1237 FLJ23604 3' AGTTCTTGGCACATCTGTA 46857 TAAGA  
 TGCAGGTGT AGGGGCT  
 ||||| |||||  
 ATGTCTACA TTCTTGA  
 CGG\_  
 GAM1237 FLJ30046 3' AGCTCATTGCACTTAATACCTG 58098 AAG\_  
 CA TGCAGGTGTTAAG GGGCT  
 ||||| |||||  
 ACGTCCATAATTC CTCGA  
 ACGTTA  
 GAM1237 FLJ30567 3' AGTTCTTTATTGTGTCTGCAGT 58824 G TG TAAG  
 G CA TGCAGG T AAGGGGCT  
 || ||||| | |||||  
 GT ACGTCT G TTTCTTGA  
 G GT TTA\_  
 GAM1237 FLJ31890 3' TTGTTAATATTTGTATTG 91343 G  
 CAGTGCAGGTGTAA AA  
 ||||| |||||  
 GTTATGTTTATAATT TT  
 G  
 GAM1237 FLJ32356 3' GGCCCCTTGGGAGCTTGCCTG 58364 T GTTAAG  
 CAG GCAGGT AAGGGGCT  
 || ||||| |||||  
 GTC CGTTCG TTCCCCGG  
 \_ AGGG\_  
 GAM1237 FLJ32884 5' GCCCAAAGCCCTGTGCTG 58459 TG T AAGAAG  
 CAG CAGG GTT GGGC  
 || ||||| |||||  
 GTC GTCC CGA CCCG  
 GT \_ AAA\_  
 GAM1237 FTS 3' TCTTCAGCCTGCACTG 42491 GTT  
 CAGTGCAGGT AAGA  
 ||||| |||||  
 GTCACGTCCG TTCT  
 AC\_  
 GAM1237 FUSIP1 3' AGTCTCTTACAGTGCCTCTG 21770 TGC TG AAG  
 CAG AGG TT AAGGGGCT  
 || ||| || |||||

GTC TCC GA TTCTCTGA  
 \_\_\_\_ GT CA\_  
 GAM1237 FYCO1 3' CCCTTTTGTCTGGCTG 44492 G GT TTAAG  
 CAGT CAG G AAGGGG  
 ||||| ||| | |||||  
 GTCG GTC T TTTCCC  
 \_ TG \_\_\_\_  
 GAM1237 FYCO1 3' GGCTCTGACCATGCTTAGTACT 44496 \_ TAAGAA  
 G CAGTGC AGGTGT GGGGCT  
 ||||| ||||| |||||  
 GTCATG TTCGTA TCTCGG  
 A CCAG\_  
 GAM1237 G2 3' GTTTCTTTGGTCTTTACTG 66663 C TGTTAA GG  
 CAGTG AGG GAAG GC  
 ||||| ||| ||| ||  
 GTCAT TTC TTTC TG  
 \_ TGG\_\_ TT  
 GAM1237 GBA2 5' CTTGAGGTACCTGCAGTG 71025 G \_  
 CA TGCAGGTG TTAAG  
 || ||||| |||||  
 GT ACGTCCAT AGTTC  
 G GG  
 GAM1237 GDAP1L1 3' GGCCTGGGGCTTGGTGTCTGAC 43833 G TG AAG\_  
 TG CAGT CAGG TTAAG GGGCT  
 ||||| ||||| |||||  
 GTCA GTCT GGTTT TCCGG  
 \_ GT GGGG  
 GAM1237 GFPT1 3' AGCCTTTTTTTTAGTAAATCCTT 9020 C TG\_  
 ATT GTG AGG TTAAGAAGGGGGCT  
 ||| ||| ||||| |||||  
 TAT TCC GATTTTTTTTCCGA  
 \_ TAAAT  
 GAM1237 GHITM 3' AGCTTCTTTGTGGCTTACACTG 26914 C GTTAA  
 CAGTG AGGT GAAGGGGGCT  
 ||||| ||||| |||||  
 GTCAC TTCG TTTCTTCGA  
 A GTG\_  
 GAM1237 GMFB 3' TAGTCTTTTGTTAAGCATGGTG 14670 TG \_\_\_\_ G  
 CTTGTACTG GG T TAA AAGGGGGCT A  
 || | ||| ||||| |  
 TC G ATT TTTTCTGA T  
 GT GTACGA G  
 GAM1237 GMPPB 3' AGCCTCTTAAGGGCTGGCACTG 95720 A G TAAG  
 CAGTGC GGT T AAGGGGGCT  
 ||||| ||| | |||||  
 GTCACG TCG G TTCTCCGA  
 G G AA\_  
 GAM1237 GMPPB 5' CTTGAGTCCTGCATTG 95738 TG  
 CAGTGCAGG TTAAG  
 ||||| |||||

GTTACGTCC AGTTC  
 TG  
 GAM1237 GOLGA1 3' TCTTGATTCTGTGCTG 9094 TG T  
 CAG CAGG GTTAAGA  
 ||| ||| |||||  
 GTC GTCT TAGTTCT  
 GT \_  
 GAM1237 GOLPH3 3' AGTAAATTAATATCTGCTCTG 42111 T GAAGGG  
 CAG GCAGGTGTAA GCT  
 ||| ||||| |||  
 GTC CGTCTATAATT TGA  
 T AAA\_\_  
 GAM1237 GOLPH3 3' GGCTTTTTCTTTTTGTAC 42114 TGTT  
 GTGCAGG AAGAAGGGGCT  
 ||||| |||||  
 CATGTTT TTCTTTTTCGG  
 T\_\_  
 GAM1237 GPR107 3' GCCAGATAACACTTCGCTG 40564 C AGAAGG  
 CAGTG AGGTGTTA GGC  
 ||||| ||||| |||  
 GTCGC TTCACAAT CCG  
 \_ AGA\_\_  
 GAM1237 GPR88 3' AGCTTTGAACATTCTGTACTG 41875 \_ AAGAAG  
 CAGTGCAGG TGTT GGGCT  
 ||||| ||| |||||  
 GTCATGTCT ACAA TTCGA  
 T GT\_\_  
 GAM1237 GR6 3' GGCTCCTCCAGGCCTCTGCGCT 23731 T AA A  
 G CAGTGCAGG GTT GA GGGGCT  
 ||||| ||| || |||||  
 GTCGCGTCT CGG CT CCTCGG  
 C AC \_  
 GAM1237 GREAT 3' AGCTTTTGGAAGATGACATCTG 55479 AGA\_\_  
 CA TGCAGGTGTTA AGGGGCT  
 ||||| ||| |||||  
 ACGTCTACAGT TTTTCGA  
 AGAAGG  
 GAM1237 GREB1 3' GTCCTTTCTTGTGTGATTG 27884 G G TGT  
 CAGT CA G TAAGAAGGGGC  
 ||| || |||||  
 GTTA GT T GTTCTTTCCTG  
 \_ G\_\_  
 GAM1237 H2AFZ 5' AGCCTTTTCTCTGCCTTGC 9170 T TA  
 GCAGG GT AGAAGGGGCT  
 ||||| || |||||  
 CGTTC CG TCTTTTCCGA  
 \_ TC  
 GAM1237 HCA4 3' GTCTTTTTCGATTGGC 77591 AG TA  
 GC GTGT AGAAGGGGC  
 || ||| |||||

			CG TACG TTTTTTCTG		
			GT _		
GAM1237 HCA66	3'	AGCCCCGTGGGCAAATTTGTAT 71774		GTTAAGAA	
	TG	CAGTGCAGGT GGGGCT			
		GTTATGTTA CCCCCA			
		AACGGGTG			
GAM1237 HEMK	3'	GGCTCCTTCTTAGTGGATT 32437	G GGTG		
		AGT CA TTAAGAAGGGGCT			
		TTA GT GATTCTTCCTCGG			
		G _			
GAM1237 HIC2	3'	GCCCTCTGGGCCTGTGTTG 65264	TG GTTA AG		
		CAG CAGGT AGA GGGC			
		GTT GTCCG TCT CCCG			
		GT GG_ _			
GAM1237 HN1L	3'	AGTCTTTTCTTGAAACATCTTG 57993	C _		
		G AGGTGT TAAGAAGGGGCT			
		G TCTACA GTTCTTTTCTGA			
		T AA			
GAM1237 HPIP	3'	GGCCTTAGCTGGACCTGCGTTG 40050	GTTA AA		
		CAGTGCAGGT AG GGGGCT			
		GTTGCGTCCA TC TTCCGG			
		GG_ GA			
GAM1237 HRIHFB2436	3'	GCCTTTGTTCAATTGTATTG 26794	G TTAAGA		
		CAGTGCAG TG AGGGGC			
		GTTATGTT AC TTTCCG			
		_ TTG_			
GAM1237 HRMT1L3	3'	AGCCCTTCACGAAGGCTTTGTG 39071	TG _ G AAGA		
	TTG	CAG CAG GT TT AGGGGCT			
		GTT GTT CG AA TTCCCGA			
		GT T G GCAC			
GAM1237 HSCBCIP1	5'	TTTAGCATTGAACTG 88799	G		
		CAGT CAGGTGTTAAG			
		GTCA GTTTACGATTT			
		A			
GAM1237 HSGP25L2G	3'	GGTTTCCAGCCATACCTGTTCT 62167	T TAAGAA GG		
	G	CAG GCAGGTGT G GCT			
		GTC TGTCCATA C TGG			
		T CCGAC_ TT			
GAM1237 HSPC009	3'	GCCCTTTCTTGTAGTTG 25830	GG GT		
		CA T TAAGAAGGGGC			

			GT G GTTCTTTCCCG		
			TT AT		
GAM1237	HSPC067	5'	AGCTCCTTTTGAAGGTGT	26334	GGTG
			GCA TTAAGAAGGGGCT		
			TGT AGTTTTTCCTCGA		
			GGAA		
GAM1237	HT002	3'	GGCTCCCAGGATAGTTGCACTG	25945	G AAGAA
			CAGTGCAG TGTT GGGGCT		
			GTCACGTT ATAG CCTCGG		
			G GAC__		
GAM1237	HT002	3'	CCTTCCAGACATCTGCG	25935	AA
			TGCAGGTGTT GAAGG		
			GCGTCTACAG CTTCC		
			AC		
GAM1237	HT008	3'	GGTTCTTGGCCGCCATCTGTAC	59803	TTAAGA
	TG		CAGTGCAGGTG AGGGGCT		
			GTCATGTCTAC TTCTTG		
			CGCCGG		
GAM1237	IMAGE145052	3'	AGTCTTTTTATAATTTGGATTG	26537	G GTTAA
			CAGT CAGGT GAAGGGGCT		
			GTTA GTTTA TTTTCTGA		
			G ATA__		
GAM1237	IRF5	3'	AGCCCCGATGAGCACCTGGCTG	50972	G AAGAA
			CAGT CAGGTGTT GGGGCT		
			GTCG GTCCACGA CCCCCA		
			_ GTAG_		
GAM1237	ITPK1	3'	AGCCGATGGCGCCTGTGCTG	26405	TG AGAAGG
			CAG CAGGTGTTA GGCT		
			GTC GTCCGCGGT CCGA		
			GT AG__		
GAM1237	ITPK1	3'	AGTTCCGCGCTGGTGTCTGGGC	26407	G TG A AA_
	TG		CAGT CAGG TTA G GGGGCT		
			GTCG GTCT GGT C CTTGA		
			G GT _GCG		
GAM1237	JAM1	3'	GCTCTTTCCTTGTGTA	33763	GGTGT _
			CAGTGCA TAAG AAGGGGC		
			GTCATGT GTTC TTTCTCG		
			_ C		
GAM1237	JAM1	3'	GCTCTTTCCTTGTGTA	57956	GGTGT _
			CAGTGCA TAAG AAGGGGC		

GTCATGT GTTC TTTCTCG  
 \_\_\_\_\_ C  
 GAM1237 JAM1 3' GCTCTTTCCTTGTGTA CTG 57883 GGTGT \_  
 CAGTGCA TAAG AAGGGGC  
 ||||| ||| |||||  
 GTCATGT GTTC TTTCTCG  
 \_\_\_\_\_ C  
 GAM1237 JAM1 3' GCTCTTTCCTTGTGTA CTG 57901 GGTGT \_  
 CAGTGCA TAAG AAGGGGC  
 ||||| ||| |||||  
 GTCATGT GTTC TTTCTCG  
 \_\_\_\_\_ C  
 GAM1237 JAM1 3' GCTCTTTCCTTGTGTA CTG 57930 GGTGT \_  
 CAGTGCA TAAG AAGGGGC  
 ||||| ||| |||||  
 GTCATGT GTTC TTTCTCG  
 \_\_\_\_\_ C  
 GAM1237 KATII 5' CTTGATGCTTGGCTG 32647 G  
 CAGT CAGGTGTTAAG  
 ||| |||||  
 GTCG GTTCGTAGTTC  
 \_\_\_\_\_  
 GAM1237 KCNH8 3' GGTTTTTCATGAGTGCCTGATT 58257 G TG AAGA  
 G CAGT CAGG TT AGGGGCT  
 ||| ||| || |||||  
 GTTA GTCC GA TTTTGG  
 \_ GT GTAC  
 GAM1237 KCNS1 3' GGTCATGTTTGGCCTTGTGTTG 9579 TG T AAGG  
 CAG CAGG GTTAAG GGCT  
 || ||| ||||| |||  
 GTT GTTC CGGTTT CTGG  
 GT \_ GTA\_  
 GAM1237 KHDRBS1 3' AGCCCCAGACATACTGTGTTG 21623 TG \_ AAGAA  
 CAG CAG GTGTT GGGGCT  
 || ||| ||||| |||||  
 GTT GTC TACAG CCCCCA  
 GT A A\_  
 GAM1237 KIAA0014 3' GCTCTGTGATGCCTGCCTG 27848 T AGAA  
 CAG GCAGGTGTTA GGGGC  
 || ||||| |||||  
 GTC CGTCCGTAGT TCTCG  
 \_\_\_\_\_ G\_  
 GAM1237 KIAA0063 3' GGTTTCTTCACTCCAGTGTTG 29638 TG A T TAA GG  
 CAG C GG GT GAAG GCT  
 || | || ||| |||  
 GTT G CC CA CTTC TGG  
 GT A T \_ TT  
 GAM1237 KIAA0087 3' TCTAGACATTTCACTG 28707 C A  
 CAGTG AGGTGTT AGA  
 |||| ||||| |||



GTCAC TTTACAG TCT  
 \_ A  
 GAM1237 KIAA0090 3' AGTCCAAAGGCGTCTGCATTG 88437 GT AAGAAG  
 CAGTGCAG GTT GGGCT  
 ||||| || ||||  
 GTTACGTC CGG CCTGA  
 TG AAA\_\_  
 GAM1237 KIAA0090 3' GCCTCGAACACCTGGGCTG 88444 G AAGAA  
 CAGT CAGGTGTT GGGGC  
 ||| ||||| ||||  
 GTCG GTCCACAA CTCCG  
 G G\_\_  
 GAM1237 KIAA0090 3' GGTACATTTGGTGTGTTTGCAC T 88447 TGTAA GGG  
 G CAGTGCAGG GAA GCT  
 ||||| || |||  
 GTCACGTTT TTT TGG  
 TGTGG\_ ACA  
 GAM1237 KIAA0092 3' TTCTTAATACCTGTTTTG 27969 T  
 CAG GCAGGTGTTAAGAA  
 ||| |||||  
 GTT TGTCCATAATTCTT  
 T  
 GAM1237 KIAA0133 3' GCCTGAGGTGTCTGCTCTG 28766 T TG AAGAAG  
 CAG GCAGG TT GGGC  
 ||| |||| || ||||  
 GTC CGTCT GG TCCG  
 T GT AG\_\_  
 GAM1237 KIAA0182 3' TTTTAGTGTTTGTACTG 72038 TG  
 CAGTGCAGG TTAAGA  
 ||||| |||||  
 GTCATGTTT GATTTT  
 GT  
 GAM1237 KIAA0212 3' AGTTTCTTCTGTTCTGTGTT 27930 TG TGTA GG  
 AG CAGG AGAAG GCT  
 || |||| |||| |||  
 TT GTCT TCTTC TGA  
 GT TG\_\_ TT  
 GAM1237 KIAA0226 3' AGCTCTTTCTCCAGGTCAC TGC 63510 G TTA\_\_  
 GCTG GTGCAG TG AGAAGGGGCT  
 ||||| || |||||  
 CGCGTC AC TCTTTCTCGA  
 \_ TGGACC  
 GAM1237 KIAA0227 3' AGTCTCCTGATGTCTGTGCT 60694 TG TG AGAA  
 AG CAGG TTA GGGGCT  
 || |||| || |||||  
 TC GTCT AGT CTCTGA  
 GT GT C\_\_  
 GAM1237 KIAA0247 3' GCCTTAGTGGCTGCACTG 28402 G GT AGAAG  
 CAGTGCAG T TA GGGC  
 ||||| | || |||

GTCACGTC G AT TCCG  
 G TG \_\_\_\_\_  
 GAM1237 KIAA0258 3' TTTTGGCCCTTGTATTG 28828 T  
 CAGTGCAGG GTTAAGA  
 ||||| |||||  
 GTTATGTTT CGGTTTT  
 C  
 GAM1237 KIAA0266 3' GTCCGCTAGCGTCTGTCTG 41334 T GT AAGA \_ T  
 CAG GCAG GTT AG GGGC  
 ||| ||| ||| |||  
 GTC TGTC CGA TC CCTG  
 \_ TG \_\_\_\_\_ G T  
 GAM1237 KIAA0296 3' GCCCCTTTTCCCTCTGC 28113 TGTTA  
 GCAGG AGAAGGGGC  
 |||| |||||  
 CGTCT TTTTCCCCG  
 CCC\_  
 GAM1237 KIAA0317 3' GCTTTTTCTTGAATTGTA 29086 GGTG  
 TGCA TTAAGAAGGGGC  
 ||| |||||  
 ATGT AGTTCTTTTTCG  
 TA\_  
 GAM1237 KIAA0317 3' GGCCTTTTCTTTTACTGTTTTG 29087 T GTGTT  
 CAG GCAG AAGAAGGGGCT  
 ||| ||| |||||  
 GTT TGTC TTCTTTTCCGG  
 T ATT\_  
 GAM1237 KIAA0318 3' GCTTACAGCATTTGCCTG 68957 T AAGAAG  
 CAG GCAGGTGTT GGGC  
 ||| ||||| |||  
 GTC CGTTTACGA TTCG  
 \_ CA\_  
 GAM1237 KIAA0323 3' GGTCTCAGCTATGCCTGTTTTG 63270 T TA AA  
 CAG GCAGGTGT AG GGGGCT  
 ||| ||||| ||| |||||  
 GTT TGTCCGTA TC CTCTGG  
 T \_ GA  
 GAM1237 KIAA0323 3' AGTCTCAGGTGTGTCTGCCTG 63255 T TG TAAGAA  
 CAG GCAGG T GGGGCT  
 ||| ||||| | |||||  
 GTC CGTCT G CTCTGA  
 \_ GT TGGG\_  
 GAM1237 KIAA0329 3' GTCCTGAGCCTGCACTG 29279 GTTAAGAA  
 CAGTGCAGGT GGGGC  
 ||||| |||||  
 GTCACGTCCG TCCTG  
 AG\_  
 GAM1237 KIAA0339 3' GTCCCTTTTGCTGGGCTG 71475 G GTGTTA  
 CAGT CAG AGAAGGGGC  
 ||| ||| |||||

GTCG GTC TTTCCCTG  
 G G\_\_\_\_  
 GAM1237 KIAA0354 3' GGCCTTTGAGGACACACCTGTC 29571 T TAAGA\_  
 TG CAG GCAGGTGT AGGGGCT  
 ||| ||||| |||||  
 GTC TGTCCACA TTTCCGG  
 \_ CAGGAG  
 GAM1237 KIAA0365 3' AGCCTAGAAGACATTTGT 78662 AAGAAG  
 GCAGGTGTT GGGCT  
 ||||| |||||  
 TGTTTACAG TCCGA  
 AAGA\_  
 GAM1237 KIAA0367 5' GCCTCAGACACTTGTCTG 67299 T AAGAA  
 CAG GCAGGTGTT GGGGC  
 ||| ||||| |||||  
 GTC TGTTCACAG CTCCG  
 \_ A\_\_\_\_  
 GAM1237 KIAA0418 3' GGTCTCTTCCTAATCTGCAC 27562 GTTAA  
 GTGCAGGT GAAGGGGCT  
 ||||| |||||  
 CACGTCTA CTTCTCTGG  
 ATC\_  
 GAM1237 KIAA0426 3' GGTCTGAGTAGGCTTGTATTG 28260 G AGAAG  
 CAGTGCAGGT TTA GGGCT  
 ||||| ||| |||||  
 GTTATGTTTCG GAT TCTGG  
 \_ GAG\_  
 GAM1237 KIAA0435 3' AGCTTCATGACCGATGTCTGGC 28969 G TG AAGAA\_  
 TG CAGT CAGG TT GGGGCT  
 ||| ||| || |||||  
 GTCG GTCT AG CTTCGA  
 \_ GT CCAGTA  
 GAM1237 KIAA0435 5' GCCTAAATACTTGCTTTG 28976 T AAGAAG  
 CAG GCAGGTGTT GGGC  
 ||| ||||| |||||  
 GTT CGTTCATAA TCCG  
 T A\_\_\_\_  
 GAM1237 KIAA0446 5' AGTCTCTGGGCATCTGCAT 68851 TAAGA  
 GTGCAGGTGT AGGGGCT  
 ||||| |||||  
 TACGTCTACG TCTCTGA  
 GG\_  
 GAM1237 KIAA0446 5' GCCCTGCTGTATTTGTCTG 68869 T TTAAGAA  
 CAG GCAGGTG GGGGC  
 ||| ||||| |||||  
 GTC TGTTTAT TCCCG  
 \_ GTCG\_  
 GAM1237 KIAA0446 3' GTCCCTGTATTTGATACT 68875 GA\_  
 GGTGTAA AGGGGC  
 ||||| |||||

TCATAGTT TCCCTG  
TATG

GAM1237 KIAA0451 5' GGCCTTTTCTTTTCTGTGTT 29112 TG TGTT  
AG CAGG AAGAAGGGGCT  
|| ||| |||||  
TT GTCT TTCTTTCCTGG  
GT TT\_\_

GAM1237 KIAA0469 3' AGTCTTTTTTGCGGCTTGCTG 29322 C G TA  
CAGTG AG TGT AGAAGGGGCT  
|||| ||| |||||  
GTCGT TC GCG TTTTTTCTGA  
T G \_

GAM1237 KIAA0537 3' GGCCTTAGGCATCTGCATTG 29251 AAGAA  
CAGTGCAGGTGTT GGGGCT  
||||||| ||||  
GTTACGTCTACGG TTCCGG  
A\_\_

GAM1237 KIAA0542 3' AGCCCATTGGCGCCTGCGTTG 66081 GAAG  
CAGTGCAGGTGTAA GGGCT  
||||||| ||||  
GTTGCGTCCGCGGTT CCCGA  
A\_\_

GAM1237 KIAA0557 3' AGCTTTTGTCTGGCCTGTGCTG 77986 TG GTTA \_  
CAG CAGGT AGA AGGGGCT  
|| ||| || |||||  
GTC GTCCG TCT TTTTCGA  
GT G\_\_ G

GAM1237 KIAA0628 3' GTCTTTACTTACTTGTCTG 28876 T TTA A  
CAG GCAGGTG AG AGGGGC  
|| ||||| || |||||  
GTC TGTTCAT TC TTTCTG  
\_ \_\_ A

GAM1237 KIAA0628 3' AGTTCTTTCCATATTCTGCAT 28863 TGTTAA  
GTGCAGG GAAGGGGCT  
||||| |||||  
TACGTCT CTTTCTTGA  
TATAC\_

GAM1237 KIAA0630 3' GGTTTCTTTTTTAACAGCTTGT 89393 \_ \_ GG  
AT GTGCAGG TGTTAAGAA G GCT  
||||| ||||| | |||  
TATGTTT ACAATTTTT C TGG  
G T TT

GAM1237 KIAA0643 3' GCCTCCTATGTTTGCATT 45600 TG TAAGA \_  
AGTGCAGG T AGG GGC  
||||| | ||| |||  
TTACGTTT A TCC CCG  
GT \_\_\_\_ T

GAM1237 KIAA0645 3' GGCCAGGCTGCACCTGTGCTG 27822 TG TA AAGG  
CAG CAGGTGT AG GGCT  
|| ||||| || |||

GTC GTCCACG TC CCGG  
 GT \_ GGA\_  
 GAM1237 KIAA0648 3' AGTTTTGCATATTCTTGTGCTG 82649 TG T TAAGAA  
 CAG CAGG GT GGGGCT  
 ||| ||| || |||||  
 GTC GTTC TA TTTTGA  
 GT T TACG\_  
 GAM1237 KIAA0660 3' AGCTCTTTAAGTGTTCATT 24511 TG TAAG  
 AGTGCAGG T AAGGGGCT  
 ||||| | |||||  
 TTACGTTT G TTTCTCGA  
 GT AA\_  
 GAM1237 KIAA0660 5' AGTCTTTCCTCTAGCATTGAC 24512 \_ \_ A  
 ATTG AGTG CAGGTGTTA AG AGGGGCT  
 ||| ||||| || |||||  
 TTAC GTTTACGAT TC TTTCTGA  
 A C C  
 GAM1237 KIAA0663 3' TCTTGATGCTTCTGCTG 29130 C  
 CAGTG AGGTGTTAAGA  
 |||| |||||  
 GTCGT TTCGTAGTTCT  
 C  
 GAM1237 KIAA0674 5' GGCTCTTTCAGAATCATGTGCT 60615 TG GGT AA  
 G CAG CA GTT GAAGGGGCT  
 ||| || ||| |||||  
 GTC GT TAA CTTTCTCGG  
 GT AC\_ GA  
 GAM1237 KIAA0682 3' GGTCTTTTTTGTCTTTTGTGC 29369 TG TGTTA  
 G CAGG AGAAGGGGCT  
 | ||| |||||  
 C GTTT TTTTTTCTGG  
 GT TCTG\_  
 GAM1237 KIAA0763 3' GCCCCAGGATGTCTGCCTG 29533 T TG AAGAA  
 CAG GCAGG TT GGGGC  
 ||| ||| || |||||  
 GTC CGTCT AG CCCCCG  
 \_ GT GA\_  
 GAM1237 KIAA0766 3' AGCTTTTTTGTCTTATCTGCGT 29001 G TTAA  
 G CA TGCAGGTG GAAGGGGCT  
 || ||||| |||||  
 GT GCGTCTAT TTTTTTCGA  
 \_ TCTG  
 GAM1237 KIAA0830 3' GGCCTTTGGTGGGGATGTCTGC 69700 TG AAGA\_  
 GCAGG TT AGGGGCT  
 |||| || |||||  
 CGTCT AG TTTCCGG  
 GT GGGTGG  
 GAM1237 KIAA0830 3' GGTCTCTAGAACCATCTGCATT 69701 TTAAGA  
 G CAGTGCAGGTG AGGGGCT  
 ||||| |||||

GTTACGTCTAC TCTCTGG  
 CAAGA\_  
 GAM1237 KIAA0892 3' CTTAACATCTGTCCTG 71010 TG  
 CAG CAGGTGTAAAG  
 ||| |||||  
 GTC GTCTACAATTC  
 CT  
 GAM1237 KIAA0937 3' TCTTGGTATTGCACTG 91592 G TT  
 CAGTGCAG TG AAGA  
 ||||| || |||  
 GTCACGTT AT TTCT  
 \_ GG  
 GAM1237 KIAA0970 3' GCATTTAGCACTGGCATTG 29962 A GAAGGG  
 CAGTGC GGTGTAA GC  
 ||||| ||||| ||  
 GTTACG TCACGATT CG  
 G TA\_\_\_\_  
 GAM1237 KIAA0976 3' GCCCCTCTAACTGTACTG 29893 GTGTTA A  
 CAGTGCAG AGA GGGGC  
 ||||| ||| |||||  
 GTCATGTC TCT CCCC  
 AA\_\_\_\_\_  
 GAM1237 KIAA0979 3' GGTCTTTTTTTTCTTCATTG 30445 C TGTT  
 CAGTG AGG AAGAAGGGGCT  
 ||||| ||| |||||  
 GTTAC TTC TTTTTTCTGG  
 \_ TT\_\_\_\_  
 GAM1237 KIAA0979 3' GGCTTTTTTCAGTGATCTTCACT 30443 C T A\_  
 G CAGTG AGG GTTA GAAGGGGCT  
 ||||| ||| ||||| |||||  
 GTCAC TTC TAGT CTTTTTCGG  
 \_ \_ GA  
 GAM1237 KIAA0993 3' GGCCCCCTTTTAACTTGTAT 64145 GTTA  
 GTGCAGGT AGAAGGGGCT  
 ||||| |||||  
 TATGTTCA TTTTCCCCGG  
 AA\_\_\_\_\_  
 GAM1237 KIAA0995 5' CCTCTTCTCTGCCTG 72876 T TGTTAA  
 CAG GCAGG GAAGGGG  
 ||| ||||| |||||  
 GTC CGTCT TTTCTCC  
 \_ C\_\_\_\_\_  
 GAM1237 KIAA1016 3' TTTTTCCTCCTGACTTTGTGTT 91736 TG T A A CT  
 G CAG CAGG GTTA GA GGGG  
 ||| ||||| ||||| |||  
 GTT GTTT CAGT CT CCTT  
 GT \_ C \_ TTTT  
 GAM1237 KIAA1023 3' AGCTTTTTCTTTGCTCGTTTGT 34254 T GG TT\_  
 CTG AG GCA TG AAGAAGGGGCT  
 || ||| || |||||

			TC TGT GC TTCTTTTTCGA		
			_ TT TCGT		
GAM1237	KIAA1023	3'	AGCCCAGGCCTGGTGTCTGCAT 34253	TG	AGAAG
		T	AGTGCAGG TTA GGGCT		
			TTACGTCT GGT CCCGA		
			GT CCGGA		
GAM1237	KIAA1028	3'	GGCTCCAGCAATATGTCTGCAT 91944	TG	TAAGAA
		TG	CAGTGCAGG T GGGGCT		
			GTTACGTCT A CCTCGG		
			GT TAACGA		
GAM1237	KIAA1028	3'	GTTCTATCCCTGCACTG 91945	TG	TAAGA
			CAGTGCAGG T AGGGGC		
			GTCACGTCC A TCCTTG		
			CT _____		
GAM1237	KIAA1028	3'	GTTCTTTCTTAGCTGC 91946	GGT	
			GCA GTTAAGAAGGGGC		
			CGT CGATTCTTTCTTG		
			_____		
GAM1237	KIAA1029	3'	AGTTCCCAAGCCAGCGCCTGGC 23470	G	AAGAA_
		TG	CAGT CAGGTGTT GGGGCT		
			GTCG GTCCGCGA CCTTGA		
			_ CCGAAC		
GAM1237	KIAA1042	3'	AGCTTCTTCAAGACCTTCACTG 30334	C	G AA
			CAGTG AGGT TT GAAGGGGCT		
			GTCAC TCCA AA CTTCTTCGA		
			T G _		
GAM1237	KIAA1061	3'	AGCTCCTTTTCACTCCTGCCTG 71173	T	T TAA
			CAG GCAGG GT GAAGGGGCT		
			GTC CGTCC CA TTTCCTCGA		
			_ T C_		
GAM1237	KIAA1076	3'	GGCTTTTTTTTTTCTTGTGC 65517	TG	TGTT
			G CAGG AAGAAGGGGCT		
			C GTTC TTTTTTTTCGG		
			GT TT_		
GAM1237	KIAA1078	3'	AGCTTTTTTTTAATTATGT 65118	GGT	
			GCA GTTAAGAAGGGGCT		
			TGT TAATTTTTTTTCGA		
			AT_		
GAM1237	KIAA1084	3'	GCTTCCATGCTTGCTTTG 29839	T	TAAGAA
			CAG GCAGGTGT GGGGC		

GTT CGTTCGTA CTTCG  
 T C\_\_\_\_  
 GAM1237 KIAA1086 3' AAATGTTTTTTAAACATTTGTGC 70739 TG GGGCT  
 T AG CAGGTGTTAAGAAG  
 || |||||  
 TC GTTTACAATTTTT  
 GT GTAAAG  
 GAM1237 KIAA1102 3' GGTTTTTTTTTTTTTTTGCAT 69013 TGTT  
 T AGTGCAGG AAGAAGGGGCT  
 ||||| |||||  
 TTACGTTT TTTTTTTTGG  
 TTTT  
 GAM1237 KIAA1107 3' AGTCCCTTTACTTTTTGCTCTG 63994 T T\_ TAA  
 CAG GCAGG GT GAAGGGGCT  
 ||| |||| || |||||  
 GTC CGTTT CA TTTCCCTGA  
 T TT \_\_\_\_  
 GAM1237 KIAA1126 3' GCCTCATGTTTGTGTCTG 71930 \_ TG TAAGAA  
 CAG TGCAGG T GGGGC  
 ||| |||| | ||||  
 GTC GTGTTT A CTCCG  
 T GT \_\_\_\_  
 GAM1237 KIAA1136 3' GCCCACAATGTCTGCCCTG 91319 T TG AAGAAG  
 CAG GCAGG TT GGGC  
 ||| |||| || ||||  
 GTC CGTCT AA CCGG  
 C GT CA\_\_\_\_  
 GAM1237 KIAA1138 3' AGTCTTTTTTTATTTTGTATTG 62137 TGT  
 CAGTGCAGG TAAGAAGGGGCT  
 ||||| |||||  
 GTTATGTTT ATTTTTTTCTGA  
 T\_\_\_\_  
 GAM1237 KIAA1190 3' AGCTCTTTTTCTTCCTTGCACT 71094 TGTTA  
 AGTGCAGG AGAAGGGGCT  
 ||||| |||||  
 TCACGTTT TTTTCTCGA  
 CTTC\_  
 GAM1237 KIAA1193 3' AGCCACTTTAGGTCTGCATTG 67628 TGTTAA G  
 CAGTGCAGG GAAG GGCT  
 ||||| ||| ||||  
 GTTACGTCT TTTC CCGA  
 GGA\_\_ A  
 GAM1237 KIAA1198 3' AGAATCTTTTAGTATCTGGGCT 63287 G A GG  
 G CAGT CAGGTGTTAAGA GG CT  
 ||| ||||| || ||  
 GTCG GTCTATGATTTT CT GA  
 G \_ AA  
 GAM1237 KIAA1203 3' GGCTCTTGGAATTTTGCCTG 71643 T AAGA  
 CAGTGCAGG GTT AGGGGCT  
 ||||| || |||||



GTCACGTTT TAA TTCTCGG  
 \_ GG\_  
 GAM1237 KIAA1210 3' CCTGGACATCTGACTG 96328 G AAGAAG  
 CAGT CAGGTGTT GGG  
 ||| ||||| ||  
 GTCA GTCTACAG TCC  
 \_ G\_\_\_\_  
 GAM1237 KIAA1317 3' AGCTCTTTCATAGACTTGTGCT 86029 TG G A  
 AG CAGGT TTA GAAGGGGCT  
 || ||||| ||| |||||  
 TC GTTCA GAT CTTTCTCGA  
 GT \_ A  
 GAM1237 KIAA1317 5' GTTTCTTGCCTGCACTG 86032 GTTAAG GG  
 CAGTGCAGGT AAG GC  
 ||||| ||| ||  
 GTCACGTCCG TTC TG  
 \_\_\_\_\_ TT  
 GAM1237 KIAA1340 3' AGCATTAAATATTTGTGCTG 69179 TG A AGGG  
 CAG CAGGTGTT AGA GCT  
 ||| ||||| ||| |||  
 GTC GTTTATAA TTT CGA  
 GT A A\_\_\_\_  
 GAM1237 KIAA1391 3' GGCTTTTTCTTATTAAAGGTTG 67264 T AGG T  
 G GC TG TAAGAAGGGGCT  
 || || ||||| |||||  
 G TG AT ATTCTTTTTCGG  
 T GAA T  
 GAM1237 KIAA1393 3' TTTTATAGTATATGTGCTG 72102 TG G  
 CAG CA GTGTTAAGAAG  
 ||| || ||||| |||||  
 GTC GT TATGATTTTTT  
 GT A  
 GAM1237 KIAA1395 3' GCCTCAGCTGTCTGTGCTG 76086 TG TGTTA AA  
 CAG CAGG AG GGGGC  
 ||| ||| || |||||  
 GTC GTCT TC CTCCG  
 GT G\_\_\_\_ GA  
 GAM1237 KIAA1456 3' CTTCTGATGCCTCACTG 66995 C A  
 CAGTG AGGTGTTA GAAG  
 ||||| ||||| |||  
 GTCAC TCCGTAGT CTTC  
 \_ C  
 GAM1237 KIAA1462 3' AGTTCCTGAAAAATTAACCTT 91382 G GA\_\_\_\_  
 G TACTG GCAGGT TTAA AGGGGCT  
 ||||| ||| |||||  
 TGTTCA AATT TCCTTGA  
 A AAAAAAG  
 GAM1237 KIAA1464 3' GCCCTGGGCCCTGTGCTG 68266 TG T TAAGAA  
 CAG CAGG GT GGGGC  
 ||| ||||| || |||||

		GTC GTCC CG TCCCG	
		GT _ GG_____	
GAM1237 KIAA1497	5'	GGCTTTTTCTTAGTGTTCTAT 67514	CA TG
	T	AGTG GG TTAAGAAGGGGCT	
		TTAT TT GATTCTTTTCGG	
		CC GT	
GAM1237 KIAA1509	3'	GGCCTTTTCTCTTGCTTGCCTG 61617	__ TA_
	CGGTG	TGCAGGT GT AGAAGGGGCT	
		GCGTCCG CG TCTTTTCGG	
		TT TTC	
GAM1237 KIAA1559	5'	GTTCTTTCCGGCTTCGCTG 73074	C G TTAA
		CAGTG AG TG GAAGGGGC	
		GTCGC TC GC CTTTCTTG	
		T G _____	
GAM1237 KIAA1559	3'	TTCTTCAGCACTTGAGCTG 73077	G AA
		CAGT CAGGTGTT GAAGGG	
		GTCG GTTCACGA CTTCTT	
		A _____	
GAM1237 KIAA1580	5'	GGTTTCTTCTTGACAGCTGAC 69448	G G GG
		GT CAG TGTTAAGAAG GCT	
		CA GTC ACAGTTCTTC TGG	
		_ G TT	
GAM1237 KIAA1635	3'	TTTTATGTTTGCCTG 67865	TG T
		CAGTGCAGG T AAGA	
		GTCACGTTT A TTTT	
		GT _____	
GAM1237 KIAA1644	3'	AGCCTCTTCTTGGAATTGCAT 85022	GTG
		GTGCAG TTAAGAAGGGGCT	
		TACGTT GGTCTTCTCCGA	
		AA_	
GAM1237 KIAA1649	3'	CTCACTGCTTGCACTG 50258	GTTAAGA _
		CAGTGCAGGT AG GGG	
		GTCACGTTTCG TC CTC	
		_____ A	
GAM1237 KIAA1649	3'	CTCACTGCTTGCACTG 66977	GTTAAGA _
		CAGTGCAGGT AG GGG	
		GTCACGTTTCG TC CTC	
		_____ A	
GAM1237 KIAA1671	3'	GGTTCTGAAAAACACCTGCATT 65685	AAGAA
		AGTGCAGGTGTT GGGGCT	

			TTACGTCCACAA	TCTTGG		
			AAAG_			
GAM1237	KIAA1674	3'	AGTCTCTTGTGCTGAGTGT	TTTG 68772	TG A	___
	C		GCAGG TT AG	AAGGGGCT		
			CGTTT GA TC	TTCTCTGA		
			GT G	GTG		
GAM1237	KIAA1674	3'	TTTTCAGCAGTCTGTGCTG	68800	TG _	A
			CAG CAGG TGTT	AGAA		
			GTC GTCT	ACGA TTTT		
			GT G	C		
GAM1237	KIAA1712	3'	CCATCTTGGCATCTGTACTG	67534		A
			CAGTGCAGGTGTTAAGA	GG		
			GTCATGTCTACGGTTCT	CC		
			A			
GAM1237	KIAA1735	3'	AGCTCTGAGATGACATCTTGTT	87623	T _	AGAA
	G		G GCA GGTGTTA	GGGGCT		
			G TGT CTACAGT	TCTCGA		
			T T	AGAG		
GAM1237	KIAA1751	3'	AGTTCCCACAGGGCACCTGGCT	71687	G	AAGAA
	G		CAGT CAGGTGTT	GGGGCT		
			GTCG GTCCACGG	CCTTGA		
			_	GACAC		
GAM1237	KIAA1776	3'	CTTTCACCTTCTGTACTG	50590	T TAA	
			CAGTGCAGG GT	GAAGG		
			GTCATGTCT CA	CTTTC		
			T	___		
GAM1237	KIAA1796	3'	TCTCCTTTTGACACTTTATTG	91456	C	A CT
			CAGTG AGGTGTTAAGA	GGGG		
			GTTAT TTCACAGTTTT	CCTC		
			_	TT		
GAM1237	KIAA1798	3'	GTCAGTGACATCTGCAGTG	60622	G	AGAAGG
			CA TGCAGGTGTTA	GGC		
			GT ACGTCTACAGT	CTG		
			G	GA___		
GAM1237	KIAA1821	3'	GGCTTCTTTTAAATCTTTTGTT	71789	T T_	
	G		G GCAGG GTTAAGAAGGGGCT			
			G TGTTT TAATTTTCTTCGG			
			T	TC		
GAM1237	KIAA1881	3'	AGCCTGGAAGGGCATCTGT	95337		AAGAAG
			GCAGGTGTT	GGGCT		

		TGTCTACGG	TCCGA		
		GAAGG_			
GAM1237	KIAA1893	3'	AGCCCCTTGTCCCCCCTGTGCT	73212	TG TGTTAAG
	G		CAG CAGG AAGGGGCT		
			GTC GTCC TTCCCCGA		
			GT CCCCTG_		
GAM1237	KIAA1908	5'	AGCTCCACGGCGTCTGCAT	73394	GT AAGAA
			GTGCAG GTT GGGGCT		
			TACGTC CGG CCTCGA		
			TG CA__		
GAM1237	KIAA1948	3'	AGTCTTTTCAACTTCTGTGTT	82398	TG T AA
			AG CAGG GTT GAAGGGGCT		
			TT GTCT CAA CTTTCTGA		
			GT T _		
GAM1237	KIAA1950	5'	GGCCCTTGGACCAGTGTCTGTC	92594	T TG AAGA_
	TG		CAG GCAGG TT AGGGGCT		
			GTC TGTCT GA TTCCCGG		
			_ GT CCAGG		
GAM1237	KIAA1966	3'	AGTTGAATTGACACTTTTATTG	55891	C GAAGG
			CAGTG AGGTGTAA GGCT		
			GTTAT TTCACAGTT TTGA		
			T AAG__		
GAM1237	KIAA1977	5'	GTCCCTTCTTTCTCACTG	74281	C TGTT
			CAGTG AGG AAGAAGGGGC		
			GTCAC TCC TTCTTCCCTG		
			_ T__		
GAM1237	KIF1C	3'	GCCCCTGTCCGTCTGTCTG	61224	T GT TTAAGA
			CAG GCAG G AGGGGC		
			GTC TGTC C TCCCCG		
			_ TG CTG__		
GAM1237	KLHL4	3'	AGTTTTTTTTTAAAAACGTAC	38918	AGGTG
	T		AGTGC TTAAGAAGGGGCT		
			TCATG AATTTTTTTTGA		
			CAAAA		
GAM1237	KPNA6	3'	GGTCCTTTTCTCTCTGC	24612	TGTTAA
			GCAGG GAAGGGGCT		
			CGTCT TTTTCTGG		
			CTCC__		
GAM1237	KRTAP1-5	3'	GTTCTCAGACTTTGCATTG	49227	T AAGAA
			CAGTGCAGG GTT GGGGC		

			GTTACGTTT CAG TCTTG		
			AC__		
GAM1237	KRTAP3-2	3'	GCTCTTGTTCCTGTACTG 49232	TGTTAAGA	
			CAGTGCAGG AGGGGC		
			GTCATGTTT TTCTCG		
			TTTG__		
GAM1237	KRTHB5	3'	GGTCCCCCAGCAAGCACTTGCC 9655	T AAGAA_	
	TG		CAG GCAGGTGTT GGGGCT		
			GTC CGTTCACGA CCCTGG		
			ACGACC		
GAM1237	LANO	3'	GGTACATATTTTAGTATTTGTG 36624	TG AGGG_	
	C		G CAGGTGTAAAGA GCT		
			C GTTTATGATTTT TGG		
			GT ATACA		
GAM1237	LHFPL2	3'	TTTTCAAACATCTGTGGTG 69958	G AA	
			CA TGCAGGTGTT GAAGG		
			GT GTGTCTACAA CTTT		
			G A_		
GAM1237	LRRFIP1	3'	TCTTTTCTCTCCACTG 16419	C GTGTTA	
			CAGTG AG AGAAGGGG		
			GTCAC TC TCTTTTCT		
			C ____		
GAM1237	LY117	5'	AGCCCTAGCAGCATCTGCCTG 97744	T AAGAA	
			CAG GCAGGTGTT GGGGCT		
			GTC CGTCTACGA TCCCGA		
			CGA__		
GAM1237	LY117	5'	AGCCCTAGCAGCATCTGCCTG 97845	T AAGAA	
			CAG GCAGGTGTT GGGGCT		
			GTC CGTCTACGA TCCCGA		
			CGA__		
GAM1237	LY117	5'	AGCCCTAGCAGCATCTGCCTG 92350	T AAGAA	
			CAG GCAGGTGTT GGGGCT		
			GTC CGTCTACGA TCCCGA		
			CGA__		
GAM1237	MADHIP	5'	GTTTCTTCTACTTTATTG 16623	C GTTA GG	
			CAGTG AGGT AGAAG GC		
			GTTAT TTCA TCTTC TG		
			TT		
GAM1237	MAL2	3'	GCCCAGACATCTGTA 53553	AAGAAG	
			TGCAGGTGTT GGGC		

ATGTCTACAG CCGG  
 A\_\_\_\_\_  
 GAM1237 MAP 3' AGTTCAAAGTGTGCTGTGTT 43054 TG TG AGAAG  
 G CAG CAGG TTA GGGCT  
 ||| ||| ||| ||||  
 GTT GTCC GAT CTTGA  
 GT GT CAAA\_  
 GAM1237 MAP-1 3' AGTTCTTTCACTATCTGTGT 42176 TG TTAA  
 G CAGGTG GAAGGGGCT  
 | ||||| |||||  
 T GTCTAT CTTTCTTGA  
 GT CA\_  
 GAM1237 MAP2K5 5' GGCTCTTTCTTAATAGCC 10866 \_  
 GG TGTTAAGAAGGGGCT  
 || |||||  
 CC ATAATTCTTTCTCGG  
 G  
 GAM1237 MAP3K2 3' GGTTTCTTCTTATATCTGTATT 21734 T GG  
 AGTGCAGGTGT AAGAAG GCT  
 ||||| ||||| |||  
 TTATGTCTATA TTCTTC TGG  
 \_ TT  
 GAM1237 MAPK8IP3 3' GCCCAGAAGCGTTTGTCTG 52986 T GG AAGAAG  
 CAG GCA TGTT GGGC  
 ||| ||| ||| |||  
 GTC TGT GCGA CCGG  
 \_ TT AGA\_  
 GAM1237 MEGF10 3' AGTTCCTTTTGATCTGTTGGTG 50581 \_\_\_\_ GTTA  
 CTG T GCAGGT AGAAGGGGCT  
 | ||||| |||||  
 G TGTCTA TTTTCTTGA  
 TGGT G\_  
 GAM1237 MESDC2 3' GCTTTTTCTGTTGTACT 72494 GGTGTTA  
 AGTGCA AGAAGGGGC  
 ||||| |||||  
 TCATGT TCTTTTTCG  
 TG\_  
 GAM1237 MGC10067 3' AGTCTCTTTTGGTGGCTAAGT 58934 \_ G GT  
 A TGC AG T TAAGAAGGGGCT  
 ||| ||| |||||  
 ATG TC G GTTTTCTCTGA  
 AA G TG  
 GAM1237 MGC10955 3' GTCTGGAATGTCTGCCTG 51046 T TG AAGAAG  
 CAG GCAGG TT GGGC  
 ||| ||||| ||| |||  
 GTC CGTCT AA TCTG  
 \_ GT GG\_  
 GAM1237 MGC10966 5' GGCTGGGGGCGTGGCACCTGCA 48896 AGAAGG\_  
 CTG CAGTGCAGGTGTTA GGCT  
 ||||| |||

GTCACGTCCACGGT TCGG  
 GCGGGGG  
 GAM1237 MGC11115 3' CCCTGCTCCTGTACTG 50237 T TAAGAA  
 CAGTGCAGG GT GGGG  
 ||||| || |||  
 GTCATGTCC CG TCCC  
 T \_\_\_\_\_  
 GAM1237 MGC13071 3' AGTTTCTTTGGTATGACCTGTG 51085 TG GT A\_ GG  
 TT AG CAGGT TA GAAG GCT  
 || |||| || ||| |||  
 TT GTCCA AT TTTC TGA  
 GT GT GG TT  
 GAM1237 MGC13183 3' AGCTGAGATGATGCTTGTAT 50389 AGAAGG  
 GTGCAGGTGTTA GGCT  
 ||||| |||  
 TATGTTCTAGT TCGA  
 AGAG\_  
 GAM1237 MGC15437 3' GGCTGCACTGCTACTTGTGCTG 51784 TG TTA AAGG  
 CAG CAGGTG AG GGCT  
 || |||| || |||  
 GTC GTTCAT TC TCGG  
 GT CG\_ ACG\_  
 GAM1237 MGC17303 5' GCCCCTTCCTCGGCGCT 57501 TA \_  
 GGTGT AG AAGGGGC  
 |||| |||||  
 TCGCG TC TTCCCCG  
 GC C  
 GAM1237 MGC20255 3' TCTTTCTTGGTGTCTGTCTG 53447 T TG  
 CAG GCAGG TTAAGAAGGG  
 || |||| |||||  
 GTC TGTCT GGTTCTTTCT  
 \_ GT  
 GAM1237 MGC21854 3' AGTTCCTTTTTTAATGTT 53489 TG  
 GG TTAAGAAGGGGCT  
 || |||||  
 TT AATTTTCCTTGA  
 GT  
 GAM1237 MGC2541 5' GGCTTTGCTGTGGGCACCTGCA 54752 AAGAA\_  
 CTG CAGTGCAGGTGTT GGGGCT  
 ||||| |||  
 GTCACGTCCACGG TTTCGG  
 GTGTCTG  
 GAM1237 MGC2705 5' GCTCCCCGCGCCTGCCTTG 51114 T TAAGAA  
 CAG GCAGGTGT GGGGC  
 || |||| |||  
 GTT CGTCCGCG CCTCG  
 C CC\_  
 GAM1237 MGC27171 3' AGCCTCTTGCCTTGACCTGCAT 58084 GT \_  
 T AGTGCAGGT TAAG AAGGGGCT  
 ||||| ||| |||||

TTACGTCCA GTTC TTCTCCGA  
 — CG  
 GAM1237 MGC2941 3' GCCCCAGTCCCTGTGCTG 44159 TG TG AAGAA  
 CAG CAGG TT GGGGC  
 ||| ||| || ||||  
 GTC GTCC GA CCCC  
 GT CT \_\_\_\_  
 GAM1237 MGC3047 3' AGCCCTTGCTCCTCTGTGTTG 50358 TG TGTTA A  
 CAG CAGG AG AGGGGCT  
 ||| ||| || |||||  
 GTT GTCT TC TTCCCGA  
 GT CC\_\_ G  
 GAM1237 MGC3047 3' GGCTACATTTGGCTTCTGTACT 50362 T AAGG  
 G CAGTGCAGG GTTAAG GGCT  
 ||||| ||||| |||  
 GTCATGTCT CGGTTT TCGG  
 T ACA\_  
 GAM1237 MGC3121 5' AGCCTCGCCCGGCGTCTGATTG 43818 G GT AAGAA  
 CAGT CAG GTT GGGGCT  
 ||| ||| ||| |||||  
 GTTA GTC CGG CTCCGA  
 \_ TG CCCG\_  
 GAM1237 MGC3279 3' GTTTCATTACCTGTATTG 43815 TTAAGAA GG  
 CAGTGCAGGTG G GC  
 ||||| ||| | ||  
 GTTATGTCCAT C TG  
 TA\_\_\_\_ TT  
 GAM1237 MGC34869 5' AGCTCCGGGCGCGGCGCTTGTT 58094 T AAGAA\_  
 TTG CAG GCAGGTGTT GGGGCT  
 ||| ||||| |||||  
 GTT TGTTGCGCGG CCTCGA  
 T CGCGGG  
 GAM1237 MGC35558 3' GGCTCTTTCAACTCCTGTGTTG 58785 TG T AA  
 CAG CAGG GTT GAAGGGGCT  
 ||| ||| ||| |||||  
 GTT GTCC CAA CTTTCTCGG  
 GT T \_  
 GAM1237 MGC4172 3' GGCCTTCACCTTATATCTGTGT 44203 TG T AA\_  
 TG CAG CAGGTGT AAG GGGGCT  
 ||| ||||| ||| |||||  
 GTT GTCTATA TTC TTCCGG  
 GT \_ CAC  
 GAM1237 MGC4189 3' GCCTGTGATACTTGGGCTG 50232 G AGAAG  
 CAGT CAGGTGTTA GGGC  
 ||| ||||| ||| |||  
 GTCG GTTCATAGT TCCG  
 G G\_\_\_\_  
 GAM1237 MGC4504 3' GGCCTCTTACCCACTTG 44111 TTAAG  
 CAGGTG AAGGGGCT  
 ||||| |||||



GTTCAC TTCTCCGG  
 CCA\_\_  
 GAM1237 MGC4655 5' GGCCCCTCGGACCCTGCGCTG 52802 T AAGA  
 CAGTGCAGG GTT AGGGGCT  
 ||||| || |||||  
 GTCGCGTCC CAG TCCCCGG  
 \_ GC\_  
 GAM1237 MGC4796 5' GCTCGGGTGGCTGCGCTG 61491 G GT AAGAAG  
 CAGTGCAG T T GGGC  
 ||||| | | |||  
 GTCGCGTC G G CTCG  
 G TG G\_\_\_\_  
 GAM1237 MIC2L1 3' GCCTCTTTGGTCTGCAT 48824 TGTTAA  
 GTGCAGG GAAGGGGC  
 ||||| |||||  
 TACGTCT TTTCTCCG  
 GG\_\_\_\_  
 GAM1237 MIL1 3' GGTTCCTCAGCCTTGGCACTAG 31095 TG A A\_\_ GG  
 TGCTG C GGTGTTAAG AG GCT  
 | ||||| || |||  
 G TCACGGTTC TC TGG  
 GT A CGAC TT  
 GAM1237 MLN64 3' GGCTCTTCATCTGCCTGCGCT 94411 GTTA \_\_  
 AGTGCAGGT AGA AGGGGCT  
 ||||| || |||||  
 TCGCGTCCG TCT TTCTCGG  
 \_\_\_\_ AC  
 GAM1237 MRPL10 3' AGCTCAACCAAGCAGTTGTGCT 59150 TG G AAGAAG  
 G CAG CAG TGTT GGGCT  
 || ||| ||| |||||  
 GTC GTT ACGA CTCGA  
 GT G ACCAA\_  
 GAM1237 MRPL19 5' AGCTGGCATGGCGGCCTGCATT 28639 \_ AGAAGG  
 G CAGTGCAGGT GTTA GGCT  
 ||||| ||| |||  
 GTTACGTCCG CGGT TCGA  
 G ACGG\_  
 GAM1237 MRPL35 3' AGCCTCCATGATGTCTTTATTG 33538 C TG AGAA  
 CAGTG AGG TTA GGGGCT  
 |||| ||| || |||||  
 GTTAT TCT AGT CTCCGA  
 T GT AC\_  
 GAM1237 MRPS18A 3' AGTTCCTCCTGCACCTGTGCTG 36269 TG TA A  
 CAG CAGGTGT AG AGGGGCT  
 || ||||| || |||||  
 GTC GTCCACG TC TCCTTGA  
 GT \_ C  
 GAM1237 MRPS5 5' AGTCCCTCACCCCGGCCTGCGC 49118 GTTAAGA  
 TG CAGTGCAGGT AGGGGCT  
 ||||| |||||

			GTCGCGTCCG	TCCCTGA		
			GCCCCAC			
GAM1237	NAP1L1	3'	AGATATTTTTGATGACTGTATT	57617	GT	GGGG
	G		CAGTGCAG GTTAAGAA	CT		
			GTTATGTC TAGTTTTT	GA		
			AG	ATA_		
GAM1237	NAP1L1	3'	GGCCTTGAGGATAACCTGCACT	57619	_	AAGAA
	G		CAGTGCAGGT GTT	GGGGCT		
			GTCACGTCCA TAG	TTCCGG		
			A	GAG_		
GAM1237	NAP1L1	3'	GGTTTCTTCTAATTCTTATTG	57620	C T A	GG
			CAGTG AGG GTTA GAAG	GCT		
			GTTAT TCT TAAT CTTC	TGG		
			_ _ _	TT		
GAM1237	NAV3	3'	GGCTTCAGTAGTGTGTGTTG	29773	TG TG	AGAA
			CAG CAGG TTA	GGGGCT		
			GTT GTTT GAT	CTTCGG		
			GT GT GA_			
GAM1237	NCE2	3'	CTTTTTTGAACCTGTACTG	54762	G	
			CAGTGCAGGT TTAAGAAGG			
			GTCATGTTCA AGTTTTTTC			
			-			
GAM1237	NET-6	5'	GGCCCCCCCACCCACGTCTGCGT	26939	GT	TAAGAA
	TG		CAGTGCAG GT	GGGGCT		
			GTTGCGTC CA	CCCCGG		
			TG CCCACC			
GAM1237	NETO2	3'	AGCTCTTTCTTTCTTTTGTTA	36115	_	TGTT
	CTG		CAGTG CAGG	AAGAAGGGGCT		
			GTCAT GTTT	TTCTTTCTCGA		
			T	TCCT		
GAM1237	NEU4	5'	AGCCCAGCGAGGCCTGTGCTG	54951	TG	G AAGAAG
			CAG CAGGT TT	GGGCT		
			GTC GTCCG AG	CCCGA		
			GT G CGA_			
GAM1237	NIN283	3'	AGCTCTCCAGAATCCTGTGTTG	50066	TG T	AAGAA
			CAG CAGG GTT	GGGGCT		
			GTT GTCC TAA	TCTCGA		
			GT _	GACC_		
GAM1237	NMT1	3'	AGCGAACTTGACAATTGTATTG	40781	G	AAGGG
			CAGTGCAG TGTTAAG	GCT		

			GTTATGTT ACAGTTC	CGA		
			A AAG__			
GAM1237	NMT2	3'	AGTCCACATGTGACATTTGTAC	16663		AGAAG
			GTGCAGGTGTTA	GGGCT		
			CATGTTTACAGT	CCTGA		
			GTACA			
GAM1237	NPD009	5'	GCTGTAGCATCTCTGCTG	95051	C	AGAAGG
			CAGTG AGGTGTTA	GGC		
			GTCGT TCTACGAT	TCG		
			C G_____			
GAM1237	NR5A1	3'	GCCACTGGCACTTGCCTG	17101	T	AGAAGG
			CAG GCAGGTGTTA	GGC		
			GTC CGTTCACGGT	CCG		
			- CA_____			
GAM1237	NTPBP	3'	AGCTTCTTGCTCTTGACCCTGC	23433	T	_____
	ACTG		GTGCAGG GTTAAGA	AGGGGCT		
			CACGTCC CAGTTCT	TCTTCGA		
			- CGT			
GAM1237	NXPB2	5'	GCCCCTGCGCCTGT	72719	TAAGA	-
			GCAGGTGT	AGGGG C		
			TGTCCGCG	TCCCC G		
			_____ T			
GAM1237	NY-REN-41	3'	GGCTTGCACTAATATTTGCCTG	54689	T	AGAAG
			CAG GCAGGTGTTA	GGGCT		
			GTC CGTTTATAAT	TTCGG		
			- CACG_			
GAM1237	OCLM	3'	GGCCCCCTAACAGCAGTTGTAC	42349	G	AAGAA
	TG		CAGTGCAG TGTT	GGGGCT		
			GTCATGTT ACGA	CCCCGG		
			G CAATC			
GAM1237	OLFM2	3'	GCCCTTTTCATTCTGCCTG	54124	T	- TTAA
			CAG GCAGG TG	GAAGGGGC		
			GTC CGTCT AC	TTTTCCCG		
			- T _____			
GAM1237	OSBPL5	3'	GGTTTTTTATTCCACGCTGTGC	72691	TG	- TTAAG
	TG		CAG CAG GTG	AAGGGGCT		
			GTC GTC CAC	TTTTTTGG		
			GT G CTTA_			
GAM1237	OVCOV1	5'	GGTCTCTGGGACTGCCTGTGC	31954	TG	- AAGA
			G CAGGT GTT	AGGGGCT		

		C GTCCG CAG TCTCTGG		
		GT T GG__		
GAM1237	P101-PI3K	3' GGCCTTTTCTCTCAACCTTGGC 26679	GC	GTTA
	TG	CAGT AGGT AGAAGGGGCT		
		GTCG TCCA TCTTTTCCGG		
		GT ACTC		
GAM1237	P2RXL1	3' AGCCCAGCAGGCACCTGTATTG 18378		AAGAAG
		CAGTGCAGGTGTT GGGCT		
		GTTATGTCCACGG CCCGA		
		ACGA__		
GAM1237	PAI-RBP1	3' TTTTAATACCTGCTTTG 31586 T		
		CAG GCAGGTGTTAAGA		
		GTT CGTCCATAATTTT		
		T		
GAM1237	PAK6	3' GGCTTCTGAGCTTCTCCTGTAC 39411		TGTTAAGA
	TG	CAGTGCAGG AGGGGCT		
		GTCATGTCC TCTTCGG		
		TCTTCGAG		
GAM1237	PALM	3' GGCCTCTTCTCCATCCTGC 10415 _ TTA		
		GCAGG TG AGAAGGGGCT		
		CGTCC AC TCTTCTCCGG		
		T C__		
GAM1237	PARVA	3' GCCTTTTTATTCTTACTG 36654 C T TAA		
		CAGTG AGG GT GAAGGGGC		
		GTCAT TCT TA TTTTCCG		
		_ T _		
GAM1237	PCDH10	3' GGTCTTTTTTCTTTGCGTCTG 40427 GT T _		
		CAG GT AAGAAG GGGCT		
		GTC CG TTCTTT TCTGG		
		TG T TT		
GAM1237	PCDH19	3' GGTTAGAGTGGCATTGGCATTG 63704 AG AGAAGG		
		CAGTGC GTGTTA GGCT		
		GTTACG TACGGT TTGG		
		GT GAGA__		
GAM1237	PCSK7	3' AGCCCCTGGACATGCCTGTCCT 16332 TG TAAGA		
	G	CAG CAGGTGT AGGGGCT		
		GTC GTCCGTA TCCCCGA		
		CT CAGG_		
GAM1237	PCYT1B	3' AGTTCCCTAGAGAGACTTGCAC 16748 G AAGA _		
	TG	CAGTGCAGGT TT AGGGG CT		

			GTCACGTTCA AG	TCCCT GA		
			G AGA_ T			
GAM1237	PDCD7	5'	GCCCTCCAACGCCTGCGC	72139	AAGAA	
			GTGCAGGTGTT	GGGGC		
			CGCGTCCGCAA	TCCCG		
			CC__			
GAM1237	PDE1C	3'	CTTCAAGGCATCTGTCTG	17219	T	AA
			CAG GCAGGTGTT	GAAGG		
			GTC TGTCTACGG	CTTTC		
			AA			
GAM1237	PDE2A	3'	TCTCTTCCCCTGTCTG	10473	T	TGTTAA
			CAG GCAGG	GAAGGGG		
			GTC TGTCC	CTTCTCT		
			C_____			
GAM1237	PDE4DIP	3'	TTTTGGTCTGCACTG	95441	TG	
			CAGTGCAGG	TTAAGA		
			GTCACGTCT	GGTTTT		
			_____			
GAM1237	PDE7B	5'	GGCTCTGTCCCAGCACTTGTCT	38449	T	AA A
	G		CAG GCAGGTGTT	GA GGGGCT		
			GTC TGTTCACGA	CT TCTCGG		
			CC G			
GAM1237	PDEF	5'	GGCCCCCAGATGCCTGGCTG	24749	G	AAGAA
			CAGT CAGGTGTT	GGGGCT		
			GTCG GTCCGTAG	CCCCGG		
			ACC__			
GAM1237	PER3	3'	AGTTTCAGTTAGCATTTGCAT	33678		GAA GG
			GTGCAGGTGTAA	G GCT		
			TACGTTTACGATT	C TGA		
			GA_ TT			
GAM1237	PER3	3'	GGCTCTTTTGTAGTTGAATTG	33681	G G	TTA
			CAGT CAG TG	AGAAGGGGCT		
			GTTA GTT AT	TTTTTCTCGG		
			A G G__			
GAM1237	PF1	5'	AGCTTTCTCAAGCGCCTGCGC	95119	AA	AG
			GTGCAGGTGTT	GA GGGCT		
			CGCGTCCGCGA	CT TTCGA		
			A_ CT			
GAM1237	PHYHIP	3'	GGCCCTTTCCTCCCCCTGTGC	28613	TG	TGTTAA
	TG		CAG CAGG	GAAGGGGCT		

GTC GTCC CTTTCCCGG  
 GT CCCTTC  
 GAM1237 PIP5K1C 3' GGCCCTTTTGGAGATATACTTG 70764 G \_ TAA\_\_\_\_  
 GTGTTG C AGGTGT GAAGGGGCT  
 | ||||| |||||  
 G TTCATA TTTTCCCGG  
 T G TAGAGG  
 GAM1237 PLA2G6 3' CCCCTTTCCTGACTG 66488 G TGTTAA  
 CAGT CAGG GAAGGGG  
 ||| ||| |||||  
 GTCA GTCC TTTCCCC  
 \_ C\_\_\_\_  
 GAM1237 PLAA 3' TTTTGATATTTGGCTG 14916 G  
 CAGT CAGGTGTTAAGA  
 ||| |||||  
 GTCG GTTTATAGTTTT  
 \_  
 GAM1237 PLAC3 3' GGCTCTTTTCTTTTGTGT 69345 TG TGTTA  
 G CAGG AGAAGGGGCT  
 | ||| |||||  
 T GTTT TTTTCTCGG  
 GT TTC\_\_\_\_  
 GAM1237 PLAGL2 3' GTCCTTTCCTCTCTGCCTG 70455 T TGTTAA  
 CAG GCAGG GAAGGGGC  
 ||| ||| |||||  
 GTC CGTCT CTTTCCTG  
 \_ CTC\_\_\_\_  
 GAM1237 PLSCR2 3' GGTTCCTTCTCTCTCTACTG 39791 C TGTTAA  
 CAGTG AGG GAAGGGGCT  
 |||| ||| |||||  
 GTCAT TTC CTTCTTGG  
 C TTC\_\_\_\_  
 GAM1237 PLU-1 3' AGCTTCTTCTGCCCCTCTACTG 21755 C T TA  
 CAGTG AGG GT AGAAGGGGCT  
 |||| ||| |||||  
 GTCAT TCC CG TCTTCTTCGA  
 C C \_\_\_\_  
 GAM1237 PLU-1 3' AGCTTCTTCTGCCCCTCTACTG 87415 C T TA  
 CAGTG AGG GT AGAAGGGGCT  
 |||| ||| |||||  
 GTCAT TCC CG TCTTCTTCGA  
 C C \_\_\_\_  
 GAM1237 PMF1 3' GCCCTTTTCCCTGCCCTG 23326 T TGTTAA  
 CAG GCAGG GAAGGGGC  
 ||| ||| |||||  
 GTC CGTCC TTTTCCCG  
 C C\_\_\_\_  
 GAM1237 PNAS-127 3' GGCCTTAAGTAAACAATCTGCA 50660 \_ AAGAA  
 TTG CAGTGCAGGT GTT GGGGCT  
 ||||| ||| |||||

GTTACGTCTA CAA TTCCGG  
 A ATGAA  
 GAM1237 POLR3K 3' CTCTTAAATATTTGTACTG 32847 AAG  
 CAGTGCAGGTGTT AAGGG  
 ||||| ||||  
 GTCATGTTTATAA TTCTC  
 A\_\_  
 GAM1237 PORIMIN 3' AGTTTCTTTTTGAATACTTGT 53597 \_ GG  
 GCAGGTGT TAAGAAG GCT  
 ||||| ||||| ||  
 TGTTCATA GTTTTTTC TGA  
 A TT  
 GAM1237 POU2F1 3' AGCCTTTTTCACTCTGCAGTG 10686 G \_ TTAA  
 CA TGCAG GTG GAAGGGGCT  
 || ||||| || |||||  
 GT ACGTC CAC TTTTCCGA  
 G T \_\_\_\_  
 GAM1237 PPP1R14C 3' GGCTTCTCTCAATGGCTTGTGT 48202 TG \_ A A  
 TG CAG CAGGT GTT AGA GGGGCT  
 || ||||| || |||||  
 GTT GTTCG TAA TCT CTTCGG  
 GT G C \_  
 GAM1237 PRDX1 5' GTTTCTGCGACTTGTGTTG 10407 TG \_ TAAGA GG  
 CAG CAGGT GT AG GC  
 || ||||| || || ||  
 GTT GTTCA CG TC TG  
 GT G \_\_\_\_ TT  
 GAM1237 PRO0246 5' GCTCTTTCTCTATTTACTG 26138 GT\_ TA  
 CAG GT AGAAGGGGC  
 || || |||||  
 GTC TA TCTTTCTCG  
 ATT TC  
 GAM1237 PRO0529 5' GGTCTCTTTTTTTGTGTTTGTG 25997 TG TG T\_  
 T G CAGG T AAGAAGGGGCT  
 | |||| | |||||  
 T GTTT G TTTTCTCTGG  
 GT GT TT  
 GAM1237 PRO1575 5' CTTAACATTTCACTG 26028 C  
 CAGTG AGGTGTTAAG  
 ||||| |||||  
 GTCAC TTTACAATTC  
 \_  
 GAM1237 PRO2893 3' GTTTTTTCTTGAATGCCTG 37804 \_  
 CAGGTGT TAAGAAGGGGC  
 ||||| |||||  
 GTCCGTA GTTCTTTTTTG  
 A  
 GAM1237 PRSS12 3' AGCCTCAAGGACATCTGCCTG 13247 T AAGAA  
 CAG GCAGGTGTT GGGGCT  
 || ||||| |||||

GTC CGTCTACAG CTCCGA  
 \_ GAA\_  
 GAM1237 PSR 3' AGTTGTTTTTGATGTGTGTACT 65173 G TG G GCT  
 G CAGTGCA G TTAAGAA GG  
 ||||| I ||||| II  
 GTCATGT T AGTTTTT TT  
 G GT G GA  
 GAM1237 PSTPIP1 3' AGCCCCTTCGGACCTGCCCTG 14281 T GTTAA  
 CAG GCAGGT GAAGGGGCT  
 ||| ||||| |||||  
 GTC CGTCCA CTTCCCCGA  
 C GG\_  
 GAM1237 PTPN9 3' AGTCCTTTCTGTCACTTCTGTGT 11076 TG \_ TTA  
 G CAGG TG AGAAGGGGCT  
 I ||| II |||||  
 T GTCT AC TCTTTCCTGA  
 GT T TG\_  
 GAM1237 PTPN9 3' GCCCTTTTTCTTTTGC 11078 TGTTA  
 GCAGG AGAAGGGGC  
 |||| |||||  
 CGTTT TTTTCCCG  
 TC\_  
 GAM1237 PXMP4 3' GCCCTGAGGTGTCTGGCTG 23376 G TG AAGAA  
 CAGT CAGG TT GGGGC  
 ||| ||| II ||||  
 GTCG GTCT GG TCCCG  
 \_ GT AG\_  
 GAM1237 PXR2b 3' AGTTTCATAATAATCTGCACTG 33336 \_ AGAA GG  
 CAGTGCAGGT GTTA G GCT  
 ||||| ||| I |||  
 GTCACGTCTA TAAT C TGA  
 A A\_\_ TT  
 GAM1237 QKI 3' GCCTTTTTTATATTGCCTG 65444 GT \_  
 CAGGT TA AGAAGGGGC  
 |||| II |||||  
 GTCCG AT TTTTTTCCG  
 TT A  
 GAM1237 RAB14 3' GTTTCAGCGCTTGTGCTG 32874 TG AAGAA GG  
 CAG CAGGTGTT G GC  
 ||| ||||| I ||  
 GTC GTTCGCGA C TG  
 GT \_ TT  
 GAM1237 RAB22A 3' AGTTTCTTTTAGCTTGTAC 59929 GTTAA GG  
 GTGCAGGT GAAG GCT  
 ||||| ||| |||  
 CATGTTCG TTTC TGA  
 AT\_\_ TT  
 GAM1237 RAB27B 3' TTTTAGATTGTCATTG 14785 G  
 CAGTGCAGGT TTAAGA  
 ||||| |||||



GTTACGTTTA GATTTT

GAM1237 RAB33B 3' GGTCATCTTGACACTTTGCTG 48500 C AGG  
CAGTG AGGTGTTAAGA GGCT  
||||| ||||| |||  
GTCGT TTCACAGTTCT CTGG  
\_ A\_  
GAM1237 RAB34 3' GACCCCTGGACATTTGCACTG 49193 AAGA CT  
CAGTGCAGGTGTT AGGGG  
||||| |||  
GTCACGTTTACAG TCCCC  
G\_\_ AGT  
GAM1237 RAB40A 5' GGTTTTTTTTTCTCTATTTGC 82070 T TT\_  
CCTG AG GCAGGTG AAGAAGGGGCT  
|| ||||| |||||  
TC CGTTTAT TTTTTTTTGG  
C CTCT  
GAM1237 RABEX5 3' CTTGACAGCTACCTGCATTG 27185 \_\_\_\_  
CAGTGCAGGT GTTAAG  
||||| |||  
GTTACGTCCA CAGTTC  
TCGA  
GAM1237 RAI15 3' CTCAGACTCTGCACTG 66668 T AAGAAG  
CAGTGCAGG GTT GGG  
||||| |||  
GTCACGTCT CAG CTC  
\_ A\_  
GAM1237 RAI16 3' GCACTTTGGCATTGTCAC 42756 AA GG T  
GTGCAGGTGTT GAAG GC  
||||| ||| ||  
CACGTTTACGG TTTC CG  
\_ A\_ T  
GAM1237 RAI17 3' GTTCTTGCTTCTTGCGTTG 91284 TGTT A  
CAGTGCAGG AAG AGGGGC  
||||| ||| |||||  
GTTGCGTTC TTC TTCTTG  
\_ G  
GAM1237 RASD2 3' AGCTCTGCATACCTGCAC 26683 TAAGAA  
GTGCAGGTGT GGGGCT  
||||| |||  
CACGTCCATA TCTCGA  
CG\_  
GAM1237 RASD2 3' GGCCCCTGCCTGCGTCTGTGCT 26688 TG GT TAAGA  
AG CAG GT AGGGGCT  
|| ||| || |||||  
TC GTC CG TCCCCGG  
GT TG TCCG\_  
GAM1237 RASGRP4 3' GGCTTCCGGCTGCCTGTACTG 53658 GTTA AA \_  
CAGTGCAGGT AG GGG GCT  
||||| || ||| |||

GTCATGTCCG TC CCT CGG  
 \_\_\_\_ GG T  
 GAM1237 RASSF2 3' AGCCGTGAGCTTGGCACATGTG 28426 TG G AAGG\_  
 CTG CAG CA GTGTTAAG GGCT  
 ||| || ||||| |||  
 GTC GT CACGGTTC CCGA  
 GT A GAGTG  
 GAM1237 RBT1 3' GGCTTTTTTTTTTTTTTTTGA 25353 G TGTT\_  
 TTG CAGT CAGG AAGAAGGGGCT  
 |||| ||| |||||  
 GTTA GTTT TTTTTTTTCGG  
 G TTTT  
 GAM1237 RIS1 3' GCCCTTCCCTCTATTG 80582 C TGTTAA  
 CAGTG AGG GAAGGGGC  
 |||| ||| |||||  
 GTTAT TCC CTTTCCCG  
 C C\_\_\_\_  
 GAM1237 RNB6 3' TTTTTTTAGATTCTGCCTG 32931 T TG  
 CAG GCAGG TTAAGAAGG  
 ||| |||| |||||  
 GTC CGTCT GATTTTTTT  
 \_ TA  
 GAM1237 RNF40 3' GCCCAGAGCACTTGACTG 28715 G AAGAAG  
 CAGT CAGGTGTT GGGC  
 ||| ||||| |||  
 GTCA GTTCACGA CCGG  
 \_ GA\_\_\_\_  
 GAM1237 RNP24 3' AGCTTCTTGATTTTCATTTTCAT 22355 C TTAAG\_  
 TG CAGTG AGGTG AAGGGGCT  
 |||| |||| |||||  
 GTTAC TTTAC TTCTTCGA  
 \_ TTTAGG  
 GAM1237 RODH 3' AGCCCTTTTTTGTATGAGACT 13572 \_\_\_\_  
 GGT GTTAAGAAGGGGCT  
 ||| |||||  
 TCA TAGTTTTTTCCCGA  
 GAG  
 GAM1237 RPP14 3' TTTTTTGGTGCCTGCAT 59503 TG  
 GTGCAGG TTAAGAAG  
 ||||| |||||  
 TACGTCC GGTTTTTT  
 GT  
 GAM1237 RPS27L 3' AGCTTCCTGAATTTTAATTTTG 31924 G T \_\_\_\_ \_  
 TGTTG CAGG GTTAAGA AGGG GCT  
 |||| ||||| ||| |||  
 GTTT TAATTTT TCCT CGA  
 T \_ AAG T  
 GAM1237 RYBP 5' AGCCTTTAAATGCAGCATCTGC 59470 AAGA\_  
 G TGCAGGTGTT AGGGGCT  
 ||||| |||||

			GCGTCTACGA	TTTCCGA	
			CGTAAA		
GAM1237	SCAMP-4	5'	CTTCAGCCTGCGCTG	54395	GTTAAGAA
			CAGTGCAGGT	GGGG	
			GTCGCGTCCG	CTTC	
			A_____		
GAM1237	SCDGF-B	5'	GGCTTTTTCTTGGAGCGACGCT	47379	CAG G
	G		CAGTG GT TTAAGAAGGGGCT		
			GTCGC CG GGTTCTTTTCGG		
			AG_ A		
GAM1237	SCDGF-B	5'	GGCTTTTTCTTGGAGCGACGCT	52451	CAG G
	G		CAGTG GT TTAAGAAGGGGCT		
			GTCGC CG GGTTCTTTTCGG		
			AG_ A		
GAM1237	SCGN	3'	AGCCCCTGTGTAGTGTCTGTGT	22785	TG TG AGA
	TG		CAG CAGG TTA AGGGGCT		
			GTT GTCT GAT TCCCCGA		
			GT GT GTG		
GAM1237	SCHIP1	3'	AGTTCCTTTTAGATGTGC	27410	G G
			GCA GT TTAAGAAGGGGCT		
			CGT TA GATTTTCCTTGA		
			G _		
GAM1237	SCYA3	5'	AGTCCTTTCTTGGCTCTGC	59844	T
			GCAGG GTTAAGAAGGGGCT		
			CGTCT CGGTTCTTCCTGA		
			—		
GAM1237	SDF1	3'	TCTTGATGCATGCACTG	90862	G
			CAGTGCA GTGTTAAGA		
			GTCACGT CGTAGTTCT		
			A		
GAM1237	SDOS	3'	GGCTTCTAGAGTGTTTGTGT	50368	TG TG AAGA
			G CAGG TT AGGGGCT		
			T GTTT GA TCTTCGG		
			GT GT GA__		
GAM1237	SEC22A	3'	AGTCTCTTTAGTACTATTGTA	24876	_ TAA
	TT		AGTGCAGGT GT GAAGGGGCT		
			TTATGTTCA CA TTTCTCTGA		
			T TGA		
GAM1237	SEC6	3'	AGCCTCTCTTGGGTGCTTGT	71593	TG _ A
			GCAGG TT AAGA GGGGCT		

			TGTTC GG TTCT CTCCGA		
			GT G _		
GAM1237	SEMA5B	3'	GTCCTTTAATCTGGGCTG 63128	G	GTTAAG
			CAGT CAGGT AAGGGGC		
			GTCG GTCTA TTTCCTG		
			G A_____		
GAM1237	SENP7	3'	AGCCCCTTACCAGCATTTGTGT 40300	TG	AAG
	T		AG CAGGTGTT AAGGGGCT		
			TT GTTTACGA TTCCCCGA		
			GT CCA		
GAM1237	SFXN5	3'	GGCCCCCTTTGGACCTGCA 58038	GTAA	
			TGCAGGT GAAGGGGCT		
			ACGTCCA TTTCCCCGG		
			GG_____		
GAM1237	SGKL	3'	GGTAAGACTTTAATATCTATAC 25145	C	AAGGG
	TG		CAGTG AGGTGTTAAG GCT		
			GTCAT TCTATAATTT TGG		
			A CAGAA		
GAM1237	SKRP1	5'	GTCTCTTGGTCTGTGGCTG 55147	_	TGTTAAG
			CAGT GCAGG AAGGGGC		
			GTCG TGTCT TTCTCTG		
			G GG_____		
GAM1237	SLAC2-B	3'	AGTCTGGGCAGTGTCTGCTCTG 30509	T	TG AAGAAG
			CAG GCAGG TT GGGCT		
			GTC CGTCT GA TCTGA		
			T GT CGGG_____		
GAM1237	SLC16A6	3'	GCTTTTTTTTTTTGCTTG 16273	TT	
			CAGGTG AAGAAGGGGC		
			GTTTCGT TTTTTTTTCG		
			TT		
GAM1237	SLC6A13	3'	GGCCCTTGATGGTGCCTGTGT 33518	TG	TG AGA
			G CAGG TTA AGGGGCT		
			T GTCC GGT TTCCCGG		
			GT GT AGG		
GAM1237	SMOC1	3'	AGTTCTTTTGTACAGGCATTGG 42148	AG	AA_____
	CATTG		TGC GTGTT GAAGGGGCT		
			ACG TACGG TTTTCTTGA		
			GT ACATG		
GAM1237	SNURF	3'	AGCTTCTGCCCAGCTTGCATTG 19051		GTTAAGA
			CAGTGCAGGT AGGGGCT		

			GTTACGTTCG	TCTTCGA	
			ACCCG__		
GAM1237	SP329	3'	AGTTCTTTCTTAGTATT	47923	
			GGTGTTAAGAAGGGGCT		
			TTATGATTCTTTCTTGA		
GAM1237	SPC18	3'	GCCCCCAGTGTGTTGTATT	26668	TG AAGAA
			AGTGCAGG TT	GGGGC	
			TTATGTTT GA	CCCCG	
			GT C__		
GAM1237	SS-56	5'	GCTACTGGGCCTGCGCTG	59605	GTTAAGA GG
			CAGTGCAGGT	AG GC	
			GTCGCGTCCG	TC CG	
			GG__ AT		
GAM1237	SSH-3	3'	AGTCCCAGGCCCATGTCTGCCT	36888	T TG TAAGAA
	G		CAG GCAGG T	GGGGCT	
			GTC CGTCT A	CCCTGA	
			_ GT CCCGGA		
GAM1237	SSH-3	3'	AGTCCCAGGCCCATGTCTGCCT	35340	T TG TAAGAA
	G		CAG GCAGG T	GGGGCT	
			GTC CGTCT A	CCCTGA	
			_ GT CCCGGA		
GAM1237	STAT5A	3'	GGCCTGGAGCAGGCCTTGCGCT	12013	T AAGAAG
	G		CAGTGCAGG GTT	GGGCT	
			GTCGCGTTC CGG	TCCGG	
			_ ACGAGG		
GAM1237	STRAIT11499	3'	AGCTTTTTTTTTTTTCTGCT	41138	G TGTT
	G		CAGT CAGG	AAGAAGGGGCT	
			GTCG GTCC	TTTTTTTTCGA	
			_ TTTT		
GAM1237	STRIN	3'	AGCTCCTTTTTTAAGACTT	32764	G
			AGGT TTAAGAAGGGGCT		
			TTCA AATTTTTCCTCGA		
			G		
GAM1237	SUPT4H1	3'	GCCATGACACCTGCCTTG	12063	T AGAAGG
			CAG GCAGGTGTTA	GGC	
			GTT CGTCCACAGT	CCG	
			C A__		
GAM1237	SYAP1	3'	TTTTCTAAATATCTGTACT	51407	A
			AGTGCAGGTGTT	AGAAGG	

TCATGTCTATAA TCTTTT

A

GAM1237 SYNPO2 3' AGCAGGAGACTTAGGATTTGTG 71892 TG G AAGGG\_  
CTG CAG CAGGT TTAAG GCT

||| ||||| ||||| |||  
GTC GTTGA GATTC CGA  
GT G AGAGGA

GAM1237 SYT6 5' GGTTCTGGGAGCAGCTGTGCTG 78772 TG G AAGAA  
CAG CAG TGTT GGGGCT

||| ||| ||||| |||||  
GTC GTC ACGA TCTTGG  
GT G GGG\_

GAM1237 T2BP 3' GGTTCTAGGCTAGTGTCTGCGC 69997 TG A AA\_  
GTGCAGG TTA G GGGGCT

|||||| ||| |||||  
CGCGTCT GAT C TCTTGG  
GT \_ GGA

GAM1237 TA-KRP 3' GGTTTCTTCTTATTGGTGTG 50694 TG AGGTGT GG  
CAG C TAAGAAG GCT

||| | ||||| |||  
GTT G ATTCTTC TGG  
GT GTT\_ TT

GAM1237 TAGAP 5' GCTCTCCAGTGTCTGGCTG 54031 G TG AAGAA  
CAGT CAGG TT GGGGC

|||| |||| || |||||  
GTCG GTCT GA TCTCG  
\_ GT CC\_

GAM1237 TBDN100 3' GTCTCTTGACCTGTATT 46957 GTTAAG  
AGTGCAGGT AAGGGGC

||||||| |||||  
TTATGTCCA TTCTCTG  
G\_

GAM1237 TCL6 3' GCTCTTGTCATCTGTCTG 26999 T TTAAGA  
CAG GCAGGTG AGGGGC

||| ||||| |||||  
GTC TGTCTAC TTCTCG  
\_ CTG\_

GAM1237 TCL6 3' GCTCTTGTCATCTGTCTG 24983 T TTAAGA  
CAG GCAGGTG AGGGGC

||| ||||| |||||  
GTC TGTCTAC TTCTCG  
\_ CTG\_

GAM1237 TEB4 3' GGTCTCGCTGGTTAGTGCCTCG 60656 C TG GAA\_  
TTG AGTG AGG TTAA GGGGCT

|||| ||| ||||| |||||  
TTGC TCC GATT CTCTGG  
\_ GT GGTCG

GAM1237 TED 3' GTCTCTGTATATGTACTG 31642 GG TAAGA  
CAGTGCA TGT AGGGGC

|||||| ||| |||||

GTCATGT ATA TCTCTG  
 \_ TG\_  
 GAM1237 TEX27 3' AGCTCCGAGAGTGATATTTGCT 41659 T AGAA\_  
 CTG CAG GCAGGTGTTA GGGGCT  
 ||| ||||| |||||  
 GTC CGTTTATAGT CCTCGA  
 T GAGAG  
 GAM1237 TIAM2 3' TCATTGGCATTGTAT 24934 \_  
 GTGCAGGTGTAA GA  
 ||||| ||  
 TATGTTTACGGTT CT  
 A  
 GAM1237 TNFAIP3 3' AGTTGATATCTTAATATTTTGT 20823 TG \_ AGG\_  
 GTTG AG CAGG TGTAA GA GGCT  
 || ||| ||||| |||  
 TT GTTTATAATTCT TTGA  
 GT T ATAG  
 GAM1237 TNRC9 3' AGTTTCATACAAACATTTGTAT 71288 AAGAA GG  
 GTGCAGGTGTT G GCT  
 ||||| | |||  
 TATGTTTACAA C TGA  
 ACATA TT  
 GAM1237 TOM1L1 3' AGCCTTTTTTCTCTTTTACT 18504 C\_ TGTT  
 G CAGTG AGG AAGAAGGGGCT  
 |||| ||| |||||  
 GTCAT TTC TTTTTTCCGA  
 TT TC\_  
 GAM1237 TOMM34 3' GTCCTTGACTCTGTGCTG 22336 TG T AGAA  
 CAG CAGG GTTA GGGGC  
 ||| ||| ||| |||||  
 GTC GTCT CAGT TCCTG  
 GT \_ \_  
 GAM1237 TP53INP1 3' AGCTTTTTTTTTTTTGCTATTG 72950 \_ TGTT  
 CAGT GCAGG AAGAAGGGGCT  
 |||| ||| |||||  
 GTTA CGTTT TTTTTTTCGA  
 T T\_  
 GAM1237 TPC2 3' AGCTTCCGTGGTGCTTTGCTG 57443 C TG AGAA  
 CAGTG AGG TTA GGGGCT  
 |||| ||| ||| |||||  
 GTCGT TCC GGT CTTCGA  
 T GT GC\_  
 GAM1237 TPC2 5' GTCTCCGCGCCTGCGC 57447 TAAGAA  
 GTGCAGGTGT GGGGC  
 ||||| |||  
 CGCGTCCGCG CTCTG  
 C\_  
 GAM1237 TSGA13 5' GGCCTTGGGTGAATACCTGCCT 53611 T AAGAA  
 TG CAG GCAGGTGTT GGGGCT  
 ||| ||||| |||||

			GTT CGTCCATAA	TTCCGG	
			C	GTGGG	
GAM1237	TU3A	3'	GGCCTCTTCTTCCTACCTTGAT	23189	GC TT
	TG		CAGT AGGTG AAGAAGGGGCT		
			GTTA TCCAT TTCTTCTCCGG		
			GT	CC	
GAM1237	TUB	3'	GGCTCCTTTGCCTCTGCTACTG	12428	_ T TAA
			CAGT GCAGG GT	GAAGGGGCT	
			GTCA CGTCT CG	TTTCCTCGG	
			T	C	___
GAM1237	TUCAN	3'	AGTCTTTTTTTTTTTTGTAT	30269	TGTT
			GTGCAGG	AAGAAGGGGCT	
			TATGTTT	TTTTTTCTGA	
			TT	___	
GAM1237	UBE2V2	3'	TTTTGATACCTGTATT	12527	
			AGTGCAGGTGTTAAGA		
			TTATGTCCATAGTTTT		
GAM1237	UBE4B	3'	GGTTTTTTTTTAATGCT	20167	
			GGTGTTAAGAAGGGGCT		
			TCGTAATTTTTTTTGG		
GAM1237	UBN1	3'	AGCTCTAGGCTGGGGCTTGCGC	33728	G A AA_
	TG		CAGTGCAGGT TTA G	GGGGCT	
			GTCGCGTTTCG GGT C	TCTCGA	
			G	_GGA	
GAM1237	UHRF1	3'	GTCTTTGTTGTTAGCACT	25220	G
			GGTGTTAA AA	GGGGC	
			TCACGATT TT	TTCTG	
			G	GT	
GAM1237	ULK2	3'	GGTTTCTTTTACTTACCTGC	28006	TTA GG
			GCAGGTG	AGAAG GCT	
			CGTCCAT	TTTTC TGG	
			TCA	TT	
GAM1237	UPB1	3'	GCTTCAGTGCCTGCCTTG	32888	T TG AAGAA
			CAG GCAGG TT	GGGGC	
			GTT CGTCC GA	CTTCG	
			C	GT	___
GAM1237	UQCR	3'	GGCTCATAAGTAGTATCTGCAG	22409	G AGAAG
	TG		CA TGCAGGTGTTA	GGGCT	



			GT ACGTCTATGAT   CTCGG		
			G      GAATA		
GAM1237	USP10	3'	GAAAAATTTTAATAATTGTACT 63945	G	AGGGGCT
	G		CAGTGCAG TGTTAAGA		
			GTCATGTT ATAATTTT		
			A      AAAAAGG		
GAM1237	USP22	3'	AGCCCCAGCAGCATCTGAACTG 68001	G	AAGAA
			CAGT CAGGTGTT   GGGGCT		
			GTCA GTCTACGA   CCCCCA		
			A      CGA__		
GAM1237	USP22	5'	AGCTCGGGGGCGATGCCTGCCT 68002	T	AAGAAG
	TG		CAG GCAGGTGTT   GGGCT		
			GTT CGTCCGTAG   CTCGA		
			C      CGGGGG		
GAM1237	USP24	3'	GCCCTGAAGTGCCTGTCTG 91152	T	TG AAGAA
			CAG GCAGG TT   GGGGC		
			GTC TGTCC GA   TCCCG		
			_      GT AG__		
GAM1237	USP3	5'	GCTCCAGCGTCTGCATTG 89677	GT	AAGAA
			CAGTGCAG GTT   GGGGC		
			GTTACGTC CGA   CCTCG		
			TG      ____		
GAM1237	VAV3	3'	GGTCTTGCAGTACATTTGTTTT 20365	T	TAAGAA
	G		CAG GCAGGTGT   GGGGCT		
			GTT TGTTTACA   TTCTGG		
			T      TGACG_		
GAM1237	VMP	3'	AGTTCCTTCTACTACCTGTGT 54897	TG	TTA
			G CAGGTG   AGAAGGGGCT		
			T GTCCAT TCTTCCTTGA		
			GT      CA_		
GAM1237	WDR12	5'	AGTTCCTCGCTTACCTGTGC 80019	TG	TTAA A
			G CAGGTG   GA GGGGCT		
			C GTCCAT   CT CCTTGA		
			GT      TCG_ _		
GAM1237	WNT10A	5'	GCTCCCGGCGCTGCGCTG 47405	G	AAGAA
			CAGTGCAG TGTT   GGGGC		
			GTCGCGTC GCGG   CCTCG		
			_      C__		
GAM1237	XYLT1	3'	CTCAGTCCCTGCACTG 77849	TGTTAA	AG
			CAGTGCAGG   GA GGG		

			GTCACGTCC	CT CTC	
			_____ GA		
GAM1237	YEA	5'	AGCTTCTTGGCAGCGTCGGTGT	51527	TG A GT AAG
	TG		CAG C G GTT AAGGGGCT		
			GTT G C CGA TTCTTCGA		
			GT G TG CGG		
GAM1237	YKT6	3'	AGTTCCTTCTTGGTCAGAGGTA	21598	AGG _
			TGC TG TTAAGAAGGGGCT		
			ATG AC GGTTCCTTCCTTGA		
			GAG T		
GAM1237	YKT6	3'	GGCCTCTGGGACACTTGCCTTG	21604	T AAGA
			CAG GCAGGTGTT AGGGGCT		
			GTT CGTTCACAG TCTCCGG		
			C GG__		
GAM1237	ZFP106	3'	GCCCTTTTCTCTGGGCTG	42470	G TGTAA
			CAGT CAGG GAAGGGGC		
			GTCG GTCT TTTTCCCG		
			G C_____		
GAM1237	ZIM2	5'	GTCCAGATACCTGTGTT	31086	TG AAGAAG
			AG CAGGTGTT GGGC		
			TT GTCCATAG CCTG		
			GT A_____		
GAM1237	ZNF220	3'	GGTTCCTTTCTTAAATTGT	22227	GGTG
			GCA TTAAGAAGGGGCT		
			TGT AATTCTTTCTTGG		
			TA__		
GAM1237	ZNF313	3'	TCTTAAATGCCTGCAT	37944	_
			GTGCAGGTGTT AAGA		
			TACGTCCGTAA TTCT		
			A		
GAM1237	ZNF313	3'	AGTTCCTTTTACCTTCTGC	37939	T_ TAA
			GCAGG GT GAAGGGGCT		
			CGTCT CA TTTTCTTGA		
			TC ____		
GAM1237	ZNF340	3'	AGTTTCTGCCTAGGCGCCTGTG	84559	TG TA A_ GG
	C		G CAGGTGT AG AG GCT		
			C GTCCGCG TC TC TGA		
			GT GA CG TT		
GAM1237	ZNF340	3'	AGCCCTTTTAGAACTACTTGTA	84558	G _ AA
	GTG		CA TGCAGGT GTT GAAGGGGCT		

GT ATGTTCA CAA TTTTCCCGA  
 G T GA  
 GAM1237 LOC113386 3' GCTGAATAATACTGCATTG 57079 G AGAAGG  
 CAGTGCAG TGTTA GGC  
 ||||| |||  
 GTTACGTC ATAAT TCG  
 \_ AAG\_  
 GAM1237 LOC114971 3' GGCTTCACATGGCATTGTCTG 73151 T AGAA  
 CAG GCAGGTGTTA GGGGCT  
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 GTC TGTTTACGGT CTTCGG  
 \_ ACA\_  
 GAM1237 LOC115265 3' AGTCTCTTTTCTTTCTGTGTT 73353 TG TGTTA  
 AG CAGG AGAAGGGGCT  
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 TT GTCT TTTTCTCTGA  
 GT TTC\_  
 GAM1237 LOC115399 5' GCCTGGGGCCTTGCACTG 73433 T AAGAAG  
 CAGTGCAGG GTT GGGC  
 ||||| ||| |||||  
 GTCACGTTT CGG TCCG  
 \_ GG\_  
 GAM1237 LOC115817 3' GTCCCTTCTTTGTGCCTTG 56617 C TG T  
 G AGG T AAGAAGGGGC  
 ||| | |||||  
 G TCC G TTCTTCCCTG  
 T GTT  
 GAM1237 LOC116437 5' GCCATGTCACCTGCGTTG 73893 TTAAGAAGG  
 CAGTGCAGGTG GGC  
 ||||| |||  
 GTTGCGTCCAC CCG  
 TGTA\_  
 GAM1237 LOC116437 3' TTTTAAAACCTGTGCTG 73895 TG G  
 CAG CAGGT TTAAGA  
 || |||| |||||  
 GTC GTCCA AATTTT  
 GT A  
 GAM1237 LOC118738 3' GCTCCCTGGGCCTGCGTTG 75491 GTTAAGA \_  
 CAGTGCAGGT AGGG GC  
 ||||| ||| ||  
 GTTGCGTCCG TCCC CG  
 GG\_ T  
 GAM1237 LOC118738 3' GGTGTGTGATGATGTCTGTACT 75493 TG AGAAG  
 AGTGCAGG TTA GGGCT  
 ||||| ||| |||||  
 TCATGTCT AGT TTTGG  
 GT AGTG\_  
 GAM1237 LOC121504 3' GGTTTTTTTTTATTTTGTAGT 74100 G TGT  
 G CA TGCAGG TAAGAAGGGGCT  
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GT ATGTTT ATTTTTTTTGG
G TT_
GAM1237 LOC122786 3' AGCTCTTTCTTTATAATATTTG 74155 ____
T GCAGGTGTTA AGAAGGGGCT
||||||| |||||||
TGTTTATAAT TCTTTCTCGA
ATT
GAM1237 LOC125061 3' GCCTTGCTGTGTCTGTCTG 74392 T TG TAAGAA
CAG GCAGG T GGGGC
||| |||| | ||||
GTC TGTCT G TTCCG
_ GT TCG__
GAM1237 LOC125268 3' AGCTCTCCGTCTAGCACTTGGA 76066 G A A__
CTG AGT CAGGTGTTA GA GGGGCT
||| ||||||| || |||||
TCA GTTCACGAT CT TCTCGA
G _ GCC
GAM1237 LOC126430 5' GGCCTTTTCCTGGCTGGCGGTT 75705 G G A__
GTGTTG CAG TGTTA GAAGGGGCT
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GTT GCGGT CTTTTCGGG
T G CGGTC
GAM1237 LOC126526 3' AGCCTGCGGGCATCTGCCCTG 74532 T AAGAAG
CAG GCAGGTGTT GGGCT
||| ||||||| ||||
GTC CGTCTACGG TCCGA
C GCG__
GAM1237 LOC126603 5' AGCCTCTTTGTCACTGCTTCGC 75392 CA__ TTAA
TG CAGTG GGTG GAAGGGGCT
||||| |||| |||||||
GTCGC TCAC TTTCTCCGA
TTCG TG__
GAM1237 LOC126603 5' AGCCAAGGTGACACTTCACTG 75391 C AGAAGG
CAGTG AGGTGTTA GGCT
||||| ||||||| ||||
GTCAC TTCACAGT CCGA
_ GGAA__
GAM1237 LOC127352 3' GGCTCCAGTCAATATCTGCATT 74661 AA A_
AGTGCAGGTGTT GA GGGGCT
||||||||| || |||||||
TTACGTCTATAA CT CCTCGG
_ GA
GAM1237 LOC127702 3' AGTTTCTTTCCCCCAAATGTCT 75457 G TG AA__ GG
GTGC CAGG TT GAAG GCT
|||| || |||| |||
GTCT AA TTTC TGA
T GT ACCCCC TT
GAM1237 LOC128308 5' GCCCCAGGCTCCTGTGCTG 74733 TG T AAGAA
CAG CAGG GTT GGGGC
||| |||| || |||||

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GTC GTCC CGG CCCC  
 GT T A\_\_\_\_  
 GAM1237 LOC128387 3' GGTTCCTGATTCTAGCCTTGTGC 74750 TG T A \_\_\_\_  
 TG CAG CAGG GTTA GAA GGGGCT  
 ||| ||| ||| ||| |||  
 GTC GTTC CGAT CTT TCTTGG  
 GT \_ \_ AG  
 GAM1237 LOC128954 5' GGTCTCGAGGCCACATCTGCAT 75801 TAAGAA  
 GTGCAGGTGT GGGGCT  
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 TACGTCTACA CTCTGG  
 CCGGAG  
 GAM1237 LOC129011 3' GGCACCTTTGTTTTTGTACTG 74868 TGTTAA GG  
 CAGTGCAGG GAAG GCT  
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 GTCATGTTT TTTC CGG  
 TTGG\_\_ A\_  
 GAM1237 LOC129102 5' GCCCCAGCCATCTGTGCTG 75806 TG TTAAGAA  
 CAG CAGGTG GGGGC  
 ||| ||| |||  
 GTC GTCTAC CCCC  
 GT CGA\_\_\_\_  
 GAM1237 LOC129607 3' GGCTTCTTCCACATCTG 74887 TAA  
 CAGGTGT GAAGGGGCT  
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 GTCTACA CTTCTTCGG  
 C\_\_\_\_  
 GAM1237 LOC130074 3' GGCTTTATGAAATAAGTTTGCA 76134 GG GTTAAGAA\_  
 TTG CAGTGCA T GGGGCT  
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 GTTACGT G TTTCGG  
 TT AATAAAGTA  
 GAM1237 LOC130074 3' GGTCTTGTTTGATCTGTGCTG 76138 TG GTTA AG  
 CAG CAGGT AGA GGGCT  
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 GTC GTCTA TTT TCTGG  
 GT GG\_\_ GT  
 GAM1237 LOC130639 3' AGTCCTGCCTGACACTGCACTG 74967 G A AA  
 CAGTGCAG TGTTA G GGGGCT  
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 GTCACGTC ACAGT C TCCTGA  
 \_ \_ CG  
 GAM1237 LOC130639 5' GCCCCTGGTGTTGTGTTG 74974 TG GTGT AGA  
 CAG CAG TA AGGGGC  
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 GTT GTT GT TCCCCG  
 GT \_\_\_\_ GG\_  
 GAM1237 LOC130733 3' AGTCTCTTCTCTGTCTTTGTAC 74978 TG TA  
 TG CAGTGCAGG T AGAAGGGGCT  
 ||||| | |||||

	GTCATGTTT G TCTTCTCTGA	
	CT TC	
GAM1237 LOC130813 3'	GCAGCTTGGGTCTGCACTG 75770	TGT AAGGG
	CAGTGCAGG TAAG GC	
	GTCACGTCT GTTC CG	
	GG_ GA__	
GAM1237 LOC130814 3'	TCCTTCAACTTTGCACTG 74988	T AA
	CAGTGCAGG GTT GAAGGG	
	GTCACGTTT CAA CTCCT	
	- -	
GAM1237 LOC133308 5'	AGTCCCGAGGAGCCTGCGCTG 75085	GTTAAGAA
	CAGTGCAGGT GGGGCT	
	GTCGCGTCCG CCCTGA	
	AGGAG__	
GAM1237 LOC134111 3'	TTTAAATATCTGTGCT 75141	TG
	AG CAGGTGTTAAGA	
	TC GTCTATAATTTT	
	GT	
GAM1237 LOC134121 3'	AGCTTGGCTATGCCTGTGTTG 75149	TG TA AAG
	CAG CAGGTGT AG GGGCT	
	GTT GTCCGTA TC TTCGA	
	GT _ GG_	
GAM1237 LOC136015 3'	GTTTCTTTTGTATCATTT 76203	_ GG
	AGGTG TTAAGAAG GC	
	TTTAC AGTTTTTC TG	
	T TT	
GAM1237 LOC136288 3'	AGCCTTTTCCAATATTTAGTAT 75250	_ AA
TG	CAGTGC AGGTGTT GAAGGGGCT	
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	A C_	
GAM1237 LOC138342 5'	AGCCTCTTCTGGAGCTTGCACT 75943	GTTA
G	CAGTGCAGGT AGAAGGGGCT	
	GTTACGTTCT TCTTCTCCGA	
	AGG_	
GAM1237 LOC138716 3'	GGCCTCTGCCAAGTTCTGCATT 75367	TGTTAAGA
G	CAGTGCAGG AGGGGCT	
	GTTACGTCT TCTCCGG	
	TGAACCG_	
GAM1237 LOC139390 5'	GGTTCTGGGAGCATGTCTGCGC 75831	_ AAGAA
TG	AGTGCAG GTGTT GGGGCT	

		TCGCGTC TACGA TCTTGG		
		TG GGG__		
GAM1237	LOC142941 5'	GGTTCTTTCGTTCCCTGCTATTG 82885	_	TGTTAA
		CAGT GCAGG GAAGGGGCT		
		GTTA CGTCC CTTTCTTGG		
		T TTG__		
GAM1237	LOC143188 5'	GTCTCAGAGCATTGACTG 82901	G	AAGAA
		CAGT CAGGTGTT GGGGC		
		GTCA GTTTACGA CTCTG		
		_ GA__		
GAM1237	LOC143274 3'	GGTTATGTTAACACCTGAATTG 76513	G	GAAGG
		CAGT CAGGTGTTAA GGCT		
		GTTA GTCCACAATT TTGG		
		A GTA__		
GAM1237	LOC144161 3'	GCCTGAGATATTTGCG 83008		AAGAAG
		TGCAGGTGTT GGGC		
		GCGTTTATAG TCCG		
		AG__		
GAM1237	LOC144165 5'	AGCCTCGCGCAGCCTGCGCTG 76678		GTTAAGAA
		CAGTGCAGGT GGGGCT		
		GTCGCGTCCG CTCCGA		
		ACGCG__		
GAM1237	LOC144262 5'	GCCCCTTCAGTCTGCG 76751		TGTTAA
		TGCAGG GAAGGGGC		
		GCGTCT CTTCCCCG		
		GA__		
GAM1237	LOC144305 3'	GGCCCTGCAGGCATTTGGCTG 83035	G	AAGAA
		CAGT CAGGTGTT GGGGCT		
		GTCG GTTTACGG TCCCGG		
		_ ACG__		
GAM1237	LOC144317 5'	GGCCCCCGGATGTTTGCG 76797	TG	AAGAA
		TGCAGG TT GGGGCT		
		GCGTTT AG CCCCCG		
		GT GC__		
GAM1237	LOC144319 5'	GGCCCTGGGAGGAGTGTGCA 83058		TG AAGAA_
	CTG	CAGTGCAGG TT GGGGCT		
		GTCACGTTT GA TCCCGG		
		GT GGAGGG		
GAM1237	LOC144438 3'	GGCTATCAGTTTGATATCTTGC 76835	C	AAGG_
	TG	CAGTG AGGTGTAAAG GGCT		

GTCGT TCTATAGTTT TCGG  
 \_ GACTA  
 GAM1237 LOC144438 3' GGCTTTTAATCAGATACCTGTG 76836 TG AAGA\_  
 TTG CAG CAGGTGTT AGGGGCT  
 ||| ||||| |||||  
 GTT GTCCATAG TTTTCGG  
 GT ACTAA  
 GAM1237 LOC144473 3' GGTTTCTTTCAGCACTCTGTAC 83073 \_ AA GG  
 TG CAGTGCAG GTGTT GAAG GCT  
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 GTCATGTC CACGA TTTC TGG  
 T C\_ TT  
 GAM1237 LOC144486 5' GCCCCGGGCACTTGCCTTG 83084 T TAAGAA  
 CAG GCAGGTGT GGGGC  
 ||| ||||| |||||  
 GTT CGTTCACG CCCCCG  
 C GG\_\_\_\_  
 GAM1237 LOC144576 3' GGCCCAGGGGTTGGCATCTGCT 83158 T GAAG\_  
 TTG CAG GCAGGTGTAA GGGCT  
 ||| ||||| |||||  
 GTT CGTCTACGGTT CCCGG  
 T GGGGA  
 GAM1237 LOC144583 3' AGCCTTGGCTGTGTCTGCCCTG 76892 T TG TA AA  
 CAG GCAGG T AG GGGGCT  
 ||| |||| | || |||||  
 GTC CGTCT G TC TTCCGA  
 C GT\_\_ GG  
 GAM1237 LOC144667 3' GGTCCCCTGGGATGCCTGCATT 83170 AAGA \_  
 AGTGCAGGTGTT AGGGG CT  
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 TTACGTCCGTAG TCCCC GG  
 GG\_\_ T  
 GAM1237 LOC144893 3' GCTCTGTCACTTGCCTG 83188 TTAAGAA  
 CAGTGCAGGTG GGGGC  
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 GTCACGTTTAC TCTCG  
 TG\_\_\_\_  
 GAM1237 LOC145135 5' GCCCTTGGACTTGTGTTG 83253 TG GTTAAGA  
 CAG CAGGT AGGGGC  
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 GTT GTTCA TTCCCG  
 GT GG\_\_\_\_  
 GAM1237 LOC145225 3' GGTCTTGGGGGTATGCCTGTGT 83307 TG TAAGAA  
 G CAGGTGT GGGGCT  
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 T GTCCGTA TCCTGG  
 GT TGGGGG  
 GAM1237 LOC145225 3' GGTCTCTTCTTGACCACACT 83308 CAGGT  
 AGTG GTTAAGAAGGGGCT  
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	TCAC CAGTTCTTCTCTGG	
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GAM1237 LOC145231 5'	AGCCCTGTGACATCTGCATT 83277	AGAA
	AGTGCAGGTGTTA GGGGCT	
	TTACGTCTACAGT TCCCGA	
	G__	
GAM1237 LOC145333 3'	GTTCTTTTTGTCTCCACTG 83331	C GT TTAA
	CAGTG AG G GAAGGGGC	
	GTCAC TC T TTTTCTTG	
	C TG__	
GAM1237 LOC145387 5'	AGTTCTGTGAGGATGGCTGCAT 83351	G AAGAA
TG	CAGTGCAG TGTT GGGGCT	
	GTTACGTC GTAG TCTTGA	
	G GAGTG	
GAM1237 LOC145453 3'	CTTTCATGTCCTGCATTG 77141	TGTTAA
	CAGTGCAGG GAAGG	
	GTTACGTCC CTTTC	
	TGTA__	
GAM1237 LOC145609 5'	AGTCCTTTGCCCAACATTGTGC 83375	TG G AAG_
TG	CAG CAG TGTT AAGGGGCT	
	GTC GTT ACAA TTTCTGA	
	GT _ CCCG	
GAM1237 LOC145622 5'	AGCCTGGAGGAAGACTTGCATT 77288	G AAGAAG
G	CAGTGCAGGT TT GGGCT	
	GTTACGTTCA AA TCCGA	
	G GGAGG_	
GAM1237 LOC145622 5'	AGCCTGGAGGAAGACTTGCGTT 77289	G AAGAAG
G	CAGTGCAGGT TT GGGCT	
	GTTGCGTTCA AA TCCGA	
	G GGAGG_	
GAM1237 LOC145622 5'	AGCCTGGAGGAAGACTTGTGTT 77290	TG G AAGAAG
G	CAG CAGGT TT GGGCT	
	GTT GTTCA AA TCCGA	
	GT G GGAGG_	
GAM1237 LOC145622 3'	AGTCTGGAGGAAGACTTGTGTT 77292	TG G AAGAAG
G	CAG CAGGT TT GGGCT	
	GTT GTTCA AA TCTGA	
	GT G GGAGG_	
GAM1237 LOC145725 3'	GTCTTTGGTACCTGTGTT 77413	TG TT GAAG
	AG CAGGTG AA GGGC	

TT GTCCAT TT TCTG  
 GT GG \_\_\_\_  
 GAM1237 LOC145732 3' GTCTTTGGTACCTGTGTT 77435 TG TT GAAG  
 AG CAGGTG AA GGGC  
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 TT GTCCAT TT TCTG  
 GT GG \_\_\_\_  
 GAM1237 LOC145781 3' GTCCCAAGCATCTGTGC 77492 TG AAGAA  
 G CAGGTGTT GGGGC  
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 C GTCTACGA CCCTG  
 GT A \_\_\_\_  
 GAM1237 LOC145826 5' AGCTTCTTTTCTCTCTCTGC 83527 TGTTA\_  
 GCAGG AGAAGGGGCT  
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 CGTCT TTTCTTCGA  
 CTCTCC  
 GAM1237 LOC145844 3' AGCCCATGTTGATGTCTCGTTG 77536 C TG GAAG  
 CAGTG AGG TTAA GGGCT  
 |||| || ||||  
 GTTGC TCT AGTT CCCGA  
 \_ GT GTA\_  
 GAM1237 LOC145900 3' AGTTCCTTTAGGATTTGTAT 77563 G GA  
 GTGCAGGT TTAA AGGGGCT  
 ||||| |||| |||||  
 TATGTTTA GATT TCCTTGA  
 G \_\_\_\_  
 GAM1237 LOC145942 3' AGTTTTTTCCTCACCGTTTGCC 77574 T \_\_\_\_ TTAA  
 TG AG GCA GGTG GAAGGGGCT  
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 TC CGT CCAC CTTTTTTGA  
 \_ TTG TC\_  
 GAM1237 LOC145945 5' GGCCTCAATTAACACTGCACTG 83578 G GAA  
 CAGTGCAG TGTTAA GGGGCT  
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 GTCACGTC ACAATT CTCCGG  
 \_ AA\_  
 GAM1237 LOC145981 5' GGCCTGGGCAGGCGCTTGTGCT 60311 TG AAGAAG  
 G CAG CAGGTGTT GGGCT  
 || ||||| ||||  
 GTC GTTCGCGG TCCGG  
 GT ACGGG\_  
 GAM1237 LOC146316 5' GGCTCCTGGCCTGCACCTGCGT 60874 \_ TAAGA  
 CTG CAG TGCAGGTGT AGGGGCT  
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 GTC GCGTCCACG TCCTCGG  
 T TCCGG  
 GAM1237 LOC146433 5' GCCCTTAGGCACCTGC 77877 AAGA  
 GCAGGTGTT AGGGGC  
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CGTCCACGG TTCCCG  
A\_\_\_\_

GAM1237 LOC146439 5' GGCTTCTTCCCCTTTGTGCTG 77889 TG TGTTAA  
CAG CAGG GAAGGGGCT  
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GTC GTTT CTTCTTCGG  
GT CCC\_\_

GAM1237 LOC146540 5' AGTCCCTTACGGACTTGTCTG 77969 T GTTAAG  
CAG GCAGGT AAGGGGCT  
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GTC TGTTC A TTCCCTGA  
\_ GGCA\_\_

GAM1237 LOC146774 3' GGCTTTTTTTTTTTCTTCTG 78097 TGTT  
CAGG AAGAAGGGGCT  
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GTCT TTTTTTTTCGG  
TCTT

GAM1237 LOC147004 3' GGCTCCTTCTGATTCTTGCATT 83903 T A  
AGTGCAGG GTTA GAAGGGGCT  
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TTACGTTC TAGT CTTCTTCGG  
T \_

GAM1237 LOC147136 3' GGCTTCTTCATGGCTGCGTTG 78266 G TAA  
CAGTGCAG TGT GAAGGGGCT  
||||| ||| |||||  
GTTGCGTC GTA CTTCTTCGG  
G \_

GAM1237 LOC147341 3' GCCTTTTTTTTTGTATC 83994 TT\_  
GGTG AAGAAGGGGC  
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CTAT TTTTTTCCG  
GTT

GAM1237 LOC147622 3' GGCTCAGCTGGCATCTGTACTG 84052 A AAG  
CAGTGCAGGTGTTA G GGGCT  
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GTCATGTCTACGGT C CTCGG  
\_GA\_

GAM1237 LOC147622 5' GTTTCTTTGCCTTGCCTG 84054 T T TAA GG  
CAG GCAGG GT GAAG GC  
||| ||||| ||| ||  
GTC CGTTC CG TTTC TG  
\_ \_ \_ TT

GAM1237 LOC147912 3' GGCCTCTCCCGACATTGGTGCT 78568 TG AG AA A  
G CAG C GTGTT GA GGGGCT  
||| | ||||| || |||||  
GTC G TACAG CT CTCCGG  
GT GT CC \_

GAM1237 LOC148089 3' GCTCACGGCACATGCATTG 78635 G AAGAAG  
CAGTGCA GTGTT GGGC  
||||| ||||| |||

GTTACGT CACGG    CTCG  
           A    CA\_\_\_\_  
 GAM1237 LOC148343 5' AGTTCTTTTTTAAAATTTTGC 78791    TG\_  
                   GCAGG TTAAGAAGGGGCT  
                   ||||| |||||  
                   CGTTT AATTTTTTCTTGA  
                   TAA  
 GAM1237 LOC148438 3' GTCCAAAACATTTGACTG    84159    G    AAGAAG  
                   CAGT CAGGTGTT    GGGC  
                   ||||| |||||  
                   GTCA GTTTACAA    CCTG  
                   \_    AA\_\_\_\_  
 GAM1237 LOC148479 3' AGTCTTTTACCAAAAGTGTCTG 78865    TG AAG\_\_\_\_  
                   TAC            TGCAGG TT    AAGGGGCT  
                   ||||| ||    |||||  
                   ATGTCT GA    TTTTCTGA  
                   GT AAACCA  
 GAM1237 LOC148490 5' AGCATACTTTGGTGTGTGTGTT 78882    TG    TG AA    GG\_  
                   G            CAG CAGG TT GAAG    GCT  
                   ||| ||||| || ||||| |||  
                   GTT GTTT GG TTTC    CGA  
                   GT    GT    \_    ATA  
 GAM1237 LOC148710 3' AGTCCCAGGGACCTTTGTGCTG 84191    TG    T    AAGAA  
                   CAG CAGG GTT    GGGGCT  
                   ||| ||||| |||    |||||  
                   GTC GTTT CAG    CCCTGA  
                   GT    C    GGA\_\_\_\_  
 GAM1237 LOC148713 3' GGCCTCCACTGGGCCCTGTGCT 78953    TG    T    TA    AA  
                   G            CAG CAGG GT AG GGGGCT  
                   ||| ||||| || || |||||  
                   GTC GTCC CG TC CTCCGG  
                   GT    \_    GG AC  
 GAM1237 LOC148758 5' AGTCCCTTTGATGTGGCTGCGT 78963    G GTTAA  
                   TG            CAGTGCAG T    GAAGGGGCT  
                   ||||||| |    |||||  
                   GTTGCGTC G    TTTCCCTGA  
                   G TGTAG  
 GAM1237 LOC148887 3' GGCTCCTGTCTGTCTCTGTGTT 84245    TG    TGTTA    \_  
                   G            CAG CAGG    AGA AGGGGCT  
                   ||| |||||    ||| |||||  
                   GTT GTCT    TCT TCCTCGG  
                   GT    CTG\_\_\_\_ G  
 GAM1237 LOC149077 3' AGCTTTTTTTTGATATATG 79158    G  
                   CA GTGTTAAGAAGGGGCT  
                   || |||||  
                   GT TATAGTTTTTTTTTCGA  
                   A  
 GAM1237 LOC149153 3' GGCCTCTTTTTTCACAGGTTTT 84368    \_\_\_\_\_ TT  
                   GCATTG            CAG    GTG AAGAAGGGGCT  
                   |||    ||| |||||

GTT CAC TTTTCTCCGG  
 TTGGA T\_  
 GAM1237 LOC149276 5' GTGCTTTGTGCTTGTGCTG 84389 TG TG TAAG G  
 CAG CAGG T AAGG GC  
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 GTC GTTC G TTTC TG  
 GT GT \_\_\_\_ G  
 GAM1237 LOC149421 5' CCTCCAATCTGCATTG 79356 GTTAAGAA  
 CAGTGCAGGT GGGG  
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 GTTACGTCTA CTCC  
 AC \_\_\_\_  
 GAM1237 LOC149566 5' AGCCCTTTTCTTGACCTGCCAC 84486 \_ GT \_  
 TG CAGTG CAGGT TAAGAAG GGGCT  
 |||| ||| |||| ||||  
 GTCAC GTCCA GTTCTTT CCCGA  
 C \_ T  
 GAM1237 LOC149566 3' GCCCCTTTGTCCTTGGCTG 84490 GC TGTTAA  
 CAGT AGG GAAGGGGC  
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 GT TG \_\_\_\_  
 GAM1237 LOC149576 5' GCTCCGACGCGCTTGCGC 79427 TAAGAA  
 GTGCAGGTGT GGGGC  
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 CGCGTTCGCG CCTCG  
 CAG \_\_\_\_  
 GAM1237 LOC149603 3' GCCTCTTCCCCCTGCCCTG 70642 T TGTTAA  
 CAG GCAGG GAAGGGGC  
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 GTC CGTCC CTTCTCCG  
 C CC \_\_\_\_  
 GAM1237 LOC149657 3' GGTGTTGTTTGCATTTGCATTG 84576 AAGG  
 CAGTGCAGGTGTTAAG GGCT  
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 GTTACGTTTACAGTTT TTGG  
 GG \_\_\_\_  
 GAM1237 LOC149668 3' GGCCTTCCAGTGATGTTTGTG 84546 TG TG AGAA\_  
 T G CAGG TTA GGGGCT  
 | ||| || |||||  
 T GTTT AGT TTCCGG  
 GT GT GACCC  
 GAM1237 LOC149670 3' GCCAGTGGTTCTTGTATTG 79491 TG AGAAGG  
 CAGTGCAGG TTA GGC  
 ||||| || |||  
 GTTATGTTT GGT CCG  
 TT GA \_\_\_\_  
 GAM1237 LOC149706 5' AGCCCTTCCCCTGGTGTCTGCA 84635 TG AGA\_  
 C GTGCAGG TTA AGGGGCT  
 ||||| || |||||

	CACGTCT GGT TTCCCGA	
	GT CCCC	
GAM1237 LOC149734 3'	AGCTTTTTTACCAAATAACTGT 84629	TG G AA__
	GTTG AG CAG TGTT GAAGGGGCT	
	TT GTC ATAA TTTTTTCGA	
	GT A ACCA	
GAM1237 LOC149832 5'	ATGCCTTTTTTTTGACACCTGCG 84696	T
	CT AGTGCAGGTGTTAAGAAGGGGC	
	TCGCGTCCACAGTTTTTTTCCG	
	TAG	
GAM1237 LOC150084 3'	AGCTCCACTGAGCACTTGGCTG 79561	G A AA
	CAGT CAGGTGTT AG GGGGCT	
	GTCG GTTCACGA TC CCTCGA	
	_ G A_	
GAM1237 LOC150166 5'	AGCTCAGGAAGTACTTGGCTG 84882	G TTAAGAAG
	CAGT CAGGTG GGGCT	
	GTCG GTTCAT CTCGA	
	_ GAAGGA__	
GAM1237 LOC150213 3'	AGCTTCAGCATGCCTGCG 74850	TAAGAA
	TGCAGGTGT GGGGCT	
	GCGTCCGTA CTTCGA	
	CGA__	
GAM1237 LOC150236 5'	AGCTTCAGCATGCCTGCG 79682	TAAGAA
	TGCAGGTGT GGGGCT	
	GCGTCCGTA CTTCGA	
	CGA__	
GAM1237 LOC150271 5'	GGCTCCCCCAGTTCTGCGCTG 84951	TGTTAAGAA
	CAGTGCAGG GGGGCT	
	GTCGCGTCT CCTCGG	
	TGACCC__	
GAM1237 LOC150378 3'	GGCTCCTGTGAGGGGCACTGTAT 79749	G AAGA_
	TG CAGTGCAG TGTT AGGGGCT	
	GTTATGTC ACGG TCCTCGG	
	_ GAGTG	
GAM1237 LOC150696 3'	GGCCCTTTTATCCTGCGC 58485	TGTTA
	GTGCAGG AGAAGGGGCT	
	CGCGTCC TTTTCCCCGG	
	TA__	
GAM1237 LOC151056 5'	GCTTCTCTGTTGGCACTG 80109	AGGTGTTA A
	CAGTGC AGA GGGGC	

	GTCACG	TCT CTTCG	
	GTTG_____		
GAM1237 LOC151473 3'	AGCCAATGTATTTGAATGCTTG	80249	AAGAAGG_____
	CACTG	TGCAGGTGTT GGCT	
	ACGTTTCGTAA	CCGA	
	GTTTATGTAA		
GAM1237 LOC151475 3'	GCCCAGAATACTTGTAT	85407	AAGAAG
	GTGCAGGTGTT	GGGC	
	TATGTTCATAA	CCCG	
	GA_____		
GAM1237 LOC151512 5'	CCTTCTGGCACCTGTGCT	85429	TG A
	AG CAGGTGTTA GAAGG		
	TC GTCCACGGT CTTCC		
	GT	-	
GAM1237 LOC151556 5'	GCTTTTTCAGCCTTACTG	80278	C GTTAA
	CAGTG AGGT	GAAGGGGC	
	GTCAT TCCG	CTTTTTCG	
	- AC_____		
GAM1237 LOC151568 3'	GCCCTAGGCTCCTGTACTG	56697	T AAGAA
	CAGTGCAGG GTT	GGGGC	
	GTCATGTCC CGG	TCCCG	
	T A_____		
GAM1237 LOC151614 5'	AGCTTCTGACATTCATTTGTAT	80300	TTAAGA
	TG	CAGTGCAGGTG AGGGGCT	
	GTTATGTTTAC	TCTTCGA	
	TTACAG		
GAM1237 LOC151643 3'	AGTTTTTTTTTAAATGACTGTGC	80324	TG GT
	T	AG CAG GTTAAGAAGGGGCT	
	TC GTC TAATTTTTTTTTTGA		
	GT AG		
GAM1237 LOC151657 3'	GTTCTTTCTTAGGCTGT	85478	GTG
	GCAG	TTAAGAAGGGGC	
	TGTC	GATTCTTCTTG	
	G_____		
GAM1237 LOC151877 3'	TTTTCTTGGCACCTGTGTTG	85512	TG
	CAG CAGGTGTTAAGAAGG		
	GTT GTCCACGGTTCTTTT		
	GT		
GAM1237 LOC151996 3'	AGTCAGAACTGAATCTGCGTTG	85529	GTTA AAGG
	CAGTGCAGGT	AG GGCT	

GTTGCGTCTA TC CTGA  
 AG\_\_ AAGA  
 GAM1237 LOC152215 3' TTTTAGCATCTGTATT 80493  
 AGTGCAGGTGTTAAGA  
 |||||  
 TTATGTCTACGATTTT

GAM1237 LOC152220 3' GGCTTTTTTTTTCTTGTTTTG 85586 T TGTT  
 CAG GCAGG AAGAAGGGGCT  
 ||| ||| |||||  
 GTT TGTC TTTTTTTCGG  
 T T\_\_

GAM1237 LOC152273 3' AGTTCCTTTTAAAATGTTTGCAT 80533 TG AA  
 T AGTGCAGG TT GAAGGGGCT  
 ||||| || |||||  
 TTACGTTT AA TTTTCTTGA  
 GT AA

GAM1237 LOC152300 3' CTTTCCACTGCCTGTATTG 80543 \_ TAA  
 CAGTGCAGGT GT GAAGG  
 ||||| || |||  
 GTTATGTCCG CA CTTTC  
 T C\_\_

GAM1237 LOC152674 3' GCTCTTGCCACTGTACTG 85836 GT TAAGA  
 CAGTGCAG GT AGGGGC  
 ||||| || |||  
 GTCATGTC CG TTCTCG  
 AC \_\_\_\_

GAM1237 LOC152674 3' GGCTTTTTTTTTTTATCTGAG 85838 G TT\_  
 CTG CAGT CAGGTG AAGAAGGGGCT  
 ||| |||| |||||  
 GTCG GTCTAT TTTTTTTCGG  
 A TTT

GAM1237 LOC152719 5' CTTGGCACCTTATTG 85849 C  
 CAGTG AGGTGTTAAG  
 |||| |||||  
 GTTAT TCCACGGTTC

GAM1237 LOC152804 3' GGCTCAGTGTTGGGTTTGC ACT 85888 GG G GAAG  
 G CAGTGCA T TTAA GGGCT  
 ||||| | ||| |||  
 GTCACGT G GGTT CTCGG  
 TT\_ GTGA

GAM1237 LOC152897 3' AGCTTTTTTTTAAATTCGGTAT 80722 A T  
 T AGTGC GG GTTAAGAAGGGGCT  
 |||| || |||||  
 TTATG CT TAATTTTTTTTCGA  
 G T

GAM1237 LOC153057 5' GGCCTTCTCCAGACATCTGTGC 85899 TG AA AG  
 T AG CAGGTGTT GA GGGCT  
 || ||||| || |||



TC GTCTACAG CT TCCGG  
 GT AC CT  
 GAM1237 LOC153146 5' GGTTTATTAACACTTGAAGT 85931 G GAAGG  
 CAGT CAGGTGTAA GGCT  
 |||| ||||| ||||  
 GTCA GTTCACAATT TTGG  
 A AT\_\_  
 GAM1237 LOC153196 3' GGCTCCTTTTGTAAATTTGTGC 85966 TG GTTA  
 G CAGGT AGAAGGGGCT  
 | |||| |||||  
 C GTTA TTTTCCTCGG  
 GT ATG\_  
 GAM1237 LOC153205 5' GCCTCTTCCTCCCTCGCTG 85946 C TGTTAA  
 CAGTG AGG GAAGGGGC  
 |||| || |||||  
 GTCGC TCC CTTCTCCG  
 \_ CTC\_\_  
 GAM1237 LOC153339 3' AGCTGATTAATACCAGCATTG 86004 A GAAGG  
 CAGTGC GGTGTAA GGCT  
 |||| ||||| ||||  
 GTTACG CCATAATT TCGA  
 A AG\_\_  
 GAM1237 LOC153711 3' TTTTCGTAATTTGTATTG 86141 TT  
 CAGTGCAGGTG AAGAA  
 ||||| ||||  
 GTTATGTTTCAAT TTTT  
 GC  
 GAM1237 LOC153910 3' GCCTCTTCGTCTGCCCTG 80997 T TAA\_  
 CAGG GT GAAGGGGC  
 |||| || |||||  
 GTCC CG CTTCTCCG  
 \_ TCTG  
 GAM1237 LOC154084 5' GGTACCTGATACTTAGTGCTG 86163 TG \_ AAGA \_  
 CAG C AGGTGTT AGG GGCT  
 || | ||||| || ||||  
 GTC G TTCATAG TCC CTGG  
 GT A \_ A  
 GAM1237 LOC154094 3' GGTTCCTTCTGATTTTGGCCAT 60433 \_ T A GG  
 TG CAGTG CAGG GTTA GAAG GCT  
 |||| |||| |||| ||||  
 GTTAC GTTT TAGT CTTC TGG  
 C T \_ TT  
 GAM1237 LOC154321 5' GCAGTGGCATTGCACTG 81065 AGAAGGG  
 CAGTGCAGGTGTAA GC  
 ||||| |||| ||  
 GTCACGTTTACGGT CG  
 GA\_\_\_\_  
 GAM1237 LOC154788 3' GTTTCTTTTGTATCATTT 86247 \_ GG  
 AGGTG TTAAGAAG GC  
 |||| ||||| ||

TTTAC AGTTTTTC TG  
 T TT  
 GAM1237 LOC154822 5' AGCCCAGGGGACATCTGGCTG 86258 G AAGAAG  
 CAGT CAGGTGTT GGGCT  
 ||| ||||| ||||  
 GTCG GTCTACAG CCCGA  
 \_ GGGA\_  
 GAM1237 LOC154860 5' GCCTTACCAGCTTGTACTG 86274 GTTAAGAA  
 CAGTGCAGGT GGGGC  
 ||||| ||||  
 GTCATGTTCTG TTCCG  
 ACCA\_  
 GAM1237 LOC154881 3' AGCCCCAAAACATGGCTCTTGT 81168 T AGAA\_  
 ATTG AGTGCAGG GTTA GGGGCT  
 ||||| ||| ||||  
 TTATGTTC CGGT CCCCCGA  
 T ACAAAA  
 GAM1237 LOC155179 3' AGCCCAGGCCTGGTGTCTGCAT 81309 TG AGAAG  
 T AGTGCAGG TTA GGGCT  
 ||||| ||| ||||  
 TTACGTCT GGT CCCGA  
 GT CCGGA  
 GAM1237 LOC155179 3' AGCTTTTTCTTTGCTCGTTTGT 81310 T GG TT\_  
 CTG AG GCA TG AAGAAGGGGCT  
 || ||| || |||||  
 TC TGT GC TTCTTTTTCGA  
 \_ TT TCGT  
 GAM1237 LOC157349 5' AGCGAGGGTTTTTAGTGTGTGT 81408 TG TG GGG\_  
 GC G CAGG TTAAGAA GCT  
 | ||| ||||| |||  
 C GTTT GATTTTT CGA  
 GT GT GGGAG  
 GAM1237 LOC157464 3' GGCTCTGCATATGCCTGTAT 86451 TAAGAA  
 GTGCAGGTGT GGGGCT  
 ||||| ||||  
 TATGTCCGTA TCTCGG  
 TACG\_  
 GAM1237 LOC157503 5' TTTTTTTTAAAGTTTGTGCTG 86470 TG TG  
 CAG CAGG TTAAGAAGGG  
 ||| ||| |||||  
 GTC GTTT AATTTTTTTT  
 GT GA  
 GAM1237 LOC157567 5' GGCTTCTTCGCGGTCTGTGT 81481 TG TGTTAA  
 G CAGG GAAGGGGCT  
 | ||| |||||  
 T GTCT CTTCTTCGG  
 GT GGCG\_  
 GAM1237 LOC157624 5' CTTTTTGACATCGTACTG 86498 A  
 CAGTGC GGTGTTAAGAAG  
 ||||| |||||

GTCATG CTACAGTTTTTC

GAM1237 LOC157627 3' AGCCTCTTTT TAGTAACTGC 81503 G  
GCAG TGTTAAGAAGGGGCT  
|||||  
CGTC ATGATTTTTCTCCGA  
A

GAM1237 LOC157918 3' AGTCATTCTTTGGCATTGTGT 86641 TG \_ GG  
T AG CAGGTGTAA GAA GGCT  
|| ||||| || ||||  
TT GTTTACGGTT CTT CTGA  
GT T A\_

GAM1237 LOC157919 5' AGTCATTCTTTGGCATTGTGT 81631 TG \_ GG  
T AG CAGGTGTAA GAA GGCT  
|| ||||| || ||||  
TT GTTTACGGTT CTT CTGA  
GT T A\_

GAM1237 LOC157927 3' GGCTTCTATGCTGCGTCTGCCT 86669 T GT TAAGA  
G CAG GCAG GT AGGGGCT  
||| ||| || |||||  
GTC CGTC CG TCTTCGG  
\_ TG TCGTA

GAM1237 LOC158170 3' GGCCTCTGCCAAGTTCTGCATT 81764 TGTTAAGA  
G CAGTGCAGG AGGGGCT  
||||| |||||  
GTTACGTCT TCTCCGG  
TGAACCG\_

GAM1237 LOC158363 3' AGTTTTGAAAAGTGACATTGTG 86777 TG G AGAA\_  
CTG AG CAG TGTTA GGGGCT  
|| ||| |||| |||||  
TC GTT ACAGT TTTTGA  
GT \_ GAAAAG

GAM1237 LOC158427 3' CTTAACACTTTTGCTG 57678 C  
CAGTG AGGTGTTAAG  
|||||  
GTCGT TTCACAATTC  
T

GAM1237 LOC158654 3' GCCCAGACACCTGTGCT 81965 TG AAGAAG  
AG CAGGTGTT GGGC  
|| ||||| ||||  
TC GTCCACAG CCCG  
GT A\_

GAM1237 LOC158722 5' AGTTTCTCCCTCCATGTTGCGC 81991 \_ TTAA A GG  
TG CAGTGCAG GTG GA G GCT  
||||| || ||| |||  
GTCGCGTT TAC CT C TGA  
G CTCC \_ TT

GAM1237 LOC158835 3' GGCACCTTGGTGCCAGCATTG 82012 A TG AA GG  
CAGTGC GG TT GAAG GCT  
||||| || || ||| |||

GTTACG CC GG TTTC CGG  
 A GT \_ A\_  
 GAM1237 LOC161635 5' AGCTCCTTCGGAGACATCTGTC 96569 T AA\_  
 TG CAG GCAGGTGTT GAAGGGGCT  
 ||| ||||| |||||  
 GTC TGTCTACAG CTCCTCGA  
 \_ AGG  
 GAM1237 LOC161829 3' GGTTTCTTTTGTCTGTCTG 82319 T TG GG  
 CAG GCAGG TTAAGAAG GCT  
 ||| |||| ||||| |||  
 GTC TGTCT GATTTTTC TGG  
 \_ \_ TT  
 GAM1237 LOC163412 3' AGCCCCACGCCCTGCGCTG 82132 T TAAGAA  
 CAGTGCAGG GT GGGGCT  
 ||||| || |||||  
 GTCGCGTCC CG CCCC GA  
 C CAC\_  
 GAM1237 LOC163682 5' AGCCTCTTCTCTCACTGCCCTG 87022 T G TTA  
 CAG GCAG TG AGAAGGGGCT  
 ||| |||| || |||||  
 GTC CGTC AC TCTTCTCCGA  
 C \_ TC\_  
 GAM1237 LOC163994 5' GGTCCAGGGGATATTGGTGTGTTG 87049 TG AG AAGAAG  
 CAG C GTGTT GGGCT  
 ||| | |||| |||||  
 GTT G TATAG CCTGG  
 GT GT GGGA\_  
 GAM1237 LOC164714 5' GCTCTCACTCCTGTGCTG 87235 TG T TAAGAA  
 CAG CAGG GT GGGGC  
 ||| |||| || |||||  
 GTC GTCC CA TCTCG  
 GT T C\_  
 GAM1237 LOC165229 5' GCCCACGCCTGCGCTG 82476 TAAGAAG  
 CAGTGCAGGTGT GGGC  
 ||||| ||||| |||||  
 GTCGCGTCCGCA CCGG  
 \_\_\_\_\_  
 GAM1237 LOC165552 3' GGCTAGGTAACATCTGTGCT 82487 TG AGAAGG  
 AG CAGGTGTTA GGCT  
 || ||||| |||||  
 TC GTCTACAAT TCGG  
 GT GGA\_  
 GAM1237 LOC166824 3' TTCTGTACTTGCATT 82665 TTA  
 AGTGCAGGTG AGAA  
 ||||| |||||  
 TTACGTTTCAAT TCTT  
 G\_  
 GAM1237 LOC167153 5' AGCCCCTACCTTTTCTTGTGTT 82674 TG TGTT A\_  
 G CAG CAGG AAG AGGGGCT  
 ||| |||| || |||||

GTT GTTC TTC TCCCCGA  
 GT TT\_\_ CA  
 GAM1237 LOC168667 5' AGTCTGGGGTGCGCTGTGTTG 92755 TG \_TG AAGAAG  
 CAG CAG G TT GGGCT  
 ||| ||| | || ||||  
 GTT GTC C GG TCTGA  
 GT G GT GG\_\_\_\_  
 GAM1237 LOC170082 3' GCCATTTAGTACCTTACTG 82561 C GAAGG  
 CAGTG AGGTGTAA GGC  
 ||||| ||||| |||  
 GTCAT TCCATGATT CCG  
 \_ TA\_\_\_\_  
 GAM1237 LOC170409 3' GTCGTCGATGCCTGCACTG 82866 AA AGG  
 CAGTGCAGGTGTT GA GGC  
 ||||| ||||| || |||  
 GTCACGTCCGTAG CT CTG  
 \_ G\_\_\_\_  
 GAM1237 LOC170409 5' TTTTAACATCAGCATTG 82870 A  
 CAGTGC GGTGTAAAGA  
 ||||| ||||| |||||  
 GTTACG CTACAATTTT  
 A  
 GAM1237 LOC195977 3' CCCAAACATCTGCCTG 87537 T AAGAAG  
 CAG GCAGGTGTT GGG  
 ||| ||||| |||  
 GTC CGTCTACAA CCC  
 \_ A\_\_\_\_  
 GAM1237 LOC196214 5' GCCTCAGCTGCCTGCATTG 89619 GTTA AA  
 CAGTGCAGGT AG GGGGC  
 ||||| || |||||  
 GTTACGTCCG TC CTCCG  
 \_ GA\_\_\_\_  
 GAM1237 LOC196264 3' TCTTGGTATCTTTACTG 87617 C TT  
 CAGTG AGGTG AAGA  
 ||||| ||||| |||||  
 GTCAT TCTAT TTCT  
 T GG  
 GAM1237 LOC196403 5' AGTTCCTTCTTGAGCAACTTG 89628 \_\_  
 CAGGT G TTAAGAAGGGGCT  
 ||||| | ||||| |||||  
 GTTCA C AGTTCTTCCTTGA  
 A G  
 GAM1237 LOC196500 3' AGTCCCTTTTGTCTTGTCTGTC 87739 TG GT TTA\_  
 CTG CAG CAG G AGAAGGGGCT  
 ||| ||| | ||||| |||||  
 GTC GTC T TTTTCCCTGA  
 CT TG TCTG  
 GAM1237 LOC197049 3' TCCTTCTTTGTACTG 89694 GGTGTT  
 CAGTGCA AAGAAGGG  
 ||||| ||||| |||||

GTCATGT TTCTTCCT

GAM1237 LOC197125 3' GCTTGTGATACCTGTTTTG 87902 T AGAAGG  
CAG GCAGGTGTTA GGC  
||| ||||| |||  
GTT TGTCCATAGT TCG  
T GT\_\_\_\_

GAM1237 LOC197342 3' GGCACAGAACTGAGCACCTGCA 88005 A AAGGG\_  
CTG CAGTGCAGGTGTT AG GCT  
||||||| || |||  
GTCACGTCCACGA TC CGG  
G AAGACA

GAM1237 LOC199692 3' GGTCTCCAGAAGCCCTGCATTG 59241 T AAGAA  
CAGTGCAGG GTT GGGGCT  
|||||| ||| |||||  
GTTACGTCC CGA CTCTGG  
\_ AGAC\_

GAM1237 LOC199699 3' GTCCTGTGGTGTCTCACTG 88312 C TG AGAA  
CAGTG AGG TTA GGGGC  
|||| ||| ||| |||||  
GTCAC TCT GGT TCCTG  
\_ GT G\_\_\_\_

GAM1237 LOC199786 3' GCCCCGAATGTCTGGCTG 88385 G TG AAGAA  
CAGT CAGG TT GGGGC  
|||| ||| || |||||  
GTCG GTCT AA CCCCCG  
\_ GT G\_\_\_\_

GAM1237 LOC200030 3' TTCCTTTTATGCATTG 79342 GGTGTTAA  
CAGTGCA GAAGGGG  
||||| |||||  
GTTACGT TTTCTT  
AT\_\_\_\_

GAM1237 LOC200030 3' TTCCTTTTATGCATTG 79343 GGTGTTAA  
CAGTGCA GAAGGGG  
||||| |||||  
GTTACGT TTTCTT  
AT\_\_\_\_

GAM1237 LOC200081 3' GGCTCCTTTGCCATCTTGATGC 88566 \_ TGTTAA  
TG CAGTG CAGG GAAGGGGCT  
|||| ||| |||||  
GTCGT GTTC TTTCTCGG  
A TACCG\_

GAM1237 LOC200081 3' GGTCTTGACTGCATTTGTCTTG 88567 T TA AA  
CAG GCAGGTGT AG GGGGCT  
||| ||||| || |||||  
GTT TGTTTACG TC TTCTGG  
C \_ AG

GAM1237 LOC200197 3' GGTCTGAAGGGCACTGTGCTG 88621 TG G AAGAAG  
CAG CAG TGTT GGGCT  
||| ||| ||| |||||

		GTC GTC ACGG TCTGG		
		GT _ GAAG__		
GAM1237	LOC200251 5'	AGTTCTTGCCTTTGTGTACTG 88664	GTGTT	A_
		CAGTGCAG AAG AGGGGCT		
		GTCATGTT TTC TTCTTGA		
		GT__ CG		
GAM1237	LOC200301 5'	GGCCTTCACAGTGACATTTTAC 88749	C	AGAA_
	TG	CAGTG AGGTGTTA GGGGCT		
		GTCAC TTTACAGT TTCCGG		
		_ GACAC		
GAM1237	LOC200317 3'	GCTCTTTCTCCATTGCCTG 88797	TTA_	
		CAGGTG AGAAGGGGC		
		GTCCGT TCTTTCTCG		
		TACC		
GAM1237	LOC200781 3'	AGCTTTTTTTCAGCTTCTGC 90137	T AA	
		GCAGG GTT GAAGGGGCT		
		CGTCT CGA TTTTTTCGA		
		T C_		
GAM1237	LOC200853 3'	CTTCTGAGTGCTTGTATTG 88912	TG A	
		CAGTGCAGG TT AGAAG		
		GTTATGTTT GA TCTTC		
		GT G		
GAM1237	LOC200953 5'	AGTCAAGGAGTGGACCTGTGCT 90206	TG G	AGAAGG
	G	CAG CAGGT TTA GGCT		
		GTC GTCCA GGT CTGA		
		GT _ GAGGAA		
GAM1237	LOC201158 3'	AGCCCCCAGCACGCCTTGCTTTG 60466	T	TAAGAA
		CAG GCAGGTGT GGGGCT		
		GTT CGTCCGCA CCCC GA		
		T CGAC__		
GAM1237	LOC201194 3'	AGTCTGATGGCGCCTTTGCTG 89775	C	AGAAG
		CAGTG AGGTGTTA GGGCT		
		GTCGT TCCGCGGT TCTGA		
		T AG__		
GAM1237	LOC201952 3'	AGTAATGTTTAATGTTTGTGCT 90268	TG TG	AAGGG
		AG CAGG TTAAG GCT		
		TC GTTT AATTT TGA		
		GT GT GTAA_		
GAM1237	LOC202126 3'	GCCCTGGGTGCCTGGCTG 90315	G TG	TAAGAA
		CAGT CAGG T GGGGC		

	GTCG GTCC G TCCCG	
	_ GT GG____	
GAM1237 LOC202333 3'	AGTCTCCCGCGCATTTGCACT 89163	TAAGAA
	AGTGCAGGTGT GGGGCT	
	TCACGTTTACG CTCTGA	
	CGCC__	
GAM1237 LOC202559 3'	AGTCCTTTTTTTGTTTGT 89195	TGTT
	GCAGG AAGAAGGGGCT	
	TGTTT TTTTTCCTGA	
	GT__	
GAM1237 LOC202754 3'	AGCTTCTTCATTTCCTGTGATTG 82703	_ TGTTAA
	CAGT GCAGG GAAGGGGCT	
	GTTA TGTCC CTTCTTCGA	
	G TTA__	
GAM1237 LOC202934 5'	AGTCTCTGGATGCACTTGTGTT 90401	TG TAAGA
G	CAG CAGGTGT AGGGGCT	
	GTT GTTCACG TCTCTGA	
	GT TAGG__	
GAM1237 LOC203378 3'	AGCTTCAGTGTTAACCTTTGTG 90592	TG T GAA_
CTG	CAG CAGG GTTAA GGGGCT	
	GTC GTTT CAATT CTTCGA	
	GT C GTGA	
GAM1237 LOC204285 5'	AGCTTGCAAGGGGTCCTTGTGCT 89455	TG TG AAGAAG
G	CAG CAGG TT GGGCT	
	GTC GTTC GG TTCGA	
	GT CT GAACG__	
GAM1237 LOC204970 3'	AGCCCCTGCCTGCGTCTGCAC 89406	GT TAAGA
	GTGCAG GT AGGGGCT	
	CACGTC CG TCCCCGA	
	TG TCCG__	
GAM1237 LOC205011 3'	AGCTCATCCATGAGCTTGTATT 90649	GTAA AG
G	CAGTGCAGGT GA GGGCT	
	GTTATGTTCG CT CTCGA	
	AGTAC A__	
GAM1237 LOC205085 5'	GCCACGCGCCCTGCGCTG 90693	T AAGAAG
	CAGTGCAGG GTT GGGC	
	GTCGCGTCC CGG CCCG	
	_ CA____	
GAM1237 LOC219541 3'	GCTTTTCCTGCTGTACTG 91569	GTGTTA A
	CAGTGCAG AG AGGGGC	



GTCATGTC TC TTTTCG  
 G\_\_\_\_\_ C  
 GAM1237 LOC219653 3' AGCCCCTTTTGTAGCAGGGTGT 91290 TG AG\_ G  
 G C GT TTAAGAAGGGGCT  
 | | || |||||  
 T G CG AGTTTTTCCCCGA  
 GT GGA \_  
 GAM1237 LOC219672 5' GGCTCCAAAGCAGGTGCCCTGT 91332 TG T TAAGAA\_\_\_\_  
 GCTG G CAGG GT GGGGCT  
 | ||| || |||||  
 C GTCC CG CCTCGG  
 GT \_ TGGACGAAA  
 GAM1237 LOC219988 3' CTTTTTGCACACTTGCCCTG 91621 T \_  
 CAG GCAGGTGT TAAGAAG  
 ||| ||||| |||||  
 GTC CGTTCACA GTTTTTC  
 C C  
 GAM1237 LOC219988 3' GGCTGGGTGATACTTCTGCTG 91624 C AGAAGG  
 CAGTG AGGTGTTA GGCT  
 |||| ||||| |||||  
 GTCGT TTCATAGT TCGG  
 C GGG\_\_\_\_  
 GAM1237 LOC219988 3' GGTTTCTTTACCTTCTGTGTT 91625 TG T\_ TAA GG  
 AG CAGG GT GAAG GCT  
 || |||| || |||||  
 TT GTCT CA TTTC TGG  
 GT TC \_\_\_\_ TT  
 GAM1237 LOC219990 3' AGTTCTTTCTGTTCTGTGT 91595 TG TGTTA  
 G CAGG AGAAGGGGCT  
 | |||| |||||  
 T GTCT TCTTTCTTGA  
 GT TG\_\_\_\_  
 GAM1237 LOC220064 3' GGTCTGGGGAAGTCTGTGCTG 93428 TG TG AAGAAG  
 CAG CAGG TT GGGCT  
 ||| |||| || |||||  
 GTC GTCT AG TCTGG  
 GT GA GGG\_\_\_\_  
 GAM1237 LOC220638 5' TTCCTTTTATGCATTG 73910 GGTGTTAA  
 CAGTGCA GAAGGGG  
 ||||| |||||  
 GTTACGT TTTCCTT  
 AT\_\_\_\_\_  
 GAM1237 LOC220739 3' AGCTGAGGGGCTAGCACCTGCA 92922 AGAAGG\_  
 TTG CAGTGCAAGGTGTTA GGCT  
 ||||| |||||  
 GTTACGTCCACGAT TCGA  
 CGGGGAG  
 GAM1237 LOC221272 3' AGCTCTTCCCTTATCACTTGC 93606 G T \_  
 AGTG A TGCAGGTG TAA GAAGGGGCT  
 | ||||| ||| |||||

T ACGTTCAC ATT CTTTCTCGA  
 G T CC  
 GAM1237 LOC221474 5' CCCGGATGCTGTATTG 92377 G AAGAAG  
 CAGTGCAG TGTT GGG  
 ||||| ||| ||  
 GTTATGTC GTAG CCC  
 \_ G\_\_\_\_  
 GAM1237 LOC221490 5' AGTACTTTCTTAATGCCTTTGT 93655 GT C GG  
 TG CA G AGGTGTTAAGAAGG CT  
 || | ||||| ||  
 GT T TCCGTAATTCTTTC GA  
 TG T AT  
 GAM1237 LOC221495 3' GGTCCCTGATGGCATCTGTGTT 93861 TG AGA  
 AG CAGGTGTTA AGGGGCT  
 || ||||| |||||  
 TT GTCTACGGT TCCCTGG  
 GT AG\_  
 GAM1237 LOC221543 5' GGCTCCTTACTGCACCTGTGGC 93745 \_ TAAG  
 TG CAGT GCAGGTGT AAGGGGCT  
 ||| ||||| |||||  
 GTCG TGTCCACG TTCCTCGG  
 G TCA\_  
 GAM1237 LOC221547 3' AGTTCAAAAATACCTTCATTG 91006 C AAGAAG  
 CAGTG AGGTGTT GGGCT  
 |||| ||||| |||||  
 GTTAC TCCATAA CTTGA  
 T AAAA\_  
 GAM1237 LOC221656 3' AGCTTCTAGGTATTTTGTATTG 92225 TGTTAAGA  
 CAGTGCAGG AGGGGCT  
 ||||| |||||  
 GTTATGTTT TCTTCGA  
 TATGGA\_  
 GAM1237 LOC221656 3' AGTTTCCAGGCACTTGAACCTG 92226 G AAGAA GG  
 CAGT CAGGTGTT G GCT  
 ||| ||||| | |||  
 GTCA GTTCACGG C TGA  
 A AC\_\_ TT  
 GAM1237 LOC221663 5' AGTCTGAGAACACCTGCATT 93809 AAGAAG  
 AGTGCAGGTGTT GGGCT  
 ||||| |||||  
 TTACGTCCACAA TCTGA  
 GAG\_  
 GAM1237 LOC221663 5' GGTTTTTTTAATCTGCGC 93820 GTTAA  
 GTGCAGGT GAAGGGGCT  
 ||||| |||||  
 CGCGTCTA TTTTTTTGG  
 A\_\_\_\_  
 GAM1237 LOC221692 3' GGTCCCGGGGCATGCCTGTCTG 92243 T TAAGAA  
 CAG GCAGGTGT GGGGCT  
 || ||||| |||||

GTC TGTCCGTA CCCTGG  
 \_ CGGG\_  
 GAM1237 LOC221751 5' GGTCCCTTTTCCCTTTCTGT 92050 TGTTA  
 GCAGG AGAAGGGGCT  
 |||| |||||  
 TGTCT TTTTCCTGG  
 TTCCC  
 GAM1237 LOC221773 3' TCTTAATACTTGAAGT 91052 G  
 CAGT CAGGTGTTAAGA  
 ||| |||||  
 GTCA GTTCATAATTCT  
 A  
 GAM1237 LOC221810 3' AGCCTTTTCAGAGCTTGTA 93930 GTTAA  
 TGCAGGT GAAGGGGCT  
 ||||| |||||  
 ATGTTCG CTTTCCGA  
 AGA\_  
 GAM1237 LOC221935 3' GCTTTTTGTAAGTTCGCTG 92624 C GTTAAG  
 CAGTG AGGT AAGGGGC  
 |||| ||| |||||  
 GTCGC TTCA TTTTTCG  
 \_ ATG\_  
 GAM1237 LOC221962 3' AGCCCCAAACACAGCTGCACTG 92678 G TAAGAA  
 CAGTGCAG TGT GGGGCT  
 ||||| ||| |||||  
 GTCACGTC ACA CCCCCGA  
 G CAAA\_  
 GAM1237 LOC222134 5' GCTTTTTCTCCTGTCTG 94141 T TGTTAA  
 CAG GCAGG GAAGGGGC  
 || |||| |||||  
 GTC TGTCC CTTTTTCG  
 \_ TC\_  
 GAM1237 LOC222160 3' CTTCTTAGCACTTAGCACTG 94126 \_  
 CAGTGC AGGTGTTAAGAAG  
 ||||| |||||  
 GTCACG TTCACGATTCTTC  
 A  
 GAM1237 LOC222234 3' GGCTTTTTCAAAATTTGTGCT 94247 TG GTTAA  
 AG CAGGT GAAGGGGCT  
 || |||| |||||  
 TC GTTAA CTTTTTCG  
 GT AAA\_  
 GAM1237 LOC222550 3' AGTTCCATGATGTCTTTATTG 94351 C TG AGAA  
 CAGTG AGG TTA GGGGCT  
 |||| ||| ||| |||||  
 GTTAT TCT AGT CCTTGA  
 T GT A\_  
 GAM1237 LOC222662 5' GCCTCTTCCCCTTGCCTTG 92844 T TGTTAA  
 CAG GCAGG GAAGGGGC  
 || |||| |||||

GTT CGTTC CTTCTCCG  
 C CC\_\_\_\_  
 GAM1237 LOC245771 3' AGCCCAGAGTGCCTTGTACTG 92881 \_ TG AAGAAG  
 CAGTGCA GG TT GGGCT  
 ||||| || || ||||  
 GTCATGT CC GA CCCGA  
 T GT GA\_\_\_\_  
 GAM1237 LOC253017 3' AGCTCTGAATGTATTTGCAT 95839 TTAAGAA  
 GTGCAGGTG GGGGCT  
 ||||| ||||  
 TACGTTTAT TCTCGA  
 GTAAG\_\_\_\_  
 GAM1237 LOC253019 3' TCTTGATGCTTCTGCTG 95368 C  
 CAGTG AGGTGTTAAGA  
 |||| |||||  
 GTCGT TTCGTAGTTCT  
 C  
 GAM1237 LOC253115 5' GGTCTGATTGAGCTTGTGTTG 94497 TG G GAAG  
 CAG CAGGT TTAA GGGCT  
 || |||| ||||  
 GTT GTTCG AGTT TCTGG  
 GT \_ AG\_\_\_\_  
 GAM1237 LOC253250 3' GCTCAATAATATTGCATTG 94702 G AGAAG  
 CAGTGCAG TGTTA GGGC  
 ||||| |||| ||||  
 GTTACGTT ATAAT CTCG  
 \_ AA\_\_\_\_  
 GAM1237 LOC253250 3' GGTTCCTTCTGCTTTTGGCTG 94704 G TGTTA  
 CAGT CAGG AGAAGGGGCT  
 |||| |||| |||||  
 GTCG GTTT TCTTCCTTGG  
 \_ TTCG\_\_\_\_  
 GAM1237 LOC253260 3' AGTTTCTTCGTGTGCATGTATT 95931 \_ TAA\_ GG  
 GCATTG GCAG GTGT GAAG GCT  
 |||| |||| ||||  
 CGTT TACG CTTC TGA  
 ATG TGTG TT  
 GAM1237 LOC253295 3' AGCTTCTTTGACTTTTCCACT 95936 C T\_ AA  
 G CAGTG AGG GTT GAAGGGGCT  
 |||| |||| |||||  
 GTCAC TTT CAG TTTCTTCGA  
 C TT \_\_\_\_  
 GAM1237 LOC253573 3' CCTTTTGTTTGCCTG 97048 TT G  
 CAGGTG AA AAGGGG  
 |||| || |||||  
 GTCCGT TT TTTTCC  
 \_ G  
 GAM1237 LOC253612 3' GGCCTTTTAAATTTGCTTTGC 96753 \_ GTTAA  
 TG AGT GCAGGT GAAGGGGCT  
 || |||| |||||

	TCG CGTTTA TTTTCCGG	
	TTT AA__	
GAM1237 LOC253675 5'	GCCTCTAGATATCTGTGT 96774 TG	AAGA
	G CAGGTGTT AGGGGC	
	T GTCTATAG TCTCCG	
	GT A__	
GAM1237 LOC253776 3'	GGCCCTTTCCTCTGTGTA CTG 97430	_ TGTTAA
	CAGTGCA GG GAAGGGGCT	
	GTCATGT TC CTTTCCCG	
	G TC__	
GAM1237 LOC253782 3'	AGCCCTATCTAGTACTTG 95695	A A
	CAGGTGTTA GA GGGGCT	
	GTTTCATGAT CT TCCCGA	
	_ A	
GAM1237 LOC253975 3'	TCTTGATGCTTCTGCTG 95998	C
	CAGTG AGGTGTTAAGA	
	GTCGT TTCGTAGTTCT	
	C	
GAM1237 LOC254105 3'	GCCCCTGGGCCTGCA CTG 94769	GTTAAGA
	CAGTGCAGGT AGGGGC	
	GTCACGTCCG TCCCG	
	GG__	
GAM1237 LOC254128 3'	AGCTCCTTGCTAGTGTATGTGT 95636	TG G TG AG
TG	CAG CA G TTA AAGGGGCT	
	GTT GT T GAT TTCCTCGA	
	GT A GT CG	
GAM1237 LOC254228 3'	GGTTCAGAGAGCTTCTGCATTG 95955	T AAGAAG
	CAGTGCAGG GTT GGGCT	
	GTTACGTCT CGA CTTGG	
	T GAGA__	
GAM1237 LOC254249 3'	AGCTCTGTCTTTTGGTGT TTG 95444	TG ____
CACT	TGCAGG TTAAGAAG GGGCT	
	ACGTTT GGTTTTTC CTCGA	
	GT TGT	
GAM1237 LOC254251 3'	AGCATTTTAGTACTTGTATT 95904	AGGG
	AGTGCAGGTGTTAAGA GCT	
	TTATGTTTCATGATTTT CGA	
	A__	
GAM1237 LOC254359 3'	GGTTGGACCTTAACATCTGCAT 94783	AAGG
TG	CAGTGCAGGTGTTAAG GGCT	

		GTTACGTCTACAATTC TTGG		
		CAGG		
GAM1237	LOC254427 3'	GTCTAGAGGTGCCTGGCTG 94707	G	TG AAGAAG
		CAGT CAGG TT GGGC		
		GTCG GTCC GG TCTG		
		_ GT AGA__		
GAM1237	LOC254532 3'	AGTCTGTGCGAGTGACACCTGCA 96630		A__ AG
	C	GTGCAGGTGTTA GA GGGCT		
		CACGTCCACAGT CT TCTGA		
		GAG G_		
GAM1237	LOC254559 5'	AGCCTAACCAACACCTGTGCTG 96593	TG	AAGAAG
		CAG CAGGTGTT GGGCT		
		GTC GTCCACAA TCCGA		
		GT CCAA__		
GAM1237	LOC254672 3'	AGTTCAAAAATGCTCTGCACTG 94639	_	AAGAAG
		CAGTGCAG GTGTT GGGCT		
		GTCACGTC CGTAA CTTGA		
		T AAA__		
GAM1237	LOC254672 3'	CTTTTCTGTGCATTG 94645	GGTGTTA	
		CAGTGCA AGAAGGGG		
		GTTACGT TCTTTTC		
		G_____		
GAM1237	LOC254740 5'	GTCTCTGTTGCTTGCG 96231	TTAAGA	
		TGCAGGTG AGGGGC		
		GCGTTCGT TCTCTG		
		TG_____		
GAM1237	LOC254842 5'	GGCTTCTGTCGCTTTTGTGCTG 97597	TG _	TTAAGA
		CAG CA GGTG AGGGGCT		
		GTC GT TCGC TCTTCGG		
		GT TT TG_____		
GAM1237	LOC254848 3'	AGTCCCTCTCTGGTGTCTGTAT 97088	TG _	A
	T	AGTGCAGG TTA AGA GGGGCT		
		TTATGTCT GGT TCT CCCTGA		
		GT C _		
GAM1237	LOC254936 3'	AGTTCCTTTAGGATTTGTAT 94971	G	GA
		GTGCAGGT TTAA AGGGGCT		
		TATGTTTA GATT TCCTTGA		
		G _		
GAM1237	LOC255031 5'	GCCCGGAACACCTGCGTG 97235	G	AAGAAG
		CA TGCAGGTGTT GGGC		

		GT GCGTCCACAA	CCCG		
		— GG_____			
GAM1237	LOC255043 3'	CTTCCTGACGCCTGTCTG	95330	T	A
		CAG GCAGGTGTTA GAAG			
		GTC TGTCCGCAGT CTTC			
		— C			
GAM1237	LOC255177 3'	GGCCCCACAGTGTGACATTTG	96607		AGAA_
		CAGGTGTTA GGGGCT			
		GTTTACAGT CCCC GG			
		GTGACA			
GAM1237	LOC255272 3'	GGCTCCTTCAGACACGTGCTTG	94600	_____ G	AA
	ATGCTG	GCA GTGTT GAAGGGGCT			
		CGT CACAG CTTCTCGG			
		AGTT G A_			
GAM1237	LOC255462 3'	GTCCTGCTGACCTGCACTG	96859		GTTAAGAA
		CAGTGCAGGT GGGGC			
		GTCACGTCCA TCCTG			
		GTCG_____			
GAM1237	LOC255520 3'	GCGTTTTACACATTTGTACTG	95857		TAAG G T
		CAGTGCAGGTGT AAGG GC			
		GTCATGTTTACA TTTT CG			
		CA_ G T			
GAM1237	LOC255589 3'	GGTTCCAGAAGTGGCGCCTGCT	96954	T	AGAA_
	CTG	CAG GCAGGTGTTA GGGGCT			
		GTC CGTCCGCGGT CCTTGG			
		T GAAGA			
GAM1237	LOC255978 5'	AGTCTTTTCTTGCTGCTGTATT	95442		GT T
		AGTGCAG GT AAGAAGGGGCT			
		TTATGTC CG TTCTTTTCTGA			
		GT _			
GAM1237	LOC256130 3'	TTTTTGCATTTGCATT	96041		T
		AGTGCAGGTGT AAGA			
		TTACGTTTACG TTTT			
		T			
GAM1237	LOC256158 5'	AGCCTGCCAGGCCCTGTGTTG	97643	TG T	AAGAAG
		CAG CAGG GTT GGGCT			
		GTT GTCC CGG TCCGA			
		GT _ ACCG_			
GAM1237	LOC256525 3'	AGCCTTTTAACTAATCTCACTG	96125	C	GTTAAG
		CAGTG AGGT AAGGGGCT			

GTCAC TCTA TTTTCCGA  
 \_ ATCAA\_  
 GAM1237 LOC256691 3' GGCTCTTTTTTCTTTTTGCAT 96199 TGTT  
 GTGCAGG AAGAAGGGGCT  
 ||||| |||||  
 TACGTTT TTTTTCTCGG  
 TTCT  
 GAM1237 LOC256730 3' GTAATTAACACCTTCATTG 95233 C GAAGGG  
 CAGTG AGGTGTAA GC  
 ||||| ||||| ||  
 GTTAC TCCACAATT TG  
 T AA\_  
 GAM1237 LOC256946 3' AGTCTCTTACAGTGCCTCTG 94543 TGC TG AAG  
 CAG AGG TT AAGGGGCT  
 ||| ||| || |||||  
 GTC TCC GA TTCTCTGA  
 \_ GT CA\_  
 GAM1237 LOC257042 3' GGCTTCCTGGGATGCTTGTGT 96898 TG AAGA \_  
 G CAGGTGTT AGGG GCT  
 | ||||| ||| |||  
 T GTTCGTAG TCCT CGG  
 GT GG\_ T  
 GAM1237 LOC257249 5' TTTCTTAATATCTGACTG 95923 G  
 CAGT CAGGTGTAAAGAAG  
 |||| |||||  
 GTCA GTCTATAATTCTTT  
 \_  
 GAM1237 LOC257408 5' GCTTCCTGTGCCTGCGCT 96069 TG TAAGA \_  
 AGTGCAGG T AGGG GC  
 ||||| | ||| ||  
 TCGCGTCC G TCCT CG  
 GT\_ T  
 GAM1237 LOC257482 3' GGCCAATTTTAACACATGCACT 94239 G AGG  
 G CAGTGCA GTGTAAAGA GGCT  
 ||||| ||||| |||  
 GTCACGT CACAATTTT CCGG  
 A AA\_  
 GAM1237 LOC257486 3' CCTGGACATCTGACTG 69245 G AAGAAG  
 CAGT CAGGTGTT GGG  
 ||| ||||| |||  
 GTCA GTCTACAG TCC  
 \_ G\_  
 GAM1237 LOC257556 5' GGTCTGATTGAGCTTGTGTTG 97710 TG G GAAG  
 CAG CAGGT TTAA GGGCT  
 ||| ||||| ||| |||||  
 GTT GTTCG AGTT TCTGG  
 GT \_ AG\_  
 GAM1237 LOC257577 3' AGTTCAAAAAATACCTTCATTG 97837 C AAGAAG  
 CAGTG AGGTGTT GGGCT  
 ||||| ||||| |||||



GTTAC TCCATAA CTTGA  
 T AAAA\_  
 GAM1237 LOC257596 5' GGCTCCTTACTGCACCTGTGGC 97938 \_ TAAG  
 TG CAGT GCAGGTGT AAGGGGCT  
 |||| ||||| |||||  
 GTCG TGTCCACG TTCCTCGG  
 G TCA\_  
 GAM1237 LOC257617 5' GGTCTGATTGAGCTTGTGTTG 97816 TG G GAAG  
 CAG CAGGT TTAA GGGCT  
 || |||| ||| ||||  
 GTT GTTCG AGTT TCTGG  
 GT \_ AG\_  
 GAM1237 LOC51000 3' AGCCTTTTCTTCAGAGCATTG 31973 \_\_\_\_  
 T GCAGGTGTT AAGAAGGGGCT  
 ||||| |||||  
 TGTTTACGA TTCTTTTCCGA  
 GAC  
 GAM1237 LOC51003 3' GCCTCAAATACTTGTGTT 32147 TG AAGAA  
 AG CAGGTGTT GGGGC  
 || ||||| ||||  
 TT GTTCATAA CTCCG  
 GT A\_  
 GAM1237 LOC51026 3' AGACATTTTGGTACTTGCATT 32165 TT GGGG  
 AGTGCAGGTG AAGAA CT  
 ||||| |||| ||  
 TTACGTTTCA TTTT GA  
 GG ACA\_  
 GAM1237 LOC51026 3' TTTTGGTACTTGCATT 32173 TT  
 AGTGCAGGTG AAGAA  
 ||||| ||||  
 TTACGTTTCA TTTT  
 GG  
 GAM1237 LOC51042 3' GGCCTCTTCTTGGTGCCCTGC 31855 \_TG  
 GCAG G TTAAGAAGGGGCT  
 |||| | |||||  
 CGTC C GGTTCCTCTCCGG  
 C GT  
 GAM1237 LOC51152 3' GTTTTTTTTTGGGACGTG 32455 G G  
 CA GT TTAAGAAGGGGC  
 || || |||||  
 GT CA GGTTTTTTTTTG  
 G G  
 GAM1237 LOC51200 3' GCTCTTTCCTACCTGTGT 33000 TG TTAA  
 G CAGGTG GAAGGGGC  
 | |||| |||||  
 T GTCCAT CTTTCTCG  
 GT C\_  
 GAM1237 LOC51267 3' GCCTCTTCATCTGCACCTG 33257 TAA\_  
 CAGGTGT GAAGGGGC  
 ||||| |||||

			GTCCACG	CTTCTCCG		
			TCTA			
GAM1237	LOC51320	3'	GGCTTTGGGATAGCACCTATAT	33546	C	AGAA
		TG	CAGTG AGGTGTTA	GGGGCT		
			GTTAT TCCACGAT	TTTCGG		
			A	AGGG		
GAM1237	LOC51696	3'	GCCCATGATACCTTACTG	32549	C	AGAAG
			CAGTG AGGTGTTA	GGGC		
			GTCAT TCCATAGT	CCCG		
			-	A		
GAM1237	LOC51701	3'	GTTAATCATGCTTGTACTG	32652		TAA AGG
			CAGTGCAGGTGT	GA GGC		
			GTCATGTTTCGTA	CT TTG		
			-	AA		
GAM1237	LOC54505	3'	AGTTCCTTTTAAATGATG	67837	GG	
			CA TGTTAAGAAGGGGCT			
			GT GTAATTTTTCCTTGA			
			A			
GAM1237	LOC56181	5'	TTTTTTGGGGCTTGTGT	95546	TG	G
			G CAGGT TTAAGAAG			
			T GTTCG GGTTTTT			
			GT	G		
GAM1237	LOC57109	5'	GGCCTGGGCAGGCGCTTGTGCT	39852	TG	AAGAAG
		G	CAG CAGGTGTT	GGGCT		
			GTC GTTCGCGG	TCCGG		
			GT	ACGGG		
GAM1237	LOC57115	3'	AGCCTTCCCCTGGTGTCTGCCT	39859	T	TG AGAA
		G	CAG GCAGG TTA	GGGGCT		
			GTC CGTCT GGT	TTCCGA		
			-	GT CCCC		
GAM1237	LOC57805	3'	GGCCCTTTTAGTCTTGTGCTG	40989	TG	TGTTAA
			CAG CAGG	GAAGGGGCT		
			GTC GTTC	TTTTCCCGG		
			GT	TGA		
GAM1237	LOC59346	3'	GCCCCTTTGTCCTCGCTG	41276	C	TGTTAA
			CAGTG AGG	GAAGGGGC		
			GTCGC TCC	TTTCCCCG		
			-	TG		
GAM1237	LOC63923	3'	GGTTCCTTCCCTCTCACCTGCA	67122		TTAA
		TT	AGTGCAGGTG	GAAGGGGCT		

TTACGTCCAC CTTCTTGG  
 TCTCC  
 GAM1237 LOC63929 3' AGTTTGTGTGATGCCTGTATT 42040 AGAAG  
 AGTGCAGGTGTTA GGGCT  
 ||||| ||||  
 TTATGTCCGTAGT TTTGA  
 GTG\_\_  
 GAM1237 LOC64116 3' AGCTTTTTTCTGACTTATGTT 42196 T GGT \_  
 G G GCA GTTA AGAAGGGGCT  
 ||| ||| |||||  
 G TGT CAGT TTTTTTTCGA  
 T ATT C  
 GAM1237 LOC84643 3' GTCCGAAATGCTGCATTG 50779 G AAGAAG  
 CAGTGCAG TGTT GGGC  
 ||||| ||| |||  
 GTTACGTC GTAA CCTG  
 \_ AG\_\_  
 GAM1237 LOC85414 3' AGCCCCCAGAGTATATCTGTGC 52392 TG TAAGAA  
 T AG CAGGTGT GGGGCT  
 || ||||| |||||  
 TC GTCTATA CCCCCGA  
 GT TGAGAC  
 GAM1237 LOC89958 3' GCCTCAGGATTTTGTGTTG 60921 TG T AAGAA  
 CAG CAGG GTT GGGGC  
 ||| ||| ||| |||||  
 GTT GTTT TAG CTCCG  
 GT \_ GA\_\_  
 GAM1237 LOC90148 3' TTTTGATACCTGTACTG 61669  
 CAGTGCAGGTGTTAAGA  
 |||||  
 GTCATGTCCATAGTTTT  
  
 GAM1237 LOC90231 3' GGCCCCCAGGGTGGCTGTGCT 61869 TG G GT AAGAA  
 G CAG CAG T T GGGGCT  
 ||| ||| | |||||  
 GTC GTC G G CCCCCG  
 GT G TG GACC\_  
 GAM1237 LOC90233 3' GCTCTTTGTTCTGTATTG 56385 TGTTA G  
 CAGTGCAGG A AAGGGGC  
 ||||| | |||||  
 GTTATGTCT T TTTCTCG  
 \_\_\_\_ G  
 GAM1237 LOC90233 3' GCTTTGTGTTCTGTATTG 56386 TGTTAAGAA  
 CAGTGCAGG GGGGC  
 ||||| |||||  
 GTTATGTCC TTTCG  
 TTGTG\_\_  
 GAM1237 LOC90233 3' GGTCTCACATGATGCTTGTA 56387 AGAA  
 TGCAGGTGTTA GGGGCT  
 ||||| |||||

ATGTTTCGTAGT CTCTGG  
 ACA\_  
 GAM1237 LOC90459 3' TTTAACATTTGCTCTG 62894 T  
 CAG GCAGGTGTTAAG  
 ||| |||||  
 GTC CGTTTACAATTT  
 T  
 GAM1237 LOC90485 3' GGCCCTACAGGTGCCTGCA 63022 TG AAGAA  
 TGCAGG TT GGGGCT  
 ||||| || |||||  
 ACGTCC GG TCCCGG  
 GT ACA\_  
 GAM1237 LOC90494 5' AGTTCTTTCTGGTGTCTGCTG 63051 TGTTA  
 GCAGG AGAAGGGGCT  
 ||||| |||||  
 CGTCT TCTTTCTTGA  
 TGTGG  
 GAM1237 LOC90495 3' AGTCCCAAGGACATCTGTGT 63059 TG AAGAA  
 G CAGGTGTT GGGGCT  
 | ||||| |||||  
 T GTCTACAG CCCTGA  
 GT GAA\_  
 GAM1237 LOC90786 5' CCTTCACATTTGTGTT 64033 TG TAA  
 AG CAGGTGT GAAGG  
 || ||||| |||||  
 TT GTTTACA CTTCC  
 GT \_  
 GAM1237 LOC90844 3' GTCCCAGGCATCTGCGCT 64209 AAGAA  
 AGTGCAGGTGTT GGGGC  
 ||||| |||||  
 TCGCGTCTACGG CCCTG  
 A\_  
 GAM1237 LOC90906 3' GGTTTGGGGAATTCTGCACTG 64309 T AAGAAG  
 CAGTGCAGG GTT GGGCT  
 ||||| || |||||  
 GTCACGTCC TAA TTTGG  
 T GGGG\_  
 GAM1237 LOC91115 3' AGTCTCCTGGGAAACGTCTGCA 64924 GT AAGA \_  
 TT AGTGCAG GTT AGG GGCT  
 ||||| || |||||  
 TTACGTC CAA TCC CTGA  
 TG AGGG T  
 GAM1237 LOC91170 5' AGCCTTTTATGGGGCTTGCACT 65135 G AG  
 G CAGTGCAGGT TTA AAGGGGCT  
 ||||| || |||||  
 GTCACGTTTCG GGT TTTTCCGA  
 G A\_  
 GAM1237 LOC91355 5' TCTTGACCTGTGTTG 65722 TG T  
 CAG CAGGTGT AAGA  
 ||| ||||| |||||

GTT GTCCACG TTCT  
 GT \_  
 GAM1237 LOC91409 3' GGTCTGCAGAGTACCTGTGCT 65958 TG AAGAA  
 G CAG CAGGTGTT GGGGCT  
 ||| ||||| |||||  
 GTC GTCCATGA TCCTGG  
 GT GACG\_  
 GAM1237 LOC91628 3' TCTTGGTATTTGTGGTG 66764 G TT  
 CA TGCAGGTG AAGA  
 || ||||| |||  
 GT GTGTTTAT TTCT  
 G GG  
 GAM1237 LOC91660 5' GTCTCTTAAATCTGTGTTG 66868 TG GTTAAG  
 CAG CAGGT AAGGGGC  
 ||| |||| |||||  
 GTT GTCTA TTCTCTG  
 GT AA\_\_\_\_  
 GAM1237 LOC91768 3' GGCTCTTTCTTAACATTCCCAC 67116 CA  
 GTG GGTGTTAAGAAGGGGCT  
 ||| |||||  
 CAC TTACAATTCTTTCTCGG  
 CC  
 GAM1237 LOC91812 5' GGCCTCGACCACTCTGCATTG 67241 \_ TTAAGAA  
 CAGTGCAG GTG GGGGCT  
 ||||| ||| |||||  
 GTTACGTC CAC CTCCGG  
 T CAG\_\_\_\_  
 GAM1237 LOC91813 5' GGCCTCGACCACTCTGCATTG 67256 \_ TTAAGAA  
 CAGTGCAG GTG GGGGCT  
 ||||| ||| |||||  
 GTTACGTC CAC CTCCGG  
 T CAG\_\_\_\_  
 GAM1237 LOC91960 3' TCTTTCTTCACCTGAACTG 67666 G TT  
 CAGT CAGGTG AAGAAGGG  
 ||| ||||| |||||  
 GTCA GTCCAC TTCTTTCT  
 A \_  
 GAM1237 LOC92080 3' AGCCTCTGCTGGTGCTGTGCTG 68038 TG G TG AGA  
 CAG CA G TTA AGGGGCT  
 ||| ||| ||| |||||  
 GTC GT C GGT TCTCCGA  
 GT \_GT CG\_  
 GAM1237 LOC92080 3' GGCCCCTGTACGGGGTGTCTGC 68054 T TG AAGA\_\_\_\_  
 CCTG AG GCAGG TT AGGGGCT  
 || |||| || |||||  
 TC CGTCT GG TCCCCGG  
 C GT GGCATG  
 GAM1237 LOC92340 3' AGCCCCTTCTTGGGCAGAGCTG 68986 GCAG G  
 CAGT GT TTAAGAAGGGGCT  
 |||| || |||||

GTCG CG GGTTCTTCCCCGA  
 AGA\_ \_  
 GAM1237 LOC92405 3' GTTTCTTGTTGCTGTGCTG 69194 TG GTGT G GG  
 CAG CAG TAA AAG GC  
 ||| ||| ||| ||| ||  
 GTC GTC GTT TTC TG  
 GT \_ G TT  
 GAM1237 LOC92521 3' GGTCCCACGATGTACCTGTCTG 69597 T TTAAGAA  
 CAG GCAGGTG GGGGCT  
 ||| ||||| |||||  
 GTC TGTCCAT CCCTGG  
 \_ GTAGCA\_  
 GAM1237 LOC92539 5' AGTCAGCACTTAATGCTTATAC 69628 C AAGG  
 TG CAGTG AGGTGTTAAG GGCT  
 ||||| ||||| |||||  
 GTCAT TTCGTAATTC CTGA  
 A ACGA  
 GAM1237 LOC92568 3' AGCTGAGCTTAGTCCTGCGCTG 69770 TGT AAGG  
 CAGTGCAGG TAAG GGCT  
 ||||| ||| |||  
 GTCGCGTCC ATTC TCGA  
 TG\_ GAG\_  
 GAM1237 LOC92597 3' AGCTTTTTTTTAAATTATTTTAC 69970 C \_ A  
 TG CAGTG AGGTG TT AGAAGGGGCT  
 ||||| ||||| ||| ||||| |||||  
 GTCAC TTTAT AA TTTTTTTCGA  
 \_ T A  
 GAM1237 LOC92661 5' GCCCAGGGGCACCTGCAT 70081 AAGAAG  
 GTGCAGGTGTT GGGC  
 ||||| |||  
 TACGTCCACGG CCGG  
 GGA\_  
 GAM1237 LOC92710 3' GGCTCTTTCTGGCGCCCTGTGC 70356 TG \_ A  
 TG CAG CAGG TGTTA GAAGGGGCT  
 ||| ||| ||||| ||||| |||||  
 GTC GTCC GCGGT CTTTCTCGG  
 GT C \_  
 GAM1237 LOC92716 3' GCCTCTGTACCTGCCCTG 70380 T TTAAGA  
 CAG GCAGGTG AGGGGC  
 ||| ||||| |||||  
 GTC CGTCCAT TCTCCG  
 C G\_  
 GAM1237 LOC96652 3' GGCCCAGGACAGTGCCTGGGCT 65470 G TG AAGAAG  
 G CAGT CAGG TT GGGCT  
 ||||| ||| |||||  
 GTCG GTCC GA CCGG  
 G GT CAGGA\_  
 GAM1237 LOC96652 3' GGTCCATCCTTGGGGCCTGC 65471 G AA\_  
 ATTG AGTGCAGGT TTAAG GGGGCT  
 ||||| ||||| |||||

TTACGTCCG GGTTC TCCTGG  
 G CTAC  
 GAM1238 DMXL1 3' TGAATTCCCATCCTAATTTTC 18579 TG TA C  
 GA GTT GA GGGAATTCA  
 || ||| || |||||  
 CT TAA CT CCCTTAAGT  
 TT TC A  
 GAM1238 PIGA 5' TGTCTAAACCGTCTCA 40008  
 TGAGATGGTTTAGACG  
 |||||  
 ACTCTGCCAAATCTGT  
 GAM1238 PIGA 5' TGTCTAAACCGTCTCA 10555  
 TGAGATGGTTTAGACG  
 |||||  
 ACTCTGCCAAATCTGT  
 GAM1238 PIGA 5' TGTCTAAACCGTCTCA 40017  
 TGAGATGGTTTAGACG  
 |||||  
 ACTCTGCCAAATCTGT  
 GAM1238 LRP1B 5' TGAATTCCCATCCGCTGGCATC 37675 GTTTA\_ C  
 TC GAGATG GA GGGAATTCA  
 |||| || |||||  
 CTCTAC CT CCCTTAAGT  
 GGTCCG A  
 GAM1238 LOC143524 3' TGAACCCCCATCTACATGCTCA 76597 \_ GTT C AA  
 TGAG ATG TAGA GGG TTCA  
 ||| ||| ||| ||| |||  
 ACTC TAC ATCT CCC AAGT  
 G \_ A CC  
 GAM1238 LOC144952 5' TGAATCTAGCACTAAACCACT 87075 A ACG\_ A  
 AG TGGTTTAG GGA TTCA  
 || ||||| || |||  
 TC ACCAAATC TCT AAGT  
 C ACGA \_  
 GAM1238 LOC153454 3' GAAGTTCGAAACCATCCCA 80833 A AGA GAA  
 TG GATGGTTT CGG TTC  
 || ||||| || |||  
 AC CTACCAA GCT AAG  
 C \_ TG\_  
 GAM1238 LOC255515 3' CCCATCTACATGCTCA 96093 \_ GTT C  
 TGAG ATG TAGA GGG  
 ||| ||| ||| |||  
 ACTC TAC ATCT CCC  
 G \_ A  
 GAM1239 BBS4 3' AGCTAGATCCTATCA 52280 TA  
 TGATAG ATCTAGCT  
 ||||| |||||

		ACTATC TAGATCGA		
		C_		
GAM1239	DAZL	3' ACTGTGAGCCATATTACTA	68138	CTA
		TAGTAAT GCTCACAGT		
		ATCATTA CGAGTGTCA		
		TAC		
GAM1239	NQO1	3' ACTGATTCTTATGATTACTATC	6146	_ CTCA
	A	TGATAGTAATC TAG CAGT		
		ACTATCATTAG ATT GTCA		
		T CTTA		
GAM1239	PAG	3' AGCTAGATCACTACA	37399	A A
		TG TAGT ATCTAGCT		
		AC ATCA TAGATCGA		
		_ C		
GAM1239	RBL2	3' AGTGATTACTGTCA	18828	TA
		TGATAGTAATC GCT		
		ACTGTCATTAG TGA		
		—		
GAM1239	TNS	5' TGAGCTGGTGCCCATCA	42631	A_ AT
		TGAT GTA CTAGCTCA		
		ACTA CGT GGTCGAGT		
		CC _		
GAM1239	CD109	3' ACTGTGAGCCAGGGATAC	56043	A_ A
		GTA TCT GCTCACAGT		
		CAT GGA CGAGTGTCA		
		AG C		
GAM1239	CPR2	3' ACTGTGAGCCAAATAAACTTC	48088	T AATCTA_
		GA AGT GCTCACAGT		
		CT TCA CGAGTGTCA		
		_ AATAAAC		
GAM1239	DZIP1	3' ACTGTAAGCATGTTACTATTA	30033	CTA C
		TGATAGTAAT GCT ACAGT		
		ATTATCATTG CGA TGTCA		
		TA_ A		
GAM1239	KIAA0310	5' ACTGTGAGCCAGAATTAC	81674	_ A
		GTAAT CT GCTCACAGT		
		CATTA GA CGAGTGTCA		
		A C		
GAM1239	KIAA1323	3' ATTGCTGCTAGATTATATCA	63039	G TCA
		TGATA TAATCTAGC CAGT		



			ACTAT ATTAGATCG GTTA		
			TC_		
GAM1239	KIAA1393	3'	ACTGTGAGCCAATTAT 72096	CTA	
			GTAAT GCTCACAGT		
			TATTA CGAGTGTCA		
			AC_		
GAM1239	ROBO2	3'	ACTGTAAGCTAGATTG 62484	C	
			TAATCTAGCT ACAGT		
			GTTAGATCGA TGTC A		
GAM1239	LOC135892	3'	ACTGTGAACTTTCAACTACTAT 75243	ATCT_ C	
			CA TGATAGTA AG TCACAGT		
			ACTATCAT TC AGTGTCA		
			CAACTT A		
GAM1239	LOC150225	3'	ACTGTGAGGCCAGCTATATCA 84978	GTAAT A _	
			TGATA CT GC TCACAGT		
			ACTAT GA CG AGTGTCA		
			ATC_ C G		
GAM1239	LOC158969	5'	ACTGCAAGGTGGTCATTGCTAT 82057	_ G CA	
			CA TGATAGTAAT CTA CT CAGT		
			ACTATCGTTA GGT GA GTCA		
			CT G AC		
GAM1239	LOC163231	3'	ACTGTGAGCCACCTGTT 82432	TAATCTA	
			GATAG GCTCACAGT		
			TTGTC CGAGTGTCA		
			CAC_		
GAM1239	LOC200488	5'	ACTGTATAAAAGATACTATCA 90079	A AGCTC	
			TGATAGTA TCT ACAGT		
			ACTATCAT AGA TGTC		
			_ AAATA		
GAM1239	LOC220980	5'	ACTGCAGCTCAGAGATTACT 93143	_ CA	
			AGTAATCT AGCT CAGT		
			TCATTAGA TCGA GTCA		
			GAC C_		
GAM1240	AP2B1	3'	GTAGTGCAGAAGGTTTACA 7064	A _	
			TGTGAAC TTCTGCAC AC		
			ACACTTG AAGACGTG TG		
			G A		
GAM1240	ARNT2	3'	TAGCTGTGTTTCTGATCCCACA 29465	AACAT TGC_	
			TGTG TC ACACAGCTA		

			ACAC	AG	TGTGTCGAT		
			CCT__	TCCT			
GAM1240	ATP8A2	3'	GCCTCAGTGCAGAATATTCCA	93511	T C	ACA_	
			TG GAA ATTCTGCAC	GC			
			AC CTT TAAGACGTG	CG			
			_ A	ACTC			
GAM1240	CIS4	3'	TGTGCAGAATAATCACA	14880	AC		
			TGTGA ATTCTGCACA				
			ACACT TAAGACGTGT				
			AA				
GAM1240	DAZ	3'	GTAGCTGTATGAGCAGTTCCA	14551	T ATT G C		
			TG GAAC CT CA ACAGCTAC				
			AC CTTG GA GT TGTGCGATG				
			_ AC_ _ A				
GAM1240	FACL3	3'	GTAGCTTACTGTCAAAATGTTT	15499	C C C__		
	A		TGAACATT TG ACA AGCTAC				
			ACTTGTAAC AC TGT TCGATG				
			A _ CAT				
GAM1240	ICOS	3'	GTAAGTGTGTGCTTATAGTTTA	23906	ATTCT C		
	CA		TGTGAAC GCACACAG TAC				
			ACATTTG CGTGTGTC ATG				
			ATATT A				
GAM1240	NEK2	3'	TGTACAAAATGTTTCA	10198	C C		
			TGTGAACATT TG ACA				
			ACACTTGTAAC AC TGT				
			A A				
GAM1240	PKDREJ	3'	GTAGCTGTACTATTTTCAC	20279	C TCTGCAC		
			GTGAA AT ACAGCTAC				
			CACTT TA TGTGCGATG				
			T TCA__				
GAM1240	SCO1	3'	TAGCTGTGGGACTGAATTTTCAC	15948	C TGCA_		
	A		TGTGAA ATTC CACAGCTA				
			ACACTT TAAG GTGTCGAT				
			_ TCAGG				
GAM1240	TDGF1	3'	GTAGAAGACAAAATGTTTCA	12201	_____		
			TGTGAACAT TCTGC				
			ACACTTGTA AGATG				
			AAACAGA				
GAM1240	FLJ13449	5'	GTGCAGAATGTTACA	44617	A		
			TGTGA CATTCTGCAC				

ACATT GTAAGACGTG

GAM1240 FLJ21126 3' GTACAGAAATGTTCCA 90328 T C  
TG GAACATTCTG AC  
|| ||||| ||  
AC CTTGTAAGAC TG

— A  
GAM1240 FLJ22004 3' GTAGCTGTGTACATATCAC 47213 ACATTC C  
GTGA TG ACACAGCTAC  
||| || |||||  
CACT AC TGTGTCGATG  
AT\_\_\_ A

GAM1240 FLJ31547 5' GCAGCCGCCGTCAATGTTTACA 58832 \_\_\_\_\_  
TGTGAACATT CTGC  
||||| |||  
ACACTTGTA GACG  
CTGCCGCC

GAM1240 GNB4 3' TAGAACAGAATGTACACA 41272 A CACACAG  
TGTG ACATTCTG CTA  
||| ||||| |||  
ACAC TGTAAGAC GAT  
A AA\_\_\_\_\_

GAM1240 KIAA0040 3' CTGTGTACCTGTGCAATGTTTA 27786 C \_\_\_\_\_  
CA TGTGAACATT TGC ACACAG  
||||| ||| |||||  
ACATTTGTAA GTG TGTGTC  
C TCCA

GAM1240 KIAA0453 3' TAGCTACATAGTGTTC A 69053 C CACAC  
TGAACATT TG AGCTA  
||||| || |||||  
ACTTGTGA AC TCGAT  
T A\_\_\_\_\_

GAM1240 KIAA0953 3' GCTAGTGCAGAATGCCACA 66786 AA AC  
TGTG CATTCTGCAC AGC  
||| ||||| |||  
ACAC GTAAGACGTG TCG  
C\_ A\_

GAM1240 KIAA1372 5' AGCTGTGTGCTCAGCCCGCA 91647 AACATTCT  
TGTG GCACACAGCT  
||| |||||  
ACGC CGTGTGTCGA  
CCGACT\_\_

GAM1240 KIAA1710 3' AGCTGTGTGGGACCACA 62516 AACAT G  
TGTG TCT CACACAGCT  
||| ||| |||||  
ACAC AGG GTGTGTCGA  
C\_\_\_\_\_

GAM1240 KIAA1729 5' GCAAAGTGCAAAGTGTTCACA 89129 C\_ ACA  
TGTGAACATT TGCAC GC  
||||| ||| |||

			ACACTTGTGA ACGTG CG		
			AA AAA		
GAM1240	LEC3	3'	CTGTGTGCAAATCATA 30860	ACATTC	
			TGTGA TGCACACAG		
			ATACT ACGTGTGTC		
			AA____		
GAM1240	MAC30	3'	CTGTGTGCCTGAGTTCCA 62678	T A CT	
			TG GAAC TT GCACACAG		
			AC CTTG AG CGTGTGTC		
			_ _ TC		
GAM1240	MGC12538	3'	CTGGATGATGTTTACA 51245	TCTG CA	
			TGTGAACAT CA CAG		
			ACACTTGTA GT GTC		
			____ AG		
GAM1240	MGC2550	3'	GTGCAATATGTTTACA 43960	TC	
			TGTGAACAT TGCAC		
			ACACTTGTA ACGTG		
			TA		
GAM1240	MYLE	3'	AGCTGCGATGGATGTTTACA 25812	TGCACA	
			TGTGAACATTC CAGCT		
			ACATTTGTAGG GTCGA		
			TAGC__		
GAM1240	RNF8	3'	GTAGGCAATATGTTTACA 14236	TC AC	
			TGTGAACAT TGC AC		
			ACACTTGTA ACG TG		
			TA GA		
GAM1240	SYT12	5'	AGCTGTGTGGGGTGCTCCA 94722	T A TG	
			TG GA CATTG CACACAGCT		
			AC CT GTGGG GTGTGTCGA		
			_ C _		
GAM1240	TMG3	3'	GTGGCCAGAATGTCCACA 43995	A CA	
			TGTG ACATTCTG CAC		
			ACAC TGTAAGAC GTG		
			C CG		
GAM1240	LOC143286	5'	AGCTTCCCAAATGTTTACA 82943	C CACAC	
			TGTGAACATT TG AGCT		
			ACACTTGTAAC TCGA		
			_ CCT__		
GAM1240	LOC144715	5'	TAGAGAAGTGCAGAATATTAC 76929	C ACAG	
			GTGAA ATTCTGCAC CTA		

CACTT TAAGACGTG GAT  
 A AAGA  
 GAM1240 LOC146332 3' AGCTGTGCAGGGCCCCACA 77820 AACCA CA  
 TGTG TTCTGCACA GCT  
 ||| ||||| ||  
 ACAC GGGACGTGT CGA  
 CC\_\_ \_\_  
 GAM1240 LOC149372 3' GTAGCTGTGTTTGTGACCACA 79328 AA TTCTGC  
 TGTG CA ACACAGCTAC  
 ||| || |||||  
 ACAC GT TGTGTCGATG  
 CA TGTT\_\_  
 GAM1240 LOC150245 3' AGCTGTACAGTTCTCA 84931 T ATTC CAC  
 TG GAAC TG ACAGCT  
 || ||| || |||||  
 AC CTTG AC TGTCGA  
 T \_\_ A\_\_  
 GAM1240 LOC154007 3' AGCCAAGAATGTTTCA 81009 GCACACA  
 TGTGAACATTCT GCT  
 ||||| |||  
 ACACTTGTAAGA CGA  
 AC\_\_\_\_  
 GAM1240 LOC157507 5' AGCTGTGTATGTGTGCTCA 81451 A TCTGC  
 TGA CAT ACACAGCT  
 ||| || |||||  
 ACT GTG TGTGTCGA  
 C TGTA\_  
 GAM1240 LOC200420 5' GCAACAAGCAGAATGTACACA 59250 A ACACA  
 TGTG ACATTCTGC GC  
 ||| ||||| ||  
 ACAC TGTAAGACG CG  
 A AACAA  
 GAM1240 LOC221830 3' GCAGAGTGGCAGATGTTTCA 92509 T A A\_\_  
 TGTGAACAT CTGC CAC GC  
 ||||| ||| ||| ||  
 ACACTTGTA GACG GTG CG  
 \_ \_ AGA  
 GAM1240 LOC221865 3' AGCTGTGCTGCTCAC 92485 ACATTCT \_  
 GTGA GCA CACAGCT  
 ||| || |||||  
 CACT CGT GTGTCGA  
 \_ C  
 GAM1241 ALDH3B1 3' GTGCTGACCCAGACCAGCAG 91532 ACCA CT  
 CTG GTCTGGGT TGC  
 ||| ||||| |||  
 GAC CAGACCCAG GTG  
 GAC\_ TC  
 GAM1241 CDH5 3' GCAGCCCAGGCCAGTCAG 8386 CA TCT  
 CTGAC GTCTGGGT TGC  
 |||| ||||| |||

			GA	CTG	CGG	ACCCG	ACG		
			AC						
GAM1241	CLK2	3'	CAAGAACCTCTGTGTC	7096		TCT			
			GAC CAG GGGTTCTTG						
			CTG GTC TCCAAGAAC						
			T						
GAM1241	DDX6	3'	GTAGCAAGAACTGCACGGTACA	15288		A CTG		C	
			TG ACC GT GGTTCTTGC AC						
			AC TGG CA TCAAGAACG TG						
			A _ CG_ A						
GAM1241	ELMO1	3'	GCAGCCCCAGACTGCCCA	55281	AC	TTC			
			TG CAGTCTGGG TTGC						
			AC GTCAGACCC GACG						
			CC C_						
GAM1241	ETV6	3'	GGCAAGCCCAGCTGGTCAG	8799	T	TT			
			CTGACCAG CTGGG CTTGCC						
			GA	CTGGTC	GACCC	GAACGG			
GAM1241	HMOX2	5'	GCAAGAACCACACCCAGCAG	65158	ACCA	CTG			
			CTG GT GGTTCTTGC						
			GAC CA CCAAGAACG						
			GACC CA_						
GAM1241	LETM1	3'	GCATGGCCAGGCTGGCCAG	24621	A	GT T			
			CTG CCAGTCTGG TC TGC						
			GAC GGTCTGGACC GG ACG						
			C _ T						
GAM1241	MLC1	5'	GAACCCAGACTATTTCAG	57592	CC				
			CTGA AGTCTGGGTTC						
			GACT TCAGACCCAAG						
			TA						
GAM1241	NAPB	3'	TGGCAAAAATTTAGAATAGCCA	70192	ACCAG		C		
	G		CTG TCTGGGTT TTGCCA						
			GAC AGATTTAA AACGGT						
			CGATA A						
GAM1241	NINJ1	3'	TGGCACTACCCAGACTGCCAG	14734	AC	TCT			
			CTG CAGTCTGGGT TGCCA						
			GAC GTCAGACCCA ACGGT						
			C_ TC_						
GAM1241	PC	3'	GGCAGGCCCCAGGCCAGCCAG	42244	ACCA	TT			
			CTG GTCTGGG CTTGCC						

			GAC CGGACCC GGACGG			
			CGAC _			
GAM1241	PC	3'	GGCAGGCCCAGGCCAGCCAG 6223	ACCA	TT	
			CTG GTCTGGG CTTGCC			
			GAC CGGACCC GGACGG			
			CGAC _			
GAM1241	PTPRK	3'	GGCCCAGCACTGGTCA 11123	_		
			TGACCAGT CTGGGT			
			ACTGGTCA GACCCGG			
			C			
GAM1241	PXF	3'	AGCACCCAAACTGGCCAG 11148	A	C	T
			CTG CCAGT TGGGT CT			
			GAC GGTCA ACCCA GA			
			C A C			
GAM1241	RAB7	3'	GGCTCACACCCAGTCTGATCAG 16157	C	T	TCTT
			CTGA CAG CTGGGT GCC			
			GACT GTC GACCCA CGG			
			A T CACT			
GAM1241	RPE	3'	TGGCAAGAAATAAACATGAC 62188	_	GG_	
			GTC TG TTCTTGCCA			
			CAG AC AAGAACGGT			
			T AAATA			
GAM1241	S100A3	5'	GTAAACACCCGAACTGGTCA 11421	C	TC	
			TGACCAGT TGGGT TTGC			
			ACTGGTCA GCCCA AATG			
			A CA			
GAM1241	SAS	5'	GGCCGGACCCAGACTGGT 38450		TT	
			ACCAGTCTGGGTTC GCC			
			TGGTCAGACCCAGG CGG			
			C_			
GAM1241	SIRT2	5'	TGGCAGAGCCAGACCGACTCAG 47593	CCA_	G	T
			CTGA GTCTGG TTCT GCCA			
			GACT CAGACC GAGA CGGT			
			CAGC _ _			
GAM1241	SMTN	3'	GGCAAGAATGTCTAGCCTG 56156	T	_	
			CAG CTGG GTTCTTGCC			
			GTC GATC TAAGAACGG			
			C TG			
GAM1241	SOX12	3'	GCAGGCCCAGGCCAGCCAG 22698	ACCA	TT	
			CTG GTCTGGG CTTGC			

GAC CGGACCC GGACG  
 CGAC \_  
 GAM1241 TCFL4 3' CAACACCTCACACTGGTCAG 63458 C \_ TC  
 CTGACCAGT TG GGT TTG  
 ||||| || ||  
 GACTGGTCA AC CCA AAC  
 C T C\_  
 GAM1241 TEM7 3' TGACAAGAGCTGCCAGC 39896 T \_ C  
 G CTGG GTTCTTG CA  
 | ||| ||||| ||  
 C GACC CGAGAAC GT  
 \_ GT A  
 GAM1241 YWHAG 3' GTAAATCCCAGACTGACAG 25021 AC TTC  
 CTG CAGTCTGGG TTGC  
 || ||||| ||  
 GAC GTCAGACCC AATG  
 A\_ TA\_  
 GAM1241 ZIC1 3' TGGCAAGAATGTTCTAG 12726 \_  
 CTGG GTTCTTGCCA  
 ||| |||||  
 GATC TAAGAACGGT  
 TTG  
 GAM1241 A4GALT 5' GGCTGCCCAGGCTGACCAG 33840 AC TCTT  
 CTG CAGTCTGGGT GCC  
 || ||||| ||  
 GAC GTCGGACCCG CGG  
 CA T\_  
 GAM1241 ARSDR1 3' AACAAAGACTGGCTCAG 32075 \_ GG  
 CTGA CCAGTCT GTT  
 ||| ||||| ||  
 GACT GGTGAGA CAA  
 C AA  
 GAM1241 DKFZP434K1772 3' GTGGCAAGGTGACTG 67716 TGGGT  
 CAGTC TCTTGCCAC  
 |||| |||||  
 GTCAG GGAACGGTG  
 T\_  
 GAM1241 DKFZP564O0423 3' TGGCAAGGCAGACTGGGCAG 91703 A GGT  
 CTG CCAGTCTG TCTTGCCA  
 || ||||| |||||  
 GAC GGTGAGAC GGAACGGT  
 G \_  
 GAM1241 DKFZP566M114 3' GACCCAGCTGGTCAG 49542 T  
 CTGACCAG CTGGGTT  
 ||||| |||||  
 GACTGGTC GACCCAG  
 \_  
 GAM1241 FLJ10159 3' GACACCAGCTGGTCAG 35862 T \_  
 CTGACCAG CTGG GTT  
 ||||| ||| ||



GACTGGTC GACC CAG  
 \_ A  
 GAM1241 FLJ12806 3' GCAAGCCGTACCCAGACCAGT 43087 CA T\_\_  
 AC GTCTGGGT CTTGC  
 || ||||| ||||  
 TG CAGACCCA GAACG  
 AC TGCC  
 GAM1241 FLJ20345 5' GTGGCAAGAAAAACCGAC 35023 T G\_\_  
 GTC GG TTCTTGCCAC  
 ||| || |||||  
 CAG CC AAGAACGGTG  
 \_ AAA  
 GAM1241 FLJ20374 5' GTAGCTGAGGACCCAGACTCGC 35080 ACC \_ C  
 CAG CTG AGTCTGGGTTCTT GC AC  
 ||| ||||| ||| ||  
 GAC TCAGACCCAGGAG CG TG  
 CGC T A  
 GAM1241 FLJ32978 3' GCAAGAATGACTGTCAG 58231 C TGG  
 CTGAC AGTC GTTCTTGC  
 |||| ||| |||||  
 GACTG TCAG TAAGAACG  
 \_ \_  
 GAM1241 JAM1 5' AGAACCCAGCCAGTCAG 57914 CA T  
 CTGAC G CTGGGTTCT  
 |||| | |||||  
 GACTG C GACCCAAGA  
 AC \_  
 GAM1241 JAM1 5' AGAACCCAGCCAGTCAG 57941 CA T  
 CTGAC G CTGGGTTCT  
 |||| | |||||  
 GACTG C GACCCAAGA  
 AC \_  
 GAM1241 K6HF 3' AGTGCCCAGACTGCCAG 16269 AC T  
 CTG CAGTCTGGGT CT  
 ||| ||||| ||  
 GAC GTCAGACCCG GA  
 C\_ T  
 GAM1241 KIAA0553 3' GCAACATCTCCAAACTGTCA 69892 C C \_ TTC  
 TGAC AGT TGG G TTGC  
 |||| ||| ||| |||  
 ACTG TCA ACC C AACG  
 \_ A T TAC  
 GAM1241 KIAA1045 3' GCAAGGCCCCAGGCCAGCCAG 71053 ACCA TT  
 CTG GTCTGGG CTTGC  
 ||| ||||| ||||  
 GAC CGGACCC GAACG  
 CGAC CG  
 GAM1241 KIAA1277 3' GCAAGCTCCTCAGACTAGTCA 64458 C \_ TT  
 TGAC AGTCTG GG CTTGC  
 |||| ||||| || ||||

ACTG TCAGAC CC GAACG  
 A T TC  
 GAM1241 KIAA1557 5' GCAGCTCTTCCAGCTGGTCAG 61136 T TTC\_  
 CTGACCAG CTGGG TTGC  
 ||||| |||| ||||  
 GACTGGTC GACCT GACG  
 \_ TCTC  
 GAM1241 KIAA1910 5' GCAAGAACTCCACCAGCAG 73327 ACCA CT  
 CTG GT GGGTTCTTGC  
 ||| || |||||  
 GAC CA CTCAAGAACG  
 GAC\_ C\_  
 GAM1241 KIAA1952 5' GCGAAGACCCAGACGAACCAG 73172 ACCA TC  
 CTG GTCTGGGT TTGC  
 ||| ||||| ||||  
 GAC CAGACCCA AGCG  
 CAAG GA  
 GAM1241 RAI16 3' TGGCTCCGAGACTGGTCAG 42759 G TTCTT  
 CTGACCAGTCT GG GCCA  
 ||||| || ||||  
 GACTGGTCAGA CC CGGT  
 G T\_\_\_\_  
 GAM1241 SYT12 3' TGGCAAGAACCAGAGGTC 94741 AG G  
 GACC TCTGG TTCTTGCCA  
 |||| |||| |||||  
 CTGG AGACC AGAACGGT  
 \_ \_  
 GAM1241 TFIP11 3' GTGGCAGGTCCAGAACCAGTCA 24055 CAG\_ TT  
 G CTGAC TCTGGG CTTGCCAC  
 |||| |||| |||||  
 GACTG AGACCT GGACGGTG  
 ACCA \_  
 GAM1241 TOR1B 3' TGACATGGGCCAGACTGAACA 27206 AC T C  
 TG CAGTCTGGGTTC TG CA  
 || ||||| ||||| ||||  
 AC GTCAGACCCGGG AC GT  
 AA T A  
 GAM1241 LOC126122 3' GTGAGGGCCCAGGCTGGTCAG 74438 TG  
 CTGACCAGTCTGGGTTCT C  
 ||||| ||||| |||||  
 GACTGGTCGGACCCGGGA G  
 GT  
 GAM1241 LOC127795 3' GTGGCAAGAACCAGCTACTTA 74691 CC T  
 G CTGA AG CTGGGTCTTGCCAC  
 |||| || ||||| |||||  
 GATT TC GACCCAAGAACGGTG  
 CA \_  
 GAM1241 LOC129831 3' CAAGAAGTGTGATGCA 74892 AC\_ CTG  
 TG CAGT GGTCTTG  
 || |||| |||||

	AC GTCG TCAAGAAC		
	GTA ____		
GAM1241 LOC146159 5'	TGGCTCCCACACTGATCAG 77686	C C	TTCTT
	CTGA CAGT TGGG GCCA		
	GA CT GTCA ACCC CGGT		
	A C T____		
GAM1241 LOC146540 3'	GCGTTCACACAACTGGTCAG 77976	C G	TCT
	CTGACCAGT TG GT TGC		
	GA CTGGTCA AC CA GCG		
	A A CTT		
GAM1241 LOC149448 3'	CAAAATACCACAACTGGTTAG 84420	C _	TC_
	CTGACCAGT TG GGT TTG		
	GA TTGGTCA AC CCA AAC		
	A A TAA		
GAM1241 LOC150150 3'	AACCCAACTGGCCAG 84865	A C	
	CTG CCAGT TGGGTT		
	GA C GGTCA ACCCAA		
	C _		
GAM1241 LOC151512 5'	GCAAGAACGTGGTTA 85432	GTCTGG	
	TGACCA GTTCTTGC		
	ATTGGT CAAGAACG		
	G____		
GAM1241 LOC152405 5'	GCAACCTAGACCAGTCAG 80579	CA	TCT
	CTGAC GTCTGGGT TGC		
	GA CTG CAGATCCA ACG		
	AC ____		
GAM1241 LOC201102 3'	TGGCAAAAACAAGCCTGCCCA 88100	AC T GG	C
	TG CAG CT GTT TTGCCA		
	AC GTC GA CAA AACGGT		
	CC C A_ A		
GAM1241 LOC220936 3'	GTGGCAAGAAGGAGCCTGGTGC 91414	_ T	GGG
AG	CTG ACCAG CT TTCTTGCCAC		
	GA C TGGTC GA AAGAACGGTG		
	G C GG_		
GAM1241 LOC221479 3'	GACCCAGGCTGGCCAG 92223	A	
	CTG CCAGTCTGGGTT		
	GA C GGTCGGACCCAG		
	C		
GAM1241 LOC256158 5'	GTGGCCTTCAGCCCAGCTGGTC 97681	T	CTT_
AG	CTGACCAG CTGGGTT GCCAC		

GACTGGTC GACCCGA CGGTG  
 \_ CTTC  
 GAM1241 LOC51204 3' GCAGGACCACCCAGCTGGTCAG 33029 T \_  
 CTGACCAG CTGGGT TCTTGC  
 ||||| ||||| |||||  
 GACTGGTC GACCCA AGGACG  
 \_ CC  
 GAM1241 LOC90317 3' TGGCAAGAATTCTACT 62257 CT  
 AGT GGGTTCTTGCCA  
 ||| |||||  
 TCA CTTAAGAACGGT  
 T\_  
 GAM1241 LOC92017 5' GCAACAAACAACCTGGCAG 67890 A C GG C  
 CTG CCAGT TG TT TTGC  
 ||| ||||| || |||||  
 GAC GGTCA AC AA AACG  
 \_ \_ A\_ C  
 GAM1242 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
 GTA GGAT GGGTTGTTT  
 ||| ||||| |||||  
 CGT CCTA CCCAACAAA  
 C CGTG\_  
 GAM1242 LCT 3' AACCGTAAAAATCCTT 9697 G  
 AAGGATTTTTA GGTT  
 ||||| |||||  
 TTCCTAAAAAT CCAA  
 G  
 GAM1242 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
 GTAAGGATTTTtagGGTTGTTT  
 ||||| ||||| |||||  
 CATTCTAAAAATCCCAACAAA  
  
 GAM1242 FBXO30 3' AACTAAAAAAATCCTGAC 49573 A AG  
 GT AGGATTTT GGTT  
 || ||||| |||||  
 CA TCCTAAAAA TCAA  
 G AA  
 GAM1242 KIAA0494 3' AACAACCCTTACTTAC 28736 GATTTT  
 GTAAG AGGGTTGTT  
 ||||| |||||  
 CATTCTCCCAACAA  
 AT\_\_\_\_  
 GAM1242 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
 TAAG TTTT GGGTTGTTT  
 ||||| ||||| |||||  
 GTTC AAAA CCCAACAAA  
 \_ C  
 GAM1242 SMT3H2 3' AACAACATAAAAAATCCTTGC 22670 GG  
 GTAAGGATTTTTA GTTGTT  
 ||||| ||||| |||||

	CGTTCCTAAAAAT CAACAA		
	A_		
GAM1242 LOC120103 3'	AACCTATGAAAAATCCTTGC	74002	A__
	GTAAGGATTTTT GGGTT		
	CGTTCCTAAAAA TCCAA		
	GTA		
GAM1242 LOC129831 3'	AAACAACCCCAATGTCC	74889	TT A
	GGAT TT GGGTTGTTT		
	CCTG AA CCCAACAAA		
	T_ C		
GAM1242 LOC133088 5'	AAACAAAATAGAAAAATCCCTG	75075	A AGGG_
C	GTA GGATTTTT TTGTTT		
	CGT CCTAAAAA AACAAA		
	C GATAA		
GAM1242 LOC148089 3'	GGCCCTAAAAATTCCTAC	78637	A
	GTA GGATTTTTTAGGGTT		
	CAT CTAAAAATCCCGG		
	C		
GAM1242 LOC154547 3'	AACAACATAAAAAATCCTTGC	76050	GG
	GTAAGGATTTTTTA GTTGTT		
	CGTTCCTAAAAAT CAACAA		
	A_		
GAM1242 LOC158104 3'	ACAGCCAAAAATCCTTA	60313	AG
	TAAGGATTTTT GGTGT		
	ATTCCTAAAAA CCGACA		
	—		
GAM1242 LOC205880 5'	AAACAACCATCATCCTGAC	90709	A TTTAG
	GT AGGAT GGTGTTT		
	CA TCCTA CCAACAAA		
	G CTA__		
GAM1242 LOC221561 3'	AACAACATAAAAAATCCTTGC	92130	GG
	GTAAGGATTTTTTA GTTGTT		
	CGTTCCTAAAAAT CAACAA		
	A_		
GAM1242 LOC257591 3'	AACAACATAAAAAATCCTTGC	97840	GG
	GTAAGGATTTTTTA GTTGTT		
	CGTTCCTAAAAAT CAACAA		
	A_		
GAM1242 LOC51145 3'	AGCTAAAATCCTTAC	32393	TAG
	GTAAGGATTTT GTT		

CATTCCTAAAA TCGA

GAM1243 AOC3 3' GTTTCAGGACAGCTGCTT 13587 CA  
AAGCAGC TCTTGAAAC  
||||| |||||||  
TTCGTCG AGGACTTTG  
AC  
GAM1243 APOB48R 3' GAGACCACCTCTCAGGGTGCCT 37960 C AACAA\_\_  
AG CATCTTGA GTCTC  
|| ||||||| |||||  
TC GTGGGACT CAGAG  
C CTCCAC  
GAM1243 ATRN 3' ACTGTTCTTGGGACTGT 57792 CCA TG\_  
GCAG TCT A AACAGT  
||| ||| | |||||  
TGTC AGG T TTGTCA  
\_\_\_ GT C  
GAM1243 CACNB2 3' ACTGTTTTGGGTAGCTGC 5577 CAT TG  
GCAGC CT AAACAGT  
||||| || |||||||  
CGTCG GG TTTGTCA  
AT\_ GT  
GAM1243 CBFB 3' TGTTTAAGATAGCTGCTT 43145 C A  
AAGCAGC ATCTTGAA CA  
||||| ||||||| ||  
TTCGTCG TAGAATTT GT  
A \_  
GAM1243 CBFB 3' TGTTTAAGATAGCTGCTT 8278 C A  
AAGCAGC ATCTTGAA CA  
||||| ||||||| ||  
TTCGTCG TAGAATTT GT  
A \_  
GAM1243 CNTN3 3' TTTCAAGATGATTGCT 66699 GC  
AGCA CATCTTGAAA  
||| |||||||  
TCGT GTAGAACTTT  
TA  
GAM1243 EGFL4 3' GAGATGACCAAGATGGCCAGC 61810 A\_ AAACA  
GC GCCATCTTG GTCTC  
|| ||||||| |||||  
CG CGGTAGAAC TAGAG  
AC CAG\_\_  
GAM1243 FZD2 3' ACCATTTCACTTTTAGGTTGCT 7595 ATCT\_\_ CA  
T AAGCAGCC TGAAA GT  
||||| ||||| ||  
TTCGTTGG ACTTT CA  
ATTTTC AC  
GAM1243 GTF2H1 3' AGACTGTTTACTGCAGTTGCT 18004 CATCTTG  
AGCAGC AAACAGTCT  
||||| |||||||

			TCGTTG	TTTGT	CAGA		
			ACGTCA_				
GAM1243	ICMT	3'	ACTGTTTCCGGTTGGCCGCT	24806	A	T	T
			AGC GCCA CT GAAACAGT				
			TCG CGGT GG CTTTGTCA				
			C T C				
GAM1243	ITGB7	3'	GAGTGACACCCAAGAGGGCTGC	6088	A	AAA_	G
	TT		AAGCAGCC TCTTG CA TC				
			TTCGTCGG AGAAC GT AG				
			G CCACA G				
GAM1243	KCNQ1	3'	AGACTGTGGAGACTGCT	4020	CCA	GAA	
			AGCAG TCTT ACAGTCT				
			TCGTC AGAG TGTCAGA				
			_ G_				
GAM1243	KIF3C	3'	TTTCAAGAGGCTGCT	9611	A		
			AGCAGCC TCTTGAAA				
			TCGTCGG AGAACTTT				
			-				
GAM1243	MBTPS1	5'	AGACTGTAAGATGGCTG	13701	GAA		
			CAGCCATCTT ACAGTCT				
			GTCGGTAGAA TGTCAGA				
			-				
GAM1243	MELK	3'	AGACTGTTATGATCGCT	28892	C	TTGA	
			AGC ATC AACAGTCT				
			TCG TAG TTGTCAGA				
			C TA_				
GAM1243	MMP2	3'	GAGACTGTCTCAAGAGGGC	15767	A	A	
			GCC TCTTGA ACAGTCTC				
			CGG AGAACT TGTCAGAG				
			G C				
GAM1243	PCLO	3'	GCCATTTCAAGACAGTGCTT	94227	G CA	CA	
			AAGCA C TCTTGAAA GT				
			TTCGT G AGAACTTT CG				
			_ AC AC				
GAM1243	PRX	3'	AGATCCTAGATGGCTGC	40515	TGAAACA		
			GCAGCCATCT GTCT				
			CGTCGGTAGA TAGA				
			TCC_				
GAM1243	SCN8A	5'	GAGCGCTCCAAGATGGCGC	26384	A	AAAC _	
			GC GCCATCTTG AGT CTC				

CG CGGTAGAAC TCG GAG  
 \_ C\_ C  
 GAM1243 SIRT1 3' AGACTGTTTTTCAGCTCTT 24264 C CATCTT  
 AAG AGC GAAACAGTCT  
 ||| ||| |||||  
 TTC TCG TTTTGTGAGA  
 \_ AC\_

GAM1243 C11orf16 3' ACTGCTTTAAGATGCCT 40214 C A  
 AG CATCTTGAA CAGT  
 || ||||| |||  
 TC GTAGAATTT GTCA  
 C C

GAM1243 C20orf36 3' GAGACTGTTTGATG 36798 TTG  
 CATC AAACAGTCTC  
 ||| |||||  
 GTAG TTTGTGAGAG

GAM1243 CSMD1 5' GAGGAGTCAAGATGCTGC 73121 C AACAG  
 GCAGC ATCTTGA TCTC  
 |||| ||||| |||  
 CGTCG TAGAACT GGAG  
 \_ GA\_

GAM1243 CXYorf1 3' GAGACTGTCAGAGCATGGCTAG 82048 \_ \_ GAA  
 CT AGC AGCCAT CTT ACAGTCTC  
 ||| ||||| ||| |||||  
 TCG TCGGTA GAG TGTCAGAG  
 A C AC\_

GAM1243 DDM36 3' CTGAATTAATGGCTGTTT 40570 C AA  
 AAGCAGCCAT TTGA CAG  
 ||||| ||| |||  
 TTTGTCGGTA AATT GTC  
 \_ AA

GAM1243 DKFZp547I014 5' GTCCCAAGATGGTTGC 39547 AA  
 GCAGCCATCTTG AC  
 ||||| |||  
 CGTTGGTAGAAC TG  
 CC

GAM1243 DKFZP564A1164 3' AGATATTTCAAGATG 70976 CA  
 CATCTTGAAA GTCT  
 ||||| |||  
 GTAGAACTTT TAGA  
 A\_

GAM1243 EVI5 3' ACTGTTTCATGACCAGCT 18987 CA\_ T  
 AGC TC TGAACAGT  
 ||| || |||||  
 TCG AG ACTTTGTCA  
 ACC T

GAM1243 FLJ10759 3' GTTCTTAAAATGGCTGC 36577 C \_  
 GCAGCCAT TTGA AAC  
 ||||| ||| |||



			CGTCGGTA AATT TTG		
			A C		
GAM1243	FLJ11175	3'	AGACTAATAAGGCTGCTT 37133	ATC	AAAC
			AAGCAGCC TTG AGTCT		
			TTCGTCCG AAT TCAGA		
			___ AA__		
GAM1243	FLJ22625	5'	GACTCCAAGATGGCGC 45257	A	AAAC
			GC GCCATCTTG AGTC		
			CG CGGTAGAAC TCAG		
			_ C__		
GAM1243	FLJ31762	3'	AGACTGTTTCAAAGAAGAGCT 58137	CA_ _	
			AGC TCTT GAAACAGTCT		
			TCG AGAA CTTTGTGTCAGA		
			AGA A		
GAM1243	FOXO3A	3'	AGACTGTTAATGGCCCCTT 7576	CA	CTTGA
			AAG GCCAT AACAGTCT		
			TTC CGGTA TTGTCAGA		
			CC A__		
GAM1243	KIAA0186	3'	GAGACTGTCTCACTATGTTGC 40752	C CT	A
			GCAGC AT TGA ACAGTCTC		
			CGTTG TA ACT TGTCAGAG		
			_ TC C		
GAM1243	KIAA0350	3'	AGAAGGCAAGTGGCTGC 61166	T	AAACAG
			GCAGCCA CTTG TCT		
			CGTCGGT GAAC AGA		
			_ GGA__		
GAM1243	KIAA0478	3'	ACTGACCAGAAGATGGTGCT 29539	G	GAAA_
			AGCA CCATCTT CAGT		
			TCGT GGTAGAA GTCA		
			_ GACCA		
GAM1243	KIAA0537	3'	ACTCAGTTCAAGATGGC 29241	AC_	
			GCCATCTTGAA AGT		
			CGGTAGAACTT TCA		
			GAC		
GAM1243	KIAA0555	3'	TTTCAAATGGCTGCTT 28891	C	
			AAGCAGCCAT TTGAAA		
			TTCGTCCGGTA AACTTT		
			-		
GAM1243	KIAA0663	5'	GTTTCAAGAAGCCACTT 29129	CA	CA
			AAG GC TCTTGAAAC		

TTC CG AGAACTTTG  
 AC A\_  
 GAM1243 KIAA1041 3' ACTGTTTTAATTGCTT 30124 CCATC  
 AAGCAG TTGAAACAGT  
 ||||| |||||  
 TTCGTT AATTTTGTCA  
  
 GAM1243 KIAA1157 3' AGACTATGCTTCAAGATG 72236 A \_  
 CATCTTGAA CA GTCT  
 ||||| || |||  
 GTAGAACTT GT CAGA  
 C AT  
 GAM1243 KREMEN2 5' GAGACTGTCAGAGGACAACGC 44454 AGCCA GAA  
 GC TCTT ACAGTCTC  
 || ||| |||||  
 CG GGAG TGTCAGAG  
 CAACA AC\_  
 GAM1243 MRP64 5' AGGCCCAAGATGGCTGT 33240 AAACA  
 GCAGCCATCTTG GTCT  
 ||||| |||  
 TGTCGGTAGAAC CGGA  
 C\_  
 GAM1243 p25 3' AGACTGTTACGCCAGAGTGCT 22844 GCCA \_ A  
 T AAGCA TCT TGAA CAGTCT  
 |||| ||| ||| |||||  
 TTCGT AGA ACTT GTCAGA  
 G\_ CCGC \_  
 GAM1243 PIGPC1 3' ACTGTTTCTCCAGGCGACTT 42093 CA ATCTT  
 AAG GCC GAAACAGT  
 ||| ||| |||||  
 TTC CGG CTTTGTCA  
 AG ACCT\_  
 GAM1243 PLEKHA3 3' CTGTCAAGATGACTGCT 38860 C AA  
 AGCAG CATCTTGA CAG  
 |||| ||||| |||  
 TCGTC GTAGAACT GTC  
 A \_  
 GAM1243 RAB34 3' GAGACTGTTCAAGAGACTGC 49194 CCA GA  
 GCAG TCTT AACAGTCTC  
 |||| ||| |||||  
 CGTC AGAG TTGTCAGAG  
 \_ AC  
 GAM1243 RAB40C 3' GAGACTGTCCACACAGCTGC 40980 CATCT AA  
 GCAGC TG ACAGTCTC  
 |||| || |||||  
 CGTCG AC TGTCAGAG  
 ACAC\_ C\_  
 GAM1243 TRIM26 3' AGACTGTTCCAACGGCT 12885 ATC A  
 AGCC TTG AACAGTCT  
 |||| ||| |||||

TCGG AAC TTGTCAGA  
C\_\_ C

GAM1243 UST 3' AGACTGCTTGGCCAGCTT 19133 A\_ TCTTGAAA  
AAGC GCCA CAGTCT  
||||| |||||  
TTCG CGGT GTCAGA  
AC TC\_\_\_\_\_

GAM1243 WASPIP 5' AGACTGTTCAACGCATAACTGC 12625 CCATC\_\_ A  
GCAG TTGAA CAGTCT  
||||| ||||| |||||  
CGTC AACTT GTCAGA  
AATACGC \_

GAM1243 LOC124145 3' ACTGCTCTCAAGATGGTGC 74251 G AA\_  
GCA CCATCTTGA CAGT  
||| ||||| |||||  
CGT GGTAAGAACT GTCA  
\_ CTC

GAM1243 LOC137991 5' GACCTCCCCAAGATGGCCGC 75290 A AAACA  
GC GCCATCTTG GTC  
|| ||||| |||||  
CG CGGTAGAAC CAG  
C CCCTC

GAM1243 LOC144742 5' ACTGTCAGATAATAGCTGTTT 76939 C\_\_ TGAA  
AAGCAGC ATCT ACAGT  
||||| ||||| |||||  
TTTGTCTG TAGA TGTCA  
ATAA C\_\_

GAM1243 LOC145899 5' AGACTGTTTCAGTTGC 83566 CATCT  
GCAGC TGAAACAGTCT  
||||| ||||| |||||  
CGTTG ACTTTGTCAGA

GAM1243 LOC146136 5' AGACTGTTCTATAGCTGC 72939 CATCTT A  
GCAGC GAA CAGTCT  
||||| ||||| |||||  
CGTCG CTT GTCAGA  
ATAT\_\_ \_

GAM1243 LOC158471 3' GATTCTCAAGATGAATGCT 57182 GC AAC  
AGCA CATCTTGA AGTC  
||||| ||||| |||||  
TCGT GTAGAACT TTAG  
AA C\_\_

GAM1243 LOC199777 3' GAGACTGCACAGTGTGGCTGCT 59246 C AAA  
T AAGCAGCCAT TTG CAGTCTC  
||||||| ||||| |||||  
TTCGTCTGGTG GAC GTCAGAG  
T AC\_

GAM1243 LOC200014 5' GAGAGTACAAAGTGGCTGC 88528 TC AA AG  
GCAGCCA TTG AC TCTC  
||||||| ||||| |||||

CGTCGGT AAC TG AGAG  
 GA A\_ \_  
 GAM1243 LOC200093 3' GAGACTGTCAGAGCATGGCTAG 63095 \_ \_ GAA  
 CT AGC AGCCAT CTT ACAGTCTC  
 ||| ||||| ||| |||||  
 TCG TCGGTA GAG TGTCAGAG  
 A C AC\_  
 GAM1243 LOC204285 3' AGACATTTCAAGATAGATGCTT 89453 GCC CA  
 AAGCA ATCTTGAAA GTCT  
 |||| ||||| ||||  
 TTCGT TAGAACTTT CAGA  
 AGA A\_  
 GAM1243 LOC219686 5' TTCAAGATGGCCGCTT 90844 A  
 AAGC GCCATCTTGAA  
 |||| |||||  
 TTCG CGGTAGAACTT  
 C  
 GAM1243 LOC220565 3' AGACTGTTCTATAGCTGC 90742 CATCTT A  
 GCAGC GAA CAGTCT  
 |||| ||| |||||  
 CGTCG CTT GTCAGA  
 ATAT\_ \_  
 GAM1243 LOC220567 3' GAGACCACCTCTCAGGGTGCCT 90738 C AACA\_  
 AG CATCTTGA GTCTC  
 || ||||| ||||  
 TC GTGGGACT CAGAG  
 C CTCCAC  
 GAM1243 LOC221964 3' GAGACTGTCTCACTCTGT 93980 CCATCT A  
 GCAG TGA ACAGTCTC  
 |||| ||| |||||  
 TGTC ACT TGTCAGAG  
 TC\_ \_ C  
 GAM1243 LOC221975 3' TGGTCCAAGATGGCTCTT 92610 C AAA  
 AAG AGCCATCTTG CA  
 ||| ||||| ||  
 TTC TCGGTAGAAC GT  
 \_ CTG  
 GAM1243 LOC253019 5' GTTTCAAGAAGCCACTT 95367 CA CA  
 AAG GC TCTTGAAAC  
 ||| || |||||  
 TTC CG AGAACTTTG  
 AC A\_  
 GAM1243 LOC253975 5' GTTTCAAGAAGCCACTT 95997 CA CA  
 AAG GC TCTTGAAAC  
 ||| || |||||  
 TTC CG AGAACTTTG  
 AC A\_  
 GAM1243 LOC255714 5' TTCAGAGATGGCTACTT 96455 C \_  
 AAG AGCCATCT TGAA  
 ||| ||||| ||||

TTC TCGGTAGA ACTT  
 A G  
 GAM1243 LOC257494 3' AGACTGTTCCAACGGCT 97789 ATC A  
 AGCC TTG AACAGTCT  
 |||| ||| |||||  
 TCGG AAC TTGTCAGA  
 C\_ C  
 GAM1243 LOC91040 3' GAGACTGTCAGAGCATGGCTAG 64719 \_ \_ GAA  
 CT AGC AGCCAT CTT ACAGTCTC  
 ||| ||||| ||| |||||  
 TCG TCGGTA GAG TGTCAGAG  
 A C AC\_  
 GAM1243 LOC92017 5' GAGACTGTCTCAGGAGTGC 67889 CA A  
 GC TCTTGA ACAGTCTC  
 || ||||| |||||  
 CG AGGACT TGTCAGAG  
 TG C  
 GAM1244 ARHGEF6 3' CAAACTTGAAGCCAGGC 68197 ACCA  
 GCCTGG CAAGTTTG  
 ||||| |||||  
 CGGACC GTTCAAAC  
 GAA\_  
 GAM1244 CNTN2 3' GTCACAACCCAGGTGA 17411 ACCACAA \_  
 TCGCCTGG GTT TGAC  
 ||||| ||| ||||  
 AGTGGACC CAA ACTG  
 \_ C  
 GAM1244 CORO2A 3' AAAGTGTGGTCCAGAGA 12642 GC A  
 TC CTGGACCACA GTTT  
 || ||||| |||||  
 AG GACCTGGTGT CAAA  
 A\_ \_  
 GAM1244 CORO2A 3' AAAGTGTGGTCCAGAGA 53398 GC A  
 TC CTGGACCACA GTTT  
 || ||||| |||||  
 AG GACCTGGTGT CAAA  
 A\_ \_  
 GAM1244 GRLF1 3' AGGTCAGAAAGTGGCCCAGG 78551 A AAG  
 CCTGG CCAC TTTGACCT  
 ||||| ||| |||||  
 GGACC GGTG AGACTGGA  
 C AA\_  
 GAM1244 LAPTM5 3' AGGCTTGTGGTCAAGC 22199 CTG  
 GC GACCACAAGTTT  
 || ||||| |||||  
 CG CTGGTGTTTCGGA  
 AA\_  
 GAM1244 POU2AF1 3' AGATTTACAGTCCAGGC 20647 CAC  
 GCCTGGAC AAGTTT  
 ||||| |||||

		CGGACCTG TTTAGA	
		ACA	
GAM1244 PTGS1	3'	GTCTCCTGTCTTATGGTCCAG 6355	C TTT__
		CTGGACCA AAG GAC	
		GACCTGGT TTC CTG	
		A TGTCT	
GAM1244 PTGS1	3'	GTCTCCTGTCTTATGGTCCAG 54574	C TTT__
		CTGGACCA AAG GAC	
		GACCTGGT TTC CTG	
		A TGTCT	
GAM1244 TRIM34	5'	AGGTCAAGTTGAGCCCAG 55224	ACCA G
		CTGG CAA TTTGACCT	
		GACC GTT GAACTGGA	
		CGA_ _	
GAM1244 TRIM9	5'	AGGCCAGGCAAGTCCAGGC 30749	CACAA A
		GCCTGGAC GTTTG CCT	
		CGGACCTG CGGAC GGA	
		AA__ C	
GAM1244 ABLIM	5'	GATATGTAACCCAGGCGG 22030	ACC A
		TCGCCTGG ACA GTT	
		GGCGGACC TGT TAG	
		CAA A	
GAM1244 AMOT	3'	AGGCATCTTCATGGTCCAGGGA 55716	G C_ TT A
		TC CCTGGACCA AAG TG CCT	
		AG GGACCTGGT TTC AC GGA	
		_ AC T_ _	
GAM1244 DKFZp434D177	5'	TTAGACCCAGGCGA 50056	ACCACAA
		TCGCCTGG GTTTGA	
		AGCGGACC CAGATT	
GAM1244 DKFZp434D177	5'	TTAGACCCAGGCGA 79443	ACCACAA
		TCGCCTGG GTTTGA	
		AGCGGACC CAGATT	
GAM1244 FLJ23420	3'	CAAGTGGGTCCAGGC 46845	A AG
		GCCTGGACC CA TTTG	
		CGGACCTGG GT GAAC	
GAM1244 HSA249128	5'	GGCGCGGTCCAGGCGG 34152	ACAA
		TCGCCTGGACC GTT	

GGCGGACCTGG CGG  
 CG\_\_  
 GAM1244 MGC15668 5' AGACCCGGTGGTCCAGACG 51277 C AA\_  
 CG CTGGACCAC GTTT  
 || ||||| |||  
 GC GACCTGGTG CAGA  
 A GCC  
 GAM1244 MGC22014 3' AGGTCCCGAGTGTAACCCAGGT 64486 ACC AGTTT  
 GA TCGCCTGG ACA GACCT  
 ||||| || ||||  
 AGTGGACC TGT CTGGA  
 CAA GAGCC  
 GAM1244 SDCCAG10 5' AGAGTTGTGGTCCAAAGA 19641 GCC G  
 TC TGGACCACAA TTT  
 || ||||| |||  
 AG ACCTGGTGTT AGA  
 AA\_ G  
 GAM1244 LOC115442 3' AGGTCAGGGATGGTCCAG 72676 CAAG  
 CTGGACCA TTTGACCT  
 ||||| |||||  
 GACCTGGT GGA CTGGA  
 AG\_\_  
 GAM1244 LOC129011 5' AGACCTGCGGTCCAGGC 74862 A A  
 GCCTGGACC CA GTTT  
 ||||| || |||  
 CGGACCTGG GT CAGA  
 C C  
 GAM1244 LOC130536 5' GCAAAGTCCAGGCG 75746 CACAAG A  
 CGCCTGGAC TTTG C  
 ||||| ||| |  
 GCGGACCTG AAAC G  
 \_\_\_\_\_ C  
 GAM1244 LOC149108 3' AGACTTCACTGTGGTCCA 84357 \_\_\_\_\_  
 TGGACCACA AGTTT  
 ||||| ||||  
 ACCTGGTGT TCAGA  
 CACT  
 GAM1244 LOC221688 5' AGACTCGGGCCAGACGA 93674 C A ACA  
 TCG CTGG CC AGTTT  
 || ||| || ||||  
 AGC GACC GG TCAGA  
 A C GC\_  
 GAM1244 LOC256228 5' AGACTTGTGGTCAAAGC 96233 CTG  
 GC GACCACAAGTTT  
 || ||||| ||||  
 CG CTGGTGTT CAGA  
 AAA  
 GAM1244 LOC257441 5' TTAGACCCAGGCGA 95566 ACCACAA  
 TCGCCTGG GTTTGA  
 ||||| ||||

AGCGGACC CAGATT

GAM1244 LOC91960 3' AGGTGCCTCTCGTGGTCCAAGC 67657 C A TTTG  
GC TGGACCAC AG ACCT  
|| ||||| || ||||  
CG ACCTGGTG TC TGGA  
A C TCCG

GAM1244 LOC92840 3' GTCCCTCGGGTCCAGGC 56435 ACA TTT  
GCCTGGACC AG GAC  
||||||| || |||  
CGGACCTGG TC CTG  
GC\_ C\_\_

GAM1245 ACTC 3' TCTCTCCATCTACCTTCCA 60187 AAAAA GA  
TGGAAGGTA GTGG GGA  
||||||| |||| |||  
ACCTTCCAT TACC TCT  
C\_\_ TC

GAM1245 ADAM19 3' TCCTCCCACCCTCCTCCA 52713 A TAAAAA  
TGGA GG GTGGGAGGA  
||| || |||||  
ACCT CC CACCCTCCT  
\_ TCC\_\_

GAM1245 AP1B1 3' CACTTTTTTCCCCTCCA 6667 A T  
TGGA GG AAAAAAGTG  
||| || |||||  
ACCT CC TTTTTTCAC  
C C

GAM1245 AQP6 3' CCCAGCTTCTTACCCACCCA 7944 AA\_ AA G A  
TGG GGTAA AAGT GG GG  
|| |||| |||| |||  
ACC CCATT TTCG CC CC  
CAC C\_ A \_

GAM1245 AQP6 3' CCCAGCTTCTTACCCACCCA 53917 AA\_ AA G A  
TGG GGTAA AAGT GG GG  
|| |||| |||| |||  
ACC CCATT TTCG CC CC  
CAC C\_ A \_

GAM1245 AR 5' CTCCCCCACCCTGCCTTCC 3491 AAAAA A  
GGAAGGTA GTGGG GGAG  
|||||| |||| ||||  
CCTTCCGT CACCC CTC  
CC\_\_ C

GAM1245 ASNS 5' CTCCTCCCCTCTCACCCGCCA 55940 AA\_ AAAAA T  
TGG GGT AG GGGAGGAG  
|| || || |||||  
ACC CCA TC CCCTCCTC  
GCC CTC\_\_ \_

GAM1245 B4GALT1 3' CTCCCCCACCCTTCTTTCA 7668 TAAAAA A  
TGGAAGG GTGGG GGAG  
|||||| |||| ||||



			ACTTTCT	CACCC CCTC	
			TCCCC_	C	
GAM1245	BAZ2A	3'	CTTTTCCCACCTCCCACCCCC	25601	AA AAAAAA
	A		TGG GGT	GTGGGAGGAG	
			ACC CCA	CACCCTTTTC	
			CC CCCTC_		
GAM1245	BIG1	5'	TCCTCCTCCTCCCCTCCA	21206	A TAAAAA TG
			TGGA GG	AG GGAGGA	
			ACCT CC	TC CCTCCT	
			C C_	CT	
GAM1245	BLMH	3'	CTCCAGCTCTTTCCTCCTTCCA	4610	TA_ A G
			TGGAAGG	AAA AGT GGAG	
			ACCTTCC	TTT TCG CCTC	
			TCC C A		
GAM1245	BSG	3'	CCTCCCACCCACCGCCA	8182	AA AAAAAA
			TGG GGT	GTGGGAGG	
			ACC CCA	CACCCTCC	
			G_ CC_		
GAM1245	BSG	3'	CCTCCCACCCACCGCCA	67797	AA AAAAAA
			TGG GGT	GTGGGAGG	
			ACC CCA	CACCCTCC	
			G_ CC_		
GAM1245	CASP2	3'	CTCCCTTCTTTACCTTC	6897	AAAGT
			GAAGGTAAA	GGGAG	
			CTTCCATTT	CCCTC	
			CTT_		
GAM1245	CASP2	3'	CTCCCTTCTTTACCTTC	52139	AAAGT
			GAAGGTAAA	GGGAG	
			CTTCCATTT	CCCTC	
			CTT_		
GAM1245	CASP2	3'	CTCCCTTCTTTACCTTC	52152	AAAGT
			GAAGGTAAA	GGGAG	
			CTTCCATTT	CCCTC	
			CTT_		
GAM1245	CASP2	3'	CTCCCTTCTTTACCTTC	52167	AAAGT
			GAAGGTAAA	GGGAG	
			CTTCCATTT	CCCTC	
			CTT_		
GAM1245	CASQ1	5'	CCTCCCACCTTGAGCCCC	6930	AA AAAA
			GG GGT	AAGTGGGAGG	

CC CCG TTCACCCTCC  
 \_ AG\_  
 GAM1245 CAV1 5' CCTCCAGCGCCTTTTTTCCCC 8259 AA T TG\_  
 CCA TGG GG AAAAAAG GGAGG  
 ||| || ||||| ||||  
 ACC CC TTTTTTC CCTCC  
 CC T CGCGA  
 GAM1245 CELSR3 3' CTCCCCCTATTCCACCCCA 7398 AA AA A T  
 TGG GGT AA AG GGGAG  
 ||| ||| || |||||  
 ACC CCA TT TC CCCTC  
 C\_ CC A C  
 GAM1245 CHC1 3' CTCCCCTTTTCCCTACCTTCCA 7022 A\_ T  
 TGGAAGGTA AAAAG GGGAG  
 ||||| |||| |||||  
 ACCTTCCAT TTTTC CCCTC  
 CCC \_  
 GAM1245 CHRNB2 5' CTCCTCCCCCTCACCGTCC 5625 A AAAAA T  
 GGA GGT AG GGGAGGAG  
 ||| ||| || |||||  
 CCT CCA TC CCCTCCTC  
 G C\_ C  
 GAM1245 CHRNB2 3' CTCCATGCTCTTTCACCCTGCC 5624 AA\_ A A \_  
 A TGG GGT AAA AGTG GGAG  
 ||| ||| ||| ||| |||  
 ACC CCA TTT TCGT CCTC  
 GTC C C A  
 GAM1245 CLCN1 3' CCTCCCACGACCTCC 3591 A AAAAAA  
 GGA GGT GTGGGAGG  
 ||| ||| |||||  
 CCT CCA CACCCTCC  
 \_ G\_  
 GAM1245 CTNS 3' CTCCTACCTCCACCTTCT 17041 AAAAAA  
 GGAAGGT GTGGGAG  
 ||||| |||||  
 TCTTCCA CATCCTC  
 CCTC\_  
 GAM1245 CTNS 3' CCTCTCTCCTACCTCCA 17039 A AAAAAAGT  
 TGGA GGTA GGGAGG  
 ||| ||| |||||  
 ACCT CCAT CTCTCC  
 \_ CCT\_  
 GAM1245 CYLN2 3' CCTCTCCTCACCTCCA 12631 A AAAAA T  
 TGG AGGT AG GGGAGG  
 ||| ||| || |||||  
 ACC TCCA TC CTCTCC  
 C C\_ \_  
 GAM1245 CYP8B1 3' TCCTCCTCTTTACCTTC 15274 AAA T  
 GAAGGT AAAG GGGAGGA  
 ||||| ||| |||||

			CTTCCA TTTC TCCTCCT		
			C_ _		
GAM1245 DACH	5'	TCCTCCTTTTACCTTC	54973	A	AAGT
		GAAGGT AAA GGGAGGA			
		CTTCCA TTT TCCTCCT			
		C _			
GAM1245 DDX3	3'	CCTCCCGCCTACCCCA	7222	AA	AAAAA
		TGG GGTA GTGGGAGG			
		ACC CCAT CGCCCTCC			
		C_ C_			
GAM1245 DFFB	3'	TCCTTCCTCAGCCTCCA	87399	A	AAAAAAGT
		TGG AGGT GGGAGGA			
		ACC TCCG CCTTCCT			
		C ACT_			
GAM1245 DIA1	3'	CTCCTTCCCTCACCCCA	23644	AA	AAAAA T
		TGG GGT AG GGGAGGAG			
		ACC CCA TC CCTTCCTC			
		C_ C_ _			
GAM1245 DPYSL2	3'	CCCATTATCTTTTACCTCCA	7293	A	A _
		TGG AGGT AAAA AGTGGG			
		ACC TCCA TTTT TTACCC			
		C C CTA			
GAM1245 DRD2	3'	CTCCTGTTTCCCTTCCCTTCCA	5844	TAAAA_	TG
		TGGAAGG AAG GGAG			
		ACCTTCC TTT CCTC			
		CTTCCC GT			
GAM1245 EGLN2	3'	TCCTCTCACTCCTCCA	53855	A	TAAAAA
		TGGA GG AGTGGGAGGA			
		ACCT CC TCACTCTCCT			
		_ _			
GAM1245 EGLN2	3'	TCCTCTCACTCCTCCA	34104	A	TAAAAA
		TGGA GG AGTGGGAGGA			
		ACCT CC TCACTCTCCT			
		_ _			
GAM1245 EGLN2	3'	TCCTCTCACTCCTCCA	54932	A	TAAAAA
		TGGA GG AGTGGGAGGA			
		ACCT CC TCACTCTCCT			
		_ _			
GAM1245 EGR3	3'	CCCACTTTTCCCCTCCA	59552	A	TAA
		TGGA GG AAAAGTGGG			

			ACCT CC TTTTCACCC		
			C C__		
GAM1245	EIF2C1	3'	TTCCTCCTACCTCCC	24183	A AAAAAAGT
			GG AGGT GGGAGGAG		
			CC TCCA TCCTCCTT		
			C _____		
GAM1245	EPHB2	3'	TCCTCCCACCTGCCACCA	15448	AA AAAAA
			TGG GGTA GTGGGAGGA		
			ACC CCGT CACCCTCCT		
			A_ C__		
GAM1245	ESRRG	3'	CTCCTTTTCTTCTTTACCTCC	66391	A _ A T
	C		GG AGGT AAA AAG GGGAGGAG		
			CC TCCA TTT TTC TTTTCCTC		
			C C C _		
GAM1245	F8	3'	CCCCTTCTTGCCCTCCA	3726	A AA T
			TGGA GGTA AAG GGG		
			ACCT CCGTT TTC CCC		
			C C_ _		
GAM1245	F8	3'	CCCCTTCTTGCCCTCCA	3727	A AA T
			TGGA GGTA AAG GGG		
			ACCT CCGTT TTC CCC		
			C C_ _		
GAM1245	F9	3'	TCTCCCTTTTACCCTCCA	3740	A AAGT
			TGGA GGTA AAA GGGAGG		
			ACCT CCATTTT CCCTCT		
			C _____		
GAM1245	FBXL11	3'	CCTCTCTCTTTTGCCCTCCA	24570	A AA T
			TGG AGGTAAA AG GGGAGG		
			ACC TCCGTTT TC CTCTCC		
			C _ T		
GAM1245	FGFR3	3'	CTCCAGGCTTTCCCACTTCC	3769	GTAAA G_
			GGAAG AAAGT GGAG		
			CCTTC TTTCG CCTC		
			ACCC_ GA		
GAM1245	FXR2	3'	CTCCTCCCATCCTGTACCCCCC	16786	AA AAAAA
	A		TGG GGTA GTGGGAGGAG		
			ACC CCAT TACCCTCCTC		
			CC GTCC_		
GAM1245	FXR2	3'	CTCCCCTGCTATCCCTCCTCCC	16785	A TAAAAA TG A
	A		TGG AGG AG GG GGAG		

		ACC TCC TC CC CCTC	
		C TCCCTA GT _	
GAM1245 FY	5'	CCTCCACCTGCCCTCA 8970	AA AAAAA
		TGG GGTA GTGGGAGG	
		ACT CCGT CACCCTCC	
		CC C__	
GAM1245 FZD4	3'	CCTCTCCCTTTCACATTCCA 24134	G AAA T
		TGGAA GT AAAG GGGAGG	
		ACCTT CA TTTC CTCTCC	
		A C__ C	
GAM1245 GPC1	3'	CTCCTCCCCTGGGACTCCCA 9101	AA AAAAA
		TGG GGT AGTGGGAGGAG	
		ACC TCA TCACCCTCCTC	
		C_ GGG__	
GAM1245 GPC4	5'	CTCCAACCTCTTCTCCCTCCA 7553	A TA AA G
		TGGA GG AA AGT GGAG	
		ACCT CC TT TCA CCTC	
		C TC CC A	
GAM1245 GRF2	3'	CTCCCCTCTTGACCTTCCA 17990	AAAAA T
		TGGAAGGT AG GGGAG	
		ACCTTCCA TC CCCTC	
		GTTC_ _	
GAM1245 GRIK3	3'	TCCTGCCCTTACCTGCCA 5891	A AAAAA T G
		TGG AGGTA AG GG AGGA	
		ACC TCCAT TC CC TCCT	
		G _ _ _ G	
GAM1245 GRINL1A	3'	TTTACTTTTTTCCCCCA 69521	AA T
		TGG GG AAAAAAGTGGG	
		ACC CC TTTTTTCATTT	
		CC _	
GAM1245 HCFC1	3'	CTCCACCTCTTCTACCCTCC 70993	A A AA_
		GGA GGTA AA GTGGGAG	
		CCT CCAT TT CACCCTC	
		C C CTC	
GAM1245 HEXA	3'	CCTCCCACTCCTGACCA 4974	A_ TAAAAA
		TGG AGG AGTGGGAGG	
		ACC TCC TCACCCTCC	
		AG _ _ _ _	
GAM1245 HHIP	5'	CTCCTCCCCTTCCCAGCC 42488	AAAA
		GGT AAGTGGGAGGAG	

CCG TTCACCCTCCTC  
 ACCC  
 GAM1245 HMGA2 5' CTCCTCTTGCTACCTCCACCTC 12998 A AAAAA\_ TG  
 CA TGA GGT AG GGAGGAG  
 ||||| || |||||  
 ACCT CCA TC TCTCCTC  
 \_ CCTCCA GT  
 GAM1245 HPCA 3' CCTCCCGGCTCTTAGCTTCCA 9253 G AAA \_  
 TGGAAG TAA AGT GGGAGG  
 ||||| ||| |||||  
 ACCTTC ATT TCG CCCTCC  
 G C\_ G  
 GAM1245 IFITM2 3' CCACTTACTCCACCTTCCA 21226 AAAA\_  
 TGGAAGGT AAGTGG  
 ||||| |||||  
 ACCTTCCA TTCACC  
 CCTCA  
 GAM1245 IGFBP5 3' CCTCCCACCCCCAGCCCCG 5191 AA AAAAAA  
 TGG GGT GTGGGAGG  
 ||| ||| |||||  
 GCC CCG CACCCTCC  
 \_ ACCCC\_  
 GAM1245 ITGA7 3' TCCTCCCACCCAATTCC 9382 GTAAAAAA  
 GGAAG GTGGGAGGA  
 ||||| |||||  
 CCTTC CACCCTCCT  
 AACC\_\_\_\_  
 GAM1245 ITS1 3' CTAAGACACTTTTCCACCCTCC 11618 A AA GG\_  
 A TGA GGT AAAAGT AG  
 ||||| ||||| ||  
 ACCT CCA TTTTAC TC  
 C CC AGAA  
 GAM1245 KAI1 3' CTCCTCCAGGCCTGCCTCCA 9498 A AAAAA G\_  
 TGG AGGTA GT GGAGGAG  
 ||| ||||| || |||||  
 ACC TCCGT CG CCTCCTC  
 C C\_ GA  
 GAM1245 KCNA7 3' TCCTCCTGTTTACCCCA 49060 AA AAAA TG  
 TGG GGTA G GGAGGA  
 ||| ||||| | |||||  
 ACC CCATT T CCTCCT  
 \_ \_ GT  
 GAM1245 KCNAB2 3' CCTCCCACCTTCCA 13302 GGTA AAAA  
 TGGA AGTGGGAGG  
 ||||| |||||  
 ACCTT TCACCCTCC  
 \_\_\_\_\_  
 GAM1245 KCNE1L 3' CTCTTCACCCCTGCACCTTCCA 24404 AAAAA T \_  
 TGGAAGGT AG GG GAGGAG  
 ||||| || |||||

ACCTTCCA TC CC CTTCTC  
 CG\_\_ C A  
 GAM1245 KRTHB1 3' CCTCCCACTCCTGGCCTCACA 9649 GA AAAAA  
 TG AGGT AGTGGGAGG  
 || ||| |||||  
 AC TCCG TCACCCTCC  
 AC GTCC\_  
 GAM1245 LRP1 5' CCTCCCCGCTCCTCCCA 9799 A TAAAAA \_  
 TGG AGG GTGGG AGG  
 ||| ||| ||||| |||  
 ACC TCC CGCCC TCC  
 C TC\_\_\_\_\_ C  
 GAM1245 LTB4R 5' CTTCTCACTCCCCA 5646 AA TAAAAA  
 TGG GG AGTGGGAGG  
 ||| ||| |||||  
 ACC CC TCACTCTTC  
 \_\_\_\_\_  
 GAM1245 MAML1 3' TCCTCCTCCTCCCTCCCA 28594 A TAAAAA TG  
 TGG AGG AG GGAGGA  
 ||| ||| ||| |||||  
 ACC TCC TC CCTCCT  
 C C\_\_\_\_\_ CT  
 GAM1245 MAP3K7IP1 3' CTCCTCCCACCATCACCTCCC 20378 A AAAAAA  
 GG AGGT GTGGGAGGAG  
 || ||| |||||  
 CC TCCA CACCCTCCTC  
 C CTAC\_  
 GAM1245 MAP4 5' CTCCTCCCGACGTCTCCTACCT 9907 A AAAAA\_ \_  
 CC GGA GGTA GT GGGAGGAG  
 ||| ||| ||| |||||  
 CCT CCAT CA CCCTCCTC  
 \_ CCTCTG G  
 GAM1245 MAP4 5' CTCCTCCCGACGTCTCCTACCT 48059 A AAAAA\_ \_  
 CC GGA GGTA GT GGGAGGAG  
 ||| ||| ||| |||||  
 CCT CCAT CA CCCTCCTC  
 \_ CCTCTG G  
 GAM1245 MFGE8 3' CTCCTCTTTCCACCTCCA 19811 A AAA T  
 TGGA GGT AAAG GGGAG  
 |||| ||| ||| |||||  
 ACCT CCA TTTC CCCTC  
 C CCC T  
 GAM1245 MGA 3' CTCCTCAGCTTCTTATCCTTCC 62807 TAAAA GG  
 A TGGAAGG AAGT GAGGAG  
 ||||| ||| |||||  
 ACCTTCC TTCG CTCCTC  
 TATTC A\_  
 GAM1245 MGST1 5' CTCCTCCTCGGCCTCACCATTTC 39697 \_ AAAAAAGT  
 CA TGGA GGT GGGAGGAG  
 ||||| ||| |||||

		ACCTT CCA TCCTCCTC	
		A CTCCGGC_	
GAM1245 MNT	3'	TCCCCCACTCTCTCACCCACCA 39718	AA AAAAA A
		TGG GGT AGTGGG GGA	
		ACC CCA TCACCC CCT	
		AC CTCTC _	
GAM1245 MPP2	3'	CTCCTCCCACCTCTCACCCC 59821	AA AAAAAA
		GG GGT GTGGGAGGAG	
		CC CCA CACCCTCCTC	
		_ CTCTC_	
GAM1245 MSF	3'	CCTCCCACCAACCCCA 88081	AA AAAAAA
		TGG GGT GTGGGAGG	
		ACC CCA CACCCTCC	
		_ C_	
GAM1245 MTCP1	5'	CCAAGTCACCTTCTTACCTCCC 26429	A A A GA_
A		TGG AGGTAA AA GTGG GG	
		ACC TCCATT TT CACT CC	
		C C C GAA	
GAM1245 MUC3B	3'	TCCTCCTCATTCCCTTCCA 94269	TAAAAA _
		TGGAAGG AGTG GGAGGA	
		ACCTTCC TTAC CCTCCT	
		C_ T	
GAM1245 MYO1C	3'	CTCCCTGCTCCTACCCTC 61205	A AAAA _
		GA GGTA AGT GGGAG	
		CT CCAT TCG CCCTC	
		C CC_ T	
GAM1245 NCOA3	3'	TTCCTTCCCCACCCCCCA 21534	AA AAAAAAGT
		TGG GGT GGGAGGAG	
		ACC CCA CCTTCCTT	
		CC CC_	
GAM1245 NDRG1	3'	CTCCTCCACAGCCCCAACCTCC 59567	A AAAAAAGTG
CA		TGG AGGT GGAGGAG	
		ACC TCCA CCTCCTC	
		C ACCCCGACA	
GAM1245 NGFR	3'	CTCAGCCCCTCTTGCCCCCA 10227	AA AAA T AG
		TGG GGTAAG AG GGG GAG	
		ACC CCGTT TC CCC CTC	
		CC C_ _ GA	
GAM1245 NOTCH3	3'	CTCCTCCCCACCCCACCTCCC 4745	A AAAAAA _
		GG AGGT GTGGG AGGAG	



		CC TCCA	CACCC TCCTC		
		C	CCC__ C		
GAM1245 NPR1	3'	TCCTCTCCTATCCCTCCA	87370	A TAAAAA	T
		TGGA GG	AG GGGAGGA		
		ACCT CC	TC CTCTCCT		
		C TA__	_		
GAM1245 NPY2R	5'	CTCCACCTTCACCCGCC	6184	AA A AAA	
		GG GGT AA	GTGGGAG		
		CC CCA TT	CACCCTC		
		GC C C__			
GAM1245 NRCAM	3'	TCCCCCACCTTTTTTGCT	17208	_ A	
		GGTAAAAAAG	TGGG GGA		
		TCGTTTTTTC	ACCC CCT		
		C C			
GAM1245 NRXN3	5'	CTCCTCTCCTCTTTCCTCCA	57277	A TAAA	T _
		TGGA GG	AAAG GG GAGGAG		
		ACCT CC	TTTC CC CTCCTC		
		C _	T T		
GAM1245 NYX	3'	CTCCCCTTCCCCTCATCTTCCA	42599	AAAA__	T
		TGGAAGGT	AAG GGGAG		
		ACCTTCTA	TTC CCCTC		
		CTCCCC	_		
GAM1245 OAS3	3'	CTCCCCTGCCTCCCA	20540	A AAAAA	T
		TGG AGGT	AG GGGAG		
		ACC TCCG	TC CCCTC		
		C _	_		
GAM1245 PACSIN1	3'	CCTCCCCTCTCGTCTCCTTCC	92258	TAAAAA_	
		GGAAGG	AGTGGGAGG		
		CCTTCC	TCACCCTCC		
		TCTGCTC			
GAM1245 PARG	3'	TCCTCCCACCTCCCACCA	13273	AA TAAAAA	
		TGG GG	GTGGGAGGA		
		ACC CC	CACCCTCCT		
		AC TC__			
GAM1245 PATE	3'	CTCCCACCCTTACCTCCA	56312	A AAAA	
		TGGA GGTAA	GTGGGAG		
		ACCT CCATT	CACCCTC		
		_ CC__			
GAM1245 PAX2	3'	TCCTCCCCTCCCCTCCCA	14329	A TAAAAA	
		TGG AGG	GTGGGAGGA		

			ACC TCC	TACCCTCCT		
			C CC_____			
GAM1245	PAX2	3'	TCCTCCCATCCCCTCCCA	14337	A	TAAAAAA
			TGG AGG	GTGGGAGGA		
			ACC TCC	TACCCTCCT		
			C CC_____			
GAM1245	PCLO	3'	CTCCTTTGTTTCCACCATCCA	94225	A	AA AGT
			TGGA GGT	AAA GGGAG		
			ACCT CCA	TTT TCCTC		
			A CC	GTT		
GAM1245	PDE4A	3'	CTCCATCCCCTTTCCCTTCCA	20584	TAAA	T _
			TGGAAGG	AAAG GGA GGAG		
			ACCTTCC	TTTC CCCT CCTC		
			C_ _	A		
GAM1245	PDE4A	3'	TTCCTCCCTAGCCTTCCA	20589	AAAAAAGT	
			TGGAAGGT	GGGAGGAG		
			ACCTTCCG	CCCTCCTT		
			AT_____			
GAM1245	PDGFRA	3'	CTCCCGTCTTCTGCCTCCCA	20597	A	AAA _
			TGG AGGTA	AAG TGGGAG		
			ACC TCCGT	TTC GCCCTC		
			C C_	T		
GAM1245	PIG8	3'	CCTTCCACCTTTCCA	16869	TAAAAAA	
			TGGAAGG	GTGGGAGG		
			ACCTTTC	CACCTTCC		
			_____			
GAM1245	PIGR	3'	CCTCTTCTTCTTTCCTTCCA	72595	T A T	
			TGGAAGG	AAA AAG GGGAGG		
			ACCTTCC	TTT TTC TTCTCC		
			_ C _			
GAM1245	PITX1	3'	CTCCTCCCACTTCCCACTCC	10597	A_	TAAAA
			GGA GG	AAGTGGGAGGAG		
			CCT CC	TTCACCTCCTC		
			CA C_			
GAM1245	PKD2L1	5'	CCTCTTCAAACCCCCACCTTCC	32262	AAAAAAG	_
	A		TGGAAGGT	TGG GAGG		
			ACCTTCCA	ACT CTCC		
			CCCCCAA	T		
GAM1245	PKM2	3'	TCCACCCTCCACCTTCCA	10603	AAAAAAGT	A
			TGGAAGGT	GGG GGA		

ACCTTCCA    CCC CCT  
           CCT\_\_\_\_\_ A  
 GAM1245 PML    3' CTCCTATTAGCCCCCTCCTTCCA 52655    TAAAAA\_  
           TGGAAGG    AGTGGGAG  
           |||||    |||||  
           ACCTTCC    TTATCCTC  
           TCCCCGA  
 GAM1245 POLR2A    5' CTCCTCCGGCTTTTTCTCCCA 6263    A TA    G  
           TGG AGG AAAAAAGT GGAGGAG  
           ||| ||| ||||| |||||  
           ACC TCC TTTTTCG CCTCCTC  
           C \_    G  
 GAM1245 POU2AF1    3' CCTTTCCTTCTTTACCTCCC 20650    A    A T GG  
           GG AGGTAAA AAG G AGG  
           || ||||| ||| |||  
           CC TCCATTT TTC C TCC  
           C    C \_ TT  
 GAM1245 PPP1R12B    3' CTCTATTCTTCTTCACCTCTCA 49467    GA    A A TG\_  
           TG AGGT AA AAG GGAG  
           || ||| || ||| |||  
           AC TCCA TT TTC TCTC  
           TC    C C TTA  
 GAM1245 PPP1R12B    3' CTCTATTCTTCTTCACCTCTCA 49478    GA    A A TG\_  
           TG AGGT AA AAG GGAG  
           || ||| || ||| |||  
           AC TCCA TT TTC TCTC  
           TC    C C TTA  
 GAM1245 PRex1    3' CTCCTCCTCATCTTAGCTTCCA 40431    G AAAAA \_  
           TGGAAG TAA GTG GGAGGAG  
           ||||| ||| ||| |||||  
           ACCTTC ATT TAC CCTCCTC  
           G C \_    T  
 GAM1245 PRKACA    3' CCTTCCTCTACTCCCA 10789    AA AAAAA T  
           TGG GGT AG GGGAGG  
           ||| ||| || |||||  
           ACC TCA TC CCTTCC  
           C\_ \_    T  
 GAM1245 PRKACA    3' CTCATCCCCCTTCACCCTCC 10790    A AAAAA T G  
           GGA GGT AAG GGGA GAG  
           ||| ||| ||| ||| |||  
           CCT CCA TTC CCCT CTC  
           C C \_ \_    A  
 GAM1245 PTK2B    3' CTCCTCTTTCTCTCCCAACCC 14628    AA AAAAA\_ TG  
           CCA    TGG GGT AG GGAGGAG  
           ||| ||| || |||||  
           ACC CCA TC TCTCCTC  
           C\_ ACCCCTC TT  
 GAM1245 PTPRN    3' CTCCTCCCACCACCCTCC 11130    A AAAAAA  
           GGA GGT GTGGGAGGAG  
           ||| ||| |||||

			CCT CCA	CACCCTCCTC		
			C C_____			
GAM1245	RAB2L	3'	CTTCCCACCTTCCA	16478	AAAAAAGT	
			TGGAAGGT	GGGAGG		
			ACCTTCCA	CCCTTC		
GAM1245	RAB5B	3'	CTCCCCCAGGACTTACCTTCC	11190	AAAAG	A
	A		TGGAAGGTAA	TGGG	GGAG	
			ACCTTCCATT	ACCC	CCTC	
			CAGG_	C		
GAM1245	RAB6A	3'	CTCTTCCTCCTCCACTTCC	11196	GTAAAAA	TG
			GGAAG	AG	GGAGGAG	
			CCTTC	TC	CCTTCTC	
			ACC_____	CT		
GAM1245	RAB6A	3'	CTCCTTGCTTTTCTCACCTCTC	11195	GA	AA_ GG
	A		TG	AGGT	AAAAGT	GAGGAG
			AC	TCCA	TTTTCG	TTCCTC
			TC	CTC	___	
GAM1245	RAI3	3'	CTCCCATCTCCATCTCCA	14284	A	AAAAAA
			TGG	AGGT	GTGGGAG	
			ACC	TCTA	TACCCTC	
			C	CCTC_		
GAM1245	RALB	3'	CTCCCCTTCTTCCCTCCA	11243	A	TAAAA T
			TGG	AGG	AAG	GGGAG
			ACC	TCC	TTC	CCCTC
			C	CTTC_		
GAM1245	RASA1	3'	CACTTTTCCACATTCCA	42634	G	AA
			TGGAA	GT	AAAAGTG	
			ACCTT	CA	TTTTCAC	
			A	CC		
GAM1245	RFX1	3'	TCCTCCCACCACCCA	11312	AA	AAAAAA
			TGG	GGT	GTGGGAGGA	
			ACC	CCA	CACCCTCCT	
			___	C_____		
GAM1245	RFX2	3'	CTCCCCTCCTACCTGCCA	5309	A	AAAA T
			TGG	AGGTA	AG	GGGAG
			ACC	TCCAT	TC	CCCTC
			G	CC_		
GAM1245	RGS19IP1	3'	CTCCCATCTCTCCTTCCA	62507		TAAAAAA
			TGGAAGG	GTGGGAG		

		ACCTTCC	TACCCTC	
		TCTC_____		
GAM1245 RS1	3'	CTTCTCACCTCCA	4392	A TAAAAAA
		TGGA GG	GTGGGAGG	
		ACCT CC	CACTCTTC	
		_____		
GAM1245 RXRA	3'	TCCTCCCCGCGCCCTCCA	11418	A AAAAAA _
		TGGA GGT	GTGGG AGGA	
		ACCT CCG	CGCCC TCCT	
		C C_____ C		
GAM1245 S100A1	3'	TTCCTCTCCACCCTCCA	20777	A TAAAAAA _
		TGG AGG	GTGG GAGGAG	
		ACC TCC	CACC CTCCTT	
		C _____ T		
GAM1245 S100A11	3'	CCACCCCCTTTCCTTCCA	18835	TAAA T A
		TGGAAGG	AAAG GGG GG	
		ACCTTCC	TTTC CCC CC	
		_____ C A		
GAM1245 SALL1	3'	CTCCTACTCCTTGCCCCCA	11432	AA AAA
		TGG GGTAAG	AGTGGGAG	
		ACC CCGTT	TCATCCTC	
		CC CC_		
GAM1245 SECTM1	3'	CTTCCCCTCCACCCCCCA	11528	AA AAAAA T
		TGG GGT	AG GGGAGG	
		ACC CCA	TC CCCTTC	
		CC CC_____		
GAM1245 SHOX	3'	CTCTCACCTCCACCTCCA	22537	A AAAAAA
		TGG AGGT	GTGGGAG	
		ACC TCCA	CACTCTC	
		C CCTC_____		
GAM1245 SLC22A12	5'	CTCCACATTCCCTACTTTCCA	58070	AAAA _
		TGGAAGGTA	AGTG GGAG	
		ACCTTTCAT	TTAC CCTC	
		CCC_ A		
GAM1245 SLC2A4	3'	TTCCTCCCCACCTTCC	6443	AAAAAAGT
		GGAAGGT	GGGAGGAG	
		CCTTCCA	CCCTCCTT	
		C_____		
GAM1245 SLC7A8	3'	CTCCCCCTTTTATCCTACCTCC	24278	A A_____ T
		GG AGGTA	AAAAG GGGAG	

			CC TCCAT TTTTC CCCTC		
			C CCTA C		
GAM1245	SMARCC1	3'	CTCCTTATACCTTCTCCCTTCC 11798	TAAAAAA	G
	A		TGGAAGG GTG GAGGAG		
			ACCTTCC CAT TTCCTC		
			CTCTTC_ A		
GAM1245	SORD	5'	CTCCCAGGCCCCACCTTCCA 11871	AAAAAAG	
			TGGAAGGT TGGGAG		
			ACCTTCCA ACCCTC		
			CCCCGG_		
GAM1245	SPARC	3'	TCCTTTTCTTCACCCTCC 11900	A AAAA	T
			GGA GGT AAG GGGAGGA		
			CCT CCA TTC TTTTCCT		
			C C_ _		
GAM1245	SPTAN1	3'	CTCCTCTGTGTGCTCTCACTTT 11936	AAAAA	_
	CCA		TGGAAGGT AGTG GGAGGAG		
			ACCTTTCA TCGT TCTCCTC		
			CTC_ GTG		
GAM1245	ST14	3'	CTCGCTTCCTCAGCCTCCA 41766	A AAAA_	
			TGGA GGT AAGTGGG		
			ACCT CCG TTCGCTC		
			_ ACTCC		
GAM1245	SYT5	3'	CCTCCCCCACCTTCCA 12074	AAAAAAGT	
			TGGAAGGT GGGAGG		
			ACCTTCCA CCCTCC		
			CCC_		
GAM1245	TAP2	3'	CCCACCTTTTTTTGACCTTCCA 5026	_ _	
			TGGAAGGT AAAAAAG TGGG		
			ACCTTCCA TTTTTTC ACCC		
			G C		
GAM1245	TBR1	3'	CCCTCGTCTTCTCTTACCTCC 21684	A AA_ _ A	
			GGA GTAA AAG TGGG GG		
			CCT CCATT TTC GCTC CC		
			_ CTC T _		
GAM1245	TEGT	3'	CTTCCTCTCCTTCCA 64623	TAAAAA	T
			TGGAAGG AG GGGAG		
			ACCTTCC TC CCTTC		
			_ T		
GAM1245	TGFBR2	3'	CCCACTTTTTTACCTTC 12266	A	
			GAAGGTAAAAA GTGGG		

CTTCCATTTT CACCC

GAM1245 TIMP3 3' CTCCTGTCTTTTACCCTCC 4507 A AA TG  
GGA GGTA AAA G GGAG  
||| ||||| | |||  
CCT CCATTTT T CCTC  
C C\_ GT

GAM1245 TMP21 3' CTCCTCCCACCTTGTACCTC 22402 A AAAAA  
GA GGTA GTGGGAGGAG  
|| ||| |||||  
CT CCAT CACCCTCCTC  
\_ GTTC\_

GAM1245 TMPRSS3 3' CCCACCCTTTCTACTTCCA 50504 GTA AA  
TGGAAG AAA GTGGG  
||||| ||| |||||  
ACCTTC TTT CACCC  
ATC CC

GAM1245 TMPRSS3 3' CCCACCCTTTCTACTTCCA 50525 GTA AA  
TGGAAG AAA GTGGG  
||||| ||| |||||  
ACCTTC TTT CACCC  
ATC CC

GAM1245 TMPRSS3 3' CCCACCCTTTCTACTTCCA 43791 GTA AA  
TGGAAG AAA GTGGG  
||||| ||| |||||  
ACCTTC TTT CACCC  
ATC CC

GAM1245 TRIM14 3' CTCCCAGTCCTCATCTTCCA 28854 AAAAAAG  
TGGAAGGT TGGGAG  
||||| |||||  
ACCTTCTA ACCCTC  
CTCCTG\_

GAM1245 TSPY 3' CTCCTCGCTTTCCCTTCCA 82106 TAAA \_  
TGGAAGG AAAGTG GGAG  
||||| ||||| |||||  
ACCTTCC TTT CGC CCTC  
C\_ T

GAM1245 UBE2V1 3' TCCCCCACCTTTATC 12521 AAA A  
GGTAAA GTGGG GGA  
||||| ||||| |||  
CTATTT CACCC CCT  
C\_ C

GAM1245 UBE2V1 3' TCCCCCACCTTTATC 41796 AAA A  
GGTAAA GTGGG GGA  
||||| ||||| |||  
CTATTT CACCC CCT  
C\_ C

GAM1245 UFD1L 3' CTCCTTCTTCCCTACTCCCCA 73285 AA AAAAAAGT  
TGG GGTA GGGAGGAG  
||| ||||| |||||

			ACC TCAT	TCTTCCTC		
			CC CCCT__			
GAM1245	WBP2	3'	CCTCCCTGCCTCCCA	73028	A	AAAAAGT
			TGG AGGTA	GGGAGG		
			ACC TCCGT	CCCTCC		
			C	_____		
GAM1245	WBSR1	3'	TCTCTCTCCTTCCTTCCA	49264		TAAAA T _
			TGGAAGG	AAG GGGAG GA		
			ACCTTCC	TTC CTCTC CT		
			_____	T		
GAM1245	WBSR1	3'	TCTCTCTCCTTCCTTCCA	42232		TAAAA T _
			TGGAAGG	AAG GGGAG GA		
			ACCTTCC	TTC CTCTC CT		
			_____	T		
GAM1245	WNT10B	3'	CTCCTCCCACTTCTCAACTCCA	12674		A GTAAAA
			TGGA G	AAGTGGGAGGAG		
			ACCT C	TTCACCCTCCTC		
			_ AACTC_			
GAM1245	ZNF216	5'	CTCCTCCCACTTCCCGAGCTCC	20020		AGGTAAAA
			GGA	AAGTGGGAGGAG		
			CCT	TTCACCCTCCTC		
			CGAGCCC_			
GAM1245	ZNF216	5'	CCCTCGCTTCCCTCCTCCCA	20019	A	TAAAA A
			TGG AGG	AAGTGGG GG		
			ACC TCC	TTCGCTC CC		
			C TCCC_	_		
GAM1245	ZNF74	5'	CTCCCGCCTCAACCTCCCA	12794	A	AAAAAA
			TGG AGGT	GTGGGAG		
			ACC TCCA	CGCCCTC		
			C ACTC_			
GAM1245	AGPAT1	5'	CTCCCACTCCACCTCCC	21148	A	AAAAA
			GG AGGT	AGTGGGAG		
			CC TCCA	TCACCCTC		
			C CCC_			
GAM1245	AIF1	3'	CCTTCCTCTTCCCCCTTCCA	16754		TAAAA T
			TGGAAGG	AAG GGGAGG		
			ACCTTCC	TTC CCTTCC		
			CCC_	T		
GAM1245	AKAP11	3'	CCTCCCCTCCTCCCA	32705	A	TAAAAA T _
			TGG AGG	AG GGGAG G		



ACC TCC TC CCCTC C  
 C \_\_\_\_\_ T  
 GAM1245 AKAP11 3' CTCCTCCCCTGTCTCTCACCT 32706 A AAAAA\_  
 CCC GG AGGT AGTGGGAGGAG  
 || ||| |||||  
 CC TCCA TCACCCTCCTC  
 C CTCTCTG  
 GAM1245 AKAP11 3' GCTCCTCCCCTCTCTTCCCCC 32711 A TA AA\_ |||  
 TCC GA GG AA AGTGGGAGGAG C  
 || || ||||| |  
 CT CC TT TCACCCTCCTC G  
 C CC CTC |||  
 GAM1245 AKT3 3' CCTCGCCACCTTTCACCCTC 18433 A A AA \_  
 GA GGT AAA GTGG GAGG  
 || ||| |||||  
 CT CCA TTT CACC CTCC  
 C C C\_ G  
 GAM1245 ARGBP2 3' CCGTCACCATCTCCACCTCCCA 40772 A AAAAAA \_ \_  
 TGG AGGT GTGG GA GG  
 ||| ||| ||||| ||  
 ACC TCCA TACC CT CC  
 C CCTC\_ A G  
 GAM1245 ARHF 3' CCTCCCATCTCCACCCCA 38740 AA AAAAAA  
 TGG GGT GTGGGAGG  
 ||| ||| |||||  
 ACC CCA TACCCTCC  
 \_ CCTC\_  
 GAM1245 ARHGEF15 3' CTCCATTTCTTCTTTACCCCC 30259 AA A\_ TG\_  
 CA TGG GGTAAG AAG GGAG  
 ||| ||||| ||| |||  
 ACC CCATTT TTC CCTC  
 CC CC TTTA  
 GAM1245 ARHGEF9 3' CCCCTCTTTTACTTTCCA 30807 A T  
 TGGAAGGTAAAA AG GGG  
 ||||| ||| |||  
 ACCTTTCATTTT TC CCC  
 C \_  
 GAM1245 ASB16 3' TCCTGCCTCTGCCTCCCA 69947 A AAAAA T G  
 TGG AGGT AG GG AGGA  
 ||| ||| || |||  
 ACC TCCG TC CC TCCT  
 C \_\_\_\_\_ T G  
 GAM1245 BICD2 3' CTCCTATTTTACCTTCC 70393 AA  
 GGAAGGTAAAA GTGGGAG  
 ||||| |||||  
 CCTTCCATTTT TATCCTC  
 \_  
 GAM1245 BRPF3 3' CTCCCCCAGGACACCACCTCCC 92316 A AAAAAAG A  
 A TGG AGGT TGGG GGAG  
 ||| ||| ||||| |||

ACC TCCA    ACCC CCTC  
           C    CCACAGG    \_  
 GAM1245 BSMAP    3' TCCTTCCTCTCCTCCCA    23995    A TAAAAA T  
                   TGG AGG    AG GGGAGGA  
                   ||| |||    || |||||  
                   ACC TCC    TC CCTTCCT  
                   C    \_\_\_\_\_ T  
 GAM1245 C(27)-3BETA-HSD 3' CTCCCTATGCTTTCACTTCC 47271    GTAAA    \_  
                   GGAAG    AAAGT GGGAG  
                   |||||    |||||    |||||  
                   CCTTC    TTTCG CCCTC  
                   AC\_\_\_\_ TAT  
 GAM1245 C17orf31 3' CCCCCACCTCTTCTACCATCCA 34119    A A AA\_ A  
                   TGGA GGTA AA GTGGG GG  
                   ||||| |||    ||||| ||  
                   ACCT CCAT TT CACCC CC  
                   A C CTC    \_  
 GAM1245 C1orf16 3' CCATTCTACTTCCCACCCTCC 29229    A AAAA    \_  
                   GGA GGT    AAGTGGGA GG  
                   ||| |||    ||||| ||  
                   CCT CCA    TTCATCTT CC  
                   C CCC\_ A  
 GAM1245 C1orf34 3' CTCCTCATCACCTCCTACTCCC 60668    AA AAAAA    \_  
                   A    TGG GGTA    GTGG GAGGAG  
                   ||| |||    ||||| |||||  
                   ACC TCAT    CACT CTCCTC  
                   C\_ CCTC\_ A  
 GAM1245 C20orf149 3' CCTCCCCACCTCCCACCCCCCA 44172    AA AAAAAA    \_  
                   TGG GGT    GTGGG AGG  
                   ||| |||    ||||| |||  
                   ACC CCA    CACCC TCC  
                   CC CCCTC\_ C  
 GAM1245 C20orf98 3' CCTCCCTAACCCTTACCTTC 71514    AAAAGT  
                   GAAGGTAA    GGGAGG  
                   |||||||    |||||  
                   CTTCCATT    CCCTCC  
                   CCCAAT  
 GAM1245 CDH26 3' CTCCCTATCCCTCTTTCCCCC 41465    AA TAAA T    \_  
                   A    TGG GG    AAAG GGA GGAG  
                   ||| ||    ||||| |||||  
                   ACC CC    TTTC CCCT CCTC  
                   CC \_\_\_\_\_ T ATC  
 GAM1245 CGB1 3' TCCCCCAGCCTTCCA 52965    AAAAAAG A  
                   TGGAAGGT    TGGG GGA  
                   |||||||    ||||| |||  
                   ACCTCCG    ACCC CCT  
                   \_\_\_\_\_ C  
 GAM1245 CGB2 3' TCCCCCAGCCTTCCA 52966    AAAAAAG A  
                   TGGAAGGT    TGGG GGA  
                   |||||||    ||||| |||

ACCTTCCG ACCC CCT  
 \_\_\_\_\_ C  
 GAM1245 CIDEB 3' CCACCTTTCTAGCCTCCCA 27042 A AA\_ A  
 TGG AGGT AAA GTGG  
 ||| ||| ||| |||  
 ACC TCCG TTT CACC  
 C ATC C  
 GAM1245 CLIC5 3' CTCCTTTTCTACCCTCC 33717 A A T  
 GGA GGTA AAAAG GGG  
 ||| ||| ||||| |||  
 CCT CCAT TTTTC CTC  
 C C \_  
 GAM1245 CLSTN3 5' CCTCCTCTTCACCCCA 28208 AA AAAA T  
 TGG GGT AAG GGGAGG  
 ||| ||| ||| |||||  
 ACC CCA TTC TCCTCC  
 C\_ C\_\_ \_  
 GAM1245 CPR2 3' CTCCCAGCTTCTTCCTCCA 48094 A TAAAA \_  
 TGGA GG AAG TGGGAG  
 |||| || ||| |||||  
 ACCT CC TTC ACCCTC  
 C TTC\_\_ G  
 GAM1245 DDX39 3' CCTCCCACCTCCCTTCC 57312 TAAAAAA  
 GGAAGG GTGGGAGG  
 ||||| |||||  
 CCTTCC CACCCTCC  
 CTC\_\_  
 GAM1245 DEFCAP 5' CTCCTCCACCCACCTCTTCT 52230 TAAAAAA  
 GGAAGG GTGGGAGGAG  
 ||||| |||||  
 TCTTCT CACCCTCCTC  
 CCACCC\_  
 GAM1245 DEFCAP 5' CTCCTCCACCCACCTCTTCT 29950 TAAAAAA  
 GGAAGG GTGGGAGGAG  
 ||||| |||||  
 TCTTCT CACCCTCCTC  
 CCACCC\_  
 GAM1245 DGKD 3' CTCCTCCCGCTCCTCCCTCC 59404 A TAAAAA  
 GGA GG AGTGGGAGGAG  
 ||| || |||||  
 CCT CC TCGCCCTCCTC  
 C TCC\_\_  
 GAM1245 DJ159A19.3 3' CTCCTGCCCTCTGCCTCCCA 31651 A AAAA T \_  
 TGG AGGTA AG GGG AGGAG  
 ||| |||| || ||| |||||  
 ACC TCCGT TC CCC TCCTC  
 C C\_\_ \_ G  
 GAM1245 DJ159A19.3 3' CCTCCCACCCATCTCCTCCA 31650 A TAAAAAA  
 TGGA GG GTGGGAGG  
 |||| || |||||

ACCT CC CACCCTCC  
 \_ TCTACC\_  
 GAM1245 dJ309H15.1 3' TCCTCCCACCCTCTTCC 56797 TAAAAA  
 GGAAGG GTGGGAGGA  
 ||||| |||||  
 CCTTCT CACCCTCCT  
 CC\_\_\_\_  
 GAM1245 DKFZp434A1010 3' TCCTCCTCTCCCTCCA 71344 A TAAAAA T  
 TGGA GG AG GGGAGGA  
 ||| || || |||||  
 ACCT CC TC TCCTCCT  
 C \_\_\_\_\_  
 GAM1245 DKFZp434I1930 3' CTCCCCTTCTTTCCCTTCCA 50033 T A T  
 TGGAAGG AAA AAG GGGAG  
 ||||| ||| ||| |||||  
 ACCTTCC TTT TTC CCCTC  
 C C \_  
 GAM1245 DKFZP434J037 3' TCCTCCCACAACCCCCCA 48220 AA AAAAAA  
 TGG GGT GTGGGAGGA  
 ||| ||| |||||  
 ACC CCA CACCCTCCT  
 CC A\_\_\_\_  
 GAM1245 DKFZP434N014 3' CTCCTGGCTCCTTATCCCCCA 60599 AA AAA \_  
 TGG GGTA AGT GGGAG  
 ||| |||| ||| |||||  
 ACC CTATT TCG TCCTC  
 CC CC\_ G  
 GAM1245 DKFZp434P0531 3' CCTCCGTTTTTTCCACCCCCA 92206 AA AA TG  
 TGG GGT AAAAG GGAGG  
 ||| ||| ||||| |||||  
 ACC CCA TTTTT CCTCC  
 \_ CC TG  
 GAM1245 DKFZp547H236 3' CTCCTGTCCCCCCTACCTCC 78543 A AAAAAGT \_  
 GGA GGTA GGA GGAG  
 ||| |||| ||| |||||  
 CCT CCAT CCCT CCTC  
 \_ CCC\_\_\_\_\_ GT  
 GAM1245 DKFZp547I224 5' CCCTCTTTTTTCCCCCA 39555 AA T T  
 TGG GG AAAAAAG GGG  
 ||| || ||||| |||  
 ACC CC TTTTTTC CCC  
 CC \_ T  
 GAM1245 DKFZP564G092 5' CTCCTCCCTCTTTACCCTCC 31535 A AAA T  
 GGA GGTA AG GGGAGGAG  
 ||| |||| || |||||  
 CCT CCATT TC CCCTCCTC  
 C \_ T  
 GAM1245 DKFZP566G1424 5' TCTCCCACACCCCCA 84791 AA AAAAAA  
 TGG GGT GTGGGAGG  
 ||| ||| |||||

ACC CCA CACCCTCT

GAM1245 DKFZP566I1024 3' CTCCCACCTCGACCTCCCA 70101 A AAAAAA  
TGG AGGT GTGGGAG  
||| ||| |||||  
ACC TCCA CACCCTC  
C GCTC\_\_

GAM1245 DKFZP586G1122 3' CCTCCCACCAAGTCACCTCCA 61285 A AAAAAA  
TGGA GGT GTGGGAGG  
|||| | |||||  
ACCT CCA CACCCTCC  
\_ CTGAC\_

GAM1245 DKFZP727C091 3' CTCTTACCCCTCCCCTCCCA 66210 A TAAAAA T \_  
TGG AGG AG GGG AGGAG  
||| || | ||| |||||  
ACC TCC TC CCC TTCTC  
C CC\_\_ C A

GAM1245 DKFZp761B0514 3' TCCTCCCAGCAGCCTCCA 50160 A AAAAAAG  
TGGA GGT TGGGAGGA  
|||| | |||||  
ACCT CCG ACCCTCCT  
\_ ACG\_\_

GAM1245 DPCR1 3' CTCCTCCCACCTTCACCCCA 55122 AA A AAA  
TGG GGT AA GTGGGAGGAG  
||| ||| || |||||  
ACC CCA TT CACCCTCCTC  
\_ C C\_

GAM1245 DSCAML1 3' TCCTCCTCACCTTCC 40362 AAAAAAGT  
GGAAGGT GGGAGGA  
||||| |||||  
CCTTCCA TCCTCCT  
C\_\_

GAM1245 E1B-AP5 3' CCTCCCCAGCCTTCCA 58566 AAAAAAGT  
TGGAAGGT GGGAGG  
||||| |||||  
ACCTTCCG CCCTCC  
AC\_\_

GAM1245 E1B-AP5 3' CCTCCCCAGCCTTCCA 22899 AAAAAAGT  
TGGAAGGT GGGAGG  
||||| |||||  
ACCTTCCG CCCTCC  
AC\_\_

GAM1245 EPB41L1 3' CTCAGTTCCATTTTACCTCCCA 70589 A AAA G\_  
TGG AGGTAAA GTGGGA GAG  
||| ||||| ||||| |||  
ACC TCCATTT TACCTT CTC  
C \_ GA

GAM1245 FATE 3' CCTTGCCCTTTTCATCTCCCA 52358 A AAA T \_  
TGG AGGT AAAG GGG AGG  
||| ||| ||||| ||| |||

ACC TCTA TTTC CCC TCC  
 C C\_\_ \_ GT  
 GAM1245 FEM-2 3' CCTCCCCTTCCTCCCA 27574 A TAAAA T  
 TGG AGG AAG GGGAGG  
 ||| ||| ||| |||||  
 ACC TCC TTC CCCTCC  
 C \_\_\_\_\_  
 GAM1245 FLJ00024 3' CTTCTCTCCCTCCACCCCCA 63761 AA AAAAA T  
 TGG GGT AG GGGAGGAG  
 ||| ||| || |||||  
 ACC CCA TC CTCTCTTC  
 C\_ CC\_\_ C  
 GAM1245 FLJ10314 3' CCTCCCCTGTCTCCTCCCA 36011 A TAAAAA T  
 TGG AGG AG GGGAGG  
 ||| ||| || |||||  
 ACC TCC TC CCCTCC  
 C TCTG\_\_ \_  
 GAM1245 FLJ10761 3' CTCCCTTTCTACCCTC 36580 A A AGT  
 GA GGTA AAA GGGAG  
 || |||| ||| |||||  
 CT CCAT TTT CCCTC  
 C C \_\_\_\_  
 GAM1245 FLJ10925 3' CTGTTCCCTCTTACACTCCA 36885 AG AAAA T G  
 TGGA GTA AG GGGAG AG  
 |||| ||| || ||||| ||  
 ACCT CAT TC CCCTT TC  
 CA \_\_\_\_ T G  
 GAM1245 FLJ11362 3' TTCCTTCCTCTCCTCCCA 41684 A TAAAAA T  
 TGG AGG AG GGGAGGAG  
 ||| ||| || |||||  
 ACC TCC TC CCTTCCTT  
 C \_\_\_\_\_ T  
 GAM1245 FLJ11539 3' CTCCACCCCTCACCTCCCA 45376 A AAAAAA  
 TGG AGGT GTGGGAG  
 ||| |||| |||||  
 ACC TCCA CACCCTC  
 C CTCC\_\_  
 GAM1245 FLJ11618 3' CCTCCCGTTCACCTACCA 42393 A A AAAG  
 TGG AGGT AA TGGGAGG  
 ||| |||| || |||||  
 ACC TCCA TT GCCCTCC  
 A C \_\_\_\_  
 GAM1245 FLJ12448 3' CTCCTCCTCTCTACACCCCCA 43177 AA AAAAA T  
 TGG GGT AG GGGAGGAG  
 ||| ||| || |||||  
 ACC CCA TC TCCTCCTC  
 C\_ CATC\_\_ \_  
 GAM1245 FLJ12541 3' TCCCCGGCTCTCCTCCCA 42329 A TAAAAA G A  
 TGG AGG AGT GG GGA  
 ||| ||| ||| ||| |||

ACC TCC TCG CC CCT  
 C TC\_\_\_\_ G \_  
 GAM1245 FLJ12650 3' TCTCCCACTACCCTCCA 44529 A AAAAA  
 TGGA GGT AGTGGGAGG  
 ||| ||| |||||  
 ACCT CCA TCACCCTCT  
 C \_\_\_\_  
 GAM1245 FLJ12788 3' CTCCCCCAACCCCTTACCTTT 42545 AAAAG\_ A  
 CA TGGAAGGTAA TGGG GGAG  
 ||||| ||| |||  
 ACTTTCCATT ACCC CCTC  
 CCCCCA \_  
 GAM1245 FLJ12921 3' CTCCTCACTCTCTACCTCCC 45910 A AAAA \_  
 GG AGGTA AGTG GGAG  
 || ||| ||| |||  
 CC TCCAT TCAC CCTC  
 C CTC\_ T  
 GAM1245 FLJ13111 3' CTCCTCCCCACCCCCCA 46938 AA TAAAAA \_  
 TGG GG GTGGG AGGAG  
 ||| || ||| |||  
 ACC CC CACCC TCCTC  
 CC \_\_\_\_\_ C  
 GAM1245 FLJ13782 3' TTTCTCACCCCTCCA 46172 A TAAAAA  
 TGGA GG GTGGGAGG  
 ||| || |||||  
 ACCT CC CACTCTT  
 C \_\_\_\_  
 GAM1245 FLJ13852 3' CTCCTCTTTCTCCTCCA 43577 A TAAA T  
 TGG AGG AAAG GGGAG  
 ||| ||| ||| |||  
 ACC TCC TTTC CCCTC  
 C \_\_\_\_ T  
 GAM1245 FLJ14107 5' CCTCCCACTCCCCA 46691 AA TAAAAA  
 TGG GG AGTGGGAGG  
 ||| || |||||  
 ACC CC TCACCCTCC  
 \_ \_  
 GAM1245 FLJ14549 3' CCCACTTCCCTCTCCTTCCA 51441 TAAAA\_  
 TGGAAGG AAGTGGG  
 ||||| |||||  
 ACCTTCC TTCACCC  
 TCTCCC  
 GAM1245 FLJ14596 3' CTCCTCCCACCTCTGTCACCAC 51459 AA AAAAAA\_  
 CA TGG GGT GTGGGAGGAG  
 ||| ||| |||||  
 ACC CCA CACCCTCCTC  
 A\_ CTGTCTC  
 GAM1245 FLJ14681 5' CTCCTATCTCTGCCTTCCA 51524 AAAAA  
 TGGAAGGTA GTGGGAG  
 ||||| |||||

ACCTTCCGT TATCCTC  
 CTC\_\_  
 GAM1245 FLJ14721 3' CCTTCCCCTACCCCA 51581 AA AAAAA T  
 TGG GGT AG GGGAGG  
 ||| ||| || |||||  
 ACC CCA TC CCTTCC  
 C\_ \_\_\_\_ C  
 GAM1245 FLJ14824 3' TCTTCCTTCTCCCCTCCA 51646 A TAAAAA T  
 TGG AGG AG GGGAGGA  
 ||| ||| || |||||  
 ACC TCC TC TCCTTCT  
 C CC\_ T  
 GAM1245 FLJ20085 3' CCCCCGCCCCCGCACCTTCCA 34514 AAAAAA A  
 TGGAAGGT GTGGG GG  
 ||||| ||||| ||  
 ACCTTCCA CGCCC CC  
 CGCCCC \_  
 GAM1245 FLJ20113 3' CCCCAGCTTCCTGCCCTCCA 34575 A AAA G A  
 TGGA GGTA AAGT GG GG  
 |||| ||| |||| ||  
 ACCT CCGT TTCG CC CC  
 C CC\_ A \_  
 GAM1245 FLJ20207 5' CTCCCGCTTCCTCCCTCCA 34736 A TAAAA  
 TGG AGG AAGTGGGAG  
 ||| ||| |||||  
 ACC TCC TTCGCCCTC  
 C CTCC\_  
 GAM1245 FLJ20308 3' TCCACTTCTCACCTGCCA 66856 A AAAA  
 TGG AGGT AAGTGGG  
 ||| ||| |||||  
 ACC TCCA TTCACCT  
 G CTC\_  
 GAM1245 FLJ20548 3' CCTGCCCCTTTTCCTTCCA 35377 TAA T \_  
 TGGAAGG AAAAG GGG AGG  
 ||||| ||||| ||| |||  
 ACCTTCC TTTTC CCC TCC  
 \_ \_ G  
 GAM1245 FLJ20568 3' CCTCCCACCTTCCTTCTTCC 35416 TAAAAAA  
 GGAAGG GTGGGAGG  
 ||||| |||||  
 CCTTCT CACCCTCC  
 TCCTTC\_  
 GAM1245 FLJ21156 3' CTTTTCCCCTCTCCCTCCA 44808 A TAAAAA T  
 TGGA GG AG GGGAGGAG  
 ||| || || |||||  
 ACCT CC TC CCCTTTTC  
 C TC\_ \_  
 GAM1245 FLJ21596 3' CTCCTCCCACCCCGTAGCTCCA 45700 A G AAAAA  
 TGGA G TA GTGGGAGGAG  
 ||| | || |||||



ACCT C AT CACCCTCCTC  
 \_ G GCCC\_  
 GAM1245 FLJ22671 3' CTCCTTCTCCTTCACCTTCCA 45865 AAAA TG  
 TGGAAGGT AAG GGAGGAG  
 ||||| || |||||  
 ACCTTCCA TTC CTCCTC  
 C\_\_ CT  
 GAM1245 FLJ23022 3' TCCTTTCTCCTTCCTTCCA 46813 TAAAA T\_ GG  
 TGGAAGG AAG G AGGA  
 ||||| || | |||  
 ACCTTCC TTC C TCCT  
 \_\_\_\_ CT TT  
 GAM1245 FLJ23416 3' TCCTCCCCTCCCCTCCCA 49955 A TAAAAA T  
 TGG AGG AG GGGAGGA  
 ||| || || |||||  
 ACC TCC TC CCCTCCT  
 C CC\_\_ \_  
 GAM1245 FLJ30058 3' CCCTGACTTTCCTACCCTCC 58639 A AA G A  
 GGA GGTA AAAGT GG GG  
 ||| ||| ||||| || ||  
 CCT CCAT TTTCA TC CC  
 C CC G \_  
 GAM1245 FLJ30532 3' TCCTGCCTCTGCCTCCCA 58553 A AAAAA T G  
 TGG AGGT AG GG AGGA  
 ||| ||| || || |||||  
 ACC TCCG TC CC TCCT  
 C \_\_\_\_ T G  
 GAM1245 FOXH1 3' CTCCCGCTCCCACCCCA 14073 AA AAAAA  
 TGG GGT AGTGGGAG  
 ||| ||| |||||  
 ACC CCA TCGCCCTC  
 C\_ CCC\_  
 GAM1245 FUK 3' CCTCCTACTCCCA 58974 AA TAAAAA  
 TGG GG AGTGGGAGG  
 ||| || |||||  
 ACC CC TCATCCTCC  
 \_\_\_\_  
 GAM1245 GBTS1 3' CTGCTCTCTCCACCCTCC 59055 A AAAAA T G  
 GGA GGT AG GGGAG AG  
 ||| ||| || ||||| ||  
 CCT CCA TC CTCTC TC  
 C CC\_\_ T G  
 GAM1245 GOLGA3 3' CTCCCGGCACTTCTACCTTCCA 19716 A AA \_  
 TGGAAGGTA AA GT GGGAG  
 ||||| || || |||||  
 ACCTTCCAT TT CG CCCTC  
 C CA G  
 GAM1245 GPS2 3' CCTTTTACTCCCCTACCCCA 50574 AA AAAA  
 TGG GGTA AGTGGGAGG  
 ||| ||| |||||

ACC CCAT TCATTTTCC  
 — CCCC  
 GAM1245 GPS2 3' CCTTTTACTCCCCTACCCCA 87156 AA AAAA  
 TGG GGTA AGTGGGAGG  
 ||| ||| |||||  
 ACC CCAT TCATTTTCC  
 — CCCC  
 GAM1245 GRASP1 3' CTCCTCCCCTTCCTACCCCC 39301 AA AAA T  
 GG GGTA AAG GGGAGGAG  
 || ||| ||| |||||  
 CC CCAT TTC CCCTCCTC  
 C\_ CC\_ \_  
 GAM1245 HARS2 3' CCTTCCCTTCCACCTCC 55033 A AAAA T  
 GGA GGT AAG GGGAGG  
 ||| ||| ||| |||||  
 CCT CCA TTC CCTTCC  
 \_ CC\_ \_  
 GAM1245 HEAB 5' CCTCCCACCTTTGGCGTC 22413 AG AA A  
 GA GT AAA GTGGGAGG  
 || || ||| |||||  
 CT CG TTT CACCCTCC  
 G\_ G\_ C  
 GAM1245 HTCD37 3' CCCCTTTTTCTACCCCA 67674 AA \_ T  
 TGG GGTA AAAAAG GGG  
 ||| ||| ||||| |||  
 ACC CCAT TTTTTC CCC  
 \_ CC \_  
 GAM1245 HU-K4 3' CTCCCACCTCTACCTCCA 24367 A AAAAA  
 TGGA GGTA GTGGGAG  
 |||| ||| |||||  
 ACCT CCAT CACCCTC  
 \_ CTC\_  
 GAM1245 IL18BP 5' CCTCCCCCACCTTTTCA 19106 AAAAAAGT  
 TGGAAGGT GGGAGG  
 ||||| |||||  
 ACTTTCCA CCCTCC  
 CC\_\_\_\_\_  
 GAM1245 KCNH8 5' CTCCCTCCATCCTTCCA 58255 TAAAAA GA  
 TGGAAGG GTGG GGAG  
 ||||| ||| |||  
 ACCTTCC TACC CCTC  
 \_\_\_\_\_ TC  
 GAM1245 KIAA0170 3' CTCCACTACCTTTTCCCTCCC 27674 A T AA GA  
 A TGG AGG AAAA GTGG GGAG  
 ||| ||| ||| ||| |||  
 ACC TCC TTTT CATC CCTC  
 C C CC A\_  
 GAM1245 KIAA0172 5' CTCCCTTTTCTTACCATCC 64969 A A T  
 GGA GGTA AAAG GGGAG  
 ||| |||| ||| |||||

CCT CCATT TTTT CCCTC  
 A C \_  
 GAM1245 KIAA0232 3' CTCCTCCCCATCTCACCCCCA 72748 AA AAAAAAGT  
 TGG GGT GGGAGGAG  
 ||| ||| |||||  
 ACC CCA CCCTCCTC  
 C\_ CTCTAC\_  
 GAM1245 KIAA0285 3' CTCCTCCCACCTTCTCACCTTT 29016 AAAAAA  
 CA TGAAGGT GTGGGAGGAG  
 ||||| |||||  
 ACTTTCCA CACCCTCCTC  
 CTCTTC  
 GAM1245 KIAA0296 3' TCCTCTCTCTCCCCCA 28119 AA TAAAAA T  
 TGG GG AG GGGAGGA  
 ||| || |||||  
 ACC CC TC CTCTCCT  
 CC TC\_\_\_\_\_ T  
 GAM1245 KIAA0367 3' CCTCCCACAGCCACCTCCA 67297 A AAAAAA  
 TGA GGT GTGGGAGG  
 ||| ||| |||||  
 ACCT CCA CACCCTCC  
 \_ CCCGA\_  
 GAM1245 KIAA0451 3' CCTCTCTCTCCTTCCA 29105 TAAAAA T  
 TGAAGG AG GGGAGG  
 ||||| || |||||  
 ACCTTCC TC CTCTCC  
 \_\_\_\_\_ T  
 GAM1245 KIAA0451 3' CTCTTCCCACCCTCC 29106 A TAAAAA  
 GGA GG GTGGGAGGAG  
 ||| || |||||  
 CCT CC CACCCTTCTC  
 \_\_\_\_\_  
 GAM1245 KIAA0514 5' TCTCCCTTCCCCTCCCA 28096 A TA AAAGT  
 TGG AGG AA GGGAGG  
 ||| ||| || |||||  
 ACC TCC TT CCCTCT  
 C CC \_\_\_\_\_  
 GAM1245 KIAA0515 3' CCCTCCGCTCCCTTCCA 63806 TAAAAA GA  
 TGAAGG AGTGG GG  
 ||||| ||||| ||  
 ACCTTCC TCGCC CC  
 C\_\_\_\_\_ TC  
 GAM1245 KIAA0532 3' CTCCCACCTCCACCTCCCA 70772 A AAAAAA  
 TGG AGGT GTGGGAG  
 ||| ||| |||||  
 ACC TCCA CACCCTC  
 C CCTC\_  
 GAM1245 KIAA0552 5' CCTCCCCTCCCCCTCCCA 28312 A TAAAAA T  
 TGG AGG AG GGGAGG  
 ||| ||| || |||||

		ACC TCC TC CCCTCC		
		C CCCC__ _		
GAM1245 KIAA0599	3'	CCCAGATTCTTTTTATCCCCC 77172	AA	_____
A		TGG GGTAAAAAAG TGGG		
		ACC CTATTTTTTC ACCC		
		CC TTAG		
GAM1245 KIAA0643	3'	CCGGGACACTTTTCTTCCCTCC 45597	A TAA	GGA_
A		TGGA GG AAAAGTG GG		
		ACCT CC TTTTCAC CC		
		C TTC AGGG		
GAM1245 KIAA0669	5'	CTCCCACTCCCACCCCCA 28788	AA	AAAAA
		TGG GGT AGTGGGAG		
		ACC CCA TCACCCTC		
		C_ CCC__		
GAM1245 KIAA0773	3'	CTCCCCCAATGCCCTGCCTTCC 28053	AAAAAG	A
A		TGGAAGGTA TGGG GGAG		
		ACCTTCCGT ACCC CCTC		
		CCCGTA _		
GAM1245 KIAA0854	3'	CCTCCCACACTGCCCCCCA 30098	AA	AAAAA
		TGG GGTA GTGGGAGG		
		ACC CCGT CACCCTCC		
		CC CA__		
GAM1245 KIAA1026	3'	CTCAACCCTTTTTATCCCCCA 71192	AA TA	T GAG
		TGG GG AAAAAG GG GAG		
		ACC CC TTTTTC CC CTC		
		CC TA _ AA_		
GAM1245 KIAA1026	3'	CTCCTCCCACACATTACCTTCC 71193	AAAA	
A		TGGAAGGTAA GTGGGAGGAG		
		ACCTTCCATT CACCCTCCTC		
		ACA_		
GAM1245 KIAA1042	3'	CTCCTCTCTTGCTCCCACCTCC 30338	A	AAAAAAGT
C		GG AGGT GGGAGGAG		
		CC TCCA CTCTCCTC		
		C CCCTCGTT		
GAM1245 KIAA1046	3'	CTCCCCAGCCCCCCTTACCTTC 29995	AAAA_ G	A
		GAAGGTAA GT GG GGAG		
		CTTCCATT CG CC CCTC		
		CCCCC A _		
GAM1245 KIAA1111	3'	CCCTCACCCCTTTACCCCCA 96207	AA	AAA A
		TGG GGTAAA GTGGG GG		

ACC CCATTT CACTC CC  
 C\_ CCC \_  
 GAM1245 KIAA1155 3' CTCCCCAATCTTACCTTCC 62231 AAAAGT  
 GGAAGGTAA GGGAG  
 ||||| ||||  
 CCTTCCATT CCCTC  
 CTAAC\_  
 GAM1245 KIAA1163 3' CTCCTCTTACCCTACCCCA 78900 AA AAAAA  
 TGG GGTA GTGGGAGGAG  
 || ||| |||||  
 ACC CCAT CATTCTCCTC  
 \_ CC\_  
 GAM1245 KIAA1169 3' CTCCTCGCTTCCCCTCCCA 35449 A TAAAA \_  
 TGG AGG AAGTG GGAG  
 || ||| |||| ||||  
 ACC TCC TTCGC CCTC  
 C CC\_ T  
 GAM1245 KIAA1205 3' CCTCCCCTCCTTTT 70043 TAAAAA  
 GGAAGG AGTGGGAGG  
 |||| |||||  
 TTTTCC TCACCCTCC  
 \_\_\_\_\_  
 GAM1245 KIAA1266 3' CCTCCTACTCCTCCA 66117 A TAAAAA  
 TGGA GG AGTGGGAGG  
 ||| || |||||  
 ACCT CC TCATCCTCC  
 \_ \_\_\_\_\_  
 GAM1245 KIAA1363 3' CCCCCATCTCCTCCTTCCA 69261 TAAAAAA A  
 TGGAAGG GTGGG GG  
 ||||| |||| ||  
 ACCTTCC TACCC CC  
 TCCTC\_ \_  
 GAM1245 KIAA1388 3' CCTCCCACCTTTGTAGTGC 93578 AA\_ \_  
 GTA AAAG TGGGAGG  
 || ||| |||||  
 CGT TTTC ACCCTCC  
 GATG C  
 GAM1245 KIAA1416 3' TCTTCTACCCATCCA 86464 A TAAAAA  
 TGGA GG GTGGGAGG  
 ||| || |||||  
 ACCT CC CATCTTCT  
 A \_\_\_\_\_  
 GAM1245 KIAA1463 3' TTCCTCCCCACTCCTCCA 72279 A TAAAAA \_  
 TGGA GG AGTGGG AGGAG  
 ||| || |||| ||||  
 ACCT CC TCACCC TCCTT  
 \_ \_\_\_\_\_ C  
 GAM1245 KIAA1538 5' TCTTCTCTCCCCCTCCA 71558 A TAAAAA T  
 TGGA GG AG GGGAGGA  
 ||| || || |||||

ACCT CC TC TCCTTCT  
 C CC\_\_\_\_ \_  
 GAM1245 KIAA1543 5' CTCCTGTCTTCACCTTCC 70984 AAAA \_  
 GGAAGGT AAG TGGGAG  
 ||||| || |||||  
 CCTTCCA TTC GTCCTC  
 C\_\_ T  
 GAM1245 KIAA1666 3' TTCCTCCCTCACCCTCCA 65252 A\_ AAAAAAGT  
 TGGA GGT GGGAGGAG  
 ||| || |||||  
 ACCT CCA CCCTCCTT  
 CA CT\_\_\_\_\_  
 GAM1245 KIAA1671 3' TCTTCCTCCTCACCTCCA 65696 A AAAAA TG  
 TGGA GGT AG GGAGGA  
 ||| || || |||||  
 ACCT CCA TC CTTCT  
 \_ C\_\_ CT  
 GAM1245 KIAA1755 3' CTCCTCTCTCTCACCTCCC 61343 A AAAAA T  
 GG AGGT AG GGGAGGAG  
 || ||| || |||||  
 CC TCCA TC CTCTCCTC  
 C C\_\_ T  
 GAM1245 KIAA1775 3' TCTCCCACCCTACCA 52385 A TAAAAA  
 TGG AGG GTGGGAGG  
 ||| || |||||  
 ACC TCC CACCCTCT  
 A \_\_\_\_\_  
 GAM1245 KIAA1811 3' CTCCTCCCCTGGTCCTCCCCC 64795 AA TAAAAA T  
 A TGG GG AG GGGAGGAG  
 ||| || || |||||  
 ACC CC TC CCCTCCTC  
 CC TCCTGG \_  
 GAM1245 KIAA1822 3' TCCTCCCCAGCCTCCA 67575 A AAAAAAGT  
 TGGA GGT GGGAGGA  
 ||| || |||||  
 ACCT CCG CCCTCCT  
 \_ AC\_\_\_\_\_  
 GAM1245 KIAA1870 5' CTCTGGCAGACCTTTTACCTTC 51830 AA\_\_ G  
 CA TGGAAGGTAAAA GT GGAG  
 ||||| || |||  
 ACCTTCCATTTT CG TCTC  
 CCAGA G  
 GAM1245 KIAA1871 3' CTCCTCCCTCCTCAGCCTCCCA 61231 A AAAAAAGT  
 TGG AGGT GGGAGGAG  
 ||| || || |||||  
 ACC TCCG CCCTCCTC  
 C ACTCCT\_\_  
 GAM1245 KIAA1949 5' CCCTCCACTTCCTCTCCTCCCA 92082 A TAAAA GA  
 TGG AGG AAGTGG GG  
 ||| || ||||| ||

			ACC TCC TTCACC CC		
			C TCTCC TC		
GAM1245 KIAA1949	5'	CCCTCCACTTCCTCTCCTCCCA 97750	A TAAAA GA		
		TGG AGG AAGTGG GG			
		ACC TCC TTCACC CC			
		C TCTCC TC			
GAM1245 KIAA1949	5'	CCCTCCACTTCCTCTCCTCCCA 97872	A TAAAA GA		
		TGG AGG AAGTGG GG			
		ACC TCC TTCACC CC			
		C TCTCC TC			
GAM1245 LYPLA2	3'	CTCCCCCAGCTGTCTCACCCC 23429	AA AAAAA _ A		
	CA	TGG GGT AG TGGG GGAG			
		ACC CCA TC ACCC CCTC			
		C_ CTCTG G C			
GAM1245 MAP2K5	5'	CCTCCCCCTCATCCTCCA 10865	A TAAAAA T		
		TGGA GG AG GGGAGG			
		ACCT CC TC CCCTCC			
		_ TAC_ C			
GAM1245 MCF2L	3'	CTCCCCACGCGCCCCCTGCCTC 60844	A AAAAA_ _ A		
	CCA	TGG AGGTA GTG GG GGAG			
		ACC TCCGT CGC CC CCTC			
		C CCCCCG A _			
GAM1245 MDS028	3'	CTCCCATTTTTCCACCCACCCA 37463	AA_ AA		
		TGG GGT AAAAGTGGGAG			
		ACC CCA TTTTACCCTC			
		CAC CC			
GAM1245 MEIS3	3'	CTCCTGTCCCCCCACCTCC 78280	A AAAAAAGT _		
		GGA GGT GGGA GGAG			
		CCT CCA CCCT CCTC			
		_ CCCC_ GT			
GAM1245 MGC10540	3'	CTCCCTTTACTTCTTACCTCCC 50381	A AA GA		
	A	TGG AGGTAA AAGTGG GGAG			
		ACC TCCATT TTCATT CCTC			
		C C_ TC			
GAM1245 MGC10540	3'	CTCCTCCCACCCCTTTAGCTGC 50382	A G AAA		
	T	GG AG TAAA GTGGGAGGAG			
		TC TC ATTT CACCCTCCTC			
		G G CCC			
GAM1245 MGC10818	3'	CCCTTCTTTCTACCTTC 47538	AA T_		
		GAAGGTA AAAG GGG			

CTTCCAT TTTC CCC  
 CC TT  
 GAM1245 MGC11316 3' TCCTCCCACCTTTCTTGGCT 51943 G A  
 AG TAA AAAGTGGGAGGA  
 || ||| |||||  
 TC GTT TTTCACCCTCCT  
 G C  
 GAM1245 MGC12966 3' TCATACCCCTTTCCTTCCA 51126 TAAA T AG\_  
 TGGAAGG AAAG GGG GA  
 ||||| ||| ||| ||  
 ACCTTCC TTTC CCC CT  
 \_\_\_\_\_ ATA  
 GAM1245 MGC13138 3' TCCTTCCTCAGCCTCCCA 53027 A AAAAAAGT  
 TGG AGGT GGGAGGA  
 ||| ||| |||||  
 ACC TCCG CCTTCCT  
 C ACT\_\_\_\_\_  
 GAM1245 MGC20235 3' CTCATCACACCCTTACCTCCCA 58893 A AAAA \_  
 TGG AGGTAA GTGG GAG  
 ||| ||||| ||| |||  
 ACC TCCATT CACT CTC  
 C CCCA A  
 GAM1245 MGC2555 3' CTCCCCACTTTCACCTCCC 51315 A AAA AG  
 GG AGGT AAAGTGGG G  
 || ||| ||||| |  
 CC TCCA TTTCACCC C  
 C C\_\_ CT  
 GAM1245 MGC2628 3' TCCTTTTTCTCTCCCTCCA 43978 A TAAAAA TG  
 TGGA GG AG GGAGGA  
 |||| || || |||||  
 ACCT CC TC TTTCCT  
 C TC\_\_ TT  
 GAM1245 MGC26684 3' CTCCTCCCGACCTTTTTTACCC 57990 AA \_  
 CCC GG GGTA AAAAAG TGGGAGGAG  
 || ||||| |||||  
 CC CCATTTTTTC GCCCTCCTC  
 CC CA  
 GAM1245 MGC2803 3' CCCCCCTTCTCACCTCC 43864 A AAAA T A  
 GGA GGT AAG GGG GG  
 ||| ||| ||| ||| ||  
 CCT CCA TTC CCC CC  
 \_ CTC\_ \_ \_  
 GAM1245 MGC29667 3' CTCCTCTTCTATCTTACCCTC 58333 A AAA T  
 GA GGTA AG GGGAGGAG  
 || |||| || |||||  
 CT CCATT TC TTCTCCTC  
 C CTA \_  
 GAM1245 MGC3200 3' CTTCCCCTCCTTCCA 50223 TAAAAA T  
 TGGAAGG AG GGGAGG  
 ||||| || |||||



ACCTTCC TC CCCTTC

GAM1245 MGC35558 5' CCTCCCGCCACCCCGCCA 58780 AA\_ AAAAAA  
TGG GGT GTGGGAGG  
||| ||| |||||  
ACC CCA CGCCCTCC  
GCC C\_\_\_\_\_

GAM1245 MGC4172 3' CTCCTTCCCTCCCCACCCTTC 44202 TAAAAA T  
GAAGG AG GGGAGGAG  
||||| || |||||  
CTTCC TC CCTTCCTC  
CACCCC \_

GAM1245 MGC4342 3' CCTCCCCGCTCCCTTCCA 44265 TAAAAA \_  
TGGAAGG AGTGGG AGG  
||||| ||||| |||  
ACCTTCC TCGCCC TCC  
C\_\_\_\_\_ C

GAM1245 MGC4549 3' CTTCTCCACCTTCTA 50463 AAAAAAGT  
TGGAAGGT GGGAGG  
||||| |||||  
ATCTTCCA TCTTCC  
CC\_\_\_\_\_

GAM1245 MGC5528 3' CCCTCTACTTTTAGCCTTCCA 44044 AA GA  
TGGAAGGT AAAAGTGG GG  
||||| ||||| ||  
ACCTCCG TTTTCATC CC  
A\_ TC

GAM1245 NALP2 3' CTCCTCCCCGGCCCCTACCCCT 35315 AA AAAAAAGT  
CA TGG GGTA GGGAGGAG  
||| ||| |||||  
ACT CCAT CCCTCCTC  
CC CCCCCGC

GAM1245 NIP30 3' CTCCTTTTCCCCTTCCA 46324 TA AAGT  
TGGAAGG AAA GGGAG  
||||| ||| |||||  
ACCTTCC TTT TCCTC  
CC \_\_\_\_\_

GAM1245 NIT1 3' CCTCCCACCCCCACCCTGCCA 18807 A TAAAAAA  
TGG AGG GTGGGAGG  
||| ||| |||||  
ACC TCC CACCCTCC  
G CACCCC\_

GAM1245 OBSCN 3' CCTCCCGCTCACCTTCC 70651 AAAAA  
GGAAGGT AGTGGGAGG  
||||| |||||  
CCTTCCA TCGCCCTCC  
C\_\_\_\_\_

GAM1245 P311 5' CTCCCTTTCCCTCTCTCTCCCC 16487 AA TAAAAA T \_  
CCA TGG GG AG GGGA GGAG  
||| || || ||||| |||

ACC CC TC CCCT CCTC  
 CC TCTC\_\_ T TTC  
 GAM1245 P311 3' CCCCCCACCTTTTTTTTC 16486 T A A  
 GAAGG AAAAA GTGGG GG  
 |||| |||| |||| ||  
 CTTTT TTTTT CACCC CC  
 \_ C C  
 GAM1245 PCDH10 5' CTCCTCCTCGTTCTCCTCCCA 40424 A TA AAAGT  
 TGG AGG AA GGGAGGAG  
 ||| ||| || |||||  
 ACC TCC TT TCCTCCTC  
 C TC GC\_\_  
 GAM1245 PCDH10 5' CTCCTCCTCGTTCTCCTCCCA 51988 A TA AAAGT  
 TGG AGG AA GGGAGGAG  
 ||| ||| || |||||  
 ACC TCC TT TCCTCCTC  
 C TC GC\_\_  
 GAM1245 PDEF 3' TCCATCCCCCTGCCTCCCA 24752 A AAAAA T \_  
 TGG AGGT AG GGA GGA  
 ||| ||| || |||||  
 ACC TCCG TC CCCT CCT  
 C \_ C A  
 GAM1245 PER3 3' TTTCACCTTCCA 33685 AAAAAAGT  
 TGGAAGGT GGGAGG  
 ||||| |||||  
 ACCTTCCA CCCTT  
 \_\_\_\_\_  
 GAM1245 PF1 3' TCCATCCCACCTTCCA 95123 AAAAAA \_  
 TGGAAGGT GTGGGA GGA  
 ||||| ||||| |||  
 ACCTTCCA TACCCT CCT  
 \_\_\_\_\_ A  
 GAM1245 phospho1 5' CCCACTTCTTACACTCCA 82369 AG AA  
 TGGA GTAA AAGTGGG  
 ||| ||| |||||  
 ACCT CATT TTCACCC  
 CA C\_  
 GAM1245 PHRET1 5' CTCCCCCTCCAGCCTCCCA 41057 A AAAAA T  
 TGG AGGT AG GGGAG  
 ||| ||| || |||||  
 ACC TCCG TC CCCTC  
 C ACC\_\_ C  
 GAM1245 PHYHIP 3' TCCTTCTCCACCTGCCCA 28615 A\_ AAAAAAGT  
 TGG AGGT GGGAGGA  
 ||| ||| |||||  
 ACC TCCA TCTTCCT  
 CG CC\_\_\_\_\_  
 GAM1245 PKNOX2 3' CCTCCCACCCACCTTCCA 90876 AAAAAA  
 TGGAAGGT GTGGGAGG  
 ||||| |||||

ACCTTCCA CACCCTCC  
 CC\_\_\_\_  
 GAM1245 PLAGL2 3' CCCTCATTGGTCTTCCTCCCA 70446 A TAAAAA A  
 TGG AGG AGTGGG GG  
 ||| ||| ||||| ||  
 ACC TCC TTA CTC CC  
 C TTCTGG \_  
 GAM1245 PPFIA4 3' TCCTTTCTCTGACCTCCCA 70333 A AAAAA T GG  
 TGG AGGT AG G AGGA  
 ||| ||| || | |||  
 ACC TCCA TC C TCCT  
 C G\_\_\_\_ T TT  
 GAM1245 PPY2 3' CTCCCGCCCCCTACCACTCCA 40821 A\_ AAAAA  
 TGGA GGTA GTGGGAG  
 ||| ||| |||||  
 ACCT CCAT CGCCCTC  
 CA CCCC\_  
 GAM1245 PRO1430 3' TTCCTTTCTATCTTCCA 37749 AAAAAAGT GG  
 TGGAAGGTA G AGGAG  
 ||||| || | |||  
 ACCTTCTAT C TCCTT  
 \_\_\_\_\_ TT  
 GAM1245 PRO2730 5' CCTTCTACCCTCCA 47414 A TAAAAAA  
 TGGA GG GTGGGAGG  
 ||| || |||||  
 ACCT CC CATCTTCC  
 \_ \_  
 GAM1245 PRO2831 5' CTCCCACCTCAACCTCCCA 37601 A AAAAAA  
 TGG AGGT GTGGGAG  
 ||| ||| |||||  
 ACC TCCA CACCCTC  
 C ACTC\_  
 GAM1245 PTPNS1 3' CCTCCCCACCACCTCTCA 54997 GA AAAAAA \_  
 TG AGGT GTGGG AGG  
 || ||| ||||| |||  
 AC TCCA CACCC TCC  
 TC C\_\_\_\_ C  
 GAM1245 QSCN6 3' CCTCCCACCCCTTGCTCC 11037 AG AAAA  
 GGA GTAA GTGGGAGG  
 ||| ||| |||||  
 CCT CGTT CACCCTCC  
 \_ CCC\_  
 GAM1245 RAB6C 3' CTCTTCCTCCTCCACTTCC 49568 GTAAAAA TG  
 GGAAG AG GGAGGAG  
 |||| || |||||  
 CCTTC TC CTTCTC  
 ACC\_\_\_\_ CT  
 GAM1245 RABEX5 3' CTCAATCTTTTTTCCCTCCA 27184 A T TGG  
 TGGA GG AAAAAAG GAG  
 |||| || ||||| |||

ACCT CC TTTTTC CTC  
 C \_ TAA  
 GAM1245 RBPMS 5' CCGTCCCCTCCTTCCA 22491 TAAAAA T \_  
 TGGAAGG AG GGA GG  
 ||||| || |||||  
 ACCTTC TC CCCT CC  
 \_\_\_\_\_ G  
 GAM1245 RIP60 3' CCTCCCACCTGCCCCC 25455 AA AAAAA  
 GG GGTA GTGGGAGG  
 || ||| |||||  
 CC CCGT CACCCTCC  
 C\_ C\_\_\_\_  
 GAM1245 RIP60 3' TCTCCCTTCCCCTCCA 25461 A TA AAAGT  
 TGG AGG AA GGGAGG  
 ||| ||| || |||||  
 ACC TCC TT CCCTCT  
 C CC \_\_\_\_\_  
 GAM1245 RNF8 3' CTCCCACCTCAACCTCCA 14223 A AAAAAA  
 TGG AGGT GTGGGAG  
 ||| ||| |||||  
 ACC TCCA CACCCTC  
 C ACTC\_\_\_\_  
 GAM1245 RNPC1 3' CTCCTGCCTCTCCACACTCCA 33988 AG AAAAA T G  
 TGGA GT AG GG AGGAG  
 ||| || || |||||  
 ACCT CA TC CC TCCTC  
 CA CC\_\_\_\_ T G  
 GAM1245 RPH3A 3' CTCCTCCCTCTTCTTCCCTTC 30242 T A T  
 CA TGGAAGG AAA AAG GGGAGGAG  
 ||||| ||| ||| |||||  
 ACCTTC TTT TTC CCCTCCTC  
 C C T  
 GAM1245 SCGF 5' CCTCCCACCCAGACATCCA 11439 AG AAAAAA  
 TGGA GT GTGGGAGG  
 ||| || |||||  
 ACCT CA CACCCTCC  
 A\_ GACCC\_  
 GAM1245 SCYA13 3' CTCTAAGCCCCCTTCCCTTCCA 18255 TAAAA T A\_\_\_\_  
 TGGAAGG AAG GGG GGAG  
 ||||| ||| ||| |||  
 ACCTTC TTC CCC TCTC  
 C\_\_\_\_ C GAA  
 GAM1245 SCYB10 3' TTTCCCATCTTCCA 7801 GTAAAAA  
 TGGAAG GTGGGAGG  
 ||||| |||||  
 ACCTTC TACCCTTT  
 \_\_\_\_\_  
 GAM1245 SIMRP7 3' CTCCCCTTCTACCCTCCA 92363 A AAA T  
 TGGA GGTA AAG GGGAG  
 ||| ||| ||| |||

			ACCT CCAT TTC CCCTC		
			C C__ _		
GAM1245	SIRPB1	3'	CTCCACACCTCTCACCTCCA	20249	A AAAAAA _
			TGGA GGT GTG GGAG		
			ACCT CCA CAC CCTC		
			_ CTCTC_ A		
GAM1245	SLC26A10	5'	CTCCCTCTTATCTCCACCCCCC	56029	AA AAAA__ T
	A		TGG GGT AAG GGGAG		
			ACC CCA TTC CCCTC		
			CC CCTCTA T		
GAM1245	SMARCF1	3'	CTCCTGTTTCTCTCTCCTCCTT	20038	TAAAAA_ TG G
	CCA		TGGAAGG AG G AGGAG		
			ACCTTCC TC T TCCTC		
			TCCTCTC TT G		
GAM1245	SMARCF1	3'	CTCCTTCCACCTCCCCTCCCTC	20039	A TAAAAA
	CA		TGGA GG GTGGGAGGAG		
			ACCT CC CACCTTCCTC		
			C TCCCCTC		
GAM1245	SMARCF1	3'	CTCCTGTTTCTCTCTCCTCCTT	37434	TAAAAA_ TG G
	CCA		TGGAAGG AG G AGGAG		
			ACCTTCC TC T TCCTC		
			TCCTCTC TT G		
GAM1245	SMARCF1	3'	CTCCTTCCACCTCCCCTCCCTC	37435	A TAAAAA
	CA		TGGA GG GTGGGAGGAG		
			ACCT CC CACCTTCCTC		
			C TCCCCTC		
GAM1245	SMARCF1	3'	CTCCTGTTTCTCTCTCCTCCTT	57484	TAAAAA_ TG G
	CCA		TGGAAGG AG G AGGAG		
			ACCTTCC TC T TCCTC		
			TCCTCTC TT G		
GAM1245	SMARCF1	3'	CTCCTTCCACCTCCCCTCCCTC	57485	A TAAAAA
	CA		TGGA GG GTGGGAGGAG		
			ACCT CC CACCTTCCTC		
			C TCCCCTC		
GAM1245	SPR1	3'	CTCGGCCCCACCTACCTCCCA	25953	A AAAAA AG_
			TGG AGGTA GTGGG GAG		
			ACC TCCAT CACCC CTC		
			C C__ CGG		
GAM1245	SRF	3'	TTCTTCCCGCCCCACCTCCCA	11953	A AAAAA
			TGG AGGT GTGGGAGGAG		

ACC TCCA CGCCCTTCTT  
 C CCC\_\_\_\_  
 GAM1245 SSBP3 3' CCTCCCACCCCATCCA 36061 A TAAAAAA  
 TGGA GG GTGGGAGG  
 ||| || |||||  
 ACCT CC CACCCTCC  
 A C\_\_\_\_\_  
 GAM1245 STI2 3' CCCCTTTTTTACTCCA 88965 AA T  
 TGG GGTA AAAAG GGG  
 || ||||| ||  
 ACC TCATTTTTTC CCC  
 C\_ \_  
 GAM1245 THG-1 5' CCTCCCGCCACCTCCC 48184 A AAAAAA  
 GG AGGT GTGGGAGG  
 || ||| |||||  
 CC TCCA CGCCCTCC  
 C C\_\_\_\_\_  
 GAM1245 TUBB5 3' CTCCA ACTTCTCTTTCACCCTC 20300 A A A T GA  
 TA TGGA GGT AAA AG GG GGAG  
 ||| ||| || || |||  
 ATCT CCA TTT TC TC CCTC  
 C C C T AA  
 GAM1245 USP22 3' TCTTCCTTTCCCCTTCCA 68030 TA AAAGT  
 TGGAAGG AA GGGAGGA  
 ||||| || |||||  
 ACCTTC TT TCCTTCT  
 CC \_\_\_\_\_  
 GAM1245 WBSCR17 3' TCCTCACCCCATCTCCA 81304 A AAAAAAGT \_  
 TGG AGGT GG GAGGA  
 || ||| || |||||  
 ACC TCTA CC CTCCT  
 C CC\_\_\_\_\_ A  
 GAM1245 ZIN 3' CTCCCCCATCCCCATCCTCC 25489 A TAAAAAA A  
 A TGGA AGG GTGGG GGAG  
 ||| ||| ||||| |||||  
 ACC TCC TACCC CCTC  
 C TACCCCC \_  
 GAM1245 ZNF213 3' CCTCCC ACTCCGTTTCCA 65096 GTAAAAA  
 TGGAAG AGTGGGAGG  
 ||||| |||||  
 ACCTTT TCACCCTCC  
 GCCC\_\_\_\_\_  
 GAM1245 ZNF238 3' CTCCCCTTCCTCCTTACCCTCC 20959 A AA\_\_\_\_ T  
 GGA GGTA AAG GGGAG  
 || |||| || |||||  
 CCT CCATT TTC CCCTC  
 C CCTCC \_  
 GAM1245 LOC112817 3' CTCCCATCCCTGCCCTCCA 56510 A AAAAA  
 TGGA GGTA GTGGGAG  
 ||| ||| |||||

ACCT CCGT TACCCTC  
 C CCC\_\_  
 GAM1245 LOC113612 3' CTCTTACCCTTCTGCCTTCCA 73084 A AA  
 TGGAAGGTA AA GTGGGAG  
 ||||| || |||||  
 ACCTCCGT TT CATTCTC  
 C CC  
 GAM1245 LOC115129 3' CTCCTCCCCAGTTCCCCTCCA 73230 A TA AAAGT  
 TGGA GG AA GGGAGGAG  
 ||| || || |||||  
 ACCT CC TT CCCTCCTC  
 \_ CC GAC\_\_  
 GAM1245 LOC115207 3' CTCCCATTCTCCCCCTCCA 56601 A TAAAAA  
 TGGA GG AGTGGGAG  
 ||| || |||||  
 ACCT CC TTACCCTC  
 C CCTC\_\_  
 GAM1245 LOC115219 5' CTCCTCTTCTCCCCACCCCA 73305 AA AAAAA TG  
 TGG GGT AG GGAGGAG  
 ||| || || |||||  
 ACC CCA TC TCTCCTC  
 C\_ CCCC\_ CT  
 GAM1245 LOC120425 5' TCCTTTTCTTATCCCTCCA 74012 A TAAAA T  
 TGGA GG AAG GGGAGGA  
 ||| || || |||||  
 ACCT CC TTC TTTTCT  
 C TA\_\_ \_  
 GAM1245 LOC123242 5' CCCCCAACCTTCCA 75597 AAAAAAG A  
 TGGAAGGT TGGG GG  
 ||||| ||| ||  
 ACCTTCCA ACCC CC  
 \_\_\_\_\_  
 GAM1245 LOC123775 3' CTCATTTCACCCACCCCCA 75624 AA AAAAAA \_  
 TGG GGT GTGGGAG GAG  
 ||| || ||||| |||  
 ACC CCA CACCCTT CTC  
 CC CC\_\_ TA  
 GAM1245 LOC124446 5' CCCCTGTTTATCTCTTCGCCTT 74287 TA A\_\_ TG A  
 CCA TGGAAGG AA AAG GG GG  
 ||||| || ||| |||  
 ACCTTCC TT TTT CC CC  
 GC CTCTA GT \_  
 GAM1245 LOC125268 3' CCTCCCTCGCCTTCCA 76074 AAAAAAGT  
 TGGAAGGT GGGAGG  
 ||||| |||||  
 ACCTCCG CCCTCC  
 CT\_\_\_\_\_  
 GAM1245 LOC126364 3' CTCCCAAATTGCTCCCCACCTC 75686 A AAA\_\_ AG  
 CCA TGG AGGT AA TGGGAG  
 ||| ||| || |||||

ACC TCCA TT ACCCTC  
 C CCCCTCG AA  
 GAM1245 LOC126669 3' TTTCTCCCTCCTTCCA 75427 TAAAAAAGT  
 TGGAAGG GGGAGGAG  
 ||||| |||||  
 ACCTTCC CCCTCTTT  
 T\_\_\_\_\_  
 GAM1245 LOC126755 3' TCCTGCCTCTTACTCTCCA 74567 AG AAAA T G  
 TGGA GTA AG GG AGGA  
 ||| || || ||||  
 ACCT CAT TC CC TCCT  
 CT \_\_\_\_ T G  
 GAM1245 LOC128387 3' TCCTCCCTCAGCCTCCCA 74754 A AAAAAAGT  
 TGG AGGT GGGAGGA  
 ||| ||| |||||  
 ACC TCCG CCCTCCT  
 C ACT\_\_\_\_\_  
 GAM1245 LOC128954 5' CTCCTCTTACTCCCTAACCTCC 75797 A AAAAA  
 CA TGG AGGT AGTGGGAGGAG  
 ||| ||| |||||  
 ACC TCCA TCATTCTCCTC  
 C ATCCC  
 GAM1245 LOC128989 3' TCTCCCTCTTCCCTCCA 74820 A TAAAA T  
 TGGA GG AAG GGGAGG  
 ||| || ||| |||||  
 ACCT CC TTC CCCTCT  
 C \_\_\_\_ T  
 GAM1245 LOC138399 5' CTCCTCTTCATCTTGTTACCT 75327 A A \_ \_  
 TCCA TGGAAGGT AA AAG TGG GAGGAG  
 ||||| || ||| ||| |||||  
 ACCTTCCA TT TTC ACT CTCCTC  
 C G T T  
 GAM1245 LOC144231 5' TCCTTCCTCCTACCACCCA 83019 AA AAAAAAGT  
 TGG GGTA GGGAGGA  
 ||| ||| |||||  
 ACC CCAT CCTTCCT  
 CA CCT\_\_\_\_\_  
 GAM1245 LOC144473 3' CTCCCCCTCTTCTACCCTCC 83071 A AAA T A  
 GGA GGTA AAG GGG GGAG  
 ||| ||| ||| ||| |||||  
 CCT CCAT TTC CCC CCTC  
 C C\_\_ T \_  
 GAM1245 LOC144501 3' CTCCTCCCCTGCGGTCCTCCCA 83107 A TAAAAA  
 TGG AGG GTGGGAGGAG  
 ||| ||| |||||  
 ACC TCC TACCCTCCTC  
 C CTGGG\_  
 GAM1245 LOC144501 3' CTCCTTCCCCTTCCTCCCTCCA 83108 A TAAAA T  
 TGGA GG AAG GGGAGGAG  
 ||| || ||| |||||



	ACCT CC	TTC CCTTCCTC	
	C TCC__ C		
GAM1245 LOC144501 3'	CTCCCCCTTCACCTTCC	83106	AAAA T
	GGAAGGT AAG GGGAG		
	CCTTCCA TTC CCCTC		
	C__ C		
GAM1245 LOC145216 3'	CTCCTGCCTTTGACCTCCCA	83264	A AA A TG
	TGG AGGT AAA G GGAG		
	ACC TCCA TTT C CCTC		
	C G_ C GT		
GAM1245 LOC145371 3'	CTCCATTCTGTACCTCCCA	77151	A AAAA TG_
	TGG AGGTA AG GGAG		
	ACC TCCAT TC CCTC		
	C C__ TTA		
GAM1245 LOC146268 3'	CCTCCCACCTCTCCA	77805	A GTAAAAA
	TGGA G AGTGGGAGG		
	ACCT C TCACCCTCC		
	— — — — —		
GAM1245 LOC146346 5'	TCCTCCCATCCTCCA	77846	A TAAAAAA
	TGGA GG GTGGGAGGA		
	ACCT CC TACCCTCCT		
	— — — — —		
GAM1245 LOC147495 3'	TCCTCTCCCTCCCTCCCA	84016	A TAAAAA T
	TGG AGG AG GGGAGGA		
	ACC TCC TC CTCTCCT		
	C C__ C		
GAM1245 LOC147622 5'	CCTCCTCACCTTCCA	84046	AAAAAAGT
	TGGAAGGT GGGAGG		
	ACCTTCCA TCCTCC		
	C_____		
GAM1245 LOC148113 3'	CTCGCTTTCCACCTCCC	78667	A AAA
	GG AGGT AAAGTGGG		
	CC TCCA TTTCGCTC		
	C CCC		
GAM1245 LOC148147 3'	CTACGCTTTCACCTTCCA	78679	AAA GG
	TGGAAGGT AAAGTG AG		
	ACCTTCCA TTTCGC TC		
	C__ A_		
GAM1245 LOC148195 5'	CTCCTCTTTCTTCACTCCTCCA	84127	A TAAAA TG
	TGGA GG AAG GGAGGAG		

		ACCT CC	TTC TCTCCTC		
		_ TCAC_	TT		
GAM1245	LOC148710 3'	CCTCCC	ACTCTCCA	84192	A GTAAAAA
		TGGA G	AGTGGGAGG		
		ACCT C	TCACCCTCC		
		-----			
GAM1245	LOC148894 5'	TCTCTCTGCTCAC	TTCCA	84260	AAAAA TG GA
		TGGAAGGT	AG G GGA		
		ACCTTCCA	TC C TCT		
		C_____	GT TC		
GAM1245	LOC149422 3'	CTCCTCTTGACTCCTGCC	CCTCC	79349	A AAAA _
	A	TGGA GGTA	AGT GGGAGGAG		
		ACCT CCGT	TCA TTCTCCTC		
		C CC_	G		
GAM1245	LOC149448 3'	CCTCCCACCACCCA		84421	AA AAAAAA
		TGG GGT	GTGGGAGG		
		ACC CCA	CACCCTCC		
		_ C_____			
GAM1245	LOC149773 5'	CTCCTCCTGCC	CCCCCTCCCTCC	79476	A TAAAAA TG
	CA	TGG AGG	G GGAGGAG		
		ACC TCC	C CCTCCTC		
		C CTCCCCC	GT		
GAM1245	LOC150170 5'	CTCCCTATTTTTACTCCA		79589	AA AGT
		TGG GGTA	AAAAA GGGAG		
		ACC TCATTTTT	CCCTC		
		C_	AT_		
GAM1245	LOC150175 5'	CTCCCTATTTTTACTCCA		79630	AA AGT
		TGG GGTA	AAAAA GGGAG		
		ACC TCATTTTT	CCCTC		
		C_	AT_		
GAM1245	LOC150215 5'	CTCCCTATTTTTACTCCA		79638	AA AGT
		TGG GGTA	AAAAA GGGAG		
		ACC TCATTTTT	CCCTC		
		C_	AT_		
GAM1245	LOC150218 5'	CTCCCTATTTTTACTCCA		79719	AA AGT
		TGG GGTA	AAAAA GGGAG		
		ACC TCATTTTT	CCCTC		
		C_	AT_		
GAM1245	LOC150407 3'	TCCTCCCTCTGCCTCCA		79834	A AAAAA T
		TGG AGGT	AG GGGAGGA		

ACC TCCG TC CCCTCCT  
 C \_\_\_\_\_ T  
 GAM1245 LOC151323 5' CTCCTAGAGATCTTTACCTCC 80218 A AAA \_\_\_\_\_  
 C GG AGGT AAAG TGGGAG  
 || ||| ||| |||||  
 CC TCCA TTTC ATCCTC  
 C C\_\_ TAGAG  
 GAM1245 LOC151361 3' TCCCCCACATTCTCCCA 85329 A TAAAAA A  
 TGG AGG GTGGG GGA  
 ||| ||| ||||| |||  
 ACC TCC CACCC CCT  
 C TTA\_\_\_\_\_ C  
 GAM1245 LOC151614 3' CTCCCACCTTGACCTTCCA 80303 AAAAAA  
 TGGAAGGT GTGGGAG  
 ||||| |||||  
 ACCTTCCA CACCCTC  
 GTTC\_\_\_\_  
 GAM1245 LOC151959 5' CCTCCCACCGCCCCA 85523 AA AAAAAA  
 TGG GGT GTGGGAGG  
 ||| ||| |||||  
 ACC CCG CACCCTCC  
 \_\_\_\_\_ C\_\_\_\_\_  
 GAM1245 LOC152179 5' CCAAATTACTTTTTTCCTTCC 85559 T GA\_\_\_\_  
 A TGGAAGG AAAAAAGTGG GG  
 ||||| ||||| ||  
 ACCTTCC TTTTTTCATT CC  
 \_\_\_\_\_ AAAA  
 GAM1245 LOC152245 5' CCTCCCCCTCTTCCCTCCCA 85599 A TAA A T  
 TGG AGG AA AG GGGAGG  
 ||| ||| || ||| |||||  
 ACC TCC TT TC CCCTCC  
 C C\_\_ C C  
 GAM1245 LOC153146 5' TCCTCCCAGATACCTCTCA 85935 GA AAAAAG  
 TG AGGTA TGGGAGGA  
 || ||||| |||||  
 AC TCCAT ACCCTCCT  
 TC AG\_\_\_\_  
 GAM1245 LOC153443 3' CTCCCACCTCTGCCTCCCA 80823 A AAAAA  
 TGG AGGTA GTGGGAG  
 ||| ||||| |||||  
 ACC TCCGT CACCCTC  
 C CTC\_\_\_\_  
 GAM1245 LOC153770 3' TCCTCCTCCTTACTCCCA 80930 AA AAAA TG  
 TGG GGTA AG GGAGGA  
 ||| ||||| || |||||  
 ACC TCAT TC CCTCCT  
 CC \_\_\_\_\_ CT  
 GAM1245 LOC154007 3' TCCTGTCCTCAGCCTCCCA 81023 A AAAAA T G  
 TGG AGGT AG GG AGGA  
 ||| ||||| || |||||

ACC TCCG TC CT TCCT  
 C AC\_\_\_ \_ G  
 GAM1245 LOC154790 5' CCACCCTTTTACCTCCA 81148 A AA  
 TGGA GGTAAAA GTGG  
 ||| ||||| |||  
 ACCT CCATTTT CACC  
 \_ CC  
 GAM1245 LOC157543 5' CTCCTACTTTTACCTGTCCA 81475 \_ AA  
 TGGA AGGTAAA AGTGGGAG  
 ||| ||||| |||||  
 ACCT TCCATT TCATCCTC  
 G \_  
 GAM1245 LOC157638 5' CTCCTCGCGCCCCACCTCCC 81512 A AAAAAA G  
 GG AGGT GTG GAGGAG  
 || ||| || |||||  
 CC TCCA CGC CTCCTC  
 C CCC\_\_\_ G  
 GAM1245 LOC158263 3' CCCCCACCTTTGCCTTCCA 81843 AAA A  
 TGGAAGGTAAA GTGGG GG  
 ||||| ||| ||  
 ACCTTCCGTTT CACCC CC  
 C\_\_\_ \_  
 GAM1245 LOC158364 3' CCCCTTTCTTACCTCACA 81874 GA A T  
 TG AGGTAA AAAG GGG  
 || ||||| ||| |||  
 AC TCCATT TTTC CCC  
 AC C \_  
 GAM1245 LOC158402 5' CTCCCGTCTCCGCCTCCCA 86804 A AAAAA \_  
 TGG AGGT AG TGGGAG  
 ||| ||| || |||||  
 ACC TCCG TC GCCCTC  
 C CC\_\_\_ T  
 GAM1245 LOC159090 5' CTCTTCCCTCCTCCCTCCA 82087 A TAAAAAAGT  
 TGGA GG GGGAGGAG  
 ||| || |||||  
 ACCT CC CCCTTCTC  
 C TCCT\_\_\_\_  
 GAM1245 LOC161570 5' CTCCCCACCTTTCCTTCCA 87093 T AAA AG  
 TGGAAGG AAA GTGGG G  
 ||||| ||| ||| |  
 ACCTTCC TTT CACCC C  
 \_ C\_\_\_ CT  
 GAM1245 LOC162962 3' CTCCCCTTTTTCCTTCCA 82375 TA T  
 TGGAAGG AAAAAG GGGAG  
 ||||| ||||| |||||  
 ACCTTCC TTTTTC CCCTC  
 \_ \_  
 GAM1245 LOC165721 5' TCCCCCACTCCTCTCA 82604 GA TAAAAA A  
 TG AGG AGTGGG GGA  
 || ||| ||||| |||

	AC TCC TCACCC CCT		
	TC _____ C		
GAM1245 LOC166793 5'	CTCCCGAGCACTTACCTTCCA 59228	AAAAG	
	TGGAAGGTAA TGGGAG		
	ACCTTCCATT GCCCTC		
	CACGA		
GAM1245 LOC166968 3'	TCTTCCTCATCTCCCA 82670	A	AAAAAAGT
	TGG AGGT GGGAGGA		
	ACC TCTA TCCTTCT		
	C C_____		
GAM1245 LOC170392 3'	TCCCCCACCGCCCTCTA 76366	A	AAAAAA A
	TGGA GGT GTGGG GGA		
	ATCT CCG CACCC CCT		
	C C_____ C		
GAM1245 LOC170393 3'	CCTCCCACCCTTGCCCCA 82845	AA	AAAA
	TGG GGTA GTGGGAGG		
	ACC CCGTT CACCCTCC		
	___ CC__		
GAM1245 LOC170393 3'	CCTCCCACCCTTGCCCCA 82846	AA	AAAA
	TGG GGTA GTGGGAGG		
	ACC CCGTT CACCCTCC		
	___ CC__		
GAM1245 LOC170393 3'	CCTCCCACCCTTGCCCCA 82849	AA	AAAA
	TGG GGTA GTGGGAGG		
	ACC CCGTT CACCCTCC		
	___ CC__		
GAM1245 LOC170393 3'	CCTCCCACCCTTGCCCCA 82848	AA	AAAA
	TGG GGTA GTGGGAGG		
	ACC CCGTT CACCCTCC		
	___ CC__		
GAM1245 LOC170393 3'	CCTCCCACCCTTGCCCCA 82847	AA	AAAA
	TGG GGTA GTGGGAGG		
	ACC CCGTT CACCCTCC		
	___ CC__		
GAM1245 LOC170393 3'	CCTCCCACCCTTGCCCCA 82844	AA	AAAA
	TGG GGTA GTGGGAGG		
	ACC CCGTT CACCCTCC		
	___ CC__		
GAM1245 LOC196500 3'	CTCCCTCCTTCCTTCCA 87740	TAAAA T_	
	TGGAAGG AAG GGGAG		

	ACCTTCC	TTC	CCCTC		
	_____	CT			
GAM1245	LOC197114	5'	CTCCCCTTTCCCTTCCA	89704	TAAA T
			TGGAAGG AAAG GGGAG		
			ACCTTCC TTTC CCCTC		
			C_____		
GAM1245	LOC200169	5'	CTCCTCTCTTCCTTACCTTCC	89948	AAAAGT
			GGAAGGTAA GGGAGGAG		
			CCTTCCATT CTCTCCTC		
			CCTT_____		
GAM1245	LOC200399	5'	CTCCTAGAGATCTTTACCTCC	88809	A AAA _____
			C GG AGGT AAAG TGGGAG		
			CC TCCA TTTC ATCCTC		
			C C_ TAGAG		
GAM1245	LOC201102	3'	CCTTCCCTTCTTCCCTCCA	88091	A TAAAA T
			TGGA GG AAG GGGAGG		
			ACCT CC TTC CCTTCC		
			C TTC_____		
GAM1245	LOC202500	5'	TCTCCCTACCTCCCA	89193	A AAAAAGT
			TGG AGGTA GGGAGG		
			ACC TCCAT CCCTCT		
			C _____		
GAM1245	LOC202908	5'	CTCCCATCTCAACCTCCCA	89233	A AAAAAA
			TGG AGGT GTGGGAG		
			ACC TCCA TACCCTC		
			C ACTC_____		
GAM1245	LOC219348	3'	TCCTCTCACTCCACTTCCA	91271	GTAAAAA
			TGGAAG AGTGGGAGGA		
			ACCTTC TCACTCTCCT		
			ACC_____		
GAM1245	LOC219654	3'	CCTCCCACGACCCCA	91301	AA AAAAAA
			TGG GGT GTGGGAGG		
			ACC CCA CACCCTCC		
			C_ G_____		
GAM1245	LOC219818	3'	CCTCCCATCCTTACCTCC	90889	A A AAA
			GGA GGT AA GTGGGAGG		
			CCT CCA TT TACCCTCC		
			_ C CC_		
GAM1245	LOC219972	3'	CTACCCCTTCATCTTCCA	91638	AAAA T A
			TGGAAGGT AAG GGG GG		

	ACCTTCTA	TTC CCC TC	
	C___ _	A	
GAM1245 LOC220705 3'	CTCCCATTCTACTCTCC	91227	AG AAA
	GGA GTA AAGTGGGAG		
	CCT CAT TTTACCCTC		
	CT C__		
GAM1245 LOC221218 3'	CCTGTCTCTCACCTCCA	91760	A AAAAA T G
	TGGA GGT AG GG AGG		
	ACCT CCA TC CT TCC		
	_ C___ T G		
GAM1245 LOC221399 5'	TCCACTTCTTCACCTCTCA	93850	GA A A
	TG AGGT AA AAGTGGG		
	AC TCCA TT TTCACCT		
	TC C C		
GAM1245 LOC221466 3'	CCTCCCGCCATCCTCCCA	93685	A TAAAAAA
	TGG AGG GTGGGAGG		
	ACC TCC CGCCCTCC		
	C TAC___		
GAM1245 LOC221876 5'	TCTTCCCCACCTTCC	93926	AAAAAAGT
	GGAAGGT GGGAGGA		
	CCTTCCA CCCTTCT		
	C_____		
GAM1245 LOC222057 5'	CTCCCACCTCAACCTCCCA	92773	A AAAAAA
	TGG AGGT GTGGGAG		
	ACC TCCA CACCCTC		
	C ACTC__		
GAM1245 LOC253001 5'	CCCCCAACCTTCCA	96255	AAAAAAG A
	TGGAAGGT TGGG GG		
	ACCTTCCA ACCC CC		
	_____ -		
GAM1245 LOC253148 5'	CCCCCACACCTCCCA	96876	A AAAAAA A
	TGG AGGT GTGGG GG		
	ACC TCCA CACCC CC		
	C _____ -		
GAM1245 LOC253613 3'	CCCCTTTCTTACCTCACA	96191	GA A T
	TG AGGTAA AAAG GGG		
	AC TCCATT TTTC CCC		
	AC C _		
GAM1245 LOC253891 3'	TTCTCTCGCCACCTTCCA	94419	AAAAAA
	TGGAAGGT GTGGGAGGAG		

ACCTTCCA CGCTCTCCTT  
 C\_\_\_\_\_  
 GAM1245 LOC253962 5' CTCCCTCTCTTCCACCTCCC 96657 A AA A T  
 GG AGGT AA AG GGGAG  
 || ||| || ||||  
 CC TCCA TT TC CCCTC  
 C CC C T  
 GAM1245 LOC254181 5' CCTTCCACACCCCA 97584 AA AAAAAA  
 TGG GGT GTGGGAGG  
 ||| ||| |||||  
 ACC CCA CACCTTCC  
 \_\_\_\_\_  
 GAM1245 LOC254268 3' TCCTCCCTCAGCCTCCCA 95414 A AAAAAAGT  
 TGG AGGT GGGAGGA  
 ||| ||| |||||  
 ACC TCCG CCCTCCT  
 C ACT\_\_\_\_\_  
 GAM1245 LOC254873 3' TTCCTCCCCACCTTCC 94573 AAAAAAGT  
 GGAAGGT GGGAGGAG  
 ||||| |||||  
 CCTTCCA CCCTCCTT  
 C\_\_\_\_\_  
 GAM1245 LOC255975 5' CTCCCATCTCAACCTCCCA 95892 A AAAAAA  
 TGG AGGT GTGGGAG  
 ||| ||| |||||  
 ACC TCCA TACCCTC  
 C ACTC\_\_\_\_\_  
 GAM1245 LOC256094 3' CTCCTCTCTGCCCCCTGCCCCC 94892 AA AAAAAAGT  
 CA TGG GGTA GGGAGGAG  
 ||| ||| |||||  
 ACC CCGT CTCTCCTC  
 CC CCCCCGT  
 GAM1245 LOC256454 3' CTCCCCAAAGGCCCCACCTTCC 96530 AAAAAAGTG A  
 A TGGAAGGT GG GGAG  
 ||||| || |||  
 ACCTTCCA CC CCTC  
 CCCCCGAAA \_  
 GAM1245 LOC256878 5' CTCCCATCTCAACCTCCCA 96903 A AAAAAA  
 TGG AGGT GTGGGAG  
 ||| ||| |||||  
 ACC TCCA TACCCTC  
 C ACTC\_\_\_\_\_  
 GAM1245 LOC257206 5' CTCATTCTCTTTACCTGCCA 97096 A A A TGG  
 TGG AGGT AAA AG GAG  
 ||| ||| ||| ||| |||  
 ACC TCCA TTT TC CTC  
 G C C TTA  
 GAM1245 LOC257364 3' CTCTTCTCTCCCTTACTTTCCA 94966 AAAAGT  
 TGGAAGGTAA GGGAGGAG  
 ||||| |||||



ACCTTTCATT CTCTTCTC  
 CCCT\_\_  
 GAM1245 LOC257468 3' CTCCTGTCCCCCCCACCTCC 95187 A AAAAAAGT \_\_  
 GGA GGT GGA GGAG  
 ||| ||| ||| |||  
 CCT CCA CCCT CTC  
 \_ CCCC\_\_ GT  
 GAM1245 LOC51093 3' CCCCTTTCTCTCCTTCCA 32043 TAAA T  
 TGGAAGG AAAG GGG  
 ||||| ||| |||  
 ACCTTC TTTC CCC  
 TCTC \_  
 GAM1245 LOC51279 3' CTCCTCACCCTCTACCTCCC 33313 A AAAA T \_  
 GG AGGTA AG GG GAGGAG  
 || ||| || |||||  
 CC TCCAT TC CC CTCCTC  
 C C\_\_ \_ A  
 GAM1245 LOC51308 3' CTCCTCCCACCCTGAGCCCCA 33494 AA AAAAAA  
 TGG GGT GTGGGAGGAG  
 ||| ||| |||||  
 ACC CCG CACCCTCCTC  
 \_ AGTCC\_  
 GAM1245 LOC51337 3' CTCCTCCTCCTCCTCTACCTCC 33586 A AAAA TG  
 A TGGA GGTA AG GGAGGAG  
 ||| ||| || |||||  
 ACCT CCAT TC CCTCCTC  
 \_ CTCC CT  
 GAM1245 LOC56267 3' CTCCCCTTTCCCCTCCCA 39011 A TAAA T  
 TGG AGG AAAG GGGAG  
 ||| ||| ||| |||||  
 ACC TCC TTTC CCCTC  
 C CC\_\_ \_  
 GAM1245 LOC56961 5' CTCCCAGCTGCTCCCCACCTCC 62907 A AAAAA\_\_ \_  
 C GG AGGT AG TGGGAG  
 || ||| || |||||  
 CC TCCA TC ACCCTC  
 C CCCCTCG G  
 GAM1245 LOC90378 3' CCTCCCCTACCACCCA 62523 AA AAAAA T  
 TGG GGT AG GGGAGG  
 ||| ||| || |||||  
 ACC CCA TC CCCTCC  
 CA \_\_\_\_ \_  
 GAM1245 LOC90494 5' CTCCTTCCATGCTCCACCCTCC 63054 A AAAAAA  
 A TGGA GGT GTGGGAGGAG  
 ||| ||| |||||  
 ACCT CCA TACCTTCCTC  
 C CCTCG\_  
 GAM1245 LOC90670 3' CTCCTTACCTTCCA 63740 AAAAAAGT  
 TGGAAGGTA GGGAG  
 ||||| |||

ACCTTCCAT TCCTC

GAM1245 LOC90785 3' TCACTTCTCTGACCTTCCA 64019 AAAA\_  
TGGAAGGT AAGTGG  
||||||| |||||  
ACCTTCCA TTCACT  
GTCTC

GAM1245 LOC90981 3' CTCCTCCCACCTTTTACC 64535 AA  
GGTAAAA GTGGGAGGAG  
||||||| |||||  
CCATTTT CACCCTCCTC  
C\_

GAM1245 LOC91252 3' CTCCAGAGCTGCCACCTCCCA 65339 A AAAAA G\_  
TGG AGGT AGT GGAG  
||| ||| ||| |||  
ACC TCCA TCG CCTC  
C CCCG\_ AGA

GAM1245 LOC91445 3' CCTCCCACTCCCCCTCTTCTTC 60549 TAAAAA\_  
C GGAAGG AGTGGGAGG  
||||||| |||||  
CCTTCT TCACCCTCC  
TCTCCCCC

GAM1245 LOC91585 5' CCTCTTCCTTGCCCTCCA 66573 A AAAA TG  
TGGA GGTA AG GGAGG  
||| ||| || |||||  
ACCT CCGT TC TCTCC  
C \_\_\_\_ CT

GAM1245 LOC92154 3' TCCTCCCCGCCCTCCA 68357 A TAAAAAA \_  
TGGA GG GTGGG AGGA  
||| || ||||| |||||  
ACCT CC CGCCC TCCT  
C C\_\_\_\_\_ C

GAM1245 LOC92303 3' TCCTCCCTCAGCCTCCCA 68828 A AAAAAAGT  
TGG AGGT GGGAGGA  
||| ||| |||||  
ACC TCCG CCCTCCT  
C ACT\_\_\_\_\_

GAM1245 LOC92579 3' CTCCCTTTCTTTCCCTCCCA 69837 A T AAAGT  
TGG AGG AAA GGGAG  
||| ||| ||| |||||  
ACC TCC TTT CCCTC  
C C CCTTT

GAM1246 GAS11 3' ACTGCCCTGTCTTT 7622 TC T  
AAAGACAG GG CAGT  
||||||| || |||||  
TTTCTGTC CC GTCA

GAM1246 LILRA1 3' ATGTTATCTGGACTGTCTGCCA 22486 AA GGT \_  
TG AGACAGTC CAG TAACAT  
|| ||||| ||| |||||

AC TCTGTCAG GTC ATTGTA  
 CG \_\_\_\_ T  
 GAM1246 BLCAP 3' ATGTTACTGACTCCTCAGTC 21977 AGTC\_  
 GAC GGTCAGTAACAT  
 ||| |||||  
 CTG TCAGTCATTGTA  
 ACTCC  
 GAM1246 FLJ22055 3' ATGTTATTGTTGACTCTCTCCC 45492 AA C T  
 A TG AGA AGTCGG CAGTAACAT  
 || ||| ||||| |||||  
 AC TCT TCAGTT GTTATTGTA  
 CC C \_  
 GAM1246 GS3955 3' ATGTTACTTGAATCTGTGCTTC 41316 AG TCGG \_  
 A TGAA ACAG TCA GTAACAT  
 |||| ||| ||| |||||  
 ACTT TGTC AGT CATTGTA  
 CG TA\_\_ T  
 GAM1246 KIAA1095 3' GTTACTGAATGTGTTTCA 67471 G GTCGG  
 TGAAA ACA TCAGTAAC  
 |||| ||| |||||  
 ACTTT TGT AGTCATTG  
 G A\_\_\_\_  
 GAM1246 MAPK8IP3 3' TGCTTTGCCGACTGTCCTTC 52997 A C\_  
 GAA GACAGTCGGT AGTA  
 ||| ||||| |||  
 CTT CTGTCAGCCG TCGT  
 C TT  
 GAM1246 QKI 3' ATGCCACTGCTTTGTCTTTC 65437 TC T AA  
 GAAAGACAG GG CAGT CAT  
 ||||| || ||| |||  
 CTTTCTGTT TC GTCA GTA  
 \_ \_ CC  
 GAM1246 LOC148195 3' GTTACTAACTTTAAATGTCTTT 84136 GTC\_\_ C  
 TA TGAAAGACA GGT AGTAAC  
 ||||| ||| |||||  
 ATTTTCTGT TCA TCATTG  
 AAATT A  
 GAM1246 LOC207085 5' GAGTTGACTGTCTTCA 90702 A \_  
 TGAA GACAGTCGG TC  
 ||| ||||| ||  
 ACTT CTGTCAGTT AG  
 \_ G  
 GAM1246 LOC221683 5' ATTAGCCTGTCTTTCA 93711 GTC TC  
 TGAAAGACA GG AGT  
 ||||| || |||  
 ACTTTCTGT CC TTA  
 \_ GA  
 GAM1246 LOC222160 5' TACCATACGTGCTGTCTTTCA 94133 \_ GTCA  
 TGAAAGACAGT CG GTA  
 ||||| || |||

ACTTTCTGTCG GC CAT  
 T ATAC  
 GAM1247 ABCA1 3' TCGTGGCTAACATCCTGCTT 18553 A GAGA  
 AAGCA GATGTTGGT GCA  
 |||| ||||| ||  
 TTCGT CTACAATCG CGT  
 C GTG\_  
 GAM1247 DPYSL2 3' CGTGCTCTCACTCTCTTTCT 7295 C TGTT  
 AG AAGA GGTGAGAGCACG  
 || ||| |||||  
 TC TTCT TCACTCTCGTGC  
 T CTC\_  
 GAM1247 FASN 5' CGCGCCCTCACCAGAGCAGC 14633 AAGATG A A  
 GC TTGGTGAG GC CG  
 || ||||| ||  
 CG GACCACTC CG GC  
 ACGA\_\_ C C  
 GAM1247 INHA 3' GCCCCACCATCATCAGCT 9336 AA T AGA  
 AGC GATG TGGTG GC  
 ||| ||| ||| ||  
 TCG CTAC ACCAC CG  
 A\_ T CCC  
 GAM1247 POLR2H 5' CGCGCTCTACCCCTTCTGCT 20643 A TGTT A  
 AGCA GA GGTGAGAGC CG  
 |||| || ||||| ||  
 TCGT CT CCACTCTCG GC  
 \_ TCC\_ C  
 GAM1247 RNH 3' TGCTCTCACCCTGCAT 59625 T\_  
 ATGT GGTGAGAGCA  
 |||| |||||  
 TACG CCACTCTCGT  
 TC  
 GAM1247 RNH 3' TGCTCTCACCCTGCAT 11370 T\_  
 ATGT GGTGAGAGCA  
 |||| |||||  
 TACG CCACTCTCGT  
 TC  
 GAM1247 SLC17A7 3' CGTGCCCACTTCACATCT 39700 T\_ AGA  
 AGATGT GGTG GCACG  
 |||| ||| ||||  
 TCTACA TCAC CGTGC  
 CT C\_  
 GAM1247 SMAC 5' CGTGAGCCACCAACACCCTGC 57209 AGA AGAG  
 GCA TGTTGGTG CACG  
 || ||||| |||  
 CGT ACAACCAC GTGC  
 CCC CGA\_  
 GAM1247 C17orf31 3' TGCTCTCAGCCTTTCTCCCT 34129 CA TGTT \_  
 AG AGA GG TGAGAGCA  
 || ||| || |||||

TC TCT CC ACTCTCGT  
 CC TT\_\_ G  
 GAM1247 C6orf9 3' TGCCCTCAACTCTTGCTT 42078 T TGG A  
 AAGCAAGA GT TGAG GCA  
 ||||| || ||| ||  
 TTCGTTCT CA ACTC CGT  
 \_ \_ \_ C  
 GAM1247 DKFZP434B195 3' GCCCACTCACCCAACATCCTG 48429 A \_ A\_  
 CA GATGTTGG TGAG GC  
 || ||||| ||| ||  
 GT CTACAACC ACTC CG  
 C C ACC  
 GAM1247 DKFZP564B167 5' GCTCCCACCCGGCTGC 31215 AGAT \_ A  
 GCA GTTGG TG GAGC  
 || |||| || |||  
 CGT CGGCC AC CTCG  
 \_ \_ \_ C C  
 GAM1247 DKFZP564I1171 3' CTCCCACCAACACCTCCTT 71587 CA A A  
 AAG AG TGTTGGTG GAG  
 || || ||||| |||  
 TTC TC ACAACCAC CTC  
 C\_ C C  
 GAM1247 FLJ13855 3' CGTGCCCCCAGCTGCTCTTGT 43585 T\_\_ TGAGA  
 GCAAGA GTTGG GCACG  
 |||| |||| ||||  
 TGTTCT CGACC CGTGC  
 CGT CC\_  
 GAM1247 FLJ20275 3' CGTGCTTGCTTAACATCCTGTT 34821 A TGA  
 AGCA GATGTTGG GAGCACG  
 ||| ||||| |||||  
 TTGT CTACAATT TTCGTGC  
 C CG\_  
 GAM1247 FLJ20436 5' TGCTCTCACCCCTCGTCT 35173 TT  
 AGATG GGTGAGAGCA  
 |||| |||||  
 TCTGC CCACTCTCGT  
 TC  
 GAM1247 FLJ23519 3' TGCTCTCACCCCTGCAT 69209 T\_  
 ATGT GGTGAGAGCA  
 ||| |||||  
 TACG CCACTCTCGT  
 TC  
 GAM1247 HSPBP1 3' TGCTCTCACTCTCATC 24364 TT  
 GATG GGTGAGAGCA  
 ||| |||||  
 CTAC TCACTCTCGT  
 TC  
 GAM1247 IRO039700 3' TGCCCAATACTCTTGC 37910 \_ TGAGA  
 GCAAGA TGTTGG GCA  
 |||| |||| |||

CGTTCT ATAACC CGT  
C \_\_\_\_\_

GAM1247 KIAA1546 3' TGCTCTCCCTATGCCAACAT 67912 \_\_\_\_\_  
ATGTTGGT GAGAGCA  
||||| |||||  
TACAACCG CTCTCGT  
TATCC

GAM1247 KIAA1710 5' CGTGCTCTCTAGAATCTTCCT 62517 C GTTGGT  
AG AAGAT GAGAGCACG  
|| ||| |||||  
TC TTCTA CTCTCGTGC  
C AGAT\_\_

GAM1247 KIAA1877 3' CTCTGCACATCTTGGCT 66171 \_ TG G  
AGC AAGATGT GT AGAG  
|| ||||| || |||  
TCG TTCTACA CG TCTC  
G \_ \_

GAM1247 MBLR 5' CGCGCTCTCCCGCCGCTCGC 49626 A A T T A  
GC AG TG TGG GAGAGC CG  
|| || || ||||| ||  
CG TC GC GCC CTCTCG GC  
C C C \_ C

GAM1247 MGC13071 3' TGCTCTCGGAACATC 51091 GG  
GATGTT TGAGAGCA  
||||| |||||  
CTACAA GCTCTCGT  
G\_

GAM1247 OSBPL5 3' GCACTCCTGGCCATCTTGC 72685 \_TG T A  
GCAAGATG T G GAG GC  
|||||| | ||| ||  
CGTTCTAC G C CTC CG  
C GT \_ A

GAM1247 PTGES2 3' GCACCCCCACCAGCCCTCTCGC 46882 A T\_ AGA\_\_  
TT AAGC AGA GTTGGTG GC  
||||| ||||| ||  
TTCG TCT CGACCAC CG  
C CC CCCC

GAM1247 SIAT4A 5' GCTATACCAACACCTTCCT 11671 C A\_ AG  
AG AAG TGTTGGTG AGC  
|| || ||||| |||  
TC TTC ACAACCAT TCG  
C CC A\_

GAM1247 TED 3' CTCCCAAGGGCCACTCTTGC 31634 \_ \_ T  
GCAAGA TG TTGG GAG  
||||| || ||| |||  
CGTTCT AC AACC CTC  
C CGGG \_

GAM1247 TRIM29 3' CGTGCTCTCTCTCGTC 23959 TT T  
GATG GG GAGAGCACG  
||| || |||||

CTGC TC CTCTCGTGC  
 \_ T  
 GAM1247 LOC152195 5' TACCCTGCCTCTTGCTT 85565 T T\_  
 AAGCAAGA GT GGTG  
 ||||| || |||  
 TTCGTTCT CG CCAT  
 C TC  
 GAM1247 LOC201191 3' TGCTCTCTCTTACCCTGT 89773 AGAT T T  
 GCA GT GG GAGAGCA  
 || || || |||||  
 TGT CA TC CTCTCGT  
 CC\_ T T  
 GAM1247 LOC255927 3' CGCGCCCGGCCAAAACCCTGCT 96008 AGATG GAGA A  
 T AAGCA TTGGT GC CG  
 |||| |||| |||  
 TTCGT AACCG CG GC  
 CCCAA GCC\_ C  
 GAM1247 LOC256777 3' GCTCCCAGTTTCCTGTTT 95137 A TG TGA  
 AAGCA GA TTGG GAGC  
 |||| || ||| |||  
 TTTGT CT GACC CTCG  
 C TT \_  
 GAM1247 LOC84570 5' CGTGCTCTCACAGCCTTTTTGC 50710 T\_ G  
 GCAAGA GTTG TGAGAGCACG  
 |||| ||| |||||  
 CGTTTT CGAC ACTCTCGTGC  
 TC \_  
 GAM1247 LOC90120 5' GCCCTCAGCCGCCTTGC 61536 ATGT \_ A  
 GCAAG TGG TGAG GC  
 |||| || ||| |||  
 CGTTC GCC ACTC CG  
 C\_ G C  
 GAM1247 LOC91450 3' TGCTCTCACGGACTTGTTT 66077 GAT G  
 AAGCAA GTT GTGAGAGCA  
 |||| ||| |||||  
 TTTGTT CAG CACTCTCGT  
 \_ G  
 GAM1248 ABL1 5' TGGGCCGGGCTCGGCCT 17680 \_  
 GGGCTGAGTCTG CCTG  
 ||||| ||| |||  
 TCCGGCTCGGGC GGGT  
 C  
 GAM1248 ADORA2A 3' GGGCACAGCAGACTGGCCTGG 5434 TG G C GA  
 C GGCT AGTCTGC TGTGCC  
 | ||| ||||| |||||  
 G CCGG TCAGACG ACACGG  
 GT \_ \_ GT  
 GAM1248 ADRBK2 3' CGGCTTGGGGTCAGCTCAG 17683 G GCCTGT  
 CTGGGCTGA TCT GCCG  
 ||||| || |||

GACTCGACT GGG CGGC  
 G TT\_\_\_\_  
 GAM1248 ANK1 3' ATCGGTCTCAGCTGGGCAGAGT 60387 TG G \_ \_\_\_\_  
 TGGCCCGG A TCTGCCT GT GCCGA T  
 | ||||| || |||| |  
 T AGACGGG CG TGGCT A  
 GT G T ACTC  
 GAM1248 ARHGEF12 3' GCAGGTGGGCTTGCCC 30999 T TG  
 GGGC GAGTC CCTGT  
 |||| |||| ||||  
 CCCG TTCGG GGACG  
 \_ GT  
 GAM1248 ATP7B 3' TCTGGGTGCAGCTGGGCTTGGC 3544 TG TG GC TG GA  
 CTGG C GGC AGTCT CTG CC  
 | ||| |||| ||| ||  
 G CCG TCGGG GAC GG  
 GT GT TC GT GTCTG  
 GAM1248 ATP8A2 3' CAGGTGCACTCGGCCAG 93510 C  
 CTGGGCTGAGT TGCCTG  
 ||||| |||||  
 GACCCGGCTCA GTGGAC  
 C  
 GAM1248 ATP8A2 3' GTACTGTGGGCTTAGTTC 93516 TG CT  
 GGGCTGAGTC C GTGC  
 ||||| |||  
 CTTGATTCGG G CATG  
 GT T\_  
 GAM1248 B3GAT1 3' TGGGTGGGTGGGACTCAGTCCA 37833 \_TG TG G A  
 G CTGGGCTGAGT C CC T CCG  
 ||||| ||| |||  
 GACCTGACTCA G GG G GGT  
 G GT GT\_  
 GAM1248 B3GAT1 3' TGGGTGGGTGGGACTCAGTCCA 53981 \_TG TG G A  
 G CTGGGCTGAGT C CC T CCG  
 ||||| ||| |||  
 GACCTGACTCA G GG G GGT  
 G GT GT\_  
 GAM1248 BACH2 3' TTGGCATGAGGTTTACCCTGG 41494 TG CTGA CT \_  
 C GG GT GCCT GTGCCGA  
 | || || ||| |||||  
 G CC CA TGGA TACGGTT  
 GT \_\_\_\_ TT G  
 GAM1248 BCL7A 3' TTGGCGCAGGTGAGGACTCAG 40647 \_  
 CTGAGTCT GCCTGTGCCGA  
 ||||| |||||  
 GACTCAGG TGGACGCGGTT  
 AG  
 GAM1248 BCL9 3' CGTGGGCATGGGTGGATTTAGC 15066 TG GA  
 C GGCTGAGTC CCTGTGCC  
 ||||| |||||



		CCGATTTAG GGGTACGG	
		GT GTGCA	
GAM1248 BCS1L	3'	CAGGCTGGGCTCAGCTCAG 15077	—
		CTGGGCTGAGTCT GCCTG	
		GACTCGACTCGGG CGGAC	
		T	
GAM1248 BIRC7	3'	TTGGCGTGGGGGATGGCTTA 57789	GA G TG
		TGGGCT GTCT CC TGCCGA	
		ATTCGG TAGG GG GCGGTT	
		— _ GT	
GAM1248 BIRC7	3'	TTGGCGTGGGGGATGGCTTA 42208	GA G TG
		TGGGCT GTCT CC TGCCGA	
		ATTCGG TAGG GG GCGGTT	
		— _ GT	
GAM1248 BMP1	3'	TTGGCCAAAGGACACGGCTCAG 20426	A GCC T
		CTGGGCTG GTCT TG GCCGA	
		GACTCGGC CAGG AC CGGTT	
		A AA_ _	
GAM1248 BRCA2	3'	GGTATACTTTTGCTTCAG 3550	_ T_ C
		CTGG GC GAGT TGCC	
		GACT CG TTCA ATGG	
		T TT T	
GAM1248 C18orf1	5'	GCACAGGCTTGTCCGG 60244	TGAGTCT
		CTGGGC GCCTGTGC	
		GGCCTG CGGACACG	
		TT_	
GAM1248 C8orf1	3'	TTGGTACAATTACTTCATCTGG 15089	TG CT CTGCC
		C GG GAGT TGTGCCGA	
		G CT TTCA ACATGGTT	
		GT AC TTA_	
GAM1248 CA4	5'	TCGGTGCGCGACCCCGGCTCAG 5553	A_ T CT TG
		CTGGGCTG GTC GC G CCGA	
		GACTCGGC CAG CG C GGCT	
		CC _ _ GT	
GAM1248 CACNB2	3'	GGGACAGATTCAGTCT 5579	—
		GGGCTGAGTCTG CCT	
		TCTGACTTAGAC GGG	
		A	
GAM1248 CAPN9	3'	TTGGTGTGGAACCATACGCCC 21753	_ GTCTG T TG
AG		CTGGGC TGA CC G CCGA	

			GACCCG ATT GG T GGTT		
			C ACCAA _GT		
GAM1248	CARKL	3'	CAGGCAGGCCTGGCCCAG 25186	GA	
			CTGGGCT GTCTGCCTG		
			GACCCGG CGGACGGAC		
			TC		
GAM1248	CARKL	3'	TTGGCGTGGGCTTTGCTGGCCC 25193	G CT_ TG	
	AG		CTGGGCT AGT GCC TGCCGA		
			GACCCGG TCG CGG GCGGTT		
			_ TTT GT		
GAM1248	CD1A	5'	TCGTGGGGTAGGTTTGTTTGG 71184	TG T GT GTGC	
			C GGC GA CTGCCT CGA		
			G TTG TT GATGGG GCT		
			GT _ TG GT__		
GAM1248	CD81	3'	GCCCAGAGACTCAGCTTGG 15136	TG GC T	
			C GGCTGAGTCT CTG GC		
			G TCGACTCAGA GAC CG		
			GT _ C		
GAM1248	CDH11	3'	TCGGCCACCACAGATTCAGACT 53364	TG _ CC_ T	
	TGG		GG CTGAGTCTG TG GCCGA		
			TC GACTTAGAC AC CGGCT		
			GT A ACC _		
GAM1248	CLTB	5'	TCGGCGGGGACGGGCTTGCGCG 23018	G TG C G	
	GG		CTG GC AGTCTG CT TGCCGA		
			GGC CG TCGGGC GG GCGGCT		
			G GT A G		
GAM1248	COX11	5'	GAGGCGGGTGGGTGTTAGTTCA 15192	_ TG GT GA	
	G		CTGGGCTGA GTC CCT GCC		
			GACTTGATT TGG GGG CGG		
			G GT _ AGA		
GAM1248	CRLF1	5'	TCGGCTGCTCAGACTTGCTCCG 16455	_ T CCTGT	
	G		CTGG GC GAGTCTG GCCGA		
			GGCC CG TTCAGAC CGGCT		
			T _ TCGT_		
GAM1248	DAAM1	3'	TTGGTGTGGGGATACAGTCT 30379	A TG TG	
			GGGCTG GTC CCTG CCGA		
			TCTGAC TAG GGGT GGTT		
			A _ GT		
GAM1248	DAZ	3'	GGTAGATACGGTTCAG 82116	A	
			CTGGGCTG GTCTGCC		

			GA	CTTGGC	TAGATGG	
			A			
GAM1248	DAZ	3'	GGTAGATACGGTTCAG	82117	A	
			CTGGGGCTG	GTCTGCC		
			GA	CTTGGC	TAGATGG	
			A			
GAM1248	DDB2	5'	TTGGCGGGAAGTTGGCTTAGCT	3661	TG__	GT
	CGG		GGGCTGAGTC	CCT GCCGA		
			CTCGATT	CGG GGG CGGTT		
			TTGAA	_		
GAM1248	DVL3	5'	GGGAGGCTCGGCCCGG	15372	G	
			CTGGGGCTGAGTCT	CC		
			GGCCCGGCTCGGA	GG		
			G			
GAM1248	EDNRB	5'	TGCAGCGACTTGGCTCGG	14338	TG	T C
			CTGGGC	AGTC GC TGTG		
			GGCTCG	TCAG CG ACGT		
			GT	_ _		
GAM1248	EIF2C1	3'	TTGGCTCATGTGGATTTGGTTT	24184	TG	TG C T
	A		TGGGC	AGTC C TG GCCGA		
			ATTTG	TTAG G AC CGGTT		
			GT	GT T T		
GAM1248	ENO1	5'	GGCGCGGGCGGCGCGG	7473	A T	
			CTG G	CTGCCTGTGCC		
			GGC C	GGCGGGCGCGG		
			G	_		
GAM1248	EPHB2	3'	TTGGTCACAGGGTGGTTTTGGT	33891	TG T TG	_ _
	TTAG		TGGGC	AG C CC TGTG CCGA		
			ATTTG	TT G GG ACAC GGTT		
			GT T	GT G T		
GAM1248	EPHB2	3'	TTGGTCACAGGGTGGTTTTGGT	15452	TG T TG	_ _
	TTAG		TGGGC	AG C CC TGTG CCGA		
			ATTTG	TT G GG ACAC GGTT		
			GT T	GT G T		
GAM1248	ETV5	5'	CGGAGCGGTTCCGCCAG	15486	T	CTGTG
			CTGGGGCTGAG	CTGC CCG		
			GACCCGGCTT	GGCG GGC		
			_	A	_	
GAM1248	FE65L2	3'	TTGGGGAGGGTGGGCCAGCTC	55681	A TG	GTG
	AG		CTGGGGCTG	GTC CCT CCGA		

GACTCGAC CGG GGG GGTT  
 C GT AGG  
 GAM1248 FNTB 3' TGGTGCACAGGCAAGACTTGCT 8957 \_ T \_ CGA  
 TCAG GG GC GAGTCT GCCTGTGC  
 || || ||||| |||||  
 CT CG TTCAGA CGGACACG  
 T \_ A TGGTT  
 GAM1248 FOLR2 3' TTGGATAACCAGGCTGGGCTCA 5860 \_ TG\_\_\_\_  
 GCTCAG GCTGAGTCT GCCTG CCGA  
 ||||| ||||| |||||  
 CGACTCGGG CGGAC GGTT  
 T CAATA  
 GAM1248 GATM 5' TCGGCACGAGCGACGCGGCCCA 7630 A T C  
 G CTGGGCTG GTC GC TGTGCCGA  
 ||||| ||||| |||||  
 GACCCGGC CAG CG GCACGGCT  
 G \_ A  
 GAM1248 GCN5L2 3' TTGGATTCTGGGCTGGGCCCA 59842 GA GCCTGTG  
 G CTGGGCT GTCT CCGA  
 ||||| ||||| |||||  
 GACCCGG CGGG GGTT  
 TC TCCTTA\_  
 GAM1248 GPR23 5' TTGGTGCCAGGATTTGGTTCG 60545 TG GCCT TG  
 TGGGC AGTCT G CCGA  
 ||||| ||||| | |||||  
 GCTTG TTAGG C GGTT  
 GT AC\_\_GT  
 GAM1248 GPX3 5' TTGGCTGCAAGGGTCTCGGCTT 9127 TG T TG \_ \_  
 GG C GGCTGAG C CCT GT GCCGA  
 | ||||| | ||||| |||||  
 G TCGGCTC G GGA CG CGGTT  
 GT T\_\_ A T  
 GAM1248 GRB10 3' TTGGCATATTTTGTGGACTCAG 17988 TG C\_\_\_\_  
 TC GGCTGAGTC C TGTGCCGA  
 ||||| ||||| |||||  
 CTGACTCAG G ATACGGTT  
 GT TTTT  
 GAM1248 GSS 3' TGTGGGTATAGCTCAG 3932 AGTC TG  
 CTGGGCTG TGCC TG  
 ||||| ||||| |||||  
 GACTCGAT ATGG GT  
 \_\_\_\_ GT  
 GAM1248 GUCY1A3 5' GTGGGTGGGACTCAGCTCAG 63492 \_ TG TG  
 CTGGGCTGAGT C CC T  
 ||||| ||||| |||||  
 GACTCGACTCA G GG G  
 G GT GT  
 GAM1248 H1F0 5' AGGCAGGCTTTGCTCAG 18013 T  
 CTGGGC GAGTCTGCCT  
 ||||| ||||| |||||

		GA	CTCG	TT	CGG	ACGGA	
			T				
GAM1248	HARS	3'	CAGGAGGCTTAGTCCAG	9173		G	
			CTGGGCTGAGTCT CCTG				
			GACCTGATTCGGA GGAC				
GAM1248	HPCA	5'	TCGCTGGGTGGGACTTGGCTCG	9257		TG _TG T CGA	
	G		CTGGGC AGT C CCTG GC				
			GGCTCG TCA G GGGT CG				
			GT G GT _ CT				
GAM1248	HRB	5'	TTGGTGTGGCCCGTCAGCCC	15707		GTCT T TG	
			GGGCTGA GCC G CCGA				
			CCCGACT CGG T GGTT				
			GCC_ _GT				
GAM1248	IDH3A	3'	GGCTTAGGCTTGGGCTCAG	18646		_ T	
			CTGAGTCT GCCTG GCC				
			GA	CTCGG	CGGAT	CGG	
			TT T				
GAM1248	IL20RA	3'	TTGGTACAGGCAGACAACCCTG	27049		TG CTGA	
	G		C GG GTCTGCCTGTGCCGA				
			G CC CAGACGGACATGGTT				
			GT CAA_				
GAM1248	IMPA2	5'	CGGCGCACCTCAGCCT	95239		TCTGCC	
			GGGCTGAG TGTGCCG				
			TCCGACTC ACGCGGC				
			C_				
GAM1248	KCNK5	3'	TTGGTCTACTCAGGCCAGCCC	13614		A CC T	
	AG		CTGGGCTG GTCTG TG GCCGA				
			GACCCGAC CGGAC AT TGGTT				
			C TC C				
GAM1248	LAIR1	5'	TGGTGCGCCTCAGGCCAG	41357		G TCT CT TG	
			CTGG CTGAG GC G CCG				
			GACC GACTC CG C GGT				
			G _ _GT				
GAM1248	LAIR1	5'	TGGTGCGCCTCAGGCCAG	41359		G TCT CT TG	
			CTGG CTGAG GC G CCG				
			GACC GACTC CG C GGT				
			G _ _GT				
GAM1248	LAIR1	5'	TGGTGCGCCTCAGGCCAG	9662		G TCT CT TG	
			CTGG CTGAG GC G CCG				

			GACC GACTC CG C GGT		
			G ____ GT		
GAM1248	LIMD1	3'	TTGGCACAGGCATTATGTTTG 26468	GG	TGAGTC
			T GC TGCCTGTGCCGA		
			G TG ACGGACACGGTT		
			TT TATT__		
GAM1248	LIPA	3'	TCGGATGCAAACCTCAGCTCAG 4083	C	CTGTG
			CTGGGCTGAGT TGC CCGA		
			GACTCGACTCA ACG GGCT		
			A TA__		
GAM1248	MAPK7	3'	GCAGGTGAGGCTCGGCTTGG 10840	TG	_
			C GGCTGAGTCT GCCTGT		
			G TCGGCTCGGA TGGACG		
			GT G		
GAM1248	MAPK7	3'	GCAGGTGAGGCTCGGCTTGG 57380	TG	_
			C GGCTGAGTCT GCCTGT		
			G TCGGCTCGGA TGGACG		
			GT G		
GAM1248	MAPK7	3'	GCAGGTGAGGCTCGGCTTGG 57383	TG	_
			C GGCTGAGTCT GCCTGT		
			G TCGGCTCGGA TGGACG		
			GT G		
GAM1248	MAPK7	3'	GCAGGTGAGGCTCGGCTTGG 57386	TG	_
			C GGCTGAGTCT GCCTGT		
			G TCGGCTCGGA TGGACG		
			GT G		
GAM1248	MASP1	3'	TGGTATAACTGAGCTTGG 57476	TG	G CTGCC
			C GGCT AGT TGTGCCG		
			G TCGA TCA ATATGGT		
			GT G ____		
GAM1248	MGAT4B	3'	CGGGCTTGGGCCCGCCTGG 26550	TG	A _
			C GGCTG GTCT GCCTG		
			G CCGGC CGGG CGGGC		
			GT _ TT		
GAM1248	MGAT4B	3'	CGGGCTTGGGCCCGCCTGG 53949	TG	A _
			C GGCTG GTCT GCCTG		
			G CCGGC CGGG CGGGC		
			GT _ TT		
GAM1248	MPP2	3'	CAGTGGGCTCAGCCCAG 59818	TG	C
			CTGGGCTGAGTC C TG		

GACCCGACTCGG G AC  
 GT \_  
 GAM1248 MTR 5' GTGTGGCAGGCTCGCCTGG 4215 TG T T TG  
 C GGC GAGTCTGCC G C  
 | ||| ||||| |  
 G CCG CTCGGACGG T G  
 GT \_ \_GT  
 GAM1248 MTRR 5' GTGCAGGTTCTGTGCCCGG 10133 \_ GTCT TG  
 CTGGGC TGA GCCTG C  
 ||||| ||| ||||| |  
 GGCCCG GCT TGGAC G  
 T \_ \_GT  
 GAM1248 MUC4 3' TTGGCATCTGCACTCCAGCCCA 56332 \_ CT CT  
 G CTGGGCTG AGT GC GTGCCGA  
 ||||| ||| || |||||  
 GACCCGAC TCA CG TACGGTT  
 C \_ TC  
 GAM1248 NCAM2 3' TTGGTGGTTGTTTGGTTTGG 15806 TG TG GT T TGT  
 C GGC A C GCC GCCGA  
 | ||| | ||| |||||  
 G TTG T G TGG TGGTT  
 GT GT TG T \_  
 GAM1248 NIPSNAP1 3' TCTGAGGGGCGAGTGCTCAGTTC 13293 \_ GTGCCGA  
 AG CTGGGCTGAGT CTGCCT  
 ||||| |||||  
 GACTTGACTCG GACGGG  
 T GAGTCT  
 GAM1248 NR1I2 3' TGGCATGACCTCATTCCGG 13975 GC \_ TGCCT  
 CTGG TGAG TC GTGCCG  
 |||| |||| || |||||  
 GGCC ACTC AG TACGGT  
 TT C \_  
 GAM1248 NR1I2 3' TTGGTGTAGGTAGGTCTGTTTG 13977 GG T G TG  
 T GC GA TCTGCCTG CCGA  
 | || ||||| |||||  
 G TG CT GGATGGAT GGTT  
 TT T \_ GT  
 GAM1248 NR1I2 3' TGGCATGACCTCATTCCGG 41831 GC \_ TGCCT  
 CTGG TGAG TC GTGCCG  
 |||| |||| || |||||  
 GGCC ACTC AG TACGGT  
 TT C \_  
 GAM1248 NR1I2 3' TTGGTGTAGGTAGGTCTGTTTG 41833 GG T G TG  
 T GC GA TCTGCCTG CCGA  
 | || ||||| |||||  
 G TG CT GGATGGAT GGTT  
 TT T \_ GT  
 GAM1248 OPA1 3' GGTATGCTCGGTTGAG 55532 G C  
 CT GGCTGAGT TGCC  
 || ||||| |||||

			GA TTGGCTCG ATGG		
			G T		
GAM1248	OPA1	3'	TTGGTATGGCCATTAGGTTTCAG 55537	G CT T	
			CTGGGGCT AGT GCC GTGCCGA		
			GACTTGG TTA CGG TATGGTT		
			A C_ _		
GAM1248	OPA1	3'	GGTATGCTCGGTTGAG 55541	G C	
			CT GGCTGAGT TGCC		
			GA TTGGCTCG ATGG		
			G T		
GAM1248	OPA1	3'	TTGGTATGGCCATTAGGTTTCAG 55546	G CT T	
			CTGGGGCT AGT GCC GTGCCGA		
			GACTTGG TTA CGG TATGGTT		
			A C_ _		
GAM1248	OPA1	3'	GGTATGCTCGGTTGAG 55550	G C	
			CT GGCTGAGT TGCC		
			GA TTGGCTCG ATGG		
			G T		
GAM1248	OPA1	3'	GGTATGCTCGGTTGAG 55568	G C	
			CT GGCTGAGT TGCC		
			GA TTGGCTCG ATGG		
			G T		
GAM1248	OPA1	3'	TTGGTATGGCCATTAGGTTTCAG 55573	G CT T	
			CTGGGGCT AGT GCC GTGCCGA		
			GACTTGG TTA CGG TATGGTT		
			A C_ _		
GAM1248	OPA1	3'	TTGGTATGGCCATTAGGTTTCAG 55555	G CT T	
			CTGGGGCT AGT GCC GTGCCGA		
			GACTTGG TTA CGG TATGGTT		
			A C_ _		
GAM1248	OPA1	3'	GGTATGCTCGGTTGAG 55559	G C	
			CT GGCTGAGT TGCC		
			GA TTGGCTCG ATGG		
			G T		
GAM1248	OPA1	3'	TTGGTATGGCCATTAGGTTTCAG 55564	G CT T	
			CTGGGGCT AGT GCC GTGCCGA		
			GACTTGG TTA CGG TATGGTT		
			A C_ _		
GAM1248	OPCML	3'	TTGGGAAGCAGATCAGCCTAG 10348	G CTGTG	
			CTGGGGCTGA TCTGC CCGA		



			GATCCGACT AGACG GGTT		
			— AAG—		
GAM1248	OPHN1	5'	TGCCCCGCGGATTCGGCC 10362	CT	
			GGCTGAGTCTGC GTG		
			CCGGCTTAGGCG CGT		
			CC		
GAM1248	OXR1	3'	TGGCACAGGTAACATTTGG 35838 TG C_		
			C AGT TGCCTGTGCCG		
			G TTA ATGGACACGGT		
			GT CA		
GAM1248	OXTR	5'	CGCCTGCGGACTCGGTGCAG 6206 G CT		
			CTG GCTGAGTCTGC GTG		
			GAC TGGCTCAGGCG CGC		
			G TC		
GAM1248	PAX2	3'	AGGGGGATTTCGGCCCAG 14330 G		
			CTGGGCTGAGTCT CCT		
			GACCCGGCTTAGG GGA		
			G		
GAM1248	PAX2	3'	AGGGGGATTTCGGCCCAG 14321 G		
			CTGGGCTGAGTCT CCT		
			GACCCGGCTTAGG GGA		
			G		
GAM1248	PCSK1	3'	GTCCCTCAGGTAGATTTTGT 4772 TG T TGCCGA		
	GG		C GGC GAGTCTGCCTG		
			G TTG TTTAGATGGAC		
			GT T TCCCTGT		
GAM1248	PIK3R1	3'	TTGGTCCAGCCTGTTTAGCCT 68583 TG GT TGC TG		
	GG		C GGCTGA C CTG CCGA		
			G CCGATT G GAC GGTT		
			GT TG TCC CT		
GAM1248	PLOD3	5'	GCGGCTGGCTCAGCCCAG 6555 T T		
			CTGGGCTGAGTC GCC GT		
			GACCCGACTCGG CGG CG		
			T —		
GAM1248	PLP2	3'	TCGGTGTGGGTGGTGGTTC 10654 AGT TG TG		
			GGGCTG C CCTG CCGA		
			CTTGGT G GGGT GGCT		
			— GT GT		
GAM1248	PMP22	5'	TTGGAAGCTGCAGGCTTAGTCT 4332 CT G_		
			GGGCTGAGTCTGC GT CCGA		

TCTGATTCTGGACG CG GGTT  
 T\_ AA  
 GAM1248 PNN 5' TCGGCGGCGCGGCATAGCCCGG 71113 A \_ TGT  
 CTGGGGCTG GTC TGCC GCCGA  
 ||||| ||| ||| ||||  
 GGCCCGAT CGG GCGG CGGCT  
 A C \_  
 GAM1248 POLS 3' AGGCAGGTTGGGCTCAG 22788 G GT  
 CTGGGGCT A CTGCCT  
 ||||| | |||||  
 GACTCGG T GACGGA  
 G TG  
 GAM1248 POR 3' TTGGCATGGGCGCAGGCCAG 94177 GA CT  
 CTGGGGCT GT GCCTGTGCCGA  
 ||||| || |||||  
 GACCCGG CG CGGGTACGGTT  
 A\_ \_  
 GAM1248 PPEF2 3' TGGCGCGATCTCGGCTCA 20678 TCTGCC  
 TGGGCTGAG TGTGCCG  
 ||||| |||||  
 ACTCGGCTC GCGCGGT  
 TA\_ \_  
 GAM1248 PRDM2 3' TTGGCGTTTGGACCCAGTTCAG 24251 A CCTG  
 CTGGGGCTG GTCTG TGCCGA  
 ||||| ||||| |||||  
 GACTTGAC CAGGT GCGGTT  
 C TT\_ \_  
 GAM1248 PRKAB1 3' TGGTATACCTGAGTTTGG 20739 TG G TCTGCC  
 C GGCT AG TGTGCCG  
 | |||| || |||||  
 G TTGA TC ATATGGT  
 GT G C\_ \_  
 GAM1248 PRKACB 3' TCGGTGCAGGTAGGTCA 10796 G TG  
 TGA TCTGCCTG CCGA  
 || ||||| |||||  
 ACT GGATGGAC GGCT  
 \_ GT  
 GAM1248 PRNP 3' TTGGGATGCAGGCTCAGCCC 4340 CT G  
 GGGCTGAGTCTGC GT CCGA  
 ||||| ||||| |||||  
 CCCGACTCGGACG TA GGTT  
 \_ G  
 GAM1248 PTGS1 3' TAGGTAGACTTTGCTTAG 6357 T  
 CTGGGC GAGTCTGCCTG  
 ||||| |||||  
 GATTCG TTCAGATGGAT  
 T  
 GAM1248 PTGS1 3' TAGGTAGACTTTGCTTAG 54576 T  
 CTGGGC GAGTCTGCCTG  
 ||||| |||||

GATTCG TTCAGATGGAT  
 T  
 GAM1248 PXMP3 5' TTGGTAATCCAGATTCGGCTAG 4350 G CCTG  
 CTGG CTGAGTCTG TGCCGA  
 |||| ||||| |||||  
 GATC GGCTTAGAC ATGGTT  
 \_ CTA\_  
 GAM1248 PYGB 3' TTGGCTGACACAGCTTAGCTTG 11179 TG T CCTGT  
 G C GGCTGAG CTG GCCGA  
 | ||||| || |||||  
 G TCGATTC GAC CGGTT  
 GT \_ ACAGT  
 GAM1248 RAB33A 5' TTGGGGCCCCGGTTCGGTCCGG 16579 T CCT G  
 CTGGGCTGAG CTG GT CCGA  
 ||||| || || |||||  
 GGCCTGGCTT GGC CG GGTT  
 \_ CC\_ G  
 GAM1248 RAP1 3' TTGGTGCTCAGAATGTAGCTCG 38584 AG\_ CCT TG  
 G CTGGGCTG TCTG G CCGA  
 ||||| ||| | |||||  
 GGCTCGAT AGAC C GGTT  
 GTA T\_\_GT  
 GAM1248 SFTPD 3' GGGCAGTGCTTGGCCCAG 11584 TG \_  
 CTGGGC AGT CTGCCT  
 ||||| || |||||  
 GACCCG TCG GACGGG  
 GT T  
 GAM1248 SH3BP2 3' CAGGTGGGCTCAGTTC 11596 TG  
 GGGCTGAGTC CCTG  
 ||||| |||||  
 CTTGACTCGG GGAC  
 GT  
 GAM1248 SH3BP2 3' GGCGTGATCTCGGCTCA 11610 \_ \_  
 TGGGCTGAG TC TGCC  
 ||||| || |||||  
 ACTCGGCTC AG GCGG  
 T T  
 GAM1248 SLC12A7 3' GGCTGGATTTACCCAG 21705 C \_  
 CTGGG TGAGTCT GCC  
 |||| ||||| |||||  
 GACCC ATTTAGG CGG  
 \_ T  
 GAM1248 SLC19A1 3' TTGGTATGTGCCAGGCTTGCCT 11760 TG T \_C  
 GG C GGC GAGTCTG C TGTGCCGA  
 | || ||||| | |||||  
 G CCG TTCGGAC G GTATGGTT  
 GT \_ C T  
 GAM1248 SLC25A14 3' TTGGTTAGCCCCAGACTTGGGC 14201 G TG C\_\_ T  
 TAG TGG C AGTCTG CTG GCCGA  
 ||| | ||||| || |||||

ATC G TCAGAC GAT TGGTT  
 G GT CCC \_  
 GAM1248 SLC25A14 3' TTGGTTAGCCCCAGACTTGGGC 43022 G TG C\_\_ T  
 TAG TGG C AGTCTG CTG GCCGA  
 ||| | |||| | ||||  
 ATC G TCAGAC GAT TGGTT  
 G GT CCC \_  
 GAM1248 SMOH 3' TCGGCTCTAGGGCCTCAGTCTG 18871 TG TCT GT\_\_  
 G C GGCTGAG GCCT GCCGA  
 | |||| | ||||  
 G CTGACTC CGGG CGGCT  
 GT \_\_\_\_ ATCT  
 GAM1248 SMURF1 5' CGGGACTGGGCTCGGCT 92451 CCT G  
 GGCTGAGTCTG GT CCG  
 |||| ||||  
 TCGGCTCGGGT CA GGC  
 \_\_\_\_ G  
 GAM1248 SNCAIP 3' TAATGTGGGCAGATTTGGCTCA 95921 TG TG CCGA  
 G CTGGGC AGTCTGCC TG  
 |||| |||| ||  
 GACTCG TTAGACGG GT  
 GT GT AAT  
 GAM1248 SOX4 5' TCGGCGTGTGCTTGGCCCGG 11879 TG CT CTGT  
 CTGGGC AGT GC GCCGA  
 |||| | || ||||  
 GGCCCG TCG TG CGGCT  
 GT TG \_\_\_\_  
 GAM1248 SPP1 5' TCGGGACCAGACTCGTCTCAG 5155 C CCT G  
 CTGGG TGAGTCTG GT CCGA  
 |||| |||| || ||||  
 GACTC GCTCAGAC CA GGCT  
 T \_\_\_\_ G  
 GAM1248 TARBP2 3' TTGGTGTGGGCTCCCGCCTGG 56172 TG T\_ TG CTGT  
 C GGC GAGTC C GCCGA  
 | || |||| | ||||  
 G CCG CTCGG G TGGTT  
 GT CC GT \_\_\_\_  
 GAM1248 TIAM1 3' TTGGCAGCTGACTTGGTTC 12289 TG T CTG  
 GGGC AGTC GC TGCCGA  
 ||| ||| || ||||  
 CTTG TCAG CG ACGGTT  
 GT T \_\_\_\_  
 GAM1248 TLR9 5' AGGCAGGTGCAGCCTAG 33849 AG  
 CTGGGCTG TCTGCCT  
 |||| ||||  
 GATCCGAC GGACGGA  
 GT  
 GAM1248 TM6SF2 5' GGCAGCCTCGGCCCGG 72364 T  
 CTGGGCTGAG CTGCC  
 |||| ||||

GGCCCCGGCTC GACGG  
C  
GAM1248 TNFAIP2 3' TCGATCTCAGGCATGACTCAGC 20835 \_ TGC\_  
CCGG TGGGCTGAGTC TGCCTG CGA  
||||||| ||||| |||  
GCCCCGACTCAG ACGGAC GCT  
T TCTA  
GAM1248 TNFRSF11A 3' TTGGCAACCTGGCTCTGGCCCA 13857 \_ TGCCTG  
G CTGGGCT GAGTC TGCCGA  
||||||| ||||| |||||  
GACCCGG CTCGG ACGGTT  
T TCCA\_\_  
GAM1248 TNNT1 3' TCGGCTCTCCTGGGCTCAGTCC 12349 GCCTGT  
GGGCTGAGTCT GCCGA  
||||||| |||||  
CCTGACTCGGG CGGCT  
TCCTCT  
GAM1248 TRPV1 5' CAGGCAGGCCTGGCCCAG 54793 GA  
CTGGGCT GTCTGCCTG  
||||||| |||||  
GACCCGG CGGACGGAC  
TC  
GAM1248 WARS 3' CTGGACGGGTGGACTTAGCTAG 67286 G TG G A  
CTGG CTGAGTC CCTGT CCG  
||||||| ||||| |||  
GATC GATTCAG GGGCA GGT  
\_ GT \_ CC  
GAM1248 ZIC3 5' TGGCGCAGCCCAGCCCGG 12731 A TCTGC  
CTGGGCTG G CTGTGCCG  
||||||| | |||||  
GGCCCGAC C GACGCGGT  
C \_\_\_\_  
GAM1248 ABHD3 3' GTGAAGGCAGCTCAGCTTAG 56375 T G  
CTGGGCTGAG CTGCCT TGC  
||||||| ||||| |||  
GATTCGACTC GACGGA GTG  
\_ A  
GAM1248 ASB13 3' TCGGCCTGGGATGTGGCCTGG 45222 TG AGTCTG T  
C GGCTG CCTG GCCGA  
| ||||| ||||| |||||  
G CCGGT GGGT CGGCT  
GT GTA\_\_ C  
GAM1248 ATP10D 3' CAGGCAGACATCAGCTCAG 73140 \_  
CTGGGCTGA GTCTGCCTG  
||||||| |||||  
GACTCGACT CAGACGGAC  
A  
GAM1248 BLP1 3' TTGGTGTGGATCGATTCTGTTT 49201 TG T TGC TG  
GG C GGC GAGTC CTG CCGA  
| ||||| ||||| |||||

G TTG CTTAG GGT GGTT  
 GT T CTA GT  
 GAM1248 C1orf25 5' CGGGCGGGCTTGGCACGG 72535 G TG  
 CTG GC AGTCTGCCTG  
 ||| || |||||  
 GGC CG TCGGGCGGGC  
 A GT  
 GAM1248 C20orf116 3' TTGGTGTGGCAGAAGGCCTGGC 43739 GA \_\_\_\_ T TG  
 CTAG GGGCT GT CTGCC G CCGA  
 |||| || |||| | |||  
 TCCGG CG GACGG T GGTT  
 TC GAA \_GT  
 GAM1248 C20orf98 3' TGGAGGACAGGTTTGGCCCAG 71517 TG GT \_ GTG  
 CTGGGC A CTG CCT CCG  
 |||| | ||| |||  
 GACCCG T GAC GGA GGT  
 GT TG A \_\_\_\_  
 GAM1248 C6orf31 3' CGCGGGGTGATTGAGTCCAG 47642 TG  
 CTGGGCTGAGTC CCTGTG  
 ||||| |||||  
 GACCTGACTTAG GGGCGC  
 TG  
 GAM1248 C9orf7 3' CGGGCCTGGCTTAGCCCAG 34168 T\_  
 CTGGGCTGAGTC GCCTG  
 ||||| |||||  
 GACCCGATTCCG CGGGC  
 TC  
 GAM1248 CAMK2G 5' GCAGCAGGCTTGGTTTGG 68965 TG TG C  
 C GGC AGTCTGC TGT  
 | ||| ||||| |||  
 G TTG TCGGACG ACG  
 GT GT \_  
 GAM1248 CAMKK1 3' CGGGCAGGCCTGGCTCAG 50170 GA  
 CTGGGCT GTCTGCCTG  
 ||||| |||||  
 GACTCGG CGGACGGGC  
 TC  
 GAM1248 CCRK 3' TGGAAGGAAGATTTGGTTTGG 24013 TG TG G GTG  
 C GGC AGTCT CCT CCG  
 | ||| |||| ||| |||  
 G TTG TTAGA GGA GGT  
 GT GT A A\_\_  
 GAM1248 CD36L2 5' GGCGGGTGCGGCCCGG 18569 AG  
 CTGGGCTG TCTGCC  
 ||||| |||||  
 GGCCCGGC GGGCGG  
 GT  
 GAM1248 CDV-1 3' AGGTAGATTTAGTTTG 25918 GG  
 T GCTGAGTCTGCCT  
 | |||||

G TGATTTAGATGGA  
 TT  
 GAM1248 CENTG1 3' GGGCGGACTTACCTGG 28711 TG C  
 C GG TGAGTCTGCCT  
 | || |||||  
 G CC ATTCAGGCGGG  
 GT \_  
 GAM1248 CLSTN2 3' TTGGCACAGGCACAGAGCT 42134 GA CT  
 GGCT GT GCCTGTGCCGA  
 |||| || |||||  
 TCGA CA CGGACACGGTT  
 GA \_  
 GAM1248 CSEN 3' TCGGCATTACACACAGCCTGG 25535 TG A C CCT  
 C GGCTG GT TG GTGCCGA  
 | |||| || |||||  
 G CCGAC CA AC TACGGCT  
 GT A C T\_  
 GAM1248 CSTF3 5' TTGGCGGTCTGGCTCAGCTGGG 7176 G T\_ TGT  
 CT GGCTGAGTC GCC GCCGA  
 || ||||| || |||||  
 GG TCGACTCGG TGG CGGTT  
 G TC \_  
 GAM1248 CSTF3 5' TTGGTGTGCGGTCTGGCTCA 7177 G T T TG  
 G CTGGGCT AG CTGCC G CCGA  
 ||||| || |||| | |||||  
 GACTCGG TC GGCGG T GGTT  
 \_ T T GT  
 GAM1248 CX46.6 3' CAGGCAGACTCTGCCCAG 39942 T  
 CTGGGC GAGTCTGCCTG  
 ||||| |||||  
 GACCCG CTCAGACGGAC  
 T  
 GAM1248 CXYorf1 5' GGGTGGCTCGGCTCGG 82050 T  
 CTGGGCTGAGTC GCCT  
 ||||| |||||  
 GGCTCGGCTCGG TGGG  
 \_  
 GAM1248 DGKD 3' TAGGCGAGTTCAGCTTGG 59411 TG TC  
 C GGCTGAG TGCCTG  
 | ||||| |||||  
 G TCGACTT GCGGAT  
 GT GA  
 GAM1248 DGS-A 3' TTGGTGCACGAACATCCAG 84904 C C CC TG  
 CTGGG TGAGT TG TG CCGA  
 |||| |||| || |||||  
 GACCT ACTCA GC AC GGTT  
 \_ A \_ GT  
 GAM1248 DKFZP434B205 3' GGCACGGGGTGGCCAG 75321 A TG  
 CTG GTC CCTGTGCC  
 ||| ||| |||||

GAC CGG GGGCACGG  
 \_ TG  
 GAM1248 DKFZP434C128 3' TGGCTTAGGCCTGGTCTGG 64847 TG G TCT T  
 C GGCT AG GCCTG GCCG  
 | ||| || |||| ||||  
 G CTGG TC CGGAT CGGT  
 GT \_ \_ \_ T  
 GAM1248 DKFZp434E0519 3' TTGGTGCACACTCTCATTTTGG 49993 TG C TC CC TG  
 C GG TGAG TG TG CCGA  
 | || |||| || || ||||  
 G TT ACTC AC AC GGTT  
 GT T TC \_ GT  
 GAM1248 DKFZP434H0820 3' CAGGCAGGCTCAGCTC 63846  
 GGGCTGAGTCTGCCTG  
 ||||| |||||  
 CTCGACTCGGACGGAC  
  
 GAM1248 DKFZP564I052 3' TTGGTCTTGGGTATGGCTTAG 66725 \_ T\_  
 CTGAGTC TGCCTG GCCGA  
 ||||| ||||| ||||  
 GATTCGG ATGGGT TGGTT  
 T TC  
 GAM1248 DKFZp586H0623 3' CAGGTGATTTGGTCCGG 34067 TG T  
 CTGGGC AGTC GCCTG  
 ||||| |||| |||||  
 GGCCTG TTAG TGGAC  
 GT \_  
 GAM1248 DKFZp761G2113 3' TCGGCGTGCAGGACTCAGACCT 69911 TG \_ \_ CTG  
 GG C GG CTGAGTC TGC TGCCGA  
 | || ||||| || |||||  
 G CC GACTCAG ACG GCGGCT  
 GT A G T\_  
 GAM1248 DKFZp762K222 5' TTGGCGCAGGTGGGCCAGGC 71121 GA TG  
 GCT GTC CCTGTGCCGA  
 ||| ||| |||||  
 CGG CGG GGACGCGGTT  
 AC GT  
 GAM1248 DKKL1-pending 5' TCGGCACGAGGCCGGGCTGTGG 27011 \_ \_ \_  
 TCTAG GGCTG AGTCTG CCT GTGCCGA  
 |||| ||||| || |||||  
 CTGGT TCGGGC GGA CACGGCT  
 G C G  
 GAM1248 ECE2 3' TAGGGGTGGA CTGCTC 28069 TG G  
 GGGCTGAGTC CCT TG  
 ||||| ||| ||  
 CTCGACTCAG GGG AT  
 GT G  
 GAM1248 EHM2 5' CGGCGCGGGCTTGCCCCGG 38915 CTGA CT  
 CTGGG GT GCCTGTGCCG  
 |||| || |||||



GGCCC CG CGGGCGCGGC  
\_\_\_\_ TT  
GAM1248 FBX30 3' TTGGCCCAGAGGCTCAGGCCGG 52588 G GC T  
CTGG CTGAGTCT CTG GCCGA  
||||| ||||| ||| |||||  
GGCC GACTCGGA GAC CGGTT  
G \_\_\_\_ C  
GAM1248 FBX02 3' TGGCATAGGTTTGCTTAG 24088 CT  
CTGAGT GCCTGTGCCG  
||||| |||||  
GATTCG TGGATACGGT  
TT  
GAM1248 FLJ10375 3' CGCAGTGGCTTGGCTCGG 36074 TG TGC  
CTGGGC AGTC CTGTG  
||||| ||| |||||  
GGCTCG TCGG GACGC  
GT T\_\_\_\_  
GAM1248 FLJ10996 5' TCGGATCATGGGTTTGCCCAG 38777 TGAGTCT \_\_\_\_  
CTGGGC GCCTGTG CCGA  
||||| ||||| |||  
GACCCG TGGGTAC GGCT  
TT\_\_\_\_ TA  
GAM1248 FLJ11539 3' TCGGTCACCTCGTAGGCCAGCC 45380 A CT\_ \_  
TAG TGGGCTG GTCTGC GTG CCGA  
||||| ||||| ||| |||||  
ATCCGAC CGGATG CAC GGCT  
\_\_\_\_ CTC T  
GAM1248 FLJ11598 3' CGGCATGTATTTCATCTAG 46379 C TC CT  
CTGGG TGAG TGC GTGCCG  
||||| ||| ||| |||||  
GATCT ACTT ATG TACGGC  
\_\_\_\_ T\_ \_\_\_\_  
GAM1248 FLJ11710 3' TCGGCATGCTCTTAGGCCAG 45833 GAGTCT CT  
CTGGGCT GC GTGCCGA  
||||| || |||||  
GACCCGG CG TACGGCT  
ATTCT\_ \_\_\_\_  
GAM1248 FLJ12389 3' TTGGTATGTACAATTCAGTTCA 60269 C CC  
G CTGGGCTGAGT TG TGTGCCGA  
||||| || |||||  
GACTTGACTTA AC GTATGGTT  
\_\_\_\_ AT  
GAM1248 FLJ12517 3' GAGGTGTGGGCGGGCTCGTCCA 43437 T TG GA  
G CTGGGC GAGTCTGCCTG CC  
||||| ||||| ||| ||  
GACCTG CTCGGGCGGGT GG  
\_\_\_\_ GT AGG  
GAM1248 FLJ12618 3' GCAGGTAGATTGTAGCCCAG 45995 \_  
CTGGGCTG AGTCTGCCTGT  
||||| ||||| |||||

GACCCGAT TTAGATGGACG  
 G  
 GAM1248 FLJ12650 3' TTGGACTTGGATTTGAGCTTGG 44533 TG \_ GCCT G  
 C GGCT GAGTCT GT CCGA  
 | ||| ||||| || ||||  
 G TCGA TTTAGG CA GGTT  
 GT G TT\_\_ \_  
 GAM1248 FLJ12650 3' TTGGACGTGGACTTGGACTTGG 44532 TG \_TG TG CT G  
 C GG C AGTC C GT CCGA  
 | ||| |||| | || ||||  
 G TC G TCAG G CA GGTT  
 GT A GT GT\_\_ \_  
 GAM1248 FLJ13102 3' TTGGCATGGCAAAGCTTGTCT 46019 CT C\_ T  
 AG CTGGG GAGT TGCC GTGCCGA  
 ||||| |||| |||| |||||  
 GATCT TTCG ACGG TACGGTT  
 TG AA \_  
 GAM1248 FLJ13110 5' GGCGGGCGCGCTCAGTCTGG 43305 TG C GT  
 C GGCTGAGT TGCCT GCC  
 | ||||| ||||| ||||  
 G CTGACTCG GCGGG CGG  
 GT C \_  
 GAM1248 FLJ13194 3' GGGCAGTTTGTTTAG 47130 TG T  
 CTGGGC AG CTGCCT  
 ||||| || |||||  
 GATTTG TT GACGGG  
 GT \_  
 GAM1248 FLJ13490 3' TTGGCATGTGTAACTTAGTTC 46304 C C  
 A TGGGCTGAGT TGC TGTGCCGA  
 ||||| ||||| ||||| |||||  
 ACTTGATTCA ATG GTACGGTT  
 A T  
 GAM1248 FLJ13590 5' TCGGCCGCCGTAGGCCGGCTTG 45788 TG A CT \_  
 G C GGCTG GTCTGC GTG CCGA  
 | ||||| ||||| ||||| |||||  
 G TCGGC CGGATG CGC GGCT  
 GT \_ C\_ C  
 GAM1248 FLJ13611 3' TGGGCAGATTTGGCCT 46297 TG  
 GGGC AGTCTGCCTG  
 |||| |||||  
 TCCG TTAGACGGGT  
 GT  
 GAM1248 FLJ13614 3' GGGTAGACTCGTCTAG 57455 T  
 CTGGGC GAGTCTGCCT  
 ||||| |||||  
 GATCTG CTCAGATGGG  
 \_  
 GAM1248 FLJ13725 5' TTGGTACCATCAAGCTCAGCCT 68289 TG TC CCT  
 GG C GGCTGAG TG GTGCCGA  
 | ||||| || |||||

G CCGACTC AC CATGGTT  
 GT GA TAC  
 GAM1248 FLJ14327 3' TCGGTGTATTTTTTTAGTCTA 46148 TCTGCC TG  
 TGGGCTGAG TG CCGA  
 ||||| || |||  
 ATCTGATTT AT GGCT  
 TTTT\_\_ GT  
 GAM1248 FLJ14327 3' TTGGTGTGTGTAGGACATGGCT 46151 A \_ C TG  
 TAG CTGGGCTG GTC TGC TG CCGA  
 ||||| || ||| || |||  
 GATTCGGT CAG ATG GT GGTT  
 A G T GT  
 GAM1248 FLJ14427 3' TTGGGTGGGGACTCAGCCCAG 51336 TG TG G  
 CTGGGCTGAGTC CC T CCGA  
 ||||| || ||| |||  
 GACCCGACTCAG GG G GGTT  
 \_\_ GT \_  
 GAM1248 FLJ14668 3' TGGGAGGTAGACTAGTTTG 51516 TG G GTG  
 C GGCT AGTCTGCCT CCG  
 | ||| ||||| |||  
 G TTGA TCAGATGGA GGT  
 GT \_ G\_\_  
 GAM1248 FLJ20034 3' TTGGTCTCTAGGTTTCAGGTTAG 34391 G GT CCTGT  
 CTGG CTGA CTG GCCGA  
 ||| ||| || |||||  
 GATT GACT GAT TGGTT  
 G TG CTC\_\_  
 GAM1248 FLJ20123 5' GCAGGCAGCTCAGCCCAG 34587 T  
 CTGGGCTGAG CTGCCTGT  
 ||||| |||||  
 GACCCGACTC GACGGACG  
 -  
 GAM1248 FLJ20147 3' TTGGTATTTCTAGACATAGTCT 34643 A CCT  
 AG CTGGGCTG GTCTG GTGCCGA  
 ||||| ||||| |||||  
 GATCTGAT CAGAT TATGGTT  
 A CTT  
 GAM1248 FLJ20446 3' CGCAGGCGGGTTTATTTTGG 35185 TG C GT  
 C GG TGA CTGCCTGTG  
 | ||| |||||  
 G TT ATT GGCGGACGC  
 GT T TG  
 GAM1248 FLJ20619 3' TGGCACGGGTGGAATCAG 35465 G TG  
 CTGA TC CCTGTGCCG  
 ||| || |||||  
 GACT AG GGGCACGGT  
 A GT  
 GAM1248 FLJ21140 3' TGGTATGA ACTCAGCC 45483 CTGCC  
 GGCTGAGT TGTGCCG  
 ||||| |||||

CCGACTCA GTATGGT  
 A\_\_\_\_  
 GAM1248 FLJ21313 5' TGGCGCGGCCCGGCCTGG 43692 TG AGTCT T  
 C GGCTG GCC GTGCCG  
 | |||| || ||||  
 G CCGC CGG CGCGGT  
 GT C\_\_\_\_\_  
 GAM1248 FLJ22002 3' TGGTGCAAGTTTCAGCTCA 45781 T CTGT  
 TGGGCTGAG CTGC GCCG  
 ||||| ||| |||  
 ACTCGACTT GACG TGGT  
 T\_\_\_\_\_  
 GAM1248 FLJ22393 5' CCCTGCGGCGGGCGCGGCCCGG 47059 A T CCGA  
 CTGGGCTG GTCTGCC GTG  
 ||||| ||||| |||  
 GGCCCGGC CGGGCGG CGT  
 G \_ CCCT  
 GAM1248 FLJ22746 3' TGAACCCAGGCAGACTTATTTT 45553 TG C TGCCGA  
 GG C GG TGAGTCTGCCTG  
 | || |||||  
 G TT ATTCAGACGGAC  
 GT T CCAAGTC  
 GAM1248 FLJ22969 5' TCGCCTGAGGCAGATCGGTCCG 68664 G GTGC  
 G CTGGGCTGA TCTGCCT CGA  
 ||||| ||||| |||  
 GGCCTGGCT AGACGGA GCT  
 \_ GTCC  
 GAM1248 FLJ23323 3' TTGGTGCAAGTTGTACTTGGTCT 45059 TG C GC TG  
 GGGC AGT T CTG CCGA  
 ||| ||| ||| |||  
 TCTG TCA G GAC GGTT  
 GT T TT GT  
 GAM1248 FLJ23471 3' TCGGGGCCATGGGCTTGGCCCG 45300 TG CCT G  
 G CTGGGC AGTCTG GT CCGA  
 ||||| ||||| || |||  
 GGCCCG TCGGGT CG GGCT  
 GT AC\_ G  
 GAM1248 FLJ23471 3' TCGGGGCCGTGGGCTCGGCCCG 45301 TG CT G  
 G CTGGGCTGAGTC C GT CCGA  
 ||||| ||| ||| |||  
 GGCCCGGCTCGG G CG GGCT  
 GT C\_ G  
 GAM1248 FLJ23476 3' TGGCAGGGGTTTCAGTCCA 44965 GTCT G  
 TGGGCTGA GCCT TGCCG  
 ||||| ||| |||  
 ACCTGACT TGGG ACGGT  
 \_ G  
 GAM1248 FLJ23510 3' TTGGTGTCCCACTGGCCTCGGT 45292 TCT T \_  
 CCAG GCTGAG GCC GTG CCGA  
 ||||| ||| ||| |||

TGGCTC CGG CAC GGT  
 \_\_\_\_ T CCTGT  
 GAM1248 FLJ32356 3' TTGGTGACAGACTCAGCCCA 58371 CCTG  
 TGGGCTGAGTCTG TGCCGA  
 ||||| ||||  
 ACCCGACTCAGAC GTGGTT  
 A\_\_\_\_  
 GAM1248 FLJ32658 3' GCGCAGGCTTACCCTAG 58409 CTGA CT  
 CTGGG GT GCCTGTGC  
 |||| || |||||  
 GATCC CA CGGACGCG  
 \_\_\_\_ TT  
 GAM1248 FOXP1 3' TTGGCATATATCCTTCAGTTTG 51074 GG TCTGCC  
 T GCTGAG TGTGCCGA  
 | |||| |||||  
 G TGACTT ATACGGTT  
 TT CCTAT\_  
 GAM1248 FOXP1 5' TTGGTGCTGGGGCTCAGC 51075 TG T TG  
 GCTGAGTC CC G CCGA  
 ||||| || ||||  
 CGACTCGG GG C GGTT  
 \_\_\_\_ T GT  
 GAM1248 GPCR150 5' CGGAGGCAGGTTTCGGCT 26877 GT GTG  
 GGCTGA CTGCCT CCG  
 |||| |||| ||  
 TCGGCT GACGGA GGC  
 TG \_\_\_\_  
 GAM1248 HCA4 3' TTGGCACAATCTTGGCTCAG 77597 TG TCTGCC  
 CTGGGC AG TGTGCCGA  
 |||| || |||||  
 GACTCG TC ACACGGTT  
 GT TA\_\_\_\_  
 GAM1248 HCDI 5' GCTGGGCGGGCTTAGTC 39491 T  
 GGCTGAGTCTGCCTG GC  
 ||||| ||||| ||  
 CTGATTCGGGCGGGT CG  
 -  
 GAM1248 HCGIV.9 5' TCGGCGTGGATCTCGGACCCAG 38614 \_ \_ TG CTGT  
 CTGGG CTGAG TC C GCCGA  
 |||| |||| || | ||||  
 GACCC GGCTC AG G CGGCT  
 A T GT\_\_\_\_  
 GAM1248 HERC1 3' TGGTGCAATTTTGTAGTTGGG 14067 G TC CTGT  
 CT GGCTGAG TGC GCCG  
 || ||||| || ||||  
 GG TTGATTT ACG TGGT  
 G TT \_\_\_\_  
 GAM1248 HGC6.1.1 3' AGTGTGGACTGGCCCGG 26826 G TG\_  
 CTGGGCT AGTC C CT  
 ||||| |||| | ||

GGCCCCG TCAG G GA  
\_ GT T  
GAM1248 HS6ST 3' CAGGCAGGCCTGGCTCAG 62026 GA  
CTGGGCT GTCTGCCTG  
||||| |||||  
GACTCGG CGGACGGAC  
TC  
GAM1248 HSJ1 3' AGGAAGGAGGACTTGGCCTAG 22123 TG G GTG GA  
CTGGGC AGTCT CCT CC  
||||| ||||| || ||  
GATCCG TCAGG GGA GG  
GT A A\_\_ AA  
GAM1248 HSPC072 5' TTGGCCCATGTAGGCTGAGCTC 26339 G C T  
AG CTGGGCT AGTCTGC TG GCCGA  
||||| ||||| || |||||  
GACTCGA TCGGATG AC CGGTT  
G T C  
GAM1248 HSPC148 3' TTGGGAATAGTTTAAACCCAG 33083 C GTCT G\_  
CTGGG TGA GCCTGT CCGA  
||||| ||| ||||| |||||  
GACCC ATT TGGATA GGTT  
A \_\_\_\_ AG  
GAM1248 ICB-1 3' GGGCGGGCTGGTTTGG 16757 TG G  
C GGCT AGTCTGCCT  
| ||||| |||||  
G TTGG TCGGGCGGG  
GT \_  
GAM1248 IDI2 3' CTGAAGCAGGCAGACTAGCCTG 52695 TG G GC A  
G C GGCT AGTCTGCCTGT CG  
| ||||| ||||| || ||  
G CCGA TCAGACGGACG GT  
GT \_ AA CC  
GAM1248 KIAA0101 3' GGTAACCTTAGCTTAG 28424 C  
CTGGGCTGAGT TGCC  
||||||| |||||  
GATTCGATTCA ATGG  
\_  
GAM1248 KIAA0121 3' CACGGCGTGTTTGGTTCCG 72655 TG TC T  
CTGGGC AG TGCC GTG  
||||| || ||||| |||||  
GGCTTG TT GCGG CAC  
GT GT \_  
GAM1248 KIAA0125 5' TGGGCAGCTGGGCTCAGCTTGG 28904 TG GC G  
C GGCTGAGTCT CTGT CCG  
| ||||| ||||| |||||  
G TCGACTCGGG GACG GGT  
GT TC \_  
GAM1248 KIAA0193 3' TTGGTACAGGTGTTATTCACTA 28668 TG \_ CT\_  
CTGG G GCTGAGT GCCTGTGCCGA  
| ||||| ||||| |||||

C T G A C T T A   T G G A C A T G G T T  
 G T A   T T G  
 GAM1248 KIAA0218 3' TCGGCACAGGCAGAAGGACTTC 28625 CTGAG  
 A G   C T G G G   T C T G C C T G T G C C G A  
 ||||| |||||  
 G A C T T   A G A C G G A C A C G G C T  
 C A G G A  
 GAM1248 KIAA0237 3' TTGGCTACTGGGCTCATCCCAG 28539 C   C C T \_  
 C T G G G T G A G T C T G   G T G C C G A  
 ||||| ||||| || |||||  
 G A C C C A C T C G G G T   C A C G G T T  
 T   \_   T  
 GAM1248 KIAA0247 3' TGGCATATGTTTGGTCT 28412 T G G T C T C  
 G G G C A   G C T G T G C C G  
 ||||| | || |||||  
 T C T G T   T G A T A C G G T  
 G T \_   T  
 GAM1248 KIAA0258 3' TTGGTCCCTTCAGGTTTGGCCC 28824 T G G T C C T G T  
 A   T G G G C A C T G   G C C G A  
 ||||| | || |||||  
 A C C C G T G A C   T G G T T  
 G T T G T T C C C  
 GAM1248 KIAA0295 3' TGGCTCCGACTCAGTTTGG 68112 T G   T G C C T G T  
 C G G C T G A G T C   G C C G  
 | ||||| |||||  
 G T T G A C T C A G   C G G T  
 G T   C C T \_  
 GAM1248 KIAA0295 3' TTGGCCACTGGCTTAGCCCAG 68113 T G C C T  
 C T G G G C T G A G T C   T G G C C G A  
 ||||| ||||| || |||||  
 G A C C C G A T T C G G   A C C G G T T  
 T C \_ \_  
 GAM1248 KIAA0354 3' GGGACACAGTGGGTTAGCCTGG 29572 T G   G T G C \_ G A  
 C G G C T G A T C C T G T G C C  
 | ||||| || |||||  
 G C C G A T T G G G A C A C G G  
 G T \_ G T \_ A G T  
 GAM1248 KIAA0415 3' GGAGGCTCAGCCCGG 92579 G  
 C T G G G C T G A G T C T C C  
 ||||| ||||| ||  
 G G C C C G A C T C G G A G G  
 \_  
 GAM1248 KIAA0435 5' TCGGCCTCCTGGATTCAAGTTC 28985 \_ G C C T G T  
 A G   C T G G G C T G A G T C T   G C C G A  
 ||||| ||||| |||||  
 G A C T T G A C T T A G G   C G G C T  
 A T C C T C \_  
 GAM1248 KIAA0444 3' TTGGCGTCTTTGGGCTGGGTTT 62350 T G G G C C T G  
 G G   C G G C T A G T C T   T G C C G A  
 | ||||| ||||| |||||

G TTGG TCGGG GCGGTT  
 GT G TTTCT  
 GAM1248 KIAA0494 3' TGGTATAGGCCAAGTCAG 28751 GTCT  
 CTGA GCCTGTGCCG  
 |||| |||||  
 GACT CGGATATGGT  
 GAAC  
 GAM1248 KIAA0555 3' TTGGCACAATCTCGGCTCA 28890 TCTGCC  
 TGGGCTGAG TGTGCCGA  
 ||||| |||||  
 ACTCGGCTC ACACGGTT  
 TA\_\_\_\_  
 GAM1248 KIAA0618 5' GCCCCGCTAGGCCCGGCCCGG 29165 A CTGT  
 CTGGGCTG GTCTGC GC  
 ||||| ||||| ||  
 GGCCCGGC CGGATG CG  
 C CCC\_  
 GAM1248 KIAA0648 3' TGGCATTGTTTCAGCATAG 82658 G GTCT CT  
 CTG GCTGA GC GTGCCG  
 ||| |||| || |||||  
 GAT CGACT TG TACGGT  
 A \_\_\_\_ T\_  
 GAM1248 KIAA0773 3' TTGGCACAGGCAGAGTTTCGG 28063 \_  
 CTGAG TCTGCCTGTGCCGA  
 |||| |||||  
 GGCTT AGACGGACACGGTT  
 G  
 GAM1248 KIAA0828 3' TTGGTTCTAAGAGTTAGTCTGG 81204 TG G GCCTGT  
 C GGCTGA TCT GCCGA  
 | ||||| ||| |||||  
 G CTGATT AGA TGGTT  
 GT G ATCT\_  
 GAM1248 KIAA0918 3' TTGGCACGGGATTTCTCAGCTT 73137 TCTG  
 GGGCTGAG CCTGTGCCGA  
 ||||| |||||  
 TTCGACTC GGGCACGGTT  
 TTTA  
 GAM1248 KIAA0972 3' TTGGCTCTGGATGTGGCCTAG 30016 A GCCTGT  
 CTGGGCTG GTCT GCCGA  
 ||||| ||| |||||  
 GATCCGGT TAGG CGGTT  
 G TCT\_  
 GAM1248 KIAA0997 3' GGTGAGATTTTAGTCTGG 30193 TG \_ \_  
 C GGCTGAG TCT GCC  
 | ||||| ||| |||  
 G CTGATTT AGA TGG  
 GT T G  
 GAM1248 KIAA1026 3' TCGGCCGACAGGCACAGCCTGG 71212 TG AGTC \_  
 C GGCTG TGCCTGTG CCGA  
 | |||| ||||| |||||



G CCGAC ACGGACGC GGCT  
 GT \_\_\_\_ C  
 GAM1248 KIAA1028 3' GGCCAGGCCAGCCAG 91943 AGTCT T  
 CTGGGCTG GCCTG GCC  
 ||||| |||||  
 GACCCGAC CGGAC CGG  
  
 GAM1248 KIAA1117 3' TTGGTTTCAGACTTGGTTCA 61123 TG CCTGT  
 TGGGC AGTCTG GCCGA  
 ||||| |||||  
 ACTTG TCAGAC TGGTT  
 GT TT\_\_\_\_  
 GAM1248 KIAA1138 3' GCGGGGCGGGCTTGTCCCAG 62139 C G  
 CTGGG TGAGTCTGCCT TGC  
 ||||| |||||  
 GACCC GTTCGGGCGGG GCG  
 T \_  
 GAM1248 KIAA1157 5' GCCGGGTGGGCTCAGTTCAG 72246 TG T  
 CTGGGCTGAGTC CCTG GC  
 ||||| |||||  
 GACTTGACTCGG GGGC CG  
 GT \_  
 GAM1248 KIAA1169 5' TTGGTGCAGAAAGTAGGTTTCAG 35453 GT \_ TG  
 CTGA CTGC CTG CCGA  
 ||||| |||||  
 GACT GATG GAC GGTT  
 TG AA GT  
 GAM1248 KIAA1228 3' TTGTGTCTGTGGACTCTGCTCA 65054 T TG CT TG CGA  
 G  
 CTGGGC GAGTC C G C  
 ||||| ||||| | | |  
 GACTCG CTCAG G T G  
 T GT TC GT TT  
 GAM1248 KIAA1257 3' TGGTGTCAATTCAGTTTG 62764 GG C CCT TG  
 T GCTGAGT TG G CCG  
 | ||||| || | |||  
 G TGA CTTA AC T GGT  
 TT \_ \_ GT  
 GAM1248 KIAA1297 5' TGGTGCAGGACCGGCTGAG 72191 G A CTG TG  
 CT GGCTG GT CCTG CCG  
 || ||||| || |||||  
 GA TCGGC CA GGAC GGT  
 G \_ \_ GT  
 GAM1248 KIAA1297 5' TTGGCTGTGCATTTCAGCTCAG 72194 TC CTGT  
 CTGGGCTGAG TGC GCCGA  
 ||||| |||||  
 GACTCGACTT ACG CGGTT  
 \_ TGT\_  
 GAM1248 KIAA1396 3' CAGGCAGATATGGTCTGG 62986 TG A  
 C GGCTG GTCTGCCTG  
 | ||||| |||||

G CTGGT TAGACGGAC  
 GT A  
 GAM1248 KIAA1719 3' TTGGCACAGGCTGCTCAGCCGA 68175 G CT  
 G CT GGCTGAGT GCCTGTGCCGA  
 || ||||| |||||  
 GA CCGACTCG CGGACACGGTT  
 G T\_  
 GAM1248 KIAA1821 3' TGTTGTGGGTGTAGCCCAG 71802 AGTC TG GC  
 CTGGGCTG TGCC T CG  
 ||||| ||| | ||  
 GACCCGAT GTGG G GT  
 \_\_\_\_\_ GT TT  
 GAM1248 KIAA1822 3' GAATACAGCAGCTTAGTTTAG 67568 T C CCGA  
 CTGGGCTGAG CTGC TGTG  
 ||||| ||| |||  
 GATTGATTC GACG ACAT  
 \_\_\_\_\_ AAGT  
 GAM1248 KIAA1862 3' TCGGTGCAGGTACAGCTCAG 68930 AGTC TG  
 CTGGGCTG TGCCTG CCGA  
 ||||| |||| |||  
 GACTCGAC ATGGAC GGCT  
 \_\_\_\_\_ GT  
 GAM1248 KIAA1924 3' GCCGTGCGGGCTCAGCCTGG 73677 TG C T  
 C GGCTGAGTCTGC TG GC  
 | ||||| || ||  
 G CCGACTCGGGCG GC CG  
 GT T \_  
 GAM1248 LSFR2 3' TCGGCATGGGCACCTGGGTGTG 60571 G G TC  
 G CTG GCT AG TGCCTGTGCCGA  
 ||| ||| || |||||  
 GGT TGG TC ACGGGTACGGCT  
 G G C\_  
 GAM1248 MAD4 3' TCGGGGCCAGGCAGGCCAGCCC 21285 A \_G  
 AG CTGGGCTG GTCTGCCTG T CCGA  
 ||||| ||||| | |||  
 GACCCGAC CGGACGGAC G GGCT  
 \_\_\_\_\_ C G  
 GAM1248 MAP1LC3A 3' AGGGGGGCTCGGCCTGG 50706 TG G  
 C GGCTGAGTCT CCT  
 | ||||| |||  
 G CCGGCTCGGG GGA  
 GT G  
 GAM1248 MAPK11 5' CGGCTCGGGCTCGGCTCGG 10847 GTCT T  
 CTGGGCTGA GCCTG GCCG  
 ||||| ||| |||  
 GGCTCGGCT CGGGC CGGC  
 \_\_\_\_\_ T  
 GAM1248 MAPK11 5' CGGCTCGGGCTCGGCTCGG 57299 GTCT T  
 CTGGGCTGA GCCTG GCCG  
 ||||| ||| |||

GGCTCGGCT CGGGC CGGC  
\_\_\_\_ T  
GAM1248 MAPK8IP3 3' CGGCACCTGCTAGTCCAG 52980 AGTCT CT  
CTGGGCTG GC GTGCCG  
||||| || |||||  
GACCTGAT CG CACGGC  
\_\_\_\_ TC  
GAM1248 MAST205 5' TTGGCGCGGCTGCGCTGCGGCC 30670 \_ CT\_ T  
CGG TGGGCTG AGT GCC GTGCCGA  
||||| ||| ||| |||||  
GCCCGGC TCG CGG CGCGGTT  
G CGT \_  
GAM1248 MCF2L 3' TCGGCCCGTCCGGCTCGGCCCA 60846 T CC T  
G CTGGGCTGAG CTG TG GCCGA  
||||||| ||| || |||||  
GACCCGGCTC GGC GC CGGCT  
\_ CT C  
GAM1248 MED8 3' TTGGCATGGGCAGGGGTTGAG 53522 G GAG  
CT GGCT TCTGCCTGTGCCGA  
|| ||| |||||  
GA TTGG GGACGGGTACGGTT  
G \_  
GAM1248 MGC10981 5' GGGCAGACGCAGCCTGG 51021 TG A  
C GGCTG GTCTGCCT  
| |||| |||||  
G CCGAC CAGACGGG  
GT G  
GAM1248 MGC14697 5' TCGGCGTGGCGTCGGTC 51248 GTC TGT  
GGCTGA TGCC GCCGA  
||||| ||| |||||  
CTGGCT GCGG CGGCT  
\_\_\_\_ TG\_  
GAM1248 MGC15619 3' TTGGTGAGAGGTTTGGTTTG 50424 GG TG GTCT G\_  
T GC A GCCT TGCCGA  
| || | ||| |||||  
G TG T TGGA GTGGTT  
TT GT \_\_\_\_ GA  
GAM1248 MGC16491 3' TTGGGGAGGGCTGGGTTTAGCC 53639 GT \_ GTG  
CGG CTGGGCTGA CT GCCT CCGA  
||||||| || ||| |||||  
GGCCCGATT GG CGGG GGTT  
TG T AGG  
GAM1248 MGC2306 3' TGGCATTGCTGGCCTGG 50966 TG AGTCT CT  
C GGCTG GC GTGCCG  
| |||| || |||||  
G CCGGT CG TACGGT  
GT \_\_\_\_ TT  
GAM1248 MGC23284 3' GGGGGACGGAGGACTTGGCCTG 58705 TG TG GC G GA  
G C GGC AGTCT CTGT CC  
| ||| |||| |||| ||

G CCG TCAGG GGCA GG  
 GT GT A\_ G GGT  
 GAM1248 MGC2477 5' TTGGATCTCAGGTTTAGCTGAG 44075 G GTCT TG\_\_  
 CT GGCTGA GCCTG CCGA  
 || ||||| |||| ||||  
 GA TCGATT TGGAC GGTT  
 G \_\_\_\_ TCTA  
 GAM1248 MGC34923 5' GGGCTCACAGACCTCAGCCTGG 58523 TG \_ CC T GA  
 C GGCTGAG TCTG TG GCC  
 | ||||| |||| || |||  
 G CCGACTC AGAC AC CGG  
 GT C \_ T GT  
 GAM1248 MGC4172 5' CGGCGCGGCCGTGGCCCGG 44201 AGTCT T  
 CTGGGCTG GCC GTGCCG  
 ||||| || |||||  
 GGCCCGGT CGG CGCGGC  
 GC\_\_ \_  
 GAM1248 MGC4677 3' TGGTCATGGGCTGGTCTGG 53511 TG AGTCT \_  
 C GGCTG GCCTGTG CCG  
 | |||| ||||| ||||  
 G CTGGT CGGGTAC GGT  
 GT \_\_\_\_ T  
 GAM1248 MGC5242 3' GGGCCTGGCAGATTCACCTCAG 43825 C TGT GA  
 CTGGG TGAGTCTGCC GCC  
 |||| ||||| ||||  
 GACTC ACTTAGACGG CGG  
 C TC\_ GT  
 GAM1248 MRAS 3' TTGGCCCAAGGACTTGGTACAG 24229 GG TG GCC T  
 CTG C AGTCT TG GCCGA  
 || | |||| || |||||  
 GAC G TCAGG AC CGGTT  
 AT GT A\_ C  
 GAM1248 MRP63 3' TTGGTGCAAGGCTTGCAATCCCA 43811 CTGA CT TG  
 G CTGGG GT GCCTG CCGA  
 |||| || ||||| ||||  
 GACCC CG CGGAC GGTT  
 TAA\_ TT GT  
 GAM1248 NBL1 3' TTGGCACTGGATGGACTTGGCT 59320 \_ TG \_ T  
 TCAG TGG GC AGTCTG CC GTGCCGA  
 ||| || ||||| || |||||  
 ACT CG TCAGGT GG CACGGTT  
 T GT A T  
 GAM1248 NUDT9 5' TCGGCGTCACGTGCTGGTCTGG 43891 TG G CT C \_  
 C GGCT AGT GC TG TGCCGA  
 | |||| || || |||||  
 G CTGG TCG TG AC GCGGCT  
 GT \_ \_ C T  
 GAM1248 OSBPL8 3' GCCAAGGTAGTTTCAGTTTAG 40457 T GT  
 CTGGGCTGAG CTGCCT GC  
 ||||| ||||| || ||

GATTTGACTT GATGGA CG  
 \_ AC  
 GAM1248 PADI1 3' GCACAGGCAGGCTGGTTCAG 61997 G  
 CTGGGCT AGTCTGCCTGTGC  
 ||||| |||||  
 GACTTGG TCGGACGGACACG

\_  
 GAM1248 PDZ-GEF1 5' ATTGGTACATGATGTGTAAATT 26493 C C\_\_\_\_  
 CAGTTCAG TGAGT TGC TGTGCCGA T  
 ||||| ||||| |  
 ACTTA ATG ACATGGTT A  
 A TGTAGT

GAM1248 PDZD2 5' TTGGTGCCTGCTGCTTGGCTC 80882 TG CT CT TG  
 GGGC AGT GC G CCGA  
 ||| ||| || | |||  
 CTCG TCG CG C GGTT  
 GT T\_ TC GT

GAM1248 PIP5K1C 3' TCCCAGTGGTGGGACTCAGCCC 70766 GC TG GCC  
 AG CTGGGCTGAGTCT C T GA  
 ||||| ||||| | | ||  
 GACCCGACTCAGG G G CT  
 GT GT ACC

GAM1248 PRDM11 3' TTGGCTTCCCTAACTTAGTCCA 39584 CTGCCTGT  
 G CTGGGCTGAGT GCCGA  
 ||||| |||||  
 GACCTGATTCA CGGT  
 ATCCCTT\_

GAM1248 PRRG2 3' TCGGTGCGGGCAGGCTCGC 6291 T TG  
 GC GAGTCTGCCTG CCGA  
 || ||||| |||||  
 CG CTCGGACGGGC GGCT  
 GT

\_  
 GAM1248 PSMD3 5' TCGTGTGCAGGCCCGGCTCGG 10974 AGTCT TG\_  
 CTGGGCTG GCCTG C CGA  
 ||||| ||||| | |||  
 GGCTCGGC CGGAC G GCT  
 C\_\_\_\_ GT T

GAM1248 PTBP2 5' CGGCACGAGCGTGGCTCGG 41035 \_ C  
 CTGAGTC TGC TGTGCCG  
 ||||| ||| |||||  
 GGCTCGG GCG GCACGGC  
 T A

GAM1248 PTD012 5' AGGCGGGGTTGGCCTAG 25889 TG G  
 CTGGGC A TCTGCCT  
 ||||| | |||||  
 GATCCG T GGGCGGA  
 GT G

GAM1248 R32184\_3 3' CGGTAGGCGGGCCTAGCCCGG 53065 A GT A  
 CTGGGCTG GTCTGCCT GCCG  
 ||||| ||||| |||

GGCCCGAT CGGGCGGA TGGC  
C \_ G  
GAM1248 REM 3' ACTGTAGACTGGTCTGG 25805 TG G CT  
C GGCT AGTCTGC GT  
| ||| ||||| ||  
G CTGG TCAGATG CA  
GT \_ T\_  
GAM1248 RI58 3' TTGGCATGGGGTGCAGTCCAG 24849 AGTCTG  
CTGGGCTG CCTGTGCCGA  
||||| |||||  
GACCTGAC GGGTACGGTT  
GTG\_  
GAM1248 RLUCL 5' TTGGCGTGGGCGTGGGCGCGG 54221 G GAGTC TG  
CTG GCT TGCC TGCCGA  
||| ||| |||||  
GGC CGG GCGG GCGGTT  
G GT\_ GT  
GAM1248 RNP24 3' TGGTATGGGGATGATCCAG 22360 CTGA TG  
CTGGG GTC CCTGTGCCG  
|||| ||| |||||  
GACCT TAG GGGTATGGT  
AG\_ \_  
GAM1248 SARM 3' GGGTGGGCTGGTCCAG 30610 G TG  
CTGGGCT AGTC CCT  
||||| ||| |||  
GACCTGG TCGG GGG  
\_ GT  
GAM1248 SBBI26 3' TTGGTGACAAAGTTTTGGTTTG 38137 TG TG T GCCTG  
G C GGC AG CT TGCCGA  
| ||| ||| |||||  
G TTG TT GA GTGGTT  
GT GT T AACA\_  
GAM1248 SEC3 5' TCGGCACAGCCAGGCTCAGTCC 36813 C  
GG CTGGGCTGAGTCTG CTGTGCCGA  
||||||| |||||  
GGCCTGACTCGGAC GACACGGCT  
C  
GAM1248 SEMA5A 5' TTGGTGTGTGAGACTTGGGCTG 14265 TG G TG \_ CT TG  
G C G C AGTCT GC G CCGA  
| | |||| | |||  
G C G TCAGA TG T GGTT  
GT G GT G \_ GT  
GAM1248 SMCR5 3' TTGGCACAGAGCATCTGCCTAG 58598 T GTC \_  
CTGGGC GA TGC CTGTGCCGA  
||||| || |||||  
GATCCG CT ACG GACACGGTT  
T \_ A  
GAM1248 SSR3 3' TTGGTATAATACAGTGTAGCTT 23042 AGT CC\_  
AG CTGGGCTG CTG TGTGCCGA  
||||| || |||||

GATTCGAT GAC ATATGGTT  
 GT\_ ATA  
 GAM1248 SYT12 3' CAGGCAGGTCTCAGCCTGG 94726 TG \_  
 C GGCTGAG TCTGCCTG  
 | ||||| |||||  
 G CCGACTC GGACGGAC  
 GT T  
 GAM1248 TGIF2 3' GGGTAGGGCAGACTCTGCTTGG 41456 TG T G GA  
 C GGC GAGTCTGCCT TGCC  
 | || ||||| ||||  
 G TCG CTCAGACGGG ATGG  
 GT T \_ GT  
 GAM1248 TIMM13 5' TGGAGCGGCCTCGGTCCGG 24942 TCT T G  
 CTGGGCTGAG GCC GT CCG  
 ||||| || ||||  
 GGCCTGGCTC CGG CG GGT  
 \_ \_ A  
 GAM1248 TSPEAR 3' CAGGTGGGCCAGCCTAG 58714 A TG  
 CTGGGCTG GTC CCTG  
 ||||| || ||||  
 GATCCGAC CGG GGAC  
 C GT  
 GAM1248 TXNDC 3' ATATTGCAGGGTTCAGTCTAG 47736 TCTG CCGA  
 CTGGGCTGAG CCTGTG  
 ||||| ||||  
 GATCTGACTT GGACGT  
 G\_ TATAA  
 GAM1248 USP19 3' TTGGCCTCAGGCTTGGCCC 88960 TG CCTGT  
 GGGC AGTCTG GCCGA  
 ||| |||| ||||  
 CCCG TCGGAC CGGTT  
 GT TC\_  
 GAM1248 VPS39 3' CAGGCAGGCTGGCTTAG 62843 G  
 CTGGGCT AGTCTGCCTG  
 ||||| |||||  
 GATTCGG TCGGACGGAC  
 \_  
 GAM1248 WBSCR21 5' TGCTGTAGATATCAGCCCAG 48478 \_ CT  
 CTGGGCTGA GTCTGC GTG  
 ||||| |||| ||||  
 GACCCGACT TAGATG CGT  
 A T\_  
 GAM1248 ZNF185 3' TTGGCATAGGCTAGTGTTTAGC 23119 GT\_ \_  
 TT GGGCTGA CT GCCTGTGCCGA  
 ||||| || |||||  
 TTCGATT GA CGGATACGGTT  
 TGT T  
 GAM1248 LOC115051 3' CAGGCAGGCCTGGCTCAG 60037 GA  
 CTGGGCT GTCTGCCTG  
 ||||| |||||

	GACTCGG CGGACGGAC	
	TC	
GAM1248 LOC115399 3'	TGGCGCAGGACGCCCCGG 73438	CTGA CTG
	CTGGG GT CCTGTGCCG	
	GGCCC CG GGACGCGGT	
	CA_	
GAM1248 LOC116411 5'	TTGGTGCTCCACTCAGCTCA 73876	CTGCCT TG
	TGGGCTGAGT G CCGA	
	ACTCGACTCA C GGTT	
	CCTC_ GT	
GAM1248 LOC122704 3'	ACTGCCTGGGAGGCTTGGCTTA 74138	TG G TGT CGA
G	CTGGGC AGTCT CC GC	
	GATTCG TCGGA GG CG	
	GT G TC_ TCAC	
GAM1248 LOC123591 5'	CCAGCTGCGGGAGGCTCAGCCC 75610	G _ CGA
AG	CTGGGCTGAGTCT CCTGT GC	
	GACCCGACTCGGA GGGCG CG	
	_ T ACCT	
GAM1248 LOC126167 5'	TGGGATGGACTCGTTCAG 74461	T _
	CTGGGC GAGTCTG CCTG	
	GACTTG CTCAGGT GGGT	
	_ A	
GAM1248 LOC126823 5'	TCGGGCCGCAGGCTCAGGCTGG 74576	TG G CT G
	C G CTGAGTCTGC GT CCGA	
	G C GACTCGGACG CG GGCT	
	GT G C_ _	
GAM1248 LOC130814 3'	TAGGTAGGTTCTGTCCAG 74987	T GT
	CTGGGC GA CTGCCTG	
	GACCTG CT GATGGAT	
	T TG	
GAM1248 LOC132299 5'	TTGGCAACGAGGGACTCGGCCT 75056	GCCTG
	GGGCTGAGTCT TGCCGA	
	TCCGGCTCAGG ACGGTT	
	GAGCA	
GAM1248 LOC133418 3'	TTGGCACATGGAGATTCCGCTC 75093	T G _
AG	CTGGGC GAGTCT CC TGTGCCGA	
	GACTCG CTTAGA GG ACACGGTT	
	C _ T	
GAM1248 LOC133686 5'	TTGGCCGATAGAGTTAGCCTGG 75128	TG G CC T
	C GGCTGA TCTG TG GCCGA	



	G CCGATT AGAT GC CGGTT	
	GT G A _ _	
GAM1248 LOC139411 3'	TGGCATATTTTCACCTTAG 75835	C TCTGCC
	CTGGG TGAG TGTGCCG	
	GATTC ACTT ATACGGT	
	C TT _ _	
GAM1248 LOC144308 3'	TTGGAGCTCAGCTTGGCCCAG 83053	TG T CCT G
	CTGGGC AG CTG GT CCGA	
	GACCCG TC GAC CG GGTT	
	GT _ T _ A	
GAM1248 LOC145501 3'	TGGGTGGGTTTCAGCACTAG 77258	_ GT TG
	CTGG GCTGA C CCTG	
	GATC CGACT G GGGT	
	A TG GT	
GAM1248 LOC145858 5'	TTGGTCTGGGGTATGGCCCGG 77548	AGTC GT _
	CTGGGCTG TGCCT GCCGA	
	GGCCCGGT ATGGG TGGTT	
	_ GTC	
GAM1248 LOC146784 5'	TGTAGGAGGACTTAGCCTGG 78129	TG G GT
	C GGCTGAGTCT CCT G	
	G CCGATTCAGG GGA T	
	GT A TG	
GAM1248 LOC148603 5'	TTGGCTGTGATTGGCTTGGTTC 78916	TG TGCCTGT
AG	CTGGGC AGTC GCCGA	
	GACTTG TCGG CGGT	
	GT TTAGTGT	
GAM1248 LOC149086 5'	TTGGTTGAAGGCTGTGGTCTGG 84340	TG AGTCT GT _
	C GGCTG GCCT GCCGA	
	G CTGGT CGGA TGGTT	
	GT GT _ AGT	
GAM1248 LOC149422 3'	AGGCGGGTCCAGCTCGG 79348	AG
	CTGGGCTG TCTGCCT	
	GGCTCGAC GGGCGGA	
	CT	
GAM1248 LOC150343 5'	TCGGCTGGTAGGTTTGGGCCAG 79678	G TG GT TGT
	CTGG C A CTGCC GCCGA	
	GACC G T GATGG CGGCT	
	G GT TG T _	
GAM1248 LOC150358 5'	TCGGCAGTCGGACACAGCCCAG 84927	A C GT
	CTGGGCTG GTCTG CT GCCGA	

GACCCGAC CAGGC GA CGGCT  
 A T \_\_\_\_  
 GAM1248 LOC150406 3' GTGTGGGCATTGGTTTCAG 79857 TG GTC TG  
 CTGGGC A TGCCTG C  
 ||||| | ||||| |  
 GACTTG T ACGGGT G  
 GT \_\_\_\_ GT  
 GAM1248 LOC150468 5' GGCAGATTTAATTTCAG 79877 C  
 CTGGG TGAGTCTGCC  
 ||||| |||||  
 GACTT ATTTAGACGG  
 A  
 GAM1248 LOC151174 5' GTGTAGGTTTCAGCCCCG 85254 T GTCT TG  
 C GGGCTGA GCCTG C  
 | ||||| ||||| |  
 G CCGGACT TGGAT G  
 C \_\_\_\_ GT  
 GAM1248 LOC151318 3' TGGAACAGGCTCAGTCC 80230 GTCT G  
 GGGCTGA GCCTGT CCG  
 ||||| ||||| |||  
 CCTGACT CGGACA GGT  
 \_\_\_\_ A  
 GAM1248 LOC152217 3' AGGTAGGCTGGGTCCAG 91232 G  
 CTGGGGCT AGTCTGCCT  
 ||||| |||||  
 GACCTGG TCGGATGGA  
 G  
 GAM1248 LOC153205 3' TTGGTGTCTATGATTCAGTTTA 85950 TGCCT TG  
 TGGGCTGAGTC G CCGA  
 ||||| ||||| | |||  
 ATTTGACTTAG T GGTT  
 TATC\_ GT  
 GAM1248 LOC153683 3' TGGCATTAAATTTGGTCTAG 86083 TG CTGCCT  
 CTGGGC AGT GTGCCG  
 ||||| ||| |||||  
 GATCTG TTA TACGGT  
 GT AT \_\_\_\_  
 GAM1248 LOC158056 5' TGGAGACAGGCTAGCCTGG 81689 TG AGTCT G\_  
 C GGCTG GCCTGT CCG  
 | ||||| ||||| |||  
 G CCGAT CGGACA GGT  
 GT \_\_\_\_ GA  
 GAM1248 LOC159184 5' AGGCAGGCTCGCTCCGG 60045 \_ T  
 CTGG GC GAGTCTGCCT  
 ||||| || |||||  
 GGCC CG CTCGGACGGA  
 T \_  
 GAM1248 LOC160646 3' TTGGTGCAATCTTGGCTCAG 82233 TG TC CTGT  
 CTGGGC AG TGC GCCGA  
 ||||| || ||| |||||

	GACTCG TC ACG TGGTT	
	GT TA ____	
GAM1248 LOC161635 5'	CACGGTAGGCTTGGCCAG 96570	TG T
	CTGGGC AGTCTGCC GTG	
	GACCCG TCGGATGG CAC	
	GT _	
GAM1248 LOC163404 5'	CGGCTCGGCTCGGCCCGG 82126	TGCCT T
	CTGGGCTGAGTC G GCCG	
	GGCCCGGCTCGG C CGGC	
	____ T	
GAM1248 LOC163682 3'	TCGGCACAGACCTAGACTTGGC 87041	TG C__
T	GGC AGTCTG CTGTGCCGA	
	TCG TCAGAT GACACGGCT	
	GT CCA	
GAM1248 LOC170106 5'	TTGGTGGGAAGGTCTGGCTCAG 82572	AG G GT
	CTGGGCTG TCT CCT GCCGA	
	GACTCGGT GGA GGG TGGTT	
	CT A _	
GAM1248 LOC170425 5'	TTGGCATGGGATGCCAGCCAG 76380	G A CTG
	CTGG CTG GT CCTGTGCCGA	
	GACC GAC CG GGGTACGGTT	
	_ _ TA_	
GAM1248 LOC196074 3'	TTGGTATAGGTTTAAAGTGTGG 87584	G GAGTCT
	CTG GCT GCCTGTGCCGA	
	GGT TGA TGGATATGGTT	
	G ATT__	
GAM1248 LOC199745 3'	TATACGTGGGCTTGGCCCAG 88353	TG TG C
	CTGGGC AGTC C TGTG	
	GACCCG TCGG G ATAT	
	GT GT C	
GAM1248 LOC199986 5'	CACAGGCAGTTTCAGCCCAG 89899	T
	CTGGGCTGAG CTGCCTGTG	
	GACCCGACTT GACGGACAC	
	T	
GAM1248 LOC200014 3'	TTGGATCTTGGGTTTGGTCTA 88546	TG GTCT TG__
	TGGGC A GCCTG CCGA	
	ATCTG T TGGGT GGT	
	GT ____ TCTA	
GAM1248 LOC200093 5'	ACGGGTGGCTCGGCTCGG 63086	T
	CTGGGCTGAGTC GCCTGT	

GGCTCGGCTCGG TGGGCA

GAM1248	LOC200310	3'	TTGACACTGTGGCTTGGCCCAG 65746	TG T CT C
			CTGGGC AGTC GC GTG CGA	
			GACCCG TCGG TG CAC GTT	
			GT _ T_ A	
GAM1248	LOC200933	3'	TTGGTGTAGAACAACCTCAGTTC 90203	CTGC TG
		GG	CTGGGCTGAGT CTG CCGA	
			GGCTTGACTCA GAT GGTT	
			ACAA GT	
GAM1248	LOC201245	5'	TTGGCATGGGCGCGCCTGCCCA 87366	TGA T
		G	CTGGGC GTC GCCTGTGCCGA	
			GACCCG CGG CGGGTACGGTT	
			TC_ C	
GAM1248	LOC201689	5'	TACCCACTGGGCAGGTTTTGCC 67151	T GT _ CCGA
		CAG	CTGGGC GA CTGCCT GTG	
			GACCCG TT GACGGG CAC	
			T TG T CCAT	
GAM1248	LOC203078	3'	TTGGATCACGGCTTGTTTCAG 89278	TG TGCCT _
			CTGGGC AGTC GTG CCGA	
			GACTTG TCGG CAC GGTT	
			GT _ _ _ TA	
GAM1248	LOC204804	3'	CGGGCCCAATTCAGCCCAG 89472	CT_
			CTGGGCTGAGT GCCTG	
			GACCCGACTTA CGGGC	
			ACC	
GAM1248	LOC204804	3'	TTGGATTTCTGACTTGGCTCAG 89491	TG TGCCTGTG
			CTGGGC AGTC CCGA	
			GACTCG TCAG GGTT	
			GT TCTTTA_	
GAM1248	LOC219445	5'	TGGCGCGATCTCGGCTCA 91581	TCTGCC
			TGGGCTGAG TGTGCCG	
			ACTCGGCTC GCGCGGT	
			TA_	
GAM1248	LOC219513	5'	GCAGGTGGACCCGGCCCGG 94329	A TG
			CTGGGCTG GTC CCTGT	
			GGCCCGGC CAG GGACG	
			C GT	
GAM1248	LOC219920	5'	AGGTGCATTTGGCCCAG 93301	TG C
			CTGGGC AGT TGCCT	

		GACCCG TTA GTGGA		
		GT C		
GAM1248	LOC220064 3'	TGGCGCGATCTCGGCTCA	93429	TCTGCC
		TGGGCTGAG TGTGCCG		
		ACTCGGCTC GCGCGGT		
		TA____		
GAM1248	LOC220081 5'	TGGCTTGGACTCAGTTTA	91747	GCCTGT
		TGGGCTGAGTCT GCCG		
		ATTTGACTCAGG CGGT		
		TT____		
GAM1248	LOC220739 3'	TTGGCCTGGAAAGGCAGGCTCA	92940	C GT____
		CCTGG G TGAGTCTGCCT GCCGA		
		C ACTCGGACGGA CGGTT		
		_ AAGGTC		
GAM1248	LOC220753 3'	TTGGTGTGTAGTTCAGTCT	92947	T CT TG
		GGGCTGAG CTGC G CCGA		
		TCTGACTT GATG T GGTT		
		_ _ GT		
GAM1248	LOC221495 5'	TTGGCATGGAGGCCACTCAGCC	93867	CT _
		CAG TGGGCTGAGT GCCT GTGCCGA		
		ACCCGACTCA CGGA TACGGTT		
		C_ GG		
GAM1248	LOC222550 3'	GGGCCTCTTAGGCTTAGTTCAG	94353	CCTGT GA
		CTGGGCTGAGTCTG GCC		
		GACTTGATTCCGAT CGG		
		TCTC_ GT		
GAM1248	LOC254100 5'	TCGGCGCAGGCGGGGCAGC	96420	AG
		GCTG TCTGCCTGTGCCGA		
		CGAC GGGCGGACGCGGCT		
		G_		
GAM1248	LOC254158 5'	TCGGTGCGGCGAAGGTTTAGTT	96314	GT _ T TG
		CA TGGGCTGA CT GCC G CCGA		
		ACTTGATT GA CGG C GGCT		
		TG AG _ GT		
GAM1248	LOC255231 3'	GCAGGCAGACTGAGCTCAG	95375	G
		CTGGGCT AGTCTGCCTGT		
		GACTCGA TCAGACGGACG		
		G		
GAM1248	LOC255465 3'	TTGGCATGGGTGGTGCCT	97310	TGAGT TG
		GGGC C CCTGTGCCGA		

TCCG G GGGTACGGTT  
 T\_\_\_\_GT  
 GAM1248 LOC256372 5' TTGGCACTGTGACACAGTTCAG 95271 A T CT  
 CTGGGGCTG GTC GC GTGCCGA  
 ||||| ||| || |||||  
 GACTTGAC CAG TG CACGGTT  
 A \_ T\_  
 GAM1248 LOC51157 3' TCGGAAC TGGTTCCAGTCCAG 32491 AGTCT \_ G  
 CTGGGGCTG GCCT GT CCGA  
 ||||| ||| || |||  
 GACCTGAC TGGG CA GGCT  
 CT\_\_\_\_T A  
 GAM1248 LOC58489 3' TTGGTTAGGGGTTTGGATTG 72530 TG \_ G \_  
 C AGTCT GCCT TG CCGA  
 | |||| ||| || |||  
 G TTAGG TGGG AT GGTT  
 GT TT G T  
 GAM1248 LOC89894 5' TCGGTACAGAGCAGGATTCAGT 60605 G \_ \_  
 ATAG TG GCTGAGTC TGC CTGTGCCGA  
 || ||||| ||| |||||  
 AT TGA CT TAG ACG GACATGGCT  
 A G A  
 GAM1248 LOC89932 5' TGGTGCAGGCAGCCCTGG 60823 TG CTGA T TG  
 C GG G CTGCCTG CCG  
 | || | ||||| |||  
 G CC C GACGGAC GGT  
 GT \_\_\_\_ GT  
 GAM1248 LOC90120 5' TTGGATTGTGTAGATGCAGTCT 61546 A CTGTG  
 AG CTGGGGCTG GTCTGC CCGA  
 ||||| |||| |||  
 GATCTGAC TAGATG GGTT  
 G TGT TA  
 GAM1248 LOC91040 5' GGGTGGCTCGGCTCGG 64721 T  
 CTGGGGCTGAGTC GCCT  
 ||||| ||||  
 GGCTCGGCTCGG TGGG  
 -  
 GAM1248 LOC91547 3' TTGGTCTAGGTTGCAGCCTGG 66408 TG AGTCT T  
 C GGCTG GCCTG GCCGA  
 | |||| |||| ||||  
 G CCGAC TGGAT TGGTT  
 GT GT\_\_ C  
 GAM1248 LOC91548 5' TCGAGTGTGCATTCGGTCCAG 66417 TC CT TG\_  
 CTGGGGCTGAG TGC G C CGA  
 ||||| ||| | |||  
 GACCTGGCTT ACG T G GCT  
 \_\_ \_\_GT A  
 GAM1248 LOC92689 3' TGGCACAATCTCGGCTCA 70232 TCTGCC  
 TGGGCTGAG TGTGCCG  
 ||||| |||||

ACTCGGCTC ACACGGT  
 TA\_\_\_\_  
 GAM1248 LOC93268 5' TTGGTTTTTCAGGGCTCAGTCT 71887 GCCTGT  
 GGGCTGAGTCT GCCGA  
 ||||| ||||  
 TCTGACTCGGG TGGTT  
 ACTTT\_  
 GAM1248 LOC93273 3' TCGGTGTCTGGGCTCAGCCAG 71888 G CCT TG  
 CTGG CTGAGTCTG G CCGA  
 ||| ||||| | |||  
 GACC GACTCGGGT T GGCT  
 \_ C\_\_GT  
 GAM1248 LOC93622 3' ATAGGCGCATTTCAGTTTGG 56930 TG C  
 C GGCTGAGT TGCCTGT  
 | ||||| |||||  
 G TTGACTTA GCGGATA  
 GT C  
 GAM1248 LOC96597 5' TTGGATCAGCAGACTCAGCTGA 66922 G C TG  
 G CT GGCTGAGTCTGC TG CCGA  
 || ||||| || |||  
 GA TCGACTCAGACG AC GGTT  
 G \_ TA  
 GAM1249 UBQLN3 3' GCCTATCTTGAGATGCAATT 33928 GGTG  
 AGTTGCATT GAGATAGGC  
 ||||| |||||  
 TTAACGTAG TTCTATCCG  
 AG\_  
 GAM1249 UNC13 3' CCCATCTCCATGCCACACCTTA 21056 T CAT \_ A  
 TAAG TG TGGT GGAGAT GG  
 ||| || ||| ||||| ||  
 ATTG AC ACCG CCTCTA CC  
 C \_ TA C  
 GAM1249 ZNF261 3' GCCCAGGAACCAATGCTACT 17496 T GGAGATA  
 AGT GCATTGGT GGC  
 || ||||| ||  
 TCA CGTAACCA CCG  
 T AGGAC\_  
 GAM1249 FLJ12525 3' GCCCACCCTTAGTACAAC 48305 C T AGATA  
 AGTTG ATTGG GG GGC  
 |||| |||| || |||  
 TCAAC TGATC CC CCG  
 A \_ CCAC\_  
 GAM1249 KRTAP3-3 3' CCTATCTCAGTACCTACAAC 52593 CATT \_  
 AGTTG GGTG GAGATAGG  
 |||| ||| |||||  
 TCAAC CCAT CTCTATCC  
 AT\_\_ GA  
 GAM1250 BAZ2A 3' CACAAGTGCAGCTGTAG 25595 AGAA C  
 CTGCAGC GC ACTTGTG  
 ||||| || |||||

			GATGTCG CG TGAACAC	
			A _ _	
GAM1250 BSCL2	5'	CCACAAGT	CACTGGAAG 51028	GCA A A C
		CT GC GA G	CACTTGTGG	
		GA TG CT C	GTGAACACC	
		AGG A _ A		
GAM1250 GABRE	5'	CGCGACCTCCGCGCAGG	41805	A A A CCAC
		CCTGC GC GA G	TTGTG	
		GGACG CG CT C	AGCGC	
		_ C _ C _		
GAM1250 GABRE	5'	CGCGACCTCCGCGCAGG	17110	A A A CCAC
		CCTGC GC GA G	TTGTG	
		GGACG CG CT C	AGCGC	
		_ C _ C _		
GAM1250 GABRE	5'	CGCGACCTCCGCGCAGG	41774	A A A CCAC
		CCTGC GC GA G	TTGTG	
		GGACG CG CT C	AGCGC	
		_ C _ C _		
GAM1250 GABRE	5'	CGCGACCTCCGCGCAGG	41783	A A A CCAC
		CCTGC GC GA G	TTGTG	
		GGACG CG CT C	AGCGC	
		_ C _ C _		
GAM1250 GAN	5'	ATTGTGGCCAGCTTCTGCTCAG	41860	C _ CTTG
		CTG AGCAGAAGC	CA T	
		GAC TCGTCTTCG	GT A	
		_ ACCIIIG	GTTC	
GAM1250 GPC1	3'	CCACCTGCGCTTCTGCTGGAGG	9099	G _ CTT
		CCT CAGCAGAAGC	CA GTGG	
		GGA GTCGTCTTCG	GT CACC	
		G C C _		
GAM1250 KAI1	3'	CCACAGCGTCCCTGGCGCAGG	9496	AG AA CAC
		CCTGC CAG GC	TTGTGG	
		GGACG GTC TG	GACACC	
		CG CC C _		
GAM1250 KCNMB1	3'	CCACGCTGTCTTCTGTTGCAGG	14708	C CT
		CCTGCAGCAGAAG	CA TGTGG	
		GGACGTTGTCTTC	GT GCACC	
		T C _		
GAM1250 LGMN	5'	CCACGGTCGCCTGCCACAGG	18816	CA AA C T
		CCTG GCAG GC	ACT GTGG	



GGAC CGTC CG TGG CACC  
AC \_ C \_  
GAM1250 MLPH 3' CCACATGGACTCCACCTGCA 44079 CA\_ AG CT  
TGCAG GA CCA TGTGG  
||||| || ||| |||||  
ACGTC CT GGT ACACC  
CACC CA \_  
GAM1250 MOCS1 3' CACTTGTGGCCTGACCTCTGCT 92033 AG\_\_\_\_\_ CTTG  
GCAG GCAGCAGA CCA TG  
||||||| ||| ||  
CGTCGTCT GGT AC  
CCAGTCC||| GTTC  
GAM1250 NR1D1 5' CACTTGTGGCCAAGACCTTGCT 41363 AAG\_\_\_\_\_ CTTG  
GCAGG GCAGCAG CCA TG  
||||||| ||| ||  
CGTCGTT GGT AC  
CCAGAACC||| GTTC  
GAM1250 PDCL 3' GGTGGCCTCTGCTGCTGG 18217 T A  
CC GCAGCAGA GCCACT  
|| ||||| |||||  
GG CGTCGTCT CGGTGG  
T C  
GAM1250 PDLIM1 3' CCAGCAGGCCTCTGCTGCAG 40633 A ACT \_  
CTGCAGCAGA GCC TG TGG  
||||||| ||| |||  
GACGTCGTCT CGG AC ACC  
C \_ G  
GAM1250 PLOD 3' AGGGACTTCTGCTTCA 4320 C \_ A  
TG AGCAGAAG CC CT  
|| ||||| |||  
AC TCGTCTTC GG GA  
T A \_  
GAM1250 PMM1 3' CAGGACGCCTGCTGCA 10668 AA CAC G  
TGCAGCAG GC TT TG  
||||||| || |||  
ACGTCGTC CG AG AC  
\_ C\_ G  
GAM1250 PTPRF 3' CACTTGTGGTATGACTTCTGCT 11105 G G\_\_\_\_\_ CTTG  
GAAGG CAGCAGAA CCA TG  
||||||| ||| ||  
GTCGTCTT GGT AC  
A CAGTAT||| GTTC  
GAM1250 PTPRF 3' CACTTGTGGTATGACTTCTGCT 55267 G G\_\_\_\_\_ CTTG  
GAAGG CAGCAGAA CCA TG  
||||||| ||| ||  
GTCGTCTT GGT AC  
A CAGTAT||| GTTC  
GAM1250 PYGM 5' AGGGCCCCGTGCTGCAGG 18820 GAA\_ A  
CCTGCAGCA GCC CT  
||||||| ||| ||

			GGACGTCGT CGG GA	
			GCCC _	
GAM1250	RALBP1	3'	CCACAAGCCCATGCTGCTGCAG 22294	AAGCCA
			CTGCAGCAG CTTGTGG	
			GACGTCGTC GAACACC	
			GTACCC	
GAM1250	RAMP3	3'	CCGGAAGCCTCTGCCTGCAGG 19588	_ A CAC G
			CCTGCAG CAGA GC TT TGG	
			GGACGTC GTCT CG AA GCC	
			C C _ G	
GAM1250	RNPEP	3'	CCACAGCTCTCCCGCTACAGG 65110	C A _ _ CACT
			CCTG AGC GA AGC TGTGG	
			GGAC TCG CT TCG ACACC	
			A CCC C _	
GAM1250	SF3B3	5'	CCACACCATCCTTCTCGCTGCA 24856	_ CCACT
	GG		CCTGCAGC AGAAG TGTGG	
			GGACGTCG TCTTC ACACC	
			C CTACC	
GAM1250	SLC14A1	5'	CCACTGCCTTCTGCTGC 31837	C CTT
			GCAGCAGAAG CA GTGG	
			CGTCGTCTTC GT CACC	
			C _	
GAM1250	SUFU	3'	CCATCTGCCTCTGCTGCA 32408	A CACTT
			TGCAGCAGA GC GTGG	
			ACGTCGTCT CG TACC	
			C TC _	
GAM1250	SURF6	3'	GGTGGCCTCTGCTGCCGG 22191	T A
			CC GCAGCAGA GCCACT	
			GG CGTCGTCT CGGTGG	
			C C	
GAM1250	TACR1	5'	CCACGACAGGACTCTGCTGCAG 31713	AG AC
			CTGCAGCAGA CC TTGTGG	
			GACGTCGTCT GG AGCACC	
			CA AC	
GAM1250	TACR1	5'	CCACAGGACTCTGCTGCAG 6470	AG ACT
			CTGCAGCAGA CC TGTGG	
			GACGTCGTCT GG ACACC	
			CA _	
GAM1250	TAF11	5'	CACTTGTGGCCGAGCTTCTGCC 18915	CA _ CTTG
	TCAGG		G GCAGAAGC CA TG	

			C CGTCTTCG	GT AC		
			TC	AGCCIIIG GTTC		
GAM1250	TAP2	3'	CACTTGTGGCTCAAGCCCTGCT	5025	AAG_____	CTTG
			GCAG	GCAGCAG CCA TG		
			CGTCGTC	GGT AC		
			CCGAACTCIII	GTTC		
GAM1250	TNFRSF7	3'	CAGCTGCGCCTGCGCTGCAGG	6955	AGAA _ C	
			CCTGCAGC	GC CA TTG		
			GGACGTCG	CG GT GAC		
			CGTC	C C		
GAM1250	TNS	5'	AGTGGCTCCTCTGCAGG	42626	C A	
			CCTGCAG AG	AGCCACT		
			GGACGTC	TC TCGGTGA		
			_ C			
GAM1250	TNXB	5'	CACTTGTGGCTCAGCCCCTGTT	38879	AA _____	CTTG
			GCAGG	GCAGCAG GC CA TG		
			CGTTGTC	CG GT AC		
			CC	ACTCIIIG GTTC		
GAM1250	TRIM14	3'	CCACACCTCTCTGCTGC	28853	_ CCACT	
			GCAGCAGA AG	TGTGG		
			CGTCGTCT	TC ACACC		
			C C	_____		
GAM1250	VIPR2	3'	CCACACCCCTCTGCTGCA	12606	AGCCACT	
			TGCAGCAGA	TGTGG		
			ACGTCGTCT	ACACC		
			CCCC	_____		
GAM1250	ZNF35	5'	CACTTGTGGCCAGCCTCCTGCT	12778	AA_ _____	CTTG
			GCAG	GCAGCAG GC CA TG		
			CGTCGTC	CG GT AC		
			CTC	ACCCIIIG GTTC		
GAM1250	APPD	3'	TGGCTTCACTGCAGG	44218	CA	
			CCTGCAG	GAAGCCA		
			GGACGTC	CTTCGGT		
			A_			
GAM1250	ARHGEF9	3'	CCTTGGGGCTTCTGCCCAGG	30808	CA A TGT	
			CCTG	GCAGAAGCC CT GG		
			GGAC	CGTCTTCGG GG CC		
			C_	_ TT_		
GAM1250	ATP10D	5'	CGAGAGCCCCCAGCTGCAGG	73144	AGAA_ CA	
			CCTGCAGC	GC CTTG		

GGACGTCG CG GAGC  
ACCCC A\_  
GAM1250 C16orf7 3' GTGGCCTCTGCTGCTGG 16942 T A  
CC GCAGCAGA GCCAC  
|| ||||| ||||  
GG CGTCGTCT CGGTG  
T C  
GAM1250 C20orf18 3' CCAGCGGGGGCTGCCGCTGCAG 48339 AGA A \_  
G CCTGCAGC AGCC CTTG TGG  
||||| ||| ||| |||  
GGACGTCG TCGG GGGC ACC  
CCG \_ G  
GAM1250 C3F 3' CCAGCTGTGCCTCTGCTGC 19288 A C TTG  
GCAGCAGA GC AC TGG  
||||| || || |||  
CGTCGTCT CG TG ACC  
C \_ TCG  
GAM1250 CNNM3 3' CACAGCCTCCCTGCAGG 34338 CA A CACT  
CCTGCAG GA GC TGTG  
||||| || || |||  
GGACGTC CT CG ACAC  
C\_ C \_\_\_\_  
GAM1250 DKFZp761D0614 3' CCACAAGTAGTTTGTACAGG 87556 CA AGCC  
CCTG GCAGA ACTTGTGG  
||| ||| |||||  
GGAC TGT TT TGAACACC  
AC GA\_\_  
GAM1250 DKFZP761I2123 3' CAAGCCTGCTGCTGCAG 48755 A CCA  
CTGCAGCAG AG CTTG  
||||| || |||  
GACGTCGTC TC GAAC  
G C\_\_  
GAM1250 EDR1 3' GGCATCTTCTGCTGCAGG 15383 \_\_\_\_  
CCTGCAGCAGAA GCC  
||||||| |||  
GGACGTCGTCTT CGG  
CTA  
GAM1250 FER1L4 3' CCACAAGTGA CTCTCGCTG 47336 \_ A C  
CAGC AGA G CACTTGTGG  
||| ||| | |||||  
GTCG TCT C GTGAACACC  
C \_ A  
GAM1250 FLJ10199 3' CCACACAGCCTCCTGCTGCAGG 71230 A CCA \_  
CCTGCAGCAG AG CT TGTGG  
||||||| || || |||||  
GGACGTCGTC TC GA ACACC  
C C\_\_ C  
GAM1250 FLJ10375 3' ATTGTGGCCAACTTTGCTGCAG 36070 AG\_\_\_\_\_ CTTG  
CTGCAGCAGA CCA T  
||||||| ||| |

		GACGTCGTTT	GGT	A	
		CAACCCIII	GTTC		
GAM1250	FLJ10737	3'	GTGCGCCTCTGCCGCAGG	36524	A A _
			CCTGC GCAGA GC CAC		
			GGACG CGTCT CG GTG		
			C C C		
GAM1250	FLJ12949	3'	CCACAAGTACTATCTGCTGCAG	43444	_ CC
			CTGCAGCAGA AG ACTTGTGG		
			GACGTCGTCT TC TGAACACC		
			A A _		
GAM1250	FLJ13055	3'	CACGCCCCCTGCTGCGGG	42709	AA CACTT
			CCTGCAGCAG GC GTG		
			GGGCGTCGTC CG CAC		
			CC _		
GAM1250	FLJ14082	5'	CAGGCAGCTTCTGCTCAGG	46672	C CA
			CCTG AGCAGAAGC CTTG		
			GGAC TCGTCTTCG GGAC		
			_ AC		
GAM1250	FLJ20040	3'	CCACCGGCCTCCCGCCTGCAGG	38629	_ A_ A ACTT
			CCTGCAG C GA GCC GTGG		
			GGACGTC G CT CGG CACC		
			C CC C C _		
GAM1250	FLJ20171	3'	ATTGTGGCCAGCTCCTGCTGCA	34677	A _ CTTG
	G		CTGCAGCAG AGC CA T		
			GACGTCGTC TCG GT A		
			C ACCIIIG GTTC		
GAM1250	FLJ20273	5'	CCGGAAGCTTCTGCAACAGG	38728	CA CAC G
			CCTG GCAGAAGC TT TGG		
			GGAC CGTCTTCG AA GCC		
			AA _ G		
GAM1250	FLJ21945	3'	CAGGTAAGTCCTACTGCAGG	47315	C AAGCC
			CCTGCAG AG ACTTG		
			GGACGTC TC TGGAC		
			A CTGAA		
GAM1250	FLJ22940	5'	CACAGATCTGCTGCAG	44696	AGCCAC
			CTGCAGCAGA TTGTG		
			GACGTCGTCT GACAC		
			A _		
GAM1250	FLJ23022	5'	CCACACATGCCCTTCTCCACAG	46811	CAGC C_ CT
	G		CCTG AGAAG CA TGTGG		

		GGAC TCTTC GT ACACC	
		ACC_ CC AC	
GAM1250 FLJ23420	5'	ATTGTGGCCAGCTTCTGCTGCA 46844	_____ CTTG
		TGCAGCAGAAGC CA T	
		ACGTCGTCTTCG GT A	
		ACCIIG GTTC	
GAM1250 GPA33	3'	CCACCTCCCACTCCTGCTGCA 19453	A CCACTT
		TGCAGCAG AG GTGG	
		ACGTCGTC TC CACC	
		C ACCCTC	
GAM1250 KIAA0356	3'	CACTTGTGGCCACCCCTCTGCT 66190	AG_____ CTTG
		GCAGG GCAGCAGA CCA TG	
		CGTCGTCT GGT AC	
		CCCCACCI GTTC	
GAM1250 KIAA0514	3'	CAGAAGCTTCTGCTGAG 28079 G	CAC G
		CT CAGCAGAAGC TT TG	
		GA GTCGTCTTCG AA AC	
		_ _ G	
GAM1250 KIAA0532	3'	CCACAAGTAGCTACGACTGCA 70771	CAGA C
		TGCAG AGC ACTTGTGG	
		ACGTC TCG TGAACACC	
		AGCA A	
GAM1250 KIAA0543	3'	ATTGTGGCCAGCTCTGCTGCAG 68933	A _____ CTTG
		G CTGCAGCAGA GC CA T	
		GACGTCGTCT CG GT A	
		_ ACCIIG GTTC	
GAM1250 KIAA0711	5'	CCACAAGTGGGAGCCACAG 29515	CA AGAAG
		CTG GC CCACTTGTGG	
		GAC CG GGTGAACACC	
		AC AG_	
GAM1250 KIAA0712	5'	CAAGAAACTGCTGCTGCAGG 28198	A CCA_
		CCTGCAGCAG AG CTTG	
		GGACGTCGTC TC GAAC	
		G AAAA	
GAM1250 KIAA0773	3'	CCACCCGTCTCCTGCTGCAGG 28048	A CC TT
		CCTGCAGCAG AG AC GTGG	
		GGACGTCGTC TC TG CACC	
		C _ CC	
GAM1250 KIAA0907	3'	GGTGGCTTATGCTGCAG 30181	G
		CTGCAGCA AAGCCACT	

		GACGTCGT TTCGGTGG		
		A		
GAM1250 KIAA0939	3'	CAGGCCACTTCTGCTGAGG 62009	G	CCA
		CCT CAGCAGAAG CTTG		
		GGA GTCGTCTTC GGAC		
		ACC		
GAM1250 KIAA1145	3'	CCACTCCCGCCATCTGCTGCAG 65621		A_ CACTT
	G	CCTGCAGCAGA GC GTGG		
		GGACGTCGTCT CG CACC		
		AC CCCT_		
GAM1250 KIAA1441	3'	ATTGTGGTATGCTCCTGCTGCA 88410		A _____ CTTG
	G	CTGCAGCAG AGC CA T		
		GACGTCGTC TCG GT A		
		C TAT   G GTTC		
GAM1250 KIAA1643	3'	ATTGTGGCTAGCCTCCCTGCAG 64547		CA A _____ CTTG
	G	CTGCAG GA GC CA T		
		GACGTC CT CG GT A		
		C_ C ATC   G GTTC		
GAM1250 KIAA1855	3'	CCAGGGTGGTGGCTTCTCTGCA 92338		C __ G
	G	CTGCAG AGAAGCCACT T TGG		
		GACGTC TCTTCGGTGG G ACC		
		TG G		
GAM1250 KIAA1981	3'	TGGCCTCGCTGCAGG 88348	A A	
		CCTGCAGC GA GCCA		
		GGACGTCG CT CGGT		
		C		
GAM1250 MGC13170	5'	ATTGTGGCTGCTCCTGCTGCAG 51144		A _____ CTTG
	G	CCTGCAGCAG AGC CA T		
		GGACGTCGTC TCG GT A		
		C TCI  G GTTC		
GAM1250 MGC15668	5'	CCACAAGTAAGCGGCCCCAG 51278		CA AGAA C_
		CTG GC GC ACTTGTGG		
		GAC CG CG TGAACACC		
		CC G__ AA		
GAM1250 MGC16703	5'	CCTTGGGGGCTTCTCCCGCAGG 73100	AGC	A T
		CCTGC AGAAGCC CTTG GG		
		GGACG TCTTCGG GGGT CC		
		CCC _ T		
GAM1250 MGC29762	5'	CGCAGCTCCTGCTGCAG 58470		A CACT
		CTGCAGCAG AGC TGTG		

			GACGTCGTC TCG ACGC		
			C ____		
GAM1250	MGC4604	3'	CCATGCGTAGACTCCCGCTGCA 48976	A_	AGCC T
			GG CCTGCAGC GA AC TGTGG		
			GGACGTCG CT TG GTACC		
			CC CAGA C		
GAM1250	MGC5338	5'	TGGCGGAGCCCTGCTGCAGG 43943	AA	_____
			CCTGCAGCAG GCCA		
			GGACGTCGTC CGGT		
			CCGAGG		
GAM1250	MVD	3'	CCACGGCGCTTCTGCTGAG 10139 G	CAC	
			CT CAGCAGAAGC TTGTGG		
			GA GTCGTCTTCG GGCACC		
			_ C_		
GAM1250	NINJ2	3'	CCACAAGTGTGGAGCTGCAG 33279	AGA	C
			CTGCAGC AGC ACTTGTGG		
			GACGTCG TTG TGAACACC		
			AGG _		
GAM1250	PADI3	3'	CCACATCCTGCTCTGCTGCAGG 32655	A	CACT
			CCTGCAGCAGA GC TGTGG		
			GGACGTCGTCT CG ACACC		
			_ TCCT		
GAM1250	PCSK7	3'	CCACCCTGTCTTCCTCTGCA 16334	CA	C CTT
			TGCAG GAAG CA GTGG		
			ACGTC CTTC GT CACC		
			TC T CC_		
GAM1250	PNMA1	5'	CAC TTGTGGCGACGCCCTGCT 20073	AA	_____ CTTG
			GCAGG GCAGCAG GC CA TG		
			CGTCGTC CG GT AC		
			CC CAGCIIIG GTTC		
GAM1250	PP1628	5'	CAGGAGGCCCTGCTGCAG 47293	AA	A
			CTGCAGCAG GCC CTTG		
			GACGTCGTC CGG GGAC		
			CC A		
GAM1250	PTPRR	3'	GGTGGCTTCTGCTCCAG 11138	C	
			CTG AGCAGAAGCCACT		
			GAC TCGTCTTCGGTGG		
			C		
GAM1250	PTPRR	3'	GGTGGCTTCTGCTCCAG 55617	C	
			CTG AGCAGAAGCCACT		



			GAC TCGTCTTCGGTGG		
			C		
GAM1250	SEPT3	3'	CCACTCAACTGGCCTCTGCTGC 38889	A	CTT__
			GCAGCAGA GCCA GTGG		
			CGTCGTCT CGGT CACC		
			C CAACT		
GAM1250	SH3BP1	5'	ACAAGCGGCTGCAGG 38534	GCAGAA	A
			CCTGCA GCC CTTGT		
			GGACGT CGG GAACA		
			_____ C		
GAM1250	SIAT4B	5'	CCACTGTCCCCTGCTGCAG 22654	AAGCC	TT
			CTGCAGCAG AC GTGG		
			GACGTCGTC TG CACC		
			CCC__ T_		
GAM1250	SLAM	5'	ACAGCCTCTGCTGCA 11708	A	CACT
			TGCAGCAGA GC TGT		
			ACGTCGTCT CG ACA		
			C _____		
GAM1250	SLC4A11	3'	CAGGGCAGCTTCTGCCAGG 49338	CA	CA_
			CCTG GCAGAAGC CTTG		
			GGAC CGTCTTCG GGAC		
			C_ ACG		
GAM1250	ZNF338	5'	CGGGGAGCCGCTGCTGCA 42011	AA	CA
			TGCAGCAG GC CTTG		
			ACGTCGTC CG GGGC		
			GC AG		
GAM1250	LOC113201	5'	GGCTTCTGCCTGCAGG 56550	_	
			CCTGCAG CAGAAGCC		
			GGACGTC GTCTTCGG		
			C		
GAM1250	LOC138389	5'	CACTGCTTCTGCCACAG 76221	CA	CACTT
			CTG GCAGAAGC GTG		
			GAC CGTCTTCG CAC		
			AC T_____		
GAM1250	LOC145800	3'	CATGGACAACCTCCTGACTGCAG 77500	_	A CCAC TG
		G	CCTGCAG CAG AG T TG		
			GGACGTC GTC TC G AC		
			A C AACA GT		
GAM1250	LOC146268	3'	AGTGCTTCTGCCAG 77799	CA	C
			CTG GCAGAAGC ACT		

GAC CGTCTTCG TGA

GAM1250 LOC146506 3' CCACAAGTAACTCTTTTCCAG 77932 C C A CC  
CTG AG AGA G ACTTGTGG  
||| || ||| | |||||  
GAC TT TCT C TGAACACC  
C T \_ AA

GAM1250 LOC147136 5' CCACTCAGCGCCCCGTTGCAG 78259 AGAA CACTT  
G CCTGCAGC GC GTGG  
||||| || |||  
GGACGTTG CG CACC  
CCCC CGACT

GAM1250 LOC147160 5' ATTGTGGCCAGTCCTGCTGCAG 83957 AAG\_\_\_\_\_ CTTG  
G CCTGCAGCAG CCA T  
||||||| || |  
GGACGTCGTC GGT A  
CTGACCI|| GTTC

GAM1250 LOC147276 3' CACTTGTGGCCAGCCTCCTGCT 78330 AA\_ \_\_\_\_\_ CTTG  
GCAGG GCAGCAG GC CA TG  
||||| || || ||  
CGTCGTC CG GT AC  
CTC ACCI||G GTTC

GAM1250 LOC147645 3' CACTTGTGGCCAAGCCTCTGCA 78420 A A \_\_\_\_\_ CTTG  
GCAG GC GCAGA GC CA TG  
|| ||||| || || ||  
CG CGTCT CG GT AC  
A C AACCI||G GTTC

GAM1250 LOC148022 5' ATTGTGGCCAGCTTCTGCTGCC 78616 T \_\_\_\_\_ CTTG  
GG C GCAGCAGAAGC CA T  
| ||||| || |  
G CGTCGTCTTCG GT A  
C ACCI||G GTTC

GAM1250 LOC148147 3' CCACAAGTGTGGTGCTGC 78674 GAA C  
GCAGCA GC ACTTGTGG  
||||| || |||||  
CGTCGT TG TGAACACC  
GG\_ \_

GAM1250 LOC151146 5' AGTCAGCTTTTGCTGCA 80135 C\_  
TGCAGCAGAAGC ACT  
||||||| |||  
ACGTCGTTTTCG TGA  
AC

GAM1250 LOC151902 3' CCACAAGAATGGTTCTGCCAG 80380 CA G \_  
CTG GCAGAA CCA CTTGTGG  
||| ||||| ||| |||||  
GAC CGTCTT GGT GAACACC  
C\_ \_ AA

GAM1250 LOC153579 5' CAGGTGGCCCCACTGCTG 80892 AA\_  
CAGCAG GCCACTTG  
||||| |||||

	GTCGTC CGGTGGAC	
	ACCCC	
GAM1250 LOC155004 5'	CACAAGTCTTTACTGAGG 81222	G CA CC
	CCT CAG GAAG ACTTGTG	
	GGA GTC TTTC TGAACAC	
	_ A _	
GAM1250 LOC158490 5'	CACTTGTGGCCGAACCTTTGCT 81934	A G_____ CTTG
	GCAG GCAGCAG A CCA TG	
	CGTCGTT T GGT AC	
	C CAAGCC    GTTC	
GAM1250 LOC166983 5'	ATTGTGGCCAGCTCTGCTGCAG 87263	A _____ CTTG
	G CTGCAGCAGA GC CA T	
	GACGTCGTCT CG GT A	
	_ ACC   G GTTC	
GAM1250 LOC196812 3'	CCTAAGTGGCCCTCCTACAG 89568	C C AA T
	CTG AG AG GCCACTTG GG	
	GAC TC TC CGGTGAAT CC	
	A C CC _	
GAM1250 LOC196988 3'	CATGGACAACCTCTGACTGCAG 87854	_ A CCAC TG
	G CCTGCAG CAG AG T TG	
	GGACGTC GTC TC G AC	
	A C AACA GT	
GAM1250 LOC197003 3'	AGTAGCTCCTCTGCAGG 87865	C A C
	CCTGCAG AG AGC ACT	
	GGACGTC TC TCG TGA	
	_ C A	
GAM1250 LOC197125 3'	CACCCCTCCTGCTGTAGG 87898	A CCACTT
	CCTGCAGCAG AG GTG	
	GGATGTCGTC TC CAC	
	C CC_____	
GAM1250 LOC199796 5'	CCAAGGTGAAGCCACTGCTGCA 74452	AA _ G
	GG CCTGCAGCAG GC CACTT TGG	
	GGACGTCGTC CG GTGGA ACC	
	AC AA _	
GAM1250 LOC200312 5'	ATTGTGGCCAGCTTCTGCTCAG 89990	C _____ CTTG
	G CTG AGCAGAAGC CA T	
	GAC TCGTCTTCG GT A	
	_ ACC   G GTTC	
GAM1250 LOC201116 3'	CGACCTCCTGCTGCAGG 88101	A CCACTTG
	CCTGCAGCAG AG TG	

GGACGTCGTC TC GC  
C CA\_\_\_\_\_  
GAM1250 LOC201382 5' CCCGAGCTCTACTGCA 88241 C A CAC T  
TGCAG AGA GC TTG GG  
||||| ||| || ||| ||  
ACGTC TCT CG AGC CC  
A \_ \_ \_ \_  
GAM1250 LOC220595 3' CACTTGTGGCCACCCCTCTGCT 91140 AG\_\_\_\_\_ CTTG  
GCAGG GCAGCAGA CCA TG  
||||||| ||| ||  
CGTCGTCT GGT AC  
CCCCACCI||| GTTC  
GAM1250 LOC221179 5' CACTTGTGGCCGAGCTTCAGCT 93547 A \_\_\_\_\_ CTTG  
GCAGG GCAGC GAAGC CA TG  
||||| ||||| || ||  
CGTCG CTTCG GT AC  
A AGCCIIIG GTTC  
GAM1250 LOC221463 3' GG TAGCTCCAGCTGCAGG 92074 AGA C  
CCTGCAGC AGC ACT  
||||||| ||| |||  
GGACGTCG TCG TGG  
ACC A  
GAM1250 LOC221935 3' GTA ACTTCGCTGCAGG 92625 A CC  
CCTGCAGC GAAG AC  
||||||| ||||| ||  
GGACGTCG CTTC TG  
\_ AA  
GAM1250 LOC222060 5' CGCTCAGCTTCTGCTCAGG 94105 C CACTT TG  
CCTG AGCAGAAGC G G  
||||| ||||| ||| |  
GGAC TCGTCTTCG C C  
\_ ACT\_ GT  
GAM1250 LOC253489 5' CACAAGTACTGCTGCG 95492 AAGCC  
TGCAGCAG ACTTGTG  
||||||| |||||  
GCGTCGTC TGAACAC  
A\_\_\_\_\_  
GAM1250 LOC254101 5' CACTTGTGGCATAACCTCTGCT 96273 AG\_\_\_\_\_ CTTG  
GCAG GCAGCAGA CCA TG  
||||||| ||| ||  
CGTCGTCT GGT AC  
CCAATACI||| GTTC  
GAM1250 LOC254266 3' CCAGAACTGCCTGCCACAGG 97350 CA AA CAC G  
CCTG GCAG GC TT TGG  
||||| ||||| || |||  
GGAC CGTC CG AA ACC  
AC \_ TC\_ G  
GAM1250 LOC254439 3' CCTAGGAGGCTTCTGCCACCAG 94747 CA\_ A T  
CTG GCAGAAGCC CTTG GG  
||| ||||| ||||| ||| ||

GAC CGTCTTCGG GGAT CC  
 CAC A \_  
 GAM1250 LOC254552 5' ATTGTGGCTTGCCCCTGCTGCA 94774 AA \_\_\_\_\_ CTTG  
 G CTGCAGCAG GC CA T  
 ||||| || || |  
 GACGTCGTC CG GT A  
 CC TTCIIIG GTTC  
 GAM1250 LOC254830 5' CCACAGGCACGGACCCCTGCTG 97638 AAG\_ A\_  
 CAGG CCTGCAGCAG CC CTTGTGG  
 ||||| || |||||  
 GGACGTCGTC GG GGACACC  
 CCCA CAC  
 GAM1250 LOC255481 3' TGCATCTTCTGCTACAG 94443 C CCACT TG  
 CTG AGCAGAAG TG G  
 || ||||| || |  
 GAC TCGTCTTC AC T  
 A T\_\_\_\_\_ GT  
 GAM1250 LOC255826 5' GGTGCTTCTGCCACAGG 97501 CA C  
 CCTG GCAGAAGC ACT  
 ||| ||||| |||  
 GGAC CGTCTTCG TGG  
 AC \_  
 GAM1250 LOC256401 5' CGCAGCTCCACGCTGCAGG 96017 AGA\_ CACT  
 CCTGCAGC AGC TGTG  
 ||||| ||| |||  
 GGACGTCG TCG ACGC  
 CACC \_\_\_\_\_  
 GAM1250 LOC256806 3' CCACTGCCTTCTGCTGCAG 96457 C CTT  
 CTGCAGCAGAAG CA GTGG  
 ||||| ||| |||  
 GACGTCGTCTTC GT CACC  
 C \_\_\_\_\_  
 GAM1250 LOC51308 3' ATTGTGGCCAGCTTCTGCCACG 33492 CA \_\_\_\_\_ CTTG  
 G CTG GCAGAAGC CA T  
 || ||||| || |  
 GGC CGTCTTCG GT A  
 AC ACCIIIG GTTC  
 GAM1250 LOC51337 3' TGGCTTCCGCTGAGG 33591 G A  
 CCT CAGC GAAGCCA  
 ||| ||| |||||  
 GGA GTCG CTTCGGT  
 \_ C  
 GAM1250 LOC89932 5' CACAGCTCCTCCTACAGG 60789 C C A CACT  
 CCTG AG AG AGC TGTG  
 ||| ||| ||| |||  
 GGAC TC TC TCG ACAC  
 A C C \_\_\_\_\_  
 GAM1250 LOC90371 5' CCAGAAGCCTCTGCTGC 62495 A CAC G  
 GCAGCAGA GC TT TGG  
 ||||| || |||

CGTCGTCT CG AA ACC  
C \_\_\_\_ G

GAM1250 LOC90522 5' CCACCCTCCTCTGCAGCAGG 63153 A AGCCACTT  
CCTGC GCAGA GTGG  
||||| ||||| ||||  
GGACG CGTCT CACC  
A CCTCC\_\_

GAM1250 LOC93444 3' GTGGCTTCTGCAGCAG 72390 A  
CTGC GCAGAAGCCAC  
||||| ||||| |||||  
GACG CGTCTTCGGTG  
A

GAM1251 OTX1 3' TGAATTTTCACCCCCCA 27309 A A  
TG GGGGTGAAAA TCA  
|| ||||| |||||  
AC CCCCAC TTTT AGT  
C A

GAM1251 C20orf188 3' ATGGGTGACCCCCACCCCCCA 31577 A AAAAA  
TG GGGGTG TCACTTAT  
|| ||||| |||||  
AC CCCCAC AGTGGGTA  
C CCCC\_

GAM1251 DKFZP434D1335 3' AAATAAGTAATCTTCCCCCCT 65113 T AAATC  
AGGGG GAA ACTTATTT  
||||| ||||| |||||  
TCCCC CTT TGAATAAA  
C CTAA\_

GAM1251 DKFZp434N0650 3' AGTGCTTCTCACCCCTCA 50046 AAAAT  
TGAGGGGTGA CACT  
||||||| |||||  
ACTCCCCACT GTGA  
CTTC\_

GAM1251 FLJ13322 3' AATAAGACCCCACCCCTC 45295 AAAAATCA  
GAGGGGTG CTTATT  
||||||| |||||  
CTCCCCAC GAATAA  
CCCA\_\_

GAM1251 KHSRP 3' AAGTCTCTATTCTTCACCCCCC 13483 A A C\_\_  
A TG GGGGTGAA AAT ACTT  
|| ||||| |||||  
AC CCCCAC TTT TTA TGAA  
C C TCTC

GAM1251 P15-2 3' AAATAAGTGATTTTTTCCC 38003 T  
GGG GAAAAATCACTTATTT  
||| ||||| ||||| |||||  
CCC TTTT TTAGTGAATAAA

GAM1251 PLA2G6 3' AAATGGGTGTCCCCCACCCTCAT 66486 \_ AAAAAT  
CA TGA GGGGTG CACTTATTT  
||| ||||| ||||| |||||

		ACT CCCAC	GTGGGTAAA	
		A	CCCCT_	
GAM1251	SFRS9	3'	AAGTTGTATATTTTCACCCCT 13657	___ _
			AGGGGTGAAAAAT CA CTT	
			TCCCCACTTTTTA GT GAA	
			TAT T	
GAM1251	LOC143308	5'	AGGCTGACTCCCACCCCTCA 82934	AAAAA _
			TGAGGGGTG TCA CTT	
			ACTCCCCAC AGT GGA	
			CCTC_ C	
GAM1251	LOC144558	3'	TGATTTTTCACCCCTTCA 83151	
			TGAGGGGTGAAAAATCA	
			ACTTCCCCACTTTTGTAGT	
GAM1252	ABP1	3'	GCAAGGTACCCCCTGGCA 63111	A G
			TGTCAGGG GTA TTTGT	
			ACGGTCCC CAT GAACG	
			C G	
GAM1252	ARF3	3'	GCACCCACCCACCCCTGACA 8001	A A_ TT_
			TGTCAGGG GT GT GTGC	
			ACAGTCCC CA CA CACG	
			_ CC CCC	
GAM1252	DMRT2	3'	CACGGACTCCCTGGCA 21615	AGT
			TGTCAGGGAGT TTGTG	
			ACGGTCCCTCA GGCAC	
GAM1252	ENTPD3	3'	ACACATTGATCCCTAGCA 6974	TC G T
			TG AGGGA TAGT TGT	
			AC TCCCT GTTA ACA	
			GA A C	
GAM1252	GSTM3	3'	GGCATTTCCTACTCCCCAAC 68069	CA TTT_
			GT GGGAGTAG GTGCC	
			CA CCCTCATC TACGG	
			AC CCTT	
GAM1252	HCFC1	3'	GGCACCGCCTCCCAAACA 70995	CA TA TT
			TGT GGGAG GT GTGCC	
			ACA CCCTC CG CACGG	
			AA _ C_	
GAM1252	HDGF	3'	AACTGCTCCCACCTCCTGACA 15678	_____
			TGTCA GGGAGTAGTT	

		ACAGT CCCTCGTCAA		
		CCTCCA		
GAM1252	HLA-DMB	3' ACATCTTCAACCCCCTGACA	9205	A ____ TT
		TGTCAGGG GT AG TGT		
		ACAGTCCC CA TC ACA		
		C ACT T_		
GAM1252	HTRA3	3' AGCTTCTTCCCCCCTGACA	89120	____ T
		TGTCAGGG AG AGTT		
		ACAGTCCC TC TCGA		
		CCCT T		
GAM1252	IKBB	3' GACTCGACCCCCTGACA	63206	A ____
		TGTCAGGG GT AGTT		
		ACAGTCCC CA TCAG		
		C GC		
GAM1252	IKBB	3' GACTCGACCCCCTGACA	63207	A ____
		TGTCAGGG GT AGTT		
		ACAGTCCC CA TCAG		
		C GC		
GAM1252	IL2RB	3' GGCACAGATCCCCCACA	6075	CA AGTA
		TGT GGG GTTTGTGCC		
		ACA CCC TAGACACGG		
		CC C____		
GAM1252	ITPA	3' GCAGGCACCCCCTGA	53091	A A
		TCAGGG GT GTTTGT		
		AGTCCC CA CGGACG		
		C _		
GAM1252	MYLK	5' GCTCTACTCCCTGCA	53832	T TTTGT
		TG CAGGGAGTAG GC		
		AC GTCCCTCATC CG		
		_ T____		
GAM1252	MYLK	5' GCTCTACTCCCTGCA	53830	T TTTGT
		TG CAGGGAGTAG GC		
		AC GTCCCTCATC CG		
		_ T____		
GAM1252	NRAS	3' GCACAAACACACCTCAACA	10273	CA A A
		TGT GGG GT GTTTGTGC		
		ACA TCC CA CAAACACG		
		AC A _		
GAM1252	NUP98	5' GCAGGGGACTCCTGACA	32862	G AG
		TGTCAGG AGT TTTGT		



			ACAGTCC TCA GGACG		
			_ GG		
GAM1252	PACE	3'	GGCACTGAGCCCCCAACA 10394	CA AGTA	_
			TGT GGG GTTT GTGCC		
			ACA CCC CGAG CACGG		
			AC CC_ T		
GAM1252	PACSIN1	3'	GGCACAGAGGGTCCTGACA 92262	AGTAG	
			TGTCAGGG TTTGTGCC		
			ACAGTCCT AGACACGG		
			GGG_		
GAM1252	PKD2L1	5'	GGCACAGACATCCCCCTACA 32264	C AGTA	
			TGT AGGG GTTTGTGCC		
			ACA TCCC CAGACACGG		
			_ CCTA		
GAM1252	PTPN7	3'	GGCAGCGCCGCCCTGACA 11072	A TA TT	
			TGTCAGGG G GT GTGCC		
			ACAGTCCC C CG CACGG		
			_ GC _		
GAM1252	PTPN7	3'	GGCAGCGCCGCCCTGACA 54554	A TA TT	
			TGTCAGGG G GT GTGCC		
			ACAGTCCC C CG CACGG		
			_ GC _		
GAM1252	PTPN7	3'	GGCAGCGCCGCCCTGACA 54565	A TA TT	
			TGTCAGGG G GT GTGCC		
			ACAGTCCC C CG CACGG		
			_ GC _		
GAM1252	PTPRA	5'	GACTTCCGCATCCCTGACA 11093	_ _	
			TGTCAGGGA GT AGTT		
			ACAGTCCCT CG TCAG		
			A CCT		
GAM1252	RS1	3'	CACAAAGCAGCCCTGATA 4388	AGTAG	
			TGTCAGGG TTTGTG		
			ATAGTCCC AAACAC		
			GACG_		
GAM1252	SH3GL3	3'	CACAAACTCTGGACA 11631	AG AGT	
			TGTC GGAGT TTGTG		
			ACAG TCTCA AACAC		
			G_ _		
GAM1252	SLC7A7	5'	GGCACTTCTCTCCCTGAC 14293	T TTT	
			GTCAGGGAG AG GTGCC		

			CAGTCCCTC TC CACGG		
			— TT—		
GAM1252 SMP1	3'	GCACAACAGCCCTGCA	26701	T	AGTA T
		TG CAGGG GTT GTGC			
		AC GTCCC CAA CACG			
		— GA— —			
GAM1252 TEAD3	3'	GCACACACACTCCCTGCCA	12210	T	A T
		TG CAGGGAGT GT TGTGC			
		AC GTCCCTCA CA ACACG			
		C — C			
GAM1252 TIMM17B	3'	GGCACCCCAGCTGCCCTGACA	19543		— AGTTT
		TGTCAGGG AGT GTGCC			
		ACAGTCCC TCG CACGG			
		G ACCC—			
GAM1252 TLL2	3'	GGCACACCTGGACTCCTTGACA	24965		AGTT—
		TGTCAGGGAGT TGTGCC			
		ACAGTTCCTCA ACACGG			
		GGTCC			
GAM1252 TNFSF4	3'	GCACATGTTTCCCTGACA	12444		TAGTT
		TGTCAGGGAG TGTGC			
		ACAGTCCCTT ACACG			
		TGT—			
GAM1252 TRPV1	3'	GGCACAATTTTGGCTCCCTGCA	54876	T	AGT—
		TG CAGGGAGT TTGTGCC			
		AC GTCCCTCG AACACGG			
		— GTTTT			
GAM1252 TRPV1	3'	GGCACAATTTTGGCTCCCTGCA	38092	T	AGT—
		TG CAGGGAGT TTGTGCC			
		AC GTCCCTCG AACACGG			
		— GTTTT			
GAM1252 TRPV1	3'	GGCACAATTTTGGCTCCCTGCA	54810	T	AGT—
		TG CAGGGAGT TTGTGCC			
		AC GTCCCTCG AACACGG			
		— GTTTT			
GAM1252 TRPV1	3'	GGCACAATTTTGGCTCCCTGCA	54843	T	AGT—
		TG CAGGGAGT TTGTGCC			
		AC GTCCCTCG AACACGG			
		— GTTTT			
GAM1252 ZNF76	3'	GGCACCAGGGACTTCCTGACA	12812		AG T
		TGTCAGGGAGT TT GTGCC			

			ACAGTCCTTCA GA CACGG		
			GG C		
GAM1252	BRAP	3'	GACTGTTCTCCCTGACA 22249	—	
			TGTCAGGGAG TAGTT		
			ACAGTCCCTC GTCAG		
			TT		
GAM1252	CACNA1I	3'	GCACAGGCGCCCGACA 40836	A	AGTA
			TGTC GGG GTTTGTGC		
			ACAG CCC CGGACACG		
			— G —		
GAM1252	CAMP-GEFII	3'	GCAAGCCCCTGACA 22828		AGTA
			TGTCAGGG GTTTGT		
			ACAGTCCC CGAACG		
			—		
GAM1252	COAS3	3'	CACAGGCCTCCCTAACA 57357	C	TA
			TGT AGGGAG GTTTGTG		
			ACA TCCCTC CGGACAC		
			A —		
GAM1252	CRTAC1	3'	GCACAAAACCTGGCA 36026		GAGTAG
			TGTCAGG TTTGTGC		
			ACGGTCC AAACACG		
			A —		
GAM1252	CST7	5'	GGCACAAACCATTGCCCGGCA 13328	A	G A
			TGTC GG AGT GTTTGTGCC		
			ACGG CC TTA CAAACACGG		
			C G C		
GAM1252	DCTD	3'	GGCACATCTGTCCTGACA 8622	AG	TT
			TGTCAGGG TAG TGTGCC		
			ACAGTCCT GTC ACACGG		
			— T —		
GAM1252	DKFZP547L112	5'	GCACTGGAGGACCCCCTGCCA 66530	T	A AG —
			TG CAGGG GT TTT GTGC		
			AC GTCCC CA AGG CACG		
			C C GG T		
GAM1252	FBXO27	3'	GCACTTGACCTCCCTGGCA 74511		TAGTTT
			TGTCAGGGAG GTGC		
			ACGGTCCCTC CACG		
			CATGTT		
GAM1252	FBXO29	3'	GCACGCATCTCCCTGAC 76756		TAGTT
			GTCAGGGAG TGTGC		

			CAGTCCCTC	GCACG		
			TAC__			
GAM1252	FLJ10326	3'	GCAAGAACCCTCCTGACA	36030	G TA	G
			TGTCAGG AG GTTT TGC			
			ACAGTCC TC CAAG ACG			
			_ C_ A			
GAM1252	FLJ10540	3'	GGCAGTGATACCTCCCTGACA	36258	TA	TG
			TGTCAGGGAG GTT TGCC			
			ACAGTCCCTC TAG ACGG			
			CA TG			
GAM1252	FLJ11850	3'	ACAAGCATCCCCTGACA	42716	AG	A
			TGTCAGGG T GTTTGT			
			ACAGTCCC A CGAACA			
			CT _			
GAM1252	FLJ12287	3'	GCACATGAGCTCTCTAACA	42315	C	AGTT
			TGT AGGGAGT TGTGC			
			ACA TCTCTCG ACACG			
			A AGT_			
GAM1252	FLJ12768	3'	GGCACTCTTCTCCCTGA	47184	T	TTT
			TCAGGGAG AG GTGCC			
			AGTCCCTC TC CACGG			
			T T__			
GAM1252	FLJ13902	3'	GCCATCTCCCTGACA	45043	TAGTT	T
			TGTCAGGGAG TG GC			
			ACAGTCCCTC AC CG			
			T____ _			
GAM1252	FLJ13912	3'	GGCATCACTGCTTCCCCCTGAC	42864	__	TT
	A		TGTCAGGG AGTAGT GTGCC			
			ACAGTCCC TCGTCA TACGG			
			CCT C_			
GAM1252	FLJ13993	3'	CACAAAACCCCTGGCA	60456	A	AG
			TGTCAGGG GT TTTGTG			
			ACGGTCCC CA AAACAC			
			- -			
GAM1252	FLJ20511	3'	ACTGTCTACTCCCTGCA	35318	T	TTT
			TG CAGGGAGTAG GT			
			AC GTCCCTCATC CA			
			_ TGT			
GAM1252	FLJ21148	3'	GGCACAAACCACCTCTC	45860	TA_	
			GGGAG GTTTGTGCC			

			CTCTC CAAACACGG		
			CAC		
GAM1252	FLJ21709	3'	GGCAGTGTGACCCCTTGACA	49843	A AGTTTG
			TGTCAGGG GT TGCC		
			ACAGTTCC CA ACGG		
			C GTGTG_		
GAM1252	FLJ22969	3'	GGCACAAACCACCATGCCC	68656	A__ A
			GGG GT GTTTGTGCC		
			CCC CA CAAACACGG		
			GTAC C		
GAM1252	FLJ31978	3'	ACACCTGCTCTCTGACA	58345	TT
			TGTCAGGGAGTAG TGT		
			ACAGTCTCTCGTC ACA		
			C_		
GAM1252	GADD45A	3'	GCAGTTACTCCCTACA	8628	C TTTG
			TGT AGGGAGTAG TGC		
			ACA TCCCTCATT ACG		
			_ G__		
GAM1252	GIT2	3'	CACCTACTCCCTGACA	28755	TTT
			TGTCAGGGAGTAG GTG		
			ACAGTCCCTCATC CAC		
			_____		
GAM1252	GIT2	3'	CACCTACTCCCTGACA	54090	TTT
			TGTCAGGGAGTAG GTG		
			ACAGTCCCTCATC CAC		
			_____		
GAM1252	GIT2	3'	CACCTACTCCCTGACA	54077	TTT
			TGTCAGGGAGTAG GTG		
			ACAGTCCCTCATC CAC		
			_____		
GAM1252	H11	5'	CACAACCGTCCCTGGCA	26847	GTA T
			TGTCAGGGA GTT GTG		
			ACGGTCCCT CAA CAC		
			GC_ _		
GAM1252	KCNT1	5'	GGCCGCATGCCACTCCCTGAC	61836	A T _
			GTCAGGGAGT GT TGTG CC		
			CAGTCCCTCA CG ACGC GG		
			C T C		
GAM1252	KIAA0143	3'	CACAAACTTTGCTCTACA	64782	C AGT
			TGT AGGG AGTTTGTG		

ACA TCTC TCAAACAC  
 \_ GTT  
 GAM1252 KIAA0258 3' GACTCACTCCCTGCCA 28816 T \_  
 TG CAGGGAGT AGTT  
 || ||||| ||||  
 AC GTCCCTCA TCAG  
 C C  
 GAM1252 KIAA0303 5' AGCTACTCTCCTGACA 69460 \_  
 TGTCAGG GAGTAGTT  
 ||||| |||||  
 ACAGTCC CTCATCGA  
 T  
 GAM1252 KIAA0618 3' GGCACAGGCATCCATGACA 29172 G GTA  
 TGTCA GGA GTTTGTGCC  
 ||||| || |||||  
 ACAGT CCT CGGACACGG  
 A A\_  
 GAM1252 KIAA0664 3' GGCTCCCTACTCCCTGCA 64286 T TTTGT  
 TG CAGGGAGTAG GCC  
 || ||||| ||  
 AC GTCCCTCATC CGG  
 \_ CCT\_  
 GAM1252 KIAA0711 5' GCACAGCGGCTTCTCCTAACA 29519 CA T \_  
 TGT GGGAG AGT TTGTGC  
 || ||||| || |||||  
 ACA TCCTC TCG GACACG  
 A\_ T GC  
 GAM1252 KIAA0748 3' GGCACAAACTGAGTCTGATA 28943 GAG  
 TGTCAGG TAGTTTGTGCC  
 ||||| |||||  
 ATAGTCT GTCAAACACGG  
 GA\_  
 GAM1252 KIAA0769 3' GGTCCCCTACTACCCTGACA 29097 AG TTGT  
 TGTCAGGG TAGT GCC  
 ||||| || ||  
 ACAGTCCC ATCA TGG  
 \_ CCC\_  
 GAM1252 KIAA0820 5' GGCCCCTACTCCCTGTCA 69026 T TTTGT  
 TG CAGGGAGTAG GCC  
 || ||||| ||  
 AC GTCCCTCATC CGG  
 T CC\_  
 GAM1252 KIAA1058 3' CACAAAGCGATATCCTGACA 82252 A AG\_  
 TGTCAGGG GT TTTGTG  
 ||||| || |||||  
 ACAGTCCT TA AAACAC  
 A GCG  
 GAM1252 KIAA1257 3' GCACAAACATTCCCTTACA 62740 C A  
 TGT AGGGAGT GTTTGTGC  
 || ||||| |||||

		ACA TCCCTTA CAAACACG		
		T _		
GAM1252 KIAA1393	5'	GCTTGGACATCCCTGACA	72099	GTA TT T
		TGTCAGGGA GT G GC		
		ACAGTCCCT CA T CG		
		A__ GG T		
GAM1252 KIAA1465	3'	GGCGTGTAGTCCCTGACA	60834	G GTT GT
		TGTCAGGGA TA T GCC		
		ACAGTCCCT AT G CGG		
		G __ TG		
GAM1252 KIAA1505	5'	GGCTCCCATTCCCTGACA	94187	AGTTTGT
		TGTCAGGGAGT GCC		
		ACAGTCCCTTA CGG		
		CCCT__		
GAM1252 KIAA1755	3'	GCACAGGTCCCCACA	61348	CA GTAG
		TGT GGGA TTTGTGC		
		ACA CCCT GGACACG		
		CC ____		
GAM1252 KIAA1863	3'	GCCTTCCCTACTCCCTGCCA	64871	T TTTGT
		TG CAGGGAGTAG GC		
		AC GTCCCTCATC CG		
		C CCTTC		
GAM1252 MAPK8IP3	3'	GGCTGGATACCCCCTCGACA	52989	_ A GTTTGT
		TGTC AGGG GTA GCC		
		ACAG TCCC CAT CGG		
		C C AGGT__		
GAM1252 MGC12981	3'	GCACAGCTGTTCTCCGACA	50385	A T
		TGTC GGGAGTAGTT GTGC		
		ACAG CTCTTGTCGA CACG		
		C _		
GAM1252 MGC2835	3'	GGCACTGGGGGCACTCCCTGCA	43962	T A _
		TG CAGGGAGT GTTT GTGCC		
		AC GTCCCTCA CGGG CACGG		
		_ _ GGT		
GAM1252 MIC2L1	3'	GGCCCTTTAATCCCTGACA	48825	G TTTGT
		TGTCAGGGA TAG GCC		
		ACAGTCCCT ATT CGG		
		A TCC__		
GAM1252 MKNK1	5'	ACACCAACTTCCTGACA	13477	AGTT
		TGTCAGGGAGT TGT		

			ACAGTCCTTCA	ACA		
			ACC_			
GAM1252	MUC13	3'	AGCTCACTCTCTGACA	52328		—
			TGTCAGGGAGT AGTT			
			ACAGTCTCTCA	TCGA		
			C			
GAM1252	POFUT1	3'	GCCCGTACACTCCCTGCCA	70472	T	A T T
			TG CAGGGAGT GT TG GC			
			AC GTCCCTCA CA GC CG			
			C _ T C			
GAM1252	PPP4R1L	5'	ACTCCTCTCCCTGACA	79499	T	TTT
			TGTCAGGGAG AG GT			
			ACAGTCCCTC TC CA			
			_ CT_			
GAM1252	RRP46	3'	GGCACAGATCCCCCAGCA	39348	CA	AGTA
			TGT GGG GTTTGTGCC			
			ACG CCC TAGACACGG			
			AC CC_			
GAM1252	SCYA22	3'	GGCCATTTCCTCCCTGA	90951	AGTT	T
			TCAGGGAGT TG GCC			
			AGTCCCTCA AC CGG			
			CTTT _			
GAM1252	TRAP25	5'	GCAGACCCCTGACA	54675	AGTA	
			TGTCAGGG GTTTGT			
			ACAGTCCC CAGACG			
			_____			
GAM1252	TRIM2	3'	GGCACAAACTGGAATGA	30943	GGGAG	
			TCA TAGTTTGTGCC			
			AGT GTCAAACACGG			
			AAG_			
GAM1252	TRIP-Br2	3'	GCACTGACCCCTGGCA	28584	A	AGTTT
			TGTCAGGG GT GTGC			
			ACGGTCCC CA CACG			
			C GT_			
GAM1252	TU12B1-TY	3'	GGCCTCTCCCTGACA	33398	T	TTT TG
			TGTCAGGGAG AG G C			
			ACAGTCCCTC TC C G			
			_ _ GT			
GAM1252	LOC114971	3'	GGCACCAGCAGCCCCTGACA	73150	A A	T
			TGTCAGGG GT GTT GTGCC			



		ACAGTCCC CG CGA CACGG		
		_ A C		
GAM1252	LOC118668 5'	GCACAGCTGCCCTGACA 75482	AG	T
		TGTCAGGG TAGTT GTGC		
		ACAGTCCC GTCGA CACG		
		— —		
GAM1252	LOC126302 3'	GGCACCAGGCACCCC 74495	A A	_
		GGG GT GTTTG TGCC		
		CCC CA CGGAC ACGG		
		_ _ C		
GAM1252	LOC126917 3'	GGCACTGGCCTCCCTGAC 74589	TA	TT
		GTCAGGGAG GT GTGCC		
		CAGTCCCTC CG CACGG		
		_ _ GT		
GAM1252	LOC130327 3'	CACACCTATTCCCTGAC 74916		TT
		GTCAGGGAGTAG TGTG		
		CAGTCCCTTATC ACAC		
		C_		
GAM1252	LOC132332 3'	ACTGCTCCCCTCTGACA 76160		—
		TGTCA GGGAGTAGT		
		ACAGT CCCTCGTCA		
		CTC		
GAM1252	LOC134121 3'	CACAAACAACCCTGACA 75151	AGTA	
		TGTCAGGG GTTTGTG		
		ACAGTCCC CAAACAC		
		AA_		
GAM1252	LOC134689 5'	GCACCAGTCCCTGCA 75932	T	AGTTT
		TG CAGGGAGT GTGC		
		AC GTCCCTCG CACG		
		_ AC_		
GAM1252	LOC143267 3'	GCACAGATTCTCCCTGA 82925		T
		TCAGGGAG AGTTTGTGC		
		AGTCCCTC TTAGACACG		
		—		
GAM1252	LOC143381 3'	CACAGGGCCCTCTGACA 76544	A	AG
		TGTCAGGG GT TTTGTG		
		ACAGTCTC CG GGACAC		
		C _		
GAM1252	LOC144473 3'	GCACAGTCTGACTCCCTGCCA 83072	T	_ T
		TG CAGGGAGT AG TTGTGC		

	AC GTCCCTCA TC GACACG	
	C G T	
GAM1252 LOC146229 3'	GGCACAAATCTCGGCTCCCTGCA 77766	T _ T
	TG CAGGGAGT AG TTGTGCC	
	AC GTCCCTCG TC AACACGG	
	_ GC T	
GAM1252 LOC148198 3'	GGCACAAACCACCATGCCT 70686	GA_ A
	AGG GT GTTTGTGCC	
	TCC CA CAAACACGG	
	GTAC C	
GAM1252 LOC150519 3'	ACACTCTAACTCCCTGA 79910	_ TT
	TCAGGGAGT AG TGT	
	AGTCCCTCA TC ACA	
	A TC	
GAM1252 LOC154761 3'	GGCACAGCTCCCCTGATA 81123	_ AGTT
	TGTCAGGG AGT TGTGCC	
	ATAGTCCC TCG ACACGG	
	C _	
GAM1252 LOC157556 3'	GCAATACTCCCTGAC 86485	GTTTG
	GTCAGGGAGTA TGC	
	CAGTCCCTCAT ACG	
	A _	
GAM1252 LOC157740 5'	GGCACAGGGTGCCCTCGACA 81564	AG A G
	TGTC GG GTA TTTGTGCC	
	ACAG CC CGT GGACACGG	
	CT _ G	
GAM1252 LOC157858 3'	ACAGCCCCTCTCTGACA 86576	AGT
	TGTCAGGGAGT TTGT	
	ACAGTCTCTCA GACA	
	CCC	
GAM1252 LOC160646 3'	GCACAGCTCCCCTGACA 82227	_ AGTT
	TGTCAGGG AGT TGTGC	
	ACAGTCCC TCG ACACG	
	C _	
GAM1252 LOC170395 3'	GGCACAAAAGCCTTAACA 76374	C AGTAG
	TGT AGGG TTTGTGCC	
	ACA TTCC AAACACGG	
	A GA _	
GAM1252 LOC196051 3'	GGCACATCTGCCACCCTGACA 87568	A_ TT
	TGTCAGGG GTAG TGTGCC	

		ACAGTCCC CGTC ACACGG		
		AC T_		
GAM1252	LOC196319 3'	CACAAACCCTACCTGA	89624	G TA
		TCAGG AG GTTTGTG		
		AGTCC TC CAAACAC		
		A C_		
GAM1252	LOC196472 5'	CACCTGTGCTCCTGACA	87718	G GTTT
		TGTCAGG AGTA GTG		
		ACAGTCC TCGT CAC		
		_ GTC_		
GAM1252	LOC200895 3'	GGCACTCTTGCCACTCCTTGAC	88920	A TT__
	A	TGTCAGGGAGT GT GTGCC		
		ACAGTTCCTCA CG CACGG		
		C TTCT		
GAM1252	LOC205100 5'	GCACAAAGGGCCCTGGCA	90698	AGTAG
		TGTCAGGG TTTGTGC		
		ACGGTCCC AAACACG		
		GGG__		
GAM1252	LOC206836 5'	GCACAGGTGTCCCCAGACA	89543	A AG G
		TGTC GGG TA TTTGTGC		
		ACAG CCC GT GGACACG		
		A CT _		
GAM1252	LOC219654 3'	GGTCTCCTAGCCCCTGACA	91310	AG TTTGT
		TGTCAGGG TAG GCC		
		ACAGTCCC ATC TGG		
		CG CTC__		
GAM1252	LOC219898 5'	CACATTTTCCTGACA	93272	TAGTT
		TGTCAGGGAG TGTG		
		ACAGTCCTTT ACAC		
		T____		
GAM1252	LOC221421 3'	GGCCTCCTACTCCCCAGCA	92279	CA TTTGT
		TGT GGGAGTAG GCC		
		ACG CCCTCATC CGG		
		AC CTC__		
GAM1252	LOC221922 5'	GCACGCGCTCCTGACA	92697	GAGT T
		TGTCAGG AGT TGTGC		
		ACAGTCC TCG GCACG		
		____ C		
GAM1252	LOC254402 5'	GACTATATCCCCGACA	97555	A _
		TGTC GGGA GTAGTT		

ACAG CCCT TATCAG  
 C A  
 GAM1252 LOC254532 5' GCACAAATGCGTGACA 96637 GGA G  
 TGTCA GTA TTTGTGC  
 |||| || |||||  
 ACAGT CGT AAACACG  
 G\_\_ \_  
 GAM1252 LOC90786 3' GGCTCTTTTACTCCCCACA 64034 CA TTTGT  
 TGT GGGAGTAG GCC  
 || ||||| ||  
 ACA CCCTCATT CGG  
 C\_ TTCT\_  
 GAM1252 LOC93496 3' ACAGTGTTACTCCCTAATA 72427 C GT\_  
 TGT AGGGAGTA TTGT  
 || ||||| ||  
 ATA TCCCTCAT GACA  
 A TGT  
 GAM1253 SLC17A4 3' CAACAGTTCTTCATGTAGC 18525 CAGT  
 GCTGC TGAAGAACTGTTG  
 |||| |||||  
 CGATG ACTTCTTGACAAC  
 T\_\_  
 GAM1253 CITED1 5' CAACAGCTCCAGCTGGCAGC 14729 AA A  
 GCTGCCAGTTG GA CTGTTG  
 ||||| || |||||  
 CGACGGTCGAC CT GACAAC  
 \_ C  
 GAM1253 FLJ10900 5' CAACAGTTCTTGCTGAAGCAGT 65590 \_ TG  
 T AGCTGC CAGT AAGAACTGTTG  
 |||| || |||||  
 TTGACG GTCG TTCTTGACAAC  
 AA \_  
 GAM1253 HS6ST 3' CAACAGTTCCTTTGCCAGCAGC 62025 CA T A  
 GCTGC GT GA GAACTGTTG  
 |||| || |||||  
 CGACG CG TT CTTGACAAC  
 AC T C  
 GAM1253 MGC4638 3' CAACAGTTCTTCAAGTG 48939 G  
 CA TTGAAGAACTGTTG  
 || |||||  
 GT AACTTCTTGACAAC  
 G  
 GAM1253 ZNF262 3' TTCCCCAATGGCAGCTT 17492 G AA  
 AAGCTGCCA TTG GAA  
 ||||| || ||  
 TTCGACGGT AAC CTT  
 \_ CC  
 GAM1253 LOC115051 3' CAACAGTTCCTTTGCCAGCAGC 60036 CA T A  
 GCTGC GT GA GAACTGTTG  
 |||| || |||||

		CGACG CG TT CTTGACAAC		
		AC T C		
GAM1253	LOC143153 3'	CAGCCTCAAGCTGGCAGC 76463	GA AA	
		GCTGCCAGTT AG CTG		
		CGACGGTCGA TC GAC		
		AC C_		
GAM1253	LOC168512 5'	CAACAGCCTCTCTGGCAGCTT 82714	TTGA A_	
		AAGCTGCCAG AGA CTGTTG		
		TTCGACGGTC TCT GACAAC		
		____ CC		
GAM1253	LOC199923 3'	AACAGTTCCAGACCAGC 88494	CCA GAA	
		GCTG GTT GAACTGTT		
		CGAC CAG CTTGACAA		
		____ AC_		
GAM1253	LOC199926 3'	TAGTCCTTCAACTCACAGCTT 89880	CC A	
		AAGCTG AGTTGAAG ACTG		
		TTCGAC TCAACTTC TGAT		
		AC C		
GAM1253	LOC202316 3'	TAGTCCTTCAACTCACAGCTT 90340	CC A	
		AAGCTG AGTTGAAG ACTG		
		TTCGAC TCAACTTC TGAT		
		AC C		
GAM1253	LOC221479 3'	CAACAACCTACAGCAGCAGC 92222	CA A AAC	
		GCTGC GTTG AG TGTG		
		CGACG CGAC TC ACAAC		
		A_ A A_		
GAM1254	ADAM21 3'	TGAGCACATTTCTGACCA 13763	ACA G	
		TG AGAAATGTG TCG		
		AC TCTTTACAC AGT		
		CAG G		
GAM1254	AP1S1 3'	TCAGGGCACTTCTTGTG 54035	AT G G	
		GACAAGAA GTG TC TGA		
		CTGTTCTT CAC GG ACT		
		____ G		
GAM1254	AQP3 3'	TCACGATCCACCCTTTC 59592	T_ _	
		GAAA GTGG TCGTGA		
		CTTT CACC AGCACT		
		CC T		
GAM1254	CHML 5'	TCACACCTCATTTCTTTCA 8431	C T C	
		TGA AAGAAATG GGT GTGA		

			ACT TTCTTTAC CCA CACT		
			— T —		
GAM1254	CHRNA3	3'	TCGTTACCCATTTCTT 5611	T	CG
			AAGAAATG GGT TGA		
			TTCTTTAC CCA GCT		
			— TT		
GAM1254	FBXL7	3'	CATGGACATTCTTGTCA 24545	AAT	GT
			TGACAAGA GTG CGTG		
			ACTGTTCT TAC GTAC		
			— AG		
GAM1254	FGF20	3'	CACAACCATTTCTTTCTTGTCA 39069	T_	C
			TGACAAGAAA GTGGT GTG		
			ACTGTTCTTT TACCA CAC		
			CT A		
GAM1254	IGFBP1	3'	TCATGAAACACTTCTCATCA 5181	CA	A GG
			TGA AGAA TGT TCGTGA		
			ACT TCTT ACA AGTACT		
			AC C A_		
GAM1254	KERA	3'	TCATTACCATTCTTGT 22871	AT	C
			ACAAGAA GTGGT GTGA		
			TGTTCTT TACCA TACT		
			— T		
GAM1254	MICB	3'	TCACGACTGCTCCTGCCA 19831	A A	AAT TG
			TG CA GA G GTCGTGA		
			AC GT CT C CAGCACT		
			C C — GT		
GAM1254	OLR1	3'	TCACAACAGTTCTTGTTA 10340	ATGTG	C
			TGACAAGAA GT GTGA		
			ATTGTTCTT CA CACT		
			GA — A		
GAM1254	PLAUR	5'	CACATTCATATTTACCGTCA 10616	AAG	TC
			TGAC AAATGTGG GTG		
			ACTG TTTATACT CAC		
			CCA TA		
GAM1254	POU4F1	3'	CACTGAAAACATTTTGTCA 20661	A	GG _
			TGACAAGAA TGT TC GTG		
			ACTGTTTTT ACA AG CAC		
			— AA T		
GAM1254	PTPN1	3'	TCACGACTCTTCCTGCA 11051	A A	ATGT
			TG CA GAA GGTCGTGA		

			AC GT CTT TCAGCACT		
			_ C C__		
GAM1254	SCN7A	3'	CACTTACCACCTCTTTTCA 11440	C AAT C_	
			TGA AAGA GTGGT GTG		
			ACT TTCT CACCA CAC		
			T C__ TT		
GAM1254	SLC4A4	3'	CCACTTATTTTTTTGTCA 13634	__	
			TGACAAGAAAT GTGG		
			ACTGTTTTTTA CACC		
			TT		
GAM1254	SMP1	3'	TCACATGAATAATTTTTGTCA 26703	A GGTC	
			TGACAAGAA TGT GTGA		
			ACTGTTTTT ATA CACT		
			A AGTA		
GAM1254	7h3	3'	CACGATTGGCCTCTAGTCA 52271	A AATGT	
			TGAC AGA GGTCGTG		
			ACTG TCT TTAGCAC		
			A CCGG_		
GAM1254	ADMP	3'	TCACAAATCATATTCTGTCA 58870	A A C_	
			TGACA GAA TGTGGT GTGA		
			ACTGT CTT ATACTA CACT		
			_ _ AA		
GAM1254	C6orf35	3'	TCAAGAGCCTTTCTTGTCA 37452	TGT CG_	
			TGACAAGAAA GGT TGA		
			ACTGTTCTTT CCG ACT		
			_ _ AGA		
GAM1254	CAPNS2	3'	TCACAACCCTACATATTTCTGA 50322	CA ____ C	
	TCA		TGA AGAAATGT GGT GTGA		
			ACT TCTTTATA CCA CACT		
			AG CATC A		
GAM1254	CLIC4	3'	ACCAATTTCTTGCA 25627	A G	
			TG CAAGAAAT TGGT		
			AC GTTCTTTA ACCA		
			_ _		
GAM1254	DCOXM	3'	TCACAATCTTTTCTTGTC 49611	TGT C	
			GACAAGAAA GGT GTGA		
			CTGTTCTTT CTA CACT		
			T__ A		
GAM1254	GORASP2	3'	CACGCAACATTTCTTGT 31382	G T	
			ACAAGAAATGT G CGTG		

			TGTTCTTTACA C GCAC		
			A _		
GAM1254	GTF2E1	3'	TACAGACCTCTTGTCA 18617	AATGT	_
			TGACAAGA GGTC GTG		
			ACTGTTCT CCAG CAT		
			_____ A		
GAM1254	KIAA0336	3'	CCACAATTCTTTTGTCA 27588	__	A
			TGACA AGAA TGTGG		
			ACTGT TCTT ACACC		
			TT A		
GAM1254	KIAA0475	3'	CAGCTTTGCATTTCTGTCA 29486	A	TG TCG
			TGACA GAAATG G TG		
			ACTGT CTTTAC T AC		
			_ GT TCG		
GAM1254	KIAA0475	3'	TCATGGCCATTTCTG 29505	A	AT
			CA GAA GTGGTCGTGA		
			GT CTT TACCGGTACT		
			C _		
GAM1254	KIAA0635	5'	TCACACAAATTTCTTGTC 27698	GTG	C
			GACAAGAAAT GT GTGA		
			CTGTTCTTTA CA CACT		
			AA_ _		
GAM1254	KIAA1320	5'	CCACATTTTGTAATTTCTTGTC 69299	_____	
	A		TGACAAGAA ATGTGG		
			ACTGTTCTT TACACC		
			TAATGTTT		
GAM1254	KIAA1813	3'	TCACACTGTAAATTTCTTGT 70307	__	TG C
			ACAAGAAAT G GT GTGA		
			TGTTCTTTA T CA CACT		
			AA GT _		
GAM1254	KIAA1821	3'	CAGAATACATTTCTTGT 71778	G	G
			ACAAGAAATGTG TC TG		
			TGTTCTTTACAT AG AC		
			A _		
GAM1254	KIAA1951	3'	CAGGCTTCTCTTGTCA 73758	AATGT	G
			TGACAAGA GGTC TG		
			ACTGTTCT TCGG AC		
			CT_ _		
GAM1254	MGC2306	3'	CACAGCCTGTCTTGTCA 50956	AATGT	C
			TGACAAGA GGT GTG		



		ACTGTTCT	CCG CAC		
		GT__	A		
GAM1254	NRN1	3'	CACTGCACATTTCTCCTCA	33433	CA GTC
			TGA AGAAATGTG GTG		
			ACT TCTTTACAC CAC		
			CC GT_		
GAM1254	PTPN9	3'	TCATGTCTCCTCTTGTCA	11081	AATGT T
			TGACAAGA GG CGTGA		
			ACTGTTCT TC GTACT		
			CC__ T		
GAM1254	RA-GEF-2	3'	CCACAGGGTTTCTTGTCA	32954	__
			TGACAAGAAA TGTGG		
			ACTGTTCTTT ACACC		
			GGG		
GAM1254	SERF2	5'	CACGTGCTTTTTCTTGTG	19307	TGT _
			GACAAGAAA GGT CGTG		
			CTGTTCTTT TCG GCAC		
			T__ T		
GAM1254	SGKL	3'	TCACAGAAGCATTCT	25147	GG _
			AGAAATGT TC GTGA		
			TCTTTACG AG CACT		
			A_ A		
GAM1254	TACTILE	5'	CACATTACTTTTCTGTG	19468	A T C
			GACA GAAA GTGGT GTG		
			CTGT CTTT CATTA CAC		
			C _ _		
GAM1254	WBP4	3'	TCACAAAATTACATTCT	23232	C__
			AGAAATGTGGT GTGA		
			TCTTTACATTA CACT		
			AAA		
GAM1254	LOC115219	3'	CACGACAACGGGTCCTCA	73296	CAA AA G
			TGA GA TGT GTCGTG		
			ACT CT GCA CAGCAC		
			C__ GG A		
GAM1254	LOC115294	3'	TCATTGCATATTTCTTGTCA	73018	G C
			TGACAAGAAATGTG T GTGA		
			ACTGTTCTTTATAC G TACT		
			_T		
GAM1254	LOC128499	3'	CACGACCACATCCTCT	74762	A_
			AGA ATGTGGTTCGTG		

		TCT TACACCAGCAC		
		CC		
GAM1254	LOC132946 3'	TCACGACTGAGATGTCA	75074	AGAAATG
		TGACA    TGGTCGTGA		
		ACTGT    GTCAGCACT		
		AGA_____		
GAM1254	LOC148426 5'	CAGGACACAATTTCTTGCCA	84150	A    GTG  G
		TG CAAGAAAT  GTC TG		
		AC GTTCTTTA  CAG AC		
		C    ACA  G		
GAM1254	LOC151195 3'	CATGTTGCATTTCTTGT	80168	TG T
		ACAAGAAATG  G CGTG		
		TGTTCTTTAC  T GTAC		
		GT _		
GAM1254	LOC152317 5'	TCACACTGACTTTTGTCA	85650	AATG  C
		TGACAAGA  TGGT GTGA		
		ACTGTTTT  GTCA CACT		
		CA__ _		
GAM1254	LOC152674 3'	TCAACCCACCCTCTTGTC	85839	AAT  TCG
		TGACAAGA  GTGG TGA		
		ACTGTTCT  CACC ACT		
		CC_  CA_		
GAM1254	LOC154428 5'	CACGTGTGCACATTTCTGACCA	86215	ACA    GT__
		TG AGAAATGTG  CGTG		
		AC TCTTTACAC  GCAC		
		CAG    GTGT		
GAM1254	LOC154743 3'	CCACATTGTCTTGTC	81115	_
		TGACAAGA AATGTGG		
		ACTGTTCT TTACACC		
		G		
GAM1254	LOC155435 3'	TCACATTCTCTTGTC	81354	_
		TGACAAGA AATGTGG		
		ACTGTTCT TTACACT		
		C		
GAM1254	LOC158263 3'	CGCCCACTTCTTGTC	81844	AT  T
		TGACAAGAA  GTGG CG		
		ACTGTTCTT  CACC GC		
		_  C		
GAM1254	LOC164955 3'	TCATGACCATTCTT	82460	AT
		AAGAA  GTGGTCGTGA		

TTCTT TACCAGTACT

GAM1254 LOC221069 5' TCACAGTTCGTTTCTTCTCA 93202 C T TC  
TGA AAGAAATG GG GTGA  
||| ||||| || ||||  
ACT TTCTTTGC TT CACT  
C \_ GA

GAM1254 LOC253228 5' TCAGGAGCATTCTTTCA 95941 C GG G  
TGA AAGAAATGT TC TGA  
||| ||||| || ||||  
ACT TTCTTTACG AG ACT

GAM1254 LOC255919 3' TCATTCTTACATTCTAATCA 95041 CA TC  
TGA AGAAATGTGG GTGA  
||| ||||| ||||  
ACT TCTTTACATT TACT  
AA CT

GAM1254 LOC56920 3' TCAGAGCACATTTCTTGT 39392 G G  
ACAAGAAATGTG TC TGA  
||||||| || ||||  
TGTTCTTTACAC AG ACT  
G \_

GAM1254 LOC91115 3' TCACGACCCTCTCATGCA 64948 A A AATGT  
TG CA GA GGTCGTGA  
|| ||| |||||  
AC GT CT CCAGCACT  
\_ A CTC\_

GAM1254 LOC91768 3' CAAGGGCCATTCTTCTCA 67111 C AT G\_  
TGA AAGAA GTGGTC TG  
||| |||| ||||| ||  
ACT TTCTT TACCGG AC  
C \_ GA

GAM1255 CHC1L 5' TTAAAGATGACTGAATA 7018 C  
TATTCAG CATCTTTGA  
||||| |||||  
ATAAGTC GTAGAAATT  
A

GAM1255 LILRB3 3' CACCTGACTCAAAGATGACTAA 22488 C C \_ T  
TA TATT AG CATCTTTGA CAG GTG  
|||| || ||||| ||| |||  
ATAA TC GTAGAAACT GTC CAC  
\_ A CA \_

GAM1255 LILRB5 3' GTCAAAGATGACTAATA 22422 C C  
TATT AG CATCTTTGAC  
|||| || |||||  
ATAA TC GTAGAAACTG  
\_ A

GAM1255 NPY1R 3' CACTGTAAAGATTACTGAATA 6177 CC A  
TATTCAG ATCTTTG CAGTG  
||||| ||||| ||||

	ATAAGTC TAGAAAT GTCAC	
	AT _	
GAM1255 AP1GBP1 3'	CAAAGATGACTGCATA 23389	T C
	TAT CAG CATCTTTG	
	ATA GTC GTAGAAAC	
	C A	
GAM1255 AP1GBP1 3'	CAAAGATGACTGCATA 54515	T C
	TAT CAG CATCTTTG	
	ATA GTC GTAGAAAC	
	C A	
GAM1255 FLJ10498 3'	CACACTGTATTGTGAAAAC TGC 36192	CA__ TTTG_
	TGAA TTCAGC TC ACAGTGTG	
	AAGTCG AG TGTCACAC	
	TCAAA TGTTA	
GAM1255 FLJ22548 3'	CTGAAAAATGGCTGAATA 42401	C GA
	TATTCAGCCAT TTT CAG	
	ATAAGTCGGTA AAA GTC	
	_ A_	
GAM1255 KIAA0174 3'	CACCAAAGATGGCTGGA 78593	ACA
	TTCAGCCATCTTTG GTG	
	AGGTCGGTAGAAAC CAC	
	_____	
GAM1255 KIAA1068 3'	CACACTGTCCCACCACAACTGA 31029	CCATCTTT_
	A TTCAG GACAGTGTG	
	AAGTC CTGTCACAC	
	AACACCACC	
GAM1255 KIAA1668 3'	ACACCTGGTGGCTGAA 66467	TTTGACA
	TTCAGCCATC GTGT	
	AAGTCGGTGG CACA	
	TC_____	
GAM1255 PRO1787 3'	CACACTGTCTCTCAGCTCAA 37767	C CATCTTT
	TT AGC GACAGTGTG	
	AA TCG CTGTCACAC	
	C ACTCT__	
GAM1255 LOC115110 3'	CACACTTGCCAATGGCTGAA 71712	CTT A _
	TTCAGCCAT TG CA GTGTG	
	AAGTCGGTA AC GT CACAC	
	__ C T	
GAM1255 LOC158230 3'	CACACTGTATAATGATGAATA 81796	GC CTTTG
	TATTCA CAT ACAGTGTG	

			ATAAGT GTA TGTCACAC		
			A_ ATA__		
GAM1256 ABCC3	3'	AGTCCTGTACTCTGGGGTG	39139	A	CAGC
		CACC CAGA TGCAGGACT			
		GTGG GTCT ATGTCCTGA			
		G C__			
GAM1256 ABCC3	3'	AGTCCTGTACTCTGGGGTG	39151	A	CAGC
		CACC CAGA TGCAGGACT			
		GTGG GTCT ATGTCCTGA			
		G C__			
GAM1256 ABCC3	3'	AGTCCTGTACTCTGGGGTG	13692	A	CAGC
		CACC CAGA TGCAGGACT			
		GTGG GTCT ATGTCCTGA			
		G C__			
GAM1256 ARVCF	3'	AGCCCTGCAGTCACGTGAGG	8026	A	GACA A
		CC CA GCTGCAGG CT			
		GG GT TGACGTCC GA			
		A GCAC C			
GAM1256 CCS	3'	AGCTGCTGTGGTGTT	17609	A	
		AACACCACAG CAGCT			
		TTGTGGTGTC GTCGA			
		—			
GAM1256 CELSR1	3'	TTTGTACTTCTGCGGTG	26492	A	C C
		CACC CAGA AG TGCAGG			
		GTGG GTCT TC ATGTTT			
		C _ _			
GAM1256 CELSR3	3'	GCAAAAGTTGTCTGTGGTG	7401		—
		CACCACAGACAGCT GC			
		GTGGTGTCTGTTGA CG			
		AAA			
GAM1256 COL19A1	3'	AGCCACCAAGCTGTCTTTGGT	8506	C	GCA_ A
		ACCA AGACAGCT GG CT			
		TGGT TCTGTCTGA CC GA			
		T ACCA _			
GAM1256 DDC	3'	CTCAGCTGTCTGTGG	5797	C	
		CCACAGACAGCTG AG			
		GGTGTCTGTCTGAC TC			
		—			
GAM1256 DLEC1	3'	AGTCCTGCACCCTGCGG	23685	A	ACAGC
		CC CAG TGCAGGACT			

			GG GTC ACGTCCTGA		
			C CC__		
GAM1256 DLEC1	3'	AGTCCTGCACCTGCGG	23696	A	ACAGC
		CC CAG TGCAGGACT			
		GG GTC ACGTCCTGA			
		C CC__			
GAM1256 DUSP2	3'	GCCCTGTCTGTGGGT	15347	A	CT
		AAC CCACAGACAG GC			
		TTG GGTGTCTGTC CG			
		— C_			
GAM1256 ERN2	5'	AGCCGTGCAGCTGCCAGG	52701	ACAGA	_ A
		CC CAGCTGCA GG CT			
		GG GTCGACGT CC GA			
		ACCC_ G _			
GAM1256 EZH1	3'	TCTGCTTTCCTGTCTGTAGTG	8830	C	CT__
		CAC ACAGACAG GCAGG			
		GTG TGTCTGTC CGTCT			
		A CTTT			
GAM1256 FUT4	3'	AGTCCTGCAGGAGTGCTG	8961	_ AG	
		CAG AC CTGCAGGACT			
		GTC TG GACGTCCTGA			
		G AG			
GAM1256 GGA3	3'	AGCCCTGGGAATGTCTGTGG	56825	GCTG	A
		CCACAGACA CAGG CT			
		GGTGTCTGT GTCC GA			
		AAGG C			
GAM1256 GGA3	3'	AGCCCTGGGAATGTCTGTGG	25741	GCTG	A
		CCACAGACA CAGG CT			
		GGTGTCTGT GTCC GA			
		AAGG C			
GAM1256 GPC1	3'	AGCCCCGCACGGGCTGTCTGGG	9098	A	__ A A
TGT		ACACC CAGACAGCT GC GG CT			
		TGTGG GTCTGTCGG CG CC GA			
		— GCA C C			
GAM1256 HMGN3	3'	AGTCCTGTGCATACTGTGGTGT	14902	ACA	T
T		AACACCACAG GC GCAGGACT			
		TTGTGGTGTGTC CG TGTCTGA			
		ATA _			
GAM1256 HPS1	3'	AGCCTCCTGTCTGCAGTG	3964	CA	CTGC A
		CAC CAGACAG AGG CT			

			GTG GTCTGTC TCC GA		
			AC C___ _		
GAM1256	IGFBP1	3'	TCAAAGCTACCTGTGGTG 5180	AC	GCAG
			CACCACAG AGCT GA		
			GTGGTGTC TCGA CT		
			CA AA__		
GAM1256	IGFBP3	3'	AGCTCACAGCCTTCTGTGGTGT 5185	CA	CA A
			ACACCACAGA GCTG GG CT		
			TGTGGTGTCT CGAC TC GA		
			TC AC _		
GAM1256	IGFBP4	3'	AGTCCTGTCTCTGCCTGCGG 7758	A A	CT
			CC CAG CAG GCAGGACT		
			GG GTC GTC TGTCCTGA		
			C C TC		
GAM1256	IL19	3'	GTCCATGTCTGTGATGT 25360 C	GCTGCA	
			ACA CACAGACA GGAC		
			TGT GTGTCTGT CCTG		
			A A___		
GAM1256	INPP5B	5'	AGTCCCGTGCGCCCTGTGGTG 95521	ACA T A	
			CACCACAG GC GC GGA CT		
			GTGGTGTC CG TG CCTGA		
			CCG _ C		
GAM1256	ISLR	3'	CTCACTGTCTGCGGTG 18669 A	C C	
			CACC CAGACAG TG AG		
			GTGG GTCTGTC AC TC		
			C _ _		
GAM1256	KAI1	3'	AGCCCTGGCTGTTCTGTGGT 9495	_ TG A	
			ACCACAGA CAGC CAGG CT		
			TGGTGTCT GTCG GTCC GA		
			T _ C		
GAM1256	KDR	3'	TGAAGCTGTGTGTGGTGT 9596	G G	
			ACACCACA ACAGCT CA		
			TGTGGTGT TGTCGA GT		
			G A		
GAM1256	MLLT4	3'	AGTTATGGGCTCTCTGCAGTGT 72482	CA C G G	
	T		AACAC CAGA AGCT CA GACT		
			TTGTG GTCT TCGG GT TTGA		
			AC C _ A		
GAM1256	MPO	3'	TCCTGGCTCTGTGG 4204	CA TG	
			CCACAGA GC CAGGA		

GGTGTCT CG GTCCT

GAM1256 PACSIN1 3' AGTCCTGCAGCACCAGGTG 92253 ACAGACA  
CACC GCTGCAGGACT  
|||| ||||||||  
GTGG CGACGTCCTGA  
ACCA\_\_

GAM1256 PCLO 3' CAGTGTCTGTGATGTT 94224 C G  
AACA CACAGACA CTG  
|||| |||||| ||  
TTGT GTGTCTGT GAC

A \_  
GAM1256 PLOD3 5' TCCTCGCCTTGTCTGTGG 6558 CT \_  
CCACAGACAG GC AGGA  
||||||| || ||||  
GGTGTCTGTT CG TCCT  
C\_ C

GAM1256 PPP1R8 5' AGCCCCGCATCCCTCTGTGGT 10722 CAGC A A  
ACCACAGA TGC GG CT  
|||||| || || ||  
TGGTGTCT ACG CC GA  
CCCT C C

GAM1256 PPP2R2B 3' TGAGGTTGTCTGTAGT 15909 C G  
AC ACAGACAGCT CA  
|| |||||||| ||  
TG TGTCTGTTGG GT  
A A

GAM1256 RAX 3' AGCCCTGCAGCTGGAGGG 25536 ACAGA A  
CC CAGCTGCAGG CT  
|| |||||||| ||  
GG GTCGACGTCC GA  
GAG\_\_ C

GAM1256 REGL 3' AGTCCTGCAGCCAGGAGGGT 21485 ACAGACA  
ACC GCTGCAGGACT  
|| ||||||||  
TGG CGACGTCCTGA  
GAGGAC\_

GAM1256 RFC1 3' GTCCTGTCCTGTGATGG 11302 CAG CT  
CCA ACAG GCAGGAC  
|| |||| ||||||  
GGT TGTC TGTCCTG  
AG\_ C\_

GAM1256 RRM2 3' AGTCCTGTCTGTTTATAGTG 6407 CAC CT  
CAC AGACAG GCAGGACT  
|| |||| ||||||  
GTG TTTGTC TGTCCTGA  
ATA \_

GAM1256 RU2 5' AGTCCTGCAAGCTCCTAGTG 33020 \_ AC \_  
CAC AG AGCT GCAGGACT  
|| || |||| ||||||



			GTG TC TCGA CGTCCTGA		
			A C_ A		
GAM1256	RXRA	3'	CCTGCAGCCATCTGTG 11407	CA	
			CACAGA GCTGCAGG		
			GTGTCT CGACGTCC		
			AC		
GAM1256	SH3BP2	3'	AGCCCTGCAGCTACAGCTG 11589	AC_	A
			CAG AGCTGCAGG CT		
			GTC TCGACGTCC GA		
			GACA C		
GAM1256	SLC1A4	3'	TTGTATGTCTGTGGT 11721	GC	
			ACCACAGACA TGCAG		
			TGGTGTCTGT ATGTT		
			—		
GAM1256	TBXA2R	5'	AGCCTGCCCTGTCTG 6478	CT	A
			CAGACAG GCAGG CT		
			GTCTGTC CGTCC GA		
			C_ _		
GAM1256	TEM7	3'	AGCCCCAGCTTCTGT 39880	C	CA A
			ACAGA AGCTG GG CT		
			TGTCT TCGAC CC GA		
			_ C_ _		
GAM1256	UNC13	3'	AGTCCTGCTCATCTGTGG 21055	CAGCT	
			CCACAGA GCAGGACT		
			GGTGTCT CGTCCTGA		
			ACT_		
GAM1256	WASF3	3'	AGCCCTGCAGCTGTAGTACAGT 21823	CACAG_	A
	G		CAC ACAGCTGCAGG CT		
			GTG TGTGACGTCC GA		
			ACATGA C		
GAM1256	ZNF138	5'	AGGCCCAGCCTCTGTGG 81184	CA	CA A
			CCACAGA GCTG GG CT		
			GGTGTCT CGAC CC GA		
			C_ _ G		
GAM1256	ABCA9	3'	AGTCCATGTTTTGTCTGTTGTG 54409	C	CT _
			CAC ACAGACAG GCA GGACT		
			GTG TGTCTGTT TGT CCTGA		
			T T_ A		
GAM1256	APCL	5'	GTTCAGCTGTCTGT 19684	CAG	
			ACAGACAGCTG GAC		

TGTCTGTCGAC TTG

GAM1256 BRD1 5' AGTCCTGCAACTGTGG 27413 ACAGC  
CCACAG TGCAGGACT  
||||| |||||  
GGTGTC ACGTCCTGA

A\_\_

GAM1256 C16orf5 3' AGTCCCCAGGCCTGTGG 25445 ACA GCA  
CCACAG GCT GGA CT  
||||| ||| |||||  
GGTGTC CGG CCTGA

\_\_ ACC

GAM1256 C1orf24 3' AGTCTCTGCTTTCTGCAGTG 53707 CA CAGCT \_  
CAC CAGA GCAG GACT  
||| ||||| ||||| |||||  
GTG GTCT CGTC CTGA  
AC TT\_\_ T

GAM1256 C1orf34 3' AGTCCCGGTCTGCTGTGGTGT 60661 A \_ CA  
AACACCACAG CAG CTG GGA CT  
||||||| ||| ||| |||||  
TTGTGGTGTC GTC GGC CCTGA

\_ T \_

GAM1256 C20orf82 5' AGTCTCTGGTCTGTCTG 84711 CTG \_  
CAGACAG CAG GACT  
||||||| ||| |||||  
GTCTGTC GTC CTGA

TG\_ T

GAM1256 DKFZP434C171 3' AGTCCTGATAGTCTGTGG 31551 AGCTG  
CCACAGAC CAGGACT  
||||||| |||||  
GGTGTCTG GTCCTGA

ATA\_\_

GAM1256 DKFZP434P211 3' AGTCCTGCGATGCTAAGTG 27260 CAC A GC  
CAC AG CA TGCAGGACT  
||| ||| |||||  
GTG TC GT GCGTCCTGA

AA\_ \_ A\_

GAM1256 DMWD 3' AGCCCCAGGTCTGCAGTGT 60876 CA AG CA A  
ACAC CAGAC CTG GG CT  
||||| ||||| ||| |||  
TGTG GTCTG GAC CC GA

AC \_ C\_ \_

GAM1256 DOCK3 3' AGTCCTGCATGTTCAAG 66495 ACA GC  
CC GACA TGCAGGACT  
|| ||||| |||||  
GG TTGT ACGTCCTGA

AC\_ \_

GAM1256 FLJ10094 3' AGTTATATCTGTGGCGTT 35807 A C\_\_  
AAC CCACAGA AGCT  
||| ||||| |||||

		TTG GGTGTCT TTGA		
		C ATA		
GAM1256	FLJ10178	3' AGCCCTATAGTTCTGTG 35869	CA	C A
		CACAGA GCTG AGG CT		
		GTGTCT TGAT TCC GA		
		__ A C		
GAM1256	FLJ10637	5' AGTCCCCTGTCTGTGG 68586	CTGCA	
		CCACAGACAG GGA CT		
		GGTGTCTGTC CCTGA		
		C__		
GAM1256	FLJ12891	5' AGTCCTGCAGCCTCGCTGG 46336	CA	CA
		CCA GA GCTGCAGGACT		
		GGT CT CGACGTCCTGA		
		CG C_		
GAM1256	FLJ12903	3' GTGCTATTGTGGTGT 42778	AC	T
		ACACCACAG AGC GC		
		TGTGGTGT TCG TG		
		A_ _		
GAM1256	FLJ13902	3' AGCCCTGTAGCATCTGTG 45038	CA	A
		CACAGA GCTGCAGG CT		
		GTGTCT CGATGTCC GA		
		A_ C		
GAM1256	FLJ20033	3' TTTTGCTAGCTGTGGTGT 34351	ACAGCT	
		AACACCACAG GCAGGA		
		TTGTGGTGTG CTTTT		
		GAT__		
GAM1256	FLJ20315	3' CCAGCTGCTGCCTGTGGCGT 34933	A	A T A
		AC CCACAG CAGC GC GG		
		TG GGTGTC GTCG CG CC		
		C C T A		
GAM1256	FLJ20374	3' AGCCCTGCAGCTGGCTGGAGT 35077	CA	A A
		AC CAG CAGCTGCAGG CT		
		TG GTC GTCGACGTCC GA		
		AG G C		
GAM1256	FLJ22127	3' AGTCCTGTGGCTGGCCCGTGAT 42881	C	AGA_ TG
	G	CA CAC CAGC CAGGACT		
		GT GTG GTCG GTCCTGA		
		A CCG GT		
GAM1256	FLJ23185	5' GTCCTGCAGTATGGCGT 46833	A	CAGACA
		AC CCA GCTGCAGGAC		

			TG GGT	TGACGTCCTG		
			C	A_____		
GAM1256	FLJ31762	5'	AGTCCTGCAGATGTGCGTG	58139	_	GACAG
			CAC CACA	CTGCAGGACT		
			GTG GTGT	GACGTCCTGA		
			C	A_____		
GAM1256	GIOT-2	3'	CCTTCAGTTATCTGCAGT	32749	CA	C C
			AC CAGA	AGCTG AGG		
			TG GTCT	TTGAC TCC		
			AC	A T		
GAM1256	HRH3	3'	AGCCCCGCCGTGTCTGTGG	23364		G T A A
			CCACAGACA	C GC GG CT		
			GGTGTCTGT	G CG CC GA		
			_	C C C		
GAM1256	HYA22	3'	TCCTACGTGTTGGTCTGTGGT	19429	_	_ C
			ACCACAGAC	AGC TG AGGA		
			TGGTGTCTG	TTG GC TCCT		
			G	T A		
GAM1256	KCNB2	5'	TCCCACAGCCCTTTGTGGTG	96102	CA	CA
			CACCACAGA	GCTG GGA		
			GTGGTGTTT	CGAC CCT		
			CC	AC		
GAM1256	KCNT1	3'	AGTCCTGCAGATCCCTCTGTGG	61826		CAG__
	T		ACCACAGA	CTGCAGGACT		
			TGGTGTCT	GACGTCCTGA		
			CCCTA			
GAM1256	KIAA0218	3'	GTCCCTCGTCTGTGGT	28623	_	CTGCA
			ACCACAGAC	AG GGAC		
			TGGTGTCTG	TC CCTG		
			C	_____		
GAM1256	KIAA0828	3'	TCCTGTGCCTGTAGTGTT	81199	C	ACA T
			AACAC ACAG	GC GCAGGA		
			TTGTG TGTC	CG TGTCT		
			A	__ _		
GAM1256	KIAA0953	3'	AGTCCTGCATGTAGTTGGTG	66780		CAG GC
			CACCA ACA	TGCAGGACT		
			GTGGT TGT	ACGTCCTGA		
			TGA	_		
GAM1256	KIAA1157	3'	AGTCCGTCCATGCTCTGTGG	72239	_	GCT A
			CCACAGA	CA GC GGA		

		GGTGTCT GT TG CCTGA		
		C ACC _		
GAM1256	KIAA1183	3' GCAGCCTGTGGTGT 62535	ACA	
		AACACCACAG GCTGC		
		TTGTGGTGTC CGACG		
		—		
GAM1256	KIAA1280	5' AGCCTGACTGTCCGTGGTG 69710	A CTG A	
		CACCAC GACAG CAGG CT		
		GTGGTG CTGTC GTCC GA		
		C A _ _		
GAM1256	KIAA1336	3' TCCTGGGTTTTGTAATGTT 72325	CC CA G	
		AACA ACAGA GCT CAGGA		
		TTGT TGTTT TGG GTCCT		
		AA _ _		
GAM1256	KIAA1505	5' AGTCCCACCCATCTGTGGT 94185	CAGC CA	
		ACCACAGA TG GGACT		
		TGGTGTCT AC CCTGA		
		ACCC _		
GAM1256	KIAA1786	3' AGTCCTTCCTTATCTGTGGT 66022	CAGCTGC	
		ACCACAGA AGGACT		
		TGGTGTCT TCCTGA		
		ATTCT _		
GAM1256	MAD4	3' CCTGTACCGGTCTGTGG 21271	AGC	
		CCACAGAC TGCAGG		
		GGTGTCTG ATGTCC		
		GCC		
GAM1256	MGC10940	3' AGCCCCCAATCTGTGGT 50214	CAGC CA A	
		ACCACAGA TG GG CT		
		TGGTGTCT AC CC GA		
		A _ CC C		
GAM1256	MGC2654	5' AGCTTGACCTGTCTGCAGT 44103	CA CTG A	
		AC CAGACAG CAGG CT		
		TG GTCTGTC GTTC GA		
		AC CAG _		
GAM1256	MVD	3' AGTCCTGCGGCCGCCCAGGTGT 10138	ACAGACA	
		ACACC GCTGCAGGACT		
		TGTGG CGGCGTCCTGA		
		ACCGC _		
GAM1256	NIN283	3' AGCCCTCTGCCGGCTGTGGTGT 50065	ACA TGC A	
		ACACCACAG GC AGG CT		

			TGTGGTGTG	CG	TCC	GA	
			GGC	TC_	C		
GAM1256	NTT5	3'	AGTCCTGCTACTTCTGGGGTG	25880	A	C	CT
			CACC	CAGA	AG	GCAGGACT	
			GTGG	GTCT	TC	CGTCCTGA	
			G	_	AT		
GAM1256	P2RX1	3'	TCCTGGGCTCCCTGCCTGTGG	67172	A	_____	G
			CCACAG	CA	GCT	CAGGA	
			GGTGTC	GT	CGG	GTCT	
			C	CCCT	_		
GAM1256	PMAIP1	5'	TGCAGCTGTCCGAGGTG	40892	ACA		
			CACC	GACAGCTGCA			
			GTGG	CTGT	CGACGT		
			AGC				
GAM1256	PMVK	3'	AGTCCCCTCAGCCTGTGGTG	21610	ACA	CA_	
			CACCACAG	GCTG	GGACT		
			GTGGTGTC	CGAC	CCTGA		
			_____	TCC			
GAM1256	PMVK	3'	AGTCCCCTCAGCCTGTGGTG	94612	ACA	CA_	
			CACCACAG	GCTG	GGACT		
			GTGGTGTC	CGAC	CCTGA		
			_____	TCC			
GAM1256	POLD3	3'	TCTGAGCTGTCTGCAAGG	91646	A__		G
			CC	CAGACAGCT	CAGG		
			GG	GTCTGT	CGA	GTCT	
			AAC	_			
GAM1256	PRO2958	3'	AGTCCTAAACTGGCATCTGT	37651	CA	C_	
			ACAGA	GCTG	AGGACT		
			TGTCT	CGGT	TCCTGA		
			A_	CAAA			
GAM1256	RAN	3'	GCAGCTGTCCTGTGATGT	20907	C	_	
			ACA	CACAG	ACAGCTGC		
			TGT	GTGTC	TGTCGACG		
			A	C			
GAM1256	RMP	3'	AGTTTTGTGCCAGCTGTG	13707	ACA	T	
			CACAG	GC	GCAGGACT		
			GTGTC	CG	TGTTTTGA		
			GAC	_			
GAM1256	RMP	3'	AGTTTTGTGCCAGCTGTG	56242	ACA	T	
			CACAG	GC	GCAGGACT		

			GTGTC CG TGTTTTGA		
			GAC _		
GAM1256	SCYD1	3'	AGTCACCCCGGCCACCTGCGGT 90924	A ACA CAG_	
	G		CACC CAG GCTG GACT		
			GTGG GTC CGGC CTGA		
			C CAC CCCA		
GAM1256	SHAPY	5'	AGTCCCGCCTGTCTGT 57108	CT A	
			ACAGACAG GC GGA		
			TGTCTGTC CG CCTGA		
			_ C		
GAM1256	SMOC1	3'	AGTCCTGCAATTGTA	A _ C	
			CTGCGG 42147		
			CC CAG ACAG TGCAGGACT		
			GG GTC TGTT ACGTCCTGA		
			C A A		
GAM1256	SRPUL	3'	TCCTGCAGTGTTTCCAGG 27101	AC_ G	
			CC AGACA CTGCAGGA		
			GG TTTGT GACGTCCT		
			ACC _		
GAM1256	SSH-3	3'	AGCCCTGCACACTCACCTGTGG 35339	AC_ C_ A	
			CCACAG AG TGCAGG CT		
			GGTGTC TC ACGTCC GA		
			CAC AC C		
GAM1256	TOSO	3'	CCCAGGCTCGGACTGTGGTG 18389	AC__ GCA	
			CACCACAG AGCT GG		
			GTGGTGTC TCGG CC		
			AGGC AC_		
GAM1256	TPC2	3'	CCTGCAGCTTCCGTGGTG 57446	A C	
			CACCAC GA AGCTGCAGG		
			GTGGTG CT TCGACGTCC		
			C _		
GAM1256	TRIM11	3'	CCATGCCTGTCTGTG 72831	CT _	
			CACAGACAG GCA GG		
			GTGTCTGTC CGT CC		
			_ A		
GAM1256	UGT2B10	3'	AGCCCCAGTAATGCTCTGTGG 6540	_ _ CA A	
			CCACAGA CA GCTG GG CT		
			GGTGTCT GT TGAC CC GA		
			C AA C_ _		
GAM1256	LOC113386	3'	AGTCCTGCATGTGTTGATG 57077	CA GC	
			CA GACA TGCAGGACT		

GT TTGT ACGTCCTGA  
 AG GT  
 GAM1256 LOC130814 3' AGTGCTCAGACATCTGCAGTGT 74984 CA CAG C G  
 T AACAC CAGA CTG AG ACT  
 |||| ||| ||| |||  
 TTGTG GTCT GAC TC TGA  
 AC ACA \_ G  
 GAM1256 LOC131870 3' AGTCCTGCAGCCTCATATGG 75013 CAGACA  
 CCA GCTGCAGGACT  
 ||| |||||  
 GGT CGACGTCCTGA  
 ATACTC  
 GAM1256 LOC133491 5' GTCTGGCGCCTGTGGCGT 75096 A ACA T A  
 AC CCACAG GC GC GGAC  
 || ||||| ||| |||  
 TG GGTGTC CG CG TCTG  
 C \_ \_ G  
 GAM1256 LOC139065 3' TCCTTTTGATTTGTGG 75817 \_ CTGC  
 CCACAGA CAG AGGA  
 ||||| ||| |||  
 GGTGTTT GTT TCCT  
 A T \_  
 GAM1256 LOC145622 5' AGTCCTGCAAAGGTGATGGTGG 77291 AGA G \_  
 T ACCAC CA CT GCAGGACT  
 |||| ||| |||||  
 TGGTG GT GA CGTCCTGA  
 GTA G AA  
 GAM1256 LOC145676 5' AGTCCTGTCCAGGGTCT 77333 AG \_  
 AGAC CTG CAGGACT  
 |||| ||| |||||  
 TCTG GAC GTCCTGA  
 G\_ CT  
 GAM1256 LOC145955 5' AGCCCTGAGATGTCCATGGT 83586 CA G G A  
 ACCA GACA CT CAGG CT  
 |||| |||| ||| |||  
 TGGT CTGT GA GTCC GA  
 AC A \_ C  
 GAM1256 LOC145957 5' CTGCTGTTGTCTGCGGT 56794 A T  
 ACC CAGACAGC GCAG  
 ||| ||||| |||  
 TGG GTCTGTTG CGTC  
 C T  
 GAM1256 LOC146287 5' TTGCAGCTGCCTCGGT 83654 AC A  
 ACC AG CAGCTGCAG  
 ||| ||| |||||  
 TGG TC GTCGACGTT  
 C\_ C  
 GAM1256 LOC146669 3' AGCCCTGCAGCCTGGG 78049 A ACA A  
 CC CAG GCTGCAGG CT  
 || ||| ||||| ||



GG GTC CGACGTCC GA  
— — C  
GAM1256 LOC147040 3' CAGTGTCTGTGATGT 78230 C G  
ACA CACAGACA CTG  
||| ||||| |||  
TGT GTGTCTGT GAC  
A —  
GAM1256 LOC147160 5' AGCCCTGCAGTGCCTGTACAGG 83956 ACAG — A  
CC ACA GCTGCAGG CT  
|| ||| ||||| ||  
GG TGT TGACGTCC GA  
ACA\_ GCG C  
GAM1256 LOC149111 3' CCTGCGTGTCTGTG 79181 GC  
CACAGACA TGCAGG  
||||| |||||  
GTGTCTGT GCGTCC  
—  
GAM1256 LOC150174 3' AGTCCTGCGATGCTAAGTG 79604 CAC A GC  
CAC AG CA TGCAGGACT  
||| ||| |||||  
GTG TC GT GCGTCCTGA  
AA\_ \_ A\_  
GAM1256 LOC150213 3' AGTCCTGCGATGCTAAGTG 74851 CAC A GC  
CAC AG CA TGCAGGACT  
||| ||| |||||  
GTG TC GT GCGTCCTGA  
AA\_ \_ A\_  
GAM1256 LOC150236 3' AGTCCTGCGATGCTAAGTG 79683 CAC A GC  
CAC AG CA TGCAGGACT  
||| ||| |||||  
GTG TC GT GCGTCCTGA  
AA\_ \_ A\_  
GAM1256 LOC154559 3' GCAGCTGTCCTGTGATGT 81096 C \_  
ACA CACAG ACAGCTGC  
||| ||||| |||||  
TGT GTGTC TGTCGACG  
A C  
GAM1256 LOC158117 3' CCTGGTCTGTTCTGTATTGTT 81703 CC \_ CTG  
AACA ACAGA CAG CAGG  
|||| |||| ||| |||  
TTGT TGTCT GTC GTCC  
TA T TG\_  
GAM1256 LOC160897 3' CCAGCTATTGTCTGTTGTGTT 82245 C CT A  
AACAC ACAGACAG GC GG  
|||| ||||| ||| |||  
TTGTG TGTCTGTT CG CC  
T AT A  
GAM1256 LOC161482 3' GCACTTACCTGTGGTGTT 87089 AC\_ C  
AACACCACAG AG TGC  
||||||| ||| |||

		TTGTGGTGTG TC ACG		
		CAT _		
GAM1256	LOC164382 3'	AGTCTCCCTGTCTGTGGT 87203		CTGCA
		ACCACAGACAG GGA		
		TGGTGTCTGTC TCTGA		
		CC__		
GAM1256	LOC200301 5'	AGCCTGTCTGTGTGTT 88736	C	_
		AACAC ACAGACAG CT		
		TTGTG TGTCTGTC GA		
		_ C		
GAM1256	LOC203275 3'	CCTGGTCTGTTCTGTATTGTT 89319	CC	_ CTG
		AACA ACAGA CAG CAGG		
		TTGT TGTCT GTC GTCC		
		TA T TG_		
GAM1256	LOC219920 5'	TTGGGCACTGCCTGTGG 93323	A C	AG
		CCACAG CAG TGC GA		
		GGTGTC GTC ACG TT		
		C _ GG		
GAM1256	LOC220932 3'	AGTCCTGTTCTCTGTTAATGT 93135	_	CT_
		ACA GACAG GCAGGACT		
		TGT TTGTC TGTCCTGA		
		AA TCT		
GAM1256	LOC221466 5'	GTCCTGTGTCCAGGGTG 93693	ACA	AGCT
		CACC GAC GCAGGAC		
		GTGG CTG TGTCCTG		
		GAC _		
GAM1256	LOC221547 3'	GCAGCTGTCCTGTGATGT 91007	C	_
		ACA CACAG ACAGCTGC		
		TGT GTGTC TGTCGACG		
		A C		
GAM1256	LOC221935 3'	AGCCGTCACCTGTCTGTG 92615	CT A	A
		CACAGACAG GC GG CT		
		GTGTCTGTC TG CC GA		
		AC _ _		
GAM1256	LOC253681 3'	CAGTGTCTGTGATGT 95127	C	G
		ACA CACAGACA CTG		
		TGT GTGTCTGT GAC		
		A _		
GAM1256	LOC257115 3'	AGTCCTGCAAGGTGAAGGCGTT 96523	A ACAGA	G _
		AAC CC CA CT GCAGGACT		

TTG GG GT GA CGTCCTGA  
 C AA\_\_ G A  
 GAM1256 LOC257577 3' GCAGCTGTCCTGTGATGT 97838 C \_  
 ACA CACAG ACAGCTGC  
 ||| |||| |||||  
 TGT GTGTC TGTCGACG  
 A C  
 GAM1256 LOC51112 5' AGTCCTGCGGGCCGTGG 32082 AGACAG  
 CCAC CTGCAGGACT  
 ||| |||||  
 GGTG GCGTCCTGA  
 CCG\_\_  
 GAM1256 LOC51236 3' TCCTGCAGCTGTCTGCAGG 33205 A\_  
 CC CAGACAGCTGCAGGA  
 || |||||  
 GG GTCTGTCGACGTCCT  
 AC  
 GAM1256 LOC51713 3' TTTGTACTGTCTGCGG 32762 A C  
 CC CAGACAG TGCAGG  
 || |||||  
 GG GTCTGTC ATGTTT  
 C \_  
 GAM1256 LOC56920 3' AGCCTTCCAGCCTGCGGTG 39379 A ACA C\_ A  
 CACC CAG GCTG AGG CT  
 ||| || ||| |||  
 GTGG GTC CGAC TCC GA  
 C \_\_ CT \_  
 GAM1256 LOC90408 3' AGTCCTGTGGTCCTGTG 62655 ACA TG  
 CACAG GC CAGGACT  
 |||| || |||||  
 GTGTC TG GTCCTGA  
 C\_\_ GT  
 GAM1256 LOC91397 5' GCAGTATCTGTGGTG 65910 CA  
 CACCACAGA GCTGC  
 ||||| ||||  
 GTGGTGTCT TGACG  
 A\_  
 GAM1257 ADCY7 3' TGGTGGGCCTGGCAATGA 6647 A TG  
 TCATTGCCAGGC T CCA  
 ||||| ||| |||  
 AGTAACGGTCCG G GGT  
 \_ GT  
 GAM1257 AICDA 3' GCAACCCTTGCAATGAA 40328 C CA  
 TTCATTGC AGG TTGC  
 ||||| ||| |||  
 AAGTAACG TCC AACG  
 T C\_  
 GAM1257 BIN3 3' GGCCCTTTGCAATGAAT 37957 C\_ CATT  
 ATTCATTGC AGG GCC  
 ||||| ||| |||

			TAAGTAACG TCC CGG	
			TT ____	
GAM1257	CLOCK	3'	TTGGCAATACCTAGTGAT 16914	TG C C
			AT C AGG ATTGCCAA	
			TA G TCC TAACGGTT	
			GT A A	
GAM1257	DMRT2	3'	GCAATGCCTGCTAAATG 21616	GC_
			CATT CAGGCATTGC	
			GTAA GTCCGTAACG	
			ATC	
GAM1257	DSG1	3'	GCAATGCCTGAGCCTGAA 8684	TT _
			TTCA GC CAGGCATTGC	
			AAGT CG GTCCGTAACG	
			C_ A	
GAM1257	FER	5'	GGCATGACCAGCAATGAA 17892	CA _ T
			TTCATTGC GG CAT GCC	
			AAGTAACG CC GTA CGG	
			A_ A _	
GAM1257	GAC1	5'	TGGGGCCTGGCAATGA 20947	ATTG
			TCATTGCCAGGC CCA	
			AGTAACGGTCCG GGT	
			G_	
GAM1257	KRAS2	3'	GCAATGCCTGTGAA 17158	TTGC
			TTCA CAGGCATTGC	
			AAGT GTCCGTAACG	
			_____	
GAM1257	KRAS2	3'	GCAATGCCTGTGAA 52958	TTGC
			TTCA CAGGCATTGC	
			AAGT GTCCGTAACG	
			_____	
GAM1257	MGAM	3'	GCCATTTCTGGCAATGAG 72362	C T
			TTCATTGCCAGG AT GC	
			GAGTAACGGTCT TA CG	
			T C	
GAM1257	MN1	3'	GGCAGGAGCCAAACAATGAAT 10094	CCA A_
			ATTCATTG GGC TTGCC	
			TAAGTAAC CCG GACGG	
			AAA AG	
GAM1257	MPST	3'	GCAATGCCTGGCCTGG 40887	TT
			TCA GCCAGGCATTGC	

		GGT CGGTCCGTAACG	
		C_	
GAM1257 NEBL	3'	CAGTGTCCATGCAATGAAT 21120	CA_
		ATTCATTGC GGCATTG	
		TAAGTAACG CTGTGAC	
		TAC	
GAM1257 NOS1	5'	CAGGCTGGCAATGAA 5244	G A
		TTCATTGCCAG C TTG	
		AAGTAACGGTC G GAC	
		--	
GAM1257 PLCG1	3'	TGGATTCCAGCAGTGAAT 10623	CA CATTG
		ATTCATTGC GG CCA	
		TAAGTGACG CC GGT	
		A_ TTA_	
GAM1257 RALB	3'	TTGGCAATACCCTGTGGAT 11247	TTGC C_
		ATTCA CAGG ATTGCCAA	
		TAGGT GTCC TAACGGTT	
		____ CA	
GAM1257 RPL15	3'	TTGGTAAGCTAGCAATGAAT 11387	CA A
		ATTCATTGC GGC TTGCCAA	
		TAAGTAACG TCG AATGGTT	
		A_ _	
GAM1257 SELE	3'	TGATCACTGGCAATGAA 4828	GC
		TTCATTGCCAG ATTG	
		AAGTAACGGTC TAGT	
		AC	
GAM1257 SLC15A1	3'	GCAGCCAGCAGTGAAT 17402	CA AT
		ATTCATTGC GGC TGC	
		TAAGTGACG CCG ACG	
		A_ _	
GAM1257 SLC38A2	3'	GGTTCCTGAACAATGAAT 38591	C_ CATT
		ATTCATTG CAGG GCC	
		TAAGTAAC GTCC TGG	
		AA T_	
GAM1257 STX8	3'	GCAGTGACACCTGGCAATGA 16766	_____
		TCATTGCCAGG CATTGC	
		AGTAACGGTCC GTGACG	
		ACA	
GAM1257 TBX5	5'	GGTATGCCTGGTAAT 3961	T
		ATTGCCAGGCAT GCC	

TAATGGTCCGTA TGG

GAM1257 TBX5 5' GGTATGCCTGGTAAT 54893 T  
ATTGCCAGGCAT GCC  
||||||| |||  
TAATGGTCCGTA TGG

GAM1257 TDGF1 5' TTGGCTGTTTGGCAATGA 12204 C T  
TCATTGCCAGG AT GCCAA  
||||||| || |||||  
AGTAACGGTTT TG CGGTT

GAM1257 TRHDE 3' TTGGATTGTCTGGCAATGA 25390 TTG  
TCATTGCCAGGCA CCAA  
||||||| |||||  
AGTAACGGTCTGT GGT

GAM1257 AP1GBP1 3' TAATGTCTGAAATGAAT 23398 GC  
ATTCATT CAGGCATTG  
||||| |||||  
TAAGTAA GTCTGTAAT

GAM1257 AP1GBP1 3' TAATGTCTGAAATGAAT 54523 GC  
ATTCATT CAGGCATTG  
||||| |||||  
TAAGTAA GTCTGTAAT

GAM1257 APOA1BP 3' TGGCAATAAAAGTCAGTGAAT 58587 CCAGGC  
ATTCATTG ATTGCCA  
||||| |||||  
TAAGTGAC TAACGGT  
TGAAAA

GAM1257 C1orf16 3' GGCAACCCAGCAATGAA 29233 CA CA  
TTCATTGC GG TTGCC  
||||| || |||||  
AAGTAACG CC AACGG  
A\_ CC

GAM1257 CSTF2 3' AATACCTGGCAAGAA 7173 A C  
TTC TTGCCAGG ATT  
||| ||||| |||  
AAG AACGGTCC TAA

GAM1257 DKFZP434J1813 5' TGGAACCAGCAGTGAAT 61793 CA CATTG  
ATTCATTGC GG CCA  
||||| || |||  
TAAGTGACG CC GGT

GAM1257 DKFZP564O0423 5' TGGCAACCAAAAGCAATGAA 91702 CA\_ CA  
TTCATTGC GG TTGCCA  
||||| || |||||

AAGTAACG CC AACGGT  
 AAAA \_\_\_\_  
 GAM1257 DKFZP761E1824 3' CAGTTCTGTGCAATGAA 66436 \_ C  
 TTCATTGC CAGG ATTG  
 ||||| ||| |||  
 AAGTAACG GTCT TGAC  
 T \_  
 GAM1257 FLJ10546 5' AGTGTCTGCAATGAA 59473 C  
 TTCATTGC AGGCATT  
 ||||| |||||  
 AAGTAACG TCTGTGA  
 \_  
 GAM1257 FLJ13693 3' TTGGCGTCCAGCAATGAA 45650 CA ATT  
 TTCATTGC GGC GCCAA  
 ||||| ||| |||  
 AAGTAACG CTG CGGTT  
 AC \_\_\_\_  
 GAM1257 FLJ22527 3' TTGACAATTAGTAAGCAATGAG 45307 CAG \_ C  
 T ATTCATTGC GC ATTG CAA  
 ||||| || ||| |||  
 TGAGTAACG TG TAAC GTT  
 AA\_ AT A  
 GAM1257 HPCAL4 3' GCAATGCCTCAAGGAT 32738 A CC  
 ATTC TTG AGGCATTGC  
 ||| ||| |||||  
 TAGG AAC TCCGTAACG  
 \_ \_  
 GAM1257 K-ALPHA-1 5' TTGGCAATGCCTGCTGGGAG 76841 ATT C  
 TTC GC AGGCATTGCCAA  
 ||| || |||||  
 GAG CG TCCGTAACGGTT  
 GGT \_  
 GAM1257 KIAA0140 3' TGGCCCCACACTGGCAATGA 27818 GCATT\_  
 TCATTGCCAG GCCA  
 ||||| |||  
 AGTAACGGTC CGGT  
 ACACCC  
 GAM1257 KIAA0561 3' TGGAGCTGGCAGTGAAT 65900 GCATTG  
 ATTCATTGCCAG CCA  
 ||||| |||  
 TAAGTGACGGTC GGT  
 GA\_\_\_\_  
 GAM1257 KIAA1055 3' TTGGCAATGCCACGGCAA 66071 A\_  
 TTGCC GGCATTGCCAA  
 ||| |||||  
 AACGG CCGTAACGGTT  
 CA  
 GAM1257 KIAA1155 3' GGTCTCCTGCAATGAA 62238 C CATT  
 TTCATTGC AGG GCC  
 ||||| ||| |||

			AAGTAACG TCC TGG		
			_ TC_		
GAM1257	KIAA1393	3'	TGGCCTTTGGCAAGAA 72101	A	CATT
			TTC TTGCCAGG GCCA		
			AAG AACGGTTT CGGT		
			_ C_		
GAM1257	KIAA1715	3'	TTGGCAGTATTGACATTGAAT 68134	T C	GC
			ATTCA TG CAG ATTGCCAA		
			TAAGT AC GTT TGACGGTT		
			T A A_		
GAM1257	MGC17330	3'	GCTTGCTGGCAATGA 53528	G	TT
			TCATTGCCAG CA GC		
			AGTAACGGTC GT CG		
			_ T_		
GAM1257	PLAGL2	3'	GCCTCTGCCAGCAATGAG 70452	CA	TT_
			TTCATTGC GGCA GC		
			GAGTAACG CCGT CG		
			A_ CTC		
GAM1257	PTK9L	3'	CAGGGGCCTGGCATGAA 23467	T	A_
			TTCAT GCCAGGC TTG		
			AAGTA CGGTCCG GAC		
			_ GG		
GAM1257	WHIP	3'	TGGCAGCTTTGTGCAATGAAT 39299	_ _	AT
			ATTCATTGC CAG GC TGCCA		
			TAAGTAACG GTT CG ACGGT		
			T T _		
GAM1257	ZFP95	3'	TTGGTACCTCAGCAATGAA 27383	C_	CAT
			TTCATTGC AGG TGCCAA		
			AAGTAACG TCC ATGGTT		
			AC _		
GAM1257	ZFP95	3'	TTGGTACCTCAGCAATGAA 59027	C_	CAT
			TTCATTGC AGG TGCCAA		
			AAGTAACG TCC ATGGTT		
			AC _		
GAM1257	LOC116228	3'	TTGGCAGTGTGGCAAAGAAT 73804	A	AG
			ATTC TTGCC GCATTGCCAA		
			TAAG AACGG TGTGACGGTT		
			A _		
GAM1257	LOC116349	3'	GCAACAAGTTGAGCAATGAA 73832	CA	A_
			TTCATTGC GGC TTGC		



AAGTAACG TTG AACG  
 AG AAC  
 GAM1257 LOC118851 5' TTGGCAATCTACCAACGAAT 75508 A CCA C  
 ATTC TTG GG ATTGCCAA  
 |||| ||| || |||||  
 TAAG AAC TC TAACGGTT  
 C CA\_ \_  
 GAM1257 LOC149182 5' TTGGACAACCCTCAGCAATGAA 84380 C\_ CA \_  
 TTCATTGC AGG TTG CCAA  
 ||||| ||| ||| |||  
 AAGTAACG TCC AAC GGTT  
 AC C\_ A  
 GAM1257 LOC149319 5' TGGCCCCGTGGCAGTGAAT 79303 \_ CATT  
 ATTCATTGCCA GG GCCA  
 ||||| || |||  
 TAAGTGACGGT CC CGGT  
 G C\_\_\_\_  
 GAM1257 LOC158235 3' TTGGCACATAGGCAATCAACGA 86703 \_\_\_\_ AGGCAT  
 AT ATTC ATTGCC TGCCAA  
 ||| ||||| |||||  
 TAAG TAACGG ACGTT  
 CAAC ATAC\_\_\_\_  
 GAM1257 LOC170409 5' GCACCTGGCAAGAA 82863 A CAT  
 TTC TTGCCAGG TGC  
 ||| ||||| |||  
 AAG AACGGTCC ACG  
 \_ \_  
 GAM1257 LOC199725 3' TTGGTGCTAGACAATGAAT 89844 CCA ATT  
 ATTCATTG GGC GCCAA  
 ||||| ||| |||||  
 TAAGTAAC TCG TGGTT  
 AGA \_\_\_\_  
 GAM1257 LOC199858 5' TGGCAAGGCTGGCAAT 88425 G A  
 ATTGCCAG C TTGCCA  
 ||||| | |||||  
 TAACGGTC G AACGGT  
 \_ G  
 GAM1257 LOC255285 3' GCAATGCTGCATGAGT 96275 T CA  
 ATTCAT GC GGCATTGC  
 ||||| || |||||  
 TGAGTA CG TCGTAACG  
 \_ \_  
 GAM1257 LOC257095 5' TGGCCCAGCAGTGAA 96945 CA CATT  
 TTCATTGC GG GCCA  
 ||||| || |||  
 AAGTGACG CC CGGT  
 A\_ \_\_\_\_  
 GAM1257 LOC257109 3' GCAATGCTGGCTAATGA 95571 \_ G  
 TCATT GCCAG CATTGC  
 |||| |||| |||||

AGTAA CGGTC GTAACG  
 T \_  
 GAM1257 LOC90509 5' AGTGCCTGGGAATGAAT 63103 G  
 ATTCATT CCAGGCATT  
 ||||| |||||  
 TAAGTAA GGTCCGTGA  
 G  
 GAM1257 LOC92912 3' TTGGCAATGTACAGTAA 70848 CAG  
 TTGC GCATTGCCAA  
 ||| |||||  
 AATG TGTAACGGTT  
 ACA  
 GAM1258 AF3P21 3' CTCTTCACCCCACACCCA 33195 AA AAGA  
 TGG TGTG GTGAGGAG  
 ||| ||| |||||  
 ACC ACAC CACTTCTC  
 C\_ CC\_  
 GAM1258 AKT1 3' TGTCCCCTCACTCTGTCAGCCA 17697 AA TGA A  
 TGG TG AGAGTGAGG GACA  
 ||| || ||||| |||  
 ACC AC TCTCACTCC CTGT  
 G\_ TG\_ C  
 GAM1258 AMPD3 3' TGTCTTTTCCCCACTATTCCA 4903 \_ AAGAGT  
 TGAAT GTG GAGGAGACA  
 ||||| ||| |||||  
 ACCTTA CAC CTTTCTGT  
 T CC\_  
 GAM1258 AP2A1 3' TGTCTCCTCCCCTCCCACCCCA 26388 AAT AA T\_  
 TGG GTG GAG GAGGAGACA  
 ||| ||| ||| |||||  
 ACC CAC CTC CTCCTCTGT  
 C\_ C\_ CC  
 GAM1258 AP2A1 3' TGTCTCCTCCCCTCCCACCCCA 55440 AAT AA T\_  
 TGG GTG GAG GAGGAGACA  
 ||| ||| ||| |||||  
 ACC CAC CTC CTCCTCTGT  
 C\_ C\_ CC  
 GAM1258 AP2B1 3' TGTCCCCTCACCCCTCTCC 7066 ATGT AGA\_ A  
 GGA GA GTGAGG GACA  
 ||| || ||||| |||  
 CCT CT CACTCC CTGT  
 \_ CCCC C  
 GAM1258 ATP10C 3' CCTCTCTCCACATTCCA 44409 AA T  
 TGAATGTG GAG GAGG  
 ||||| ||| |||  
 ACCTTACAC CTC CTCC  
 \_ T  
 GAM1258 BAI2 3' TCTCTCTATTTTCACACTCCA 8121 A G AG  
 TGGA TGTGAAGA TG GAGA  
 ||| ||||| || |||

ACCT ACACTTTT AT CTCT  
 C \_ CT  
 GAM1258 CAPON 3' CCTCACTCTCCCCGTCTCC 63962 \_ TGA  
 GGA ATG AGAGTGAGG  
 ||| ||| |||||  
 CCT TGC TCTCACTCC  
 C CCC  
 GAM1258 CELSR3 3' CTCCTCACCCACCACCCCA 7399 AAT AAGA  
 TGG GTG GTGAGGAG  
 ||| ||| |||||  
 ACC CAC CACTCCTC  
 C\_ CACC  
 GAM1258 CERD4 3' TGTCTCTTTTACCTCACACTC 23857 A A A \_  
 GA TGTGA G GTGAG GAGACA  
 || |||| | |||| |||||  
 CT ACACT C CATTT CTCTGT  
 C \_ \_ T  
 GAM1258 CLC 3' GTCTCCTCCCCACCTCC 25109 AT AAGAGT  
 GGA GTG GAGGAGAC  
 ||| ||| |||||  
 CCT CAC CTCCTCTG  
 C\_ CC\_\_\_\_  
 GAM1258 COL5A3 3' TGCCCTCCTACTCCTCCGTC 31698 A T A A  
 GA TG GA GAGTGAGGAG CA  
 || ||| ||||| ||  
 CT GC CT CTCACTCCTC GT  
 \_ \_ C C  
 GAM1258 COX10 3' TCCTCCCTTCACCCCA 7125 AAT AGT  
 TGG GTGAAG GAGGA  
 ||| ||||| |||||  
 ACC CACTTC CTCCT  
 CC\_ C\_  
 GAM1258 DNLC2A 3' TCTCCTCACTTCCA 26364 ATGTGAAG  
 TGGA AGTGAGGAGA  
 |||| |||||  
 ACCT TCACTCCTCT  
 \_\_\_\_\_  
 GAM1258 EHD2 3' TGTCCGCCCTTCACACCTCCA 27502 A\_ A AGGA  
 TGGA TGTGAAG GTG GACA  
 |||| ||||| ||| |||||  
 ACCT ACACTTC CGC CTGT  
 CC C \_\_\_\_\_  
 GAM1258 ELK1 3' CCTCCTCCCCACTCCA 17839 AT AA T  
 TGGA GTG GAG GAGG  
 |||| ||| ||| |||||  
 ACCT CAC CTC CTCC  
 \_ CC \_  
 GAM1258 FSTL1 3' TCTAAAACTCTTCAAACCTCCA 23015 ATG GAGG  
 TGGA TGAAGAGT AGA  
 |||| ||||| |||

			ACCT ACTTCTCA TCT			
			CAA AAAA			
GAM1258	GRIN2A	3'	TCTTCCTTCACATCCA 5900	A	AGT	
			TGGA TGTGAAG GAGGA			
			ACCT ACACTTC CTTCT			
			— —			
GAM1258	INSM1	3'	CACTCTTGACATTCCA 9349	G		
			TGGAATGT AAGAGTG			
			ACCTTACA TTCTCAC			
			G			
GAM1258	KHK	3'	CCGGCTCCTCACACACCA 21401	AA	A GA	
			TGG TGTGA GAGT GG			
			ACC ACACT CTCG CC			
			AC C G_			
GAM1258	KHK	3'	CCGGCTCCTCACACACCA 4031	AA	A GA	
			TGG TGTGA GAGT GG			
			ACC ACACT CTCG CC			
			AC C G_			
GAM1258	KNSL4	3'	GTCTCCTCACTCGCCTTTTCA 23620	T_	AA	
			TGGAA GTG GAGTGAGGAGAC			
			ACTTT CGC CTCACTCCTCTG			
			TC —			
GAM1258	MAP4	3'	CCTCCTCTCACTCCCCA 48058	AAT	A T	
			TGG GTGA GAG GAGG			
			ACC CACT CTC CTCC			
			CCT — —			
GAM1258	MAP4	3'	CCTCCTCTCACTCCCCA 9906	AAT	A T	
			TGG GTGA GAG GAGG			
			ACC CACT CTC CTCC			
			CCT — —			
GAM1258	MNT	3'	CCAGCTCCACACATTCCA 39707	AA	GA	
			TGGAATGTG GAGT GG			
			ACCTTACAC CTCG CC			
			AC A_			
GAM1258	NR3C1	3'	CACCCTTCTCATTCCA 3922	T	A	
			TGGAATG GAAG GTG			
			ACCTTAC CTTC CAC			
			T C			
GAM1258	PGD	3'	TCACCCTCCACGATTCCA 78799	_	A A	
			TGGAAT GTG AG GTGA			

ACCTTA CAC TC CACT  
 G C C  
 GAM1258 RNH 5' CACTCTTCACCTCCA 11362 AT  
 TGGG GTGAAGAGTG  
 ||| |||||  
 ACCT CACTTCTCAC  
 C\_  
 GAM1258 RNH 5' CACTCTTCACCTCCA 59617 AT  
 TGGG GTGAAGAGTG  
 ||| |||||  
 ACCT CACTTCTCAC  
 C\_  
 GAM1258 SACM2L 3' CCTGCCTTCACTCCCA 42589 AAT A G  
 TGG GTGAAG GT AGG  
 || ||||| ||  
 ACC CACTTC CG TCC  
 CT\_ \_ \_  
 GAM1258 SACM2L 3' CCTGCCTTCACTCCCA 54543 AAT A G  
 TGG GTGAAG GT AGG  
 || ||||| ||  
 ACC CACTTC CG TCC  
 CT\_ \_ \_  
 GAM1258 SERPIND1 3' CTCCCCACTCTTCACAGCAAAC 3945 AA\_\_\_ A  
 C GG TGTGAAGAGTG GGAG  
 || ||||| ||  
 CC ACACTTCTCAC CCTC  
 AAACG C  
 GAM1258 SERPINE1 3' CCCAGCTCTTCACCCCCCA 5194 AAT GA  
 TGG GTGAAGAGT GG  
 || ||||| ||  
 ACC CACTTCTCG CC  
 CCC AC  
 GAM1258 SLC9A1 3' TGCCTCTAACTCCCTCCTCACA 70414 A A T \_\_\_ A  
 CTCCA TGGG TGTGA GAG GAG GAG CA  
 ||| ||||| ||| ||  
 ACCT ACACT CTC CTC CTC GT  
 C C C AAT C  
 GAM1258 SMOH 3' TCTCTTCCTCACACCCA 18872 AAT AA T  
 TGG GTG GAG GAGGAGA  
 ||| ||| ||| |||||  
 ACC CAC CTC CTTCTCT  
 \_\_\_ A\_ \_  
 GAM1258 ST7 3' CTCACTCCCCACATCCCA 41583 A AA  
 TGG ATGTG GAGTGAG  
 ||| ||||| |||||  
 ACC TACAC CTCACTC  
 C CC  
 GAM1258 STAT4 3' TCTGAAGCTCTCTTCACACTCC 12007 A TGA\_\_\_  
 GGA TGTGAAGAG GGA  
 ||| ||||| |||

			CCT ACACTTCTC	TCT		
			C	TCGAAG		
GAM1258	TRIM8	3'	CCTCCCCTCTTCCTCATTCCA	48114	T_	T_
			TGGAATG GAAGAG GAGG			
			ACCTTAC CTTCTC CTCC			
			TC	CC		
GAM1258	ZNF26	5'	TCTCCTTGTTACATCCG	72982	A	AGA TG
			TGGA TGTGA G AGGAGA			
			GCCT ACACT T TCCTCT			
			-	___GT		
GAM1258	AMOTL1	3'	TGTCTCCTCACCCACCCCCA	73657	AAT	AAGA
			TGG GTG GTGAGGAGACA			
			ACC CAC CACTCCTCTGT			
			CC_ C_			
GAM1258	ARNTL2	3'	CACTCTTCCCACTCCA	39456	A	T
			TGGA TG GAAGAGTG			
			ACCT AC CTTCTCAC			
			C C			
GAM1258	C20orf112	3'	TCCCCATACCTAACATTCCA	54645	GA	A A A
			TGGAATGT AG GTG GG GA			
			ACCTTACA TC CAT CC CT			
			A_ _ A C			
GAM1258	CD109	3'	TGTCTCCTTCCCACATCC	56051	A	AAGAGT
			GGA TGTG GAGGAGACA			
			CCT ACAC TTCCTCTGT			
			-	CC_		
GAM1258	CRMP5	3'	TGTCTAGTTTCCCACATTCCA	39297	AA	TGAGG
			TGGAATGTG GAG AGACA			
			ACCTTACAC CTT TCTGT			
			C_ TGA_			
GAM1258	CXorf1	3'	CCCTCTTCACCCTCCA	16303	AT	TGA
			TGGA GTGAAGAG GG			
			ACCT CACTTCTC CC			
			CC	___		
GAM1258	DGKZ	3'	CCTCACTGCCACATTCCA	13323	AAG	
			TGGAATGTG AGTGAGG			
			ACCTTACAC TCACTCC			
			CG_			
GAM1258	DKFZp434C0328	3'	TGCCTCCTCACTTAGAATACCA	34139	AA	GAA A
			TGG TGT GAGTGAGGAG CA			

ACC ATA TTCACTCCTC GT  
 \_\_ AGA C  
 GAM1258 DKFZP547E1010 5' GTCTTGTCTTCACACCCC 66937 AA GTGAG  
 GG TGTGAAGA GAGAC  
 || ||||| ||||  
 CC ACACTTCT TTCTG  
 CC G\_\_

GAM1258 DKFZP547E1010 5' GTCTTGTCTTCACACCCC 31544 AA GTGAG  
 GG TGTGAAGA GAGAC  
 || ||||| ||||  
 CC ACACTTCT TTCTG  
 CC G\_\_

GAM1258 DKFZP564C103 3' GTCTGTTCTCACCCTCCA 31611 AT AGA T G  
 TGA GTGA G GAG AGAC  
 ||| ||| | ||| |||  
 ACCT CACT C CTT TCTG  
 CC \_\_ G

GAM1258 DKFZP566G1424 5' TCCCCATACCTAACATTCCA 84789 GA A A A  
 TGAATGT AG GTG GG GA  
 ||||| || ||| |||  
 ACCTTACA TC CAT CC CT  
 A\_ \_ A C

GAM1258 ELOVL1 3' CTCACTCCTCCACCCCA 43060 AA T A  
 TGG TG GA GAGTGAG  
 ||| ||| |||||  
 ACC AC CT CTCACTC  
 CC \_ C

GAM1258 FLJ00012 3' TCTCCTCACTTTTTTCTCC 73999 ATGT  
 GGA GAAGAGTGAGGAGA  
 ||| ||||| |||||  
 CCT TTTTCACTCCTCT  
 C\_\_

GAM1258 FLJ11274 3' CCTGTCTCCACATTCC 37199 AA TG  
 GGAATGTG GAG AGG  
 ||||| ||| |||  
 CCTTACAC CTC TCC  
 \_\_ TG

GAM1258 FLJ20294 3' CTCCTCACCCCAGCCCTCCA 34874 AT GAAGA  
 TGA GT GTGAGGAG  
 ||| || |||||  
 ACCT CG CACTCCTC  
 CC ACCC\_

GAM1258 FLJ20373 3' TGTCCCCCACCCTTTTTTCC 35075 TGT A A A  
 GGAA GAAG GTG GG GACA  
 ||| ||| ||| ||| |||  
 CCTT TTTC CAC CC CTGT  
 T\_\_ C C C

GAM1258 FLJ20374 5' CTCACTCCTCACGTCCCA 35079 A A  
 TGG ATGTGA GAGTGAG  
 ||| ||||| |||||

ACC TGC ACT CTC ACT C  
 C C  
 GAM1258 FLJ20920 3' GTCCATCCCCACATTCC 47140 AAGA AGGA  
 GGAATGTG GTG GAC  
 ||||| ||| |||  
 CCTTACAC TAC CTG  
 CCCC \_\_\_\_  
 GAM1258 FLJ22055 3' TCTTCACTCTCCACCCCCA 45500 AAT A  
 TGG GTG AGAGTGAGGA  
 ||| ||| |||||  
 ACC CAC TCTCACTTCT  
 CC\_ C  
 GAM1258 FLJ22282 3' TGCCTCCTCCACTCAGCATTCC 45593 GAA \_ A  
 A TGAATGT GAGTG AGGAG CA  
 ||||| ||||| ||||| ||  
 ACCTTACG CTCAC TCCTC GT  
 A\_ C C  
 GAM1258 FLJ23519 3' CACTCTTCACCTCCA 49962 AT  
 TGA GTGAAGAGTG  
 ||| |||||  
 ACCT CACTTCTCAC  
 C\_  
 GAM1258 FLJ23519 5' CACTCTTCACCTCCA 69200 AT  
 TGA GTGAAGAGTG  
 ||| |||||  
 ACCT CACTTCTCAC  
 C\_  
 GAM1258 GMPPB 5' GTCTCCCTGCTTCCCAAACCCC 95750 AATG AA GA  
 A TGG TG GAGT GGAGAC  
 ||| || ||||| |||||  
 ACC AC TTCG CCTCTG  
 CCAA CC TC  
 GAM1258 GTF3C1 3' CCTGTGCACACCTCACATTCCA 7718 AGA \_\_\_\_  
 TGAATGTGA GTG AGG  
 ||||| ||| |||  
 ACCTTACACT CAC TCC  
 CCA GTG  
 GAM1258 HSRNAFEV 3' GTCTCCCCACCACTCCA 34024 AT AAGA A  
 TGA GTG GTG GGAGAC  
 ||| ||| ||| |||||  
 ACCT CAC CAC CCTCTG  
 \_ \_ C  
 GAM1258 KIAA0193 3' TCCCCCACTCCTCACACC 28661 AA A A A  
 GG TGTGA GAGTG GG GA  
 || ||||| ||||| |||  
 CC AACT CTCAC CC CT  
 \_ C C C  
 GAM1258 KIAA0247 3' TCCTTACTCCTCACCCCCA 28411 AAT A  
 TGG GTGA GAGTGAGGA  
 ||| ||||| |||||



ACC CACT CTCATTCCT  
 CC\_ C  
 GAM1258 KIAA0721 3' CCTTATTCCTCCACCCCA 95966 AA T A  
 TGG TG GA GAGTGAGG  
 ||| ||| |||||  
 ACC AC CT CTTATTCC  
 CC \_ C  
 GAM1258 KIAA0721 3' CCTTATTCCTCCACCCCA 41339 AA T A  
 TGG TG GA GAGTGAGG  
 ||| ||| |||||  
 ACC AC CT CTTATTCC  
 CC \_ C  
 GAM1258 KIAA0916 5' CCTCCTCCTCACATTCC 30492 A T  
 GGAATGTGA GAG GAGG  
 ||||| ||| |||  
 CCTTACACT CTC CTCC  
 C \_  
 GAM1258 KIAA1737 3' CCCATTTTCTTCACATCCCA 67352 A \_ A  
 TGG ATGTGAAGA GTG GG  
 ||| ||||| ||| ||  
 ACC TACACTTCT TAC CC  
 C TT \_  
 GAM1258 KIAA1786 3' CCTTCCTCACATTCTA 66024 AGA TG  
 TGAATGTGA G AGG  
 ||||| | |||  
 ATCTTACACT C TCC  
 \_ CT  
 GAM1258 LASP1 3' CCCAGCTCCTCACATACC 20451 A A GA  
 GG ATGTGA GAGT GG  
 || ||||| ||| ||  
 CC TACACT CTCG CC  
 A C AC  
 GAM1258 MGC14480 3' GCTCCTGCCCACATTCC 58748 AAGA G A  
 GGAATGTG GT AGGAG C  
 ||||| || |||||  
 CCTTACAC CG TCCTC G  
 C \_ \_ C  
 GAM1258 MGC26954 3' GTCTCCTCACTCTCCA 58839 A  
 TG AGAGTGAGGAGAC  
 || ||||| |||||  
 AC TCTCACTCCTCTG  
 C  
 GAM1258 MGC4707 3' TCTCCTCACAGCAACTCCA 44123 ATG AAGA  
 TGGA TG GTGAGGAGA  
 ||| || |||||  
 ACCT AC CACTCCTCT  
 CA\_ GA\_  
 GAM1258 moblak 3' TGTCCCCTCCACCCTCACTCCA 55519 AT A A \_ A  
 TGGA GTGA G GTG AGG GACA  
 ||| ||| | ||| |||

ACCT CACT C CAC TCC CTGT  
 — \_ C C C  
 GAM1258 PI4KII 3' TGCTGCCTCACTCCCCACCCCC 37348 AAT AA \_ A  
 A TGG GTG GAGTGAGG AG CA  
 ||| ||| ||||| || ||  
 ACC CAC CTCACTCC TC GT  
 CC\_ CC G \_  
 GAM1258 PRIC285 3' CCCACCTTCTACATTCCA 61433 \_ A A  
 TGGAATGT GAAG GTG GG  
 ||||| ||| ||| ||  
 ACCTTACA CTTC CAC CC  
 T \_ \_  
 GAM1258 RDHL 3' TCTCCTTTTCAACCCCA 60066 AATG T  
 TGG TGAAGAG GAGG  
 ||| ||||| |||  
 ACC ACTTTTC CTCT  
 CCA\_ \_  
 GAM1258 SEMA4G 5' TCTCATCTGCCACATTCCA 94687 A\_ G  
 TGGAATGTG AGA TGAGG  
 ||||| ||| |||  
 ACCTTACAC TCT ACTCT  
 CG \_  
 GAM1258 SOX7 3' TCCCCTTCCCCACGTTCCA 48725 AA TGA  
 TGGAATGTG GAG GGA  
 ||||| ||| |||  
 ACCTTGAC CTT CCT  
 CC CC\_  
 GAM1258 STK39 3' CCTCACTCCCATTTC 25075 T AA  
 GGAA GTG GAGTGAGG  
 ||| ||| |||||  
 CCTT TAC CTCACTCC  
 \_ C\_  
 GAM1258 SYAP1 3' TCTGTACTCCACATTCCA 51406 AA A  
 TGGAATGTG GAGTG GGA  
 ||||| ||| |||  
 ACCTTACAC CTCAT TCT  
 \_ G  
 GAM1258 SZF1 3' GTCTCTCCTCACACTCCA 32234 A A GTGAG  
 TGA TGTGA GA GAGAC  
 ||| |||| || ||||  
 ACCT AACT CT CTCTG  
 C C \_  
 GAM1258 TMLHE 3' GTCTCCTTATCCCATCCCA 36516 A T AGAG  
 TGG ATG GA TGAGGAGAC  
 ||| ||| || |||||  
 ACC TAC CT ATTCCTCTG  
 C C \_  
 GAM1258 WBSCR17 3' TCTCCTCACCCCATCTCC 81305 AT AAGA  
 GGA GTG GTGAGGAGA  
 ||| ||| |||||

CCT TAC CACTCCTCT  
 C\_ CC\_  
 GAM1258 LOC115574 3' TGTCTCCTTGGCTTCCAACCCC 73470 AA\_ T AG  
 A TGG TG GAAG TGAGGAGACA  
 ||| || ||| |||||  
 ACC AC CTTC GTTCCTCTGT  
 CCA \_ G\_  
 GAM1258 LOC115574 3' CCTGCTCTTCACCTCC 73465 AT G  
 GGA GTGAAGAGT AGG  
 ||| ||||| |||  
 CCT CACTTCTCG TCC  
 C\_ \_  
 GAM1258 LOC118738 5' TCTTGCTCCACATCTCCA 75496 \_ AA TG  
 TGGA ATGTG GAG AGG  
 ||| ||||| ||| |||  
 ACCT TACAC CTC TCT  
 C \_ GT  
 GAM1258 LOC121036 3' TGTCCCTGCCCTCCTCACCCCA 74038 AAT A TG\_ A  
 TGG GTGA GAG AGG GACA  
 ||| ||||| ||| |||||  
 ACC CACT CTC TCC CTGT  
 C\_ C CCG \_  
 GAM1258 LOC124997 3' TCCCTGCGACCTCACATTCTA 74388 AGA\_ GA  
 TGGAATGTGA GT GGA  
 ||||| || |||  
 ATCTTACACT CG CCT  
 CCAG TC  
 GAM1258 LOC133634 5' TCCTGTCTTCCACCCCA 75109 AA T GTG  
 TGG TG GAAGA AGGA  
 ||| ||||| |||  
 ACC AC CTTCT TCCT  
 CC \_ G\_  
 GAM1258 LOC145739 3' TGTCTCCTGTTCATCATCCCA 77446 A \_ GAGTG  
 TGG ATG TGAA AGGAGACA  
 ||| ||||| |||||  
 ACC TAC ACTT TCCTCTGT  
 C T G\_  
 GAM1258 LOC145761 5' TGTCTCCCAGCCCCACATACC 83478 A AAGA GA  
 GG ATGTG GT GGAGACA  
 || |||| || |||||  
 CC TACAC CG CCTCTGT  
 A CC\_ AC  
 GAM1258 LOC146229 3' CCCACCTCCACACCCA 77734 AA A A A  
 TGG TGTG AG GTG GG  
 ||| |||| || ||| ||  
 ACC ACAC TC CAC CC  
 C\_ C \_ \_  
 GAM1258 LOC147622 5' CTCCTCACCTTCCA 84047 T A  
 TG GAAG GTGAGGAG  
 || |||| |||||

AC CTTC CACTCCTC

GAM1258 LOC149464 5' TGTCTCCACCCCCACATTCC 84437 AAGA GA  
GGAATGTG GT GGAGACA  
||||||| || |||||  
CCTTACAC CA CCTCTGT  
CCCC \_

GAM1258 LOC150848 3' TCTTTACCTCTACATTCCA 85132 A A  
TGGAATGTG AG GTGAGGA  
||||||| || |||||  
ACCTTACAT TC CATTTCT  
C \_

GAM1258 LOC157653 5' GTCTCCTCACCTGCACCCA 81528 AAT A A  
TGG GTG AG GTGAGGAGAC  
||| ||| || |||||  
ACC CAC TC CACTCCTCTG  
\_ G \_

GAM1258 LOC202458 5' TGCCTCCTTACCCTCACACTCC 89175 A A A A  
GGA TGTGA G GTGAGGAG CA  
||| ||||| | ||||| ||  
CCT ACACT C CATTCCTC GT  
C \_ C C

GAM1258 LOC222493 5' TCTCCCCACCTCCACCC 94348 AAT A\_ A A  
GG GTG AG GTG GGAGA  
|| ||| || ||| |||||  
CC CAC TC CAC CCTCT  
\_ CC \_ C

GAM1258 LOC253737 5' TCCAGTTCCTCACATCCC 96241 A A TGA  
GG ATGTGA GAG GGA  
|| ||||| ||| |||  
CC TAACT CTT CCT  
C C GA\_

GAM1258 LOC255096 5' TTCCTCCTCACACTC 97626 A A  
GA TGTGA GAGTGAG  
|| ||||| |||||  
CT AACT CTCATT  
C C

GAM1258 LOC255121 5' CCAGCTCTTCACATCCC 97559 A GA  
GG ATGTGAAGAGT GG  
|| ||||| ||| ||  
CC TAACTTCTCG CC  
C A\_

GAM1258 LOC255652 3' CCTTCTCTTCACTCCCA 96720 AAT T  
TGG GTGAAGAG GAGG  
||| ||||| ||| |||  
ACC CACTTCTC TTCC  
CT\_ \_

GAM1258 LOC51236 3' CCTCACTCCACACCCTA 33201 AA AA  
TGG TGTG GAGTGAGG  
||| ||||| |||||

ATC ACAC CTCACTCC  
 CC \_  
 GAM1258 LOC90719 3' TGTCTCCTCACCCCCAGCTGCC 63891 AAT GAAGA  
 A TGG GT GTGAGGAGACA  
 ||| || |||||  
 ACC CG CACTCCTCTGT  
 GT\_ ACCCC  
 GAM1258 LOC96597 3' CCCGGCTTCACATGCCA 66909 A AG A  
 TGG ATGTGAAG TG GG  
 ||| ||||| ||  
 ACC TACACTTC GC CC  
 G G\_ \_  
 GAM1259 HSPA5 3' TTGTTATTTACACTGGTCTA 18083 C A TG  
 TAG ACCAGT TAAATAG A  
 ||| ||||| ||||| |  
 ATC TGGTCA ATTTATT T  
 \_ C GT  
 GAM1259 LDB3 3' ACTACTTTATACTAGTG 76403 C \_  
 CAC AGTATAAA TAGT  
 ||| ||||| ||||  
 GTG TCATATTT ATCA  
 A C  
 GAM1259 RFX1 3' AAATCACTATTTTGTGTGCT 11307 \_ GTAT  
 AGCAC CA AAATAGTGATTT  
 ||||| || |||||  
 TCGTG GT TTTATCACTAAA  
 T \_  
 GAM1259 DKFZP564D172 3' AAATCACTATTTAATTGCCTCT 49382 CAC A  
 A TAG CAGT TAAATAGTGATTT  
 ||| ||||| |||||  
 ATC GTTA ATTTATCACTAAA  
 TCC \_  
 GAM1259 DKFZP586I2223 3' ACTGTCTTCCACACTGGTGCTA 31266 ATAA\_  
 TAGCACCAGT ATAGT  
 ||||| ||||  
 ATCGTGGTCA TGTCA  
 CACCTTC  
 GAM1259 DKFZP586I2223 3' ACTGTCTTCCACACTGGTGCTA 54908 ATAA\_  
 TAGCACCAGT ATAGT  
 ||||| ||||  
 ATCGTGGTCA TGTCA  
 CACCTTC  
 GAM1259 DKFZP586I2223 3' ACTGTCTTCCACACTGGTGCTA 54916 ATAA\_  
 TAGCACCAGT ATAGT  
 ||||| ||||  
 ATCGTGGTCA TGTCA  
 CACCTTC  
 GAM1259 ELF2 3' TCACTTAACTGGTGCTA 22501 ATAAAT  
 TAGCACCAGT AGTGA  
 ||||| ||||

			ATCGTGGTCA	TC	ACT	
			AT_____			
GAM1259	FLJ20139	3'	TC	ACTCTGGTGCTA	34630	TATAAAT
				TAGCACCAG	AGTGA	
			ATCGTGGTC	TC	ACT	
			_____			
GAM1259	KIAA1622	3'	TTATTTG	TACTAATGCTA	54262	CC
				TAGCA	AGTATAAATAG	
			ATCGT	TCATGTTTATT		
			AA			
GAM1259	p25	3'	TATTTATA	CTGGACTA	22855	CA
				TAG	CCAGTATAAATA	
			ATC	GGTCATATTTAT		
			A_			
GAM1259	TRAF6	3'	AAATCACTACCGCCTTGTGCTA	16093		C TATAAA
				TAGCAC	AG TAGTGATTT	
			ATCGTG	TC ATCACTAAA		
			T	CGCC_		
GAM1259	ZFP91	3'	AAATCACTACAATAGCCTAGTG	53816		C TA AA_
	CT			AGCAC	AG TA TAGTGATTT	
			TCGTG	TC AT ATCACTAAA		
			A	CG AAC		
GAM1259	LOC151273	3'	TC	ACTTAACTGGTGCTA	67018	ATAAAT
				TAGCACCAGT	AGTGA	
			ATCGTGGTCA	TC	ACT	
			AT_____			
GAM1259	LOC81034	3'	AAATCACTTATTACAGATGCTA	47838		CCA TAAAT
				TAGCA	GTA AGTGATTT	
			ATCGT	CAT TCACTAAA		
			AGA	TAT_		
GAM1260	DXYS155E	3'	CATCTTTCTCCACTCACC	GCAG	17450	A_ CT
				CTGCGGTGA	AGAAA TG	
			GACGCCACT	TCTTT AC		
			CACC	CT		
GAM1260	EXO1	5'	CGGGTTTCTCCAACCGCA	55230		GAA
				TGCGGT	AGAAACTTG	
			ACGCCA	TCTTTGGGC		
			ACC			
GAM1260	JAM3	3'	CACAGACACCACCGCAGT	51421		AAAGAAAC A
				ACTGCGGTG	TTGT G	

			TGACGCCAC	GACA C	
			CACA_____	C	
GAM1260	KIF13A	3'	CCCAGAGGCCCTTCACCGCA	42085	AGAAA GTA
			TGCGGTGAA	CTT GG	
			ACGCCACTT	GAG CC	
			CCCG_ AC_		
GAM1260	PAWR	5'	CCTACAAGCTCCTCCAAGCCCC	10429	TGAAA_ AA_
	GC		GCGG	GA CTTGTAGG	
			CGCC	CT GAACATCC	
			CCGAAC	CCTC	
GAM1260	BC-2	3'	CAGGATCTTTTACCACA	27084 C	AA
			TG GGTGAAAGA	CTTG	
			AC CCATTTTCT	GGAC	
			A	A_	
GAM1260	C22orf4	3'	CCACAGTGCTCTTCTCACCGCA	60641	_ A_ T A
	G		CTGCGGTGA	AAGA ACT GT GG	
			GACGCCACT	TTCT TGA CA CC	
			C	CG _ _	
GAM1260	FLJ10199	5'	CCGCGGGGCCCTTCCACCGCAG	71231	A AAA A
			CTGCGGTG	AAG CTTGT GG	
			GACGCCAC	TTC GGGCG CC	
			C	CC_ _	
GAM1260	FLJ20813	3'	CCTATAGGTTCCCTCCACCAC	35680 C	AAAGA
			G GGTG	AACTTGTAGG	
			C CCAC	TTGGATATCC	
			A	CTCCC	
GAM1260	FLJ20871	3'	CCCACACCTCCCTCACCGC	42026	AA AACT A
			GCGGTGA	GA TGT GG	
			CGCCACT	CT ACA CC	
			CC	CC_ C	
GAM1260	FLJ22405	5'	CAAGACCTCATCCACCGCAG	42518	AAA AA_
			CTGCGGTG	GA CTTG	
			GACGCCAC	CT GAAC	
			CTA	CCA	
GAM1260	FLJ32356	3'	TTTCTTCTCACACAGT	58372 C	_
			ACTG GGTGA	AAGAAA	
			TGAC	CCACT TTCTTT	
			A	C	
GAM1260	KIAA0471	3'	CCTAAACTCTCCTTCACTGCA	29391	A AACTTG
			TGCGGTGAA	GA TAGG	

		ACGTC	ACTT	CT	ATCC	
			C	CTCAA	_	
GAM1260	KIAA0471	5'	CCTGGCTCCCCTCCCACCGCAG	29392		AA AA
		T	ACTGCGGTG	AG	TAGG	
			TGACGCCAC	TC	GTCC	
			CC	CCCTCG	_	
GAM1260	KIAA1538	5'	CAAGTTCCCTGCTCACC	GCAG	71531	A_ A_
			CTGCGGTGA	AG	AACTTG	
			GACGCCACT	TC	TTGAAC	
			CG	CC		
GAM1260	KIAA1691	3'	CCTACAAGCCCTGGCCGCA	92554		GAA AAA
			TGCGGT	AG	CTTGTAGG	
			ACGCCG	TC	GAACATCC	
			G	CC	_	
GAM1260	PURB	3'	CTACAGGCCTCCACCCA	52639	C	AAA AA
			TG	GGTG	GA	CTTGTAG
			AC	CCAC	CT	GGACATC
			-	CC		
GAM1260	SDC3	3'	CCTGCTTCCTCCCCACCGCAG	27746		AAA AACTT
			CTGCGGTG	GA	G	TAGG
			GACGCCAC	CT	CGTCC	
			CC	CCTT	_	
GAM1260	SHANK3	3'	CTGCCGCTCCACCGCAG	65495		AA AA
			CTGCGGTG	AG	G	TAG
			GACGCCAC	TC	CGTC	
			C	GC	___	
GAM1260	TSPEAR	3'	CTATTTCTACACCGCAG	58721		AAA ACTT
			CTGCGGTG	GAA	G	TAG
			GACGCCAC	CTT	TATC	
			ATC	___		
GAM1260	WBSCR17	3'	CACAAGTTTCCTGCACC	81297	AAA	A
			GGTG	GAAACTTGT	G	
			CCAC	CTTTGAACA	C	
			GTC	C		
GAM1260	LOC124695	5'	CCCAGAGCTCTCCACCGCAG	75657		AA AA
			CTGCGGTG	AGA	CTT	GG
			GACGCCAC	TCT	GAG	CC
			C	C	AC	_
GAM1260	LOC125268	3'	CCTACACCACCTCCCTCACCGC	76073		AA AACT
		A	TGCGGTGA	GA	TGTAGG	



	ACGCCACT CT ACATCC	
	CC CCACC	
GAM1260 LOC144262 5'	CAAGTGTAGCCCCTCCCACCGC 76748	AA AA_____
AG	CTGCGGTG AG ACTTG	
	GACGCCAC TC TGAAC	
	CC CCGATG	
GAM1260 LOC145761 5'	CGACTTTCCCTCACCGCAG 83474	AA C
	CTGCGGTGA GAAA TTG	
	GACGCCACT CTTT AGC	
	CC C	
GAM1260 LOC148987 3'	CACATTTTTACCGCAGT 79120	AAACT A
	ACTGCGGTGAAAG TGT G	
	TGACGCCATTTTT ACA C	
	_____ C	
GAM1260 LOC153937 5'	TTTGTTCACCGCAGT 81008	A G
	ACTGCGGTG AA AAA	
	TGACGCCAC TT TTT	
	C G	
GAM1260 LOC205011 3'	CCTACAAGCTCCATGCCCA 90651	C AAA AA
	TG GGTG GA CTTGTAGG	
	AC CCGT CT GAACATCC	
	_ AC_ C_	
GAM1260 LOC253263 3'	CCCACAATAATCCTTCATCGC 97029	A AAC_ A
AG	CTGCGGTGAA GA TTGT GG	
	GACGCTACTT CT AACA CC	
	C AATC C	
GAM1260 LOC51690 3'	CTGCTGCTCCACCGCAGT 32478	AA AAACCT
	ACTGCGGTG AG GTAG	
	TGACGCCAC TC CGTC	
	CC GT_____	
GAM1260 LOC91301 5'	CCTACAAGAAACCTCACCGCA 65541	AAGAAA
	TGCGGTGA CTTGTAGG	
	ACGCCACT GAACATCC	
	CCAAA_	
GAM1261 AR 5'	GAGCTAGCCGCTCCAGTG 3493	A ACA
	TACT GA GCTAGCTC	
	GTGA CT CGATCGAG	
	C CGC	
GAM1262 ATP1A1 3'	CCTGAAAACCATCCAT 5517	A
	ATG ATGGTTTTTAGG	

			TAC TACCAAAAGTCC		
			C		
GAM1262 EMP1	3'	AATCCCAAACCAT	7441	TTAG	
		AATGGTTT GGGATT			
		TTACCAAA CCCTAA			
GAM1262 EPB72	3'	TGAACCCCCTAAGCACC	14613	T A	
		GGT TTTAGGGG TTCA			
		CCA GAATCCCC AAGT			
		C C			
GAM1262 IVD	5'	CCGCTAAAAACACTCAT	9462	ATG G	
		ATGA GTTTTTAG GG			
		TACT CAAAAATC CC			
		CA_ G			
GAM1262 SPRR1B	3'	TGAATCCCCTATCCCATTC	87406	TTTT	
		GAATGG TAGGGGATTCA			
		CTTACC ATCCCCTAAGT			
		CT__			
GAM1262 WHSC1L1	3'	CCAGCCTAAAAACCACCAT	35030	AA	
		ATG TGGTTTTTTAGG GG			
		TAC ACCAAAAATCC CC			
		C_ GA			
GAM1262 CDC14B	3'	TTCCTAAAAACCACCCA	52864	AA	
		TG TGGTTTTTTAGGGG			
		AC ACCAAAAATCCTT			
		CC			
GAM1262 CNNM1	3'	AATCTCCAAACCATTC	39765	TTA	
		GAATGGTTT GGGGATT			
		CTTACCAAA CCTCTAA			
GAM1262 DIO2	3'	AATTCTATAAAAACCACCCA	25674	AA G	
		TG TGGTTTTTA GGGATT			
		AC ACCAAAAAT TCTTAA			
		CC A			
GAM1262 DIO2	3'	AATTCTATAAAAACCACCCA	5822	AA G	
		TG TGGTTTTTA GGGATT			
		AC ACCAAAAAT TCTTAA			
		CC A			
GAM1262 FLJ23462	3'	TTCATGAAAAACCATTC	45808	AGG	
		TGAATGGTTTTT GGA			

		ACTTACCAAAAA CTT		
		GTA		
GAM1262	JDD1	3' TCATCCTAAACACCATTTCAT 63221	T	_
		ATGAATGGT TTTAGGG GA		
		TACTTACCA AAATCCT CT		
		C A		
GAM1262	KIAA0057	3' TTGAAGAGGAAAAAACCATTC 24448		AGGGGA
		GAATGGTTTTT TTCAA		
		CTTACCAAAAA AAGTT		
		AGGAG_		
GAM1262	LANO	3' TTGAATCCCCCAAGTTCC 36627	TT A	
		GG TTT GGGGATTCAA		
		CC GAA CCCCTAAGTT		
		TT C		
GAM1262	RIP5	3' TGAAACTTTTTTAAAAACCACCC 38127	AA	_ A
	A	TG TGGTTTTTAGGG G TTCA		
		AC ACCAAAAATTTT C AAGT		
		CC T A		
GAM1262	SDF1	3' AATCCCCTAAGCAGACCA 90853	___	
		TGGTTT TTAGGGGATT		
		ACCAGA AATCCCCTAA		
		CG		
GAM1262	SLC17A3	5' CCAAGGGTGAAAACCATTC 21809		GG___
		TGAATGGTTTTTA GG		
		ACTTACCAAAAGT CC		
		GGGAA		
GAM1262	ST13	3' AATCCTTTAAAAACACTCA 14113	ATG	
		TGA GTTTTTTAGGGGATT		
		ACT CAAAAATTCCTAA		
		CA_		
GAM1262	LOC126302	3' AATCCCAGCTCCACCATTCA 74488		TTTTAG
		TGAATGGT GGGATT		
		ACTTACCA CCCTAA		
		CCTCGA		
GAM1262	LOC126302	3' AATCCCAGCTCCACCATTCA 74489		TTTTAG
		TGAATGGT GGGATT		
		ACTTACCA CCCTAA		
		CCTCGA		
GAM1262	LOC129052	5' AATCCACCAACCATTC 75804	TTTA _	
		GAATGGTT GG GGATT		

CTTACCAA CC CCTAA  
 \_\_\_\_\_ A  
 GAM1262 LOC143437 5' TGACGTCCCTAAAAACCATTC 82957 AT  
 GAATGGTTTTTTAGGGG TCA  
 ||||| |||  
 CTTACCAAAAATCCCT AGT  
 GC  
 GAM1262 LOC222662 3' TGAATCCTTTAACATCCA 92846 TTT  
 TGG TTAGGGGATTCA  
 || |||||  
 ACC AATTCCTAAGT  
 TAC  
 GAM1262 LOC253531 5' TGACGTCCCTAAAAACCATTC 96472 AT  
 GAATGGTTTTTTAGGGG TCA  
 ||||| |||  
 CTTACCAAAAATCCCT AGT  
 GC  
 GAM1263 AQP3 3' TTCACGATCCACCCTTTC 59593 T\_ \_  
 GAAA GTGG TCGTGAA  
 ||| ||| |||||  
 CTTT CACC AGCACTT  
 CC T  
 GAM1263 ARSB 3' TCACGACTCTTGTC 3502 AATGTG  
 GACAAGA GTCGTGA  
 ||||| |||||  
 CTGTTCT CAGCACT  
 \_\_\_\_\_  
 GAM1263 B4GALT5 3' TTTTCACAAAAATAGTCCTTTG 16519 AAA\_ GGTC  
 TCA TGACAAG TGT GTGAAAA  
 ||||| || |||||  
 ACTGTTT ATA CACTTTT  
 CCTG AAAA  
 GAM1263 CHRNA3 3' TCGTTACCCATTTCTT 5610 T CG  
 AAGAAATG GGT TGA  
 ||||| ||| |||  
 TTCTTTAC CCA GCT  
 \_ TT  
 GAM1263 DRD1 3' TTACAACCACATTTCTGGCCA 5840 ACA C  
 TG AGAAATGTGGT GTGA  
 || ||||| |||  
 AC TCTTTACACCA CATT  
 CGG A  
 GAM1263 FUT1 3' TCTGATCACATCCCCTGTC 3798 AGAA T  
 GACA ATGTGGTCTG GA  
 ||| ||||| ||  
 CTGT TACACTAGT CT  
 CCCC \_  
 GAM1263 IRF1 3' GCCACATTTCTGATCA 64345 CA  
 TGA AGAAATGTGGT  
 ||| |||||

ACT TCTTTACACCG  
 AG  
 GAM1263 MAP3K8 5' TCACGACCACCTCATG 17791 A AAT  
 CA GA GTGGTCGTGA  
 || || |||||  
 GT CT CACCAGCACT  
 A C\_\_  
 GAM1263 NGFR 3' TTCTGACCACACTTCCTGTC 10231 A A T  
 GACA GAA TGTGGTCG GAA  
 |||| || ||||| |||  
 CTGT CTT ACACCAGT CTT  
 C C \_  
 GAM1263 OLR1 3' TTCACAACAGTTCTTGTTA 10341 ATGTG C  
 TGACAAGAA GT GTGAA  
 ||||| || ||||  
 ATTGTTCTT CA CACTT  
 GA\_\_ A  
 GAM1263 POU4F1 3' CACTGAAAACATTTTTGTCA 20660 A GG \_  
 TGACAAGAA TGT TC GTG  
 ||||| || || |||  
 ACTGTTTTT ACA AG CAC  
 \_ AA T  
 GAM1263 SMP1 3' TTTACATGAATAATTTTTGTC 26705 A GGTC  
 A TGACAAGAA TGT GTGAAA  
 ||||| || ||||  
 ACTGTTTTT ATA CACTTT  
 A AGTA  
 GAM1263 ZNF264 3' TTCTATTAACATTTCTTTTCA 12769 C GGTCGT  
 TGA AAGAAATGT GAA  
 || ||||| |||  
 ACT TTCTTTACA CTT  
 T ATTAT\_  
 GAM1263 C20orf175 3' CGAGCTCCACGTTTCCTGCCA 55063 A A \_\_\_\_  
 TG CA GAAATGTGG TCG  
 || || ||||| |||  
 AC GT CTTTGCACC AGC  
 C C TCG  
 GAM1263 CAPNS2 3' TTTCACAACCCTACATATTCT 50323 CA \_\_\_\_ C  
 GATCA TGA AGAAATGT GGT GTGAAA  
 || ||||| || |||||  
 ACT TCTTTATA CCA CACTTT  
 AG CATC A  
 GAM1263 CLDN6 3' TTTACACTCACATTTTATCA 41041 CA \_ C  
 TGA AGAAATGTG GT GTGAA  
 || ||||| || ||||  
 ACT TTTTACAC CA CATT  
 A\_ T\_  
 GAM1263 DKFZP564L0864 3' GCACCAATTTCTTGCCA 72555 A G C  
 TG CAAGAAAT TGGT GT  
 || ||||| |||| ||

AC GTTCTTTA ACCA CG  
 C \_ \_  
 GAM1263 DKFZP566B183 3' TTTCCATAAACATTTCTTTTCA 31330 C GGTCGT  
 TGA AAGAAATGT GAAA  
 ||| ||||| |||  
 ACT TTCTTTACA CTTT  
 T AATAC\_  
 GAM1263 GTF2E1 3' TACAGACCTCTTGTCA 18616 AATGT \_  
 TGACAAGA GGTC GTG  
 ||||| ||| |||  
 ACTGTTCT CCAG CAT  
 \_ A  
 GAM1263 KIAA0089 3' TTTTAATTCACATTTCTT 69967 TCG  
 AAGAAATGTGG TGAAA  
 ||||| |||  
 TTCTTTACACT ATTTT  
 TA\_  
 GAM1263 KIAA0373 5' TTTTCAAAGTAACATTTCTT 28015 GGTCG  
 AAGAAATGT TGAAAA  
 ||||| |||  
 TTCTTTACA ACTTTT  
 ATGAA  
 GAM1263 KIAA1813 3' TTTTCACACTGTAAATTTCTTG 70314 \_ TG C  
 T ACAAGAAAT G GT GTGAAAA  
 ||||| | |||||  
 TGTTCCTTA T CA CACTTTT  
 AA GT \_  
 GAM1263 KIAA1951 3' TTCCAGGCTTCTCTTGTCA 73766 AATGT GT  
 TGACAAGA GGTC GAA  
 ||||| ||| |||  
 ACTGTTCT TCGG CTT  
 CT\_ AC  
 GAM1263 MGC4170 3' TTCACCATTTCTTGTC 44227 TGGTC  
 GACAAGAAATG GTGAA  
 ||||| |||  
 CTGTTCTTTAC CACTT  
 \_  
 GAM1263 NRN1 3' CACTGCACATTTCTCCTCA 33432 CA GTC  
 TGA AGAAATGTG GTG  
 ||| ||||| |||  
 ACT TCTTTACAC CAC  
 CC GT\_  
 GAM1263 PLA2G12 3' TTTTCACAACCACATTT 48028 C  
 AAATGTGGT GTGAAAA  
 ||||| |||||  
 TTTACACCA CACTTTT  
 A  
 GAM1263 PPY2 3' CACTCCACATTCCTGGCCA 40819 ACA A TC  
 TG AG AATGTGG GTG  
 || ||||| |||

			AC TC TTACACC CAC		
			CGG C T_		
GAM1263	ZNF31	3'	TTTGTAGACCACATTTCTGTGTT	64992	A _TG
	A		TGACA GAAATGTGGTC G AA		
			ATTGT CTTTACACCAG T TT		
			C A GT		
GAM1263	LOC115219	3'	CACGACAACGGGTCCTCA	73295	CAA AA G
			TGA GA TGT GTCGTG		
			ACT CT GCA CAGCAC		
			C_ GG A		
GAM1263	LOC120376	5'	TTCAGAGCATTCTTTCA	75986	C GG G
			TGA AAGAAATGT TC TGAA		
			ACT TTCTTTACG AG ACTT		
			- - -		
GAM1263	LOC133418	3'	TTTCATATACATTTTTTGCCA	75094	A GTC
			TG CAAGAAATGTG GTGAAA		
			AC GTTTTTTACAT TACTTT		
			C A_		
GAM1263	LOC151199	3'	TTAAAACACAGCTCTTGCCA	80174	A AA CG
			TG CAAGA TGTGGT TGA		
			AC GTTCT ACACCA ATT		
			C CG AA		
GAM1263	LOC152317	5'	TCACACTGACTTTTGTCA	85649	AATG C
			TGACAAGA TGGT GTGA		
			ACTGTTTT GTCA CACT		
			CA_ -		
GAM1263	LOC152674	3'	TTCAACCCACCCTCTTGTC	85841	AAT TCG
			TGACAAGA GTGG TGAA		
			ACTGTTCT CACC ACTT		
			CC_ CA_		
GAM1263	LOC152845	5'	CATGACCACATTTTTCA	60330	CAA
			TGA GAAATGTGGTCGTG		
			ACT TTTACACCAGTAC		
			-		
GAM1263	LOC154743	3'	TTTAGTCCACATTGTCTTGTC	81118	_ TCG
			TGACAAGA AATGTGG TGAA		
			ACTGTTCT TTACACC ATTT		
			G TG_		
GAM1263	LOC165476	5'	TTCACGGCACCTTCT	87201	AT G
			AGAA GTG TCGTGAA		

TCTT CAC GGCACCTT  
 C\_ \_  
 GAM1263 LOC254266 5' TTTTCGGTCACACATCTTATCA 97356 C AA GT T  
 TGA AAGA TGTG CG GAA  
 ||| ||| ||| |||  
 ACT TTCT ACAC GC TTT  
 A AC TG T  
 GAM1263 LOC255919 3' TTTCATTCTTACATTTCTAATC 95043 CA TC  
 A TGA AGAAATGTGG GTGAAA  
 ||| ||||| |||||  
 ACT TCTTTACATT TACTTT  
 AA CT  
 GAM1263 LOC51754 5' CACGGCCACATCTCTGTCA 71027 A A  
 TGACA GA ATGTGGTCGTG  
 ||||| || |||||  
 ACTGT CT TACACCGGCAC  
 \_ C  
 GAM1263 LOC55862 3' ACCTCATTCTTGCCA 37485 A T  
 TG CAAGAAATG GGT  
 || ||||| |||  
 AC GTTCTTTAC CCA  
 C T  
 GAM1263 LOC55954 3' CACGTGGTCACTTTTCTCATCA 38877 CA T GT \_  
 TGA AGAAA GTG C GTG  
 ||| ||||| ||| | |||  
 ACT TCTTT CAC G CAC  
 AC T TG TG  
 GAM1264 BIG1 3' AGAAAATTTTTTCAGATGG 21202 TAC  
 CCATCTGAAA GTTTTCT  
 ||||| |||||  
 GGTAGACTTT TAAAAGA  
 TT\_  
 GAM1264 CYP4B1 3' AGAATGGGGTCCCAGATGGCTC 5758 T AA A\_  
 A C AGCCATCTG AT CGTTTT  
 | ||||| || |||||  
 A TCGGTAGAC TG GTAAGA  
 C CC GG  
 GAM1264 DLEC1 3' AGAAGGTCCTTCTGATGGCTAG 23695 T AT G  
 CTAGCCATC GAA AC TTTT  
 ||||| ||| || |||  
 GATCGGTAG CTT TG AAGA  
 T CC G  
 GAM1264 FSTL1 3' GAAATGTCAGATGGC 23011 AATA  
 GCCATCTGA CGTTTT  
 ||||| |||||  
 CGGTAGACT GTAAAG  
 \_  
 GAM1264 KCNK10 3' AGAACTTCATTTTCAGATAGC 40968 C AC\_  
 GC ATCTGAAAT GTTTT  
 || ||||| |||||



			CG TAGACTTTA CAAGA		
			A CTT		
GAM1264	KCNK10	3'	AGAACTTCATTTTCAGATAGC	56337	C AC_
			GC ATCTGAAAT GTTTT		
			CG TAGACTTTA CAAGA		
			A CTT		
GAM1264	KCNK10	3'	AGAACTTCATTTTCAGATAGC	56342	C AC_
			GC ATCTGAAAT GTTTT		
			CG TAGACTTTA CAAGA		
			A CTT		
GAM1264	MAT2A	3'	GAAGCCATCACCTCAGATGGC	19785	AATAC__
			GCCATCTGA GTTTT		
			CGGTAGACT CGAAG		
			CCACTAC		
GAM1264	PPP1R3D	3'	AAAAGTAGCCTCAGGTGGCCAG	20700	A AA_ G
			CT GCCATCTGA TAC TTTT		
			GA CGGTGGACT ATG AAAA		
			C CCG _		
GAM1264	ZNF35	3'	AGAAAAGCATTTCAGAGGCTA	12776	A ACG
			TAGCC TCTGAAAT TTTTCT		
			ATCGG AGACTTTA AAAAGA		
			_ CG_		
GAM1264	ATP10D	3'	AAAACATTGTAGATGGTTA	73138	A AC
			TAGCCATCTG AAT GTTTT		
			ATTGGTAGAT TTA CAAAA		
			G _		
GAM1264	FLJ13373	5'	AAACTTATTTTCAGATAGC	46573	C C
			GC ATCTGAAATA GTTTT		
			CG TAGACTTTAT CAAAA		
			A T		
GAM1264	FLJ20534	3'	GTATTTCAAAGGACTAG	35361	_ ATC
			CTAG CC TGAAATAC		
			GATC GG ACTTTATG		
			A AA_		
GAM1264	HPCAL4	3'	AAGGCTACTTCAGATGGC	32727	A C
			GCCATCTGAA TA GTTTT		
			CGGTAGACTT AT CGGAA		
			C _		
GAM1264	JWA	3'	AAAACGTCTTTAGATG	21138	AT
			CATCTGAA ACGTTTT		

GTAGATTT TGCAAAA  
 C\_  
 GAM1264 KIAA0171 3' GTATTTTCAGAGGCCAG 27856 A A  
 CT GCC TCTGAAATAC  
 || ||| |||||  
 GA CGG AGACTTTATG  
 C G  
 GAM1264 KIAA0798 3' AGAACAAGTTTCAGATGGC 27714 AC  
 GCCATCTGAAAT GTTTT  
 ||||| ||||  
 CGGTAGACTTTG CAAGA  
 AA  
 GAM1264 KIAA0924 3' AAAAGGTGCTTCAGAGACTAG 29710 CCA A G  
 CTAG TCTGAA TAC TTTT  
 ||| ||||| ||| ||||  
 GATC AGACTT GTG AAAA  
 AG\_ C G  
 GAM1264 KIAA1145 3' TGTATTTTCGATGGCCAG 65628 A T  
 CT GCCATC GAAATACG  
 || ||||| |||||  
 GA CGGTAG CTTTATGT  
 C \_  
 GAM1264 MDN1 5' GGAACTTCAGATGGGC 62681 \_ ATAC  
 GCC ATCTGAA GTTTT  
 ||| ||||| ||||  
 CGG TAGACTT CAAGG  
 G \_  
 GAM1264 MGC26914 3' AGAAGATACCCAGATGGC 58663 AAATAC  
 GCCATCTG GTTTTCT  
 ||||| |||||  
 CGGTAGAC TAGAAGA  
 CCA\_  
 GAM1264 MOCS3 3' TATTTTCAGATGATAG 27156 GC  
 CTA CATCTGAAATA  
 ||| |||||  
 GAT GTAGACTTTAT  
 A\_  
 GAM1264 MY014 3' AGAACATTTTCCAGATGGC 48137 \_ TAC  
 GCCATCTG AAA GTTTT  
 ||||| ||| ||||  
 CGGTAGAC TTT CAAGA  
 C TA\_  
 GAM1264 POMT1 3' GTATTTTCAGAGGCCAG 23154 A A  
 CT GCC TCTGAAATAC  
 || ||| |||||  
 GA CGG AGACTTTATG  
 C \_  
 GAM1264 PSMD10 3' TGTATTTTCAGAAACTA 10994 CCA  
 TAG TCTGAAATACG  
 ||| |||||

ATC AGACTTTATGT  
 AA\_  
 GAM1264 LOC151877 3' TGTATATCCCTGATGGCTA 85510 T\_\_ A  
 TAGCCATC GA ATACG  
 ||||| || ||||  
 ATCGGTAG CT TATGT  
 TCC A  
 GAM1264 LOC158476 3' TGTATTTTCAGATGACTG 86858 C  
 TAG CATCTGAAATACG  
 || |||||  
 GTC GTAGACTTTATGT  
 A  
 GAM1264 LOC161784 3' AAAACGTATTCCAGATTGTT 82298 C A  
 AGC ATCTG AATACGTTTT  
 || |||| |||||  
 TTG TAGAC TTATGCAAAA  
 T C  
 GAM1264 LOC255229 3' AAAACGTATTCCAGATTGTT 95436 C A  
 AGC ATCTG AATACGTTTT  
 || |||| |||||  
 TTG TAGAC TTATGCAAAA  
 T C  
 GAM1265 ADAM19 3' CAGGAAGAAGACTGGCCATTAT 52703 C CTGAG  
 G CATGA GGCT TTCTTCCTG  
 |||| || |||||  
 GTATT CCGG AAGAAGGAC  
 A TCAG\_  
 GAM1265 FACL5 5' CAGGAAGAACTCAGAGCCG 64186  
 CGGCTCTGAGTTCTTCCTG  
 |||||  
 GCCGAGACTCAAGAAGGAC  
 GAM1265 GNAL 5' CAGGAAAGAGAGGAGCCGTCG 9058 GAG TC  
 TGACGGCTCT T TTCCTG  
 ||||| | ||||  
 GCTGCCGAGG A AAGGAC  
 AG\_ GA  
 GAM1265 KAL1 3' CAGGAAGAACTTCTGTCA 4013 CTCT  
 TGACGG GAGTTCTTCCTG  
 |||| |||||  
 ACTGTC TTCAAGAAGGAC  
 \_\_\_\_\_  
 GAM1265 MYO1E 3' CAGGAGGACAAAACCACCATG 17187 AC CTC AGT  
 CATG GG TG TCTTCCTG  
 ||| || || |||||  
 GTAC CC AC AGGAGGAC  
 CA AAA \_\_\_\_  
 GAM1265 PRKAR2B 3' CAGAAAGAACTCAGATGT 10804 \_ C  
 GC TCTGAGTTCTT CTG  
 || ||||| ||

			TG AGACTCAAGAA GAC		
			T      A		
GAM1265	PUM2	3'	AGGATCAAAGCTGTCATG	31014	C GTTCT
			CATGACGGCT TGA TCCT		
			GTACTGTCGA ACT AGGA		
			A _____		
GAM1265	SKI	3'	CAGGAAGTGCAGAGCCGCA	11701	A AGTT
			TG CGGCTCTG CTCCTG		
			AC GCCGAGAC GAAGGAC		
			— GT—		
GAM1265	TEM8	3'	AGGAAGATGCAACCCCATG	36326	AC CTC AGT
			CATG GG TG TCTTCCT		
			GTAC CC AC AGAAGGA		
			C_ A_ GT_		
GAM1265	ARHGEF4	5'	AGAAAAAACTCAGGGC	52207	C C
			GCTCTGAGTT TT CT		
			CGGGA CTCAA AA GA		
			A A		
GAM1265	FLJ31978	3'	CAGGAAGGAACAAGCGCC	58348	T GAG
			GGC CT TTCTTCCTG		
			CCG GA AGGAAGGAC		
			C ACA		
GAM1265	HSU24186	5'	AGAACTCAAAGCCGTC	25324	C
			GACGGCT TGAGTTCT		
			CTGCCGA ACTCAAGA		
			A		
GAM1265	KCNT1	3'	AGCTCCAGGGCCGCCA	61825	A —
			TG CGGCTCT GAGTT		
			AC GCCGGGA CTCGA		
			C CC		
GAM1265	KIAA1867	3'	CAGGAAGAACCCAAGAGCTCAT	94822	CG GA_
			ATGA GCTCT GTTCTTCCTG		
			TACT CGAGA CAAGAAGGAC		
			— ACC		
GAM1265	KIAA1878	3'	AATTCAGAGAATCGTCATG	91707	—
			CATGACGG CTCTGAGTT		
			GTACTGCT GAGACTTAA		
			AA		
GAM1265	MFN1	3'	CAGGAAGAACTCATGA	35541	_
			TC TGAGTTCTTCCTG		

AG ACTCAAGAAGGAC  
 T  
 GAM1265 MIDORI 3' CAGGGCCCTTCCAGAGCCTGTC 73784 \_ AGTTCT  
 ATG CATGAC GGCTCTG TCCTG  
 ||||| ||||| |||||  
 GTACTG CCGAGAC GGGAC  
 T CTTCCC  
 GAM1265 MYH7B 3' CAGGAAGAACCTGGCTCGCATG 70530 A \_ CTGA  
 CATG CG GCT GTTCTTCCTG  
 |||| || ||| |||||  
 GTAC GC CGG CAAGAAGGAC  
 \_ T TC\_  
 GAM1265 RNAHP 3' AGAAAGCAGCAGCCGTCAT 23761 \_ AG  
 ATGACGGCT CTG TTCT  
 ||||| ||| |||||  
 TACTGCCGA GAC AAGA  
 C GA  
 GAM1265 SLC37A1 3' AGACGGAGCTCAGACCC 38561 C TC  
 GG TCTGAGTTCT CT  
 || ||||| ||  
 CC AGACTCGAGG GA  
 C CA  
 GAM1265 LOC116236 3' CAGGAAAAGCACAAACCTCAT 73809 C CTC A C  
 ATGA GG TG GTT TTCCTG  
 |||| || || ||| |||||  
 TACT CC AC CGA AAGGAC  
 \_ AA\_ A A  
 GAM1265 LOC124801 3' CAGGAAGAACTCTCTTGCATG 74336 A CTCT  
 CATG CGG GAGTTCTTCCTG  
 |||| ||| |||||  
 GTAC GTT CTCAAGAAGGAC  
 \_ CT\_  
 GAM1265 LOC222160 5' AGGAAGAACTCACCCC 94117 CTC  
 GG TGAGTTCTTCCT  
 || |||||  
 CC ACTCAAGAAGGA  
 CC\_  
 GAM1265 LOC51094 3' CAGGAAGAATAAAGCC 32045 CTGA  
 GGCT GTTCTTCCTG  
 |||| |||||  
 CCGA TAAGAAGGAC  
 AA\_  
 GAM1265 LOC92078 3' CAGGAAGAAGAATCGACCGTC 67977 C T G\_  
 GACGG TC GA TTCTTCCTG  
 |||| || || |||||  
 CTGCC AG CT AAGAAGGAC  
 \_ \_ AAG  
 GAM1266 ALX4 3' CCACGCCCATGTTTCCA 41629 A AGTTT A  
 TG AAGACATG GTG TGG  
 || ||||| ||| |||

			AC TTTTGTAC CGC ACC		
			C C_____		
GAM1266 BCLG	3'	CCATCTCTGGACTCACAGCTTC 56985	A ACA GT_		
CA		TG AAG TGAGTTT GATGG			
		AC TTC ACTCAGG CTACC			
		C GAC TCT			
GAM1266 CHGB	3'	GCCATCACATGATCTGTTTTTC 8430	T GTT		
A		TGAAAGACA GA TGTGATGGC			
		ACTTTTGT CT ACACTACCG			
		_ AGT			
GAM1266 HUNK	3'	CAAACATGTTTTCA 27442	A		
		TGAA GACATGAGTTTG			
		ACTT TTGTACTCAAAC			
		-			
GAM1266 KIF3C	3'	CCAACATAGCTCATGCCCTTCA 9599	AGA T A		
		TGAA CATGAGTT GTG TGG			
		ACTT GTACTCGA TAC ACC			
		CCC _ A			
GAM1266 PAG	3'	CCCAGAACTCATTCTTCA 37402	A C GTGAT		
		TGAA GA ATGAGTTT GG			
		ACTT CT TACTCAAG CC			
		C _ AC_			
GAM1266 RGL	3'	CCATCACACTCTTCCTTC 30731	A CAT TT		
		GAA GA GAGT GTGATGG			
		CTT CT CTCA CACTACC			
		C T_ _			
GAM1266 SNX5	3'	GCCATCACCTGGCCCATGTC 27035	A T_		
		GACATG GTT GTGATGGC			
		CTGTAC CGG CACTACCG			
		C TC			
GAM1266 FLJ10738	3'	CACAACTCCATCTCCCA 36528	AA CAT		
		TG AGA GAGTTTGTG			
		AC TCT CTCAAACAC			
		CC AC_			
GAM1266 HABP2	3'	CCATCACATCTTTATTCCTCA 14695	AA C TT		
		TGA GA ATGAG TGTGATGG			
		ACT CT TATTT ACACTACC			
		C_ _ CT			
GAM1266 HIF1AN	3'	GCCATCATTACATCTATTCA 61975	_ CA GTTT		
		TGAA AGA TGA GTGATGGC			

ACTT TCT ACT TACTACCG  
 A AC \_\_\_\_  
 GAM1266 KIAA1937 5' CCATCACATATCCCCTTCCA 73696 A ACAT GTT  
 TG AAG GA TGTGATGG  
 || ||| || |||||  
 AC TTC CT ACACTACC  
 C CC\_\_ AT\_  
 GAM1266 TRIM2 3' GCCATCATATCATATCCTATCA 30942 AA\_ C GTT  
 TGA GA ATGA TGTGATGGC  
 ||| || ||| |||||  
 ACT CT TACT ATACTACCG  
 ATC A \_\_\_\_  
 GAM1266 LOC120973 5' CATCACCAATCTTTCA 75553 CA AGTTT  
 TGAAAGA TG GTGATG  
 ||||| || |||||  
 ACTTTCT AC CACTAC  
 A\_ \_\_\_\_  
 GAM1266 LOC122830 3' CCACACAGTACTCAGCCTTTCA 74164 ACA \_ A  
 TGAAAG TGAGT TTGTG TGG  
 ||||| ||||| ||||| |||  
 ACTTTC ACTCA GACAC ACC  
 CG\_ T \_  
 GAM1266 LOC146337 3' GCCATCACCCCATGCCGTC 83661 AAGA AGTTT  
 GA CATG GTGATGGC  
 || ||| |||||  
 CT GTAC CACTACCG  
 GCC\_ CC\_\_  
 GAM1266 LOC149566 3' CCATCACAACCCTCTTTCA 84487 CATGAGT  
 TGAAAGA TTGTGATGG  
 ||||| |||||  
 ACTTTCT AACACTACC  
 CCC\_\_  
 GAM1266 LOC151405 5' CCATCACCAAACATCTTATC 85335 CAT \_ \_  
 GA GA GTTTG TGATGG  
 || || ||||| |||||  
 CT CT CAAAC ACTACC  
 ATT A C  
 GAM1266 LOC197335 5' GCCACCTATGACCTCGTGTC 87976 T TG A\_  
 GACATGAG T TG TGGC  
 ||||| | || |||  
 CTGTGCTC A AT ACCG  
 C GT CC  
 GAM1266 LOC253272 5' CCATCACAGAATATCTTT 95360 CATGAG  
 AAAGA TTTGTGATGG  
 |||| |||||  
 TTTCT AGACACTACC  
 ATA\_\_  
 GAM1266 LOC254440 3' GCCATCACAAATGGGTCCTTTC 97070 \_ ATGA  
 A TGAAAG AC GTTTGTGATGGC  
 ||||| || |||||

				ACTTTC TG TAAACACTACCG			
				C GG_			
GAM1266	LOC255736	5'	GCTGGTAAATTACACGTCTTTC	95334	A		GTGA
	A		TGAAAGAC TGAGTTT TGGC				
			ACTTTCTG ACTTAA GTCG				
			C ATG_				
GAM1266	LOC57019	3'	CCACCCTCTTGTCTTTCA	39723	T		TTTGTGA
			TGAAAGACA GAG TGG				
			ACTTTCTGT CTC ACC				
			T CC_____				
GAM1267	ADH1B	3'	CTTAGACATAAAGTAAAAT	72644	C		CAC
			ATTT ACTTT TGTCTGAG				
			TAAA TGAAA ACAGATTC				
			A T_				
GAM1267	AHR	3'	ATCTCAGATGTTAAATAAATG	7875	CAC	C	T
			CATTT TTT AC GTCTGAGAT				
			GTAAA AAA TG TAGACTCTA				
			TA_ T _				
GAM1267	FDFT1	3'	TAGGAAAGTGAAATG	15518	A		
			CATTTCACTTTC CTG				
			GTAAAGTGAAAG GAT				
			—				
GAM1267	JTB	3'	ATCTCAGACAGTGAAAGTGAAA	21959			
	TG		CATTTCACTTTCACTGTCTGAGAT				
			GTAAAGTGAAAGTGACAGACTCTA				
GAM1267	KLF4	3'	TCCCAGACAGTGGATATG	14891	CT		A
			CA TTCACTGTCTG GA				
			GT AGGTGACAGAC CT				
			AT C				
GAM1267	PHYH	3'	ACAGTAAAAGTGAAAT	20608	C		
			ATTTCACTTT ACTGT				
			TAAAGTGAAA TGACA				
			A				
GAM1267	PKD2	3'	TCCAGGTTGAAAGTGAAA	60096	CTG		A
			TTTCACTTTCA TCTG GA				
			AAAGTGAAAGT GGAC CT				
			T_ _				
GAM1267	WRN	3'	GGGCAGTGAAAATGAAA	5098	C		
			TTTCA TTTCACTGTCT				



AAAGT AAAGTGACGGG  
 A  
 GAM1267 ZNF216 3' ATCTGCACAGCAAAGTGAAA 20017 CA CTG  
 TTTCAC TTT CTGT AGAT  
 ||||| ||| |||  
 AAAGTGAAA GACA TCTA  
 C\_ CG\_  
 GAM1267 CG012 5' CTCAC TCTGAAAAGTGAA 83218 CT CT  
 TTCAC TTTCA GT GAG  
 ||||| || |||  
 AAGTGAAAGT CA CTC  
 CT \_  
 GAM1267 EIF2C2 3' ATCTTCTGAGAGTGAAAG 71946 G T\_  
 CTTTCACT TC GAGAT  
 ||||| || |||  
 GAAAGTGA AG TTCTA  
 G TC  
 GAM1267 FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802 ACTTTCACT  
 G CATTTC GTCTGAGAT  
 ||||| |||||  
 GTAAAG CAGACTCTA  
 AAACATTT\_  
 GAM1267 FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281 CTT  
 CATTTCA TCACTGTCTGAGAT  
 ||||| |||||  
 GTAAAGT AGTGACAGACTCTA  
 C\_  
 GAM1267 KIAA0984 3' TTTGTCCAGTGAAAATGAA 65534 C TC  
 TTCA TTTCAC TGAG  
 ||| ||||| |||  
 AAGT AAAGTGAC GTTT  
 A CT  
 GAM1267 KLHL6 3' ATCTCAGAGCAGGAAA 55299 A \_  
 TTTC CTG TCTGAGAT  
 ||| ||| |||||  
 AAAG GAC AGACTCTA  
 \_ G  
 GAM1267 NIR3 3' GCAGTGAAAAGTGCAAT 66242 T  
 ATT CACTTTCACTGT  
 ||| |||||  
 TAA GTGAAAAGTGACG  
 C  
 GAM1267 PORIMIN 3' ATCTCAGAGGGCCAAAGTGAA 53598 CA G  
 TTCACTTT CT TCTGAGAT  
 ||||| || |||||  
 AAGTGAAA GG AGACTCTA  
 CC G  
 GAM1267 PP35 3' ATCTCAGACTGAAA 22814 CT  
 TTTC A GTCTGAGAT  
 ||||| |||||

AAAGT CAGACTCTA

GAM1267 PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148 TCAC C\_  
CATTTCACCTT TGT TGAG  
||||||| ||| |||  
GTAAAGTGAA ACG ACTC  
TA\_\_ TT

GAM1267 SEP15 3' TCCTACAGTAAGAGTGAAA 14934 C CT  
TTTCACTTT ACTGT GA  
||||||| ||||| ||  
AAAGTGAGA TGACA CT  
A TC

GAM1267 SFXN2 3' CTCAGGGGAAAAAAGTGAAA 73941 CACTG  
TTTCACTTT TCTGAG  
||||||| |||||  
AAAGTGAAA GGA CTC  
AAAGG

GAM1267 LOC149703 3' ATCTCAGACAGCCGTTTGAAA 84647 ACTTTCA  
TTTC CTGTCTGAGAT  
||| |||||  
AAAG GACAGACTCTA  
GTTTGCC

GAM1267 LOC154007 3' ATCTCAAACCCTTTAGTGAAA 81015 TTCACT C  
TTTCACT GT TGAGAT  
||||| || |||||  
AAAGTGA CA ACTCTA  
TTTCC\_ A

GAM1267 LOC155004 3' TCATTTAAGTGAAAGGAAA 81226 A GTC\_  
TTTC CTTTCACT TGA  
||| ||||| |||  
AAAG GAAAGTGA ACT  
\_ ATTT

GAM1267 LOC222134 5' ACAGTGAAGTGAAATG 94136 T  
CATTTCACCTT CACTGT  
||||||| |||||  
GTAAAGTGAA GTGACA

GAM1268 ARF3 3' CCCACTCACTCTTAT 7999 AG TT  
ATGAGAGT GAGT GGG  
||||||| ||| |||  
TATTCTCA CTCA CCC

GAM1268 ATRN 3' AGACCCCTCCTCTCAT 57793 T A  
ATGAGAG AGG GTTT  
||||||| ||| |||  
TACTCTC TCC CAGA  
C C

GAM1268 CD8A 3' AGCCCAAACCTGCTGTCCCA 8330 A G G  
TG GA TAG AGTTTGGGCT  
|| || ||| |||||

			AC CT GTC TCAAACCCGA		
			C _ G		
GAM1268	CST2	3'	CCACCTCCTACTCCCA 7171	A	TT
			TG GAGTAGGAG TGG		
			AC CTCATCCTC ACC		
			C C_		
GAM1268	DLST	3'	AGCCCAGGCCTGCCCTCA 8642	A	AG
			TGAG GTAGG TTTGGGCT		
			ACTC CGTCC GGACCCGA		
			C _		
GAM1268	EGLN1	5'	AGCCCAAAATTTCTTCAT 41893	GAGT	_
			ATGA AGGAGTTT GGGCT		
			TACT TCTTTAA CCCGA		
			_ A		
GAM1268	FBXL7	3'	AGCCCAAAGATTAGCTTCAT 24541	G	AG AG
			ATGA AGT G TTTGGGCT		
			TACT TCG T AAACCCGA		
			_ AT AG		
GAM1268	FGD1	5'	AGCCCAGATCTATTCCCAT 15520	A	GA
			ATG GAGTAG GTTTGGGCT		
			TAC CTTATC TAGACCCGA		
			C _		
GAM1268	FGFR1	3'	AGCCCAAAGTGGGGGCTCT 43625	AGG_	
			AGAGT AGTTTGGGCT		
			TCTCG TCAAACCCGA		
			GGGG		
GAM1268	GM2A	3'	AGGCCAAAGTCCCACTCTC 67770	A	G
			GAGAGT GGAGTTTGG CT		
			CTCTCA CCTCAAACC GA		
			C G		
GAM1268	GNAI1	3'	CCCCACCCACCCCTCAT 9052	A A A	TT
			ATGAG GT GG GT GGG		
			TACTC CA CC CA CCC		
			C C _ C_		
GAM1268	GPR61	3'	GCCTTCCTACTCCCAT 78912	A	GTTT
			ATG GAGTAGGA GGGC		
			TAC CTCATCCT TCCG		
			C _		
GAM1268	GPX2	3'	GATCTCCTACTCCAT 9117	A	T
			ATG GAGTAGGAG TT		

			TAC CTCATCCTC AG	
			— T	
GAM1268 HAP1	3'	AGCCTGTCCCCATTCTCAT	14164	A AG TT
		ATGAGAGT GG T GGGCT		
		TACTCTTA CC G TCCGA		
		C CT__		
GAM1268 KMO	3'	AGCCCAGAGTTACCCTCT	13443	TAG G
		AGAG GA TTTGGGCT		
		TCTC TT AGACCCGA		
		CCA G		
GAM1268 MAGP2	3'	AGCTTTTACCCCTACTCTC	12990	A TT
		GAGAGTAGG GT GGGCT		
		CTCTCATCC CA TTCGA		
		C TT		
GAM1268 NDRG3	3'	AGCCCAAGAACCACTTCCAT	49291	AG A AG
		ATG AGT GG TTTGGGCT		
		TAC TCA CC GAACCCGA		
		CT _ AA		
GAM1268 NDRG3	3'	AGCCCAAGAACCACTTCCAT	42492	AG A AG
		ATG AGT GG TTTGGGCT		
		TAC TCA CC GAACCCGA		
		CT _ AA		
GAM1268 PRPH	3'	AGCCCAAACCCTAAGACCA	20757	AGAG A
		TG TAGG GTTTGGGCT		
		AC ATCC CAAACCCGA		
		CAGA _		
GAM1268 PSME3	3'	AGACTCCTACTCCAT	19367	A
		ATG GAGTAGGAGTTT		
		TAC CTCATCCTCAGA		
		_		
GAM1268 RPP20	3'	AGCCCAAAGGACTCTGCAT	19548	_ AGGAG
		ATG AGAGT TTTGGGCT		
		TAC TCTCA AAACCCGA		
		G GG__		
GAM1268 SLC4A10	3'	CCCAAATCCACTTTTCAT	41910	A G
		ATGAGAGT GGA TTTGGG		
		TACTTTCA CCT AAACCC		
		_ _		
GAM1268 SLC6A8	3'	AGCCCAAACCATCCTCTC	18848	T _
		GAG AGGA GTTTGGGCT		

			CTC TCCT CAAACCCGA		
			— AC		
GAM1268	SLC9A3R1	3'	CTTTTGTTCCTACTCCCA	70422	A TT
			TG GAGTAGGAGT GGG		
			AC CTCATCCTTG TTC		
			C TT		
GAM1268	SOCS5	3'	AGCCGAATCCACTCTCAT	25794	A GT G
			ATGAGAGT GGA TT GGCT		
			TACTCTCA CCT AA CCGA		
			— — G		
GAM1268	SUOX	5'	TTTGGACTCCCACTCTCA	4852	A TG
			TGAGAGT GGAGTT GG		
			ACTCTCA CCTCAG TT		
			C GT		
GAM1268	TCN1	3'	AGCCCAAACCTTTCCTCA	6511	AGTA
			TGAG GGAGTTTGGGCT		
			ACTC TTTCAAACCCGA		
			C__		
GAM1268	TRAF1	3'	AGCCCAGAAAGTCTCTCAT	18970	TAGGAG
			ATGAGAG TTTGGGCT		
			TACTCTC AGACCCGA		
			TGAA__		
GAM1268	VDR	3'	AGACCCCCACTCTCAT	4565	A A
			ATGAGAGT GG GTTT		
			TACTCTCA CC CAGA		
			C C		
GAM1268	WHSC1	3'	GGTTCCTCCCACTCT	29915	A TTT
			AGAGT GGAG GGGCT		
			TCTCA CCTC CTTGG		
			C C__		
GAM1268	WHSC1	3'	GGTTCCTCCCACTCT	55833	A TTT
			AGAGT GGAG GGGCT		
			TCTCA CCTC CTTGG		
			C C__		
GAM1268	WHSC1	3'	GGTTCCTCCCACTCT	55850	A TTT
			AGAGT GGAG GGGCT		
			TCTCA CCTC CTTGG		
			C C__		
GAM1268	WHSC1	3'	GGTTCCTCCCACTCT	55859	A TTT
			AGAGT GGAG GGGCT		

TCTCA CCTC CTTGG  
 C C\_\_  
 GAM1268 ABLIM 3' CCCTTTTCCTGACTCTCAT 9763 \_ TTT  
 ATGAGAGT AGGAG GGG  
 ||||| |||| ||  
 TACTCTCA TCCTT CCC  
 G TT\_  
 GAM1268 ABLIM 3' CCCTTTTCCTGACTCTCAT 22024 \_ TTT  
 ATGAGAGT AGGAG GGG  
 ||||| |||| ||  
 TACTCTCA TCCTT CCC  
 G TT\_  
 GAM1268 ADPRTL3 5' AGCCAGGACCTCTCCCAT 18499 A T AG TG  
 ATG GAG AGG TT GGCT  
 || ||| || ||  
 TAC CTC TCC AG CCGA  
 C \_ \_ GA  
 GAM1268 AHCYL1 3' AGCCCTTCCTCCACTCCCA 21761 A A TTT  
 TG GAGT GGAG GGGCT  
 || ||| ||| ||||  
 AC CTCA CCTC CCCGA  
 C \_ CTT  
 GAM1268 C20orf108 3' AGCCCCAACCCCACTCCA 55041 A A A T  
 TG GAGT GG GTT GGGCT  
 || ||| || ||||  
 AC CTCA CC CAA CCCGA  
 \_ C \_ C  
 GAM1268 C6orf37 3' CTCCTCCTACTACCAT 67478 AG TTT  
 ATG AGTAGGAG GGG  
 || ||||| ||  
 TAC TCATCCTC CTC  
 CA \_  
 GAM1268 C8orf17 3' CCCAAACTCGACTCTT 39596 AG  
 GAGAGT GAGTTTGGG  
 |||| |  
 TTCTCA CTCAAACCC  
 G\_  
 GAM1268 COE2 5' CCCAAACTTTGACTACAT 64249 AG AG  
 ATG AGT GAGTTTGGG  
 || || |  
 TAC TCA TTCAAACCC  
 A\_ GT  
 GAM1268 DGS-A 3' CCCAAACTCCTTCCTTT 84896 T\_  
 AGAG AGGAGTTTGGG  
 ||| |||||  
 TTTC TCCTCAAACCC  
 CT  
 GAM1268 DKFZP564M082 3' AGCCCAAACCTACCCTGC 25896 \_  
 GTAGG AGTTTGGGCT  
 |||| |

CGTCC TCAAACCCGA  
CA  
GAM1268 DKFZP586J1624 3' AGCCCACCCAGCACTCTCAT 31390 A\_\_ A TT  
ATGAGAGT GG GT GGGCT  
||||||| || || |||||  
TACTCTCA CC CA CCCGA  
CGA \_ \_  
GAM1268 DKFZp761G0313 3' AGCCCAAACCCACATTC 65812 A A A  
GAG GT GG GTTTGGGCT  
||| || || |||||  
CTT CA CC CAAACCCGA  
A \_ \_  
GAM1268 DOCK3 3' AGCCGTCTCCTACTCCA 66494 A TTTG  
TG GAGTAGGAG GGCT  
|| ||||| |||  
AC CTCATCCTC CCGA  
\_ TG\_  
GAM1268 EPN2 3' AGCCTGGCCTGCTCTCA 30320 AGT TG  
TGAGAGTAGG T GGCT  
||||||| | |||  
ACTCTCGTCC G CCGA  
\_ GT  
GAM1268 FHX 3' AGCCCAAACCTCTGCTTCTAT 37298 AG G  
ATG AGTAG AGTTTGGGCT  
||| ||||| |||||  
TAT TCGTC TCAAACCCGA  
CT \_  
GAM1268 FLJ10815 5' AGCCCAAACCTCTTCCCTCT 36692 T\_  
AGAG AGGAGTTTGGGCT  
||||| |||||  
TCTC TTCTCAAACCCGA  
CC  
GAM1268 FLJ13842 3' AGCCACACCCTACTCT 44983 A TTG  
AGAGTAGG GT GGCT  
||||||| || |||  
TCTCATCC CA CCGA  
\_ CA\_  
GAM1268 FLJ14084 3' AGCCCAAAGTTGCCTCA 41296 A AG G  
TGAG GT GA TTTGGGCT  
||||| || |||||  
ACTC CG TT AAACCCGA  
\_ \_ G  
GAM1268 FLJ20419 3' CCCAAACTCCCGCCTCA 35140 A TA  
TGAG G GGAGTTTGGG  
||||| | |||||  
ACTC C CCTCAAACCC  
\_ GC  
GAM1268 FLJ21432 3' AGCCCAAACCCTGGCTTAT 44630 AG A  
ATGAG TAGG GTTTGGGCT  
||||| ||||| |||||

TATTC GTCC CAAACCCGA  
 G\_ \_  
 GAM1268 FLJ23548 5' CTGGTACCCCACTCTCAT 44748 A A \_ TG  
 ATGAGAGT GG GT T G  
 ||||| || || |  
 TACTCTCA CC CA G C  
 C \_ T GT  
 GAM1268 FLJ30681 3' TCCTTCCTATTCTCAT 91790 TTT  
 ATGAGAGTAGGAG GGG  
 ||||| ||||| |||  
 TACTCTTATCCTT CCT  
  
 GAM1268 GPR88 3' CCCTTTCCACTTTCAT 41879 A TTT  
 ATGAGAGT GGAG GGG  
 ||||| ||||| |||  
 TACTTTCA CCTT CCC  
 \_ T \_  
 GAM1268 HSPBAP1 3' AGCTTTTGTTCCTCTCTCAT 44836 T TT  
 ATGAGAG AGGAGT GGGCT  
 ||||| ||||| |||||  
 TACTCTC TCCTTG TTCGA  
 \_ TT  
 GAM1268 HSPBAP1 5' AGTTTGGCCCTACTCT 44837 A T TG  
 AGAGTAGG G T GGCT  
 ||||| || |||||  
 TCTCATCC C G TTGA  
 C \_ GT  
 GAM1268 HSPC072 3' AGGCTCCTCTCCCAT 26337 A T  
 ATG GAG AGGAGTTT  
 ||| ||| |||||  
 TAC CTC TCCTCGGA  
 C \_  
 GAM1268 HUMZD58C02 3' AGCCCGGGGCTACTTCCA 79764 AG GAG  
 TG AGTAG TTTGGGCT  
 || ||||| |||||  
 AC TCATC GGGCCCGA  
 CT G \_  
 GAM1268 KIAA0152 3' AGCTTTGGTTTCTATCCCAT 28292 A G GT TG  
 ATG GA TAGGA T GGCT  
 ||| || ||||| | |||||  
 TAC CT ATCCT G TCGA  
 C \_ TG TT  
 GAM1268 KIAA0738 3' AGCCCTCTCCTACTCTC 28214 TTT  
 GAGAGTAGGAG GGGCT  
 ||||| ||||| |||||  
 CTCTCATCCTC CCCGA  
 T \_  
 GAM1268 KIAA0930 3' AGCCCAAAGTGAAGTGCCTC 70536 A GG \_  
 GAG GTA AGTTTGGGCT  
 ||| ||| |||||



CTC CGT TCAAACCCGA  
 \_ GAAG  
 GAM1268 KIAA1030 3' AGCCCTAGACTAGCTCTCA 93330 AGG \_  
 TGAGAGT AGTTT GGGCT  
 ||||| |||| ||||  
 ACTCTCG TCAGA CCCGA  
 A\_ T  
 GAM1268 KIAA1199 3' GCCCAAAGCCTTCAT 72516 GAGT AG  
 ATGA AGG TTTGGGC  
 ||| || |||||  
 TACT TCC AAACCCG  
 \_ G\_  
 GAM1268 KIAA1789 3' AGCCCAAACCTTAACCTCT 67095 TAG  
 AGAG GAGTTTGGGCT  
 ||| |||||  
 TCTC TTCAAACCCGA  
 CAA  
 GAM1268 KIAA1813 5' AGGCTCCCACCACTCTCAT 70290 A\_  
 ATGAGAGT GGAGTTT  
 ||||| |||||  
 TACTCTCA CCTCGGA  
 CCAC  
 GAM1268 KIAA1863 3' GGACCCCCAGCTCTCA 64873 A AGTTT \_  
 TGAGAGT GG GGG CT  
 ||||| || ||| ||  
 ACTCTCG CC CCC GG  
 A \_ A  
 GAM1268 KIAA1870 5' AGCCCAAACCCCGCTGCT 51824 \_ TA A  
 AG AG GG GTTTGGGCT  
 || || || |||||  
 TC TC CC CAAACCCGA  
 G GC \_  
 GAM1268 MGC11034 3' AGCCCAAACCTCCTAGGACTCTT 48786 \_  
 GAGAGT AGGAGTTTGGGCT  
 ||||| |||||  
 TTCTCA TCCTCAAACCCGA  
 GGA  
 GAM1268 MGC20253 3' AGTCTGACTCCTACCCT 58060 A T TG  
 AG GTAGGAG T GGCT  
 || ||||| | |||  
 TC CATCCTC A CTGA  
 C \_ GT  
 GAM1268 MGC20481 3' CCCAAATTTCCACTCCA 62713 A A  
 TG GAGT GGAGTTTGGG  
 || ||| |||||  
 AC CTCA CTTTAAACCC  
 \_ C  
 GAM1268 MGC35558 3' CCCACGCTTTCCCACCCTC 58779 A A \_ T  
 GAG GT GGA GT TGGG  
 ||| || ||| || |||

			CTC CA CCT CG ACCC		
			C C TT C		
GAM1268	MGC861	3'	AGCCCCCTCCCACTCCCA	43901	A A TTT
			TG GAGT GGAG GGGCT		
			AC CTCA CCTC CCCGA		
			C C C__		
GAM1268	NSE1	5'	AGCCCAGGACCCACTC	59072	A AG
			GAGT GG TTTGGGCT		
			CTCA CC GGACCCGA		
			_ CA		
GAM1268	PHF5A	3'	GCCCACTAGTCTCAT	51285	G GAGTT
			ATGAGA TAG TGGGC		
			TACTCT ATC ACCCG		
			G _____		
GAM1268	REM	5'	GGCACCTCCTACTCCCAT	25809	A TTTGG
			ATG GAGTAGGAG GCT		
			TAC CTCATCCTC CGG		
			C CA__		
GAM1268	RPP14	3'	GTTTCATCCACTCTCAT	59502	A GTT
			ATGAGAGT GGA TGGGC		
			TACTCTCA CCT ACTTG		
			- -		
GAM1268	SEMA6C	3'	AGCTGGCGGACTCCCACTC	48117	A _
			GAGT GGAGTTTG GGCT		
			CTCA CCTCAGGC TCGA		
			C GG		
GAM1268	SFXN2	5'	AGCCCAGGTCCTCCTCTCA	73938	T G
			TGAGAG AGGA TTTGGGCT		
			ACTCTC TCCT GGACCCGA		
			C _		
GAM1268	Spir-1	3'	CCATCATCCCTGCTCTCAT	64696	AG T_
			ATGAGAGTAGG T TGG		
			TACTCTCGTCC A ACC		
			CT CT		
GAM1268	STK22D	5'	AGCCCAAAGGACTCTC	49321	AGGAG
			GAGAGT TTTGGGCT		
			CTCTCA AAACCCGA		
			GG__		
GAM1268	TA-PP2C	3'	AGTATCTCTCCTACTCTCA	57756	TTTGG
			TGAGAGTAGGAG GCT		

		ACTCTCATCCTC	TGA		
		TCTA_			
GAM1268	TERA	3' CCCAAACCAGAGTACTCTTA	41134	GGA__	
		TGAGAGTA	GTTTGGG		
		ATTCTCAT	CAAACCC		
		GAGAC			
GAM1268	TU3A	3' CCTTTTGCTCCTATCCCAT	23187	A G	TT_
		ATG GA	TAGGAGT GGG		
		TAC CT	ATCCTCG TCC		
		C _	TTT		
GAM1268	LOC115399	3' GCCCAAGACTCCCTC	73432	TA	_
		GAG	GGAGTTT GGGC		
		CTC	CCTCAGA CCCG		
		_	A		
GAM1268	LOC124626	5' CGTGCGTCCTACTCTC	74314	_ T	
		GAGAGTAGGA	GT TG		
		CTCTCATCCT	CG GC		
		G T			
GAM1268	LOC138389	5' AGCCCAGGCACCCTCCA	76216	A TA A	
		TG GAG	GG GTTTGGGCT		
		AC CTC	CC CGGACCCGA		
		_ _	A		
GAM1268	LOC138639	3' AGCCTTATTCCCCTC	75362	A	TT
		GAGT	GGAGT GGGCT		
		CTCA	CCTTA TCCGA		
		C	T_		
GAM1268	LOC144600	5' AGCCCAAAGTGAAGTGCCTC	83159	A	GG__
		GAG GTA	AGTTTGGGCT		
		CTC CGT	TCAAACCCGA		
		_	GAAG		
GAM1268	LOC145693	5' AGCCCAGGGGAGTCTCTCA	77347		TAGGAG
		TGAGAG	TTTGGGCT		
		ACTCTC	GGACCCGA		
		TGAGG_			
GAM1268	LOC145757	3' AGCCCAGGCACCTCCTCCCA	77451	A T A	
		TG GAG	AGG GTTTGGGCT		
		AC CTC	TCC CGGACCCGA		
		C C	A		
GAM1268	LOC146455	3' AGCCACCGTGCCCAACCTCA	77902	A A A	TTG__
		TGAG	GT GG GT GGCT		

		ACTC CA CC CG	CCGA		
		_ A _	TGCCA		
GAM1268	LOC146488 3'	AGCCCAAACCATCCTCTC	70808	T	__
		GAG AGGA	GTTTGGGCT		
		CTC TCCT	CAAACCCGA		
		_ AC			
GAM1268	LOC147004 3'	AGCCCCTGTCACTCTCAT	83900	A	AGTTT
		ATGAGAGT GG	GGGCT		
		TACTCTCA CT	CCCGA		
		_ GTC__			
GAM1268	LOC148109 5'	CAGGCCCTACTCTCA	78657	A	
		TGAGAGTAGG	GTTTG		
		ACTCTCATCC	CGGAC		
		-			
GAM1268	LOC148137 3'	AGCCCGAGGTCCCACTCTC	58419	A	G
		GAGAGT GGA	TTTGGGCT		
		CTCTCA CCT	GAGCCCGA		
		C G			
GAM1268	LOC148137 3'	CTTGGGCTCCTACCTCAT	58428	A	TG
		ATGAG GTAGGAGTT	GG		
		TACTC CATCCTCGG	TC		
		- GT			
GAM1268	LOC148696 5'	AGCCTCTGCCTCCACTCTCAT	84186	A	_ TT
		ATGAGAGT GGAG T	GGGCT		
		TACTCTCA CCTC G	TCCGA		
		- C TC			
GAM1268	LOC148809 5'	AGCCCTCAGACTCCTCCCTCA	78999	AGT	__
		TGAG AGGAGTTT	GGGCT		
		ACTC TCCTCAGA	CCCGA		
		CC_ CT			
GAM1268	LOC154442 3'	AGCCCAGATTCACTCCCA	86218	A	AG
		TG GAGT GAGTTTGGGCT			
		AC CTCA CTTAGACCCGA			
		C _			
GAM1268	LOC154860 3'	AGCCCAAACATGCTCT	86272	GGA	
		AGAGTA GTTTGGGCT			
		TCTCGT CAAACCCGA			
		A__			
GAM1268	LOC170063 3'	CCCAAGACTTTCAT	87245	AGGAG	
		ATGAGAGT	TTTGGG		

TACTTTCA GAACCC

GAM1268 LOC196510 3' CCCAAACCCTTTCACTCA 87748 AGT\_ A  
TGAG AGG GTTTGGG  
|||| ||| |||||  
ACTC TCC CAAACCC  
ACTT \_

GAM1268 LOC200010 3' AGTTCCCCTGCTCCCAT 89919 A TT  
ATG GAGTAGGAGT GGGCT  
||| ||||| |||||  
TAC CTCGTCCTCA CTTGA  
C CC

GAM1268 LOC200597 5' AGCCCCAGCCTACTCTC 88837 AGTTT  
GAGAGTAGG GGGCT  
||||| |||||  
CTCTCATCC CCCGA  
GACC\_

GAM1268 LOC200726 3' CCCAAATTCTCTCA 90112 GTAG  
TGAGA GAGTTTGGG  
|||| |||||  
ACTCT CTAAACCC

GAM1268 LOC220180 5' CTTACCTCCTACTCTCG 92809 TT  
TGAGAGTAGGAG TGGG  
||||||| |||||  
GCTCTCATCCTC ATTC  
C\_

GAM1268 LOC254016 5' AGCCCAGGGATGCAATCTCA 96921 \_ GGAG  
TGAGA GTA TTTGGGCT  
|||| ||| |||||  
ACTCT CGT GGACCCGA  
AA AG\_

GAM1268 LOC254973 5' AGCCCCAAATGTAACCCTC 96293 A AGGA  
GAG GT GTTTGGGCT  
||| ||| |||||  
CTC CA TAAACCCGA  
C ATG\_

GAM1268 LOC255423 5' AGCTGACCCCACTCTTA 97582 A A TG  
TGAGAGT GG GTT GGCT  
||||| || ||| |||||  
ATTCTCA CC CAG TCGA  
C \_ \_

GAM1268 LOC256310 5' AGCCCAGAAGTACTCTC 96344 GGAG  
GAGAGTA TTTGGGCT  
||||| |||||  
CTCTCAT AGACCCGA  
GA\_

GAM1268 LOC257482 3' AGCCCCAACTGAAGACTGC 94237 G\_\_\_\_  
GTAG AGTTTGGGCT  
||| |||||

CGTC TCAAACCCGA  
 AGAAG  
 GAM1268 LOC83468 5' AGCCCAAAGCCCTACCCTCA 48515 A AG  
 TGAG GTAGG TTTGGGCT  
 |||| |||| |||||  
 ACTC CATCC AAACCCGA  
 C CG  
 GAM1268 LOC90573 3' CCCTTACCCTCTCCCAT 63273 A T A TT  
 ATG GAG AGG GT GGG  
 ||| ||| ||| || |||  
 TAC CTC TCC CA CCC  
 C \_ \_ TT  
 GAM1268 LOC91149 3' CTCCTCCTACTCTCAT 65075 TTT  
 ATGAGAGTAGGAG GG  
 ||||| ||  
 TACTCTCATCCTC TC  
 CT\_  
 GAM1268 LOC91179 3' AGCCCGGGGCTACTTCCA 65168 AG GAG  
 TG AGTAG TTTGGGCT  
 || |||| |||||  
 AC TCATC GGGCCCGA  
 CT G\_  
 GAM1268 LOC91409 3' AGCCCAGCCCTAACCCTCA 65950 A \_ A T  
 TGAG GT AGG GTT GGGCT  
 |||| || ||| ||| |||||  
 ACTC CA TCC CGA CCCGA  
 C A \_ \_  
 GAM1268 LOC92305 3' AGCCCAGGCTACCCACTC 56411 A \_  
 GAGT GG AGTTTGGGCT  
 |||| || |||||  
 CTCA CC TCGGACCCGA  
 C A  
 GAM1269 ADH1B 5' GACTCACAGTCTGCTGGTGG 72645 G C\_  
 TCACTAG CAGACTGTG TC  
 ||||| ||||| ||  
 GGTGGTC GTCTGACAC AG  
 \_ TC  
 GAM1269 APG5L 3' TACAGTCTGTCTATTGG 16762 C  
 TCA TAGGCAGACTGTG  
 ||| |||||  
 GGT ATCTGTCTGACAT  
 T  
 GAM1269 CENTD1 3' GTTTGAGCTCATTGTTGGTGG 30855 G AC T  
 TCACTAG CAG TG GCTCAAAC  
 ||||| ||| || |||||  
 GGTGGTT GTT AC CGAGTTTG  
 \_ \_ T  
 GAM1269 CENTD1 3' GTTTGAGCTCATTGTTGGTGG 57565 G AC T  
 TCACTAG CAG TG GCTCAAAC  
 ||||| ||| || |||||

GGTGGTT GTT AC CGAGTTTG  
 \_ \_ T  
 GAM1269 CLCA3 3' GTGTAGTCTGTTTGGT 16994 TG  
 ACTAGGCAGACTG C  
 ||||| I  
 TGGTTTGTCTGAT G  
 GT  
 GAM1269 CLOCK 3' GTCACAGTTTGTTCAGTGA 16910 AG \_  
 TCACT GCAGACTGTG C  
 |||| ||||| I  
 AGTGA TGTTTGACAC G  
 CT T  
 GAM1269 DDX9 3' GTGTAGTTTGTGTTTGA 88549 C TG  
 TCA TAGGCAGACTG C  
 ||||| I  
 AGT GTTTGTTTGAT G  
 T GT  
 GAM1269 EN2 3' TTTGTGTTGGCTTGGTGA 7472 AGACTGT T  
 TCACTAGGC GC CAAA  
 ||||| |||||  
 AGTGGTTCG TG GTTT  
 GT \_ T  
 GAM1269 LDB1 5' GTTTGAGTGTGCGAGTGTGAGT 13986 AGG G \_ \_  
 GA CACT CA ACT GT GCTCAAAC  
 |||| |||||  
 GTGA GT TGA CG TGAGTTTG  
 \_ G G TG  
 GAM1269 MCCC2 3' GTTTTGCTGGTTATGCTTGGTG 42139 \_ T TC  
 A TCACTAGGCA GACTG GC AAAC  
 ||||| |||||  
 AGTGGTTCGT TTGGT CG TTTG  
 A \_ T  
 GAM1269 METTL1 3' GTTTGAGCGTGTGCCTCTGGA 43511 ACT G TGT  
 TC AGGCA AC GCTCAAAC  
 || |||||  
 AG TCCGT TG CGAGTTTG  
 GTC G \_  
 GAM1269 NT5C3 3' GTTTGGTTATTTTGTCTGGGGA 33235 A CTGT T  
 TC CTAGGCAGA GC CAAAC  
 || ||||| |||||  
 AG GGTCTGTTT TG GTTTG  
 G TAT \_  
 GAM1269 PITX2 3' GTTTTAGAATAGTTTCTCTGGT 4381 C G C  
 GG TCACTAGG AGACTGT CT AAAC  
 ||||| ||||| |||||  
 GGTGGTCT TTTGATA GA TTTG  
 C A T  
 GAM1269 PRDM2 3' ATATTTGTTTGGTGA 31843 C  
 TCACTAGGCAGA TGT  
 ||||| |||||

AGTGGTTTGT TT ATA

GAM1269 PRPSAP2 3' GTTTGGGTGTTTGTGAGTTTGG 10906 AG T\_ TG  
CTAGGC AC G CTCAAAC  
||||| || | |||||  
GGTTTG TG T GGGTTTG  
AG TT GT

GAM1269 PYGO2 3' GCAGTTTCTTGGTGA 63986 C  
TCACTAGG AGACTGT  
||||| |||||  
AGTGGTTC TTTGACG

GAM1269 SERPINB13 3' TTTGACTTTGTTTGGTGA 24776 CTGTGC  
TCACTAGGCAGA TCAAA  
||||||| ||||  
AGTGGTTTGT TT AGTTT  
C\_\_\_\_\_

GAM1269 SGCG 5' GTTTGAAACATTCTGTCTGTGG 4062 T C GC  
TCAC AGGCAGA TGT TCAAAC  
||| ||||| || |||||  
GGTG TCTGTCT ACA AGTTTG  
\_ T A\_

GAM1269 TAL1 3' GTTTGGGCTTCAGCCTAGTGG 12112 A CTGT  
TCACTAGGC GA GCTCAAAC  
||||||| || |||||  
GGTGATCCG CT CGGGTTTG  
A T\_\_\_\_

GAM1269 TNFSF10 3' GATCGCAGTTTGCCTGGTG 13748 C  
CACTAGGCAGACTGTG TC  
||||||| ||||| ||  
GTGGTCCGTTTGACGC AG  
T

GAM1269 TRAF5 3' TCATGGCATGGTTTGCTTAGGA 16087 A CAAAC  
TC CTAGGCAGACTGTGCT  
|| ||||| |||||  
AG GATTCGTTTGGTACGG  
\_ TACTG

GAM1269 ABCA5 3' GTTCGGTCTGCTTACTGG 37915 C T  
TCA TAGGCAGACTG GC  
||| ||||| ||  
GGT ATTCGTCTGGC TG  
C T

GAM1269 ARF4 5' GTTTAGTTTGCCTGGGA 82814 A T  
TC CTAGGCAGACTG GC  
|| ||||| ||  
AG GGTCCGTTTGAT TG  
\_ T

GAM1269 BM-009 3' GAATGCAGTTTTTTAGTGA 61702 C GC  
TCACTAGG AGACTGT TC  
||||| ||||| ||



AGTGATTT TTTGACG AG  
 \_ TA  
 GAM1269 C21orf25 3' TTTGGGTTTGTGGTGG 63561 GCA TGT  
 TCACTAG GAC GCTCAAA  
 ||||| || |||||  
 GGTGGTT TTG TGGGTTT  
 \_ TT\_  
 GAM1269 CHORDC1 5' TTTGGGCCTTGCCTGTGA 24021 T ACTGT  
 TCAC AGGCAG GCTCAAA  
 ||| ||||| |||||  
 AGTG TCCGTT CGGGTTT  
 \_ C\_  
 GAM1269 COTL1 3' GACGAGGTCTGCCTAGTGA 87956 G C  
 TCACTAGGCAGACT TG TC  
 ||||| ||||| |||||  
 AGTGATCCGTCTGG GC AG  
 A \_  
 GAM1269 DNM1L 3' GCAAAGCAGTTTGCCTGTGG 23802 T \_  
 TCAC AGGCAGACTGT GC  
 ||| ||||| ||||| |||||  
 GGTG TCCGTTTGACG CG  
 \_ AAA  
 GAM1269 FLJ11795 3' GTTTGGTTTGCTTTGTGG 45131 T T  
 TCAC AGGCAGACTG GC  
 ||| ||||| ||||| |||||  
 GGTG TTCGTTTGGT TG  
 T T  
 GAM1269 FLJ12122 3' GTTTGGGTGTGTTTGGTCTGGT 46464 \_ T TG  
 ACTAGGC AGAC G CTCAAAC  
 ||||| ||||| ||||| |||||  
 TGGTCTG TTTG T GGGTTTG  
 G \_GT  
 GAM1269 FLJ14281 3' TGCAGTTTCTTGGTGA 46215 C  
 TCACTAGG AGACTGTG  
 ||||| ||||| |||||  
 AGTGGTTC TTTGACGT  
 \_  
 GAM1269 FLJ21313 3' GTTTGAGTGCACCCTGCTGGT 43690 G AC TG  
 ACTAG CAG TG CTCAAAC  
 ||||| ||||| ||||| |||||  
 TGGTC GTC AC GAGTTTG  
 \_ CC GT  
 GAM1269 GRO2 3' TTTGAGCATCACTTAGGA 59518 A CAGACT  
 TC CTAGG GTGCTCAAA  
 || ||||| ||||| |||||  
 AG GATTC TACGAGTTT  
 \_ AC\_  
 GAM1269 HSPC195 3' GCATAGTTTGCCTGGAGA 80966 A  
 TC CTAGGCAGACTGTGC  
 || ||||| ||||| |||||

		AG GGTCCGTTTGATACG		
		A		
GAM1269	KCNS1	3' GTTTGC GTGTGTTTTTTGGTGA 9582	C	T TG T
		TCACTAGG AGAC G C CAAAC		
		AGTGGTTT TTTG T G GTTTG		
		_ _GT C		
GAM1269	KIAA0087	3' GTATTAAGCAGTATGTTTAGTG 28701	G	GCTCAAAC
	A	TCACTAGGCA ACTGT		
		AGTGATTTGT TGACG		
		A AATTATG		
GAM1269	KIAA0447	3' GTTTGGA TTTTCTGTTTGTGG 71676	T	CT G T
		TCAC AGGCAGA GT C CAAAC		
		GGTG TTTGTCT TA G GTTTG		
		_ TT _ _		
GAM1269	KIAA0459	3' TTACAGTTGGTCTGTTTAGTG 61012	T	CAAAC
		CACTAGGCAGACTG GCT		
		GTGATTTGTCTGGT TGA		
		_ CATTG		
GAM1269	KIAA0523	5' GCTCCGTCTCTTGGTGA 67739	C	TGT
		TCACTAGG AGAC GC		
		AGTGGTTC TCTG CG		
		_ CCT		
GAM1269	KIAA0663	3' GTTGCC CAGTATTTGTTTGGTG 29128	_	T TCAAAC
	G	TCACTAGGCAG ACTG GC		
		GGTGGTTTGTT TGAC CG		
		TA C TTG		
GAM1269	KIAA0844	3' GTTTGATTGAGGTTTTTTGGTG 30205	C	GTGC
	G	TCACTAGG AGACT TCAAAC		
		GGTGGTTT TTTGG AGTTTG		
		_ AGTT		
GAM1269	KIAA0945	3' TTTGGGTGAGGCCTGG 30220	AGACTG	
		CTAGGC TGCTCAA		
		GGTCCG GTGGGTTT		
		GA_		
GAM1269	KIAA1023	3' GCTGTGGTCTGTCTGCTGA 34263	C	TG_
		TCA TAGGCAGAC T GC		
		AGT GTCTGTCTG G CG		
		C GT T		
GAM1269	KIAA1240	3' GTTGGCTATGGTCTGTTCTGGT 66736	_	_ T AC
	GG	TCACTAGG CAGACTGT GC CAA		

GGTGGTCT GTCTGGTA CG GTT  
T T \_ G  
GAM1269 KIAA1486 3' TTTGGGTACGTGGTTGTGG 67388 T G GAC  
TCAC AG CA TGTGCTCAAA  
||||| ||| |||||  
GGTG TT GT GCATGGGTTT  
\_ G \_  
GAM1269 KIAA1492 3' TTTGGGTTGTGTTTGGT 64513 GACTGT  
ACTAGGCA GCTCAAA  
||||| |||||  
TGGTTTGT TGGGTTT  
GT\_\_\_\_  
GAM1269 KIAA1932 3' GTTTAGACGCATGGTTCTGTCT 73447 \_ \_ \_  
GGTGA CTAGGCAGA CTGTGC TC AAAC  
||||| ||||| || |||  
GGTCTGTCT GGTACG AG TTTG  
T C A  
GAM1269 MAT2B 3' GTTTGAGTATAGTAAATTATGA 25226 C GCAG  
TCA TAG ACTGTGCTCAAAC  
||| ||| |||||  
AGT ATT TGATATGAGTTTG  
\_ AAA\_  
GAM1269 MBLL39 3' GTTTGGTTTGCCTGGAGA 19251 A T  
TC CTAGGCAGACTG GC  
|| ||||| ||  
AG GGTCCGTTTGGT TG  
A T  
GAM1269 MBLL39 3' GTTTGGTTTGCCTGGAGA 58610 A T  
TC CTAGGCAGACTG GC  
|| ||||| ||  
AG GGTCCGTTTGGT TG  
A T  
GAM1269 MGC4251 3' CATGGTTGGCCTGGTGG 50457 A  
TCACTAGGC GACTGTG  
||||| |||||  
GGTGGTCCG TTGGTAC  
G  
GAM1269 NXN 3' GTTTGGAGACTCTGTTTGGGA 42423 A CT GC  
TC CTAGGCAGA GT TCAAAC  
|| ||||| || |||||  
AG GGTTTGTCT CA GGTTTG  
\_ \_ GA  
GAM1269 p25 3' TTTGGGCGCAGATGGTGG 22858 GGCAGA  
TCACTA CTGTGCTCAAA  
||||| |||||  
GGTGGT GACGCGGGTTT  
A\_\_\_\_  
GAM1269 POFUT1 3' CACAGTCTTTTGGTGG 70466 C  
TCACTAGG AGACTGTG  
||||| |||||

GGTGGTTT TCTGACAC

GAM1269 QSCN6 3' TGAGTGGCTTGCTTGGTGG 11041 GA GT  
TCACTAGGCA CT GCTCA  
||||||| || |||||  
GGTGGTTCGT GG TGAGT  
TC \_

GAM1269 SARCOSIN 3' GAGGTGGTTTGTGTTGGTGA 20233 TG G  
TCACTAGGCAGAC T CTC  
||||||| |||||  
AGTGGTTTGTGTTG G GAG  
GT \_

GAM1269 SSR3 3' GACCATAGTTTGACTGGTGG 23039 G C  
TCACTAG CAGACTGTG TC  
||||| ||||| ||  
GGTGGTC GTTTGATAC AG  
A C

GAM1269 X123 5' GACCACCACCGTCTGCTTGGTG 69925 T CTCAAAC  
G  
TCACTAGGCAGAC GTG  
||||||| |||||  
GGTGGTTCGTCTG CAC  
C CACCAG

GAM1269 YWHAQ 3' GTCCAGTTTGTCTAGTGA 22395 TG  
TCACTAGGCAGACTG C  
||||||| |||||  
AGTGATCTGTTTGAC G  
CT

GAM1269 ZNF287 3' GCACGGTCAGCCTGGTGG 40298 A  
TCACTAGGC GACTGTGC  
||||||| |||||  
GGTGGTCCG CTGGCACG  
A

GAM1269 ZNF387 3' GTTTGAGCAGGATGTTTTGTGA 27998 T GA GT  
TCAC AGGCA CT GCTCAAAC  
||| |||| || |||||  
AGTG TTTGT GA CGAGTTTG  
T AG \_

GAM1269 LOC121536 3' TGCAGTATGTCTGGTGG 74090 G  
TCACTAGGCA ACTGTG  
||||||| |||||  
GGTGGTCTGT TGACGT  
A

GAM1269 LOC126964 3' TTTGAGTGCACCTTGGA 74625 A CAGAC TG  
TC CTAGG TG CTCAA  
|| |||| || |||||  
AG GGTTC AC GAGTTT  
\_ C \_ GT

GAM1269 LOC130074 3' GTTTGAGTGCTGTGGGCTCTGG 76140 \_ AG T TG  
TGG  
TCACTAG GC AC G CTCAAAC  
||||||| || || |||||

GGTGGTC CG TG C GAGTTTG  
T GG T GT

GAM1269 LOC138389 5' GTTTGGGAGTCGGTTTGCTAGT 76232 G TG\_  
GA TCACTAG CAGACTG CTCAAAC  
||||| ||||| |||||  
AGTGATC GTTTGGC GGGTTTG  
\_ TGA

GAM1269 LOC143884 3' GCACTGCAGTTTGCTCAGTGG 76656 AG \_\_\_\_  
TCACT GCAGACTGT GC  
|||| ||||| ||  
GGTGA CGTTTGACG CG  
CT TCA

GAM1269 LOC146237 3' GTTTGAGTGTGGGAGCACCAGT 83633 AG\_ AGA TG  
GA TCACT GC CTG CTCAAAC  
|||| || ||| |||||  
AGTGA CG GGT GAGTTTG  
CCA AG\_ GT

GAM1269 LOC146603 5' TCCTTTCCGCAGTCTGTTTACT 78020 C CTCAAAC  
GA TCA TAGGCAGACTGTG  
||| |||||  
AGT ATTTGTCTGACGC  
C CTTTCCTG

GAM1269 LOC147804 5' GG TAGTCTGCCTGGT 78485 GT  
ACTAGGCAGACT GCT  
||||||| |||  
TGGTCCGTCTGA TGG

GAM1269 LOC148089 3' CCCAGGCACTCTGCCTGGTGG 78630 CT CAAAC  
TCACTAGGCAGA GTGCT  
||||||| |||||  
GGTGGTCCGTCT CACGG  
\_ ACCCT

GAM1269 LOC148932 3' TGAGCAGTCTGCCTGTGA 79113 T GT  
TCAC AGGCAGACT GCTCA  
||| ||||| |||||  
AGTG TCCGTCTGA CGAGT

GAM1269 LOC149722 3' GTTTGAGTATCAGATTTAGT 84606 CAGA \_  
ACTAGG CTG TGCTCAAAC  
|||| ||| |||||  
TGATTT GAC ATGAGTTTG  
A\_ T

GAM1269 LOC152200 3' ACAGTTTTTTAGTGG 85571 C  
TCACTAGG AGACTGT  
||||| |||||  
GGTGATTT TTTGACA

GAM1269 LOC152793 3' GCTATGGTCTGTGTGGTGA 80666 G \_  
TCACTA GCAGACTGT GC  
||||| ||||| ||

AGTGGT TGTCTGGTA CG  
 G T  
 GAM1269 LOC155179 3' GCTGTGGTCTGTCTGCTGA 81317 C TG\_  
 TCA TAGGCAGAC T GC  
 ||| ||||| | ||  
 AGT GTCTGTCTG G CG  
 C GT T  
 GAM1269 LOC158584 5' ATTTGTAGATTTGCTTGGTGA 81959 \_ TGCT C  
 TCACTAGGCAGA CTG CAAA  
 ||||| ||| |||  
 AGTGGTTCGTTT GAT GTTT  
 A \_ AA  
 GAM1269 LOC158972 3' GTTTGGACTCTTGCCTGGTGG 86956 ACT G T  
 TCACTAGGCAG GT C CAAAC  
 ||||| || |||||  
 GGTGGTCCGTT CA G GTTTG  
 CT\_ \_  
 GAM1269 LOC199725 3' CACAGTTTGCCTGTTGA 89835 C  
 TCA TAGGCAGACTGTG  
 ||| |||||  
 AGT GTCCGTTTGACAC  
 T  
 GAM1269 LOC200301 3' GTTTGAGTTTTGCTGCTAGGTG 88751 A ACTGT  
 A TCACT GGCAG GCTCAAAC  
 |||| ||| |||||  
 AGTGG TCGTC TGAGTTTG  
 A GTTT\_  
 GAM1269 LOC204804 3' TTTGGTTTCTGCTTATGG 89492 C CTGT T  
 TCA TAGGCAGA GC CAAA  
 ||| ||||| || |||||  
 GGT ATTCGTCT TG GTTT  
 \_ T \_  
 GAM1269 LOC255463 5' TGCAGTTTGCTTGGTG 94885  
 CACTAGGCAGACTGTG  
 |||||  
 GTGGTTCGTTTGACGT  
 GAM1269 LOC257451 3' GCAGTTTCTTGGTGA 95556 C  
 TCACTAGG AGACTGT  
 ||||| |||||  
 AGTGGTTC TTTGACG  
 \_  
 GAM1269 LOC51619 3' TTATGATCTGCAGTCTTCCTGG 32018 C C\_ AAC  
 TGA TCACTAGG AGACTGTG TCA  
 ||||| ||||| |||  
 AGTGGTCC TCTGACGT AGT  
 T CT ATTG  
 GAM1269 LOC90288 3' TTTGAGTGCAGTGGTGTGA 62113 TAG AG TG  
 TCAC GC ACTG CTCAAA  
 ||| || |||||

		AGTG TG TGAC GAGTTT	
		___ G_ GT	
GAM1270 CRY1	3'	GAAATATGTTGTTTCTAA 14521	C
		TTAGGAACAACA ATTTT	
		AATCTTTGTTGT TAAAG	
		A	
GAM1270 EIF5A2	3'	TGCAAAAATAATTTGGTTCTAA 39857	A CAC
		TTAGGA CAA ATTTTGTGCA	
		AATCTT GTT TAAAAACGT	
		G TAA	
GAM1270 IL1RAP	3'	GTCAGAAGTGCTGCTCCTAA 56244	A ACA _
		TTAGGA CA CATTTTGT C	
		AATCCT GT GTGAAGAC G	
		C C_ T	
GAM1270 IL21R	3'	TGCAAGAAGTCCATATTGTTCC 41435	CACA_
T		AGGAACAA TTTTGTGCA	
		TCCTTGTT AAGAACGT	
		ATACCTG	
GAM1270 KIF3B	3'	GTTGAACGTGCTGTTCTAA 16611	A A TT
		TTAGGAACA CAC TTT GC	
		AATCCTTGT GTG AAG TG	
		C C T_	
GAM1270 PCM1	5'	TGCAAAAAGTAGTTTCTAA 20571	AACACA
		TTAGGAAC TTTTGTGCA	
		AATCTTTG AAAAACGT	
		ATC_	
GAM1270 POLA	3'	TGCAAAAATGTTGAGTCTAA 33740	AA AC
		TTAGG CA ACATTTTGTGCA	
		AATCT GT TGTAAAAACGT	
		GA _	
GAM1270 QDPR	3'	CAGAATGTTGTTCTAA 4357	CAT
		TTAGGAACAACA TTTTG	
		AATCCTTGTGT AAGAC	
		___	
GAM1270 RECK	3'	GTTAAAATGTGTTGTTCC 40871	T
		GGAACAACACATTTT GC	
		CCTTGTTGTGTAAAA TG	
		T	
GAM1270 VCL	3'	GCTGTGTGTTAGTTCC 12578	_ TTTT
		GGAAC AACACAT GC	

CCTTG TTGTGTG CG  
 A T\_\_\_\_  
 GAM1270 VCL 3' GCTGTGTGTTAGTTCC 25737 \_ TTTT  
 GGAAC AACACAT GC  
 ||||| ||||| ||  
 CCTTG TTGTGTG CG  
 A T\_\_\_\_  
 GAM1270 C20orf72 3' GTTGAAATGTGTTGTTACC 53499 \_ T  
 GG AACAACACATTTT GC  
 || ||||| ||||| ||  
 CC TTGTTGTGTAAAG TG  
 A T  
 GAM1270 CXorf1 3' GTTGCAAATAATTGTTCT 16304 CACATT  
 GGAACAA TTTGCAAC  
 ||||| |||||  
 TCTTGTT AAACGTTG  
 AAT\_\_\_\_  
 GAM1270 DAPK2 3' GCTGAGTGTGTCTCCCTAA 26740 AACA TT  
 TTAGG ACACATTT GC  
 ||||| ||||| ||  
 AATCC TGTGTGAG CG  
 CTC\_ T\_  
 GAM1270 EPN2 3' TGCACCCACTCATGCTGTTCCCT 30330 A CATTTT\_\_\_\_  
 GA TTAGGAACA CA TGCA  
 ||||| || ||||  
 AGTCCTTGT GT ACGT  
 C ACTCACCC  
 GAM1270 KIAA0830 3' TGCTGGCCTGTTCCCTAA 69705 ACA TTTTT  
 TTAGGAACA CA GCA  
 ||||| || ||||  
 AATCCTTGT GT CGT  
 CCG \_\_\_\_\_  
 GAM1270 KIAA1265 3' GTCATTTTATGTATGTTCCCTAA 70792 AC TTT\_ \_  
 TTAGGAACA ACAT TG C  
 ||||| |||| |||  
 AATCCTTGT TGTA AC G  
 A\_ TTTT T  
 GAM1270 MGC2452 5' GCCAAGCCTGTGTTGTCCC 50985 A TT \_  
 GG ACAACACA TTTG C  
 || ||||| |||||  
 CC TGTTGTGT GAAC G  
 C CC C  
 GAM1270 MGC2488 3' GCAATGGTTGTTCCCTAA 43870 A TTT  
 TTAGGAACAAC CAT TGC  
 ||||| |||| ||||  
 AATCCTTGTTG GTA ACG  
 \_ \_  
 GAM1270 MRPL11 3' TTGCAAAAAGCTGTGCC 32122 AACAA \_  
 GG CACA TTTTGTCAA  
 || ||||| |||||



		CC GTGT GAAAACGTT		
		C_____ C		
GAM1270	OSBPL8	3' TAGGAATATGTTGTTCT	40460	C
		GGAACAACA ATTTTGT		
		TCTTGTTGT TAAGGAT		
		A		
GAM1270	RBM11	3' TTGCATATTGTTTCCTAA	58584	CACATTTT
		TTAGGAACAA TGCAA		
		AATCCTTGTT ACGTT		
		AT_____		
GAM1270	LOC145773	3' CAGGAATGTGTTGCTCCT	77496	A
		AGGA CAACACATTTTGT		
		TCCT GTTGTGTAAGGAC		
		C		
GAM1270	LOC146243	3' GTTACAAAAATGGTGCACCCTA	83641	AACA A C
		TAGG AC CATTTTGT AAC		
		ATCC TG GTAAAAAC TTG		
		CACG _ A		
GAM1270	LOC147524	5' GCTAAATGTGTCATTCT	78374	CA TT
		GGAA ACACATTT GC		
		TCTT TGTGTAAA CG		
		AC T_		
GAM1270	LOC154813	3' GTTATATGATGCTGTTTCCTAA	81163	A _ TTTT
		TTAGGAACA CA CAT GC		
		AATCCTTGT GT GTA TG		
		C A TAT_		
GAM1270	LOC51320	3' TGCGTGTACTGTTTCTAA	33547	AC TTTT
		TTAGGAACA ACAT GCA		
		AATCTTTGT TGTG CGT		
		CA _____		
GAM1270	LOC90841	3' TTGCAATTTTCATGGTTCCTAA	64204	AACACATTT
		TTAGGAAC TTGCAA		
		AATCCTTG AACGTT		
		GTACTTT_		
GAM1270	LOC92293	3' TTGCAAAAATGCATTCATCC	68766	ACAACA
		GGA CATTTTGTCAA		
		CCT GTAAAAACGTT		
		ACTTAC		
GAM1271	CLCN5	5' TGAAATACCTAAGCTGCTCCAA	3595	_____
		TTGGAGCAG GTTTCA		

			AACCTCGTC	TAAAGT		
			GAATCCA			
GAM1271	FLRT2	5'	ATTGAAAAATGAGGTCTGC	25056	GT	CTC
			GCAG TTCATT CAAT			
			CGTC GAGTAA GTTA			
			TG AAA			
GAM1271	IL17	3'	TGGGGAAAATGAAACCCTCC	9333	CA	—
			GGAG GGTTCAT TCTCCA			
			CCTC CCAAAGTA AGGGGT			
			— AA			
GAM1271	NLGN1	5'	TGAAGATGCTGCTCCAA	30026	G	—
			TTGGAGCAG TTTCA			
			AACCTCGTC GAAGT			
			GTA			
GAM1271	POLG	3'	GTGATAAACCTGCTCCAA	10682		—
			TTGGAGCAGGTT TCAT			
			AACCTCGTCCAA AGTG			
			AT			
GAM1271	TPK1	3'	GGAGAACCTGTCCAA	42384	G	TTCAT
			TTGGA CAGGT TCTCC			
			AACCT GTCCA AGAGG			
			— ———			
GAM1271	C1orf8	5'	GAGAATGAAACCCTC	16832	CA	
			GAG GGTTTCATTCTC			
			CTC CCAAAGTAAGAG			
			—			
GAM1271	CLIC6	3'	TGGAGAACATGTTCCAA	82536	G	TTCAT
			TTGGAGCA GT TCTCCA			
			AACCTTGT CA AGAGGT			
			A ———			
GAM1271	CLIPR-59	3'	TGGAGAATTTCAATGCCCCGA	31374	A	GGTTTC
			TTGG GCA ATTCTCCA			
			AGCC CGT TAAGAGGT			
			C AACTT_			
GAM1271	DKFZP547L112	3'	TGGAGAACTCTTGCTCCA	66532		TTTCA
			TGGAGCAGG TTCTCCA			
			ACCTCGTTC AAGAGGT			
			TC_			
GAM1271	EPS8R3	5'	GGACCACCTGCTCCAA	55701		TTCATTC
			TTGGAGCAGGT TCC			

			AACCTCGTCCA	AGG	
			CC_____		
GAM1271	EPS8R3	5'	GGACCACCTGCTCCAA	57404	TTCATTC
			TTGGAGCAGGT	TCC	
			AACCTCGTCCA	AGG	
			CC_____		
GAM1271	FLJ20552	3'	AGAACAAAACCTGCTCCAA	35389	G CA
			TTGGAGCAG TTT TTCT		
			AACCTCGTC AAA AAGA		
			— AC		
GAM1271	FLJ22865	5'	TGGAGAAAACCTGCTCTAA	47071	GTTTCA
			TTGGAGCAG TTCTCCA		
			AATCTCGTC AAGAGGT		
			AA_____		
GAM1271	KIAA0372	5'	ATTGAAATTTGTTACCTACTCC	27663	C TT TTCTC
			AA TTGGAG AGGT CA CAAT		
			AACCTC TCCA GT GTTA		
			A TT TTAAA		
GAM1271	PRO0132	5'	ATGAAACCACTCCAA	26101	CA
			TTGGAG GGTTTCAT		
			AACCTC CCAAAGTA		
			A_		
GAM1271	TEX27	3'	AGAGTGGAACCCGCTGCAA	41658	G A
			TTG AGC GGTTTCATTCT		
			AAC TCG CCAAGGTGAGA		
			G C		
GAM1271	LOC149373	3'	ATTGGGGTGATGATACCCACCC	79312	AGCA T _
			CAA TTGG GGT TCATT CTCCAAT		
			AACC CCA AGTAG GGGGTTA		
			CCAC T T		
GAM1271	LOC152687	3'	TTGGAGAATATTGCTCC	80643	GTTTC
			GGAGCAG ATTCTCCAA		
			CCTCGTT TAAGAGGTT		
			A_____		
GAM1271	LOC51202	3'	ATTGGAGAATGAAACCTGCTCC	33017	
			AA TTGGAGCAGGTTTCATTCTCCAAT		
			AACCTCGTCCAAAGTAAGAGGTTA		
GAM1272	ABCC3	3'	AGAAGCTGCTACCCCTACATCA	39148	TA__ T GTG
			TGATGTAG AGC GT CT		

			ACTACATC TCG CG GA		
			CCCA T AA_		
GAM1272	NBS1	3'	GAGGCTGGCCTCTACATCA	69499	TAA T G
			TGATGTAG GCTG GT CTC		
			ACTACATC CGGT CG GAG		
			TC_ _ _		
GAM1272	PIP5K1A	3'	AGCACACAGCACACA	13054	A AA
			TGT GT GCTGTGTGCT		
			ACA CA CGACACACGA		
			_ _		
GAM1272	PLN	3'	TGCAGCTTGCCACATCA	10650	A
			TGATGT GTAAGCTGTG		
			ACTACA CGTTCGACGT		
			C		
GAM1272	RAG2	3'	AGCAAGATCTACTACATC	82200	AG_ GTG
			GATGTAGTA CT TGCT		
			CTACATCAT GA ACGA		
			CTA _		
GAM1272	TSN	3'	AGCACACACAAAATAAATCA	16103	G GTAAGC
			TGAT TA TGTGTGCT		
			ACTA AT ACACACGA		
			A AAAAC_		
GAM1272	ZNF236	3'	GGAGCACATGCAGACACACCA	23715	A A AA T
			TG TGT GT GC GTGTGCTCC		
			AC ACA CA CG TACACGAGG		
			C _ GA _		
GAM1272	BIKE	3'	GAAAACATGGGCTACTACATTA	34185	AG GC
			TGATGTAGTA CTGTGT TC		
			ATTACATCAT GGTACA AG		
			CG AA		
GAM1272	C11orf15	3'	AGCACACAGCTCAAAGTCA	40219	G TAGTA
			TGAT AGCTGTGTGCT		
			ACTG TCGACACACGA		
			AAAC_		
GAM1272	C17orf31	5'	GAGAACCTTCTACATCA	34124	T CTGT G
			TGATGTAG AAG GT CTC		
			ACTACATC TTC CA GAG		
			_ _ _ A		
GAM1272	DKFZP586D2223	3'	GAGCAGTTGCCTACCACAT	37682	A A TGTG
			ATGT GTA GC TGCTC		

TACA CAT CG ACGAG  
 C C TTG\_  
 GAM1272 FLJ11722 3' AGCAGGAATCCTACATCA 46388 TAAG GTG  
 TGATGTAG CT TGCT  
 ||||| || |||  
 ACTACATC GG ACGA  
 CTAA \_\_\_\_  
 GAM1272 GENX-3414 3' AGCACTTTTTACTACAT 14145 CTGT  
 ATGTAGTAAG GTGCT  
 ||||| |||  
 TACATCATTT CACGA  
 TT\_\_\_\_  
 GAM1272 JM11 3' GGAGCACACAGCTGAC 53265 A  
 GT AGCTGTGTGCTCC  
 || |||||  
 CA TCGACACACGAGG  
 G  
 GAM1272 KIAA0261 3' ACAGTTACTACATCA 68176 G  
 TGATGTAGTAA CTGT  
 ||||| |||  
 ACTACATCATT GACA  
 -  
 GAM1272 KIAA0416 3' AGCACACACACACACACA 31463 A A AAGC  
 TG TGT GT TGTGTGCT  
 || ||| || |||||  
 AC ACA CA ACACACGA  
 - \_ CAC\_  
 GAM1272 KIAA1635 3' AGCACAAGTAAATTATACATCA 67859 GTAA\_\_ G  
 TGATGTA GCT TGTGCT  
 ||||| || |||||  
 ACTACAT TGA ACACGA  
 ATTAAA \_  
 GAM1272 KIAA1644 3' CACACAAGTACATACATGCA 85025 \_ \_ AGC  
 TG ATGTA GTA TGTGTG  
 || |||| || |||||  
 AC TACAT CAT ACACAC  
 G A GA\_  
 GAM1272 LHFP 3' AGCACACAAGCACATACA 19334 GTAA \_  
 TGTA GCT GTGTGCT  
 ||| || |||||  
 ACAT CGA CACACGA  
 ACA\_ A  
 GAM1272 MGC5601 5' ATCCAACCTTACTACATCA 47505 C TG  
 TGATGTAGTAAG TG T  
 ||||| ||| ||  
 ACTACATCATTC AC A  
 A CT  
 GAM1272 PRO0611 5' ACCAGCTTATTACACCA 26005 A T  
 TG TGTAAGTAAGCTG GT  
 || ||||| ||

AC ACATTATTCGAC CA  
 C \_  
 GAM1272 SFXN2 3' GAGCACACAGGCACACAT 73945 A AAG  
 ATGT GT CTGTGTGCTC  
 ||| || |||||  
 TACA CA GACACACGAG  
 \_ CG\_  
 GAM1272 SYNPO2 3' GAGCACACAATTATTAGCATCA 71894 \_ GC  
 TGATGT AGTAA TGTGTGCTC  
 ||||| |||| |||||  
 ACTACG TTATT ACACACGAG  
 A A\_  
 GAM1272 LOC138654 5' GAGCCTCATTCTGACTACATCA 75948 A CT T\_  
 TGATGTAGT AG GTG GCTC  
 ||||| || ||| |||  
 ACTACATCA TC TAC CGAG  
 G T\_ TC  
 GAM1272 LOC145815 5' AGAACACAAACTACATC 83516 AAGC G  
 GATGTAGT TGTGT CT  
 ||||| |||| ||  
 CTACATCA ACACA GA  
 A \_ A  
 GAM1272 LOC145980 5' CACACAGCTCCATTTCAT 83599 T A\_  
 ATG AGT AGCTGTGTG  
 ||| || |||||  
 TAC TTA TCGACACAC  
 T CC  
 GAM1272 LOC151568 5' GGGAGCACGGGCTTCTACACC 56702 A TAA G  
 A TG TGTAG GCT TGTGCTCCC  
 || |||| || |||||  
 AC ACATC CGG GCACGAGGG  
 C TTC \_  
 GAM1272 LOC200953 5' AGCACACAGTGGACACG 90205 A AA  
 TGT GT GCTGTGTGCT  
 ||| || |||||  
 GCA CA TGACACACGA  
 \_ GG  
 GAM1272 LOC90139 3' GGAACACACAGAGGTGCACATC 55403 A AG\_ C  
 A TGATGT GTA CTGTGTG TCC  
 ||||| || ||||| |||  
 ACTACA CGT GACACAC AGG  
 \_ GGA A  
 GAM1273 ABCF1 3' ATTCAGGCACATGAAGGTGGAG 6566 C\_ AT  
 TG CATTTCACTTTCA TGTCTGAG  
 ||||| |||||  
 GTGAGGTGGAAGT ACGGACTT  
 AC A  
 GAM1273 ACVRL1 5' GCGGTGGAGGGGAGGTG 3418 A  
 CATTTT CTTTCACTGT  
 ||||| |||||

		GTGGAG GGAGGTGGCG		
		G		
GAM1273 ADRA1A	3'	TCTTGATGGAAGTGAGG 5448	CTG	T
		TTTCACTTTCA TC GAGA		
		GGAGTGAAGGT AG TTCT		
		— —		
GAM1273 AGT	3'	ATTTTAGAGAATGGGGGTGGGG 3453	TT	TT CTG
		T CACT CA TCTGAGAT		
		G GTGG GT AGATTTTA		
		GG GG AAG		
GAM1273 AIM1	3'	ATCTCAGGCTGGAGTGCAGTG 91816	T	CACT
		CATT CACTTT GTCTGAGAT		
		GTGA GTGAGG CGGACTCTA		
		C T—		
GAM1273 AKAP13	3'	GTTTTGGGCATGGATAAAGTGA 22144	—	C TG
AG		TTTCACT TTCA TGTC AGAT		
		GAAGTGA AGGT ACGG TTTG		
		AAT _ GT		
GAM1273 AKAP13	3'	GTTTTGGGCATGGATAAAGTGA 23248	—	C TG
AG		TTTCACT TTCA TGTC AGAT		
		GAAGTGA AGGT ACGG TTTG		
		AAT _ GT		
GAM1273 AKAP13	3'	GTTTTGGGCATGGATAAAGTGA 58580	—	C TG
AG		TTTCACT TTCA TGTC AGAT		
		GAAGTGA AGGT ACGG TTTG		
		AAT _ GT		
GAM1273 ATP11B	3'	ATTCAGGTGTGGCTGTGGAAT 80315	TT	TGT
G		CATTTAC TCAC CTGAGAT		
		GTAAGGTG GGTG GACTTTA		
		TC TG_		
GAM1273 B4GALT4	3'	TAGCAGGAGGGTGGAGTG 13674	A	T
		CATTTCACTTTC CTG CTG		
		GTGAGGTGGGAG GAC GAT		
		— —		
GAM1273 BLAME	3'	ATCTGGGAGTGAGGGTGGAG 39239	TG	G
		TTTCACTTTCAC TCT AGAT		
		GAGGTGGGAGTG AGG TCTA		
		— G		
GAM1273 C20orf1	5'	ATTCAGAAAAGGGGTGAAA 23999	CACTG	
		TTTCACTTT TCTGAGAT		

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AAAGTGGGG AGACTTTA
AAA__
GAM1273 C21orf5 3' TTTCAGGCTAGGTGCGGTG 17614 TT __
      CACT CACT GTCTGAGA
      ||| ||| |||||
      GTGG GTGG CGGACTTT
      C_ AT
GAM1273 CAPN10 3' GTCTCAGAACCGAGTGAGGTG 43604 TCACTG
      CATTTCACTT TCTGAGAT
      ||||| |||||
      GTGGAGTGAG AGACTCTG
      CCA__
GAM1273 CARPX 3' ATTCAGATAGTGCCTAGGA 39415 A TT__
      TC CT CACTGTCTGAGAT
      || || |||||
      AG GA GTGATAGACTTTA
      _ TCCT
GAM1273 CARPX 5' TCGGGTGGGAGTGCGAGTG 39426 _ TT TGT
      CATTT CACT CAC CTGA
      |||| ||| ||| |||
      GTGAG GTGA GTG GGCT
      C GG __
GAM1273 CASP10 3' TTTTGGACTGGGTGCGGTG 52111 TT __ TG
      CACT CACT GTC AGA
      ||| ||| ||| |||
      GTGG GTGG CAG TTT
      C_ GT GT
GAM1273 CASP10 3' TTTTGGACTGGGTGCGGTG 52127 TT __ TG
      CACT CACT GTC AGA
      ||| ||| ||| |||
      GTGG GTGG CAG TTT
      C_ GT GT
GAM1273 CCND1 3' GTGGTGGCAGTGAGGTGGGGT 53891 TT TGAGAT
      G CAT CACTTTCACTGTC
      ||| |||||
      GTG GTGGAGGTGACGG
      GG TGGTG
GAM1273 CDK4 5' GTCACATGGTGAGGGTGGGG 53763 TT C GAT
      T CACTTTCACTGT TGA
      | ||||| |||
      G GTGGGAGTGGTA ACT
      GG C G
GAM1273 CDK4 5' GTCACATGGTGAGGGTGGGG 3573 TT C GAT
      T CACTTTCACTGT TGA
      | ||||| |||
      G GTGGGAGTGGTA ACT
      GG C G
GAM1273 CDKN2A 5' GTCCGGGTGGGAGTGGGGGTGG 54229 TT TT G__ A
      GGTG T CACT CACT TCTG GAT
      | ||| ||| ||| |||

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G GTGG GTGA GGGC CTG  
 GG GG GGGT \_  
 GAM1273 CDKN2A 5' TATCTTGGAGGTCCGGGTGGGA 54230 TT G\_\_\_\_\_ TG  
 GTGGGG ACT CACT TC AGAT A  
 ||| ||| || ||| |  
 TGA GTGG AG TCTA T  
 GG GCCTGG GT  
 GAM1273 CDKN2B 3' AGGTGGTGGAGTGGAGTG 54353 T TG  
 CATTTCACTT CAC TCT  
 ||||| ||| |||  
 GTGAGGTGAG GTG GGA  
 \_ GT  
 GAM1273 CERD4 3' ATCTCAGAGCAGAGGAGGTGGG 23849 TT A \_  
 G T CACTTC CTG TCTGAGAT  
 | ||||| ||| |||||  
 G GTGGAGG GAC AGACTCTA  
 GG A G  
 GAM1273 CHRM1 3' TTTTCCTGGGAGTGGGAGTCAA 94794 C TT G T\_ T  
 GTG CATTT ACT CACT TC GAGA  
 ||||| ||| ||| ||| |||  
 GTGAA TGA GTGA GG CTTT  
 C GG G TC TA  
 GAM1273 CLASP1 3' GGGGGTGGGGTGGGGTG 65305 TT T G  
 CAT CACTT CACT TC  
 ||| ||||| ||| |||  
 GTG GTGGG GTGG GG  
 GG \_ G  
 GAM1273 CMAR 5' ATTTTGGACGGTGCTCTGA 17772 CTTT TG  
 TCA CACTGTC AGAT  
 ||| ||||| |||  
 AGT GTGGCAG TTTA  
 CTC\_ GT  
 GAM1273 COL1A1 3' ATCTATGTGATGGGTGGGGTG 3601 TT \_ TGTCTG  
 CAT CACTT TCAC AGAT  
 ||| ||||| ||| |||  
 GTG GTGGG AGTG TCTA  
 GG T TA\_\_\_\_  
 GAM1273 COL4A4 5' CAGGCGGGGAAGTGGGGTG 3626 TT A  
 CAT CACTTTC CTGTCTG  
 ||| ||||| |||||  
 GTG GTGAAGG GGCGGAC  
 GG \_  
 GAM1273 COL4A6 3' GTCTTAGGCAGGCAAGAGAATT 8473 \_\_\_\_ CA\_  
 GAAATG TCA CTTT CTGTCTGAGAT  
 ||| ||| ||||| |||||  
 AGT GAGA GACGGATTCTG  
 TAA ACG  
 GAM1273 CPT1B 3' GCCCAGGTGGTGGAGGTGGGGT 15199 TT TG AGAT  
 AT CACTTTCAC TCTG  
 || ||||| |||

			TG GTGGAGGTG GGAC		
			GG GT CCG		
GAM1273 D10S170	3'	GTTTTGTACTTTGGTAGTGAAG 18367		T	CT CT
	TG	CATTTCACT TCA GT GAGAT			
		GTGAAGTGA GGT CA TTTTG			
		T TT TG			
GAM1273 DDEF2	3'	ATTTTAGGCGGCCAGTGAAGTGA 13952	T		TTCA
		CA TTCACCT CTGTCTGAGAT			
		GT AAGTGA GGCGGATTTTA			
		C CC__			
GAM1273 DES	3'	TCTCAGGCTGGTGGGAG 72132	TT		_
		CT CACT GTCTGAGA			
		GA GTGG CGGACTCT			
		GG T			
GAM1273 DLEC1	3'	TAGAGAGAGTGAGGTG 23706		A	
		CATTTCACTTTC CTG			
		GTGGAGTGAGAG GAT			
		A			
GAM1273 DPYSL3	3'	ATCTCAGCTTATATGAAAGTCA 7311	C	C	__
	AGTG	TTT ACTTTCA TGT CTGAGAT			
		GAA TGAAAGT ATA GACTCTA			
		C _ TTC			
GAM1273 DRIL1	3'	GTTTTGGACATTCAGAGAGATG 17831	A	TTCAC	TG
		CATTTTC CT TGTC AGAT			
		GTAGAG GA ACAG TTTG			
		A CTT__ GT			
GAM1273 DXS1283E	3'	GTTTTAGATAGTTTTTGTATGGA 70836		CTTTC_	
	A	TTTCA ACTGTCTGAGAT			
		AAGGT TGATAGATTTTG			
		AGTTTT			
GAM1273 EHF	3'	GTCTCAGATGGTTAGGACAAAG 24063		__	__
	TGGA	CACTT TC ACTGTCTGAGAT			
		GTGAA AG TGGTAGACTCTG			
		AC GAT			
GAM1273 EIF2B1	5'	CTGCGGAAGTGGAGTG 59658	T	G	_
		CACTT CACT TCTG AG			
		GTGAG GTGA AGGC TC			
		_ _ G			
GAM1273 EPHA1	3'	GTTTTAAAAGGGAGGTGGGG 17861	TT	A	GTC
		T CACTTTC CT TGAGAT			

			G GTGGAGG GA ATTTTG		
			GG _ AA_		
GAM1273	ESRRA	3'	ATCTCAGGGAGGGAAGGGGATG 15479	TT A	A G
			CAT C CTTTC CT TCTGAGAT		
			GTA G GAAGG GA GGA CTCTA		
			GG _ _ G		
GAM1273	FCAR	3'	GCACTGAGAGTGAAGTG 55798	C	
			CATTTCACTTTCA TGT		
			GTGAAGTGAGAGT ACG		
			C		
GAM1273	FCAR	3'	GCACTGAGAGTGAAGTG 55814	C	
			CATTTCACTTTCA TGT		
			GTGAAGTGAGAGT ACG		
			C		
GAM1273	FGF2	3'	GTCTCAGATACTTGGGAGGCTG 8873	_	AC__
			AGGTG TTCA CTTTC TGTCTGAGAT		
			GAGT GGAGG ATAGACTCTG		
			C GTTC		
GAM1273	FRAT2	3'	GGCTGGTGAAGGTGGGA 23881	TT	_
			T CACTTTCACT GTC		
			A GTGGAAGTGG CGG		
			GG T		
GAM1273	GCKR	3'	ATTCAGAAATAAAATGAAATG 7635	C	CACTG
			CATTTCA TTT TCTGAGAT		
			GTAAAGT AAA AGACTTTA		
			A TAA__		
GAM1273	GNPI	3'	GTCTTAGGCCTTCATGGAGTGG 18448	CACT__	
	A		TTCAC TTT GTCTGAGAT		
			AGGTGAGG CGGATTCTG		
			TACTTC		
GAM1273	GPR61	3'	TGGGCTGGTGGGAGTGGGAT 78914	TT TT	_
			AT CACT CACT GTCTG		
			TA GTGA GTGG CGGGT		
			GG GG T		
GAM1273	GUCY1B3	3'	ATCTTGATTATGGGGTGAAG 5963	T CT	TG
			TTTCACTT CA GTC AGAT		
			GAAGTGGG GT TAG TCTA		
			_ AT GT		
GAM1273	GYG2	3'	ATTCAGGTGAGTCAGGGTTGG 14047	TC	C _ GT
	ATG		CATT ACTTT AC T CTGAGAT		

		GTAG TGGGA TG G GACTTTA		
		GT C A TG		
GAM1273 HHEX	3'	ATTCAGGCAGCCTTGGAGT 10784	CA__	
		ACTTT CTGTCTGAGAT		
		TGAGG GACGGACTTTA		
		TTCC		
GAM1273 HMGA2	3'	TCTGGGGTGGGGTGGGGTG 13004	TT TTCA TG G	
		CAT CACT C TCT AGA		
		GTG GTGG G GGG TCT		
		GG ____ GT G		
GAM1273 HOXD4	5'	TTTTGGGGTACTAGGGAGTGAG 27534	TT AC_ GT G T	
GT		ATTTCACT C T CT AGA		
		TGGAGTGA G A GG TTT		
		GG ATC TG G TG		
GAM1273 HPCAL1	3'	TTATGTATGGTGAAGTGGAGTG 9272	T CTGAGAT	
		CATTTCACTT CACTGT		
		GTGAGGTGAA GTGGTA		
		_ TGTATTA		
GAM1273 HPCAL1	5'	GTGGTGACAGGTGAAATG 56190	_ TG	
		CATTTCACTT TCAC T		
		GTAAAGTGGA AGTG G		
		C GT		
GAM1273 HPCAL1	3'	TTATGTATGGTGAAGTGGAGTG 56191	T CTGAGAT	
		CATTTCACTT CACTGT		
		GTGAGGTGAA GTGGTA		
		_ TGTATTA		
GAM1273 IGF1R	3'	TTCTCTCAGTGAAGGTGGGG 6049	TT TCT T	
		T CACTTTCACTG GAGA		
		G GTGGAAGTGAC CTCT		
		GG T__ TT		
GAM1273 IL11	3'	ATTCAGGAGCAGGGGTGGGA 5324	TT CA G	
		T CACTTT CT TCTGAGAT		
		A GTGGGG GA GGA CTTTA		
		GG AC _		
GAM1273 IL13RA1	3'	TTAGGGGCAGTGGAGGTAGAAT 7782	TC GAGAT	
G		CATT ACTTTCACTGTCT		
		GTAA TGGAGGTGACGGG		
		GA GATTG		
GAM1273 IL1F5	3'	ATTTCTGTGGGGGTGGGGTG 24377	TT TT TGTCT	
		CAT CACT CAC GAGAT		

		GTG GTGG GTG CTTTA	
		GG GG T_____	
GAM1273 IL1RN	3'	GATGGTGAAAGTAAGTG 5143	C
		CATTT ACTTTCACTGTC	
		GTGAA TGAAAGTGGTAG	
		—	
GAM1273 IL24	3'	TTGGGGTGGGGGTAAGGTG 22447	C TT GT TG
		CATTT ACT CACT C A	
		GTGGA TGG GTGG G T	
		A GG _GT	
GAM1273 IRS1	3'	ATCTTTTTTTTGGATGTGGGAT 18662	TT T CTGTCT
G		CAT CAC TTCA GAGAT	
		GTA GTG AGGT TTCTA	
		GG T TTTT_	
GAM1273 IRS2	3'	TCTCAATGGAAGTGAAAT 59723	CTGTC
		ATTTCACTTTCA TGAGA	
		TAAAGTGAAGGT ACTCT	
		A_____	
GAM1273 JTB	3'	CTATCTCAGACAGTGAAAGTGA 21961	
AATG		CATTTCACTTTCACTGTCTGAGAT	
		GTAAAGTGAAAGTGACAGACTCTA	
		TCC	
GAM1273 KCNA7	3'	TCTCAGAGCAGGGGAGTG 49061	TT A _
		CACT C CTG TCTGAGA	
		GTGA G GAC AGACTCT	
		GG _ G	
GAM1273 KCNK6	3'	ATGGAGGAGGTGAGGTG 16690	A
		CATTTCACTTTC CTGT	
		GTGGAGTGGAGG GGTA	
		A	
GAM1273 KCNK6	3'	TTTCAGGCTGAGTGTGGTG 16699	TT _
		CACT CACT GTCTGAGA	
		GTGG GTGA CGGACTTT	
		T_ GT	
GAM1273 LAMC1	3'	GTCTCAGGCCACAATGGGGTG 9677	TT CTTTCACT
		CAT CA GTCTGAGAT	
		GTG GT CGGACTCTG	
		GG AACAC_____	
GAM1273 MALT1	3'	ATTTTAGATGCCTGTGAAAT 22291	TTTCACT
		ATTTCAC GTCTGAGAT	

			TAAAGTG TAGATTTTA		
			TCCG__		
GAM1273	MAPK14	3'	TCCTCCATGGTGGGAAGGGGGTG 7161	TT A	CT AT
			CAT C CTTTCACTGT GAG		
			GTG G GAAGGTGGTA CTC		
			GG_ C_ CTT		
GAM1273	MAPK14	3'	TCCTCCATGGTGGGAAGGGGGTG 57335	TT A	CT AT
			CAT C CTTTCACTGT GAG		
			GTG G GAAGGTGGTA CTC		
			GG_ C_ CTT		
GAM1273	MAPK14	3'	TCCTCCATGGTGGGAAGGGGGTG 57346	TT A	CT AT
			CAT C CTTTCACTGT GAG		
			GTG G GAAGGTGGTA CTC		
			GG_ C_ CTT		
GAM1273	MAPRE1	3'	ATTTTTTGGGGAAGTGAGGTG 24661	A	GTCT
			CATTTCACTTTC CT GAGAT		
			GTGGAGTGAAGG GG TTTTA		
			_ TT_		
GAM1273	MBP	5'	TTTTGGAAGGTGGAGTG 89783	T	G TG
			CACTT CACT TC AGA		
			GTGAG GTGG AG TTT		
			_ A GT		
GAM1273	MGAT5	5'	TGCCTCATGGTGGGAGTGAAA 10030	TT	TC AT
			TTTCACT CACTG TGAG		
			AAAGTGA GTGGT ACTC		
			GG _ CGTT		
GAM1273	MGEA5	3'	GTTTCAGAAGTGTGAGGGTGGA 24218	_	G
	GTG		ATTTCACTTT CACT TCTGAGAT		
			TGAGGTGGGA GTGA AGACTTTG		
			CT _		
GAM1273	MMP19	3'	TCAATGGTGGAGGGAGATG 10086	A	C
			CATTTC CTTTCACTGT TGA		
			GTAGAG GGAGGTGGTA ACT		
			_ _		
GAM1273	MMP19	3'	TCAATGGTGGAGGGAGATG 42975	A	C
			CATTTC CTTTCACTGT TGA		
			GTAGAG GGAGGTGGTA ACT		
			_ _		
GAM1273	MMP19	3'	TCAATGGTGGAGGGAGATG 42981	A	C
			CATTTC CTTTCACTGT TGA		

GTAGAG GGAGGTGGTA ACT

GAM1273 MMP19 3' TCAATGGTGGAGGGAGATG 42985 A C  
CATTTC CTTTCACTGT TGA  
||||| ||||||| |||  
GTAGAG GGAGGTGGTA ACT

GAM1273 MOG 3' TCTTGGCAGGGGTGGAG 10107 TCA T TG  
TTTCACTT CTG C AGA  
|||||| ||| |||  
GAGGTGGG GAC G TCT

GAM1273 MPP4 5' TATCGGGAGCAGTGAGGTG 52347 T \_ GAT  
CACTT CACTGT CTGA  
||||| ||||| |||  
GTGGA GTGACG GGCT

GAM1273 MS4A1 3' ATTTTGGGGAGACAAAGGGAAA 3748 A CA G TG  
TG CATTTC CTTT CT TC AGAT  
||||| |||| || || |||||  
GTAAAG GAAA GA GG TTTA  
G CA G GT

GAM1273 MTNR1A 3' ACAATGAAAGTGGGGTG 19887 TT C  
CAT CACTTTCA TGT  
||| ||||||| |||  
GTG GTGAAAGT ACA  
GG A

GAM1273 MYOZ1 5' ATCTCAGGCTCTAGGTGCAATG 41149 T TCACT  
CATT CACTT GTCTGAGAT  
||||| ||||| |||||||  
GTAA GTGGA CGGACTCTA  
C TCT\_

GAM1273 NAV2 3' TTTCATTAGGGGTGGGGTG 60162 TT TCA TC  
CAT CACTT CTG TGAGA  
||| ||||| ||| |||||  
GTG GTGGG GAT ACTTT  
GG \_ T\_

GAM1273 NDST2 3' ATCTTGGGAGGTGGGGAGGAAT 13296 AC TT GT TG  
G CATTTC T CACT C AGAT  
||||| | |||| | |||||  
GTAAGG G GTGG G TCTA  
A\_ GG AG GT

GAM1273 NEBL 3' TTTTGTGGTAGGGAAGTGGGA 21126 TT A GT \_ T  
TG CAT CACTTTC CT C TGAGA  
||| ||||||| || | |||||  
GTA GTGAAGG GA G GTTTT  
GG \_ TG T TA

GAM1273 NEU1 3' GTCTTGGGCAGGTCTAGTGAGC 4742 T TTCA TG  
TG CA TTCACT CTGTC AGAT  
|| ||||| ||||| |||||

GT GAGTGA GACGG TCTG  
 C TCTG GT  
 GAM1273 NEUROD2 3' ATTTTGGCGGGAGGGGAAGTG 20478 A A T TG  
 CATTTC CTTTC CTG C AGAT  
 ||||| ||||| ||| | ||||  
 GTGAAG GGGAG GGC G TTTA  
 \_ \_ \_ GT  
 GAM1273 NFE2L1 3' TGTCTGCCCCAGACAAGTGGGA 12177 TT \_ \_\_\_\_  
 GTGAAATG ACT CACT GTCTG AGAT G  
 ||| ||||| |||| |  
 TGA GTGA CAGAC TCTG T  
 GG A CCCG  
 GAM1273 NFRKB 5' GTCTTAAGGGAAGTGAAAGAGG 20497 A G\_ \_  
 AGTG ATTTTC CTTTCACT TCT GAGAT  
 ||||| ||||| ||| |||||  
 TGAGG GAAAGTGA GGA TTCTG  
 A AG A  
 GAM1273 NGB 3' GTTTTGGTGGCAGAGGTGGGAT 41188 TT CA T TG  
 G CAT CACTTT CTG C AGAT  
 ||| ||||| ||| | ||||  
 GTA GTGGAG GGT G TTG  
 GG AC \_ GT  
 GAM1273 NLGN1 3' CCTTTTGGTAAGGTGAAGTG 30024 C GTCT AT  
 CATTTCACTTT ACT GAG  
 ||||| ||||| ||| |||  
 GTGAAGTGGAA TGG TTC  
 \_ TT\_ CT  
 GAM1273 NPC2 3' GTCTTAGGTGGTTTCATTAAAT 21223 CACTTTC TG  
 G CATTT AC TCTGAGAT  
 |||| | |||||  
 GTAAA TG GGATTCTG  
 TTACTT\_ GT  
 GAM1273 OCRL 3' GTTTCTTGGTGGGGGTGGGG 4264 TT TT GTCT  
 T CACT CACT GAGAT  
 | |||| |||| ||||  
 G GTGG GTGG CTTTG  
 GG GG TT\_  
 GAM1273 OCRL 3' GTTTCTTGGTGGGGGTGGGG 7830 TT TT GTCT  
 T CACT CACT GAGAT  
 | |||| |||| ||||  
 G GTGG GTGG CTTTG  
 GG GG TT\_  
 GAM1273 PER2 3' TTTTGTATGGAGGTGAAAT 43051 CTG T  
 ATTTCACTTTCA TC GAGA  
 ||||| ||||| ||| |||  
 TAAAGTGGAGGT AG TTTT  
 \_ T  
 GAM1273 PGAM1 3' TTTCATGGCAGTGAAA 76276 \_  
 TTTCAGTCTC TGAGA  
 ||||| |||||



AAAGTGACGG ACTTT  
 T  
 GAM1273 PIGN 5' GTCTCAGTCCTGTGCAAAGTGA 24672 \_ TGT\_  
 GATG ATTTCACTTT CAC CTGAGAT  
 ||||| ||| |||||  
 TAGAGTGAAA GTG GACTCTG  
 C TCCT  
 GAM1273 PKP4 3' GAAATGTGAAAGTGAAGTG 13266 TG\_  
 CATTTCACTTTTCA C TC  
 ||||| ||  
 GTGAAGTGAAAGTG AG  
 TAA  
 GAM1273 PRDM2 3' GTCTCGGAGAAACGGGTGAGCT 24250 T TCACTG  
 G CA TTCACTT TCTGAGAT  
 || ||||| |||||  
 GT GAGTGGG AGGCTCTG  
 C CAAAG\_  
 GAM1273 PSEN1 5' ATAGTGAGGCTGGGATG 23621 TT \_  
 CAT CA CTTTCACTGT  
 ||| || |||||  
 GTA GT GGAGGTGATA  
 GG C  
 GAM1273 RALB 3' GTTTTGGAGGAGGGAGTGGAGT 11245 TT A G TG  
 ATTTCACT C CT TC AGAT  
 ||||| | || ||||  
 TGAGGTGA G GG AG TTTG  
 GG A \_ GT  
 GAM1273 RAMP3 3' CGGTGAGATGGAGTG 19589 C  
 CATTTCA TTTCACTG  
 ||||| |||||  
 GTGAGGT AGAGTGGC  
 -  
 GAM1273 RANBP7 3' ATTTTGGGGGTGGGGGGGA 21113 A TT G TG  
 TTC CT CACT TC AGAT  
 ||| || |||| || ||||  
 AGG GG GTGG GG TTTA  
 \_ GG \_ GT  
 GAM1273 RGS19IP1 3' GATGGTGAGGGGAGGTG 62509 A  
 CATTT CTTTCACTGTC  
 ||||| |||||  
 GTGGAG GGGAGTGGTAG  
 -  
 GAM1273 RNASE1 3' ATTTTGGGGGTGAAGAGTGGGT 63875 T \_ G TG  
 TG CA TTCACTTT CACT TC AGAT  
 || ||||| |||| || ||||  
 GT GGGTGAGA GTGG GG TTTA  
 T A \_ GT  
 GAM1273 RNGTT 3' ATTTTGGACATTGTGAAGGAAA 13729 A T \_ TG  
 TG CATTT CTT CAC TGTC AGAT  
 ||||| ||| ||| |||| ||||

			GTAAAG GAA GTG ACAG TTTA		
			— — TT GT		
GAM1273	RXRB	3'	CAGTGGTGGAGGTGGG 41758	T	
			TTCAC TTTCACTG CTG		
			GGGTGGAGGTGGT GAC		
			—		
GAM1273	SEDL	3'	ATTCTGCAGTTGGGAGTGAAAT 27322	TT _ CT AT	
	G		CATTTCACT CA CTGT GAG		
			GTAAAGTGA GT GACG CTT		
			GG T T_ A		
GAM1273	SH3BP4	3'	CAGTAGAGTGAGGTG 27232	C	
			CATTTCACTTT ACTG		
			GTGGAGTGAGA TGAC		
			—		
GAM1273	SIGLEC6	3'	ATTTTAAGACTGAAAGTGAAAT 59926	CT _	
			ATTTCACTTTCA GTCT GAGAT		
			TAAAGTGAAAGT CAGA TTTTA		
			_ A		
GAM1273	SLC17A2	5'	TTTAATGGTGAAGGTAAGTG 19546	C C	
			CATTT ACTTTCACTGT TGAG		
			GTGAA TGGAAGTGGTA ATTT		
			— —		
GAM1273	SLC19A1	5'	GTCTCGGGGCCCTGGGGTGAG 11758	T CT _	
			TTCAC TT CA GTCT GAGAT		
			GAGTGGG GT CGGG CTCTG		
			_ CC G		
GAM1273	SLC38A2	3'	TCTCGGGTTAAGGGAAGTG 38593	A G_	
			CAC TTTC CT TCTGAGA		
			GTGAAGG GA GGGCTCT		
			_ ATT		
GAM1273	SLC6A4	3'	TTTTGGACGTGTGAGGATG 6452	CT _ TG	
			CA TTCAC TGTC AGA		
			GT GAGTG GCAG TTT		
			AG T GT		
GAM1273	SLC7A8	3'	GTCTTGGGGCAGGGTGAAA 24282	TTCA _ TG	
			TTTCACT CTGT C AGAT		
			AAAGTGG GACG G TCTG		
			_ G GT		
GAM1273	SMARCB1	3'	TCGGGTGGGGGTGGAGTG 65586	TT TGT	
			CATTTCACT CAC CTGA		

		GTGAGGTGG GTG GGCT		
		GG ____		
GAM1273 SNCA	3'	TTAATTATTGAAAGTGGGGTG 4433	TT	C TC
		CAT CACTTTCA TG TGA		
		GTG GTGAAAGT AT ATT		
		GG T TA		
GAM1273 SRRM2	3'	TTTGGGGTGGGAGGGAATG 32918	A TT	GT TG
		CATTTC CT CACT C AG		
		GTAAGG GA GTGG G TT		
		_ GG _ GT		
GAM1273 SSPN	3'	GTCTTAGAAGAAAGTGGAAT 17445	ACTG	
		ATTTCACTTTC TCTGAGAT		
		TAAGGTGAAAG AGATTCTG		
		A__		
GAM1273 STAR	3'	ATCTCCATCTGGTGACAGTGGG 4443	TT T	GTCT_
	ATG	CAT CACT TCACT GAGAT		
		GTA GTGA AGTGG CTCTA		
		GG C TCTAC		
GAM1273 T	3'	GTCTCAGGTTAAGAAGGAAATG 12077	A	CACTG
		CATTTC CTTT TCTGAGAT		
		GTAAAG GAAG GGA CTCTG		
		_ AATT_		
GAM1273 TAF1C	3'	TGGTGAGGGTGGAGTG 19060		
		CATTTCAC TTTCACTG		
		GTGAGGTGGGAGTGGT		
GAM1273 TIMP3	3'	GTTTTAGTGTCAAAAGTGAGAT 4517	CACTGT	
	G	CATTTCAC TTT CTGAGAT		
		GTAGAGTGAAA GATTTTG		
		ACTGT_		
GAM1273 TMOD4	5'	TACCACACAGTGGGAGGGGGTG 25331	TT A TT	C AGAT
		CAT C CT CACTGT TG		
		GTG G GA GTGACA AC		
		GG_ GG C CATG		
GAM1273 TNFRSF4	3'	ATCTTGGCCAGGGTGGAGTG 12451	TTCA	T TG
		CATTTCAC T CTG C AGAT		
		GTGAGGTGG GAC G TCTA		
		__ C GT		
GAM1273 TRH	3'	CAGCCAGTGAGGGTGGGGTG 23051	TT	T
		CAT CACTTTCAC T G CTG		

		GTG GTGGGAGTGAC GAC		
		GG C		
GAM1273 TRHDE	3'	TTTTGGGCAATGTGAGAG 25393	___	TG
		CTTTCAC TGTC AGA		
		GAGAGTG ACGG TTT		
		TA GT		
GAM1273 TRIM9	3'	GTTTCAAATGGGTGGTGGGGTG 53761	TT	TTCA C
		CAT CACT CTGT TGAGAT		
		GTG GTGG GGTA ACTTTG		
		GG TG__ A		
GAM1273 TSG	3'	ATTCCTACTGTGAGTGGAGTG 40231	TT	T CT
		CATTCAC TCAC GT GAGAT		
		GTGAGGTG AGTG CA CTTTA		
		__ T TC		
GAM1273 TSLP	5'	TTTAGTGTGAACTGGGGTG 52310	TT C	TGT
		CAT CA TTTTAC CTGAG		
		GTG GT AAAGTG GATTT		
		GG C T__		
GAM1273 VDAC1	3'	TTTGGGGTGGAGAAGGTGGA 12583	A TG	G T
		TTCAC TTTC C TCT AGA		
		AGGTGGAAG G GGG TTT		
		A GT G T		
GAM1273 VDR	3'	TCTTTGTGAGAGTGAGCTG 4571	T	TGTCT
		CA TTCAC TTTCAC GAGA		
		GT GAGTGAGAGTG TTCT		
		C T__		
GAM1273 WNT10B	3'	GGGTGGTGGGGGTCAGGTG 12675	C TT	TG
		CATTT ACT CAC TCT		
		GTGGA TGG GTG GGG		
		C GG GT		
GAM1273 ZNF239	5'	GTCAGGATAATGGTGGGAATGG 19042	TT C TT	___ GAT
		GGTG CAT CACTGT CTGA		
		GT A GTGGTA GACT		
		GG A GG ATAG G		
GAM1273 AKAP6	5'	GTTTTGGAAAGAAGTGAGGT 14996	CACTG	TG
		ATTTCACTTT TC AGAT		
		TGGAGTGAAG AG TTTG		
		AA__ GT		
GAM1273 APXL2	3'	TAGGTGGAGAGGGTGGGGTG 75196	TT	A TG
		CAT CACTTTC C TCTG		

		GTG GTGGGAG G GGAT	
		GG A GT	
GAM1273	ARFGAP3	3' ATCTCAGGCGGCAGTGAAGT 27385	TTCA
		ATTTCACT CTGTCTGAGAT	
		TGAAGTGA GGCGGACTCTA	
		C__	
GAM1273	ARHGEF9	3' TTTTAGGTACTGTGAAGG 30827	__ GT
		CTTTCAC T CTGAGA	
		GGAAGTG A GATTTT	
		TC TG	
GAM1273	ARHGEF9	3' TTTTGGGGAAGTGAAAT 30829	ACTGT TG
		ATTTCACTTTC C AGA	
		TAAAGTGAAGG G TTT	
		____ GT	
GAM1273	BCL2L1	3' GTCTGTGTGAAGGTGAAA 56807	TGTCTG
		TTTCACTTTCAC AGAT	
		AAAGTGGAAGTG TCTG	
		TG__	
GAM1273	C19orf7	3' AGACAGTGAGAGTGAAA 61124	
		TTTCACTTTCACTGTCT	
		AAAGTGAGAGTGACAGA	
GAM1273	C1orf17	3' TTTCAGAGTGGGGAAGTG 68219	A _
		CACTTTC CTG TCTGAGA	
		GTGAAGG GGT AGACTTT	
		_ G	
GAM1273	C1orf34	3' GCAGTGAGGGTGAGCTG 60673	T
		CA TTCACTTTCACTGT	
		GT GAGTGGGAGTGACG	
		C	
GAM1273	C20orf151	3' TCTGGCAGTGAGGGTGGAG 88703	T
		TTTCACTTTCACTGTC GA	
		GAGGTGGGAGTGACGG CT	
		T	
GAM1273	C20orf21	3' TCTCAGGACAAGTGGAAG 35117	_ _
		CTTTCAC T GTC TGAGA	
		GAAGGTGA CAG ACTCT	
		A G	
GAM1273	C20orf29	3' GTCTCAGACTCCCCTGAGGGTG 37129	CT__
	GAG	TTTCACTTTCA GTCTGAGAT	

			GAGGTGGGAGT	CAGACTCTG	
			CCCCT		
GAM1273	C20orf60	3'	TAGGGGTGGGGGTGGGATG	53738	TT TT G
			CAT CACT CACT TCTG		
			GTA GTGG GTGG GGAT		
			GG GG _		
GAM1273	C22orf5	5'	GACAGTGAGGGGGGGATG	24342	TT A
			CAT C CTTTCACTGTC		
			GTA G GGGAGTGACAG		
			GG _		
GAM1273	C8orf2	3'	ATAGTGAAAGTAAGATG	23157	C
			CATTT ACTTTCACTGT		
			GTAGA TGAAAGTGATA		
			A		
GAM1273	CCR5	3'	ATTTCAGACTGAATGGGGGTGG	5147	TT TT CT__
	GG		T CACT CA GTCTGAGAT		
			G GTGG GT CAGACTTTA		
			GG GG AAGT		
GAM1273	CCR6	3'	TCTCTTCAGGGTGGGGTG	15173	TT TTCA TCT
			CAT CACT CTG GAGA		
			GTG GTGG GAC CTCT		
			GG ____ TT_		
GAM1273	CCR6	3'	TCTCTTCAGGGTGGGGTG	48589	TT TTCA TCT
			CAT CACT CTG GAGA		
			GTG GTGG GAC CTCT		
			GG ____ TT_		
GAM1273	CECR7	5'	ATAGTGGGAATGAAATG	79615	C TT
			CATTTCA T CACTGT		
			GTAAAGT A GTGATA		
			A GG		
GAM1273	CENTA2	3'	TCTCAGATGGCTGAAATGT	37269	_ _
			AC TTTCA CTGTCTGAGA		
			TG AAAGT GGTAGACTCT		
			T C		
GAM1273	CEP3	3'	ATCTTGGCAAAAAAGGAAGTG	21247	A CAC T TG
			CATTTCTCTTT TG C AGAT		
			GTGAAG GAAA AC G TCTA		
			_ AAA _ GT		
GAM1273	CHSY1	3'	TTGGGGACAAAAGTGAAATG	29905	CAC GA T
			CATTTCACTTT TGTCT GA		

			GTAAAGTGAAA ACAGG TT		
			___ GG T		
GAM1273	CNNM2	3'	GGACAGTGAGGGAGGAATG 34461	A	
			CATTTC CTTTCACTGTCT		
			GTAAGG GGGAGTGACAGG		
			A		
GAM1273	COLEC10	3'	TTTCAGACCATGTGGAATG 21230	TTTCACT	
			CATTTCAC GTCTGAGA		
			GTAAGGTG CAGACTTT		
			TAC___		
GAM1273	CRR9	3'	ATTCAGGTGGTTTTCTAAGTG 47878	TC___ TG	
			CACTT AC TCTGAGAT		
			GTGAA TG GGACTIONA		
			TCTTT GT		
GAM1273	CYYR1	3'	ATTTTAGGTGGGTGTGAAGTG 53670	TTTCA TG	
			CATTTCAC C TCTGAGAT		
			GTGAAGTG G GGATTTTA		
			TG___ GT		
GAM1273	DAPK3	3'	GTCGTGGGACGGGGAGGGTGGG 7211	TT A GA_	
	ATG		CAT CACTTTC CTGTCT GAT		
			GTA GTGGGAG GGCAGG CTG		
			GG G GTG		
GAM1273	DDX8	3'	GGATGGGAAGGTGGAGTG 17053	A	
			CATTTCACCTTTC CTGTCT		
			GTGAGGTGGAAG GGTAGG		
			—		
GAM1273	DKFZp434B217	3'	GGGTTTGGGCGGGAGTGGGCTG 70701	T TCA TG AT	
			CA TTCACCTT CTGTC AG		
			GT GGGTGAG GGCGG TT		
			C ___ GT GGGT		
GAM1273	DKFZP434K028	3'	CTTACAGTGGAGGTAAAGTG 93231	C CT	
			CATTT ACTTTCACTGT GAG		
			GTGAA TGGAGGTGACA TTC		
			A ___		
GAM1273	DKFZp434O0320	3'	GGTGGCAGGTGGAGTG 83696	—	
			CATTTCACCTT TCACT		
			GTGAGGTGGA GGTGG		
			C		
GAM1273	DKFZP434O047	5'	ATTTTGGACAAGGTGCTGAAGT 31503	CTTT ___ TG	
	G		CATTTCA CACT GTC AGAT		

GTGAAGT GTGG CAG TTTA  
 C\_\_\_ AA GT  
 GAM1273 DKFZp547F072 5' TCCATGGGCGGGGGTGGGGTG 50094 TT TT A GTC A T  
 CAT CACT C CT TG GA  
 ||| ||| | || ||  
 GTG GTGG G GG AC CT  
 GG GG C GT\_ \_ T  
 GAM1273 DKFZP564C103 3' TCTTAGATAAGTAAGGTG 31612 C \_  
 CACTTT ACT GTCTGAGA  
 ||||| ||| |||||  
 GTGGAA TGA TAGATTCT  
 \_ A  
 GAM1273 DKFZP564I052 3' GTTTTAGGTGGTGATCTTAAAT 66718 CACTT TG  
 G CATT TCAC TCTGAGAT  
 |||| ||| |||||  
 GTAAA AGTG GGATTTTG  
 TTCT\_ GT  
 GAM1273 DKFZP564I052 3' GTTTTGAGAGGGGAGTAGAAGT 66719 \_ TT A G T  
 G CATTT C ACT C CT TC GAGAT  
 ||||| ||| | ||| |||||  
 GTGAAG TGA G GA AG TTTTG  
 A GG\_ G \_  
 GAM1273 DKFZP566G1424 3' ATTTTGGAAGTCAAGTGAAGTG 84773 \_ TG  
 CACTTTCAT GTC AGAT  
 ||||| ||| |||  
 GTGAAAGTGA CAG TTTA  
 CT GT  
 GAM1273 DKFZp761N1114 3' GTTTCAGAAAGCTGGGTGGTGG 79022 \_ \_ G  
 TCACT TTCA CT TCTGAGAT  
 |||| ||| || |||||  
 GGTGG GGGT GA AGACTTTG  
 T C A  
 GAM1273 DKFZp762P2111 3' GTCTCAGGTGTTCTGGGGATG 86361 TT ACTTT TGT  
 CAT C CAC CTGAGAT  
 || | ||| |||||  
 GTA G GTG GACTCTG  
 GG GTCTT \_  
 GAM1273 DKFZp762P2111 3' TGAGAAACAGTGGAGTGGAGTG 86365 T CTGAGAT  
 CATTTCAT CACTGT  
 ||||| |||||  
 GTGAGGTGAG GTGACA  
 \_ AAGAGTA  
 GAM1273 DMRTA2 3' GTTTTGTTTAGGAGGGTGGG 60660 A TC  
 TTCATTTTC CTG TGAGAT  
 ||||| ||| |||||  
 GGGTGGGAG GAT GTTTTG  
 \_ TT  
 GAM1273 DRIL2 3' ATCGTGGGGGCGGGGAGGTGGA 21322 A GA\_  
 GTG ATTTCACTTTC CTGTCT GAT  
 ||||| ||||| |||



			TGAGGTGGAGG GGCGGG CTA		
			— GGTG		
GAM1273	EAT2	3'	TCAGGTGAAGGTGAGG 79281	TGT	
			TTTCACTTTTCAC CTGA		
			GGAGTGGAAGTG GACT		
GAM1273	EPS8R1	5'	TAGAACATGAAGGTGGGATG 34803	TT	C _
			CAT CACTTTCA TGT CTG		
			GTA GTGGAAGT ACA GAT		
			GG _ A		
GAM1273	FBXL3B	5'	ATCTTCTGTATGTAGGAGGTGG 24070	_ TGTCT_	
	AATG		ATTTCACTTTC AC GAGAT		
			TAAGGTGGAGG TG TTCTA		
			A TATGTC		
GAM1273	FHX	3'	TCAAGGGTGAAAGTGATGATG 37307	_	GTC
			CATT TCACTTTTCACT TGA		
			GTAG AGTGAAAGTGG ACT		
			T GA_		
GAM1273	FKSG42	3'	GTCTCAGGGTGGGAAGTGGGA 49335	TT	_ GT
			T CACTTTC ACT CTGAGAT		
			A GTGAAGG TGG GACTCTG		
			GG G _		
GAM1273	FLJ00024	3'	GTCTTGGGAGAAGGGTGAGG 63765	CA	G TG
			TTTCACTTT CT TC AGAT		
			GGAGTGGGA GA GG TCTG		
			A_ _ GT		
GAM1273	FLJ10052	3'	ATCTCAGGCTCCACAGTGAGG 35771	TTCACT	
			TTTCACT GTCTGAGAT		
			GGAGTGA CGGACTCTA		
			CACCT_		
GAM1273	FLJ11506	3'	TGGGTGGGGAAGTGAAATG 45115	A TG	
			CATTTCACTTTC C TCTG		
			GTAAAGTGAAGG G GGGT		
			_ GT		
GAM1273	FLJ12056	3'	TTTGGGGGCAGGGAGGTTGGGT 46258	TC	A GA T
	G		CATT ACTTTC CTGTCT GA		
			GTGG TGGAGG GACGGG TT		
			GT _ GG TT		
GAM1273	FLJ12121	3'	GTTTTGGACAGTCATTTGGAAT 46458	CTTTC	TG
			ATTTCA ACTGTC AGAT		

			TAAGGT	TGACAG	TTTG		
			TTAC_	GT			
GAM1273	FLJ12547	3'	ATCTCAGCCAGAGAGAGTGAAC	46489	T	A	T
		TG	CA TTCACTTTC	CTG CTGAGAT			
			GT AAGTGAGAG	GAC GACTCTA			
			C	A C			
GAM1273	FLJ12581	3'	TCTCATGGAGGGTGGAGT	45881		ACTGTC	
			ATTTCACTTTC	TGAGA			
			TGAGGTGGGAG	ACTCT			
			GT_____				
GAM1273	FLJ12787	3'	TTTCAGGTCAGAGGAA	49756	A	_	
			TTTC CTG TCTGAGA				
			AAGG GAC	GGA CTTT			
			A	T			
GAM1273	FLJ12891	3'	ACTGTGGAGGTGGAGTG	46335		T	
			CATTTCACTTTTCA	GT			
			GTGAGGTGGAGGTG	CA			
			T				
GAM1273	FLJ13072	5'	GACAGTGAGAGTGAAA	89814			
			TTTCACTTTTCACTGTC				
			AAAGTGAGAGTGACAG				
GAM1273	FLJ13852	3'	TGGGCAGTGGTAGGTGGGGTG	43579	TT	_	
			CAT CACTT TCACTGTCTG				
			GTG GTGGA GGTGACGGGT				
			GG	T			
GAM1273	FLJ14107	3'	GCAGGGGAGGTGAAATG	46693		A	
			CATTTCACTTTC	CTGT			
			GTAAAGTGGAGG	GACG			
			G				
GAM1273	FLJ14346	3'	GGCAGGGAAGTGAGATG	46714		A	
			CATTTCACTTTC	CTGTC			
			GTAGAGTGAAGG	GACGG			
GAM1273	FLJ14502	3'	GTTTTGGGCTTAATAAATGGGG	62717	TT	C TCACT	TG
		TG	CAT CA TT	GTC AGAT			
			GTG GT AA	CGG TTTG			
			GG A TAATT	GT			
GAM1273	FLJ14641	5'	CGGGGAAGTGGAATG	51483		A	
			CATTTCACTTTC	CTG			

GTAAGGTGAAGG GGC

GAM1273 FLJ14743 3' GCTCTGGGGTGGGGGTGGGGTG 68064 TT TT G T AT  
CAT CACT CACT TC GAG  
||| |||| ||| || |||  
GTG GTGG GTGG GG CTC  
GG GG \_ T GT

GAM1273 FLJ20034 3' TTTGTACGTGAGGGTGGA 34392 T CT  
TTCACCTTTCAC GT GAG  
||||||| || |||  
AGGTGGGAGTG CA TTT  
\_ TG

GAM1273 FLJ20043 3' GTTTTGGGAAAGGAGTGGGAT 34406 TT CACTG TG  
AT CACTTT TC AGAT  
|| |||| || |||  
TA GTGAGG GG TTTG  
GG AAA\_ GT

GAM1273 FLJ20306 3' GAAGGTGGAGGTGGAA 34916 G  
TTTCACTTTCACT TC  
||||||| ||  
AAGGTGGAGGTGG AG  
A

GAM1273 FLJ20340 3' TTGGAGTGGAGTGGGGTG 34980 TT T TG TG  
CAT CACTT CAC TC A  
||| |||| || || |  
GTG GTGAG GTG AG T  
GG \_ \_ GT

GAM1273 FLJ20400 3' TTCTTGACTGAAGGTGAGATG 66514 CT T T  
CATTTCACTTTCA GTC GAGA  
||||||| || |||  
GTAGAGTGGAAGT CAG TTCT  
\_ \_ TT

GAM1273 FLJ20729 3' GTCTTGAGTGCAAGTGGTATG 35649 T T TG TG  
CAT TCACTT CAC TC AGAT  
||| |||| || || |||  
GTA GGTGAA GTG AG TCTG  
T C \_ GT

GAM1273 FLJ21125 3' GTTTGATGCAGGAAGGTGGGA 44892 TT A \_ TG AT  
TG CAT CACTTTC CTGT C AG  
||| |||| ||| | ||  
GTA GTGGAAG GACG G TT  
GG \_ TA GT G

GAM1273 FLJ21162 3' TCTTGGGCTGGGTGCAGTG 45896 TT \_ TG  
CACT CACT GTC AGA  
|||| ||| || |||  
GTGA GTGG CGG TCT  
C\_ GT GT

GAM1273 FLJ21324 5' ATCTGCAGGTGGAAGGAGGTG 91189 A TGT \_  
CATTTC CTTTCAC CTG AGAT  
|||| |||| || |||

GTGGAG GAAGGTG GAC TCTA  
 — — G  
 GAM1273 FLJ21736 3' TTTCAGATGGAAGTGAGA 46234 CTG  
 TTTCACTTTCA TCTGAGA  
 ||||| |||||  
 AGAGTGAAGGT AGACTTT

—  
 GAM1273 FLJ22378 3' GTCTCGGGTCCAGGGAGTGGAG 46905 TT ACTG  
 TTTCAC T C TCTGAGAT  
 ||||| | |||||  
 GAGGTGA G GGGCTCTG  
 GG ACCT

GAM1273 FLJ22659 5' GTGGTGAAGGTTAAATG 46261 C TG  
 CATTT ACTTTCAC T  
 |||| ||||| |  
 GTAAA TGGAAGTG G  
 T GT

GAM1273 FLJ23059 3' ATCTCAGAACAGAAGGGTGGGA 49933 TT CA \_  
 T CACTTT CTGT CTGAGAT  
 | |||| ||| |||||  
 A GTGGGA GACA GACTCTA  
 GG A\_ A

GAM1273 FLJ23091 3' ACCTCATGTGGGGGTGGGGTG 46124 TT TT TGTC AT  
 CAT CACT CAC TGAG  
 ||| ||| ||| |||  
 GTG GTGG GTG ACTC  
 GG GG T\_\_ CAA

GAM1273 FLJ23185 3' TTTCAGGCAGGTGGAG 46837 CA  
 CTTT CTGTCTGAGA  
 |||| |||||  
 GAGG GACGGACTTT  
 TG

GAM1273 FLJ23309 3' ATCTTGGGTGATGGAGGAAATG 46061 A T C GT TG  
 CATTTC CTT CA T C AGAT  
 ||||| ||| || | |||||  
 GTAAAG GAG GT G G TCTA  
 \_ \_ A TG GT

GAM1273 FLJ23476 3' GTCTCAGGTGGCTGCGTGTGGT 44962 TT TTT \_ TG  
 G CAT CAC CA C TCTGAGAT  
 ||| ||| || | |||||  
 GTG GTG GT G GGA CTCTG  
 GT C\_\_ C GT

GAM1273 FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281 CTT  
 CATTTCA TCACTGTCTGAGAT  
 ||||| |||||  
 GTAAAGT AGTGACAGACTCTA  
 C\_\_

GAM1273 FLJ23556 3' GTTTTAATAAGGGAGGTGGAA 45956 A GTC  
 TTTCACTTTC CT TGAGAT  
 ||||| || |||||

AAGGTGGAGG GA ATTTTG  
 \_ ATA  
 GAM1273 FLJ31762 3' TCTTCTGGGGGTGAGATG 58145 TT CTGTCT  
 CATTTCACCT CA GAGA  
 ||||| || |||  
 GTAGAGTGG GT TTCT  
 GG C\_\_\_\_  
 GAM1273 FTSJ3 3' GTCTGAAGAACAGTGAGGTGGA 34455 T \_ G\_  
 GTG ATTTCACTT CACTGT CT AGAT  
 ||||| ||||| || |||  
 TGAGGTGGA GTGACA GA TCTG  
 \_ A AG  
 GAM1273 G4 5' ATCTCAGATTGTGGGGGTGTGG 90991 \_ TT T  
 ATG CATTT CACT CAC GTCTGAGAT  
 |||| ||| ||| |||||  
 GTAGG GTGG GTG TAGACTCTA  
 T GG T  
 GAM1273 GBTS1 3' TTAGTGAGGGAAGGTGAGATG 59064 A GT\_  
 CATTTCACTTTC CT CTGA  
 ||||| || |||  
 GTAGAGTGGGAAG GG GATT  
 \_ AGT  
 GAM1273 GBTS1 3' ATTTTGGGGAGTGGGTGATATG 59050 T TT G TG  
 CAT TCACT CACT TC AGAT  
 || |||| ||| || |||  
 GTA AGTGG GTGA GG TTTA  
 T \_ G GT  
 GAM1273 GK001 3' TTTCTGGTGGGAGTGGGGTG 39503 TT TT TCT T  
 CAT CACT CACTG GAGA  
 || |||| |||| |||  
 GTG GTGA GTGGT CTTT  
 GG GG \_ T  
 GAM1273 GPS2 5' GTCTTTGAGGTGAAAGTGGAA 15671 G T  
 TTTCACTTTCACT TC GAGAT  
 ||||| || |||||  
 AAGGTGAAAGTGG AG TTCTG  
 \_ T  
 GAM1273 GPT2 3' TTTCAGATCTGGAGAAATG 55962 ACT CT  
 CATTTC TTCA GTCTGAGA  
 |||| ||| |||||  
 GTAAAG AGGT TAGACTTT  
 \_ C\_  
 GAM1273 GRSF1 3' ATTTTAGAACAAGTAGGGGTG 9139 TC \_ \_  
 CACTT ACT GT CTGAGAT  
 |||| ||| || |||||  
 GTGGG TGA CA GATTTTA  
 GA A A  
 GAM1273 HBXAP 5' CAGTGAAATGAAGTG 33420 C  
 CATTTCATTTCACTG  
 ||||| |||||

GTGAAGT AAAGTGAC

GAM1273 HIC 5' GTTTCAGGATTGTAGGAGTGGA 67452 TC TG\_  
A TTTCACTT AC TCTGAGAT  
||||||| || |||||||  
AAGGTGAG TG GGACTTTG  
GA TTA

GAM1273 HIF1AN 3' ATCTATTCAAGTGGGAGTGGGGT 61968 TT TT TCTG  
AT CACT CACTG AGAT  
|| ||| ||||| ||||  
TG GTGA GTGAC TCTA  
GG GG TTA\_  
GAM1273 HSF2 3' TCGGGGGTGGGATGGGATG 15710 TT C TT G  
CAT CA T CACT TCTGA  
||| ||| ||||| |||||  
GTA GT A GTGG GGGCT  
GG \_ GG \_  
GAM1273 HSPC054 3' TTTTACAGCTGTGGAAAGTGAA 26264 \_ T T \_ T  
GTG ATTTCACTTTC AC G CTG AGA  
||||||| ||| ||| |||  
TGAAGTGAAAG TG C GAC TTT  
G T \_ A TG  
GAM1273 HXCP2 3' ATCTCAGTTTGGGAAGTGGGAT 50832 TT ACTGT  
G CAT CACTTTC CTGAGAT  
||| ||||| |||||  
GTA GTGAAGG GACTCTA  
GG GTTT\_  
GAM1273 HYPK 3' TCTTGGGTCAAGTAGAGTG 33080 C \_ \_ TG  
CACTTT ACT G TC AGA  
||||| ||| ||| |||  
GTGAGA TGA C GG TCT  
\_ A T GT  
GAM1273 IL18BP 3' TCTTGGGCAGAGGAGGTG 19113 A TG  
CACTTTC CTGTC AGA  
||||| ||||| |||  
GTGGAGG GACGG TCT  
A GT  
GAM1273 IL22R 3' GTGGTGAAGATGAAATG 41192 C TG  
CATTTCA TTTCAC T  
||||| ||||| |  
GTAAAGT GAAGTG G  
A GT  
GAM1273 IMAGE3451454 3' GTTTTAGCCAAAAGTGAAAT 53873 CAC T  
ATTTCACTTT TG CTGAGAT  
||||||| || |||||  
TAAAGTGAAA AC GATTTTG  
\_ C  
GAM1273 KIAA0092 3' ATTTTGGAATAAAGTGAGA 27967 CACTG TG  
TTTCACTTT TC AGAT  
||||||| || |||||

AGAGTGAAA AG TTTA  
 TA\_\_ GT  
 GAM1273 KIAA0174 5' ATTTTGGATGGTGAACCCTGAA 78592 CT\_ TG  
 GT ATTTCA TTCACTGTC AGAT  
 ||||| ||||| ||||  
 TGAAGT AAGTGGTAG TTTA  
 CCC GT  
 GAM1273 KIAA0212 3' GTGAGACCGTGGTGAAAGGGGG 27940 TT A \_\_ GAGAT  
 ATG T C CTTTCACT GTCT  
 | | ||||| ||||  
 A G GAAAGTGG CAGA  
 GG G TGC GTG  
 GAM1273 KIAA0284 3' TGGTGGGGGTGGACGTG 63119 \_ TT  
 CAT TTCACT CACTG  
 ||| ||||| ||||  
 GTG AGGTGG GTGGT  
 C GG  
 GAM1273 KIAA0285 5' GGCAGTGGAGGTGAGA 29020  
 TTTCACTTTCACTGTC  
 ||||| |||||  
 AGAGTGGAGGTGACGG  
 GAM1273 KIAA0419 5' ATTTCAGATAGTGTGTGA 28187 TTT  
 TCAC CACTGTCTGAGAT  
 |||| ||||| ||||  
 AGTG GTGATAGACTTTA  
 T\_\_  
 GAM1273 KIAA0426 3' GTTTTAGATGGTGTTACTGAGA 28261 CTTT  
 TTTCA CACTGTCTGAGAT  
 |||| ||||| ||||  
 AGAGT GTGGTAGATTTTG  
 CATT  
 GAM1273 KIAA0453 3' GTCTTGCTGGGGGGTGGTGATG 69049 \_ TT ACT CT  
 CATT TCACT C GT GAGAT  
 |||| |||| | || ||||  
 GTAG GGTGG G CG TTCTG  
 T GG GT\_ \_\_  
 GAM1273 KIAA0459 3' ATTTCAGATGGGATGCAGGTG 60983 T \_\_  
 CACTT CA CTGTCTGAGAT  
 |||| || ||||| ||||  
 GTGGA GT GGTAGACTTTA  
 C AG  
 GAM1273 KIAA0523 3' ATCTTGGGCTCACAAGTGAGG 67728 TCACT TG  
 TTTCACTT GTC AGAT  
 ||||| || ||||  
 GGAGTGAA CGG TCTA  
 CACT\_ GT  
 GAM1273 KIAA0552 3' GTTTTGGGGGGCAAGGTGGAG 28320 CA G TG  
 TTTCACTTT CT TC AGAT  
 ||||| || || ||||

		GAGGTGGAA GG GG TTTG		
		C_ G GT		
GAM1273	KIAA0660	3' GTTTCAGGCAGGAGTGGGGT 24515	TT	TCA
		AT CACTT CTGTCTGAGAT		
		TG GTGAG GACGGACTTTG		
		GG _		
GAM1273	KIAA0759	3' GTTTCCTGTTTTGAAAGTGAAAT 67329		CTGTCT
	G	CATTTCACTTTCA GAGAT		
		GTAAAGTGAAAGT CTTTG		
		TTTGT_		
GAM1273	KIAA0795	3' ATTTCAGGGAAGAGGTGGGAT 46588	TT	CA GT
		AT CACTTT CT CTGAGAT		
		TA GTGGAG GG GACTTTA		
		GG AA _		
GAM1273	KIAA0830	3' ATTTCAGCAGTGTGAAGGTAAA 69694	CA	_ T
	TG	CATTT CTTT CACTG CTGAGAT		
		GTAAA GAAG GTGAC GACTTTA		
		TG T _		
GAM1273	KIAA0871	3' ATTTCAGAATAGGAAGTAAATG 30299	C	ACTG
		CATTT ACTTTC TCTGAGAT		
		GTAAA TGAAGG A GACTTTA		
		_ ATA_		
GAM1273	KIAA0893	3' GTTTCAGGCTAAAAGGTAAATG 30360	C	CACT
		CATTT ACTTT GTCTGAGAT		
		GTAAA TGGAA CGGACTTTG		
		_ AAT_		
GAM1273	KIAA0918	3' GTTTC AACGTTTAGGGTGAAGT 73134	CAC	C
	G	CATTTCACTTT TGT TGAGAT		
		GTGAAGTGGA GCA ACTTTG		
		TTT _		
GAM1273	KIAA0931	3' ATCTCAGACTAATGGGGTGTGA 67412	_ TT	CT_
		TCAC T CA GTCTGAGAT		
		AGTG G GT CAGACTCTA		
		T GG AAT		
GAM1273	KIAA0934	3' GGCATGGGGGTGAAATG 64223	TT	C
		CATTTCACT CA TGTC		
		GTAAAGTGG GT ACGG		
		GG _		
GAM1273	KIAA0978	3' CTCGACGTGAGGGTGAAATG 70480	T	T
		CATTTCACTTTCACT GTC GAG		



GTAAAGTGGGAGTG CAG CTC

GAM1273 KIAA1036 3' TGATGGGGGGTGGGGGTGGGGT 29831 TT TT G AGAT  
G CAT CACT CACT TCTG

||| |||| |||| ||||  
GTG GTGG GTGG GGGT  
GG GG G AGTG

GAM1273 KIAA1046 3' ATCTTAGAAGAGGGGTGGG 29990 CACTG  
TTCAC TTT TCTGAGAT  
|||||| ||||||  
GGGTGGGG AGATTCTA  
AGA\_\_

GAM1273 KIAA1046 3' TTTCAGATGTTGGAAATG 30002 C CT  
CA TTTCA GTCTGAGA  
|| |||| ||||||  
GT AAGGT TAGACTTT  
A TG

GAM1273 KIAA1237 3' TTTTGGATGAAGTGAGGG 80476 \_\_ TG  
CTTTCAC T GTC AGA  
|||||| ||| |||  
GGGAGTGA TAG TTT  
AG GT

GAM1273 KIAA1257 3' GTTGGCACGACTGAGAGTGGGA 62755 TT CT \_ A\_  
TG CAT CACTTTCA GTC TG GAT  
||| |||||| ||| |||  
GTA GTGAGAGT CAG AC TTG  
GG \_\_ C GG

GAM1273 KIAA1456 3' GTTTTGGAGGAAGGAGGAAATG 67006 A\_ A TG TG  
CATTTT CTTTC C TC AGAT  
||||| |||| | |||  
GTAAAG GGAAG G AG TTTG  
GA \_\_ GT

GAM1273 KIAA1538 3' GTTTTAGACAGGCTCCCTGAA 71556 CTTTCA  
TTCA CTGTCTGAGAT  
||| ||||||||  
AAGT GACAGATTTTG  
CCCTCG

GAM1273 KIAA1559 3' TTGGAGACAGTGAGGGAAGTG 73078 A T GAGAT  
CATTTT CTT CACTGTCT  
||||| ||| ||||||  
GTGAAG GGA GTGACAGA  
\_\_ G TTT

GAM1273 KIAA1560 3' TTTGGGAGAGGGAGGGA 64183 A A G G  
TC CTTTC CT TCT AGA  
|| |||| || ||| |||  
AG GGAGG GA AGG TTT  
\_\_ G G

GAM1273 KIAA1655 5' ATCTCACCTCCAGTGGGAGGGA 66590 A TT TC\_\_  
AGTG ATTTC CT CACTG TGAGAT  
||||| || |||| |||||

		TGAAG GA GTGAC ACTCTA	
		G GG CTCC	
GAM1273 KIAA1655	5'	TCTCACTGAGAGTGAGA 66634	CTGTC
		TTTCACTTTCA TGAGA	
		AGAGTGAGAGT ACTCT	
		C____	
GAM1273 KIAA1729	3'	GTCTTAGGCGATTTGTGGGGTG 89130	TT TTTCAC
		CAT CAC TGTCTGAGAT	
		GTG GTG GCGGATTCTG	
		GG TTTA__	
GAM1273 KIAA1799	5'	ATCTTATTTCCGGTGGCGGTGA 74634	T TC__
		GGTG ATTTCACT TCACTG TGAGAT	
		TGGAGTGG GGTGGC ATTCTA	
		C CTTT	
GAM1273 KIAA1808	5'	CATTGAGGGTGAGGTG 85861	C
		CATTTCACTTTCA TG	
		GTGGAGTGGGAGT AC	
		T	
GAM1273 KIAA1811	3'	ATCTCTCTGCGGGGTGGGGTG 64793	TT TTCA CT_
		CAT CACT CTGT GAGAT	
		GTG GTGG GGCG CTCTA	
		GG ____ TCT	
GAM1273 KIAA1821	3'	GGGCAGTGAGGGTGAGG 71790	
		TTTCACTTTCACTGTCT	
		GGAGTGGGAGTGACGGG	
GAM1273 KIAA1893	3'	GTCTCGGGCAGCACGTGAGGT 73217	TTTCA
		ATTTCAC CTGTCTGAGAT	
		TGGAGTG GACGGGCTCTG	
		CAC__	
GAM1273 KPNA6	3'	GCAGAGGAGGGTGAGTG 24609	A_
		CATTTCACTTTC CTGT	
		GTGAGGTGGGAG GACG	
		GA	
GAM1273 LMOD1	3'	ATCTTTGAGGTGAGGGTGGGGT 24038	TT G T
		G CAT CACTTTCACT TC GAGAT	
		GTG GTGGGAGTGG AG TTCTA	
		GG _ T	
GAM1273 LY6G5B	5'	TTTCAGGCTCAGAGAAGTG 41131	CACT_
		CACTTT GTCTGAGA	

			GTGAAG CGGACTTT		
			AGACT		
GAM1273	MAGE-E1	3'	GATTGGACGGTGGAGCTGGGAT 47945	TT C	TG GAT
	G		CAT CA TTTCACTGTC A		
			GTA GT GAGGTGGCAG T		
			GG C GT AG		
GAM1273	MGC10960	3'	ATCTCCCCAGGAGGGTGAGATG 51003	A	TCT
			CATTTCACTTTC CTG GAGAT		
			GTAGAGTGGGAG GAC CTCTA		
			_ CC_		
GAM1273	MGC2628	3'	ATTCCTGGGTTAGGGTGGAATG 43968	C	GT T
			CATTTCACTTT ACT C GAGAT		
			GTAAGGTGGGA TGG G CTTTA		
			T _ C		
GAM1273	MGC27044	5'	CTTGGTGTTGAAAGTGAAATG 58673	CTGT	TG
			CATTTCACTTTCA C AG		
			GTAAAGTGAAAGT G TC		
			TGT_ GT		
GAM1273	MGC35558	3'	TCTCAGGTGGGTGAGGG 58787	_ TG	
			CTTTCA C TCTGAGA		
			GGGAGT G GGA CTCT		
			G GT		
GAM1273	MGC4251	3'	GTTGGCCTGGTGGGGTGAGT 50460	TT _	TGAGAT
			ATTTCACT CACT GTC		
			TGAGGTGG GTGG CGG		
			GG TC TTG		
GAM1273	MLLT10	5'	AGGCGGTGGAGGGGAGGTG 16166	A	
			CATTTC CTTTCACTGTCT		
			GTGGAG GGAGGTGGCGGA		
			G		
GAM1273	MOCS3	3'	TCTTGACATGTGAGATGT 27161	_ _	TG
			AC TTTCAC TGTC AGA		
			TG AGAGTG ACAG TCT		
			T T GT		
GAM1273	NR6A1	3'	ATTTTGAGGGAGAGGGTGGGAT 52867	TT	A G T
	G		CAT CACTTTC CT TC GAGAT		
			GTA GTGGGAG GG AG TTTTA		
			GG A G _		
GAM1273	NR6A1	3'	ATTTTGAGGGAGAGGGTGGGAT 52879	TT	A G T
	G		CAT CACTTTC CT TC GAGAT		

			GTA GTGGGAG GG AG TTTTA		
			GG A G _		
GAM1273 NR6A1	3'	ATTTTGAGGGAGAGGGTGGGAT 7642	TT	A G T	
G		CAT CACTTTC CT TC GAGAT			
		GTA GTGGGAG GG AG TTTTA			
		GG A G _			
GAM1273 P450RAI-2	3'	TGGTGGAGATGGAATG 39107	C		
		CATTTCA TTTCAGT			
		GTAAGGT GAGGTGGT			
		A			
GAM1273 PALM	3'	TCTCAGGCAGTTGGGGTGA 10417	TC		
		TCACTT ACTGTCTGAGA			
		AGTGGG TGACGGAAGTCT			
		GT			
GAM1273 PB1	3'	ATTTTAGTTACTGGGGGTGGGG 36368	TT TT C T		
		T CACT CA TG CTGAGAT			
		G GTGG GT AT GATTTTA			
		GG GG C T			
GAM1273 pcnp	3'	GTTTTGAAATTGGGGTGTGGGG 39789	TT _ TT CTG T		
TG		CAT CAC T CA TC GAGAT			
		GTG GTG G GT AG TTTTG			
		GG T GG TAA _			
GAM1273 PEF	3'	TCTGTGGAGAGTGGAGTG 24754	T G _		
		CACTT CACT TCTG AGA			
		GTGAG GTGA AGGT TCT			
		_ G G			
GAM1273 PGGT1B	3'	ATTTTAGATTGGGAGGGTGGGG 17231	TT ACT		
		T CACTTTC GTCTGAGAT			
		G GTGGGAG TAGATTTTA			
		GG GGT			
GAM1273 PINK1	3'	GTCTGTGAATGGTGAGGGTGGG 50543	TT _ TG		
A		T CACTTTCAGT C AGAT			
		A GTGGGAGTGGTA G TCTG			
		GG A TG			
GAM1273 PP1057	5'	GTTTTGTGGGGGTGGGAGTGGA 48435	TT G _		
G		TTTCACT CACT TC TGAGAT			
		GAGGTGA GTGG GG GTTTTG			
		GG G T			
GAM1273 PRMT3	3'	GTTTTTAATGTGGGGGTAGAGT 65025	TC TT TGTCT		
G		CATT ACT CAC GAGAT			

		GTGA TGG GTG TTTTG	
		GA GG TAAT_	
GAM1273 PRMT6	3'	GTTTCGCGGGGGAGTGAGG 36272	TT A CT
		TTTCACT C CTGT GAGAT	
		GGAGTGA G GGCG CTTTG	
		GG _ _	
GAM1273 PRO2900	5'	TTCAACTGAGAGTGAGGTG 37809	CT C
		CATTTCACTTTCA GT TGAG	
		GTGGAGTGAGAGT CA ACTT	
		— —	
GAM1273 PSMF1	3'	GTCTTAGGTGTTCTATGGGAGG 22354	A TT C _ _ GT
		AAGTG TC CT CA T CTGAGAT	
		AG GA GT G GATTCTG	
		_ GG ATCTT TG	
GAM1273 PXR2b	3'	ATTTTAACTTGGGGGTGAAA 33338	TT CT CT
		TTTCACT CA GT GAGAT	
		AAAGTGG GT CA TTTTA	
		GG T_ AT	
GAM1273 RAB6B	3'	GTCTTTAGGAGTAGGGTGGGAT 33414	TT C G _
		G CAT CACTTT ACT TCTGA GAT	
		GTA GTGGGA TGA GGATT CTG	
		GG _ _ T	
GAM1273 RACGAP1	3'	GTCTCAGGGTGGGAAGTGGA 25200	TT _ GT
		T CACTTTC ACT CTGAGAT	
		A GTGAAGG TGG GACTCTG	
		GG G _	
GAM1273 RAD51	3'	TTTCAGGCCAGTGTGGTG 56023	TT _
		CACT CACTG TCTGAGA	
		GTGG GTGAC GGACTTT	
		T_ C	
GAM1273 RAD51	3'	TTTCAGGCCAGTGTGGTG 11229	TT _
		CACT CACTG TCTGAGA	
		GTGG GTGAC GGACTTT	
		T_ C	
GAM1273 RASSF2	3'	GTTTCAGGTTGAAGGGAAATG 28443	A CTG
		CATTTT CTTTCA TCTGAGAT	
		GTAAAG GGAAGT GGACTTTG	
		_ T_	
GAM1273 RBM7	3'	ATTTTAGACACTTTAGGAGGGG 32235	TT A CAC_
		GTG AT C CTTT TGTCTGAGAT	

			TG G GAGG ACAGATTTTA		
			GG_ ATTC		
GAM1273 RIL	3'	GGGGGTGGTGGTGGGGTG	13488	TT T G	
		CAT CACT TCACT TC			
		GTG GTGG GGTGG GG			
		GG T G			
GAM1273 RILP	5'	GTCCCAGTGGAGGGTGGGGTG	48694	TT ACTGT A	
		CAT CACTTTC CTG GAT			
		GTG GTGGGAG GAC CTG			
		GG GT__ C			
GAM1273 RNO2 G	5'	ATTTTTTTAGTGGAGATGGGGT	52762	TT C TCT	
		CAT CA TTCTACTG GAGAT			
		GTG GT GAGGTGAT TTTTA			
		GG A TT_			
GAM1273 RoXaN	3'	ACAGTGGGTGTGAGATG	46627	T	
		CATTTTCACTTCACTGT			
		GTAGAGTG GGGTGACA			
		T			
GAM1273 SAE1	3'	TTTTGGGAGAAAGGAGATG	18537	A ACTG TG	
		CATTTTCTTTTC TC AGA			
		GTAGAG GAAAG GG TTT			
		_ A__ GT			
GAM1273 SDS3	3'	ATTTTCCATTGAAGGTGGAGT	69223	C TCT	
		ATTTCACTTTTCA TG GAGAT			
		TGAGGTGGAAGT AC TTTTA			
		T CT_			
GAM1273 SEMA4C	3'	ACATATGGAGGTGGGGTG	35052	TT C_	
		CAT CACTTTTCA TGT			
		GTG GTGGAGGT ACA			
		GG AT			
GAM1273 SFXN5	3'	TCTTAGGGTAGGGGAAGTG	58040	A GT_	
		CACTTTC CT C TGAGA			
		GTGAAGG GA G ATTCT			
		G TG G			
GAM1273 SGT1	3'	ATTTCAAGACATGGTGAACTG	21992	C _	
		CA TTCTACT GTCTGAGAT			
		GT AAAGTGG CAGACTTTA			
		C TA			
GAM1273 SH3BGL2	3'	ATCTCAGACAGTGATCAGGA	48883	ACTT	
		TC TCACTGTCTGAGAT			

AG AGTGACAGACTCTA  
 GACT  
 GAM1273 SMC1L1 3' GTCTTAGGCAGTTACCTGAAA 71960 CTTTC  
 TTTCA ACTGTCTGAGAT  
 |||| |||||  
 AAAGT TGACGGATTCTG  
 CCAT\_  
 GAM1273 SPTLC2 5' GTTTCGGGGAGGTGGGTGGGGT 16809 TT TCA G  
 G CAT CACTT CT TCTGAGAT  
 || |||| || |||||  
 GTG GTGGG GA GGGCTTTG  
 GG TG\_ G  
 GAM1273 STK29 3' GTCTCAGGCAGTGGGGG 87579 TT  
 CT CACTGTCTGAGAT  
 || |||||  
 GG GTGACGGACTCTG  
 GG  
 GAM1273 TA-PP2C 3' GTAGACGCGGTGGGGGCGGGGT 57759 TT A TT \_ AGAT  
 G CAT C CT CACT GTCTG  
 || | || ||||  
 GTG G GG GTGG CAGAT  
 GG C GG CG G  
 GAM1273 THEA 3' TTTTAGGCCAGGTGTGGTG 66305 TT \_  
 CACT CACT GTCTGAGA  
 |||| |||| |||||  
 GTGG GTGG CGGATTTT  
 T\_ AC  
 GAM1273 TIAM2 3' ATCTTGGGCTGTATCAAGGGAG 24931 A TC\_ T TG  
 TG CATTTT CTT AC GTC AGAT  
 ||||| || || ||||  
 GTGAGG GAA TG CGG TCTA  
 \_ CTA T GT  
 GAM1273 TP53TG3 3' ATCTTGACATCTTGAGATG 31102 ACTTTCAC TG  
 CATTTT TGTC AGAT  
 |||| |||| ||||  
 GTAGAG ACAG TCTA  
 GTTCT\_\_ GT  
 GAM1273 TRIP3 3' GTTTCAGGCAGACTTGGGGT 78220 TT CTTTCA  
 AT CA CTGTCTGAGAT  
 || || |||||  
 TG GT GACGGACTTTG  
 GG TCA\_\_  
 GAM1273 VIAAT 3' GTTTTGGGGGAGGCGGGGTG 54541 TT A A GT TG  
 CAT C CTTTC CT C AGAT  
 || | |||| || | ||||  
 GTG G GGAGG GG G TTTG  
 GG C \_ \_ GT  
 GAM1273 VPS39 3' GTCTTTGATGGTGGTGAGGGTG 62849 \_ T  
 GG TTCACTTTCAT GTC GAGAT  
 ||||| || ||||

GGGTGGGAGTGG TAG TTCTG  
TGG T

GAM1273 ZAP3 3' GTTTTGGGGAGGGAGGGAG 77224 A A G TG  
TTC CTTTC CT TC AGAT  
||| |||| || || ||||  
GAG GGAGG GA GG TTTG  
\_ \_ G GT

GAM1273 ZNF297B 3' ATTTCACTACTAAGGTGGTGA 25775 T ACT \_  
TCACT TC GT CTGAGAT  
||||| || || |||||  
AGTGG GG CA GACTTTA  
T AAT T

GAM1273 ZNF323 5' ATCTTAAGATTGTGAAAGTGGA 48077 T \_  
G TTTCACTTTTAC GTCT GAGAT  
||||||| ||| |||||  
GAGGTGAAAGTG TAGA TTCTA  
T A

GAM1273 ZNF84 3' TCTTGGACTTCAGGAAATG 12817 A TTCACT TG  
CATTTTC CT GTC AGA  
||||| || ||| |||  
GTAAAG GA CAG TCT  
\_ CTT\_ GT

GAM1273 LOC114987 3' TCTTGAGGGGAGTGGGATG 59124 TT TT A GTC  
CAT CACT C CT TGAGA  
||| |||| | || |||||  
GTA GTGA G GA GTTCT  
GG GG \_ \_

GAM1273 LOC115219 5' GGCGGTGGAGGGGAGATG 73312 A  
CATTTTC CTTTCACTGTC  
||||| |||||  
GTAGAG GGAGGTGGCGG  
G

GAM1273 LOC115297 3' ATCTCAGATATCCTACGGTGAG 72884 TTCAC\_  
A TTTCACT TGTCTGAGAT  
||||| |||||  
AGAGTGG ATAGACTCTA  
CATCCT

GAM1273 LOC116150 3' TCTTACTTGAGAGTGAG 56638 CT CT  
TTCACTTTCA GT GAGA  
||||||| || |||  
GAGTGAGAGT CA TTCT  
T\_ \_

GAM1273 LOC124446 3' TTTTAGAAAAAGTGAAG 74293 CACTG  
TTTCACTTT TCTGAGA  
||||||| |||||  
GAAGTGAAA AGATTTT  
A\_

GAM1273 LOC126964 3' GTTTTGGTGGGATGGGGGGAGG 74622 A TT \_ GT TG  
TG CATTTTC CT CA CT C AGAT  
||||| || || || | |||



		GTGGAG GG GT GG G TTTG		
		_ GG A GT GT		
GAM1273	LOC128977 3'	GTCTGTGAACAGTGGGGGTGGG 74827	TT TT	_TG
	G	T CACT CACTGT C AGAT		
		G GTGG GTGACA G TCTG		
		GG GG A TG		
GAM1273	LOC130940 5'	GTCTCGGGCGCGGGAGGGGGTG 57139	TT A TT AC	
		CAT C CT C TGTCTGAGAT		
		GTG G GA G GCGGGCTCTG		
		GG_ GG C_		
GAM1273	LOC131368 3'	ATTTTCAGATACTTTAAGTGAAT 75858	T	TCAC
	TG	CA TTCACTT TGTCTGAGAT		
		GT AAGTGAA ATAGACTTTA		
		T TTTC		
GAM1273	LOC134288 3'	TCCACAGAGGTGAGAGTCGGGT 75178	TC	G AGAT
	G	CATT ACTTTCACT TCTG		
		GTGG TGAGAGTGG AGAC		
		GC _ ACCTT		
GAM1273	LOC142948 3'	GTCTTGGCAGCATGGAAGTGAG 82891	_	T TG
	A	TTTCACTTTCA CTG C AGAT		
		AGAGTGAAGGT GAC G TCTG		
		AC _GT		
GAM1273	LOC143279 5'	GTCCTGGTGGTGGAGGTGGGG 76511	TT	TG TGA
		T CACTTTTAC TC GAT		
		G GTGGAGGTG GG CTG		
		GG GT TC_		
GAM1273	LOC144483 3'	TTTCATGGCAGTGAAA 60179	_	
		TTTCACTGTC TGAGA		
		AAAGTGACGG ACTTT		
		T		
GAM1273	LOC144486 3'	TTTTGGTGTGAAGGTGAAAT 83090	TGT TG T	
		ATTTCACTTTTAC C AGA		
		TAAAGTGGAAGTG G TTT		
		T_ GT T		
GAM1273	LOC144845 5'	GTGGGGCAAGGTGGGGGTGAAG 56664	TT _	GAGAT
	TG	CATTTCACT CACT GTCT		
		GTGAAGTGG GTGG CGGG		
		GG AA GTG		
GAM1273	LOC144845 5'	TCGCTCAGGGAGGTGGAGTG 56665	A TC	
		CATTTCACTTTTCTG TGA		

	GTGAGGTGGAGG GAC GCT		
	— TC		
GAM1273 LOC145828 5'	GTTTTGGAAGGGAGAGGAGGTG 83538	A A G TG	
	CATTTC CTTTC CT TC AGAT		
	GTGGAG GAGAG GG AG TTTG		
	— — A GT		
GAM1273 LOC146050 3'	ATCTCAGATGATTTAGGAAGTG 77625	ACT__	
	CACTTTC GTCTGAGAT		
	GTGAAGG TAGACTCTA		
	ATTTAG		
GAM1273 LOC146229 3'	GTGGTAGAGTGGAATG 77769	C TG	
	CATTTCACTTT AC T		
	GTAAGGTGAGA TG G		
	— GT		
GAM1273 LOC146336 3'	GACAGTGAGGCTGAAATG 77832	C	
	CATTTCA TTTCAGTGC		
	GTAAAGT GGAGTGACAG		
	C		
GAM1273 LOC146728 5'	TCGGAGTGGGGTGGAGTG 83753	T TG	
	CATTTCACTT CAC TCTGA		
	GTGAGGTGGG GTG AGGCT		
	— —		
GAM1273 LOC146990 5'	ATCTCGGGCGGCTGGAGGGGTG 83884	— —	
AGG	TTCACT TTCA CTGTCTGAGAT		
	GAGTGG AGGT GGCGGGCTCTA		
	GG C		
GAM1273 LOC147632 5'	TGGTGGAATGAGATG 56670	C	
	CATTTCA TTTCAGT		
	GTAGAGT AAGGTGGT		
	—		
GAM1273 LOC148413 3'	GCAGTGAGGATGGAGTG 78830	CT	
	CATTTCA TTCACTGT		
	GTGAGGT GAGTGACG		
	AG		
GAM1273 LOC148479 3'	GTTCCCTGCAGTGGAGGTGGAC 78879	T CT_ AT	
TG	CA TTCACTTTCACTGT GAG		
	GT AGGTGGAGGTGACG CTT		
	C TCC G		
GAM1273 LOC148529 5'	TCTTAGGCGAGTGGGAG 84172	TT _	
	CT CACT GTCTGAGA		

	GA GTGA CGGATTCT		
	GG G		
GAM1273 LOC149076 3'	ATCTTGAGGGCAGGGAGGTGAG 79148	A	___
G	TTTCACTTTC CTGTCT GAGAT		
	GGAGTGGAGG GACGGA TTCTA		
	___ GG		
GAM1273 LOC149182 5'	TCTTGTGCAGGGTGAGATG 84379	TTCA	CT
	CATTTCAC CTGT GAGA		
	GTAGAGTGG GACG TTCT		
	___ TG		
GAM1273 LOC149711 3'	ATTTCACCTGCTTGGAAAGTGA 84673	ACT C	___
GATG	ATTTCACTTTC GT TGAGAT		
	TAGAGTGAAAG CG ACTTTA		
	GTT TCC		
GAM1273 LOC149837 5'	GTTTTGAGGGTGGAATGAGGTG 84745	C	G T
	CATTTCATTTTCACT TC GAGAT		
	GTGGAGT AAGGTGG AG TTTTG		
	___ G _		
GAM1273 LOC149844 5'	GGTGGTGGGGGTGGTGGTG 79519	_	TT TG
	CATT TCACT CAC TC		
	GTGG GGTGG GTG GG		
	T GG GT		
GAM1273 LOC149844 3'	TGGTGAGTGAGATG 79521	TT	
	CATTTTCACTCACTG		
	GTAGAGTG AGTGGT		
	___		
GAM1273 LOC150225 3'	GTCTTTTGCAGGTGAAGGTGGG 85009	TT	_ CT
A	T CACTTTCAC TGT GAGAT		
	A GTGGAAGTG ACG TTCTG		
	GG G TT		
GAM1273 LOC150351 5'	TTTGTAGATAGTACGAAGT 60249	C	_
	ACTTT ACTGTCTGAGA		
	TGAAG TGATAGATTTT		
	CA		
GAM1273 LOC150358 3'	TCTCAGAGAGTGAAGTGA 84928	T	G
	TCACTT CACT TCTGAGA		
	AGTGAA GTGA AGACTCT		
	___ G		
GAM1273 LOC150819 5'	GTTAGGGAGCAGTGAAAGTGAG 85122	___	GAT
G	TTTCACTTTCACCTGT CTGA		

		GGAGTGAAAGTGACG	GATT	
		AGG	G	
GAM1273	LOC150933 3'	AT TTCAGTCACAGGAAATGGGG	85156	TT C A _
	TG	CAT CA TTTC CTGT CTGAGAT		
		GTG GT AAAG GACA GACTTTA		
		GG _ _ CT		
GAM1273	LOC151056 3'	ATCTTTTGGGAGTGAAGTGA	80106	T TT CTGTCT
		CA TTCACT CA GAGAT		
		GT AAGTGA GT TTCTA		
		C GG TTT_		
GAM1273	LOC151176 3'	GTTTTGATAAGGGGGTGATGTG	85263	T TT AC T
		CAT TCACT C TGTC GAGAT		
		GTG AGTGG G ATAG TTTTG		
		T GG A_ _		
GAM1273	LOC151194 3'	ATTTTAGATGGTGAAATTAGAA	59213	AC_
	GT	ATTTC TTTCAGTGTCTGAGAT		
		TGAAG AAAGTGGTAGATTTTA		
		ATT		
GAM1273	LOC151414 3'	ATTTTGGCATATGGGGGTGGAG	80235	TT C _ TG
		TTTCACT CA TGT C AGAT		
		GAGGTGG GT ATA G TTTA		
		GG _ C GT		
GAM1273	LOC151438 5'	TTTTCGGTGTGAAGGTGGGATG	85373	TT TGT T
		CAT CACTTTCAC CTGAGA		
		GTA GTGGAAGTG GGCTTT		
		GG T_ TT		
GAM1273	LOC151610 3'	GGATGGTGGGAGTGAAG	80288	TT
		TTTCACT CACTGTCT		
		GAAGTGA GTGGTAGG		
		GG		
GAM1273	LOC151658 5'	GTGGTGGAGTGGAGTG	85481	T TG
		CATTTCAC TT CAC T		
		GTGAGGTGAG GTG G		
		_ GT		
GAM1273	LOC151826 3'	TTT TAGGCTAGTGAAA	80370	_
		TTTCACT GTCTGAGA		
		AAAGTGA CGGATTTT		
		T		
GAM1273	LOC151904 5'	CCCTGCGTGGTGGAGGGAGGTG	80387	A TG CTGAGAT
		CATTTC CTTTCAC T		

GTGGAG GGAGGTG G  
 \_ GT CGTCCCT  
 GAM1273 LOC152274 3' TCTTGGATTGGATGAGATG 80509 CT CT TG  
 CATTTC A TTCA GTC AGA  
 ||||| ||| ||| |||  
 GTAGAGT AGGT TAG TCT  
 \_ \_ GT  
 GAM1273 LOC152275 3' GGGGGCGACAGGGAGGTGGGAT 85620 TT A TGAGAT  
 G CAT CACTTTC CTGTC  
 ||| ||||| |||||  
 GTA GTGGAGG GACAG  
 GG \_ CGGGGGT  
 GAM1273 LOC152633 5' GTCTTGCTGTGCTGGGGGTGGG 85817 TT TT CTGTCT\_  
 GTG CAT CACT CA GAGAT  
 ||| ||| || |||||  
 GTG GTGG GT TTCTG  
 GG GG CGTGTCTG  
 GAM1273 LOC152805 5' TCTCAGGATGAGTGAGG 80689 TCACTG  
 TTTCACTT TCTGAGA  
 ||||| |||||  
 GGAGTGAG GGA CTCT  
 TA\_\_\_\_  
 GAM1273 LOC153196 5' GTCTTAGAGCTAGAGATGAGGT 85975 C ACTG  
 G CATTTC A TTTC TCTGAGAT  
 ||||| ||| |||||  
 GTGGAGT AGAG AGATTCTG  
 \_ ATCG  
 GAM1273 LOC153222 3' TTTTGGAGGAGTGAAAT 80791 CACTG TG  
 ATTTCACTTT TC AGA  
 ||||| || |||  
 TAAAGTGAGG AG TTT  
 \_ GT  
 GAM1273 LOC153339 5' GTTTTGGTGGGGTGGTGGGATG 86012 TT T A T TG  
 CAT CACT TC CTG C AGAT  
 ||| ||| || ||| |||  
 GTA GTGG GG GGT G TTTG  
 GG T \_ \_ GT  
 GAM1273 LOC153651 3' TTTTAGATGGTGATTGT 80918 TT  
 AC TCACTGTCTGAGA  
 || |||||  
 TG AGTGGTAGATTTT  
 TT  
 GAM1273 LOC153711 3' TCGGGTGGGAGAGGGA 86138 A A TG  
 TTC CTTTC C TCTGA  
 ||| ||| || |||||  
 AGG GAGAG G GGGCT  
 \_ \_ GT  
 GAM1273 LOC153811 3' GCAGTGGGGGTAAGGTG 80950 C TT  
 CATTT ACT CACTGT  
 ||||| ||| |||||

	GTGGA TGG GTGACG		
	A GG		
GAM1273 LOC154386 3'	GTTTCAGTTCTGGAAGGTGAAA 81084	ACTGT	
	TTTCACTTTC CTGAGAT		
	AAAGTGAAG GACTTTG		
	GTCTT		
GAM1273 LOC154792 3'	TTTTGGATATGTGAGAG 86250	_ TG	
	CTTTCAC TGTC AGA		
	GAGAGTG ATAG TTT		
	T GT		
GAM1273 LOC154877 3'	GTCTTTACTGAGGGTGGCAGTG 86306	T G T__	
	CACT TCACT TC GAGAT		
	GTGA GGTGG AG TTCTG		
	C G TCAT		
GAM1273 LOC157623 5'	CAACGAGGCGGTGTGGGTGGAG 81493	TT GAGAT	
TG	CATTTCACT CACTGTCT		
	GTGAGGTGG GTGGCGGA		
	GT GCAACT		
GAM1273 LOC157693 3'	TCTTGGACGCAGTGAAGT 81558	TTCAC TG	
	ATTTCACT TGTC AGA		
	TGAAGTGA GCAG TCT		
	C__ GT		
GAM1273 LOC157918 3'	GTCTTGGGCACAGGTGGGGT 86649	TT TCAC TG	
	AT CACTT TGTC AGAT		
	TG GTGGA ACGG TCTG		
	GG C__ GT		
GAM1273 LOC157919 3'	GTTTCAGACAGTGGAA 81637		
	TTTCACTGTCTGAGAT		
	AAGGTGACAGACTTTG		
GAM1273 LOC158117 3'	GGCGTGGTGGGAATGGAATG 81709	C _	
	CATTTCA TTTCAT GTC		
	GTAAGGT AAGGTGG CGG		
	_ TG		
GAM1273 LOC158382 5'	ACGGGGGAAGTGAGGTG 86782	A	
	CATTTCACTTTC CTGT		
	GTGGAGTGAAGG GGCA		
	G		
GAM1273 LOC158382 5'	GTGGTGGGAAGATGAAGTG 86789	_ TG	
	CATTTCA CTTTCAC T		

	GTGAAGT GAAGGTG G	
	A GT	
GAM1273 LOC158954 3'	TTTTGGGTGGGGGGGAAGTG 60437	A TT TGT TG
	CATTTC CT CAC C AGA	
	GTGAAG GG GTG G TTT	
	G GG ___ GT	
GAM1273 LOC159184 5'	TCAATGGTGAAGGTGAAGT 60051	C
	ATTTCACTTTCACTGT TGA	
	TGAAGTGGAAGTGGTA ACT	
	—	
GAM1273 LOC163882 3'	ATGCTGGCAGTGAGAGTGAAA 82163	TGAGAT
	TTTCACTTTCACTGTC	
	AAAGTGAGAGTGACGG	
	TCGTA	
GAM1273 LOC166983 5'	GTCTGGCCCAAGGGGAGGTGGA 87266	A ___ T GAT
	GTG TTTCACTTTC CT GTC GA	
	GAGGTGGAGG GA CGG CT	
	G ACC T G	
GAM1273 LOC169436 5'	GGGGTAGATGTGGGGGTGGAAT 82743	TT T AGAT
	G CATTTCACT CAC GTCTG	
	GTAAGGTGG GTG TAGAT	
	GG _ GGGGT	
GAM1273 LOC196761 3'	GTTTTGGGCAGTGGAG 89556	TG
	TTTCACTGTC AGAT	
	GAGGTGACGG TTTG	
	GT	
GAM1273 LOC197379 3'	GATGGTGAGGGTGGGGT 89742	TT
	AT CACTTTCACTGTC	
	TG GTGGGAGTGGTAG	
	GG	
GAM1273 LOC197414 3'	ATTTTGGGCAGGCGCTGAGTGG 88061	TT TCA__ TG
	GG T CACTT CTGTC AGAT	
	G GTGAG GACGG TTTA	
	GG TCGCG GT	
GAM1273 LOC201203 3'	ATCTCAGATTGTGAGGTAAATG 88140	C T T
	CATTT ACTT CAC GTCTGAGAT	
	GTAAA TGGA GTG TAGACTCTA	
	_ _ T	
GAM1273 LOC201895 3'	TCTTAGGCCAGTGCAGTG 89094	TT _
	CACT CACTG TCTGAGA	

	GTGA GTGAC GGATTCT		
	C_ C		
GAM1273 LOC202152 3'	ATCTCAGATTTAAAAACGTGGG 89157	TT _	CACT
	ATG CAT CAC TTT GTCTGAGAT		
	GTA GTG AAA TAGACTCTA		
	GG C AATT		
GAM1273 LOC203275 3'	GGCGTG GTGGAATGGAATG 89325	C _	
	CATTTCA TTTCAC T GTC		
	GTAAGGT AAGGTGG CGG		
	_ TG		
GAM1273 LOC203317 5'	GTCTTGCCAATGGAAGTTGGAG 89333	_	C TC
	TG CATTTCA CTTTCA TG TGAGAT		
	GTGAGGT GAAGGT AC GTTCTG		
	T A C_		
GAM1273 LOC219333 3'	GTCAGGGCAGTGGAAAGTGGA 93542		GA
	TTCACTTTCACTGTCT GAT		
	AGGTGAAGGTGACGGG CTG		
	A_		
GAM1273 LOC219529 3'	GTCTCAGGTGAGTGGAGG 92972	_ GT	
	CTTTCAC T CTGAGAT		
	GGAGGTG G GACTCTG		
	A TG		
GAM1273 LOC220143 5'	GCGGGAGGGTGAAATG 93589		A
	CATTTCACTTTC CTGT		
	GTAAAGTGGGAG GGCG		
	_		
GAM1273 LOC220549 5'	GCGGTGAGAGAGAGGTG 92919		A
	CATTTC CTTTCACTGT		
	GTGGAG GAGAGTGGCG		
	A		
GAM1273 LOC220739 5'	ATTTCCCATGGGAGTGGAGT 92925	TT C	TCT
	ATTTCACT CA TG GAGAT		
	TGAGGTGA GT AC CTTTA		
	GG _ C_		
GAM1273 LOC221400 3'	GTCTCAGGTTGATGGTGGGGTG 92299	TT T	CTG
	CAT CACT TCA TCTGAGAT		
	GTG GTGG AGT GGACTCTG		
	GG T T_		
GAM1273 LOC221405 3'	TTT TAGATTAGTGGA 93892	_	
	TTTCACTG TCTGAGA		



		AAGGTGAT AGATTTT	
		T	
GAM1273	LOC221415 3'	TTTCCTGGGGGTTGAGGTG 93878	C G T_
		CACTTT ACT TC GAGA	
		GTGGAG TGG GG CTTT	
		T G TC	
GAM1273	LOC221584 3'	TCTCGAGAGAAAAGGGAGTG 93833	A A GTC
		CATTTC CTTTC CT TGAGA	
		GTGAGG GAAAG GA GCTCT	
		_ A _	
GAM1273	LOC221683 5'	GTCTTAGGTTTTGGTGTGA 93717	TT CT
		TCAC TCA GTCTGAGAT	
		AGTG GGT TGGATTCTG	
		T_ TT	
GAM1273	LOC221865 3'	ATTTTGGGTATATGGGGTGAAA 92486	CAC GT TG
	T	ATTTCACTTT T C AGAT	
		TAAAGTGGGG A G TTTA	
		TAT TG GT	
GAM1273	LOC222134 5'	ACAGTGAAGTGAAATG 94136	T
		CATTTCACTT CACTGT	
		GTAAAGTGAA GTGACA	
		_	
GAM1273	LOC245728 5'	TTCAGGCAATGAAGTG 91135	T C
		CACTT CA TGTCTGAG	
		GTGAA GT ACGGACTT	
		_ A	
GAM1273	LOC253115 3'	ATTTTTATTGTGGGGTGGGATG 94494	TT T TGTCT
		CAT CACTT CAC GAGAT	
		GTA GTGGG GTG TTTTA	
		GG _ TTAT_	
GAM1273	LOC254485 3'	CTGGGAAGTGAGGTG 95013	T G G
		CACTT CACT TCT AG	
		GTGGA GTGA AGG TC	
		_ _ G	
GAM1273	LOC254755 3'	GCAGGGAGGTGGGGTG 97369	TT A
		CAT CACTTTC CTGT	
		GTG GTGGAGG GACG	
		GG _	
GAM1273	LOC254756 3'	GCAGGGAGGTGGGGTG 97363	TT A
		CAT CACTTTC CTGT	

	GTG GTGGAGG GACG		
	GG _		
GAM1273 LOC255391 5'	TCTCTGGGGGTGCGGTG 97614	TT	G T
	CACT CACT TC GAGA		
	GTGG GTGG GG CTCT		
	C_ G T		
GAM1273 LOC255394 3'	GTTTCAGACACTGCTTAGGTGC 94886	T	T_ C
AGTG	ATT CACTT CA TGTCTGAGAT		
	TGA GTGGA GT ACAGACTTTG		
	C TTC C		
GAM1273 LOC255452 5'	GTCTCTATCCGAGAGGGTGGAG 97543		ACTGTCT
TG	CATTTCACTTTC GAGAT		
	GTGAGGTGGGAG CTCTG		
	AGCCTAT		
GAM1273 LOC255480 3'	TCTTGAGGAGGTGAAGG 96521	GT	_
	CTTTCACT CT GAGA		
	GGAAGTGG GA TTCT		
	AG G		
GAM1273 LOC255779 3'	ATTTCCCATGCAAAGTGGGAT 96013	TT	_ C TCT
G	CAT CACTTT CA TG GAGAT		
	GTA GTGAAA GT AC CTTTA		
	GG C _ CC_		
GAM1273 LOC256145 5'	GTCTCGGGCATCGTGGG 96543		_
	TTCAC TGTCTGAGAT		
	GGGTG ACGGGCTCTG		
	CT		
GAM1273 LOC256405 5'	ATCTCAGGACCAGATAGTGGAG 95872	T	ACTG
TG	CATTTCACT TC TCTGAGAT		
	GTGAGGTGA AG GGA CTCTA		
	T ACCA		
GAM1273 LOC256639 5'	GTCTTGCTTCAGGAAGGTGAAG 96219	A	TC_
TG	CATTTCACTTTC CTG TGAGAT		
	GTGAAGTGGAAG GAC GTTCTG		
	_ TTC		
GAM1273 LOC257048 3'	TATGTAGGTAGTGGGGGGAAAT 96216	A TT	GT AGAT
G	CATTTTC CT CACT CTG		
	GTAAAG GG GTGA GAT		
	_ GG TG GTATT		
GAM1273 LOC257554 5'	ATCTCAGATTGTGGGGGTGTGG 97691	_	TT T
ATG	CATTT CACT CAC GTCTGAGAT		

	GTAGG GTGG GTG TAGACTCTA		
	T GG T		
GAM1273 LOC257556 3'	ATTTTTATTGTGGGGTGGGATG 97707	TT	T TGTCT
	CAT CACTT CAC GAGAT		
	GTA GTGGG GTG TTTTA		
	GG _ TTAT_		
GAM1273 LOC257617 3'	ATTTTTATTGTGGGGTGGGATG 97813	TT	T TGTCT
	CAT CACTT CAC GAGAT		
	GTA GTGGG GTG TTTTA		
	GG _ TTAT_		
GAM1273 LOC51107 3'	TTTCTGCTGAGGGTGGAGTG 32064	CT	CT
	CATTTCACTTTCA GT GAGA		
	GTGAGGTGGGAGT CG CTTT		
	_ T_		
GAM1273 LOC51152 3'	GTCTCAAAGGAGAAAGTGAGGT 32454	A	GTC
G	CATTTCACTTTC CT TGAGAT		
	GTGGAGTGAAAG GG ACTCTG		
	A AA_		
GAM1273 LOC51716 3'	GCAGTGAAGGTGAGGT 32792		
	ATTTCACTTTTCACTGT		
	TGGAGTGGAAGTGACG		
GAM1273 LOC56912 5'	CTCACGAGAGTGGAAG 39336	G	_
	CTTTCAC TC TGAG		
	GAAGGTGA AG ACTC		
	G C		
GAM1273 LOC56959 5'	TCTTGACCGGAGGTGGAA 81927	ACT	T
	TTTCACTTTC GTC GAGA		
	AAGGTGGAGG CAG TTCT		
	C_ _		
GAM1273 LOC89135 3'	TGGTGAGTGAGATG 60319	TT	
	CATTTCAC TCACTG		
	GTAGAGTG AGTGGT		
GAM1273 LOC90170 5'	GGTGGTGAGGGTTAAATG 61710	C	TG
	CATTT ACTTTCAC TC		
	GTAAA TGGGAGTG GG		
	T GT		
GAM1273 LOC90826 5'	GTCTTGGGTTTGGGAATGTGAAA 64095	_	CTG TG
TG	CATTTCAC TTTCA TC AGAT		

GTAAAGTG AAGGT GG TCTG  
 T TT\_ GT  
 GAM1273 LOC91363 3' ATCTCAGAACAGAAAGGGTGGGA 65776 TT CA \_  
 T CACTTT CTGT CTGAGAT  
 | ||||| ||| |||||  
 A GTGGGA GACA GACTCTA  
 GG A\_ A  
 GAM1273 LOC91450 3' GTTTTGGGCAGAGGAGTGGGG 66076 TT CA TG  
 T CACTTT CTGTC AGAT  
 | ||||| |||| |||  
 G GTGAGG GACGG TTTG  
 GG A\_ GT  
 GAM1273 LOC91628 3' GCAGTGGATGTGGGATG 66760 TT T  
 CAT CAC TTCACTGT  
 ||| ||| |||||  
 GTA GTG AGGTGACG  
 GG T  
 GAM1273 LOC92305 3' GTCTCAGACTCCTGGGTAGGGG 56418 TT\_ TCACT  
 TG CAT C ACTT GTCTGAGAT  
 ||| | ||| |||||  
 GTG G TGGG CAGACTCTG  
 GG A TCCT\_  
 GAM1273 LOC93349 3' CTTAGGCGGATGGAGG 56457 \_  
 CTTTCA CTGTCTGAG  
 ||||| |||||  
 GGAGGT GGCGGATTC  
 A  
 GAM1273 LOC93587 3' TAGGAGAAAAGTGAGGTG 72648 A\_  
 CATTTCACTTTC CTG  
 ||||| |||  
 GTGGAGTGAAAG GAT  
 AG  
 GAM1274 EDNRA 3' CTACATCTTTTCAACAAGT 64108 GTC TT  
 GCT TG AAAGATGTAG  
 ||| || |||||  
 TGA AC TTTCTACATC  
 ACA T\_  
 GAM1274 FGF12 3' CTCCAACAGACAGGAT 40721 G AA  
 ATC CTGTCTGTT AG  
 ||| ||||| ||  
 TAG GACAGACAA TC  
 \_ CC  
 GAM1274 AKAP6 3' ACTGAATGTTAACAGACAG 14987 AGATG  
 CTGTCTGTTAA TAGT  
 ||||| |||  
 GACAGACAATT GTCA  
 GTAA\_  
 GAM1274 DKFZP564D0372 3' ACTACATCTTTAGAGGAAGC 48513 G G  
 GCT TCT TTAAAGATGTAGT  
 ||| ||| |||||

CGA AGG GATTTCTACATCA  
 \_ A  
 GAM1274 FLJ12552 3' CTACATCTTTCCAGC 43091 TCTGTT  
 GCTG AAAGATGTAG  
 ||| |||||  
 CGAC TTTCTACATC  
 C\_\_\_\_

GAM1274 KIAA0544 3' CACATCCTGGACAGCAGC 70891 T AAA A  
 GCTG CTGTT GATGT G  
 ||| ||| |||||  
 CGAC GACAG CTACA C  
 \_ GTC C

GAM1274 WDR7 3' ACTACATCTCTATTTGGAATGA 30954 CTG TGT A  
 T ATCG TC TA AGATGTAGT  
 ||| || |||||  
 TAGT GG AT TCTACATCA  
 AA\_ TTT C

GAM1274 LOC221715 3' CTACATCAAGACAGCGAT 93752 GTTAAA  
 ATCGCTGTCT GATGTAG  
 ||||| |||||  
 TAGCGACAGA CTACATC  
 A\_\_\_\_

GAM1275 ADH1B 3' CTTAGACATAAAGTAAAAT 72644 C CAC  
 ATTT ACTTT TGTCTGAG  
 ||| ||| |||||  
 TAAA TGAAA ACAGATTC  
 A T\_\_

GAM1275 AHR 3' ATCTCAGATGTTAAATAAATG 7875 CAC C T  
 CATTT TTT AC GTCTGAGAT  
 |||| ||| |||||  
 GTAAA AAA TG TAGACTCTA  
 TA\_ T \_

GAM1275 FDFT1 3' TAGGAAAGTGAAATG 15518 A  
 CATTTCACTTTC CTG  
 ||||| |||  
 GTAAAGTGAAAG GAT

GAM1275 JTB 3' ATCTCAGACAGTGAAAGTGAAA 21959  
 TG CATTTCACTTTCACTGTCTGAGAT  
 |||||  
 GTAAAGTGAAAGTGACAGACTCTA

GAM1275 KLF4 3' TCCCAGACAGTGGATATG 14891 CT A  
 CA TTCACTGTCTG GA  
 || ||||| ||  
 GT AGGTGACAGAC CT  
 AT C

GAM1275 PHYH 3' ACAGTAAAAGTGAAAT 20608 C  
 ATTTCACTTT ACTGT  
 ||||| |||||

			TAAAGTGAAA TGACA		
			A		
GAM1275	PKD2	3'	TCCAGGTTGAAAAGTGAAA 60096	CTG	A
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T__ _		
GAM1275	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1275	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA	CTG
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1275	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT	CT
			TTCAC TTTCA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1275	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G	T_
			CTTTCACT TC GAGAT		
			GAAAGTGA AG TTCTA		
			G TC		
GAM1275	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT 45802	ACTTTCACT	
	G		CATTTT GTCTGAGAT		
			GTAAAG CAGACTCTA		
			AAACATTT_		
GAM1275	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281	CTT	
			CATTTCA TCACTGTCTGAGAT		
			GTAAAGT AGTGACAGACTCTA		
			C_		
GAM1275	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C	TC
			TTCA TTTCACTG TGAG		
			AAGT AAAGTGAC GTTT		
			A CT		
GAM1275	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A	_
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1275	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T	
			ATT CACTTTCACTGT		

		TAA GTGAAAGTGACG		
		C		
GAM1275	PORIMIN	3' ATCTCAGAGGGCCAAAGTGAA	53598	CA G
		TTCACTTT CT TCTGAGAT		
		AAGTGAAA GG AGACTCTA		
		CC G		
GAM1275	PP35	3' ATCTCAGACTGAAA	22814 CT	
		TTTCA GTCTGAGAT		
		AAAGT CAGACTCTA		
		—		
GAM1275	PRTD-NY3	3' CTCATTGCAATAAGTGAAATG	48148	TCAC C_
		CATTTCACTT TGT TGAG		
		GTAAAGTGAA ACG ACTC		
		TA__ TT		
GAM1275	SEP15	3' TCCTACAGTAAGAGTGAAA	14934	C CT
		TTTCACTTT ACTGT GA		
		AAAGTGAGA TGACA CT		
		A TC		
GAM1275	SFXN2	3' CTCAGGGGAAAAAAGTGAAA	73941	CACTG
		TTTCACTTT TCTGAG		
		AAAGTGAAA GGA CTC		
		AAAGG		
GAM1275	LOC149703	3' ATCTCAGACAGCCGTTTGAAAA	84647	ACTTTCA
		TTTC CTGTCTGAGAT		
		AAAG GACAGACTCTA		
		GTTTGCC		
GAM1275	LOC154007	3' ATCTCAAACCCTTTAGTGAAA	81015	TTCACT C
		TTTCACT GT TGAGAT		
		AAAGTGA CA ACTCTA		
		TTTCC_ A		
GAM1275	LOC155004	3' TCATTTAAGTGAAAGGAAA	81226	A GTC_
		TTTC CTTTCACT TGA		
		AAAG GAAAGTGA ACT		
		_ ATTT		
GAM1275	LOC222134	5' ACAGTGAAGTGAAATG	94136	T
		CATTTCACTT CACTGT		
		GTAAAGTGAA GTGACA		
		—		
GAM1276	ARNT2	3' AAACAACCCGTGCATCCCTGC	29450	A TTTTA
		GTA GGAT GGGTTGTTT		

CGT CCTA CCCAACAAA  
C CGTG\_  
GAM1276 LCT 3' AACCGTAAAAATCCTT 9697 G  
AAGGATTTTTTA GGTT  
||||||| |||  
TTCCTAAAAAT CCAA  
G  
GAM1276 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
GTAAGGATTTTTAGGGTTGTTT  
|||||||  
CATTCCTAAAAATCCCAACAAA  
  
GAM1276 FBXO30 3' AACTAAAAAAATCCTGAC 49573 A AG  
GT AGGATTTTT GGTT  
|| ||||| |||  
CA TCCTAAAAA TCAA  
G AA  
GAM1276 KIAA0494 3' AACAACCCTTACTTAC 28736 GATTTTT  
GTAAG AGGGTTGTT  
|||| |||||  
CATTC TCCCAACAA  
AT\_\_\_\_  
GAM1276 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
TAAG TTTT GGGTTGTTT  
||| ||| |||||  
GTTC AAAA CCCAACAAA  
\_\_\_\_ C  
GAM1276 SMT3H2 3' AACAACATAAAAAATCCTTGC 22670 GG  
GTAAGGATTTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_  
GAM1276 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
GTAAGGATTTTTT GGGTT  
||||||| |||||  
CGTTCCTAAAAA TCCAA  
GTA  
GAM1276 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
GGAT TT GGGTTGTTT  
||| || |||||  
CCTG AA CCCAACAAA  
T\_ C  
GAM1276 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
C GTA GGATTTTT TTGTTT  
|| ||||| |||||  
CGT CCTAAAAA AACAAA  
C GATAA  
GAM1276 LOC148089 3' GGCCCTAAAAATTCCTAC 78637 A  
GTA GGATTTTTAGGGTT  
|| |||||



		CAT CTTAAAAATCCCGG		
		C		
GAM1276	LOC154547 3'	AACAACATAAAAAATCCTTGC	76050	GG
		GTAAGGATTTTGA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1276	LOC158104 3'	ACAGCCAAAAATCCTTA	60313	AG
		TAAGGATTTT GGTGT		
		ATTCCTAAAAA CCGACA		
		—		
GAM1276	LOC205880 5'	AAACAACCATCATCCTGAC	90709	A TTTAG
		GT AGGAT GGTGT		
		CA TCCTA CCAACAAA		
		G CTA_		
GAM1276	LOC221561 3'	AACAACATAAAAAATCCTTGC	92130	GG
		GTAAGGATTTTGA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1276	LOC257591 3'	AACAACATAAAAAATCCTTGC	97840	GG
		GTAAGGATTTTGA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1276	LOC51145 3'	AGCTAAAATCCTTAC	32393	TAG
		GTAAGGATTTT GGT		
		CATTCCTAAAA TCGA		
		—		
GAM1277	TGFA 3'	CCTAGCTTATTACATCGT	12250	TC TG
		ACG GTA ATAAGCTAGG		
		TGC CAT TATTCGATCC		
		TA _		
GAM1277	FLJ10620 3'	GCCTAGCTCATCAGTGGC	36359	GTA A
		GTC TGAT AGCTAGGC		
		CGG ACTA TCGATCCG		
		TG_ C		
GAM1277	SOUL 3'	GTTTATCATAGACATC	26718	C G
		GA GTC TATGATAAGC		
		CT CAG ATACTATTTG		
		A _		
GAM1278	ABCC11 3'	GTGGGGATTGCTGGATGGA	52506	_ TG CGTTC
		TCC TCCAG G TTTTAC		

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AGG AGGTC T AGGGGTG
T GT _____
GAM1278 ABCD1 5' CCCCGGGGAGGGGCGCCACCGG 3462 A ACT
GGGA TCCTCC GTGGCGTTCTTTTT
||||| |||||||||
AGGGGG CACCGCGGGGAGGG
C GCCCCG
GAM1278 ACVR1 5' GTGAGAGCTGCTGGAG 6611 TG GTTCT
CTCCAG GC TTTTAC
||||| || |||||
GAGGTC CG AGAGTG
GT _____
GAM1278 ADCY8 5' AGTAAAGAGGCTCCTGTAGGA 6649 C TG GTT
TCCT CAG GC CTTTTTACT
||||| || |||||||
AGGA GTC CG GAGAAATGA
T CT ____
GAM1278 ADRA2B 3' AGTGGGGCCTGCTGCTGAGGGG 5458 _ TG _ TTTTACT
G CCTC CAG GC GTTCT
||||| || |||||
GGGG GTC CG CGGGG
A GT TC TGA T
GAM1278 AGPAT2 3' GGTGGAAGCCGATGGCTGGAGG 21157 _ G TTTTACT
A CTCCAGT GGC TTCT
||||| || |||||
GAGGTCG CCG AAGG
GTAG _ TGG T
GAM1278 AGPAT2 3' GGTGGAAGCCGATGGCTGGAGG 65825 _ G TTTTACT
A CTCCAGT GGC TTCT
||||| || |||||
GAGGTCG CCG AAGG
GTAG _ TGG T
GAM1278 AMFR 3' AGTGGGAAGAGTGTGGGGGAGG 57241 AGTG
CCTCC GCGTTCTTTTACT
||||| |||||||||
GGAGG TGTGAGAAGGGTGA
GGG_
GAM1278 AMFR 3' AGTGGGAAGAGTGTGGGGGAGG 6694 AGTG
CCTCC GCGTTCTTTTACT
||||| |||||||||
GGAGG TGTGAGAAGGGTGA
GGG_
GAM1278 AMN 3' GTGAGGGGAGGGTGAGGA 48193 CAGTG G
TCCTC GC TTCTTTTAC
||||| || |||||||
AGGAG TG GAGGGGAGTG
_ G
GAM1278 ANK1 3' AGGAGCCGTTAGGGGA 60386 C G
TCCTC AGTGGC TTCT
||||| ||||| |||

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AGGGG TTGCCG AGGA  
 A \_  
 GAM1278 ANK1 3' AGGAGCCGTTAGGGGA 40024 C G  
 TCCTC AGTGGC TTCT  
 |||| |||| ||  
 AGGGG TTGCCG AGGA  
 A \_  
 GAM1278 ANK1 3' AGGAGCCGTTAGGGGA 3470 C G  
 TCCTC AGTGGC TTCT  
 |||| |||| ||  
 AGGGG TTGCCG AGGA  
 A \_  
 GAM1278 ANKRA2 5' AGTAGGAGGTGTGACCGGAGGG 43525 A G TT  
 TCCTCC GT GCG CTTTTTACT  
 |||| || || |||||  
 GGGAGG CA TGT GGAGGATGA  
 C G \_  
 GAM1278 AQP2 3' GGTAAGAGGGAAACTCTGGAG 4910 T CG  
 CTCCAG GG TTCTTTTACT  
 |||| || |||||  
 GAGGTC TC AGGGAGAATGG  
 \_ AA  
 GAM1278 ARHGEF5 3' GGTGGGGGGGATTTCGAGGGA 18364 AG C  
 TCC TGG GTTCTTTTACT  
 || || |||||  
 AGG GCT TAGGGGGGGTGG  
 GA T  
 GAM1278 ASB2 3' GGTAGGGGGAGCCTGGGTCTTG 32358 T \_  
 GAGGG CCAG GGC GTTCTTTTACT  
 |||| || |||||  
 GGTT CTG CGAGGGGGATGG  
 \_ GGTC  
 GAM1278 ATP1A2 3' AGGGCTGGCTGGAGGA 5520 GGC  
 TCCTCCAGT GTTCT  
 ||||| ||||  
 AGGAGGTCTG CGGGA  
 GT\_  
 GAM1278 ATP1B1 3' GGTGGGGGTTTGTGCATGGGGGA 8042 G TT T  
 TCCTCCA TGGCG CTTTT ACT  
 ||||| |||| |||| ||  
 AGGGGGT ACTGT GGGGG TGG  
 \_ TT \_  
 GAM1278 ATP2B2 5' GAGGGTGTGCTGAGGA 8066 C G TT  
 TCCTC AGTG CG CTT  
 |||| |||| || ||  
 AGGAG TCGT GT GAG  
 \_ \_ GG  
 GAM1278 ATP5G3 5' GGTGGGAAGAAGCCCTGG 8075 T \_  
 AGGG CCTCCAG GGC GTTCTTTTACT  
 ||||| || |||||

			GGAGGTC CCG CAAGAAGGGTGG		
			C GA		
GAM1278	ATP6V1A1	3'	GGCCTGCTATTGAGGA 8081	C	TT
			TCCTC AGTGGCG CT		
			AGGAG TTATCGT GG		
			_ CC		
GAM1278	AXL	5'	GGAGTTCTGGAGGA 8104	T	G
			TCCTCCAG GGC TTC		
			AGGAGGTC TTG AGG		
			- -		
GAM1278	AXL	5'	GGAGTTCTGGAGGA 41601	T	G
			TCCTCCAG GGC TTC		
			AGGAGGTC TTG AGG		
			- -		
GAM1278	BAIAP3	3'	AGTGAAAAGGGTGCCACTGG 14122		TT
			CCAGTGGCG CTTTTTACT		
			GGTCACCGT GAAAAGTGA		
			GG		
GAM1278	BAK1	3'	AGTAGGGAGTTCATCTGGAGGG 91987	_	CGTT
			TCCTCCAG TGG CTTTTTACT		
			GGGAGGTC ACT GAGGGATGA		
			T T__		
GAM1278	BAT5	3'	GTGAGAGGAGACATGAGGA 40967	CA	GCGT
			TCCTC GTG TCTTTTAC		
			AGGAG TAC AGGAGAGTG		
			_ AG__		
GAM1278	BAZ1B	3'	AGTGGTCAGTGTCGGTGGGGGG 50537	G	TT TT
			TCCTCCA TGGCG CT TTACT		
			GGGGGGT GCTGT GA GGTGA		
			G _ CT		
GAM1278	BMP1	3'	GGAGTCCCTGGGGGA 20424	T	G
			TCCTCCAG GGC TTC		
			AGGGGGTC CTG AGG		
			C _		
GAM1278	BRCA2	3'	GGTGGGAGGAGTGCTTGAGG 3551		CAGT
			CCTC GGCGTTCTTTTACT		
			GGAG TCGTGAGGAGGGTGG		
			T__		
GAM1278	BTEB1	3'	GGTAGGGAGTGGGTGGGGGG 6849		GTGGCGTT
			TCCTCCA CTTTTTACT		

			GGGGGGT	GAGGGATGG	
			GGGT_____		
GAM1278	CALM2	5'	AGTGGAGAGAGCGAGCTGAGTG 8226	TC_ GG	
	G		CC CAGT CGTTCTTTTACT		
			GG GTCG GCGAGAGAGGTGA		
			TGA A_		
GAM1278	CARP	3'	AGTGAAGAGAACGTCATGAG 26898	CA	
			CTC GTGGCGTTCTTTTACT		
			GAG TACTGCAAGAGAAGTGA		
			_____		
GAM1278	CARPX	5'	GGTGAGGGGGGCGGACTTCGAG 39424	C_ GG	
	GG		TCCTC AGT CGTTCTTTTACT		
			GGGAG TCA GCGGGGGGAGTGG		
			CT G_		
GAM1278	CCNG1	3'	TGGTATTGAAAATGCTATTGGA 14486	C TT	
	GGA		TCCTCCAGTGGCGTT TT TACT		
			AGGAGGTTATCGTAA AG ATGG		
			A TT TG		
GAM1278	CDC6	5'	GGTGGAAGAAGAGGATTGCTC 6985	C TG CG_	
	GAGGA		TC AG G TTCTTTTACT		
			AG TC T AAGAAAGGTGG		
			C GT AGGAG		
GAM1278	CDH7	5'	GGGCTGTGATTGGAGGA 15152	G _	
			TCCTCCAGT GC GTTC		
			AGGAGGTTA TG CGGG		
			G T		
GAM1278	CDX2	5'	AGTGGAAGGAGGTGGGAGGA 7009	AGTG G	
			TCCTCC GC TTCTTTTACT		
			AGGAGG TG AGGAAGGGTGA		
			G_ G		
GAM1278	CFTR	3'	TAAGGGGAATTGAGGA 4929	CAGTGGC	
			TCCTC GTTCTTTTAA		
			AGGAG TAAGGGGAAT		
			T_____		
GAM1278	CGB	5'	AGTGAGAGGAGAGGGCTGGGG 5599	GGCG	
			CTCCAGT TTCTTTTACT		
			GGGGTCG GAGGAGAGTGA		
			GGA_		
GAM1278	CHC1	3'	GGTGGGGAGAGAGGGTGGAGGG 7023	GTGGCG	
			TCCTCCA TTCTTTTACT		

			GGGAGGT GAGAGGGGTGG		
			GGGA__		
GAM1278	CHST5	3'	GGTGGAGAGGGAGCTGGGG 24030	GGCGT	
			CTCCAGT TCTTTTACT		
			GGGGTCG GGAGAGGTGG		
			AG__		
GAM1278	CHST6	3'	GGTAGGAGGAGAGAAGGCTGGG 41232	T GGCG_	
	GA		TCC CCAGT TTCTTTTACT		
			AGG GGTCTG GAGGAGGATGG		
			_ GAAGA		
GAM1278	CHST6	3'	GGTGAGAAGGAGGATGAAGGG 41233	C GTGGCG	
			TCCT CA TTCTTTTACT		
			GGGA GT AGGAAGAGTGG		
			A AGG__		
GAM1278	CKTSF1B1	3'	TGAAAAATCTGGAGGA 25371	TGGCGTTC	
			TCCTCCAG TTTTTA		
			AGGAGGTC AAAAGT		
			TA_____		
GAM1278	CLN5	5'	GGTAAAAGTTCGGTGTGTTGGGAG 21431	_GT G TT T	
	GA		TCCTCC A G CG CTTTT ACT		
			AGGAGG T T GC GAAAA TGG		
			G TG G TT _		
GAM1278	CLN6	3'	GGTGGGAGGGTGGGCCATGGAG 35410	G GT_	
	GG		TCCTCCA TGGC TCTTTTACT		
			GGGAGGT ACCG GGGAGGGTGG		
			_ GGT		
GAM1278	CLN6	3'	GTAGGGGGGGGTGTGGG 35411	AGTG TT	
			TCC GCG CTTTTTAC		
			GGG TGT GGGGGATG		
			___ GG		
GAM1278	CNN1	3'	GGGGGGCCCATTGGGGGG 7116	C	
			TCCTCCAGTGG GTTCTTT		
			GGGGGGTTACC CGGGGGG		
			_		
GAM1278	CNN2	3'	AGTGGAGAGAGTGCTAGGA 15174	AG	
			TCC TGGCGTTCTTTTACT		
			AGG ATCGTGAGAGAGGTGA		
			___		
GAM1278	COL4A6	3'	AGTAGAGGGGGTGGGTGCGTAG 53317	CCA GG_ TT	
	GA		TCCT GT CG CTTTTTACT		

			AGGA CG GT GGGAGATGA		
			TG_ TGG GG		
GAM1278 COL5A3	3'	GGTGGGAGGGACCGTGAGGG	31696	CAGTG _	
		TCCTC GCG TTCTTTTACT			
		GGGAG TGC AGGGAGGGTGG			
		_____ C			
GAM1278 COMP	3'	AGTGAGAAGGGCTCAGAGAGGA	3635	CAG C	
		TCCTC TGG GTTCTTTTACT			
		AGGAG ACT CGGGAAGAGTGA			
		AG_ _			
GAM1278 CRYZL1	5'	GGTGAAGGTGCAGGCCGTTGGG	17580	__ TC	
G		CTCCAGTGGC GT TTTTACT			
		GGGGTTGCCG CG GGAAGTGG			
		GA T_			
GAM1278 CSF1R	5'	GTGAGGAGAAGGTGGAG	17803	AGTG G	
		CTCC GC TTCTTTTAC			
		GAGG TG AAGAGGAGTG			
		_____ G			
GAM1278 CST	3'	GGTGAGGGGGGGCTCCCTGGGG	16791	T C _	
GG		TCCTCCAG GG GTTCTT TACT			
		GGGGGGTC CC CGGGGGG AGTGG			
		_ T G			
GAM1278 CTSH	3'	GGTGAAATCCTGCCCTGGAGG	15248	T TTC	
A		TCCTCCAG GGCG TTTTACT			
		AGGAGGTC CCGT AAAGGTGG			
		_ CCT			
GAM1278 CYP19	5'	GGAGTGTCTTGGGGGG	48336	TG	
		TCCTCCAG GCGTTCT			
		GGGGGGTT TGTGAGG			
		CT			
GAM1278 CYP51	3'	GGTGAAACAATTGTTGAGGGGG	5786	AG TTCT	
		CCTCC TGGCG TTTTACT			
		GGGGG GTTGT AAAGTGG			
		A_ TAAC			
GAM1278 DAXX	5'	AGTGGAAGGAAGGCGGAGGG	7212	AGTG G_	
		TCCTCC GC TTCTTTTACT			
		GGGAGG CG AGGAAGGGTGA			
		_____ GA			
GAM1278 DDAH2	5'	AGTGGGGGTGGCCGCTGGAG	25661	_ TT TTT	
		CTCCAGTGGC G CT TACT			

			GAGGTCGCCG T GG GTGA		
			G GG ____		
GAM1278	DGAT2	5'	ACCTAGAGGATGCCACTAGAGG 50786	C	TTACT
	A		TCCTC AGTGGCGTTCTTT		
			AGGAG TCACCGTAGGAGA		
			A TCCA		
GAM1278	DLG4	5'	GGTGAGAGGAGGCCAGGAGGA 7256	AGT G	
			TCCTCC GGC TTCTTTTACT		
			AGGAGG CCG GAGGAGAGTGG		
			AC_ _		
GAM1278	DPYS	5'	GGTGGGGACCTTGCAGGAGGG 7285	A TG C	TTT
			TCCTCC G G GTTCT TACT		
			GGGAGG C T CAGGG GTGG		
			A GT C ____		
GAM1278	DPYSL3	3'	AGTGGAAGGGTGTGTTGGGA 7310	AGT TT	
			TCC GGCG CTTTTTACT		
			AGG TTGT GAAAGGTGA		
			GT_ GG		
GAM1278	DSCR1	3'	GGTAAGAGGGAGCCGGTTTGGG 15336	CT _ G	
	AGA		C CCAG TGGC TTCTTTTACT		
			G GGTT GCCG AGGGAGAATGG		
			AG TG _		
GAM1278	DTR	3'	AGAGTGCCACTGCGGGA 8688	C	
			TCCT CAGTGGCGTTCT		
			AGGG GTCACCGTGAGA		
			C		
GAM1278	ELK1	3'	GGTGGGAAGGAAGGGATTTGGG 17844	TGGCG_	
	GGG		TCCTCCAG TTCTTTTACT		
			GGGGGGTT AGGAAGGGTGG		
			TAGGGA		
GAM1278	EPB49	3'	GTGAGAGGAATGAGGGG 8790	AGTGG	
			CTCC CGTCTTTTAC		
			GGGG GTAAGGAGAGTG		
			A____		
GAM1278	EPHA1	3'	AGTAAAAGGATGATCATGGGAG 17858	A _ T	
	GG		TCCTCC GTGG CGT CTTTTTACT		
			GGGAGG TACT GTA GGAAAATGA		
			G A _		
GAM1278	EPHB2	3'	AGTAAAAGGGATACAGGGGA 15441	CAG GC	
			TCCTC TG GTTCTTTTACT		



AGGGG AC TAGGGAAAATGA  
 \_\_\_\_ A\_  
 GAM1278 EPHB6 5' AGAAAAAGGGGTGGCTGTTGGA 15464 TG \_ TT ACT  
 GGA TCCTCCAG GC G CTTTTT  
 ||||| || |||||  
 AGGAGGTT CG T GGAAAA  
 GT G GG AGA  
 GAM1278 ERBB2IP 3' GGTGAAGGTGGTGGCTGGTGGG 37986 T G TTC  
 TCC CCAGTG CG TTTTACT  
 || ||||| || |||||  
 GGG GGTCGT GT GGAAGTGG  
 T G \_\_\_\_  
 GAM1278 EXTL3 3' GAATGTCACTGGTGGGA 7531 T  
 TCC CCAGTGGCGTTC  
 || |||||  
 AGG GGTCAGTGTAAAG  
 T  
 GAM1278 EZH1 3' AGTAGAAAGGGTGTGGGCGGG 8812 T AGTG TT  
 TCC CC GCG CTTTTACT  
 || || || |||||  
 GGG GG TGT GAAAGATGA  
 C G \_\_\_\_ GG  
 GAM1278 F2RL3 3' TGGTGGGGGTGGACAGTGTGTG 14196 \_\_\_\_ \_ \_  
 CTGGGGGG AGTG GC GTTC TTTTACT G  
 || || || ||||| |  
 TCGT TG CAGG GGGGGTGG T  
 GTG A T  
 GAM1278 FCN2 3' GGTAAGTCCAGGCCTTTGGG 31733 T GTTC\_  
 GGA TCCTCCAG GGC TTTTACT  
 ||||| || |||||  
 AGGGGGTT CCG GAAAATGG  
 T GACCT  
 GAM1278 FCN2 3' GGTAAGTCCAGGCCTTTGGG 31743 T GTTC\_  
 GGA TCCTCCAG GGC TTTTACT  
 ||||| || |||||  
 AGGGGGTT CCG GAAAATGG  
 T GACCT  
 GAM1278 FCN2 3' GGTGGGGGTGACACTGGGAGG 31744 \_ G TT TTT  
 CCTCC AGTG CG CT TACT  
 |||| |||| || || ||||  
 GGAGG TCAC GT GG GTGG  
 G A GG \_\_\_\_  
 GAM1278 FGF2 5' AGTAGGGGGCGGCGCGCAGGAG 8867 A G \_  
 GG TCCTCC GTG CGTT CTTTTTACT  
 |||| || || || |||||  
 GGGAGG CGC GCGG GGGGGATGA  
 A \_ C  
 GAM1278 FOSB 3' GGTGGGAGGTAGGCTGTGGGG 22109 G GTT  
 CTCCA TGGC CTTTTTACT  
 |||| || || |||||

		GGGGT GTCG GGAGGGTGG	
		_ GAT	
GAM1278 FRZB	5'	TGGTAAAGCTCGTGGGACCCCA 7593	C _____
		TTGGGGGA	AGTGG GTTCT TTTTACT G
		TTACC CAGGG GAAATGG T	
		C TGCTC	
GAM1278 GEM	5'	AGTAAGGGGGACGGCCCGAG 17928	CAGT _
		CTC GGC GTTCTTTTACT	
		GAG CCG CAGGGGGAATGA	
		C__ G	
GAM1278 GJB1	3'	GGTAAGAGGAGCAGAGGGCAGG 59972	_ AGTGGC
G		TCCT CC GTTCTTTTACT	
		GGGA GG CGAGGAGAATGG	
		C GAGA__	
GAM1278 GLUL	3'	AGTGGGGAGGAGGGTGGGGAG 9040	AGTG G _
		CTCC GC TTCTTTTT ACT	
		GAGG TG GAGGAGGG TGA	
		GG__ G G	
GAM1278 GNPI	3'	AGTGGGAGGTCCACTGGGG 18444	CGTT
		CTCCAGTGG CTTTTTACT	
		GGGGTCACC GGAGGGTGA	
		T__	
GAM1278 GPT	3'	GTGGGGGGGGGTGCTGGG 17966	GTG TT
		TCCA GCG CTTTTTAC	
		GGGT CGT GGGGGGTG	
		__ GG	
GAM1278 GSS	3'	GGTAGGAGGAGGGGGAGTGGAG 3931	GTGGCG
GG		TCCTCCA TTCTTTTACT	
		GGGAGGT GAGGAGGATGG	
		GAGGGG	
GAM1278 GTF2IRD1	5'	GGGGCGCCGCTGGCAGGA 32894	_
		TCCT CCAGTGGCGTTCT	
		AGGA GGTCGCCGCGGGG	
		C	
GAM1278 GZMM	3'	GGTGGGAGGGACAGGGAGGG 18012	AGTGGC
		TCCTCC GTTCTTTTACT	
		GGGAGG CAGGGAGGGTGG	
		GA__	
GAM1278 HDGF	3'	GGTGGGGGCAGCACAGGAGGG 15684	A GC TTT
		TCCTCC GTG GTTCT TACT	

		GGGAGG CAC CGGGG GTGG	
		A GA ____	
GAM1278 HK2	3'	GGTGGAGGGGTGACAGTGGAGG 3953	G GCGT
A		TCCTCCA TG TCTTTTACT	
		AGGAGGT AC GGGGAGGTGG	
		G AGT_	
GAM1278 HKE4	3'	GGTGCTGGGGCTGCTGGGGGG 22731	TG GTT TT
		TCCTCCAG GC CTT TACT	
		GGGGGGTC CG GGG GTGG	
		GT ____ TC	
GAM1278 HOXB13	3'	GGTGGGAGGAGCGAAAGTGGGG 21013	GTGG
G		CCTCCA CGTTCTTTTACT	
		GGGGGT GCGAGGAGGGTGG	
		GAAA	
GAM1278 HOXB13	5'	GGTGGGGAGAGCGAGCTGGG 21014	GG
		TCCAGT CGTTCTTTTACT	
		GGGTCTG GCGAGAGGGGTGG	
		A_	
GAM1278 HOXB9	3'	GTGGGGAGGGCGAGGGG 43778	AGTGG
		CTCC CGTTCTTTTAC	
		GGGG GCGGGAGGGGTG	
		A____	
GAM1278 HPCA	5'	GGTGTCTCCGCGTCTGGGTG 9256	_ TCTTTT
G		CC TCCAGTGGCGT TACT	
		GG GGGTCGCTGCG GTGG	
		T CCTCT_	
GAM1278 HSD17B1	5'	GGTGGGGAGAGCGGGCCAGGGA 4689	AG _
		TCC TGGC GTTCTTTTACT	
		AGG ACCG CGAGAGGGGTGG	
		G_ GG	
GAM1278 IER3	3'	GGTAGAGGGGTGGGGGTTGGTG 13997	T TGCGT
GG		TCC CCAG TCTTTTACT	
		GGG GGTT GGGGAGATGG	
		T GGGGGT	
GAM1278 IFNW1	5'	AGTAAGGAGGGTAAAAATGGAG 9299	GTGGC TT
G		CCTCCA G CTTTACT	
		GGAGGT T GAGGAATGA	
		AAAAA GG	
GAM1278 IL1F5	3'	GTGAGGGGTGAGTGGAGGA 24383	GTGG TT TT
		TCCTCCA CG CT TTAC	

			AGGAGGT GT GG AGTG		
			GA__ GG __		
GAM1278	IL1RAP	3'	GTAAAAAGAACAAGGGG 9314	AGTGGC	
			CTCC GTTCTTTTAC		
			GGGG CAAGAAAAATG		
			AA__		
GAM1278	INHBA	3'	AGTGAAGAGACAGATTGGGAGG 9337	AGTGGCGT	
	G		TCCTCC TCTTTTACT		
			GGGAGG AGAGAAGTGA		
			GTTAGAC_		
GAM1278	JAM3	3'	GGTAAATTGGTTGCTGGAAGA 51425 C	TG GTT TT	
			TC TCCAG GC C TTTACT		
			AG AGGTC TG G AAATGG		
			A GT __ TT		
GAM1278	JUN	5'	GGTGAGGAGGGCGCAGCGGGGA 9480	T A G	
			TCC CC GT GCGTTCTTTTACT		
			AGG GG CG CGCGGGAGGAGTGG		
			_ _ A		
GAM1278	KCNA7	3'	GGTGGAGGGCAAGGCTGGGGGG 49059	AGT G _	
	A		TCCTCC GGC TT CTTTTTACT		
			AGGGGG TCG AA GGGAGGTGG		
			G__ G C		
GAM1278	KCND2	5'	AGTGAAGGGGCGATTGGGCGA 24392 C	G GTT	
			TC TCCAGT GC CTTTTTACT		
			AG GGGTTA CG GGGAAGTGA		
			C G _		
GAM1278	KCNH2	3'	AGTGAGAGGGGCAGGGGCAGGG 4093	_ AGTGGC	
			TCCT CC GTTCTTTTACT		
			GGGA GG CGGGGAGAGTGA		
			C GGA__		
GAM1278	KCNK4	5'	GTAAGGGGAAGGCTGGAG 52808	GTG G	
			CTCCA GC TTCTTTTAC		
			GAGGT CG AAGGGGAATG		
			_ G		
GAM1278	KCNN3	5'	GGGGGCTTGTGCTGCAGGG 9562 C	_ G	
			TCCT CAGT GGC TTC		
			GGGA GTCG TCG GGG		
			C TGT G		
GAM1278	KISS1	3'	GTGGGGGGGACGTAGGG 9613	AGTG	
			CC GCGTTCTTTTAC		

			GG TGCAGGGGGGGTG	
			GA__	
GAM1278 KITLG	5'	AGTGGAGAGGGCGCTGCGCTCG 14340	TCCA TG	
GG		TCC G GCGTTCTTTTACT		
		GGG C CGCGGGAGAGGTGA		
		CTCG GT		
GAM1278 KITLG	5'	AGTGGAGAGGGCGCTGCGCTCG 6128	TCCA TG	
GG		TCC G GCGTTCTTTTACT		
		GGG C CGCGGGAGAGGTGA		
		CTCG GT		
GAM1278 KLF8	5'	GTAAAAGGGGAACGGAGGA 23406	A GGC GT	
		TCCTCC GT TCTTTTAC		
		AGGAGG CA GGGAAAATG		
		_ AG__		
GAM1278 KNSL2	3'	GGTGAGGGGTGGGAGGGTTGCT 73850	TG G ____	
GGAGGG		CCAG GC TTCTT TTTACT		
		GGTC TG GAGGG GAGTGG		
		GT G TGGG		
GAM1278 KNSL2	3'	GGTGGGAGGGTTGCTGGAGGG 73851	TG G TTT	
		TCCTCCAG GC TTCT TACT		
		GGGAGGTC TG GAGG GTGG		
		GT G ____		
GAM1278 KRT16	5'	GGTGCGTGCTCTGGAGGA 95199	TG_ T	
		TCCTCCAG GCGT CT		
		AGGAGGTC TGCG GG		
		TCG T		
GAM1278 LAMC2	3'	GTGGGAATTGCTGGAGGA 18714	TG CGTTC	
		TCCTCCAG G TTTTAC		
		AGGAGGTC T AAGGGTG		
		GT ____		
GAM1278 LANGERIN	3'	AGTGGGAGGGGTGGGTAGAGAG 31689	CAGTGG TT	
GA		TCCTC CG CTTTTTACT		
		AGGAG GT GGAGGGTGA		
		AGATGG GG		
GAM1278 LFG	3'	GGATGTTCTGGGGGA 76725	T	
		TCCTCCAG GGCGTTC		
		AGGGGGTC TTGTAGG		
		-		
GAM1278 LFG	3'	GTAGGAAGGGCAGGGGA 76726	CAGTGGC	
		TCCTC GTTCTTTTAC		

		AGGGG	CGGGAAGGATG	
		A_____		
GAM1278	LIMK1	3'	GGTGAAGGGGGTCCCTTGAGGG 9788	C T C TT
			TCCTC AG GG G CTTTTACT	
			GGGAG TC CC T GGGAAGTGG	
			T _ _ GG	
GAM1278	LIMK1	3'	GGTGAAGGGGGTCCCTTGAGGG 33650	C T C TT
			TCCTC AG GG G CTTTTACT	
			GGGAG TC CC T GGGAAGTGG	
			T _ _ GG	
GAM1278	LPL	3'	GGTGGAGAGGTTCTGGGGTGG 4090	_ TG GTT
			TC CTCCAG GC CTTTTACT	
			GG GGGGTC TG GAGAGGTGG	
			T CT _ _	
GAM1278	MADH6	5'	AGTAAGAAGGGAGCTGGGGG 18764	GGCGT
			CCTCCAGT TCTTTTTACT	
			GGGGGTCG GGAAGATGA	
			AG _ _	
GAM1278	MAFF	3'	GGCTTAGAGAACAGCTGTTGGG 24652	TG _ TTACT
	GGA		TCCTCCAG GC GTTCTTT	
			AGGGGGTT CG CAAGAGA	
			GT A TTCGG	
GAM1278	MAGEA8	3'	GGGGCAGGTTGTGGGAGGG 18106	A TG _
			TCCTCC G GC GTTCT	
			GGGAGG T TG CGGGG	
			G GT GA	
GAM1278	MAGEB3	3'	AGTGAAGGACTGGGTGTTACTG 9886	TT _
	GAGGG		TCCAGTGGCG C TTTTTACT	
			AGGTCATTGT G GGAAGTGA	
			GG TCA	
GAM1278	MAGEB3	3'	GGGTGTTACTGGAGGG 9887	TT
			TCCTCCAGTGGCG C	
			GGGAGGTCATTGT G	
			GG	
GAM1278	MAP3K12	3'	GGTGGGGGGAGGGGCGGTGGGA 20863	AG G G _
	GGA		TCCTCC T GC T TCTTTTTACT	
			GGGAGG G CG G AGGGGGGTGG	
			GT G G G	
GAM1278	MAP3K12	3'	GTGGGAGGGGCAGGAGAGA 20864	_ AGTGGC
			TC CTCC GTTCTTTTTAC	

			AG GAGG	CGGGGAGGGTG		
			A A_____			
GAM1278 MBP	3'	GGTGA	ACTCAGCCATTAGAGGA	89781	C	GTTCTT
			TCCTC AGTGGC	TTTACT		
			AGGAG TTACCG	AAGTGG		
			A ACTC__			
GAM1278 MEN1	5'	TGAGAC	CTCTGGAGGA	93381	T	CGTTCT
			TCCTCCAG GG	TTTTA		
			AGGAGGTC CC	AGAGT		
			T _____			
GAM1278 METTL1	3'	AGTGA	AAGACCCCGTTGTGGGA	43508	TC	C CTT
			TCC CAGTGG GTT	TTTACT		
			AGG GTTGCC CAG	AAGTGA		
			GT C ____			
GAM1278 METTL1	3'	AGTGA	AAGACCCCGTTGTGGGA	43514	TC	C CTT
			TCC CAGTGG GTT	TTTACT		
			AGG GTTGCC CAG	AAGTGA		
			GT C ____			
GAM1278 MGAT4B	5'	GGTAG	CCCCACCCGCTGGAGGG	53951		C TCTTT
			TCCTCCAGTGG GT	TTACT		
			GGGAGGTCGCC CA	GATGG		
			_ CCC__			
GAM1278 MLLT7	3'	GTGGG	GAGAGGTGGGGAG	19869	AGTG	G
			CTCC GC TTCTTTTAC			
			GAGG TG GAGAGGGGTG			
			GG__ _			
GAM1278 MMP14	3'	AGTGG	AGGGAGCAAGAGGAGAG	17168		CAGTGGC
GG			TCCTC GTTCTTTTACT			
			GGGAG CGAGGGAGGTGA			
			AGGAGAA			
GAM1278 MMP25	3'	GGTGA	AATCAGTGGCTGGAGGG	42445	G	GTTCT
			TCCTCCAGT GC	TTTTACT		
			GGGAGGTCG TG	AAGGTGG		
			G ACT__			
GAM1278 MMP26	3'	AGGG	AGTTTATTGGAGGA	41437	CG	
			TCCTCCAGTGG TTCTT			
			AGGAGGTTATT AGGGA			
			TG			
GAM1278 MPDU1	3'	TGGAG	GGGACTGGGAGG	16828	AGTGG	T
			CCTCC CG TCTTTTAA			

			GGAGG	GT AGGGAGGT		
			_____ C			
GAM1278	MPP2	3'	GTGGGAAGGAAATGGGG	59828	GTGGCG	
			CTCCA	TTCTTTTAC		
			GGGGT	AGGAAGGGTG		
			AA_____			
GAM1278	MRC1	5'	GGTGGAGAGGCAGTTGGGGGG	10114	TG GTT	
			TCCTCCAG GC	CTTTTACT		
			GGGGGGTT CG	GAGAGGTGG		
			GA _____			
GAM1278	MTA1L1	3'	AGTGAGTGTGTGTCCCTGGAGG	16443	T TTCTT	
	G		TCCTCCAG GGCG	TTTACT		
			GGGAGGTC CTGT	GAGTGA		
			C GTGT_			
GAM1278	MTR	3'	GTGGAAGGGACAGGAG	4214	AGTGGC	
			CTCC	GTTCTTTTAC		
			GAGG	CAGGGAAGGTG		
			A_____			
GAM1278	MYCL2	3'	GGTGGTGGATGTTGTTGGGGG	18186	TG TTT	
			CCTCCAG GCGTTC	TTACT		
			GGGGGTT TGTAGG	GGTGG		
			GT T__			
GAM1278	MYO10	3'	AGTGGGAAGGGGGATGGAG	24700	GTGGCG	
			CTCCA	TTCTTTTACT		
			GAGGT	GGGAAGGGTGA		
			AGG_____			
GAM1278	NCOA6	5'	AGTGAAAGGAAAATGAGGGGA	25954	_ GTGGCG	
			TCCTC CA	TTCTTTTACT		
			AGGGG GT	AAGGAAAGTGA		
			A AA_____			
GAM1278	NDRG3	3'	AGACAGAGAGTATTGCTGGAGG	49290	TG CG TTACT	
	G		TCCTCCAG G	TTCTTT		
			GGGAGGTC T	GAGAGA		
			GT AT	CAGA		
GAM1278	NDST2	3'	GTGGGGAGGAATGAGAGGG	13297	CA GGCG	
			TCCTC GT	TTCTTTTAC		
			GGGAG TA	AGGAGGGGTG		
			AG _____			
GAM1278	NGFRAP1	5'	GGTAAGGGGAGAAAGCTGGAGG	26884	GGCG	
	G		TCCTCCAGT	TTCTTTTACT		



		GGGAGGTCG GAGGGGAATGG	
		AAA_	
GAM1278 NPTX1	3'	GGTGGGAAGGTCCTTTTGGGG 10265	TGGCGT
GA		TCCTCCAG TCTTTTACT	
		AGGGGGTT GGAAGGGTGG	
		TTTCCT	
GAM1278 NR0B2	3'	GGTGACCCAATGCTCCTGGAGG 41741	TG CTTT
G		TCCTCCAG GCGTT TTA	
		GGGAGGTC CGTAA AGTGG	
		CT CCC_	
GAM1278 NRXN2	3'	GGGGAAGCTGCTGGAGGA 30630	TG G
		TCCTCCAG GC TTCTTT	
		AGGAGGTC CG AAGGGG	
		GT _	
GAM1278 NRXN2	3'	GGTGGGAAGGAAGGCTGGGGG 30631	GGCG
		CCTCCAGT TTCTTTTACT	
		GGGGGTCG AGGAAGGGTGG	
		GA_	
GAM1278 NRXN2	3'	GGGGAAGCTGCTGGAGGA 57016	TG G
		TCCTCCAG GC TTCTTT	
		AGGAGGTC CG AAGGGG	
		GT _	
GAM1278 NRXN2	3'	GGTGGGAAGGAAGGCTGGGGG 57017	GGCG
		CCTCCAGT TTCTTTTACT	
		GGGGGTCG AGGAAGGGTGG	
		GA_	
GAM1278 NRXN2	3'	GGGGAAGCTGCTGGAGGA 57027	TG G
		TCCTCCAG GC TTCTTT	
		AGGAGGTC CG AAGGGG	
		GT _	
GAM1278 NRXN2	3'	GGTGGGAAGGAAGGCTGGGGG 57028	GGCG
		CCTCCAGT TTCTTTTACT	
		GGGGGTCG AGGAAGGGTGG	
		GA_	
GAM1278 NUP98	3'	AGTGAATGCCTGTCACGGAGGG 32859	A TTCTT
		TCCTCC GTGGCG TTTACT	
		GGGAGG CACTGT AAGTGA	
		_ CCGT_	
GAM1278 NYX	3'	GGTGAAAATCCCAGTGGAGGG 42604	G CGTTC
		TCCTCCA TGG TTTTACT	

			GGGAGGT ACC AAAAGTGG		
			G CT__		
GAM1278	OASL	3'	GTGGGAGGAGCGCTTGAG 13581	CAGT	
			CTC GGC GTTCTTTTAC		
			GAG TCGCGAGGAGGGTG		
			T__		
GAM1278	OLIG2	3'	GGGGAGGGGGTGTATGGGAGG 19413	A TT ACT	
	G		TCCTCC GTGGCG CTTTTT		
			GGGAGG TATTGT GGGAGG		
			G GG GG		
GAM1278	OXTR	3'	GGTAGAAATTTAAATTGTTGGT 6214	_ TG CGTTC_	
	GGGA		CCT CCAG G TTTTACT		
			GGG GGTT T AAAGATGG		
			T GT AAATTT		
GAM1278	PACSIN1	3'	AGTGAAAGGACCTTTGGGGG 92254	T CGT	
			CCTCCAG GG TCTTTTACT		
			GGGGGT CC AGGAAAGTGA		
			T __		
GAM1278	PAX2	3'	GCGCCAGGAGCTTCGCTGGAGG 14324	C TTTACT	
	G		TCCTCCAGTGG GTTCTT		
			GGGAGGTCGCT CGAGGA		
			T CCGCGG		
GAM1278	PAX2	3'	GCGCCAGGAGCTTCGCTGGAGG 14333	C TTTACT	
	G		TCCTCCAGTGG GTTCTT		
			GGGAGGTCGCT CGAGGA		
			T CCGCGG		
GAM1278	PAX7	5'	GGTAGGGAGTGTGTGTGGAGGG 10435	GTG TT	
			TCCTCCA GCG CTTTTTACT		
			GGGAGGT TGT GAGGGATGG		
			G__ GT		
GAM1278	PAX7	5'	GGTGAAGGGAGCGGACGGGA 10436	A GG	
			TCC GT CGTTC TTTTACT		
			AGG CA GCGAGGGAAGTGG		
			G G_		
GAM1278	PAX7	5'	GGTAGGGAGTGTGTGTGGAGGG 25639	GTG TT	
			TCCTCCA GCG CTTTTTACT		
			GGGAGGT TGT GAGGGATGG		
			G__ GT		
GAM1278	PAX7	5'	GGTGAAGGGAGCGGACGGGA 25640	A GG	
			TCC GT CGTTC TTTTACT		

AGG CA GCGAGGGAAGTGG  
 G G\_  
 GAM1278 PBX2 3' GGTGGGAGGCATGGGCCGGGGG 10447 A GG T  
 G TCCTCC GT CGT CTTTTTACT  
 ||||| || ||| |||||  
 GGGGGG CG GTA GGAGGGTGG  
 C G\_ C  
 GAM1278 PCK1 5' AGTAGGGGGAACGAGTGGTGA 52259 CT GTGG  
 TC CCA CGTTCTTTTTACT  
 || ||| |||||  
 AG GGT GCAAGGGGGATGA  
 T\_ GA\_  
 GAM1278 PDE4A 3' GGTGGGGGGCAGTCACTGTGGG 20587 TC GTT  
 A TCC CAGTGGC CTTTTTACT  
 ||| ||||| |||||  
 AGG GTCAGTG GGGGGGTGG  
 GT AC\_  
 GAM1278 PDGFRB 5' AGTAAGGAGGACTTCCTGGAGG 65968 T C  
 G TCCTCCAG GG GTTCTTTTTACT  
 ||||| || |||||  
 GGGAGGTC CT CAGGAGGAATGA  
 \_ T  
 GAM1278 PIK3C2B 3' AGTAGGAGGCTGGATTGGAGTG 10560 \_ \_ G TTTTACT  
 G C CTCCAGT GGC TTCT  
 | ||||| ||| |||  
 G GAGGTTA TCG AGGA  
 T GG G TGA T  
 GAM1278 PIN1 3' GGTGGGAGGGGTGTTCCAAAGA 20616 CAG \_ TT  
 G CTC TGG CG CTTTTTACT  
 ||| ||| || |||||  
 GAG ACC GT GGAGGGTGG  
 AA\_ TT GG  
 GAM1278 PIN1L 3' GGTGGGAGGAGTGTTCCAAAGA 20624 CAG \_  
 G CTC TGG CGTTCTTTTTACT  
 ||| ||| |||||  
 GAG ACC GTGAGGAGGGTGG  
 AA\_ TT  
 GAM1278 PIP5K1A 3' GGTGGGAGGGAATATTTGAGGG 13057 TC TGGCG  
 A TCC CAG TTCTTTTTACT  
 ||| ||| |||||  
 AGG GTT AGGGAGGGTGG  
 GA TATA\_  
 GAM1278 PML 3' AGTGAAAGGTTGGAAGTGGTGG 52664 \_ GGCGTT  
 CC TCCAGT CTTTTTACT  
 || ||||| |||||  
 GG GGGTCA GGAAAGTGA  
 T GGT\_  
 GAM1278 PML 3' AGTGAAAGGTTGGAAGTGGTGG 52670 \_ GGCGTT  
 CC TCCAGT CTTTTTACT  
 || ||||| |||||

			GG GGGTCA GGAAAGTGA		
			T GGT__		
GAM1278	PODXL	3'	GGTAGGGGGAGGGGCTGGGGA 18237	T	GGCG
			TCC CCAGT TTCTTTTACT		
			AGG GGTCG GAGGGGGATGG		
			_ GG__		
GAM1278	POLR2E	3'	GGTGCAGGGGACGTGCTGGAGG 59921	G	T
	G		TCCTCCAGTG CGTTCCTT TACT		
			GGGAGGTCGT GCAGGGGA GTGG		
			_ C		
GAM1278	PPARBP	3'	GGTGGGAGGGGTGTAGGGAG 16491	AGTG	TT
			CTCC GCG CTTTTTACT		
			GAGG TGT GGAGGGTGG		
			GA__ GG		
GAM1278	PPFIA3	3'	GGTGAGGACCGTGCTGGGCGA 61016	C	G T TT
			TC TCCAGTG CG TCT TTA		
			AG GGGTCGT GC AGG AGTGG		
			C _ C _		
GAM1278	PPT2	5'	AGTGGGGAGAATCAAGGCGGGG 57228	CAG_	GC
	A		TCCTC TG GTTCTTTTACT		
			AGGGG AC TAAGAGGGGTGA		
			CGGA _		
GAM1278	PPT2	3'	GGTGAGAGGCTGTCATCTGGAG 57233	_	TT
	GG		TCCTCCAG TGGCG CTTTTTACT		
			GGGAGGTC ACTGT GGAGAGTGG		
			T C_		
GAM1278	PPT2	5'	AGTGGGGAGAATCAAGGCGGGG 17668	CAG_	GC
	A		TCCTC TG GTTCTTTTACT		
			AGGGG AC TAAGAGGGGTGA		
			CGGA _		
GAM1278	PRPS1	3'	GGTGGGGGGTGGTTGAGGGGG 10899	AG	GTT
			CCTCC TGGC CTTTTTACT		
			GGGGG GTTG GGGGGGTGG		
			A_ GT_		
GAM1278	PTGFRN	3'	AGTAAGAAGGGCTGCAAGGAAG 67184	_	AGTG _
	GG		TCCT CC GC GTTCTTTTACT		
			GGGA GG CG CGGGAAGAATGA		
			A AA_ T		
GAM1278	RAB13	3'	GTAAAGAGAATGAGGAG 11203	AGTGG	
			CTCC CGTTCCTTTTAC		

GAGG GTAAGAGAAATG  
 A\_\_\_\_  
 GAM1278 RAB27A 3' GGTGGGAAGGGGATTGGGGTGG 15926 \_ GGCG  
 TC CTCCAGT TTCTTTTACT  
 || ||||| |||||  
 GG GGGGTTA GGGAAGGGTGG  
 T G\_\_\_\_  
 GAM1278 RAB33A 5' TGCAAGGAGGGTGCGCTGGAGG 16578 G TT ACT  
 A TCCTCCAGTG CG CTTTT  
 ||||| || |||||  
 AGGAGGTCGC GT GAGGAA  
 \_ GG CGTC  
 GAM1278 RAB5C 3' GGTAAGGGGGGAGTGGGAGGG 59835 AGTG G\_  
 TCCTCC GC TTCTTTTACT  
 |||| || |||||  
 GGGAGG TG GGGGGGAATGG  
 G\_\_\_\_ AG  
 GAM1278 RDS 5' GGTGGGAGCTGTGCTGTGGGA 4362 TC GC TTT  
 TCC CAGTG GTTCT TACT  
 || |||| |||| ||||  
 AGG GTCGT CGAGG GTGG  
 GT GT \_\_\_\_  
 GAM1278 RNF28 3' GGTGGGAGGGGTGCGGGGCCCT 50862 T \_\_\_\_ TT  
 GGAGGG CCAG GGC G CTTTTTACT  
 |||| || | |||||  
 GGTC CCG T GGAGGGTGG  
 C GGGC GG  
 GAM1278 RNH 5' GGTGGGGAGGGTGCTGAAGAGG 59623 CAG TT  
 A TCCTC TGGCG CTTTTTACT  
 |||| |||| |||||  
 AGGAG GTCGT GAGGGGTGG  
 AA\_ GG  
 GAM1278 RNH 5' GGTGGGGAGGGTGCTGAAGAGG 11368 CAG TT  
 A TCCTC TGGCG CTTTTTACT  
 |||| |||| |||||  
 AGGAG GTCGT GAGGGGTGG  
 AA\_ GG  
 GAM1278 RS1 3' GGTGGGGGGGGGGGTGGGGGGA 4398 AGTG G  
 TCCTCC GC TTCTTTTACT  
 |||| || |||||  
 AGGGGG TG GGGGGGGGTGG  
 G\_\_\_\_ G  
 GAM1278 RTKN 5' AGTGGGAGGAGGAAGTGTGGGA 52324 TC GGCG  
 TCC CAGT TTCTTTTACT  
 || |||| |||||  
 AGG GTCA GAGGAGGGTGA  
 GT AG\_\_\_\_  
 GAM1278 SALL2 5' GTGATTGCGCTGGGGGA 63862 G TTCTTT  
 TCCTCCAGTG CG TTAC  
 ||||| || ||||

AGGGGGTTCGC GT AGTG  
 \_ TT\_\_\_\_  
 GAM1278 SDC4 3' GGTAGGGGGGGGGGAATGGGGG 11481 GTGGCG  
 A TCCTCCA TTCTTTTACT  
 ||||| |||||  
 AGGGGT GGGGGGATGG  
 AAGG\_  
 GAM1278 SEMA3F 3' GGGGGGTGATTGGAAGGG 14821 \_ G G  
 TCCT CCAGT GC TTCT  
 ||| |||| || |||  
 GGA GTTA TG GGG  
 A G G  
 GAM1278 SERPINA5 3' AGTAGGAGGATGTTCCAGTGG 5268 G \_  
 A TCCA TGG CGTTCTTTTACT  
 ||| ||| |||||  
 AGGT ACC GTAGGGAGGATGA  
 G TT  
 GAM1278 SERPINF2 3' GGTGGGGGGGGGCGCGGCTGGG 6258 \_ G \_  
 AGGA CCTCC AGT GCGTTCTTTT ACT  
 |||| ||| |||||  
 GGAGG TCG CGCGGGGGGGG TGG  
 G G G  
 GAM1278 SFRS1 3' GGTAAAAGGAGCAAAGCGAGGA 22639 CA GGC  
 TCCTC GT GTTCTTTTACT  
 |||| || |||||  
 AGGAG CG CGAGGAAAATGG  
 \_ AAA  
 GAM1278 SLC19A2 3' AGTAGAAAAGTGCTGTTTGAGG 68977 C TG C  
 G TCCTC AG GCGTT TTTTACT  
 |||| || |||| |||||  
 GGGAG TT CGTGA AAAGATGA  
 T GT \_  
 GAM1278 SLC1A2 3' TTGAATGGATGCTGCTGGAGGA 61931 TG TT CT  
 TCCTCCAG GCGTTC TTTA  
 ||||| |||| |||  
 AGGAGGTC CGTAGG AAGT  
 GT T\_ TT  
 GAM1278 SLC22A2 5' AAGAATTTGTTGGGCGGA 59529 \_ TG C  
 TCC TCCAG G GTTCTT  
 || |||| | |||||  
 AGG GGGTT T TAAGAA  
 C GT\_  
 GAM1278 SLC5A5 5' AGTGAGAGGGGAGGTGGCAGGA 4844 A G G\_  
 TCC GT GC TTCTTTTACT  
 || || || |||||  
 AGG CG TG GGGGAGAGTGA  
 A G GA  
 GAM1278 SLC7A6 3' GGTGGGGGGAAGATTGGGGA 14313 T GGCG  
 TCC CCAGT TTCTTTTACT  
 || |||| |||||

AGG GGTTA AAGGGGGGTGG  
 \_ G\_\_  
 GAM1278 SLIT2 5' GGTGGAGAGGGCGGTGGGAGG 16553 AGTGG  
 CCTCC CGTTCTTTTACT  
 |||| |||||  
 GGAGG GCGGGAGAGGTGG  
 GTG\_\_  
 GAM1278 SNAI2 3' TATGTGCCTTGGGGA 11777 T TTCTTTT  
 TCCTCCAG GGCG TA  
 ||||| ||| ||  
 AGGGGGTT CCGT AT  
 \_ GT\_\_\_\_  
 GAM1278 SOST 3' ACTAAAGAATATTATTGGGGG 47465 CG TACT  
 A TCCTCCAGTGG TTCTTTT  
 ||||| |||||  
 AGGGGGTTATT AAGAAAA  
 AT TCA  
 GAM1278 SOX9 3' AGTGAGGGAGGCTACCTGGAGG 4436 \_ G TT  
 G TCCTCCAG TGGC TTCT TTA  
 ||||| ||| ||| ||||  
 GGGAGGTC ATCG AGGG AGTGA  
 C G \_  
 GAM1278 SPAG8 3' GGTGAGGAGGGAAGTGGGG 24903 GTGGCG  
 CTCCA TTCTTTTACT  
 |||| |||||  
 GGGGT GGGAGGAGTGG  
 GAA\_\_  
 GAM1278 STAC 3' AGTGGGGAGGAGAAGTGGGGA 11988 T GTGGCG  
 TCC CCA TTCTTTTACT  
 ||| ||| |||||  
 AGG GGT AGGAGGGGTGA  
 \_ GAAG\_\_  
 GAM1278 STAT6 3' GGGAGCATAGGAGGG 12023 A G G  
 TCCTCC GTG C TTCT  
 |||| ||| |||  
 GGGAGG TAC G AGGG  
 A \_\_  
 GAM1278 SYBL1 3' AGTAGAGGGGGTGGGGAGG 18891 AGTGG TT  
 CCTCC CG CTTTACT  
 |||| || |||||  
 GGAGG GT GGGAGATGA  
 G\_\_ GG  
 GAM1278 TBX5 5' TGGGATAGTTGGAGGG 54894 GTG GTTCT  
 TCCTCCA GC TTTA  
 ||||| || |||  
 GGGAGGT TG AGGGT  
 \_\_ AT\_\_  
 GAM1278 TCF20 3' AGTGGAAGGTTTTGGGGGA 66953 TGGCGT  
 TCCTCCAG TCTTTTACT  
 ||||| |||||

			AGGGGGTT	GGAAGGGTGA		
			TT____			
GAM1278	TCF20	3'	GGTGGGGGGAATTAAGGGAG	66958	AGTGGC	
	GG		TCCTCC	GTTCTTTTACT		
			GGGAGG	TAAGGGGGGTGG		
			GAAAAT			
GAM1278	TFEB	3'	AGTGAAGGACATGCTTGAGGG	92124	C GC TT	
			TCCTC AGTG GTTCT TTACT			
			GGGAG TCGT CAGGA AGTGA			
			T A_ _			
GAM1278	TFEB	3'	GGTGAGAAGAGGGCCTGGTGGA	92128	T GT G	
			TCC CCA GGC TTCTTTTACT			
			AGG GGT CCG GAGAAGAGTGG			
			T _ G			
GAM1278	TGM2	3'	GGTAGAGAGGGGACTGGGGGA	16056	GGCG	
			TCCTCCAGT TTCTTTTACT			
			AGGGGGTCA GGGAGAGATGG			
			G_			
GAM1278	THY1	3'	GGTGGGGTACCAGCCACTGGAG	20813	GTTCT	
	GG		TCCTCCAGTGGC TTTTACT			
			GGGAGGTCACCG GGGGTGG			
			ACCAT			
GAM1278	TM7SF3	3'	AAGGGTGTACTAGGGGA	59664	C G TT	
			TCCTC AGTG CG CTT			
			AGGGG TCAT GT GAA			
			A _ GG			
GAM1278	TMEPAI	3'	GTGAGAGGAAGGCGGGGGG	39449	AGTG G	
			TCCTCC GC TTCTTTTAC			
			GGGGGG CG AAGGAGAGTG			
			_ G			
GAM1278	TNFRSF14	3'	GGGGCCCCTGCTGGGG	13784	_ C	
			CTCCAGT GG GTTCT			
			GGGGTCG CC CGGGG			
			T C			
GAM1278	TNFSF11	3'	AGTGGAGAGGGTGTCAT	13509	TT	
			GTGGCG CTTTTTACT			
			TACTGT GAGAGGTGA			
			GG			
GAM1278	TNFSF11	3'	AGTGGAGAGGGTGTCAT	52237	TT	
			GTGGCG CTTTTTACT			



TACTGT GAGAGGTGA  
 GG  
 GAM1278 TPSB1 5' GGTAGAAGGAACAGGGAGCGG 12376 \_ AGTGGC  
 TC CTCC GTTCTTTTACT  
 || ||| |||||  
 GG GAGG CAAGGAAGATGG  
 C GA\_\_\_\_  
 GAM1278 TPX1 5' GGTGAGAGGGGCGCGCA 12379 \_  
 TG GCGTTCTTTTACT  
 || |||||  
 AC CGCGGGGAGAGTGG  
 G  
 GAM1278 TRADD 3' GGTGGGGGGGACCTGCTTTGGA 13700 \_\_ TG C  
 G CTCCA G G GTTCTTTTACT  
 |||| | |||||  
 GAGGT C C CAGGGGGGGTGG  
 TT GT\_  
 GAM1278 TRPC1 3' GGTGGGAAGAAAATATGGAGGA 12391 GTGGCG  
 TCCTCCA TTCTTTTACT  
 ||||| |||||  
 AGGAGGT AAGAAGGGTGG  
 ATAA\_\_\_\_  
 GAM1278 TRPC5 5' GGTGGGGAGGATAAAGGGAG 25001 AGTGGC  
 CTCC GTTCTTTTACT  
 ||| |||||  
 GAGG TAGGAGGGGTGG  
 GAAA\_\_\_\_  
 GAM1278 TSPY 3' GTGGAAGGAAGATGGTGGG 82108 T GTGGCG  
 TCC CCA TTCTTTTAC  
 ||| |||||  
 GGG GGT AAGGAAGGTG  
 T AG\_\_\_\_  
 GAM1278 TUFT1 3' AGTGATTGGAGAATGTCCTGGG 39251 T \_  
 GGA CCTCCAG GCGTTCTTT TACT  
 ||||| ||||| |||||  
 GGGGGTC CTGTAAGAGG AGTGA  
 \_ TT  
 GAM1278 USP11 5' GGGAGGCATACTGCAGGG 16204 C \_ G  
 TCCT CAGTG GC TTCT  
 ||| |||| || |||  
 GGA GTCAT CG AGGG  
 C A G  
 GAM1278 VANGL2 3' GGGAAACTCTGGGGGG 71652 T CG  
 TCCTCCAG GG TTCT  
 ||||| || |||  
 GGGGGGTC TC AGGG  
 \_ AA  
 GAM1278 VAPB 3' GGTGAACTGGTATTGCTGCTGG 16440 TG TT\_ T\_  
 AGGG CCTCCAG GCG CT TTTACT  
 ||||| ||| || |||||

		GGAGGTC CGT GG AAGTGG		
		GT TAT TC		
GAM1278 VPS26	5'	AGTAGGGGGGACGCGGCGGCGG 16906	T A G	
		CC CC GT GCGTTCTTTTACT		
		GG GG CG CGCAGGGGGGATGA		
		C _ G		
GAM1278 WASF3	5'	AGTGGTGATGCTACTTGAGGG 21825	C	CTTT
		TCCTC AGTGGCGTT TTACT		
		GGGAG TCATCGTAG GGTGA		
		T T__		
GAM1278 WNT15	3'	GTGAGAAAGACATGGAGGG 12679	GTGGC	TC
		TCCTCCA GT TTTTAC		
		GGGAGGT CA AAGAGTG		
		A__ GA		
GAM1278 WRN	5'	GGGGACGGCGCTGGAGGG 5099	G	
		TCCTCCAGTG CGTTCTT		
		GGGAGGTCGC GCAGGGG		
		G		
GAM1278 ZIC1	5'	GGTGGGGGGGGCGGGGGGAGG 12723	AGTGG	
		CCTCC CGTTCTTTTACT		
		GGAGG GCGGGGGGGGTGG		
		GG__		
GAM1278 ZNF278	3'	GTGGAAGGGAACAGGAGGG 49440	A	GGCG
		TCCTCC GT TTCTTTTAC		
		GGGAGG CA AGGGAAGGTG		
		A __		
GAM1278 ZNF35	3'	GGTAATGATGCTATTTGGGGA 12780	C	CTTT
		TCCTC AGTGGCGTT TTACT		
		AGGGG TTATCGTAG AATGG		
		T T__		
GAM1278 ZRF1	5'	AGTGAGAGGTAGAGCTGGAGGG 94288	GGCGT	
		TCCTCCAGT CTTTTTACT		
		GGGAGGTCG GGAGAGTGA		
		AGAT__		
GAM1278 ABCA9	3'	GGGGCCTGTTGGGGGG 54411	TG	C
		TCCTCCAG G GTTCT		
		GGGGGGTT C CGGGG		
		GT _		
GAM1278 ABIN-2	5'	AGTGGACGCGCTGCTGGAG 44206	TG	TCTT
		CTCCAG GCGT TTTACT		

GAGGTC CGCG AGGTGA  
 GT C\_\_\_  
 GAM1278 ACTR2 3' GGTGGGTTTTGTTGCGGGGGGG 19151 A TG TTCTT  
 TCCTCC G GCG TTTACT  
 ||||| I ||| |||||  
 GGGGGG C TGT GGGTGG  
 G GT TTT\_\_\_  
 GAM1278 AF9Q34 3' GGATGTGCTGGAGGG 50739 G  
 TCCTCCAGTG CGTTC  
 ||||| |||||  
 GGGAGGTCGT GTAGG  
 —  
 GAM1278 AF9Q34 3' GGTAAGAAGGGTGGGAGTGGGG 50740 GTGG TT  
 CTCCA CG CTTTTTACT  
 |||| || |||||  
 GGGGT GT GAAGAATGG  
 GAGG GG  
 GAM1278 AGS3 3' GGTGAGGTGACCTGCTTCTGGA 73114 T T\_ T  
 GGG TCCTCCAG GGCG TC TTTTACT  
 ||||| ||| || |||||  
 GGGAGGTC TCGT AG GGAGTGG  
 T CC T  
 GAM1278 ALS2CR19 3' GGTGGAAGGGGCGCTGCCGCGA 54113 CA\_ TG  
 G CTC G GCGTTCTTTTACT  
 ||| I |||||  
 GAG C CGCGGGGAAGGTGG  
 CGC GT  
 GAM1278 AMOTL1 3' AGTGAGAAGAAGCATCGAGGG 73647 CAGTG G  
 TCCTC GC TTCTTTTACT  
 |||| || |||||  
 GGGAG CG AAGAAGAGTGA  
 CTA\_ \_  
 GAM1278 ARF6 5' GTGAGAGGAAGGCGGAGGA 8013 AGTG G  
 TCCTCC GC TTCTTTTAC  
 |||| || |||||  
 AGGAGG CG AAGGAGAGTG  
 \_ G  
 GAM1278 ARHGAP11A 5' GGTAAGGAGGCTGATGGGGG 28797 GT G C  
 A TCCTCCA GGC TT TTTTACT  
 ||||| ||| || |||||  
 AGGGGGT TCG GA GGAGATGG  
 AG \_ C  
 GAM1278 ARHGEF15 5' AGTGGAGGGGATTCAAGGGGGA 30256 AG C  
 TCCTCC TGG GTTCTTTTACT  
 |||| ||| |||||  
 AGGGGG ACT TAGGGGAGGTGA  
 A\_ \_  
 GAM1278 ARHGEF9 5' GTAAAGGGAGTAGGGGAG 30817 AGTG GT  
 CTCC GC TCTTTTAC  
 ||| || |||||

			GAGG TG AGGGAAATG		
			GGA_ _		
GAM1278 ASP	5'	GGTCTAGGGTGTGTGGAG	49167	TG TT TTTT	
		CTCCAG GCG CT ACT			
		GAGGTT TGT GA TGG			
		GT GG TC_			
GAM1278 BATF	5'	GTGAGGAGGACGCAGGGG	21131	AGTG	
		CTCC GCGTTCTTTTAC			
		GGGG CGCAGGAGGAGTG			
		A_			
GAM1278 BDH	5'	GCCGCAGGAGTGCTGGTGGAGG	14476	G TTTACT	
G		TCCTCCA TGGCGTTCTT			
		GGGAGGT GTCGTGAGGA			
		G CGCCGG			
GAM1278 BET3	3'	GGTGGAGGGAGGAAGGGCTGGG	26965	_ GGCG_	
AGGG		CCTCC AGT TTCTTTTACT			
		GGAGG TCG GAGGGAGGTGG			
		G GGAAG			
GAM1278 BICD2	3'	GGTAAAGAGTCACATTGGTAGG	70400	_ GCGTT	
A		TCCT CCAGTG CTTTTTACT			
		AGGA GGTTAC GAGAAATGG			
		T ACT_			
GAM1278 C11orf21	3'	GGAAGCCATTGGGGTGA	26242	_ G	
		TC CTCCAGTGGC TTCT			
		AG GGGGTTACCG AAGG			
		T _			
GAM1278 C11orf9	3'	GTTTCAGGTGCCCTGGAGGG	25213	T TT TTT	
		TCCTCCAG GGCG CTT AC			
		GGGAGGTC CCGT GGA TG			
		_ _ CT_			
GAM1278 C12orf22	3'	AGTGAAAACTGTGTTGGGGGG	47976	GT G TTC	
		TCCTCCA G CG TTTTACT			
		GGGGGGT T GT AAAAGTGA			
		TG_ CA_			
GAM1278 C14orf4	3'	GGTAAGGGGGTGTGCGGGGGG	67340	AG TT T	
		CCTCC TGGCG CTTTT ACT			
		GGGGG GCTGT GGGAA TGG			
		G_ GG _			
GAM1278 C1orf25	3'	AGTGGGGGGAAGGGGGTGGAGG	72531	GTGGCG	
G		TCCTCCA TTCTTTTACT			

GGGAGGT AAGGGGGGTGA  
GGGGG\_  
GAM1278 C1QR1 3' AGTGAAAGGAAAGATGGAGG 23835 GTGGCG  
CCTCCA TTCTTTTACT  
||||| |||||  
GGAGGT AAGGAAAGTGA  
AGA\_\_  
GAM1278 C20orf141 5' GGTGAGGAGGGTTTGCTGGGTG 54949 \_ TG C TT  
GG TCC TCCAG G G CTTTTTACT  
||| ||||| || |||||  
GGG GGGTC T T GAGGAGTGG  
T GT \_ GG  
GAM1278 C20orf151 3' GGTGGAGGGAGACAGTGGGCGG 88702 \_ G GCGT  
CC TCCA TG TCTTTTACT  
|| ||||| || |||||  
GG GGGT AC AGGGAGGTGG  
C G AG\_\_  
GAM1278 C20orf188 3' AGTGGGGAGGAAGATATGGGTG 31576 C GTGGCG  
A TC TCCA TTCTTTTACT  
|| ||||| || |||||  
AG GGGT AGGAGGGGTGA  
T ATAGA\_  
GAM1278 C20orf35 3' GTGGGAAGGATGGTGGGA 37481 CCAGT G  
TCCT G CGTTCTTTTAC  
||||| | |||||  
AGGG T GTAGGAAGGGTG  
\_\_\_\_ G  
GAM1278 C20orf7 3' GTGAGAAGAACATAGAGGA 44144 CAG GC  
TCCTC TG GTTCTTTTAC  
||||| || |||||  
AGGAG AT CAAGAAGAGTG  
\_\_\_\_ A\_  
GAM1278 C22orf5 3' GGTGGGGGGGAGCTCAGTGGCAG 24347 \_ G C  
GG TCCT CCA TGG GTTCTTTTACT  
||||| ||| |||||  
GGGA GGT ACT CGAGGGGGGTGG  
C G \_  
GAM1278 C5orf7 5' GGTGGTTGGTGGTGGCTGTTGG 63870 TG GTT\_\_ TT  
GGGG CCTCCAG GC CT TTACT  
||||| || || |||||  
GGGGGT CG GG GGTGG  
GT GTGGT TT  
GAM1278 C6orf9 3' AGTAAGAAGGGAAGGTGGGTGG 42075 T AGTGGCG  
G TCC CC TTCTTTTACT  
||| || |||||  
GGG GG GGGAAGAATGA  
T GTGGAA\_  
GAM1278 CAT56 3' GTGAGAGCTGTTGGAG 47519 TG GTTCT  
CTCCAG GC TTTTAC  
||||| || |||||

			GAGGTT CG AGAGTG		
			GT _____		
GAM1278	CBCIP2	3'	AGTGGGGTTCAGGCCCTGGGGGA 51587	T G CT	
			TCCTCCAG GGC TT TTTTACT		
			AGGGGGTC CCG GA GGGGTGA		
			__ _ CT		
GAM1278	CCR5	3'	GGTGGGGGGGGGCGCCTTAGG 5150 AGT		
			CC GCGTTCTTTTACT		
			GG CCGCGGGGGGGGTGG		
			ATT		
GAM1278	CDCA4	3'	AGTAGCATTGCTGCTGGATGA 35655 C TG TTCTTT		
			TC TCCAG GCG TTACT		
			AG AGGTC CGT GATGA		
			T GT TAC__		
GAM1278	CECR2	3'	AGTGGGAAGGGTGGGTGGGGA 48607 T GTGG TT		
			TCC CCA CG CTTTTTACT		
			AGG GGT GT GAAGGGTGA		
			__ GG__ GG		
GAM1278	CECR6	3'	GAGGACGGCTTGGAGGG 49087 GT _		
			TCCTCCA GGC GTTCTT		
			GGGAGGT TCG CAGGAG		
			__ G		
GAM1278	CG018	3'	GGTGGAGAGAAAGTGGTGGGGGG 53395 G G G		
			TCCTCCA T GC TTCTTTTACT		
			GGGGGGT G TG AAGAGAGGTGG		
			__ G _		
GAM1278	CGB5	5'	AGTGAGAGGAGAGGGCTGGGG 52314 GGCG		
			CTCCAGT TTCTTTTACT		
			GGGGTCG GAGGAGAGTGA		
			GGA_		
GAM1278	CGB8	5'	AGTGAGAGGAGAGGGCTGGGG 52589 GGCG		
			CTCCAGT TTCTTTTACT		
			GGGGTCG GAGGAGAGTGA		
			GGA_		
GAM1278	CGI-01	3'	GTGGAGGGAGTGTATGGA 31944 GTG		
			TCCA GCGTTCTTTTAC		
			AGGT TGTGAGGGAGGTG		
			A__		
GAM1278	CLDN7	3'	GGTGGGGGGGTGCCGTTGGTGG 7141 _ TT T		
	GA		TCCT CCAGTGGCG CTTTT ACT		

			AGGG GGTGCCGT GGGGG TGG		
			T GG _		
GAM1278	CLDN7	3'	GGTGGGGGGGTGCCGTTGGTGG 94585	_	TT T
	GA		TCCT CCAGTGGCG CTTTT ACT		
			AGGG GGTGCCGT GGGGG TGG		
			T GG _		
GAM1278	CLIC4	5'	AGAGTGCCGCGGGGGG 25628	A	
			TCCTCC GTGGCGTTCT		
			GGGGGG CGCCGTGAGA		
			-		
GAM1278	CLTH	5'	GGTAGGGGGTGCGGTGGGGGG 23146	G G	TT TT
			TCCTCCA T GCG CT TTACT		
			GGGGGGT G CGT GG GATGG		
			_ G GG _		
GAM1278	CMRF-35H	3'	AGTGAAGAGAGTGCCAAAGCGG 70417	AG	_
	AG		CTCC TGGCGTTCTTTTACT		
			GAGG ACCGTGAGAGAAGTGA		
			CGAA		
GAM1278	CNNM4	3'	AGTGGAGGCTTATCTGTTGGGA 39473	_ TG	CGTTC
	GGA		TCCTCC AG G TTTTACT		
			AGGAGG TT C GGAGGTGA		
			G GT TATTC		
GAM1278	CTCF	5'	GGGCGCCGCGGGGGG 21635	A	
			TCCTCC GTGGCGTTC		
			GGGGGG CGCCGCGGG		
			-		
GAM1278	DDR1	3'	GGTGAGGAGGACAAGAAGGAG 25697	AGTGGC	
			CTCC GTTCTTTTACT		
			GAGG CAGGAGGAGTGG		
			AAGAA_		
GAM1278	DDR1	3'	GGTGAGGAGGACAAGAAGGAG 25706	AGTGGC	
			CTCC GTTCTTTTACT		
			GAGG CAGGAGGAGTGG		
			AAGAA_		
GAM1278	DDR1	3'	GGTGAGGAGGACAAGAAGGAG 8724	AGTGGC	
			CTCC GTTCTTTTACT		
			GAGG CAGGAGGAGTGG		
			AAGAA_		
GAM1278	DDX34	3'	GTAGGAGGGGCGTTAGAG 27988	CAG	
			CTC TGGCGTTCTTTTAC		

GAG ATTGCGGGGAGGATG

GAM1278 DGKD 3' GGTGGGGAGGGGACATGAGGA 59409 CA GCG  
TCCTC GTG TTCTTTTACT  
||||| ||| |||||  
AGGAG TAC GGGAGGGGTGG  
\_ AG\_  
GAM1278 DGKZ 3' GGGACGGCCACGGGGGA 13324 A \_  
TCCTCC GTGGC GTTCT  
||||| ||||| |||||  
AGGGGG CACCG CAGGG  
G G  
GAM1278 DKFZp434A1520 3' AGTGAGGAATTTTATTGGTGA 61113 T C TT  
TCC CCAGTGG GTTCT TTA  
||| ||||| ||||| |||||  
AGG GGTTATT TAAGG AGTGA  
T T \_  
GAM1278 DKFZP434D146 3' AGTAGAAAGCCTTACTGTAGGA 31520 C CGTT  
TCCT CAGTGG CTTTTTACT  
||| ||||| |||||  
AGGA GTCATT GAAAGATGA  
T CC\_  
GAM1278 DKFZP434F1735 5' AGTGAAGAGATGAGGCTGGAG 31495 GG T  
CTCCAGT CGT CTTTTTACT  
||||| ||| |||||  
GAGGTCG GTA GAGAAGTGA  
GA \_  
GAM1278 DKFZP434H0820 3' GGTGGAGAGATGAGATTTAGGG 63853 \_ GG T  
GG CCTCC AGT CGT CTTTTTACT  
||||| ||| ||| |||||  
GGGGG TTA GTA GAGAGGTGG  
AT GA \_  
GAM1278 DKFZP434I0714 5' GGTGAGAGGGGCAAAGGAGGA 85800 AGTGGC  
TCCTCC GTTCTTTTACT  
||||| |||||  
AGGAGG CGGGGAGAGTGG  
AAA\_  
GAM1278 DKFZP434N178 3' GTGGGGGGGCGCTTGGGAGG 71910 AGT G TTT  
CCTCC GGC TTCT TAC  
||||| ||| ||||| |||  
GGAGG CCG GGGG GTG  
GTT G \_  
GAM1278 DKFZp547J036 5' GGTGGGGGGGGGCCAGGGAG 50129 AG C  
CTCC TGG GTTCTTTTACT  
||| ||| |||||  
GAGG ACC CGGGGGGGGTGG  
G\_ \_  
GAM1278 DKFZP564B1162 3' AGTGGGAGGGGGCCAGGCTGCA 48528 C \_ G  
GGA CCT CAGT GGC TTCTTTTACT  
||| ||||| ||| |||||



		GGA GTCG CCG GGGGAGGGTGA		
		C GA _		
GAM1278	DKFZp566D234 3'	CTTGAAGGGAATGTCACAGGAG 61863	A	CT
	GA	TCCTCC GTGGCGTTCTTTTTA		
		AGGAGG CACTGTAAGGGAAGT		
		A TCC		
GAM1278	DKFZP566J091 3'	GGAGCCTGCTGGGGGG 48123	TG C	
		TCCTCCAG G GTTCT		
		GGGGGGTC C CGAGG		
		GT _		
GAM1278	DKFZP586N0721 3'	AGTTCTGAATGTTGGTGGAGGG 31201	G	TTTTT
		TCCTCCA TGGCGTTC ACT		
		GGGAGGT GTTGTAAG TGA		
		G TCT__		
GAM1278	DKFZP667O116 3'	GTGAGAGGGAGTGGGGAGG 94286	AGTG G	
		CCTCC GC TTCTTTTACT		
		GGAGG TG AGGGAGAGTG		
		GG__ _		
GAM1278	DKFZP727G051 5'	GTGGAGAGCATGTGGAGGG 69477	AGTG T	
		TCCTCC GCGT CTTTTACT		
		GGGAGG TGTA GAGAGGTG		
		___ C		
GAM1278	DKFZp761H079 5'	GGTGGGAGGAGCGACCCGGGA 58736	AGT _	
		TCC GG CGTTCTTTTACT		
		AGG CC GCGAGGAGGGTGG		
		GC_ A		
GAM1278	DKFZP762N2316 3'	GGTAGAAGACTTCTCATTGGGG 67129	T	CGTTC
	A	TCC CCAGTGG TTTTACT		
		AGG GGTTACT GAAGATGG		
		_ CTTCA		
GAM1278	DNAJB5 3'	AGTGGGAGGGAGGTGGGGAG 24353	AGTG G	
		CTCC GC TTCTTTTACT		
		GAGG TG AGGGAGGGTGA		
		GG__ G		
GAM1278	DNAJC5 3'	AGGCTGCCACTGGAGGG 61446	TT	
		TCCTCCAGTGGCG CT		
		GGGAGGTCACCGT GA		
		CG		
GAM1278	DOCK3 3'	AGTGGAGAGGAGGGAAGTGGTG 66496	T	GGCG
	GA	TCC CCAGT TTCTTTTACT		

AGG GGTCA AGGAGAGGTGA  
 T AGGG  
 GAM1278 DOCK3 3' GGTAAAGAGGGTGGGAGGG 66506 AGTGG TT  
 TCCTCC CG CTTTTTACT  
 ||||| || |||||  
 GGGAGG GT GAGAAATGG  
 \_\_\_\_ GG  
 GAM1278 DT1P1A10 3' AGTGAGTGTGGGTGTGGCTGGA 61564 G TT TT\_  
 GGA TCCTCCAGT GCG C TTTACT  
 ||||| ||| | |||||  
 AGGAGGTCG TGT G GAGTGA  
 G GG TGT  
 GAM1278 EBF2 5' AGTGAAGGCTGGACCACAGGAG 42643 A CGTTC  
 GA TCCTCC GTGG TTTTACT  
 ||||| ||| |||||  
 AGGAGG CACC GGAAGTGA  
 A AGGTC  
 GAM1278 ELF2 3' AGTGGGAGGGGTTGGGATGGG 22497 \_ AGTGGC TT  
 TCC TCC G CTTTTTACT  
 ||| ||| | |||||  
 GGG AGG T GGAGGGTGA  
 T GT\_\_\_\_ GG  
 GAM1278 ERF 3' TGGTGGGGGGAGTAGAGGGGCC 21440 G \_\_\_\_\_  
 GCTGGAG GTGGC T TCTTTTACT G  
 ||||| | ||||| |  
 CGCCG G AGGGGGGTGG T  
 G GAGATG  
 GAM1278 EZF-2 5' AGTGAGGACAGGCTGCGGGAGG 37095 A TG G C  
 A TCCTCC G GC TT TTTTACT  
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 AGGAGG C CG GA AGGAGTGA  
 G GT \_ C  
 GAM1278 EZFIT 3' GGAGCTGGTGGAGGG 41110 G G  
 TCCTCCA TGGC TTC  
 ||||| ||| |||  
 GGGAGGT GTCG AGG  
 G \_  
 GAM1278 FER1L4 5' AGTACTATGCGTCGCTGCAGGA 47332 C TCTTTT  
 TCCT CAGTGGCGT TACT  
 ||| ||||| |||  
 AGGA GTCGCTGCG ATGA  
 C TATC\_\_\_\_  
 GAM1278 FKBP8 5' AGTGAGCTGCCACCGCTGGAGG 24099 C\_ TCTT  
 A TCCTCCAGTGG GT TTTACT  
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 AGGAGGTCGCC CG GAGTGA  
 AC TC\_\_\_\_  
 GAM1278 FLJ10315 3' GGTAAGAAGTGGTGGTGGGGGG 36021 G G TTC  
 TCCTCCA TG CG TTTTACT  
 ||||| || |||||

GGGGGGT GT GT GAAGATGG  
G G \_\_\_\_  
GAM1278 FLJ10483 5' GAGGGCGCCGCTGGGCGG 36170 \_  
CC TCCAGTGGCGTTCTT  
|| |||||  
GG GGGTCGCCGCGGGAG  
C  
GAM1278 FLJ10525 3' GGTAGGGGGAGGAGTTGTGGGG 36225 A TG G\_  
GA TCCTCC G GC TTCTTTTACT  
||||| | || |||||  
AGGGGG T TG GAGGGGGATGG  
\_ GT AG  
GAM1278 FLJ10702 5' GCACCAAGGAGCCGTTGGAGGG 36441 G TTTACT  
TCCTCCAGTGGC TTCTT  
||||||| ||||  
GGGAGGTTGCCG AGGAA  
\_ CCACGG  
GAM1278 FLJ10898 5' GGTGAAGGGCAGACTGCTAGAG 59437 C TG CGTT  
GA TCCTC AG G CTTTTTACT  
||||| || | |||||  
AGGAG TC C GGGAAGTGG  
A GT AGAC  
GAM1278 FLJ10933 3' GTAAGACATTGTTGGTGGA 36903 T TG C CTTT  
TCC CCAG G GTT TTAC  
||| ||| | ||| ||||  
AGG GGTT T CAG AATG  
T GT A \_\_\_\_  
GAM1278 FLJ11017 5' AGAGAAGGAATGTTGCTGGGGA 36985 T TG ACT  
TCC CCAG GCGTTCTTTT  
||| ||| |||||  
AGG GGTC TGTAAGGAAGA  
\_ GT GA  
GAM1278 FLJ11186 5' GTTAGAGAACGTCGCGGAGGA 37144 A TT  
TCCTCC GTGGCGTTCTTT AC  
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AGGAGG CGCTGCAAGAGA TG  
\_ T\_  
GAM1278 FLJ11996 3' GTGGAAAGGGTGGGTGGA 46444 T AGTGG TT  
TCC CC CG CTTTTTAC  
||| || || |||||  
AGG GG GT GAAAGGTG  
T \_\_\_\_ GG  
GAM1278 FLJ12294 3' AGTGGAAGGCCACAGCTGGAG 47006 \_\_\_\_ G TTTTACT  
CTCCAGT GGC TTCT  
||||| ||| ||||  
GAGGTCG CCG AAGG  
ACA G TGA T  
GAM1278 FLJ12377 5' GGTAGAGGGGGCGGCGGCGGCG 46485 T AG G  
G CC CC TG CGTTCTTTTACT  
|| || || |||||

GG GG GC GCGGGGGAGATGG  
C CG G  
GAM1278 FLJ12572 3' GTAGGAGGGGCAGGAGG 43254 AGTGGC  
CCTCC GTTCTTTTAC  
||||| |||||  
GGAGG CCGGGAGGATG  
A\_\_\_\_\_  
GAM1278 FLJ12770 5' GGGGCCCGTTGGGGG 49742 C  
TCCTCCAGTGG GTTCT  
||||||| |||||  
GGGGGGTTGCC CGGGG  
-  
GAM1278 FLJ12973 3' AGTAAGGGAGAAGTCTTGGAGG 46101 T G \_  
G TCCTCCAG GGC TTCTTT TACT  
||||||| ||| ||||| |||||  
GGGAGGTT CTG AAGAGG AATGA  
- - G  
GAM1278 FLJ13181 5' GTGGAGGGAGCGAGAGG 47241 CAGTGG  
CCTC CGTTCTTTTAC  
||||| |||||  
GGAG GCGAGGGAGGTG  
A\_\_\_\_\_  
GAM1278 FLJ13291 3' AGTGAAACTTATGTTAGGGGA 49778 CAG TC\_  
TCCTC TGGCGT TTTTACT  
||||| ||||| |||||  
AGGGG ATTGTA AAAAGTGA  
- TTC  
GAM1278 FLJ13639 3' GGGACTGTCCCCTGGGGGG 45235 T \_  
TCCTCCAG GG C GTTCT  
||||||| ||| |||||  
GGGGGGTC CC G CAGGG  
C T T  
GAM1278 FLJ13769 3' GAGAATGACATGGGGGA 46612 G G  
TCCTCCA TG CGTTCTT  
||||||| ||| |||||  
AGGGGGT AC GTAAGAG  
- A  
GAM1278 FLJ13769 3' TAAGGGGGACAGAGGG 46625 CAGTGGC  
TCCTC GTTCTTTTAA  
||||| |||||  
GGGAG CAGGGGGAAT  
A\_\_\_\_\_  
GAM1278 FLJ13798 3' GGTGGGGAGAGCCCAAGGA 87109 CCAG C  
TCCT TGG GTTCTTTTACT  
||||| ||| |||||  
AGGA ACC CGAGAGGGGTGG  
AG\_\_ \_  
GAM1278 FLJ14326 3' GTGGAGGGGGTGTCTG 49818 T TT  
CAG GGCG CTTTTTAC  
||| ||| |||||

GTC TTGT GGGAGGTG  
 \_ GG  
 GAM1278 FLJ14346 3' GTGGAGAGGGGCTGAGGGA 46720 TC GGCG  
 TCC CAGT TTCTTTTAC  
 ||| ||| |||||  
 AGG GTCG GGGAGAGGTG  
 GA \_\_\_\_  
 GAM1278 FLJ14827 5' GGTGGGAAGAAGGTGCGGGGA 51653 T A G G  
 TCC CC GTG C TTCTTTTACT  
 ||| ||| | |||||  
 AGG GG CGT G AAGAAGGGTGG  
 \_ \_ \_ G  
 GAM1278 FLJ14855 3' TAGAGTTCCTGGAGGG 52620 TG GTTCTT  
 TCCTCCAG GC TTTA  
 ||||| || |||  
 GGGAGGTC TG AGAT  
 CT \_\_\_\_  
 GAM1278 FLJ14927 3' AGTAGCCTTGCTGTTGGGTGA 51704 C TG TTCTTT  
 TC TCCAG GCG TTACT  
 || |||| || ||||  
 AG GGGTT CGT GATGA  
 T GT TCC\_\_\_\_  
 GAM1278 FLJ20036 5' CCTGCGGAGGGGCGTTATCTGG 34397 \_ TACT  
 AGGG CCTCCAG TGGCGTTCTTTT  
 ||||| |||||  
 GGAGGTC ATTGCGGGGAGG  
 T CGTCCG  
 GAM1278 FLJ20040 5' GGTGGAAGGGAGCTGTTGCGGG 38634 \_ TG G  
 G CCTC CAG GC TTCTTTTACT  
 ||| ||| || |||||  
 GGGG GTT CG AGGGAAGGTGG  
 C GT \_  
 GAM1278 FLJ20311 3' GGGGGTTATGGAGGA 34924 G G  
 TCCTCCA TGGC TTC  
 ||||| ||| |||  
 AGGAGGT ATTG GGG  
 \_ G  
 GAM1278 FLJ20321 3' GGTGGAAGGGACCCTCCTCACT 34950 C\_\_\_\_  
 GGATGG CCAGTGG GTTCTTTTACT  
 ||||| |||||  
 GGTCAC T CAGGGAAGGTGG  
 CCTCC  
 GAM1278 FLJ20464 5' TGGGGGTGCCGGAGGA 35236 AGT TT TTT  
 TCCTCC GGCG CT TA  
 ||||| ||| || |||  
 AGGAGG CCGT GG GT  
 \_ GG \_  
 GAM1278 FLJ20583 5' GGTGGAGGGGACGCGGCGG 35425 A G  
 CC GT GCGTTCTTTTACT  
 || || |||||

GG CG CGCAGGGGAGGTGG  
\_ G  
GAM1278 FLJ20967 5' GGTGGAGGGACACCTGGAGG 41964 GT C T  
CCTCCA GG GT CTTTTTACT  
||||| || || |||||  
GGAGGT CC CA GGGAGGTGG  
\_ A \_  
GAM1278 FLJ21438 5' GGTGGGGAGAAGGCGGCTGGAG 61526 G G  
GG TCCTCCAGT GC TTCTTTTACT  
||||||| || |||||  
GGGAGGTCG CG AAGAGGGGTGG  
G G  
GAM1278 FLJ21870 3' GGACCCAGAGCAGCCGCTGGAG 43461 \_ TTTTACT  
GG TCCTCCAGTGGC GTTCT  
||||||| |||||  
GGGAGGTGCGCCG CGAGA  
A CCCAGG  
GAM1278 FLJ21924 5' TAGTGAGAGAGTGCTACATCA 45479 CA\_  
GAG TC GTGGCGTTCTTTTACT A  
|| ||||| ||||| |  
AG CATCGTGAGAGAGGTGA T  
ACTA  
GAM1278 FLJ21945 3' GGT TGAGGAGTCTGCTGGGGGG 47318 TG C TT  
TCCTCCAG G GTTCTT ACT  
||||| | ||||| |||  
GGGGGGTC C TGAGGAG TGG  
GT\_ T\_  
GAM1278 FLJ22054 5' GG TAGAAAATCCATTAGAGGA 94399 C CGTTC  
TCCTC AGTGG TTTTACT  
||||| ||||| |||||  
AGGAG TTACC AAAGATGG  
A TA\_  
GAM1278 FLJ22167 3' GGTGGAGAGGGAGCTGGGG 44582 GGCGT  
CTCCAGT TCTTTTACT  
||||| |||||  
GGGGTCG GGAGAGGTGG  
AG\_  
GAM1278 FLJ22378 3' AGTGGGGAGGACGAGGATGTGG 46894 TC GTGG  
GA TCC CA CGTTCTTTTACT  
||| || |||||  
AGG GT GCAGGAGGGGTGA  
GT AGGA  
GAM1278 FLJ22386 5' GGTGGGGAGGGCGCTCGGCGGC 44744 T A \_  
GG CC CC GT GGCGTTCTTTTACT  
|| || |||||  
GG GG CG TCGCGGAGGGGTGG  
C \_ GC  
GAM1278 FLJ22405 5' GGGGAGCTGCTGGAGGA 42522 TG G  
TCCTCCAG GC TTCTT  
||||| || |||

AGGAGGTC CG AGGGG  
 GT \_  
 GAM1278 FLJ22596 5' GTAGAAAGGATGTCGGGG 46963 AGT  
 CTCC GCGCTTCTTTTAC  
 ||| |||||  
 GGGG CTGTAGGAAAGATG  
 —  
 GAM1278 FLJ22655 3' GGTAAAAAGAATTCTCTTGGAG 45312 T C  
 CTCCAG GG GTTCTTTTACT  
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 GAGGTT TC TAAGAAAAATGG  
 C T  
 GAM1278 FLJ22679 3' AGTGAAGAGAATGTGATAGG 49920 A G  
 CC GT GCGTTCTTTTACT  
 || || |||||  
 GG TA TGTAAGAGAAGTGA  
 A G  
 GAM1278 FLJ22679 3' AGTGAAGAGAATGTGATAGG 34678 A G  
 CC GT GCGTTCTTTTACT  
 || || |||||  
 GG TA TGTAAGAGAAGTGA  
 A G  
 GAM1278 FLJ22690 3' GGTGGAGACAGTGCTGGGAG 45249 AGT C  
 CTCC GCGTT TTTTACT  
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 GAGG TCGTGA AGAGGTGG  
 G\_ C  
 GAM1278 FLJ23091 3' GGTGGGGGTGTATTCCTTGGGG 46125 T C TC\_  
 GA TCCTCCAG GG GT TTTTACT  
 ||||| || || |||||  
 AGGGGGTT CC TA GGGGGTGG  
 \_ T TGT  
 GAM1278 FLJ23185 3' AGTGATCAGGCCACTGGAGGA 46825 GTT TT  
 TCCTCCAGTGGC CT TTACT  
 ||||| || |||||  
 AGGAGGTCACCG GA AGTGA  
 \_ CT  
 GAM1278 FLJ23185 3' GGTGGAGAGGATGAGGTTTGAG 46832 CAGTGG  
 GA TCCTC CGTTCTTTTACT  
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 AGGAG GTAGGAGAGGTGG  
 TTTGGA  
 GAM1278 FLJ23231 3' GGTGGGGAGGGAGGTGGGGG 46914 GTGGCG  
 CCTCCA TTCTTTTACT  
 |||| |||||  
 GGGGGT GGGAGGGGTGG  
 GGA\_  
 GAM1278 FLJ23375 3' GGTGGAGGGCCAGGATTGGTGG 46358 T \_ G TTTTACT  
 G CC CCAG TGGC TTCT  
 || ||| ||| |||

GG GGTT ACCG GAGG  
T AGG G TGG T  
GAM1278 FLJ23510 3' GGTGGAATGGTGTATGCTGTTG 45288 T TG \_\_\_\_ T  
GTGGA CCAG GCGT TC TTTTACT  
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GGTT CGTA GG AAGGTGG  
T GT TGT T  
GAM1278 FLJ23519 5' GGTGGGGGAGGGTGCTGAAGAGG 69206 CAG TT  
A TCCTC TGGCG CTTTTTACT  
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AGGAG GTCGT GAGGGGTGG  
AA\_ GG  
GAM1278 FLJ30567 3' GGATGTTACTGGAGGG 58828  
TCCTCCAGTGGCGTTC  
|||||  
GGGAGGTCATTGTAGG  
  
GAM1278 FLJ31455 5' GGTGAGGGGATCAGTCTGGTGG 58631 T TG GT\_  
A TCC CCAG GC TCTTTTACT  
||| ||| || |||||  
AGG GGTC TG AGGGGAGTGG  
T \_ ACT  
GAM1278 FLJ31455 5' TGGAAAGGACAGAGGA 58632 CAGTGGC  
TCCTC GTTCTTTTAA  
||||| |||||  
AGGAG CAGGAAAGGT  
A\_\_\_\_\_  
GAM1278 FOXO3A 5' GGGGGGTGACGGGGGG 7577 A G G  
TCCTCC GT GC TTCT  
||||| || |||  
GGGGGG CA TG GGGG  
\_ G G  
GAM1278 GALNT6 3' AGTAGGGAAGGCAGCTGGGGGA 23289 G G TT  
TCCTCCAGT GC TTCT TTA  
||||| || ||| |||  
AGGGGGTCG CG AAGG GATGA  
A G \_  
GAM1278 GIT2 3' GGTGGAATGACGTGGCCATTGG 54097 GT\_\_ T  
AGGG CCTCCAGTGGC TC TTTTACT  
||||| || |||||  
GGAGGTTACCG AG AAGGTGG  
GTGC T  
GAM1278 GIT2 3' GGTGGAATGACGTGGCCATTGG 54084 GT\_\_ T  
AGGG CCTCCAGTGGC TC TTTTACT  
||||| || |||||  
GGAGGTTACCG AG AAGGTGG  
GTGC T  
GAM1278 GIT2 3' GGTGGAATGACGTGGCCATTGG 28762 GT\_\_ T  
AGGG CCTCCAGTGGC TC TTTTACT  
||||| || |||||



			GGAGGTTACCG	AG AAGGTGG		
			GTGC	T		
GAM1278	GPA33	5'	GGTGAGAAGAGGGGAAAATTGCA	19458	C	GGCG_
	GGG		TCCT CAGT	TTCTTTTACT		
			GGA GTTA	GAGAAGAGTGG		
			C	AAAGG		
GAM1278	GPS2	5'	GGGGGCTCTGGGGGA	87161	T	G
			TCCTCCAG	GGC TTC		
			AGGGGGTC	TCG GGG		
			-	G		
GAM1278	GTF3C4	3'	TGAAGAGAAGGATGCACTGGAG	24195	G	ACT
	GA		TCCTCCAGTG	CGTTCTTTT		
			AGGAGGTCAC	G TAGGAAGAG		
			-	AAGTC		
GAM1278	H2AFY	5'	GGTGAGGAGGATTAAGTGAAGG	16891	C	GGC
	A		TCCT CAGT	GTTCTTTTACT		
			AGGA GTCA	TAGGAGGAGTGG		
			A	AT_		
GAM1278	HAPIP	3'	AGTGAAGAGGTTAATTAGAGGG	14159	C	GGCGT
			TCCTC AGT	TCTTTTACT		
			GGGAG TTA	GGAGAAGTGA		
			A	ATT_		
GAM1278	HEMK	3'	GGTGGGGAGGGCGAAGGGGG	32438	AGTGG	
			CCTCC	CGTTCTTTTACT		
			GGGGG	GCGGGAGGGGTGG		
			AA_			
GAM1278	HES2	3'	TGGGAAGAATGGGGAG	38857	AGTGG	
			CTCC	CGTTCTTTTA		
			GAGG	GTAAGAAGGGT		
			G_			
GAM1278	HNRPA3	3'	GGTGGATATGGTGGCGGTGTTG	19255	GT G	_ T_
	GAGGA		TCCA	G CGTT CT TTTACT		
			AGGT	T GCGG GG AGGTGG		
			TG G	T TAT		
GAM1278	HTATIP	3'	AGTGAGAAGGGATCCGGATGGG	21105	G_	CG
	GGA		TCCTCCA	TGG TTCTTTTACT		
			AGGGGGT	GCC GGGAAGAGTGA		
			AG	TA		
GAM1278	IMPACT	3'	GGATGCTGTTTGGAGGA	37392	_TG	
			TCCTCCA	G GCGTTC		

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AGGAGGT T CGTAGG
T GT
GAM1278 INSM2 3' GGTGGGGAGGATGCTACTTTAC 50869 _____
TGGAG CAGT GCGTTCTTTTACT
||||| |||||||
GTCA TCGTAGGAGGGGTGG
TTTCA
GAM1278 KCNJ9 3' GTGGAGGGGTGTCTGGA 17156 TG TT
TCCAG GCG CTTTTTAC
||||| ||| |||||||
AGGTC TGT GGGAGGTG
_ GG
GAM1278 KCNK16 3' GTAGAGGGATTTCGGGGG 49507 AGT CGT
CCTCC GG TCTTTTAC
||||| || |||||||
GGGGG CT AGGGAGATG
_ TT_
GAM1278 KCNV1 5' GGTGGAGAGGGGTGCGCCAAGGA 26883 AG _
G CTCC TGGCGT TCTTTTACT
||||| ||||||| |||||||
GAGG ACCGCG GGAGAGGTGG
A_ TG
GAM1278 KIAA0089 3' AGTGAATCATGCAACGTGTTGG 69963 GT G CTT___
GGGA CTCCA G CGTT TTTACT
||||| | ||| |||||||
GGGGT T GCAA AAGTGA
TG_ CGTACT
GAM1278 KIAA0100 3' TGAAAGGGTAGGGGGA 27973 AGTG GCGT
TCCTCC TCTTTTAA
||||| |||||||
AGGGGG GGGAAAGT
AT_____
GAM1278 KIAA0143 3' AGTGGAGTCGTTACCGCTGGAG 64779 CGTTCT
GA TCCTCCAGTGG TTTTACT
||||||||| |||||||
AGGAGGTCGCC GAGGTGA
ATTGCT
GAM1278 KIAA0247 3' GGTAGGGAGCTGGTTGGAG 28408 TGGC TT
CTCCAG GTTCT TTA
||||| ||||| |||||
GAGGTT CGAGG GATGG
GGT_ _
GAM1278 KIAA0247 3' GTAGAAGGGGATGCAGGG 28409 AGTG _
CC GCGTTCT TTTTAC
|| ||||||| |||||||
GG CGTAGGG AAGATG
GA_ G
GAM1278 KIAA0261 3' GGTGGGGGGAGGTGGTGGGGGA 68182 G G G
TCCTCCA T GC TTCTTTTACT
||||||| | || |||||||

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			AGGGGGT G TG GAGGGGGGTGG		
			_ G _		
GAM1278	KIAA0323	3'	GGTAAAAATACCTGTTGGGAGG 63269	_	TG C TC
	A		TCCTCC AG G GT TTTTACT		
			AGGAGG TT C CA AAAAATGG		
			G GT _ T_		
GAM1278	KIAA0352	3'	CCTCCAGGGGGCGCTATTGGAT 29154	_	TTACT
	GG		CC TCCAGTGGCGTTCTTT		
			GG AGGTTATCGCGGGGA		
			T CCTCA		
GAM1278	KIAA0354	3'	TGTGGGAAAGAGCCCATTGGAG 29573	C	ACT
	GA		TCCTCCAGTGG GTTCTTTT		
			AGGAGGTTACC CGAGAAAGG		
			_ GTGTA		
GAM1278	KIAA0367	3'	AGTGAGAAAGTTTGTGTTGAGGG 67291	CAGT	TT _
			TCCTC GGCG CTT TTTACT		
			GGGAG TTGT GAA GAGTGA		
			T__ TT A		
GAM1278	KIAA0367	3'	GGTGGAATAATTCATTGGGGA 67301	T	CGTTC
			TCC CCAGTGG TTTTACT		
			AGG GGTTACT AAAGGTGG		
			_ TA__		
GAM1278	KIAA0431	3'	GGTGAGAGGATCACTCGAGGA 30894	C	CGT
			TCCTC AGTGG TCTTTTACT		
			AGGAG TCACT AGGAGAGTGG		
			C _		
GAM1278	KIAA0446	5'	AGTGAGGGACAATTCTGGAGG 68852	TGGC_	TT
	A		TCCTCCAG GTTCT TTACT		
			AGGAGGTC CAGGG AGTGA		
			TTTAA _		
GAM1278	KIAA0472	3'	AGTGGGGAGGGTGAAGGGAGG 71855	AGTGG	TT
	G		TCCTCC CG CTTTTTACT		
			GGGAGG GT GAGGGGTGA		
			GAAG_ GG		
GAM1278	KIAA0472	3'	GAGATTGTGGCTGGAGGA 71864	G	T
			TCCTCCAGT GCG TCTT		
			AGGAGGTCG TGT AGAG		
			G T		
GAM1278	KIAA0495	5'	GGTGAGACCCTTTACTGCAGG 62598	C	CGTTC
	G		TCCT CAGTGG TTTTACT		

		GGGA GTCATT AGAGGTGG	
		C TCCC_	
GAM1278	KIAA0522	3' AGTGGGAGGGGCTGTATGGAG 71964	GTGGC
		CTCCA GTTCTTTTACT	
		GAGGT CGGGGAGGGTGA	
		ATGT_	
GAM1278	KIAA0557	3' AGTGGAGGGGGCAGGGGAGGG 77988	AGTGGC
		TCCTCC GTTCTTTTACT	
		GGGAGG CGGGGGAGGTGA	
		GGA_	
GAM1278	KIAA0563	5' AAGAACGGCTGTGGGGGA 29177	G _
		TCCTCCA TGGC GTTCTT	
		AGGGGGT GTCG CAAGAA	
		_ G	
GAM1278	KIAA0596	3' AGCTGTGGGATGTTGCTGCAGG 62824	C TG TTTTACT
	A	TCCT CAG GCGTTCT	
		AGGA GTC TGTAGGG	
		C GT TGTCGA	
GAM1278	KIAA0620	3' GGTGGAGGGGAGGGATGGGGGG 62122	GTGGCG
		TCCTCCA TTCTTTTACT	
		GGGGGGT AGGGGAGGTGG	
		AGGG_	
GAM1278	KIAA0664	3' GTGGGGAGGGGTGGGGAG 64287	AGTG G
		CTCC GC TTCTTTTAC	
		GAGG TG GGGAGGGGTG	
		GG_ _	
GAM1278	KIAA0677	3' GGTGGGGGGGTGGGACTAGAGGG 27830	C GG TT TT
		TCCTC AGT CG CTT TACT	
		GGGAG TCA GT GGG GTGG	
		A GG GG _	
GAM1278	KIAA0767	3' GGTGCCGGGGGTGCTTTGGGGG 60630	T TT TT
	G	TCCTCCAG GGCG CTT TACT	
		GGGGGGTT TCGT GGG GTGG	
		_ GG CC	
GAM1278	KIAA0773	3' AGTGAGAAGGTTGAGAGTTGGG 28045	GG_ TT
	G	CTCCAGT CG CTTTTTACT	
		GGGGTTG GT GAAGAGTGA	
		AGA TG	
GAM1278	KIAA0773	3' AGTGGGAGGGATGTGATGCTGG 28046	_
	AG	CTCCAGTG GCGTTCTTTTACT	

		GAGGTCGT TGTAGGGAGGGTGA	
		AG	
GAM1278 KIAA0773	3'	GGTGGGGAGGGGCATGTGCAGG 28060	C GTG G
	A	TCCT CA GC TTCTTTTACT	
		AGGA GT CG GGGAGGGGTGG	
		C GTA _	
GAM1278 KIAA0774	5'	GGATGTCATTGAGGA 91754	C
		TCCTC AGTGGCGTTC	
		AGGAG TTAGCTGTAGG	
		-	
GAM1278 KIAA0775	3'	GGTGGGGGGAAGGTGTTAGAGG 28283	CAGTG G
	A	TCCTC GC TTCTTTTACT	
		AGGAG TG AAGGGGGGTGG	
		ATTG_ G	
GAM1278 KIAA0794	3'	AGTAAGGAGGATGGCGGAGG 80407	AGT G
		CCTCC G CGTTCTTTTACT	
		GGAGG C GTAGGAGGAATGA	
		_ G	
GAM1278 KIAA0821	3'	AGTGAGGAGGGAGAACTTGGAA 29940	_ _ GGCG
	GGG	CCT CCA GT TTCTTTTACT	
		GGA GGT CA GGGAGGAGTGA	
		A T AGA_	
GAM1278 KIAA0841	3'	AGTGATGTAATGTCATTGGGGA 71375	T CTTT
		TCC CCAGTGGCGTT TTAGCT	
		AGG GGTACTGTAA AGTGA	
		- TGT_	
GAM1278 KIAA0863	3'	GTAGAAATATTTGGAGGA 95247	TGGCGTTC
		TCCTCCAG TTTTAC	
		AGGAGGTT AAAGATG	
		TAT_	
GAM1278 KIAA0869	3'	AGTGAGGGGAGGGCTGTGGGGA 70855	T G G
		TCC CCA TGGC TTCTTTTACT	
		AGG GGT GTCG GAGGGGAGTGA	
		- _ G	
GAM1278 KIAA0888	3'	GTAAACTGCCTTTGGGGGA 63231	T TTCTT
		TCCTCCAG GGCG TTTAC	
		AGGGGGTT CCGT AAATG	
		T C_	
GAM1278 KIAA0903	3'	AGTGGGAGGGGTACAAGGGGA 71405	T AG GC TT
		TCC CC TG G CTTTTTACT	

AGG GG AC T GGAGGGTGA  
 \_ A\_ A\_ GG  
 GAM1278 KIAA0960 3' AGTGAAAATCATACTGCCACTG 92654 \_ TC\_\_  
 GAG CTCCAGTGGC GT TTTTACT  
 ||||| || |||||  
 GAGGTCACCG CA AAAAGTGA  
 T TACT  
 GAM1278 KIAA0972 3' GTGGAAAGAGCACGAGGA 30015 CAGT GC  
 TCCTC G GTTCTTTTACT  
 |||| | |||||  
 AGGAG C CGAGAAAGGTG  
 \_\_\_\_ A\_  
 GAM1278 KIAA0992 3' AGTAGGGAGGAGAATGAAGGA 32203 C GTGGCG  
 TCCT CA TTCTTTTACT  
 ||| || |||||  
 AGGA GT AGGAGGGATGA  
 A AAG\_\_  
 GAM1278 KIAA1032 3' GGACCAGGATGCTGGTTGGAGG 66157 GT\_ TTTTACT  
 G TCCTCCA GGC GTTCT  
 ||||| |||||  
 GGGAGGT TCGTAGGA  
 TGG CCAGG  
 GAM1278 KIAA1036 3' AGTAGAGAGAGCTCGTGCTGGG 29812 T GC\_  
 GA TCC CCAGTG GTTCTTTTACT  
 || ||||| |||||  
 AGG GGTCGT CGAGAGAGATGA  
 \_ GCT  
 GAM1278 KIAA1036 3' GGTGAGAAGGAGGCCTGAAGGG 29828 C GT G  
 TCCT CA GGC TTCTTTTACT  
 ||| || || |||||  
 GGGA GT CCG AGGAAGAGTGG  
 A \_ G  
 GAM1278 KIAA1056 3' AGTGGGGGTACATGCTGGAAGG 29691 \_ GC TC  
 A TCCT CCAGTG GT TTTTACT  
 ||| ||||| || |||||  
 AGGA GGTCGT CA GGGGGTGA  
 A A\_ T\_  
 GAM1278 KIAA1077 3' AGTAGAAAGAAAGGCTGGGGA 72901 T GGCG  
 TCC CCAGT TTCTTTTACT  
 || ||||| |||||  
 AGG GGTCG AAGAAAGATGA  
 \_ GA\_  
 GAM1278 KIAA1110 3' GGTGGGAGGAGTGAGGAGGG 61848 AGTGG  
 TCCTCC CGTTCTTTTACT  
 ||||| |||||  
 GGGAGG GTGAGGAGGGTGG  
 A\_\_\_\_  
 GAM1278 KIAA1130 3' AGTGAGAATCCCGCTGTTTGGG 62411 \_ C TTTACT  
 GA CCTC CAGTGG GTTCTT  
 ||| ||||| |||||

GGGG GTCGCC TAAGAG  
TTT C TGA  
GAM1278 KIAA1130 3' GTGAGGAGGGTGCCTGGG 62426 GT TT  
TCCA GGCG CTTTTTAC  
|||| ||| |||||  
GGGT CCGT GAGGAGTG  
\_ GG  
GAM1278 KIAA1181 3' GTGGGGGGAAAGTAGAGGA 68377 CAGTG G  
TCCTC GC TTCTTTTAC  
|||| || |||||  
AGGAG TG AAGGGGGGTG  
A\_ A  
GAM1278 KIAA1190 3' GGTGAGGGGGGTGCTGGGGG 71103 GTG TT  
CCTCCA GCG CTTTTTACT  
|||| ||| |||||  
GGGGGT CGT GGGGAGTGG  
\_ GG  
GAM1278 KIAA1196 3' GCTCTGAGTGGCCACTGGGGGA 61470 GTT TTTACT  
TCCTCCAGTGGC CTT  
||||||| |||  
AGGGGGTCACCG GAG  
GT\_ TCTCGG  
GAM1278 KIAA1219 3' AGAATAGCACTGGAGGA 61364 GC  
TCCTCCAGTG GTTCT  
||||||| ||||  
AGGAGGTCAC TAAGA  
GA  
GAM1278 KIAA1244 3' AGTACTCCACAGTTTACTGGGG 71987 \_ GTTCTTTT  
GA TCCTCCAGTGG C TACT  
||||||| | |||  
AGGGGGTCATT G ATGA  
T ACACCTC\_  
GAM1278 KIAA1259 3' GGTGAAGAGGGCGGAGAGAGGG 49831 AGTGG\_  
GG CCTCC CGTTCTTTTACT  
|||| |||||  
GGGGG GCGGGAGAAGTGG  
AGAGAG  
GAM1278 KIAA1277 3' GAGAACGCTGGGGCGG 64457 T AG  
CC CC TGGCGTTCTT  
|| || |||||  
GG GG GTCGCAAGAG  
C G\_  
GAM1278 KIAA1297 3' GGACCAGGTGCTGCTGGAGGG 72183 TG \_\_\_\_  
TCCTCCAG GC GTTC  
|||| || |||  
GGGAGGTC CG CAGG  
GT TGGAC  
GAM1278 KIAA1319 3' GGTGAGGGGAATGTTATGGG 40408 G  
TCCA TGGCGTTCTTTTACT  
|||| |||||

GGGT ATTGTAAGGGGAGTGG

GAM1278 KIAA1337 3' GGATGTTTTGGGGGA 72681 T  
TCCTCCAG GGCGTTC  
||||||| |||||||  
AGGGGGT TGTAGG

GAM1278 KIAA1344 3' AGTGGGGAGAGGAATCTTGAGG 72446 C TGGCG  
G TCCTC AG TTCTTTTACT  
||||| || |||||||||  
GGGAG TC GAGAGGGGTGA  
T TAAG\_

GAM1278 KIAA1416 5' AAAGGAGCGCCGCGGAGGA 86452 A  
TCCTCC GTGGCGTTCTTTT  
||||| |||||||||  
AGGAGG CGCCGCGAGGAAA

GAM1278 KIAA1456 3' AGTTTGGGGGTTTATTGGAGGA 66987 C TT TTT  
TCCTCCAGTGG G CTT ACT  
||||||||| | ||| |||  
AGGAGGTTATT T GGG TGA  
\_GG TT\_

GAM1278 KIAA1463 3' GGTAAGCATCCTGTGGAGGG 72278 GT CGTTCT  
TCCTCCA GG TTTTACT  
||||||| || |||||||  
GGGAGGT CC GAAATGG  
GT TAC\_\_

GAM1278 KIAA1464 3' AGTGGGAAAGGCACCTGGGGGA 68260 GT C TC  
TCCTCCA GG GT TTTTACT  
||||||| || || |||||||  
AGGGGGT CC CG AAGGGTGA  
\_ A GA

GAM1278 KIAA1497 3' GTGGAGAGGACGGGTGGA 67517 T AGTGG  
TCC CC CGTTCTTTTAC  
||| || |||||||||  
AGG GG GCAGGAGAGGTG  
T \_\_\_\_\_

GAM1278 KIAA1503 5' GGTAGGAAGGGACAGTTGTTGG 68351 T TG \_ \_  
GGA CC CCAG GC GTTCTTTT TACT  
|| ||| || ||||||| |||  
GG GGTT TG CAGGGAAG ATGG  
\_ GT A G

GAM1278 KIAA1538 3' GGTGAGGGGGACCGGATGGAGG 71554 GTGGC  
G TCCTCCA GTTCTTTTACT  
||||||| |||||||||  
GGGAGGT CAGGGGGAGTGG  
AGGC\_

GAM1278 KIAA1538 3' GGTGGGGAGGACCAGCTCTGGA 71555 T \_  
GG CCTCCAG GGC GTTCTTTTACT  
||||||| ||| |||||||||



GGAGGTC TCG CAGGAGGGGTGG  
\_ AC  
GAM1278 KIAA1582 5' AGTGGGGGCAGTGCTGAAGGA 65367 C GC TTT  
TCCT CAGTG GTTCT TACT  
||||| ||||| ||||| |||||  
AGGA GTCGT CGGGG GTGA  
A GA \_\_\_\_  
GAM1278 KIAA1614 3' GGTGGGGAGTGTGCGGGAGGG 70123 AGTG TT  
TCCTCC GCG CTTTTTACT  
||||| ||| |||||  
GGGAGG CGT GAGGGGTGG  
G\_\_ GT  
GAM1278 KIAA1622 3' AGTAAGAAGATATGAAGTTGGA 40558 GG \_  
G CTCCAGT CGT TCTTTTACT  
||||| ||| |||||  
GAGGTTG GTA AGAAGAATGA  
AA T  
GAM1278 KIAA1712 5' GGA CTGGCCATTGAGGA 67541 C \_  
TCCTC AGTGGC GTTC  
||||| ||||| |||||  
AGGAG TTACCG CAGG  
\_ GT  
GAM1278 KIAA1755 3' GTGGGGGTGCATTTGGGGA 61353 T TG TT TTT  
TCC CCAG GCG CT TAC  
||| |||| ||| || |||  
AGG GGTT CGT GG GTG  
\_ TA GG \_\_\_\_  
GAM1278 KIAA1821 3' GGTGAGGAGAGGGGATCTGGGG 71793 T TGGCG  
A TCC CCAG TTCTTTTACT  
||| |||| |||||  
AGG GGTC GAGAGGAGTGG  
\_ TAGGG  
GAM1278 KIAA1831 3' GGTGGGAGGAGGCACTTCTGGG 63785 TG\_\_ G  
GGA CCTCCAG GC TTCTTTTACT  
||||| || |||||  
GGGGGTC CG GAGGAGGGTGG  
TTCA \_  
GAM1278 KIAA1857 3' GGTGAGAAGGGTGCGGCCCGAG 50720 CA G TT  
G CCTC GT GCG CTTTTTACT  
||||| || ||| |||||  
GGAG CG CGT GAAGAGTGG  
CC G GG  
GAM1278 KIAA1889 5' AGTGGGGAGAATGACAGATGGA 73501 G\_ G  
GG CCTCCA TG CGTTCTTTTACT  
||||| || |||||  
GGAGGT AC GTAAGAGGGGTGA  
AG A  
GAM1278 KIAA1906 3' GTAGGAAGGATCTGCAGGG 73197 C TGGC  
TCCT CAG GTTCTTTTAC  
||||| ||| |||||

GGGA GTC TAGGAAGGATG  
C \_\_\_\_

GAM1278 KIAA1906 3' GGTAGGGGGGTGTAAGTGGGGA 73196 T G TT TT  
TCC CCAGT GCG CT TTACT  
||| ||||| ||| || |||||  
AGG GGTCA TGT GG GATGG  
\_ A GG \_

GAM1278 KIAA1938 3' GGTGGAGGGGGGCCACCGGGG 92199 A GT  
CTCC GTGGC TCTTTTACT  
||||| ||||| |||||  
GGGG CACCG GGGGAGGTGG  
C \_

GAM1278 KIAA1938 3' GGTGGGGGGGACCTGTGTTGGAG 92200 \_TG C T  
GA CCTCCA G G GT CTTTTTACT  
||||| | ||| |||||  
GGAGGT T C CA GGGGGGTGG  
TG GT \_ \_

GAM1278 KIAA1938 3' GGTGGGTAGGCCATGGGAGGG 92201 A GTT T  
TCCTCC GTGGC CT TTTACT  
||||| ||||| || |||||  
GGGAGG TACCG GA GGGTGG  
G \_ T

GAM1278 KIAA1941 3' GGTGGAGGTTGTTGGTGGAGGA 74843 G TT TT  
TCCTCCA TGGCG CTT TACT  
||||||| ||||| ||| |||||  
AGGAGGT GTTGT GAG GTGG  
G TG \_

GAM1278 KIAA1952 5' GTGGAAACTGCTGGAG 73173 TG CGTTC  
CTCCAG G TTTTAC  
||||| | |||||  
GAGGTC C AAAGGTG  
GT \_\_\_\_

GAM1278 LENG1 5' GGGAGCTGCTGGAGGA 84075 TG G  
TCCTCCAG GC TTCT  
||||||| || |||||  
AGGAGGTC CG AGGG  
GT \_

GAM1278 LGI3 3' GTCTCCTCAGGGTGGCCACTGG 57748 \_TT TTTTACT  
AGGA CCTCCAGTGGC G CT  
||||||| ||| |||  
GGAGGTCACCG T GA  
G GG CTCCTCTGG

GAM1278 LGI4 5' TGGGGGGGGGCAGGAG 57766 AGTGGC  
CTCC GTTCTTTTTA  
||| |||||  
GAGG CGGGGGGGGT  
A \_\_\_\_

GAM1278 LIN-28 3' AGTAAAGAGATGCAATTGGGGG 45145 G T  
CCTCCAGT GCGT CTTTTTACT  
||||||| ||||| |||||

			GGGGGTTA CGTA GAGAAATGA	
			A _	
GAM1278 LSM1	5'	GTAAGGGTAATATGGAGGA	27096	GTG_ GTTCT
		TCCTCCA GC TTTTAC		
		AGGAGGT TG GGAATG		
		ATAA _____		
GAM1278 MAD4	3'	GGTGAGGGGGGCGTGCGCTAGA	21281	C _
		GGG CCTC AGTG GCGTTCTTTTACT		
		GGAG TCGC TGCGGGGGGAGTGG		
		A G		
GAM1278 MAD4	3'	GGTGAGGGGTTGCCCACTGGGT	21282	_ C T_
		GG CC TCCAGTGG GT CTTTTACT		
		GG GGGTCACC CG GGGGAGTGG		
		T _ TT		
GAM1278 MADHIP	3'	GGTGGGAAAGGGTGGTTGGGGG	16621	TG G C
		G TCCTCCAG GC TT TTTTTACT		
		GGGGGGTT TG GA AAGGGTGG		
		GG G _		
GAM1278 MADHIP	3'	GGTGGGAAAGGGTGGTTGGGGG	23639	TG G C
		G TCCTCCAG GC TT TTTTTACT		
		GGGGGGTT TG GA AAGGGTGG		
		GG G _		
GAM1278 MANBAL	3'	AGTGAGAGGGTTCCTGGGGGA	41977	TG GTT
		TCCTCCAG GC CTTTTACT		
		AGGGGGTC TG GGAGAGTGA		
		CT _____		
GAM1278 MAPK8	3'	TGGGAGGGATGGGGAG	10843	AGTGG
		CTCC CGTTCTTTTAA		
		GAGG GTAGGGAGGGT		
		G_____		
GAM1278 MAPK8	3'	TGGGAGGGATGGGGAG	57393	AGTGG
		CTCC CGTTCTTTTAA		
		GAGG GTAGGGAGGGT		
		G_____		
GAM1278 MAPK8	3'	TGGGAGGGATGGGGAG	57394	AGTGG
		CTCC CGTTCTTTTAA		
		GAGG GTAGGGAGGGT		
		G_____		
GAM1278 MAPK8	3'	TGGGAGGGATGGGGAG	57399	AGTGG
		CTCC CGTTCTTTTAA		

GAGG GTAGGGAGGGT  
 G\_\_\_\_  
 GAM1278 MESDC2 3' GTGACGCGCTGTGGGGGGA 72497 A TG TCTTT  
 TCCTCC G GCGT TTAC  
 ||||| | ||| |||  
 AGGGGG T CGCG AGTG  
 G GT C\_\_\_\_  
 GAM1278 MFN2 3' GGTAGAAAGGATGCTGCTGAGG 29604 C TG  
 CCTC AG GCGTTCTTTTACT  
 ||| || |||||  
 GGAG TC CGTAGGAAAGATGG  
 \_ GT  
 GAM1278 MGC10966 5' GGGACCTGCTGCTGGAGGA 48897 TG \_\_\_\_  
 TCCTCCAG GC GTTCT  
 ||||| || |||  
 AGGAGGTC CG CAGGG  
 GT TC  
 GAM1278 MGC12335 3' GGTGGAGGGAGGTGGTGGAGGA 51238 G G G  
 TCCTCCA T GC TTCTTTTACT  
 ||||| | || |||||  
 AGGAGGT G TG GAGGGAGGTGG  
 \_ G \_  
 GAM1278 MGC14258 3' AGATAGAACCTGTTGGGGGA 51859 TG C T  
 TCCTCCAG G GTTCT TTT  
 ||||| | ||| |||  
 AGGGGGTT C CAAGA AGA  
 GT \_ T  
 GAM1278 MGC16384 5' GTAGAAATTTGTGGAGGA 53867 AGTG TTC  
 TCCTCC GCG TTTTAC  
 |||| | || |||||  
 AGGAGG TGT AAAGATG  
 \_\_\_\_ TT\_  
 GAM1278 MGC17303 5' GGTAGGAGGGGCGAGCGCGAG 57502 CA G\_  
 CTC GTG CGTTCTTTTACT  
 || | |||||  
 GAG CGC GCGGGGAGGATGG  
 \_ GA  
 GAM1278 MGC20255 3' GTGAGACAGCATTGGAGGG 53445 G GTTCT  
 TCCTCCAGTG C TTTTAC  
 ||||| | |||  
 GGGAGGTAC G AGAGTG  
 \_ AC\_\_\_\_  
 GAM1278 MGC20496 3' GGGAGCTTGGAGGA 53434 GT G  
 TCCTCCA GGC TTCT  
 |||| | |||  
 AGGAGGT TCG AGGG  
 \_ \_  
 GAM1278 MGC20647 3' AGTGAGGGGGGAGGGTGGGGAG 95605 AGTGGCG  
 CTCC TTCTTTTACT  
 || | |||||

GAGG GGGGGGAGTGA  
 GGTGGGA  
 GAM1278 MGC2477 5' GTGGGATTGCTAGGGGGA 44068 AG T TTT  
 TCCTCC TGGCG TCT TAC  
 ||||| ||||| ||| |||  
 AGGGGG ATCGT AGG GTG  
 \_ T \_  
 GAM1278 MGC2668 3' AGAAGCCTGGGGGG 60572 GT G  
 TCCTCCA GGC TTCT  
 ||||| ||| |||  
 GGGGGGT CCG AAGA  
 \_ \_  
 GAM1278 MGC2705 3' GGTGGGGGAAGGTTGGGGGG 51117 GTG G  
 TCCTCCA GC TTCTTTTACT  
 ||||| || |||||  
 GGGGGGT TG AAGGGGGGTGG  
 \_ G  
 GAM1278 MGC3123 3' GGTGGAAAGGATGTGATGGA 44099 G G  
 TCCA T GCGTTCTTTTACT  
 ||| | |||||  
 AGGT A TGTAGGAAAGGTGG  
 \_ G  
 GAM1278 MGC4415 3' GTAGGGGGGAGATGGGGAG 48953 AGTGGCG  
 CTCC TTCTTTTAC  
 ||| |||||  
 GAGG GAGGGGGATG  
 GGTA\_  
 GAM1278 MGC5508 3' TAAGGGGACCTGAGGA 44040 CAGT CGT  
 TCCTC GG TCTTTTA  
 |||| | |||||  
 AGGAG CC AGGGGAAT  
 T \_ \_  
 GAM1278 MGC8407 3' AGTGGAGAGAATGAGTAGGAGG 43888 AG GG  
 G TCCTCC T CGTTCTTTTACT  
 |||| | |||||  
 GGGAGG G GTAAGAGAGGTGA  
 AT A\_  
 GAM1278 MGC9753 5' GGTGGTCTTGCTGCTGCAGGG 53057 C TG TTCTTT  
 TCCT CAG GCG TTACT  
 ||| ||| ||| |||  
 GGGA GTC CGT GGTGG  
 C GT TCT\_  
 GAM1278 MLLT10 5' GGTGGAGGGGAGGTGGGGGA 16169 AGTG G  
 TCCTCC GC TTCTTTTACT  
 |||| | |||||  
 AGGGGG TG AGGGGAGGTGG  
 G \_ G  
 GAM1278 MLLT10 5' GGTGGGGAGGGAAGACGCTGAG 16170 C GCG\_  
 GA TCCTC AGTG TTCTTTTACT  
 |||| ||| |||||

		AGGAG TCGC GGGAGGGGTGG	
		— AGAA	
GAM1278 MRPL16	5'	GGAGTCGCTGGGGGA 35244	G
		TCCTCCAGTGGC TTC	
		AGGGGGTCGCTG AGG	
		—	
GAM1278 MRPS7	3'	GTGAAACTGGCTGGAGGA 31997	GGC CTTT
		TCCTCCAGT GTT TTAC	
		AGGAGGTCG CAA AGTG	
		GT_ ____	
GAM1278 MRVI1	3'	AGTGACTTGATGTTCTTGAGG 20272	TG CTTT
A		TCCTCCAG GCGTT TTACT	
		AGGAGGTT TGTAG AGTGA	
		CT TTC_	
GAM1278 MRVI1	3'	AGTGACTTGATGTTCTTGAGG 55219	TG CTTT
A		TCCTCCAG GCGTT TTACT	
		AGGAGGTT TGTAG AGTGA	
		CT TTC_	
GAM1278 MYLE	3'	GAGGAAGCTGTTGGGGGG 25814	TG G
		TCCTCCAG GC TTCTTT	
		GGGGGGTT CG AAGGAG	
		GT _	
GAM1278 MYT1	3'	GGTGGAGTCCTGTTGCTGTGAG 15780	_ TG TTCT
GG		TCCTC CAG GCG TTTTACT	
		GGGAG GTC TGT GAGGTGG	
		T GT CCT_	
GAM1278 NAF1	5'	GCCCTAGGAGTGCTACGGGGGG 20224	A TTTACT
		TCCTCC GTGGCGTTCTT	
		GGGGGG CATCGTGAGGA	
		— TCCCGA	
GAM1278 NASP	3'	AGTGGAGGGGACAGTGGAGG 67967	G GGC
		CCTCCA T GTTCTTTTACT	
		GGAGGT A CAGGGGAGGTGA	
		G ____	
GAM1278 NCOR1	3'	AGTGAGGGGAACAGGGTGCAGG 20878	C GTGGC
A		TCCT CA GTTCTTTTACT	
		AGGA GT CAAGGGGAGTGA	
		C GGGA_	
GAM1278 NFAT5	5'	GGTAGGAGGGGAGTGTAGGGG 56948	CAG _
A		TCCTC TGGCG TTCTTTTACT	

			AGGGG ATTGT GGGGAGGATGG		
			___ GA		
GAM1278	NFKBIE	3'	GGTGAAAGGGCCTGAGGGGTG 92023	_	AGT GT
	A		TC CTCC GGC TCTTTTACT		
			AG GGGG CCG GGAAAGGTGG		
			T AGT ___		
GAM1278	NMP200	3'	GGTGGGGGGAATCTATGGGGGG 27175	A	C
	A		TCCTCC GTGG GTTCTTTTACT		
			AGGGGG TATC TAAGGGGGGTGG		
			G _		
GAM1278	NMT1	3'	GTGGGAGGAGTCGGAGAGG 40790	CAG	GT
			CCTC TGGC TCTTTTAC		
			GGAG GCTG AGGAGGGTG		
			AG_ _		
GAM1278	NPFF	5'	AGTCCTGGGGGCGCCATGGGAG 13553	A	TTT
	GA		TCCTCC GTGGCGTTCTT ACT		
			AGGAGG TACCGCGGGGG TGA		
			G TCC		
GAM1278	NSG-X	3'	GGTAGAAATGTACCATGGGGGA 26972	G	CG TC
			TCCTCCA TGG T TTTTACT		
			AGGGGGT ACC G AAAGATGG		
			_ AT T_		
GAM1278	NXPB2	5'	AGTGGTGCATGCCACGGAGGG 72718	A	TCTTT
			TCCTCC GTGGCGT TACT		
			GGGAGG CACCGTA GGTGA		
			_ CGT_		
GAM1278	OS-9	3'	GGTAGAGAGAGCAAGGAGGG 22343	AGTGGC	
			TCCTCC GTTCTTTTACT		
			GGGAGG CGAGAGAGATGG		
			AA_		
GAM1278	OS4	5'	AGCCCGGAGCTGCCGCTGGGGG 19175	_	TTTTACT
	A		TCCTCCAGTGGC GTTCT		
			AGGGGGTCGCCG CGAGG		
			T CCCGA		
GAM1278	OSBPL5	3'	GTGGGAGGGCCTGTGGGGG 72692	GT G	TTT
			CCTCCA GGC TTCT TAC		
			GGGGGT CCG GAGG GTG		
			GT G _		
GAM1278	P2RXL1	3'	GGTAGAAAGAGGAGTGATGGGG 18384	G G G_	
	GA		TCCTCCA T GC TTCTTTTACT		

			AGGGGGT A TG GAGAAAGATGG	
			_ G AG	
GAM1278	P450RAI-2	3'	GGTAGAAACCTGTGTGTGGGAG 39105	AGTG_ TTC
		GG	TCCTCC GCG TTTTACT	
			GGGAGG TGT AAAGATGG	
			GTGTG CC_	
GAM1278	P66	3'	GCTGCCAGAGTGCAGTGGGGG 40367	G TTTTACT
			TCCTCCAGTG CGTTCT	
			GGGGGGTCAC GTGAGA	
			_ CCGTCGA	
GAM1278	P8	3'	AGTGAGAGGCTGGGAATGGAGG 24742	GTGGCGTT
		G	TCCTCCA CTTTTTACT	
			GGGAGGT GGAGAGTGA	
			AAGGGTC_	
GAM1278	PASK	5'	GGGAGCTGTTGGAGGG 30722	TG G
			TCCTCCAG GC TTCT	
			GGGAGGTT CG AGGG	
			GT _	
GAM1278	PCL1	5'	TGGGAGGACTGCGGGG 32826	AGTG T
			CTCC GCG TCTTTTTA	
			GGGG CGT AGGAGGGT	
			_ _ C	
GAM1278	PCQAP	3'	AGTGGAGCGGGTTGCTTGGGGG 31895	_ TG _ TTTTACT
		G	CCTCCA G GC GTTCT	
			GGGGGT C TG CGAGG	
			T GT GG TGA T	
GAM1278	PDZD2	5'	AGTGGGAAGGTCCGACTGCGGG 80861	C _ CGT
		A	TCCT CAGT GG TCTTTTACT	
			AGGG GTCA CC GGAAGGGTGA	
			C G T_	
GAM1278	PDZD2	5'	GTGAAAAGCGCAGGGGGG 80877	AGTG TT
			CCTCC GCG CTTTTTAC	
			GGGGG CGC GAAAAGTG	
			GA_ _	
GAM1278	PHRET1	3'	GTGGGGGAGAACAGGAG 41063	AGTGGC
			CTCC GTTCTTTTAC	
			GAGG CAAGAGGGGTG	
			A_	
GAM1278	PI4KII	3'	AGTAAAAAGGGTGCCATCTG 37340	_ TT
			CAG TGGCG CTTTTTACT	



		GTC ACCGT GAAAAATGA	
		T GG	
GAM1278	PI4KII	3' GGTGGGAGGAAGCCTGGGGAG 37346	AGT G
		CTCC GGC TTCTTTTACT	
		GAGG CCG AAGGAGGGTGG	
		GGT _	
GAM1278	PIP5K2A	5' GGTGGAGGGGACATAGGAGG 17262	A GGC
		CCTCC GT GTTCTTTTACT	
		GGAGG TA CAGGGGAGGTGG	
		A _	
GAM1278	PMF1	3' AGTGATGGAATTTGCTGGAGGA 23324	TG C TT
		TCCTCCAG G GTTCT TTACT	
		AGGAGGTC T TAAGG AGTGA	
		GT_ T_	
GAM1278	PNMA5	3' GGTGGGGGGGGGCCACACTGAGG 73599	TC GC
	GA	TCC CAGTG GTTCTTTTACT	
		AGG GTCAC CGGGGGGGGTGG	
		GA AC	
GAM1278	POR1	3' GGTGGGAAGAGTGCCTGGAGG 24805	GT
		CCTCCA GCGTTCTTTTACT	
		GGAGGT CCGTGAGAAGGGTGG	
		_	
GAM1278	PP1628	5' GGTGGAGACCCCTGTGGGGGA 47305	GT C CTT
		TCCTCCA GG GTT TTTACT	
		AGGGGGT CC CAG AGGTGG	
		GT C _	
GAM1278	PP591	5' GGTCTGGGTGGCTACTGGAGGG 47373	GT TTTT
		TCCTCCAGTGGC TCT ACT	
		GGGAGGTCATCG GGG TGG	
		GT TC_	
GAM1278	PRAC	5' AGAGCGCCACTGGGAGG 50499	_
		CCTCC AGTGGCGTTCT	
		GGAGG TCACCGCGAGA	
		G	
GAM1278	PRIC285	3' TCCTTCAGGGGCTGCTGGAGGG 61438	TG G TTTTACT
		TCCTCCAG GC TTCT	
		GGGAGGTC CG GGGA	
		GT _ CTTCTG	
GAM1278	PRKWNK2	3' GGAGCTCGCGGAGGA 90538	A C
		TCCTCC GTGG GTTCT	

AGGAGG CGCT CGAGG

GAM1278	PRO0132	5'	AGTGAAAAAGGTCCTTGGAGGA	26100	T G CT
			TCCTCCAG GGC TT TTTTACT		
			AGGAGGTT CTG AA AAAGTGA		
			C G _		
GAM1278	PRTD-NY3	5'	GGTAGAAGGCCTGTTGTGGAGG	48149	A TG TT
	G		TCCTCC G GCG CTTTTTACT		
			GGGAGG T TGT GGAAGATGG		
			_GT CC		
GAM1278	PSKH1	3'	GGTAGGAGTTGCCGCCCTGGGG	68242	T _TC
	GA		TCCTCCAG GGCG T TTTTACT		
			AGGGGGTC CCGC G GAGGATGG		
			_ C TT		
GAM1278	RAB11B	3'	GGTGGGGAGGGCGGCAGGATGG	73906	_ AG G
	A		TCC TCC TG CGTTCTTTTACT		
			AGG AGG AC GCGGGAGGGGTGG		
			T _ G		
GAM1278	RAB35	3'	GGTGGGAAGGAATGGCTGGGGC	22482	_ GGCG
	GG		TC CTCCAGT TTCTTTTACT		
			GG GGGGTCG AGGAAGGGTGG		
			C GTA_		
GAM1278	RAB35	3'	TGGGAAGGAGGGTGCTGTGGAG	22483	G TT ACT
	GG		TCCTCCA TGGCG CTTTTT		
			GGGAGGT GTCGT GAGGAA		
			_ GG GGGTC		
GAM1278	RAD52B	5'	GTGAAGGGAGGATGGCGGA	88227	T GTGGCG
			TCC CCA TTCTTTTACT		
			AGG GGT GAGGGAAGTG		
			C AG_		
GAM1278	RAI17	3'	GGTAGGGAGGGTGACCAAGTG	91283	G _ TT
			CA TG GCG CTTTTTACT		
			GT AC CGT GAGGGATGG		
			G CA GG		
GAM1278	RBM12	3'	AGAACTCATTGAGGG	20158	C C
			TCCTC AGTGG GTTCT		
			GGGAG TTA CT CAAGA		
			_ _		
GAM1278	RELB	3'	GGTGGGGAGGGAGGTGGAGGA	21488	GTGGCG
			TCCTCCA TTCTTTTACT		

			AGGAGGT GGGAGGGGTGG		
			GGA__		
GAM1278	REM	3'	GCTCCAGGGACGCCACTGCGGG 25808	_	TTTACT
	G		CCTC CAGTGGCGTTCTT		
			GGGG GTCACCGCAGGGA		
			C CCTCGG		
GAM1278	REPRIMO	3'	GGTGGAGAGGGCGGGCAGGGGA 39054	_	AG G_
	GAGA		C CTCC TG CGTTCTTTTACT		
			G GAGG AC GCGGGAGAGGTGG		
			A GG GG		
GAM1278	RICH1	3'	AGTGAAAAGCTTTTCAGTGGAGG 36007	G	CGTT
	A		TCCTCCA TGG CTTTTTACT		
			AGGAGGT ACT GAAAAGTGA		
			G TTC_		
GAM1278	RILP	5'	AGTGGAGGGTGGGGTGGGGGG 48691	GTGG TT TT	
			TCCTCCA CG CTT TACT		
			GGGGGGT GT GAG GTGA		
			GGG_ GG _		
GAM1278	RODH-4	3'	GTGGAAATGGCCTGGAGGA 13539	TGGC TC	
			TCCTCCAG GT TTTTAC		
			AGGAGGTC CG AAAGGTG		
			_ GT		
GAM1278	RPIA	3'	GGTGGGGGGAAGAGTGGGAGGG 57969	AGTG G_	
			TCCTCC GC TTCTTTTACT		
			GGGAGG TG AAGGGGGGTGG		
			G_ AG		
GAM1278	RTN4IP1	5'	AGTGGAGGGGGTGAAGTGAGG 51191	CAGTGG TT	
	G		TCCTC CG CTTTTTACT		
			GGGAG GT GGGAGGTGA		
			TGAAA_ GG		
GAM1278	SBB103	3'	GGTAGGGGTTAATCTGTTGGGG 19361	TG CGTTC	
	G		CCTCCAG G TTTTACT		
			GGGGGTT C GGGGATGG		
			GT TAATT		
GAM1278	SDC3	5'	GGTAAAGAGAGGGGGTTGGGAG 27760	AGTGGCG	
			CTCC TTCTTTTACT		
			GAGG GAGAGAAATGG		
			GTTGGGG		
GAM1278	SDF1	3'	GGTGGGGAGACTGGGCTGAGGG 90859	TC GG T	
	A		TCC CAGT CG TCTTTTACT		

			AGG GTCG GT AGAGGGGTGG		
			GA G_ C		
GAM1278	SDNSF	5'	GGTGAGGCCCGAGGCGTTGGAG 57752	GTG T ____	
	GG		CTCCA GCGT CTT TTTACT		
			GAGGT TGCG GAG GAGTGG		
			____ _ CCCG		
GAM1278	SEC14L1	3'	GTGGGGGTGCTGGGGGGA 11507	AGT TT TTT	
			TCCTCC GGCG CT TAC		
			AGGGGG TCGT GG GTG		
			G__ GG ____		
GAM1278	SEC63L	5'	GGTGAGAAGAGCGAGGCGGAGG 23304	A GG	
	A		TCCTCC GT CGTTCTTTTACT		
			AGGAGG CG GCGAGAAGAGTGG		
			_ GA		
GAM1278	SEMA5A	3'	GGTGAGGGCATCCCTGCTGGGG 14260	T TG C__ TTTACT	
	A		C CCAG G GTTCTT		
			G GGTC C CGGGAG		
			_ GT CCTA TGG T		
GAM1278	SHANK3	3'	GGTGAATCCCTGCTGCTTGGGG 65503	C TG TTCTT	
	A		TCCTC AG GCG TTTACT		
			AGGGG TC CGT AAGTGG		
			T GT CCCT_		
GAM1278	ShrmL	5'	ATCTTCAGAGCGCCACTGAAGG 40465	C TTTTACT	
	A		TCCT CAGTGCGTTCT		
			AGGA GTCACCGCGAGA		
			A CTTCTA		
GAM1278	SLC19A3	3'	AGTGAGAGGTTAATTTGAGGG 47481	C GGCGTT	
			TCCTC AGT CTTTTTACT		
			GGGAG TTA GGAGAGTGA		
			T ATT__		
GAM1278	SLC26A10	5'	GGGGCTGTTGCCTGGAGGG 56032	_ TG _	
			TCCTCCA G GC GTTCT		
			GGGAGGT C TG CGGGG		
			C GT T		
GAM1278	SLC37A1	3'	GGTGGGGGGGGGTGCACAGG 38568	A G TT	
			CC GTG CG CTTTTTACT		
			GG CAC GT GGGGGGTGG		
			A _ GG		
GAM1278	SMARCF1	5'	GGTGGGGAGGGCAGCCCGGGGG 20043	AGT _	
	A		TCCTCC GGC GTTCTTTTACT		

			AGGGGG CCG CGGGAGGGGTGG		
			C__ A		
GAM1278	SMARCF1	5'	GGTGGGGAGGGCAGCCCGGGGG 37440	AGT	_
	A		TCCTCC GGC GTTCTTTTACT		
			AGGGGG CCG CGGGAGGGGTGG		
			C__ A		
GAM1278	SMARCF1	5'	GGTGGGGAGGGCAGCCCGGGGG 57489	AGT	_
	A		TCCTCC GGC GTTCTTTTACT		
			AGGGGG CCG CGGGAGGGGTGG		
			C__ A		
GAM1278	SPIB	3'	GGTAAGGGGAGTGCTGC 11911 TG		
			G GCGTTCTTTTACT		
			C CGTGAGGGGAATGG		
			GT		
GAM1278	SR-A1	3'	GGGATGACTGGGGGA 70047 GG		
			TCCTCCAGT CGTTCT		
			AGGGGGTCA GTAGGG		
			—		
GAM1278	STIM2	3'	GGTGAGAAGGGAGCTCTGGAG 40478 T G		
			CTCCAG GGC TTCTTTTACT		
			GAGGTC TCG GGGAAGAGTGG		
			_ A		
GAM1278	SWAP2	3'	GGTGGGGAGGACAAGGGGG 22933 AGTGGC		
			CCTCC GTTCTTTTACT		
			GGGGG CAGGAGGGGTGG		
			AA__		
GAM1278	SYNCOILIN	3'	AGTGAAAAACATACTGGGGA 47894 T GC CT		
			TCC CCAGTG GTT TTTTACT		
			AGG GGTCAT CAA AAAGTGA		
			_ A_ _		
GAM1278	SYT12	3'	GGTAGGAGCTGTGCTTGAGGG 94735 GT TC		
			TCCTCCA GCGT TTTTACT		
			GGGAGGT TCGTG GAGGATGG		
			_ TC		
GAM1278	SYT12	3'	GGTGGAAGGGCGGCTTGAGGG 94737 C G GTT		
			TCCTC AGT GC CTTTTTACT		
			GGGAG TCG CG GGAAGGTGG		
			T G _		
GAM1278	TAO1	3'	GGAGCCTGACCCTGGAGGG 16547 T _ _		
			TCCTCCAG GG C GTTCT		

GGGAGGTC CC G CGAGG  
\_ A TC  
GAM1278 TBX21 3' GGTGGGAGGGGTACAGGTGTGGG 25327 TC G\_ GT  
A TCC CA TGGC TCTTTTACT  
||| || ||| |||||  
AGG GT ACTG GGGAGGGTGG  
GT GG \_  
GAM1278 TBX4 3' GGTGGGAAGATTCTCGCTGCTG 37495 TG T\_\_  
GGG TCCAG GCG TCTTTTACT  
||||| ||| |||||  
GGGTC CGC AGAAGGGTGG  
GT TCTT  
GAM1278 TCL6 3' AGTGGGAAGGGGTGATGGATGA 40093 C G G G  
TC TCCA T GC TTCTTTTACT  
|| ||| | || |||||  
AG AGGT A TG GGGAAGGGTGA  
T \_ G \_  
GAM1278 TCL6 3' AGTGGGAAGGGGTGATGGATGA 40122 C G G G  
TC TCCA T GC TTCTTTTACT  
|| ||| | || |||||  
AG AGGT A TG GGGAAGGGTGA  
T \_ G \_  
GAM1278 THTPA 5' AGTGGGAAGGGATTCTTACTGGAG 44259 C  
CTCCAGTGG GTTCTTTTACT  
||||||| |||||  
GAGGTCATT TAGGGAAGGTGA  
T  
GAM1278 TLK1 5' GGAAGTTTGGAGGG 24455 TG G  
TCCTCCAG GC TTCT  
||||||| || |||  
GGGAGGTT TG AAGG  
\_ \_  
GAM1278 TMG3 3' GGTGGGGAGGGGTGGGGGTAGGG 43994 \_ AGTGG TT  
TCCT CC CG CTTTTTACT  
||| || || |||||  
GGGA GG GT GAGGGGTGG  
T GG\_\_ GG  
GAM1278 TMLHE 3' AGTAAGGGAGACTTGTTGGAG 36510 TG C TC  
CTCCAG G GT TTTTACT  
||||| | || |||||  
GAGGTT T CA GGGAATGA  
GT \_ GA  
GAM1278 TOLLIP 3' AGTGGGGGCCAGCCTCGCTGGA 38678 \_ GTTC  
GGG CCTCCAGT GGC TTTTACT  
||||||| ||| |||||  
GGAGGTCG CCG GGGGGTGA  
CT ACC\_  
GAM1278 TRAF2 3' AGTGAAGGGAGAGGCCCTGGGT 40927 \_ T G\_  
GGG CC TCCAG GGC TTCTTTTACT  
|| ||||| ||| |||||

GG GGGTC CCG GAGGGAAGTGA  
T \_ GA  
GAM1278 TREX1 5' AGTGGGAGGGGTGGAGCAGGA 53277 A GG TT  
TCC GT CG CTTTTTACT  
||| || || |||||  
AGG CG GT GGAGGGTGA  
A AG GG  
GAM1278 TREX1 5' AGTGGGAGGGGTGGAGCAGGA 53287 A GG TT  
TCC GT CG CTTTTTACT  
||| || || |||||  
AGG CG GT GGAGGGTGA  
A AG GG  
GAM1278 TREX1 5' AGTGGGAGGGGTGGAGCAGGA 33057 A GG TT  
TCC GT CG CTTTTTACT  
||| || || |||||  
AGG CG GT GGAGGGTGA  
A AG GG  
GAM1278 TUSP 5' GAAAAGGGGAGTGCTAACTGGG 39634 \_ ACT  
GGA TCCTCCAGT GCGTTCTTTTT  
||||| |||||  
AGGGGGTCA TCGTGAGGGGAA  
A AAGA  
GAM1278 UGT2B10 3' GAGAACTTGGAGGA 6542 TGGC  
TCCTCCAG GTTCTT  
||||| |||||  
AGGAGGTT CAAGAG  
  
GAM1278 UPB1 3' GTGGGAAGAGGGTGAGGG 32890 CAGTG G  
TCCTC GC TTCTTTTAC  
|||| || |||||  
GGGAG TG GAGAAGGGTG  
\_ G  
GAM1278 VPS33B 5' GGAGTGCTGCTGAGGA 37904 C TG  
TCCTC AG GCGTTCT  
|||| || |||||  
AGGAG TC CGTGAGG  
\_ GT  
GAM1278 VPS4A 3' GGGAGGTTGATTGGGG 25104 \_ G  
CTCCAGT GGC TTCT  
||||| ||| |||||  
GGGGTTA TTG AGGG  
G G  
GAM1278 VPS4B 3' AGTAAAAAGGATGTCA 16820  
TGGCGTTCTTTTTACT  
|||||||  
ACTGTAGGAAAAATGA  
  
GAM1278 VPS4B 5' GGTGGAGAGAGTGTTGT 16824 TG  
G GCGTTCTTTTTACT  
| |||||

T TGTGAGAGAGGTGG  
 GT  
 GAM1278 WFDC2 5' GTGAGGGGCAGTGGGGGG 54937 G GCGTT  
 TCCTCCA TG CTTTTTAC  
 ||||| || |||||  
 GGGGGGT AC GGGGAGTG  
 G \_\_\_\_  
 GAM1278 ZAP3 3' GGGGGTCTGCTGGAGGA 77223 \_ G  
 TCCTCCAGT GGC TTC  
 ||||| || ||  
 AGGAGGTCG CTG GGG  
 T G  
 GAM1278 ZF5128 3' GGTGAGAGGGATGCAGGCATGG 26808 \_ G\_  
 CCA GT GCGTTCTTTTACT  
 || || |||||  
 GGT CG CGTAGGGAGAGTGG  
 A GA  
 GAM1278 ZNF282 3' GGTGGACCCAGCTGCTGGGGA 89218 T TG GTTCTT  
 TCC CCAG GC TTTACT  
 || || || |||||  
 AGG GGTC CG AGGTGG  
 \_ GT ACCC\_  
 GAM1278 ZNF384 3' GGTAAGAAGGAGATTTGGGG 55986 TGGCG  
 CTCCAG TTCTTTTACT  
 |||| |  
 GGGGTT GAGGAAGATGG  
 TA\_\_\_\_  
 GAM1278 LOC115207 3' GGTAGGAAGGGTGGGAAGGGAG 56602 AGTGG TT  
 CTCC CG CTTTTTACT  
 || || |||||  
 GAGG GT GAAGGATGG  
 GAAGG GG  
 GAM1278 LOC115207 3' GTTTGGATCTATTGGGGGA 56605 C TTTT  
 TCCTCCAGTGG GTTC AC  
 ||||| || ||  
 AGGGGGTTATC TAGG TG  
 \_ TT\_\_\_\_  
 GAM1278 LOC115219 5' GGTGGAGGGGAGATGGGGG 73316 GTGGCG  
 CCTCCA TTCTTTTACT  
 |||| |  
 GGGGGT AGGGGAGGTGG  
 AG\_\_\_\_  
 GAM1278 LOC115399 3' GTGGAAGGAGTGCCTGG 73437 GT  
 CCA GCGTTCTTTTAC  
 || |||||  
 GGT CCGTGAGGAAGGTG  
 \_\_\_\_  
 GAM1278 LOC116150 5' AGTGGAAGGGGTTCTGGGCTCG 56629 \_ \_ G  
 GGGGG CC AGT GGC TTCTTTTACT  
 || || || |||||



		GG TCG TTG GGGAAAGGTGA		
		C GGC _		
GAM1278	LOC116173 3'	AGAGGAGGGGAAC TTATTGGGG 56640	C	ACT
	GA	TCCTCCAGTGG GTTCTTTTT		
		AGGGGGTTATT CAAGGGGAG		
		_ GAGAC		
GAM1278	LOC118668 5'	GGGATGCTGCTGGCGGG 75483	T	TG
		TCC CCAG GCGTTCT		
		GGG GGTC CGTAGGG		
		C GT		
GAM1278	LOC118812 5'	GGGGCAATCGCTGGTGGA 73933	T	C_
		TCC CCAGTGG GTTCT		
		AGG GGTCGCT CGGGG		
		T AA		
GAM1278	LOC121219 5'	AGTGGAAGGAGCAGAACGTGAG 74041	CA	GGC
	GG	TCCTC GT GTTCTTTTACT		
		GGGAG CA CGAGGAAGGTGA		
		TG AGA		
GAM1278	LOC123591 5'	GAGAGCGTCGTGGAGGA 75611	G	
		TCCTCCA TGGCGTTCTT		
		AGGAGGT GCTGCGAGAG		
		-		
GAM1278	LOC123591 3'	GTGGGAGGGTCCTAGAGGG 75614	C T G	TTT
		TCCTC AG GGC TTCT TAC		
		GGGAG TC CTG GAGG GTG		
		A _ G _		
GAM1278	LOC124222 3'	GAAGGCCTGCAGGAGGG 74272	A _ G	
		TCCTCC GT GGC TTC		
		GGGAGG CG CCG AAG		
		A T G		
GAM1278	LOC124402 3'	AGGGGTGCCGTGGAGGA 59148	G	TT
		TCCTCCA TGGCG CTT		
		AGGAGGT GCCGT GGA		
		_ GG		
GAM1278	LOC124446 3'	AGTGAAGAGCTGGAATGTGGGG 74286	AGTG	_
	GA	CTCC GCGTTCT TTTTACT		
		GGGG TGTAAGG GAAGTGA		
		_ TCGA		
GAM1278	LOC125268 3'	TGGAGACCTGGGGGG 76082	TGGCGTTC	
		TCCTCCAG TTTTAA		

GGGGGGTC AGAGGT  
C\_\_\_\_\_

GAM1278 LOC125875 5' AGTAAGGGGAACGAGGTCTGGA 74416 TGG\_  
GGG TCCTCCAG CGTTCTTTTACT  
||||| |||||  
GGGAGGTC GCAAGGGGAATGA  
TGG

GAM1278 LOC125943 5' TAGTGGGAAGGGCCGGGTTCG 74422 \_  
TTGGGG AGTGG C GTTCTTTTACT A  
||||| |||||  
TTGCT G CGGGAAGGGTGA T  
TGGG

GAM1278 LOC126208 3' GTGGGGGGTGCTGCGAGGA 74464 CA TG TT TT  
TCCTC G GCG CTT TAC  
||||| ||| |||  
AGGAG C CGT GGG GTG  
\_\_GT GG \_\_

GAM1278 LOC126299 3' GGTGGGAGGAGGGGGCTGAGGA 74485 C GGCG  
TCCTC AGT TTCTTTTACT  
||||| |||||  
AGGAG TCG GAGGAGGGTGG  
\_ GGG\_

GAM1278 LOC126917 3' TGGGGAGTCTGGAGGG 74596 TGGCGTT  
TCCTCCAG CTTTTTA  
||||| |||||  
GGGAGGTC GAGGGGT  
T\_\_\_\_\_

GAM1278 LOC126964 3' TGAGAAGTGTGGAGGG 74624 GTGGCGTT  
TCCTCCA CTTTTTA  
||||| |||||  
GGGAGGT GAAGAGT  
GT\_\_\_\_\_

GAM1278 LOC127255 3' GGTAAAGAGGATGTCGC 59164  
GTGGCGTTCTTTTACT  
|||||  
CGCTGTAGGAGAAATGG

GAM1278 LOC127294 5' GGAAGGTCACGGAGGA 74656 A G  
TCCTCC GTGGC TTCT  
||||| |||||  
AGGAGG CACTG AAGG  
\_ G

GAM1278 LOC127534 3' GGTGAGGAGGGTGGCTGTGGGG 75440 G \_TT  
G CCTCCA TGGC G CTTTTTACT  
||||| ||| | |||||  
GGGGGT GTCG T GAGGAGTGG  
\_ GGG

GAM1278 LOC128665 5' AAGAGGGACGCCGCTGAGGG 74791 C  
TCCTC AGTGGCGTTCTTTT  
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GGGAG TCGCCGCAGGGAGAA

GAM1278 LOC128954 5' GGTGGAGGGAATGCCAGCCGG 75802 A \_  
CC G TGGCGTTCTTTTACT  
||| |||||  
GG C ACCGTAAGGGAGGTGG  
C G

GAM1278 LOC129198 5' GTGGAAAGAGGATGGGCGA 76121 C GTGGCG  
TC TCCA TTCTTTTAC  
|| ||| |||||  
AG GGGT GAGAAAGGTG  
C AG\_\_

GAM1278 LOC130951 3' AGTGTGTGTGCTGGGGGG 57141 \_ TT  
TCCTCCAGTG GCG CT  
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GGGGGGTCGT TGT GA  
G GT

GAM1278 LOC131478 5' AGTGGGAAGGGGCACCGGGGGG 75863 A G G  
TCCTCC GTG C TTCTTTTACT  
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GGGGGG CAC G GGGAAGGGTGA  
C \_\_

GAM1278 LOC132228 3' GTGTGTGTTGGTGGGGGA 75045 G TTCTTTT  
TCCTCCA TGGCG TAC  
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AGGGGGT GTTGT GTG  
G GT\_\_

GAM1278 LOC132617 5' AGTGATAAGTGCTGCTGCAGGA 75890 C TG TT T  
TCCT CAG GCG CTT TTACT  
||||| ||| ||| |||||  
AGGA GTC CGT GAA AGTGA  
C GT \_ T

GAM1278 LOC132927 5' AGTGTCCGGTTCTGCTGGGGGG 75919 TG C TT TTTT  
TCCTCCAG G G C TACT  
||||| ||| ||| |||||  
GGGGGGTC C T G GTGA  
GT T GG CT\_\_

GAM1278 LOC138639 5' GTGGAGAGGCTGGGAGGG 75364 AGT GTT  
TCCTCC GGC CTTTTTAC  
||||| ||| |||||  
GGGAGG TCG GAGAGGTG  
G\_\_ \_\_

GAM1278 LOC138729 3' TGGGAGGGTGGGAGGG 76238 AGTGCGCT  
TCCTCC TCTTTTAA  
||||| |||||  
GGGAGG GGGAGGGT  
GT\_\_

GAM1278 LOC139904 5' GGTGGATGCGCTGCTGGAG 75852 TG TCTT  
CTCCAG GCGT TTTACT  
||||| ||| |||||

GAGGTC CGCG AGGTGG  
 GT T\_\_\_  
 GAM1278 LOC142893 5' GGTGGGAAGGATGGGTTGGGTG 82877 C TGG  
 A TC TCCAG CGTTCTTTTACT  
 || |||| ||||||||  
 AG GGGTT GTAGGAAGGGTGG  
 T GG\_  
 GAM1278 LOC143287 5' GGTGGAGGGAAGTGGGGAGGA 82932 AGTGGC  
 TCCTCC GTTCTTTTACT  
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 AGGAGG CAAGGGAGGTGG  
 GGT\_\_\_  
 GAM1278 LOC144473 3' AGGATGTTGTTGGGGA 83067 T TG  
 TCC CCAG GCGTTCT  
 ||| ||| |||||  
 AGG GGTT TGTAGGA  
 \_ GT  
 GAM1278 LOC144486 5' AGTGATGCGCGTCGTTGGAG 83080 TCTTT  
 CTCCAGTGGCGT TACT  
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 GAGGTTGCTGCG AGTGA  
 CGT\_\_\_  
 GAM1278 LOC144486 3' GGTAATGGAATGTTGCTGGATG 83087 \_ TG TT  
 G CC TCCAG GCGTTCT TACT  
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 GG AGGTC TGTAAGG AATGG  
 T GT T\_  
 GAM1278 LOC144509 5' GAAGGTGTATTGGGGA 76860 T \_ G  
 TCC CCAGTG GC TTC  
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 AGG GGTTAT TG AAG  
 \_ G G  
 GAM1278 LOC144587 3' GGTGGAAAGGATGTGATGGA 67029 G G  
 TCCA T GCGTTCTTTTACT  
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 GAM1278 LOC144603 5' ATGTGGAGGACGTACGGAGGA 60366 A TTACT  
 TCCTCC GTGGCGTTCTTT  
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 \_ TGTAG  
 GAM1278 LOC144893 5' GGTAGAGGGGATGGCTGGTGA 83189 CT GG  
 TC CCAGT CGTTCTTTTACT  
 || |||| |||||||||  
 AG GGTCG GTAGGGGAGATGG  
 T\_ \_  
 GAM1278 LOC145483 3' AGTGGGGAGGCTCAGGTGGAGG 77239 G\_ C T  
 G TCCTCCA TGG GT CTTTACT  
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GG \_ \_  
GAM1278 LOC145601 3' GGTGGGGAGGGGGCTGGTTGGG 83368 AG\_\_ G  
AG CTCC TGGC TTCTTTTACT  
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GAGG GTCG GGGAGGGGTGG  
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GAM1278 LOC145624 5' GTAGGATTCCTTGAGGA 83409 T CGTTCT  
TCCTCCAG GG TTTTAC  
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\_ TTT\_\_  
GAM1278 LOC145786 5' AGTGGTTATGTTGCTGGGGA 83489 T TG TCTTT  
TCC CCAG GCGT TTTACT  
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AGG GGTC TGTA GGTGA  
\_ GT TT\_\_  
GAM1278 LOC145980 5' GGA CTGTCGCTGGCGGG 83606 T \_  
TCC CCAGTGGC GTTC  
||| ||||| |||  
GGG GGTCGCTG CAGG  
C T  
GAM1278 LOC146071 5' GGTAAGGGGCACTGCCACTGTG 77662 \_ \_ T  
GGG CCTC CAGTGGC GT CTTTTTACT  
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GGGG GTCACCG CA GGGGAATGG  
T T C  
GAM1278 LOC146138 3' AGTGAGAGGGGCACCTGAAGGA 83614 C GT C  
TCCT CA GG GTTCTTTTACT  
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AGGA GT CC CGGGGAGAGTGA  
A \_ A  
GAM1278 LOC146174 5' GGTGGGGGGAGCGGGGCGGGGA 77703 A\_ GG  
G CTCC GT CGTTCTTTTACT  
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GAGG CG GCGAGGGGGGTGG  
GG GG  
GAM1278 LOC146224 5' AGTGGAAGCTTCCTGGGGGA 77706 T CGTT  
TCCTCCAG GG CTTTTTACT  
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AGGGGGTC CT GAAGGGTGA  
\_ TC\_\_  
GAM1278 LOC146517 3' GGTATGAAATGCTGCTGGTGGG 77946 T TG CTTTT  
TCC CCAG GCGTT TACT  
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GGG GGTC CGTAA ATGG  
T GT AGT\_\_  
GAM1278 LOC146909 3' GGTGGGAGGTGGGCTGGAGGA 78181 GGCGTT  
TCCTCCAGT CTTTTTACT  
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AGGAGGTCG GGAGGGTGG  
 GGT\_\_\_\_  
 GAM1278 LOC147071 5' AAGAACGGCTGTGGGGGA 72988 G \_  
 TCCTCCA TGGC GTTCTT  
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 AGGGGGT GTCG CAAGAA  
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 GAM1278 LOC147160 5' GGTGGGGAGAGAGAAAAGTGGGG 83969 GTGGCG  
 GG TCCTCCA TTCTTTTACT  
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 GAM1278 LOC147160 5' TAGTGGGGGGCAAAGGCGCCA 83971 \_\_\_\_\_  
 TTGGGCGG AGTGGCGTT CTTTTTACT A  
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 TTACCGCGG GGGGGGTGA T  
 AAAAC  
 GAM1278 LOC147515 3' AGGAGCCTTGGAGGG 84019 T G  
 TCCTCCAG GGC TTCT  
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 GGGAGGTT CCG AGGA  
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 GAM1278 LOC147965 5' GTGAAGGGGTAGTGGAGGG 78600 G GCGT  
 TCCTCCA TG TCTTTTAC  
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 GGGAGGT AT GGGGAAGTG  
 G \_\_\_\_  
 GAM1278 LOC148147 3' AGAGTCCCCTGGAGGA 78671 CG  
 TCCTCCAGTGG TTCT  
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 AGGAGGTCACC GAGA  
 CT  
 GAM1278 LOC148354 3' GGTGGAGGGAAGTGTGTGGGG 78802 GTG \_  
 CTCCA GC GTTCTTTTACT  
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 GGGT TG CAAGGGAGGTGG  
 G\_ T  
 GAM1278 LOC148426 5' GGTAGGGCACAGGTCTTGGGGG 84151 T GTTCT  
 A TCCTCCAG GGC TTTTACT  
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 AGGGGGT CTG GGGATGG  
 \_ GACAC  
 GAM1278 LOC148529 5' GGTGGGGAGAGGGATGGGGG 84170 GTGGCG  
 TCCTCCA TTCTTTTACT  
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 GGGGGT GAGAGGGGTGG  
 AGG\_\_\_\_  
 GAM1278 LOC148697 5' GGTAAGAAGAGTGTGACCAGGA 78929 A\_ G  
 G CTCC GT GCGTTCTTTTACT  
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	GAGG CA TGTGAGAAGAATGG AC G	
GAM1278 LOC148709 3'	GGTGAGGACATGCTTGTGGGAG 78948 GG TCCTCC GGCCT TTTTACT                  GGGAGG TCGTA AGGAGTGG GTGT C_	AGT_ TC
GAM1278 LOC148753 3'	AGGGTGCCGCTGGGGGA 84210 TCCTCCAGTGGCG CT            AGGGGGTCGCCGT GA GG	TT
GAM1278 LOC148758 5'	GGTGGGGAGTGTGCGGGAGGG 78975 TCCTCC GCG CTTTTTACT                GGGAGG CGT GAGGGGTGG G_ GT	AGTG TT
GAM1278 LOC148930 3'	GGTGGAGGGGGTGGGAATGGGG 79099 GA TCCTCCA CG CTTTTTACT                AGGGGGT GT GGGAGGTGG AAGG GG	GTGG TT
GAM1278 LOC148981 5'	GGTGGAACTTTGGTGGAGGA 84316 TCCTCCA TGG GTT TTTACT                   AGGAGGT GTT CAA AGGTGG G T _	G C CTT
GAM1278 LOC149111 3'	GGTGGGAGTTATGCTGGGGG 79186 CCTCCA GCGT TTTTACT                GGGGGT CGTA GAGGGTGG _ TT	GTG TC
GAM1278 LOC149420 3'	AGTGAAATTCCTTCATTGGGGG 79367 CCTCCAGTGG TTTTACT               GGGGGTTACT AAAGTGA TTCTT_	CGTTCT
GAM1278 LOC149498 3'	TGGGAAGGTGGGAGGG 79408 TCCTCC TCTTTTAA             GGGAGG GGAAGGGT GT_	AGTGCGCT
GAM1278 LOC149501 3'	AGGAAGCTACTGGAGGG 75272 TCCTCCAGTGGC TTCTT               GGGAGGTCATCG AAGGA _	G
GAM1278 LOC149657 3'	GTCCACGGGCCTACTGGGGGG 84577 TCCTCCAGTGG GTTC 	C TTTTACT

GGGGGGTCATC CGGG  
\_ CACCCTGA  
GAM1278 LOC149668 5' GGTGAGGGGGACTCTAGTGCTG 84549 \_\_\_\_ C  
GAGG TCCAGT GG GTTCTTTTACT  
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AGGTCG TC CAGGGGGAGTGG  
TGA T  
GAM1278 LOC149706 5' AGGGGCCACTGGGGGG 84636 G  
TCCTCCAGTGGC TTCT  
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GGGGGGTCACCG GGGA  
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GAM1278 LOC149706 5' GGTGGAAGGAGCAGGGCTCTGG 84645 T \_\_\_\_  
AGGG TCCAG GGC GTTCTTTTACT  
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AGGTC TCG CGAGGAAGGTGG  
\_ GGA  
GAM1278 LOC149722 3' GGGGCCTCACTGGGGA 84604 T C  
TCC CCAGTGG GTTCT  
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AGG GGTCACT CGGGG  
\_ C  
GAM1278 LOC149840 5' AGTTTTCTGGAGTGCTTTGGAG 79524 T TTTT\_  
GA TCCTCCAG GGC GTTCT ACT  
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AGGAGGTT TCGTGAGG TGA  
\_ TCTTT  
GAM1278 LOC149995 3' AGGAGCCTTGAGGG 84841 T G  
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GAM1278 LOC150271 5' AGTGGGAGGGGAAATGGGTGA 84948 C GTGGCG  
TC TCCA TTCTTTTACT  
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AG GGGT GGGGAGGGTGA  
T AAA\_  
GAM1278 LOC150279 5' AGTGGGAAGGAGATGTGGGGTGG 79665 T AGTG \_  
CC CC GCGT TCTTTTACT  
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GG GG TGTA AGGAAGGTGA  
T GG\_ G  
GAM1278 LOC150370 3' GGATTGTCTCTGGAGGG 84942 T T  
TCCTCCAG GGCG TCT  
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GGGAGGTC CTGT AGG  
T T  
GAM1278 LOC150605 5' TCCTGAGTGGGGAATGTTGCTGG 85085 TG TTTACT  
AGGG TCCTCCAG GCGTTCTT  
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	GT TGAGTCCTT	
GAM1278 LOC150759 3'	GGTAGAGGGAGGAATGATGGAG 80008	GTGGCG
GG	TCCTCCA TTCTTTTACT	
	GGGAGGT GAGGGAGATGG	
	AGTAAG	
GAM1278 LOC150935 3'	GGTGAGAAGAAGCGTGAAGGG 80036	C GTG G
	TCCT CA GC TTCTTTTACT	
	GGGA GT CG AAGAAGAGTGG	
	A G _ _	
GAM1278 LOC150951 5'	AGTGAGAGGGTCCCTGCGGGA 85166	C T CGT
	TCCT CAG GG TCTTTTACT	
	AGGG GTC CC GGGGAGGTGA	
	C _ T _	
GAM1278 LOC151031 5'	GGTGGAAGTCTTCGCCGAGGA 87189	AGT TTC_
	TCCTCC GGCG TTTTACT	
	AGGAGG CCGC GAAGGTGG	
	_ TTCT	
GAM1278 LOC151040 3'	GGTGGGGGGAGCGGGGAGGG 80103	AGTGG
	TCCTCC CGTTCTTTTACT	
	GGGAGG GCGAGGGGGGTGG	
	G _ _	
GAM1278 LOC151188 5'	GGTAGAGAGGTGCCCTTAATGG 80161	GT_ C _
GGGA	CTCCA GG GT TCTTTTACT	
	GGGGT CC CG GGAGAGATGG	
	AATT _ T	
GAM1278 LOC151273 3'	AGTGGGAGGGGTTGGGATGGG 67015	_ AGTGGC TT
	TCC TCC G CTTTTTACT	
	GGG AGG T GGAGGGTGA	
	T GT _ _ GG	
GAM1278 LOC151323 3'	GGTAGAGGGAGGAATGATGGAG 80220	GTGGCG
GG	TCCTCCA TTCTTTTACT	
	GGGAGGT GAGGGAGATGG	
	AGTAAG	
GAM1278 LOC151360 3'	GGTGGGGAGGGTCCGAGGGGA 85314	T AG C TT
	TCC CC TGG G CTTTTTACT	
	AGG GG GCC T GAGGGGTGG	
	_ A _ _ GG	
GAM1278 LOC151361 3'	GGTGGGGAGGGTCCGAGGGGA 85328	T AG C TT
	TCC CC TGG G CTTTTTACT	

		AGG GG GCC T GAGGGGTGG	
		_ A_ _ GG	
GAM1278	LOC151429 3'	GGTGGGGGCCCCGCACTCGGGGA 85360	C G TT T
		TCCTC AGTG CG CTTTT ACT	
		AGGGG TCAC GC GGGGG TGG	
		C _ CC _	
GAM1278	LOC151438 5'	GGTGGAAGGGGTGTGCCAGGAG 85368	AG _ TT
	GG	CCTCC TGGC G CTTTTTACT	
		GGAGG ACCG T GGAAGGTGG	
		_ TG GG	
GAM1278	LOC151475 3'	GAGTATGTGTGCTGGGGGG 85404	_ T
		TCCTCCAGTG GCGT CTT	
		GGGGGGTCGT TGTA GAG	
		G T	
GAM1278	LOC151701 3'	GGAAAGCGACTGGAGG 85487	G G
		CCTCCAGT GC TTCT	
		GGAGGTCA CG AAGG	
		G A	
GAM1278	LOC151742 5'	GTAGGAGGGATGCTGGTG 57670	G
		CA TGGCGTTCTTTTAC	
		GT GTCGTAGGGAGGATG	
		G	
GAM1278	LOC151878 3'	GAGAATGTGGGAGGA 80375	AGTG
		TCCTCC GCGTTCTT	
		AGGAGG TGTAAGAG	
		G_	
GAM1278	LOC152008 3'	AGTGAAGAGGATGTGTAGTGG 80433	G _
		CCA TG GCGTTCTTTTACT	
		GGT AT TGTAGGAAAAGTGA	
		G G	
GAM1278	LOC152110 3'	GGATTGGGTGCTGCTAGAGGG 80456	C TG TT TT
		TCCTC AG GCG C TTT	
		GGGAG TC CGT G AGG	
		A GT GG TT	
GAM1278	LOC152185 5'	GTGGGGGAGAACGGTGGTGG 58526	G G
		CCA TG CGTTCTTTTAC	
		GGT GT GCAAGAGGGGTG	
		G G	
GAM1278	LOC152502 3'	AGTGAAGAGGCTTATGCTGAGG 59313	C GCGT
	A	TCCTC AGTG TCTTTTACT	

		AGGAG TCGT GGAGAAGTGA	
		_ ATTC	
GAM1278	LOC152579 3'	AGTGGGAAGGTGGTTGATTGGA 80622	_ GT
		GGG TCCTCCAGT GGC TCTTTTACT	
		GGGAGGTTA TTG GGAAGGGTGA	
		G GT	
GAM1278	LOC153114 5'	GCTCATGGAATGTGTTGGAGGA 85921	GT G TTTTACT
		TCCTCCA G CGTTCT	
		AGGAGGT T GTAAGG	
		TG_ TACTCGA	
GAM1278	LOC153196 5'	AGTGAGGGGACTGGGCTGCGGG 85955	C GG T
	A	TCCT CAGT CG TCTTTTACT	
		AGGG GTCG GT AGGGGAGTGA	
		C G_ C	
GAM1278	LOC153196 3'	GGGGGGCACACTGGGGA 85969	T _ G
		TCC CCAGTG GC TTCT	
		AGG GGTCAC CG GGGG	
		_ A G	
GAM1278	LOC153196 5'	GGTGGAGCATCCTGCTGCTTGG 85971	_ TG TTCT_
	AGGA	CCTCCA G GCG TTTTACT	
		GGAGGT C CGT GAGGTGG	
		T GT CCTAC	
GAM1278	LOC153196 3'	GGTGGGGAGAGTGGGGAGAGGG 85973	AGTGG_
	GG	CCTCC CGTTCTTTTACT	
		GGGGG GTGAGAGGGGTGG	
		AGAGGG	
GAM1278	LOC153243 3'	AAGAAGCTGCTGGAGGG 80792	TG G
		TCCTCCAG GC TTCTT	
		GGGAGGTC CG AAGAA	
		GT _	
GAM1278	LOC155036 5'	GAGAGGTCGGTGGAGGA 86341	G G
		TCCTCCA TGGC TTCTT	
		AGGAGGT GCTG GAGAG	
		G _	
GAM1278	LOC155038 3'	GGAGGGTGGCAGGAGGG 81259	A G G
		TCCTCC GT GC TTCT	
		GGGAGG CG TG GAGG	
		A G G	
GAM1278	LOC155063 3'	GGTGAAGAGGTAGCTTGGGAG 86369	AGT GT
		CTCC GGC TCTTTTACT	

		GAGG TCG GGAGAAAGTGG	
		GT_ AT	
GAM1278	LOC155064 3'	GGTGGAAAGAAAGTGCTTGGGG 81250	TG G
	G	CCTCCAG GC TTCTTTTACT	
		GGGGGTT TG AAGAAAGGTGG	
		CG A	
GAM1278	LOC155066 5'	AGTGAGGAGAACGCGTGCTGAG 81278	C _
	GA	TCCTC AGTG GCGTTCTTTTACT	
		AGGAG TCGT CGCAAGAGGAGTGA	
		_ G	
GAM1278	LOC155072 5'	GTGGAAGGGGTGAGGGG 86386	AGTGG TT
		CTCC CG CTTTTTAC	
		GGGG GT GGAAGGTG	
		A__ GG	
GAM1278	LOC157349 5'	GGTAAAAACATGCTGGGGAGG 81421	AG TC
		CCTCC TGGCGT TTTTACT	
		GGAGG GTCGTA AAAAATGG	
		G_ C_	
GAM1278	LOC157693 5'	GGGGAGAGTCTGCTGGAGGA 81557	_ G
		TCCTCCAGT GGC TTCTTT	
		AGGAGGTCG CTG GAGGGG	
		T A	
GAM1278	LOC157848 3'	ACAGGAAGGGTCCCACTGGAGG 81615	C TT ACT
	G	TCCTCCAGTGG G CTTTTT	
		GGGAGGTCACC T GAAGGA	
		C GG CA	
GAM1278	LOC157848 3'	GGTAGGGGGTGGGCTGGGGGA 81623	GG TT TT
		TCCTCCAGT CG CT TTACT	
		AGGGGGTCG GT GG GATGG	
		G_ GG _	
GAM1278	LOC157860 3'	AGTGAAGGGGTGGAGGGGCTGG 86564	GGCGT__
	AGGA	CCTCCAGT TCTTTTACT	
		GGAGGTCG GGGGAAGTGA	
		GGGAGGT	
GAM1278	LOC158046 5'	GGGGCGCAGTTGGGGGA 59216	TG
		TCCTCCAG GCGTTCT	
		AGGGGGTT CGCGGGG	
		GA	
GAM1278	LOC158107 5'	AGTTGCCGGGTCTGCTGGGGG 86684	TG C TT TTTT
	A	TCCTCCAG G G CT ACT	

		AGGGGGTC C T GG TGA	
		GT _ GG CCGT	
GAM1278 LOC158187 3'	AGTAGAGAGAACTGAATTAGAG 86686	C GGC	
GA	TCCTC AGT GTTCTTTTACT		
	AGGAG TTA CAAGAGAGATGA		
	A AGT		
GAM1278 LOC158288 5'	GGTGGCTGTGCCATGGGAGGA 86720	A TTCTTT	
	TCCTCC GTGGCG TTACT		
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	G GTC__		
GAM1278 LOC158431 5'	AGTAGAGGGGGCGCAGCTGGGG 86830	G	
	CTCCAGT GCGTTCTTTTACT		
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	A		
GAM1278 LOC158434 3'	GTGAAGGGCAATTGGGAGA 86823	CT G GTTC	
	TC CCAGT GC TTTTAC		
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	AG A ____		
GAM1278 LOC158535 5'	GGTAAAAAGGAATTTGAGAGGA 87242	_ TGGCG	
	TCCTC CAG TTCTTTTACT		
	AGGAG GTT AGGAAAAATGG		
	A TA__		
GAM1278 LOC159036 3'	AGTAGGAAGAATGCAGGAGGA 86968	AGTG	
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	AGGAGG CGTAAGAAGGATGA		
	A__		
GAM1278 LOC159199 5'	GTGGAGGGAGCGCCAGG 82186	AG	
	CC TGGCGTTCTTTTAC		
	GG ACCGCGAGGGAGGTG		
	—		
GAM1278 LOC161734 3'	AGTAAAGATCCCTGTTATTGGA 87096	TTC_	
GG	CCTCCAGTGGCG TTTTACT		
	GGAGGTTATTGT AGAAATGA		
	CCCT		
GAM1278 LOC162333 5'	GGGACCCGCTGGAGGA 87136	C	
	TCCTCCAGTGG GTTCT		
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	—		
GAM1278 LOC162461 3'	AGTAGAATGGGCTACTGTGAGG 82357	_ GT T	
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GGGAG GTCATCG GG AAGATGA  
 T \_ T  
 GAM1278 LOC164397 5' GATGCCATTGTGGGGG 82526 \_  
 TCCTC CAGTGGCGTT  
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 T  
 GAM1278 LOC195977 5' TGAAAGGGCAGGAGGA 87541 AGTG GTT  
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 A \_ \_  
 GAM1278 LOC196047 5' GGTGAGAAGGAGCCTTCGGAGG 89607 AGT G  
 G TCCTCC GGC TTCTTTTACT  
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 GGGAGG CCG AGGAAGAGTGG  
 CTT \_  
 GAM1278 LOC196205 3' GGGGGCCACTGGAGGG 87591 G  
 TCCTCCAGTGGC TTC  
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 GAM1278 LOC196283 3' GAGAAGCTGCTGGAGGA 87619 TG G  
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 AGGAGGTC CG AAGAG  
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 GAM1278 LOC196500 3' GGTGGGAGGTGAGCTGGGGG 87743 GGC GTT  
 CCTCCAGT CTTTTTACT  
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 GAM1278 LOC196549 3' GGTGGGGACAGACTTGCTGGAG 59233 TG C C\_  
 GA TCCTCCAG G GTT TTTTTACT  
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 AGGAGGTC T CAG AGGGGTGG  
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 GAM1278 LOC197117 3' GGTAAAGGGGTGACTGGGGA 89721 T G GTT  
 TCC CCAGT GC CTTTTTACT  
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 GAM1278 LOC197363 3' GGTGGGAGGGTAATTGGAGGG 88057 GGC GT  
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 AT \_  
 GAM1278 LOC199678 3' GTGACTTGCTTTGGGGGA 89793 T TTCTTT  
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 ||||| |||| ||||

AGGGGGTT TCGT AGTG  
 \_ TC\_\_\_\_  
 GAM1278 LOC199787 3' GGTGAGGACCATGTCGCTGGAT 88397 \_ TC  
 GG CC TCCAGTGGCGT TTTTACT  
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 GG AGGTCGCTGTA AGGAGTGG  
 T CC  
 GAM1278 LOC200125 5' GTAGTACTGTTATTGGAG 89929 TTCTTT  
 CTCCAGTGGCG TTAC  
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 GAGGTTATTGT GATG  
 CAT\_\_\_\_  
 GAM1278 LOC200197 3' GGATGCCCCTGGAGGG 88619 T  
 TCCTCCAG GCGTTC  
 ||||| |||||  
 GGGAGGTC CCGTAGG  
 C  
 GAM1278 LOC200312 3' GTGGGAGGAAGGATGAGGG 89997 CAGTGGCG  
 TCCTC TTCTTTTAC  
 |||| |||||  
 GGGAG AAGGAGGGTG  
 TAGG\_\_\_\_  
 GAM1278 LOC200399 3' GGTAGAGGGAGGAATGATGGAG 88811 GTGGCG  
 GG TCCTCCA TTCTTTTACT  
 ||||| |||||  
 GGGAGGT GAGGGAGATGG  
 AGTAAG  
 GAM1278 LOC200982 3' GGTGAAGAGGAGATGCTGGGGA 90224 T GCG  
 TCC CCAGTG TTCTTTTACT  
 || ||||| |||||  
 AGG GGTCTG AGGAGAAGTGG  
 \_ AG\_  
 GAM1278 LOC201102 3' GGTGGAGGGGCAATTGGAAGG 88096 \_ G GTT  
 CCT CCAGT GC CTTTTTACT  
 || |||| || |||||  
 GGA GGTTA CG GGGAGGTGG  
 A A \_\_\_\_  
 GAM1278 LOC201139 3' GGTGCGTGCTCTGGAGGA 88132 TG\_ T  
 TCCTCCAG GCGT CT  
 ||||| ||| ||  
 AGGAGGTC TGCG GG  
 TCG T  
 GAM1278 LOC201173 5' AAGAACGGCTGTGGGGGA 87318 G \_  
 TCCTCCA TGGC GTTCTT  
 ||||| ||| |||||  
 AGGGGGT GTCG CAAGAA  
 \_ G  
 GAM1278 LOC201220 5' AAGAACGGCTGTGGGGGA 87338 G \_  
 TCCTCCA TGGC GTTCTT  
 ||||| ||| |||||

		AGGGGGT GTCG CAAGAA	
		— G	
GAM1278	LOC201705 3'	AGTGAGGAGGCCAGTGCTGCTG 90251	TG T__
	GAG	TCCAG GCG TCTTTTACT	
		AGGTC CGT GGAGGAGTGA	
		GT GACC	
GAM1278	LOC201910 3'	AGTGGGAGTCAGTTATGGGAGG 89098	A GTTC
	A	TCCTCC GTGGC TTTTACT	
		AGGAGG TATTG GAGGGTGA	
		G ACT_	
GAM1278	LOC202781 5'	GGGGACGTGCTGGGGGG 90368	G
		TCCTCCAGTG CGTTCTT	
		GGGGGGTTCGT GCAGGGG	
		—	
GAM1278	LOC202868 5'	GTGGAAGGGGTGAGGGG 90384	AGTGG TT
		CTCC CG CTTTTTAC	
		GGGG GT GGAAGGTG	
		A__ GG	
GAM1278	LOC203197 3'	GGTGAGGAGAGAAGCATCTGGG 89294	TG G_
	GG	CCTCCAG GC TTCTTTTACT	
		GGGGGTC CG GAGAGGAGTGG	
		TA AA	
GAM1278	LOC203668 5'	GGTGGGGAGCCGGAGCTGGAAG 89436	C GG TT
	A	TC TCCAGT CG CTTTTTACT	
		AG AGGTCG GC GAGGGGTGG	
		A AG C_	
GAM1278	LOC204689 5'	GGTGCCTGTGAGTGATGCTGGG 90662	GG TTTT_
	GGA	TCCTCCAGT CGTTC TACT	
		AGGGGGTTCG GTGAG GTGG	
		TA TGTCC	
GAM1278	LOC204820 5'	GTGGGGAGGGCGAGTGGA 90664	GTGG
		TCCA CGTTCTTTTAC	
		AGGT GCGGGAGGGGTG	
		GA__	
GAM1278	LOC219513 3'	GAGGACGACTACTGGGGGG 94328	—
		TCCTCCAGTGG CGTTCTT	
		GGGGGGTTCATC GCAGGAG	
		A	
GAM1278	LOC219842 5'	GGTAGAGAGAGCCAACAAGGTG 93269	T AG__ GT
	GA	TCC CC TGGC TCTTTTACT	



	AGG GG ACCG AGAGAGATGG		
	T AACA _		
GAM1278 LOC219920 5'	AGAGGGCCTGGGGGA 93298	GT G	
	TCCTCCA GGC TTCT		
	AGGGGGT CCG GAGA		
	_ G		
GAM1278 LOC220038 5'	AGTGGGGGGCAGGGTTAGAGGG 91718	CAG G _	
	TCCTC TGGC TT CTTTTTACT		
	GGGAG ATTG GA GGGGGGTGA		
	_ G C		
GAM1278 LOC220058 3'	AGTGACACTGCTTTACTGGAGG 91724	C TCTTT	
A	TCCTCCAGTGG GT TTACT		
	AGGAGGTCATT CG AGTGA		
	T TCAC_		
GAM1278 LOC220070 3'	GGTAAAAGCAGCCGTATTGGGG 59261	_ GTTC	
GA	TCCTCCAGT GGC TTTTACT		
	AGGGGGTTA CCG GAAAATGG		
	TG AC_		
GAM1278 LOC220549 5'	AGTCATTAGGAGTACCACTGGA 92914	CG TTT_	
GGA	TCCTCCAGTGG TTCTT ACT		
	AGGAGGTCACC GAGGA TGA		
	AT TTAC		
GAM1278 LOC220705 3'	AGAGTGTGCTGGAGGA 91225	G	
	TCCTCCAGTG CGTTCT		
	AGGAGGTCGT GTGAGA		
	-		
GAM1278 LOC221088 5'	AGTGGAAGGAGACCTCGGGGA 93264	CAGT CG	
	TCCTC GG TTCTTTTACT		
	AGGGG CC GAGGAAGGTGA		
	CT_ A_		
GAM1278 LOC221312 3'	GTGAAGAGATTTTGAAGGG 91908	C TGGCGT	
	TCCT CAG TCTTTTAC		
	GGGA GTT AGAGAAGTG		
	A TT_		
GAM1278 LOC221466 5'	GATGGGGGGATGCTGCTGGAGG 93688	TG TACT	
	CCTCCAG GCGTTCTTTT		
	GGAGGTC CGTAGGGGGG		
	GT TAGG		
GAM1278 LOC221466 5'	GGTGAAAAGGACTCCGGGGG 93691	AGT C	
	CCTCC GG GTTCTTTTACT		

	GGGGG CC CAGGAAAAGTGG	
	___ T	
GAM1278 LOC221466 5'	GGTGGAGGGGGGATGGGGGG 93692	GTGGCG
	TCCTCCA TTCTTTTACT	
	GGGGGGT GGGGAGGTGG	
	AG___	
GAM1278 LOC221773 3'	AGTAGAGGGGACGTGAGAGAAG 91036	CCAGTG
GG	TCCT GCGTTCTTTTACT	
	GGA TGCAGGGGAGATGA	
	AGAGAG	
GAM1278 LOC221833 3'	GGTGGAGAGGGAGAGGCTGGAG 92541	GGCG
G	CCTCCAGT TTCTTTTACT	
	GGAGGTCG GGGAGAGGTGG	
	GAGA	
GAM1278 LOC221876 5'	TGGGAGGGGCGGTGGA 93928	GTGG
	TCCA CGTTCTTTTTA	
	AGGT GCGGGGAGGGT	
	G___	
GAM1278 LOC221922 5'	GGTGGAGGCCCATGCCGAGG 92702	AGT TC___
G	TCCTCC GCGT TTTTACT	
	GGGAGG CCGTA GGAGGTGG	
	___ CCCC	
GAM1278 LOC221922 5'	GTGAGGAGAGCAGGAG 92703	AGTGGC
	CTCC GTTCTTTTAC	
	GAGG CGAGAGGAGTG	
	A___	
GAM1278 LOC221922 5'	GTGAGGGGGAGCAGGAGG 92704	AGTG G
	TCCTCC GC TTCTTTTAC	
	GGGAGG CG AGGGGGAGTG	
	A___ _	
GAM1278 LOC221922 5'	GGTGAAGGGGGGCTGGAGGG 92699	GTG G
	TCCTCCA GC TTCTTTTACT	
	GGGAGGT CG GGGGAAGTGG	
	___ G	
GAM1278 LOC221922 5'	GGTGAGGAGAGCAAGAGGGCAG 92700	_ AGTGGC
GG	TCCT CC GTTCTTTTACT	
	GGGA GG CGAGAGGAGTGG	
	C GAGAA_	
GAM1278 LOC221922 5'	GGTGAGGAGGGAGCAGGAGGG 92701	AGTG G
	TCCTCC GC TTCTTTTACT	

GGGAGG CG GGGAGGAGTGG  
A\_\_ A  
GAM1278 LOC222112 5' GTGGGAGGGGCGCCAGG 92806 AG  
CC TGGCGTTCTTTTAC  
|| |||||  
GG ACCGCGGGGAGGGTG  
—  
GAM1278 LOC222178 3' GGTGAGAAGGCGTGGCTGAGGG 94173 TC G T  
A TCC CAGT GCGT CTTTTACT  
||| ||| ||| |||||  
AGG GTCG TGCG GAAGAGTGG  
GA G \_  
GAM1278 LOC245728 5' GGTGGGCAGCTTGATGGCTGCT 91134 TG \_ \_ T  
GGAGGG CCAG GC GTT CT TTTACT  
|||| ||| |||||  
GGTC CG TAG GA GGGTGG  
GT G TTC C  
GAM1278 LOC253001 3' GAAGGGTGCTGCTGGGGTGG 96256 \_ TG TT  
TC CTCCAG GCG CTTT  
|| ||||| ||| |||  
GG GGGGTC CGT GAAG  
T GT GG  
GAM1278 LOC253150 3' GGTGAAGGGGCGCCCAGGG 95518 AGT  
CC GGCGTTCTTTTACT  
|| |||||  
GG CCGCGGGGGAAGTGG  
GAC  
GAM1278 LOC253299 5' AGTGAGAGGGACATGGTGGCAG 96452 \_ G GC  
GG TCCT CCA TG GTTCTTTTACT  
|||| ||| || |||||  
GGGA GGT GT CAGGGAGAGTGA  
C G A\_  
GAM1278 LOC253893 3' ACAGGAAGGGTCCCACTGGAGG 96109 C TT ACT  
G TCCTCCAGTGG G CTTTTT  
||||||| | |||||  
GGGAGGTCACC T GAAGGA  
C GG CA  
GAM1278 LOC253893 3' GGTAGGGGGTGGGCTGGGGGA 96117 GG TT TT  
TCCTCCAGT CG CT TTTACT  
||||||| || || |||||  
AGGGGGTCG GT GG GATGG  
G\_ GG \_  
GAM1278 LOC253962 5' GGTGTGCTGGGCGCCGGTGGAG 96658 G TTTT  
GG TCCTCCA TGGCGTTC TACT  
||||||| ||||| |||  
GGGAGGT GCCGCGGG GTGG  
G TCGT  
GAM1278 LOC254266 5' TGAGGGGGTAGGGGGA 97355 AGTGGCGT  
TCCTCC TCTTTTA  
||||| |||||

		AGGGGG	GGGGGAGT		
		AT_____			
GAM1278	LOC254559 5'	AGTAGGAGGGCCCGCCGAGGA	96594	A C T	
		TCCTCC GTGG GT CTTTTTACT			
		AGGAGG CGCC CG GGAGGATGA			
		C _ _			
GAM1278	LOC254835 3'	AGTGGAGAGGAAATTGGAGGG	96929	GGCG	
		TCCTCCAGT TTCTTTTACT			
		GGGAGGTTA AGGAGAGGTGA			
		A_____			
GAM1278	LOC254901 5'	TGGGAGGAGCGGGGAG	96264	AGTGG	
		CTCC CGTTCTTTTAA			
		GAGG GCGAGGAGGGT			
		G_____			
GAM1278	LOC254944 3'	GGTGGAGGGGGCATGTCTGGAG	97209	TGGC	
	GG	TCCTCCAG GTTCTTTTACT			
		GGGAGGTC CGGGGGAGGTGG			
		TGTA			
GAM1278	LOC255043 3'	GTGGGGGGATTTCGGGGGA	95331	AGTGG T_	
		TCCTCC CG TCTTTTAC			
		AGGGGG GC AGGGGGGTG			
		_____ TT			
GAM1278	LOC255328 3'	AGCAGAGGGGGCCCATTTGGAGG	96556	C A	
	G	TCCTCCAGTGG GTTCTTTT CT			
		GGGAGGTTACC CGGGGGAGA GA			
		- C			
GAM1278	LOC255461 5'	AGTGGCACACATGCCGTTGGGG	97316	T TCTTT	
	A	TCC CCAGTGGCGT TTACT			
		AGG GGTGCCGTA GGTGA			
		- CACAC			
GAM1278	LOC255465 3'	GTGAGGCTTTGCTGAGGA	97299	C TG C TCTT	
		TCCTC AG G GT TTTAC			
		AGGAG TC T CG GAGTG			
		_ GT T _____			
GAM1278	LOC255480 3'	GGTGAAGGGAGGTAGGTGGGGG	96520	GTG G	
		CCTCCA GC TTCTTTTACT			
		GGGGGT TG GAGGGAAGTGG			
		GGA _			
GAM1278	LOC255516 5'	AGTGGCACACATGCCGTTGGGG	97329	T TCTTT	
	A	TCC CCAGTGGCGT TTACT			

		AGG GGTGCCGTA	GGTGA		
		— CACAC			
GAM1278	LOC255650	3'	GGAGCTCTGGGGGG	96713	T G
			TCCTCCAG GGC TTC		
			GGGGGGTC TCG AGG		
			— —		
GAM1278	LOC256273	3'	GGGACACAGCTGGGGGA	96406	GGC
			TCCTCCAGT GTTCT		
			AGGGGGTCG CAGGG		
			ACA		
GAM1278	LOC256598	5'	GACCGCTACTTGAGGA	96351	— T
			TCCTCCA GTGGCG TC		
			AGGAGGT CATCGC AG		
			T C		
GAM1278	LOC256867	5'	GGAGCCTCCTGGGGGG	94865	TG C
			TCCTCCAG G GTTCT		
			GGGGGGTC C CGAGG		
			CT _		
GAM1278	LOC257127	3'	GGTGAAGGGAGCCACGTGGAG	96673	— C
			CTCCA GTGG GTTCTTTTACT		
			GAGGT CACC CGAGGGAAGTGG		
			G _		
GAM1278	LOC51136	3'	AGTGAAGATTAATTTACTGAGG	32323	C CGTTC
	A		TCCTC AGTGG TTTTACT		
			AGGAG TCATT AGAAGTGA		
			_ TAATT		
GAM1278	LOC51146	5'	GGTGAGGAAAGCACTGCAGGA	32402	C G G TT
			TCCT CAGTG C TTCT TACT		
			AGGA GTCAC G AAGG AGTGG		
			C _ A _		
GAM1278	LOC51161	3'	AGTGGGAGGGATTGGGGGAGGA	32507	AGTGGC
			TCCTCC GTTCTTTTACT		
			AGGAGG TAGGGAGGGTGA		
			GGGT_		
GAM1278	LOC51182	5'	GGTAGCTGTTGCTGTTGGGGGA	32827	TG TTCTTT
			TCCTCCAG GCG TACT		
			AGGGGGTT CGT GATGG		
			GT TGTC_		
GAM1278	LOC51279	3'	AGTGAGGACTGAACACTGGGG	33306	GC_ TTTACT
			CTCCAGTG GTTCTT		

		GGGGTCAC CAGGAG		
		AAGT TGA		
GAM1278	LOC51725	3' GGTGAAGGGAACAAAGCTGGAG	69867	GGC
		G CCTCCAGT GTTCTTTTACT		
		GGAGGTCG CAAGGGAAGTGG		
		AAA		
GAM1278	LOC55908	5' GGGATCCACTGGGGA	37954	T C
		TCC CCAGTGG GTTCT		
		AGG GGTACC TAGGG		
		— —		
GAM1278	LOC56959	5' AGTAAAAGTCCATTGTGAGGA	81925	— CGTTC
		TCCTC CAGTGG TTTTACT		
		AGGAG GTTACC GAAAATGA		
		T T—		
GAM1278	LOC57019	3' GAAGCTGGCTGGGGGG	39724	— G
		TCCTCCAGT GGC TTC		
		GGGGGGTCG TCG AAG		
		G —		
GAM1278	LOC57105	3' AGTAGGAGGAGGATCTGGGG	39817	TGGCG
		CTCCAG TTCTTTTACT		
		GGGGTC GAGGAGGATGA		
		TAG—		
GAM1278	LOC58525	5' AGGATGATACTGGAGGG	78642	G
		TCCTCCAGTG CGTTCT		
		GGGAGGTCAT GTAGGA		
		A		
GAM1278	LOC64182	5' GGTGGAGAGAGAATGGGGA	42298	T GTGGCG
		TCC CCA TTCTTTTACT		
		AGG GGT GAGAGAGGTGG		
		— AA—		
GAM1278	LOC85569	3' AGTGAGGAGAGGCAGTTTGGAG	52408	TG_ G
		CTCCAG GC TTCTTTTACT		
		GAGGTT CG GAGAGGAGTGA		
		TGA —		
GAM1278	LOC89919	3' AGTAAAGGGAATGTATCATGTG	60717	— GTG_
		A TC CA GCGTCTTTTACT		
		AG GT TGTAAGGGAATGA		
		T ACTA		
GAM1278	LOC90050	3' AGTGGAGGGCAGGATTGGGG	56379	GGC TT
		CTCCAGT GTTCTT TACT		

GGGGTTA CGGGAG GTGA  
GGA \_  
GAM1278 LOC90190 3' GTGGGAAGAGGATGAGGA 61781 CAGTGGCG  
TCCTC TTCTTTTAC  
||||| |||||  
AGGAG GAGAAGGGTG  
TAG\_\_\_\_  
GAM1278 LOC90309 5' GGTAATTATGGTACTGGGGGA 62183 G TCTTT  
TCCTCCAGTG CGT TTACT  
||||||| ||| |||||  
AGGGGGTCAT GTA AATGG  
G TT\_\_\_\_  
GAM1278 LOC90317 3' GGGGCCCATTTGGGAGG 62250 \_ C  
CCTCC AGTGG GTTCT  
||||| ||||| |||||  
GGAGG TTACC CGGGG  
G \_  
GAM1278 LOC90378 5' AGGGGCTGCTGGAGGA 62520 TG G  
TCCTCCAG GC TTCT  
||||||| || |||||  
AGGAGGTC CG GGGA  
GT \_  
GAM1278 LOC90408 5' GTCGGAGGGATGACTGCTGGAG 62665 TG\_ TT T  
GA TCCTCCAG G CGTTCTTT AC  
||||||| | ||||| ||  
AGGAGGTC C GTAGGGAG TG  
GT A GC  
GAM1278 LOC90719 3' GTGGAGGGGGGGGGTGGGGA 63887 T GTGGCG  
TCC CCA TTCTTTTAC  
||| ||| |||||  
AGG GGT GGGGGAGGTG  
\_ GGG\_\_\_\_  
GAM1278 LOC90784 5' AGTGGAGAGGACAGTGGGGAGG 63997 AGTG \_  
CCTCC GC GTTCTTTTACT  
||||| || |||||  
GGAGG TG CAGGAGAGGTGA  
GG\_ A  
GAM1278 LOC91064 5' GGTGGGGAGGGTGGCAGCGGG 64766 AG G TT  
TCC TG CG CTTTTTACT  
||| ||| |||||  
GGG AC GT GAGGGGTGG  
CG G GG  
GAM1278 LOC91149 3' AGTATGCTTGGTGTGTTGGAGG 65068 GTG TT TTT\_  
A TCCTCCA GCG CT TACT  
||||||| ||| || |||||  
AGGAGGT TGT GG ATGA  
\_ GT TTCGT  
GAM1278 LOC91266 5' AGTAAGGAGGATGCTACAGAAA 65408 CCA\_  
GGA TCCT GTGGCGTTCTTTTACT  
||||| |||||

AGGA CATCGTAGGAGGAATGA

AAGA

GAM1278 LOC91300 3' GTAATTGTGTTTTGGGGGA 57071 T TTCTTT  
TCCTCCAG GGCG TTAC  
||||||| ||| |||  
AGGGGGTT TTGT AATG  
\_ GTT\_

GAM1278 LOC91300 3' GTAATTGTGTTTTGGGGGA 94598 T TTCTTT  
TCCTCCAG GGCG TTAC  
||||||| ||| |||  
AGGGGGTT TTGT AATG  
\_ GTT\_

GAM1278 LOC91301 5' AGTAAAGGGAGGACCTGCGGGG 65538 A TG C \_  
G CCTCC G G GTTCTT TTTACT  
||||| | ||||| |||||  
GGGGG C C CAGGAG AAATGA  
\_ GT \_ GG

GAM1278 LOC91308 3' GTGGAAAGAATGCTTTG 65562 T  
CAG GGCGTTCTTTTAC  
||| |||||  
GTT TCGTAAGAAAGGTG

GAM1278 LOC91565 5' GGGAGGCTGGGCTGGGAGA 66464 CT \_ G  
TC CCAGT GGC TTCT  
|| ||||| ||| |||  
AG GGTCG TCG AGGG  
AG GG G

GAM1278 LOC91689 5' GGTGAGGGGCGGAGCTGGGGG 52823 GG TT  
CCTCCAGT CGTTCT TTTACT  
||||||| ||||| |||||  
GGGGGTCG GCGGGG AGTGG  
AG \_

GAM1278 LOC91812 5' AGGGAGGAGAAGGCAGGAGGA 67237 AGTG G TA  
TCCTCC GC TTCTTTT CT  
||||| || ||||| ||  
AGGAGG CG AAGAGGA GA  
A\_ G GG A

GAM1278 LOC91813 5' AGGGAGGAGAAGGCAGGAGGA 67244 AGTG G TA  
TCCTCC GC TTCTTTT CT  
||||| || ||||| ||  
AGGAGG CG AAGAGGA GA  
A\_ G GG A

GAM1278 LOC91907 3' GTGGAGAGGACGGGTGGA 67495 T AGTGG  
TCC CC CGTTCTTTTAC  
||| || |||||  
AGG GG GCAGGAGAGGTG  
T \_

GAM1278 LOC91974 5' AGTGAGAAGGTAGATGCCAACT 67750 \_ \_  
GGAGGG CCAGT GGC GTT CTTTTTACT  
||||| ||||| |||||



GGTCA CCGTAG GAAGAGTGA  
A ATG  
GAM1278 LOC92017 5' GTGGAGAGGAGGATGGGGA 67894 T GTGGCG  
TCC CCA TTCTTTTAC  
||| ||| |||||  
AGG GGT AGGAGAGGTG  
\_ AGG\_  
GAM1278 LOC92270 5' AGTGAAGAGAAAGAGTGGGAG 68628 AGTGGCG  
CTCC TTCTTTTACT  
|||| |||||  
GAGG AAGAGAAGTGA  
GTGAGA\_  
GAM1278 LOC92578 3' AGTGAGGAGAGAGCCTGGGGG 69822 GT G  
CCTCCA GGC TTCTTTTACT  
|||| ||| |||||  
GGGGGT CCG GAGAGGAGTGA  
\_ A  
GAM1278 LOC92912 5' GGTGAGGGGGACGGGGGCGGGG 70846 A GG\_  
CTCC GT CGTTCTTTTACT  
|||| ||| |||||  
GGGG CG GCAGGGGGAGTGG  
\_ GGG  
GAM1278 LOC92997 5' AGTGGAAGGAGCCTGGGAG 71085 AGT GT  
CTCC GGC TCTTTTACT  
|||| ||| |||||  
GAGG CCG AGGAAGGTGA  
GT\_ \_  
GAM1278 LOC93109 3' GGGCCCTGTGCTGGGGG 71416 \_ C  
TCCTCCAGT GG GTTC  
||||| || |||  
GGGGGGTCG CC CGGG  
TGT \_  
GAM1278 LOC93109 3' GGTGGGAGTGAACACTGGGGTG 71417 \_ GGC \_  
A TC CTCCAGT GTTC TTTTACT  
|| ||||| ||| |||||  
AG GGGGTCA CAAG GAGGGTGG  
T \_ T  
GAM1278 LOC93132 5' GGTAACAGTAGATGCCTTGGGG 71498 T CT \_  
GA TCCTCCAG GCGT TT TTACT  
||||| |||| || |||  
AGGGGGTT CCGTAG GA AATGG  
\_ AT C  
GAM1278 LOC96810 3' GTGAGGAGAGCAAGAGGA 70564 CAGTGGC  
TCCTC GTTCTTTTAC  
|||| |||||  
AGGAG CGAGAGGAGTG  
AA\_  
GAM1279 CLCN5 5' TGAAATACCTAAGCTGCTCAA 3595 \_  
TTGGAGCAG GTTCA  
||||| |||||

			AACCTCGTC	TAAAGT		
			GAATCCA			
GAM1279	FLRT2	5'	ATTGAAAAATGAGGTCTGC	25056	GT	CTC
			GCAG TTCATT CAAT			
			CGTC GAGTAA GTTA			
			TG AAA			
GAM1279	IL17	3'	TGGGGAAAATGAAACCCTCC	9333	CA	—
			GGAG GGTTCAT TCTCCA			
			CCTC CCAAAGTA AGGGGT			
			— AA			
GAM1279	NLGN1	5'	TGAAGATGCTGCTCCAA	30026	G	—
			TTGGAGCAG TTTCA			
			AACCTCGTC GAAGT			
			GTA			
GAM1279	POLG	3'	GTGATAAACCTGCTCCAA	10682		—
			TTGGAGCAGGTT TCAT			
			AACCTCGTCCAA AGTG			
			AT			
GAM1279	TPK1	3'	GGAGAACCTGTCCAA	42384	G	TTCAT
			TTGGA CAGGT TCTCC			
			AACCT GTCCA AGAGG			
			— ———			
GAM1279	C1orf8	5'	GAGAATGAAACCCTC	16832	CA	
			GAG GGTTTCATTCTC			
			CTC CCAAAGTAAGAG			
			—			
GAM1279	CLIC6	3'	TGGAGAACATGTTCCAA	82536	G	TTCAT
			TTGGAGCA GT TCTCCA			
			AACCTTGT CA AGAGGT			
			A ———			
GAM1279	CLIPR-59	3'	TGGAGAATTTCAATGCCCCGA	31374	A	GGTTTC
			TTGG GCA ATTCTCCA			
			AGCC CGT TAAGAGGT			
			C AACTT_			
GAM1279	DKFZP547L112	3'	TGGAGAACTCTTGCTCCA	66532		TTTCA
			TGGAGCAGG TTCTCCA			
			ACCTCGTTC AAGAGGT			
			TC_			
GAM1279	EPS8R3	5'	GGACCACCTGCTCCAA	57404		TTCATTC
			TTGGAGCAGGT TCC			

			AACCTCGTCCA	AGG	
			CC_____		
GAM1279	EPS8R3	5'	GGACCACCTGCTCCAA	55701	TTCATTC
			TTGGAGCAGGT	TCC	
			AACCTCGTCCA	AGG	
			CC_____		
GAM1279	FLJ20552	3'	AGAACAAAACCTGCTCCAA	35389	G CA
			TTGGAGCAG TTT TTCT		
			AACCTCGTC AAA AAGA		
			— AC		
GAM1279	FLJ22865	5'	TGGAGAAAACCTGCTCTAA	47071	GTTTCA
			TTGGAGCAG TTCTCCA		
			AATCTCGTC AAGAGGT		
			AA_____		
GAM1279	KIAA0372	5'	ATTGAAATTTGTTACCTACTCC	27663	C TT TTCTC
		AA	TTGGAG AGGT CA CAAT		
			AACCTC TCCA GT GTTA		
			A TT TTAAA		
GAM1279	PRO0132	5'	ATGAAACCACTCCAA	26101	CA
			TTGGAG GGTTTCAT		
			AACCTC CCAAAGTA		
			A_		
GAM1279	TEX27	3'	AGAGTGGAACCCGCTGCAA	41658	G A
			TTG AGC GGTTTCATTCT		
			AAC TCG CCAAGGTGAGA		
			G C		
GAM1279	LOC149373	3'	ATTGGGGTGATGATACCCACCC	79312	AGCA T _
		CAA	TTGG GGT TCATT CTCCAAT		
			AACC CCA AGTAG GGGGTTA		
			CCAC T T		
GAM1279	LOC152687	3'	TTGGAGAATATTGCTCC	80643	GTTTC
			GGAGCAG ATTCTCCAA		
			CCTCGTT TAAGAGGTT		
			A_____		
GAM1279	LOC51202	3'	ATTGGAGAATGAAACCTGCTCC	33017	
		AA	TTGGAGCAGGTTTCATTCTCCAAT		
			AACCTCGTCCAAAGTAAGAGGTTA		
GAM1280	CCR2	3'	GCCTGGACAAAGACAAA	5388	CCC
			TTTG TTGTCCAGGC		

AAAC AACAGGTCCG  
 AGA  
 GAM1280 DEC1 5' AACATGCCCAGAGCAGA 33797 CCTTG CA  
 TTTGC TC GGCATGTT  
 |||| || |||||  
 AGACG AG CCGTACAA  
 \_\_\_\_ AC  
 GAM1280 M17S2 3' CTTGGACAGGGGCAAA 49034  
 TTTGCCCTTGTCCAGG  
 |||||  
 AAACGGGGACAGGTTT  
  
 GAM1280 M17S2 3' CTTGGACAGGGGCAAA 19733  
 TTTGCCCTTGTCCAGG  
 |||||  
 AAACGGGGACAGGTTT  
  
 GAM1280 M17S2 3' CTTGGACAGGGGCAAA 49021  
 TTTGCCCTTGTCCAGG  
 |||||  
 AAACGGGGACAGGTTT  
  
 GAM1280 ARG99 3' AAACAGCAAACAAGGGCAAG 49168 CCAG A  
 TTTGCCCTTGT GC TGTT  
 ||||| || ||||  
 GAACGGGAACA CG ACAA  
 AA\_\_ \_  
 GAM1280 DKFZp434A171 5' GCACTGGACAAGGACAA 70799 C \_  
 TTG CCTTGTCCAG GC  
 || ||||| ||  
 AAC GGAACAGGTC CG  
 A A  
 GAM1280 FLJ20203 3' GCCAGGACAAGGACAAA 34734 C A  
 TTTG CCTTGTCC GGC  
 ||| ||||| ||  
 AAAC GGAACAGG CCG  
 A A  
 GAM1280 MGC29891 5' AAACATGCACACATGAAAAGGG 58193 G CAG\_\_  
 CAAA TTTGCCCTT TC GCATGTTT  
 ||||| || |||||  
 AAACGGGAA AG CGTACAAA  
 A TACACA  
 GAM1280 LOC149705 3' AAACATGCCTACTGTTTCAGG 84621 TC \_\_\_\_  
 CTTG CA GGCATGTTT  
 ||| || |||||  
 GGAC GT CCGTACAAA  
 TT CAT  
 GAM1280 LOC222484 5' AACAGCACTGGACAAG 94339 \_ A  
 CTTGTCCAG GC TGTT  
 ||||| || |||

GAACAGGTC CG ACAA

A \_

GAM1281 ABR 3' AGGATATATTTTTTTGTCTATG 6568 T T\_\_\_\_  
TTCT AATGTA ATAGAAG TGCCT

||||| ||||| |||||

TTGTAT TGTTTTT ATAGGA

C TTAT

GAM1281 ABR 3' AGGATATATTTTTTTGTCTATG 41720 T T\_\_\_\_  
TTCT AATGTA ATAGAAG TGCCT

||||| ||||| |||||

TTGTAT TGTTTTT ATAGGA

C TTAT

GAM1281 ADAM8 3' TGGGACAGCCCCAGCTTTGTGT 6617 G A\_\_\_\_  
GTGTTT TATATAGA GTTGCCT G

||||| ||||| |

GTGTGTTT CGACAGGG T

T CGACCC

GAM1281 ADAMTS3 3' GGGATAACTTATTTGTATGTT 26479 TAG

AATGTATA AAGTTGCCT

||||| |||||

TTGTATGT TTCAATAGGG

TTA

GAM1281 ADD1 3' CTTCTGTGTCGTTTT 26379 T  
GGAATG ATATAGAAG

||||| |||||

TTTTGC TGTGTCTTC

GAM1281 ADD1 3' CTTCTGTGTCGTTTT 26373 T  
GGAATG ATATAGAAG

||||| |||||

TTTTGC TGTGTCTTC

GAM1281 AGA 3' GGCTGTATTTTGTATATATTT 3443 GTT\_ CT  
GAATGTATATAGAA GTC

||||| ||||| |||

TTTATATATGTTTT CGG

ATGT

GAM1281 ALP 3' TCTGCAGTTGTCTGTATGTGTT 27128 TG AG\_ CCT  
TTA TGGAA TATATAGA TTGT

||||| ||||| |||

ATTTT GTATGTCT GACG

GT GTT TCTA

GAM1281 ANPEP 3' AGGGCAGCAGATCTGTATATTT 6711 T A\_\_\_\_  
TT GAA GTATATAGA GTTGCCT

||| ||||| |||||

TTT TATATGTCT CGACGGGA

T AGA

GAM1281 AOC3 3' AGGACAGCTGCTTCTGTGCATT 13582 T\_ A  
T GAATGTATA AG AGTTGCCT

||||| || |||||

			TTTACGTGT TC TCGACAGGA		
			CT G		
GAM1281	APAF1	3'	TTTCTGTGTAATTCCA 6742	G	
			TGGAAT TATATAGAAG		
			ACCTTA ATGTGTCTTT		
			—		
GAM1281	APAF1	3'	TTTCTGTGTAATTCCA 25051	G	
			TGGAAT TATATAGAAG		
			ACCTTA ATGTGTCTTT		
			—		
GAM1281	APOBEC1	3'	AGGATGATTCCGTGTGTGTACT 19700	A TG TA G TG	
			GG A TATA GAA T TCCT		
			TC T GTGT CTT A AGGA		
			A GT GC _ GT		
GAM1281	APOBEC1	3'	AGGATGATTCCGTGTGTGTACT 7914	A TG TA G TG	
			GG A TATA GAA T TCCT		
			TC T GTGT CTT A AGGA		
			A GT GC _ GT		
GAM1281	APPBP2	3'	AGGATAGGCTTTGTATACTTTT 21071	T AG	
	A		TGGAA GTATATAGA TTGTCCT		
			ATTTT CATATGTTT GATAGGA		
			— CG		
GAM1281	APPBP2	5'	GGGCGGCCGTGCCTTCT 21078	T ATAGAA	
			GGAA GTAT GTTGTCC		
			TCTT CGTG CGGCGGG		
			C C _		
GAM1281	ARF4L	5'	GGGCGGCTGCGGTGTTTCA 69814	TG ATATAGA	
			TGGAA T AGTTGTCC		
			ACTTT G TCGGCGGG		
			GT GCG _		
GAM1281	ARHGAP6	3'	GTATAATTTTTATGTATTTTTC 6769	T CCT	
	A		TGGAA GTATATAGAAGTTGT		
			ACTTT TATGTATTTTAAATA		
			T TG		
GAM1281	ARHGAP6	3'	GTATAATTTTTATGTATTTTTC 25520	T CCT	
	A		TGGAA GTATATAGAAGTTGT		
			ACTTT TATGTATTTTAAATA		
			T TG		
GAM1281	ARHGEF6	3'	AGGAGTTACTTTATGTACGTTG 68195	G A TG_	
	CA		TG AATGTATATAGA GT TCCT		

AC TTGCATGTATTT CA AGGA  
 G \_ TTG  
 GAM1281 ATM 5' AGGACAGTGATGTGTGTTCT 3509 TG AGAAG  
 GGAA TATAT TTGTCCT  
 ||| ||| |||||  
 TCTT GTGTA GACAGGA  
 GT GT\_\_  
 GAM1281 ATP8A2 3' TTTCTGCATATATTCTA 93522 A  
 TGAATGTAT TAGAAG  
 ||||| |||||  
 ATCTTATATA GTCTTT  
 C  
 GAM1281 ATP8A2 3' GGGGCAGCAGAACAAATGCAATT 93515 A ATAGAA  
 CA TGA TGTAT GTTGTCT  
 ||| ||| |||||  
 ACTT ACGTA CGACGGGG  
 A ACAAGA  
 GAM1281 B4GALT1 3' GGTAACCTTCTGTGTTATTTTA 7673 T T T  
 TGAATG ATATAGAAGTTG CC  
 ||||| ||||| ||||| ||  
 ATTTTAT TGTGTCTTCAAT GG  
 \_ \_ T  
 GAM1281 B4GALT6 3' ATTTTATATATATTTTA 59863  
 TGAATGTATATAGAAGT  
 ||||| ||||| |||||  
 ATTTTATATATATTTTA  
 GAM1281 B4GALT6 3' CTTTTCATTTTATATATATTT 59864 TGTCCT  
 TA TGAATGTATATAGAAGT  
 ||||| ||||| ||||| |||||  
 ATTTTATATATATTTTA  
 CTTTCT  
 GAM1281 BCAR1 3' GGAATCTGTATATATTT 63964 AGTTG  
 GAATGTATATAGA TCC  
 ||||| |||  
 TTTATATATGTCT AGG  
 A\_\_  
 GAM1281 BCL11A 3' GGGGCAATACTATTGCATTTTA 43167 T AA  
 TGAATGTA ATAG GTTGTCT  
 ||||| ||| |||||  
 ATTTTACGT TATC TAACGGGG  
 \_ A\_  
 GAM1281 BNC 3' AGGAACATTTGTACATATTCT 8160 A A TG  
 GGAATGT TATAGA GT TCCT  
 ||||| ||||| || |||  
 TCTTATA ATGTTT CA AGGA  
 C A \_  
 GAM1281 CACNA1G 3' AATCTCTATGTATATTCTA 38156 AG  
 TGAATGTATATAGA TT  
 ||||| ||||| || ||

		ATCTTATATGTATCT AA	
		CT	
GAM1281	CBFB	3' AGCTGCTTTTATGTGTATTTTA 8270	T CCT
		TGGAATGTATATAGAAGT GT	
		ATTTTATGTGTATTTTCG CG	
		T A	
GAM1281	CBFB	3' ATAGCTGCTTTTATGTGTATTT 43138	T CCT
	TA	TGGAATGTATATAGAAGT GT	
		ATTTTATGTGTATTTTCG CG	
		T ATAG	
GAM1281	CBFB	3' AGCTGCTTTTATGTGTATTTTA 43137	T CCT
		TGGAATGTATATAGAAGT GT	
		ATTTTATGTGTATTTTCG CG	
		T A	
GAM1281	CBFB	3' ATAGCTGCTTTTATGTGTATTT 8271	T CCT
	TA	TGGAATGTATATAGAAGT GT	
		ATTTTATGTGTATTTTCG CG	
		T ATAG	
GAM1281	CCNT1	5' GGGGTGTAGCGAGGTGCATTCC 6954	ATAGAA _
		GGAATGTAT GTTG TCCT	
		CCTTACGTG CGAT GGGG	
		GAG_ GT	
GAM1281	CD2AP	3' AGGGTGAATTTATATATATATT 24015	GAAG_ TG
	TT	GGAATGTATATA T TCCT	
		TTTTATATATAT A GGGA	
		ATTTA GT	
GAM1281	CD53	3' AGGGCCTTATTGATGTGTTCTA 5109	TG ATAG TT
		TGGAA TAT AAG GTCCT	
		ATCTT GTA TTC CGGGA	
		GT GTTA _	
GAM1281	CDH20	3' AGGGTGGCTTTTCTCTGCCATT 49094	_ TAT TG
	C	GAATG TA AGAAGT TCCT	
		CTTAC GT TTTTCG GGGA	
		C CTC GT	
GAM1281	CDH3	3' AGGACAATCGTGTATATGTACT 8379	A GAA
	A	TGG ATGTATATA GTTGTCCT	
		ATC TGTATATGT TAACAGGA	
		A GC_	
GAM1281	CDH8	3' AGCATTCTGTAATATTCTA 8390	A _
		TGGAATGT TATAGAA GTT	



			ATCTTATA ATGTCTT CGA	
			— A	
GAM1281	CDKN2A	5'	GGGGCGACTTCAGGTGTGC 3578	A_
			GTATAT GAAGTTGTCCT	
			CGTGTG CTTCAGCGGGG	
			GA	
GAM1281	CDKN2A	5'	GGGGCGACTTCAGGTGTGC 54237	A_
			GTATAT GAAGTTGTCCT	
			CGTGTG CTTCAGCGGGG	
			GA	
GAM1281	CDY1	3'	AGGTTACTTTAGTGTATGTTCT 16259	A TGT
	A		TGGAATGTATAT GAAGT CCT	
			ATCTTGTATGTG TTTCA GGA	
			A TT_	
GAM1281	CDY1	3'	AGGTTACTTTAGTGTATGTTCT 60264	A TGT
	A		TGGAATGTATAT GAAGT CCT	
			ATCTTGTATGTG TTTCA GGA	
			A TT_	
GAM1281	CHD2	3'	GGGTCTTTTATATATGTTCT 7032	TTGT
			GGAATGTATATAGAAG CCT	
			TCTTGTATATATTTT GGG	
			CT__	
GAM1281	CLASP2	3'	AGGGTGATTTTCTGTTACTTTT 64591	T T _TG
	TA		TGGAA GTA ATAGAAG T TCCT	
			ATTTT CAT TGTCTTT A GGGA	
			T _ TGT	
GAM1281	CLCA1	3'	GGGGCGATATACTAAATGTATT 7071	A AA_
	TTA		TGGAATGTAT TAG GTTGCCT	
			ATTTTATGTA ATC TAGCGGGG	
			A ATA	
GAM1281	COL9A2	3'	GGCGGCTTTCCTTCCA 8489	TGTATATA
			TGGAA GAAGTTGTC	
			ACCTT TTTCGGCGG	
			CC_____	
GAM1281	COLQ	3'	GGGGCGGCTCTTGTGGTTTCA 54490	GTA GA
			TGGAAT TATA AGTTGTCCT	
			ACTTTG GTGT TCGGCGGGG	
			___ TC	
GAM1281	COLQ	3'	GGGGCGGCTCTTGTGGTTTCA 54484	GTA GA
			TGGAAT TATA AGTTGTCCT	

			ACTTTG GTGT TCGGCGGGG		
			___ TC		
GAM1281	COLQ	3'	GGGGCGGCTCTTGTGGTTTCA 54478	GTA	GA
			TGGAAT TATA AGTTGTCCT		
			ACTTTG GTGT TCGGCGGGG		
			___ TC		
GAM1281	COLQ	3'	GGGGCGGCTCTTGTGGTTTCA 19049	GTA	GA
			TGGAAT TATA AGTTGTCCT		
			ACTTTG GTGT TCGGCGGGG		
			___ TC		
GAM1281	COLQ	3'	GGGGCGGCTCTTGTGGTTTCA 54472	GTA	GA
			TGGAAT TATA AGTTGTCCT		
			ACTTTG GTGT TCGGCGGGG		
			___ TC		
GAM1281	COLQ	3'	GGGGCGGCTCTTGTGGTTTCA 54498	GTA	GA
			TGGAAT TATA AGTTGTCCT		
			ACTTTG GTGT TCGGCGGGG		
			___ TC		
GAM1281	CORO1C	3'	GGGACAGCACTGTGTATGTTT 26733		AA
			GAATGTATATAG GTTGCCT		
			TTTGTATGTGTC CGACAGGG		
			A_		
GAM1281	CPSF6	3'	GGAATACTATGTATATTC 22801	AAGTTG	
			GAATGTATATAG TCC		
			CTTATATGTATC AGG		
			ATA_		
GAM1281	CXCL16	3'	TTGGACAAATTCTATGTGTATT 41929	G	T
	TT		GGAATGTATATAGAA TTGTCC		
			TTTTATGTGTATCTT AACAGG		
			A TTC		
GAM1281	CYB561	5'	GGGGCGGCTGTGCGCATTTT 8603	TA	AGA
			GGAATG TAT AGTTGTCCT		
			CTTTAC GTG TCGGCGGGG		
			GC _		
GAM1281	CYB561	5'	GGGTGCTGTGTGCATCTC 8604	GA	AAGT GT
			G ATGTATATAG T CC		
			C TACGTGTGTC G GG		
			TC _ TG		
GAM1281	CYBB	3'	AGGAGTAGCTATATATTTCTA 76353	T	AAGTTG
			TGGAA GTATATAG TCCT		

			ATCTT TATATATC	AGGA		
			— GATG—			
GAM1281	CYP4F3	3'	GTGATTTTTATGTGAATTCTA	6122	G	TG
			TGGAAT TATATAGAAGT	T		
				I		
			ATCTTA GTGTATTTTA	G		
			A GT			
GAM1281	DAAM2	3'	GGGGCGGGCGGTGTGTGTGTGT	92291	TG	GAA_ _
	TCT		GGAA TATATA GTT GTCCT			
			TCTT GTGTGT CGG CGGGG			
			GT GTGG G			
GAM1281	DDOST	3'	GGGATAATTTTATATA	17819		
			TATATAGAAGTTGTCCT			
			ATATATTTTAAATAGGG			
GAM1281	DFNA5	3'	GGGACCCTAGCTATATGCATTT	15305		AAGTT
	TA		TGGAATGTATATAG GTCCT			
			ATTTTACGTATATC CAGGG			
			GATCC			
GAM1281	DMC1	3'	GGGATATGTATATGTATGTTT	22978		GAAGT
			GAATGTATATA TGTCCT			
			TTTGTATGTAT ATAGGG			
			ATGT_			
GAM1281	ECM2	3'	GGGGTAGCTTTTCATTTCTTCCA	7332	TGTAT AG	GT
			TGGAA AT AAGTT CCT			
			ACCTT TA TTCGA GGG			
			CTT_ CT TG			
GAM1281	EDG6	3'	GCTTCTGTGTGATTCT	13667	G	
			GGAAT TATATAGAAGT			
			TCTTA GTGTGTCTTCG			
GAM1281	EFNA1	3'	AGGGCAGTGCCCATGTGTACAT	15389		GAA _
	TCT		GGAATGTATATA GT TGTCCT			
			TCTTACATGTGT CG ACGGGA			
			ACC TG			
GAM1281	EGFL5	5'	GGGCTGTATATATGTACC	86625	A	GAAGTT
			GG ATGTATATA GTCC			
			CC TGTATATAT CGGG			
			A GT_			
GAM1281	EGLN1	3'	GGATAATTTTCTATATTA	41896	T T	
			A GTATA AGAAGTTGTCC			

			A TATAT TTTTAAATAGG	
			T C	
GAM1281	EIF3S6	3'	GGGTGACTTACATTTT 7806	TATAGA TG
			GGAATGTA AGT TCC	
			TTTTACAT TCA GGG	
			_____ GT	
GAM1281	ELK1	5'	GGGGCGGCTTCTAGGTGCTGCC 17842	AAT A
			GG GTAT TAGAAGTTGTCCT	
			CC CGTG ATCTTCGGCGGGG	
			GT_ G	
GAM1281	EMD	3'	GGGGCAGGGGCTTTATGTGTTT 3683	TG T AAG
	T		GGAA TATA AG TTGTCCT	
			TTTT GTAT TC GACGGGG	
			GT T GGG	
GAM1281	EMX2	3'	AGGTTCTGTGTGCTTTTTA 87561	T G
			TGGAA GTATATAGAA TT	
			ATTTT CGTGTGTCTT GA	
			T G	
GAM1281	EN2	5'	GGGGCGGCTCGTGGTGTTC 7468	TG ATATA A
			GGAA T GA GTTGTCT	
			CTTT G CT CGGCGGGG	
			GT GTG__ _	
GAM1281	EPM2A	3'	GGGATGACTTTTCGATTATGC 19033	TA__ TG
			GTATA GAAGT TCCT	
			CGTAT TTTCA AGGG	
			TAGC GT	
GAM1281	FABP2	3'	GGAATATGGGTACATTCCA 3745	ATAGAA T
			TGGAATGTAT GT GTCC	
			ACCTTACATG TA CAGG	
			GG__ T	
GAM1281	FANCF	3'	AGGGCAATTTATTCATTTT 42669	TATATAG
			GGAATG AAGTTGTCCT	
			TTTTAC TTAAACGGGA	
			TTA__	
GAM1281	FGF5	3'	AGGATAGCTACTAAATATATAT 15531	__ A
	T		AATGTATA TAG AGTTGTCCT	
			TTATATAT ATC TCGATAGGA	
			AA A	
GAM1281	FGF5	3'	AGGATAGCTACTAAATATATAT 52477	__ A
	T		AATGTATA TAG AGTTGTCCT	

			TTATATAT ATC TCGATAGGA		
			AA A		
GAM1281	FGFR3	3'	GGGACGGCCAAGAATGTACGTC 3774	A	AGAA_
	CA		TGGA TGTATAT GTTGCCT		
			ACCT GCATGTA CGGCAGGG		
			_ AGAAC		
GAM1281	FOXO1A	3'	AGGATAACTTAATATGTTTTT 8901	TG	AG
			GAA TATAT AAGTTGCCT		
			TTT GTATA TTCAATAGGA		
			TT A_		
GAM1281	FUT9	3'	AGGGTAACGTGTATATTTT 67843	AGAA	GT
			GGAATGTATAT GTT CCT		
			TTTTATATGTG CAA GGA		
			_____ TG		
GAM1281	G6PC	3'	AGGGCGACTCTGGTGGTGCTTT 3820	T	A_ A
	T		GAA GTAT TAGA GTTGCCT		
			TTT CGTG GTCT CAGCGGGA		
			T GTG _		
GAM1281	GALNT1	3'	TATCAAATTTCTATATAGATTT 40020	G	GTCCT
	TA		TGGAAT TATATAGAAGTT		
			ATTTTA ATATATCTTTAA		
			G ACTATG		
GAM1281	GARS	5'	GGGGTGGCTTGACGCACTTCT 8987	_	ATATAG TG
			GGAA TGT AAGT TCCT		
			TCTT ACG TTCG GGGG		
			C CAG_ GT		
GAM1281	GASC1	3'	AGGGCGATAATTTATATATTTT 64242	T	A_
	CCA		TGGAA GTATATAGA GTTGCCT		
			ACCTT TATATATTT TAGCGGGA		
			T AA		
GAM1281	GLDC	3'	AGGGCAAATGTTTACATTTT 64238	T	GAAG
			GGAATGTA ATA TTGCCT		
			TTTTACAT TGT AACGGGA		
			T A_		
GAM1281	GLP1R	3'	GGGAGCTTGATATACTTC 9032	T	G G
			GAA GTATATA AAGTT TCC		
			CTT CATATAT TTCGA GGG		
			_ G _		
GAM1281	GNE	3'	GGAAGGCTAATATATTCCA 18482	ATAGA	TG
			TGGAATGTAT AGT TCC		

			ACCTTATATA	TCG AGG		
			A____	GA		
GAM1281	GRLF1	3'	GGGGCAGTTTCTGTCGCGGGTC	78559	A_	AT GT
	C		GGA TGT ATAGAA TGCCT			
			CCT GCG TGTCTT ACGGGG			
			GG C_	TG		
GAM1281	GTF2H1	3'	TTTCTGTGTACATTTT	18010		
			GGAATGTATATAGAAG			
			TTTTACATGTGTCTTT			
GAM1281	H3F3B	3'	GGCAGTTTTTATGGCGTTTT	18022	A	GT
			GGAATGT TATAGAA TGTC			
			TTTTGCG GTATTTT ACGG			
			_	TG		
GAM1281	HADHSC	3'	ATTTCTGTGTATTTTCTA	18030	T	
			TGGAA GTATATAGAAGT			
			ATCTT TATGTGTCTTTA			
			T			
GAM1281	HCS	3'	GGGACGATTAGATAGGTGTTTT	38478	TG A	AGA
	A		TGGAA T TAT AGTTGTCCT			
			ATTTT G ATA TTAGCAGGG			
			GT G GA_			
GAM1281	HHIP	3'	AGGTCTGCTTTTATTGTATATT	42487	_	TGT
	TTA		TGGAATGTATA TAGAAGT CCT			
			ATTTTATATGT ATTTTCG GGA			
			T TCT			
GAM1281	HIF1A	3'	TTTCTATGTACATTGTA	7735	G	
			TG AATGTATATAGAAG			
			AT TTACATGTATCTTT			
			G			
GAM1281	HMG3	3'	GGGACAACCTTTTAAAAGCTATT	14904	_	ATA
	TT		GGAAT GT TAGAAGTTGTCCT			
			TTTTA CG ATTTTCAACAGGG			
			T AAA			
GAM1281	HNRPK	3'	AGGAATGTTTGTGTACAATTCA	9247	A	AGTTG
			TGGA TGTATATAGA TCCT			
			ACTT ACATGTGTTT AGGA			
			A GTA_			
GAM1281	HNRPK	3'	AGGAATGTTTGTGTACAATTCA	48357	A	AGTTG
			TGGA TGTATATAGA TCCT			

			ACTT ACATGTGTTT	AGGA	
			A	GTA__	
GAM1281	HPGD	3'	CTTCAATATACATTCT	5980	A
			GGAATGTATAT	GAAG	
			TCTTACATATA	CTTC	
			A		
GAM1281	HRH1	3'	AGGACGAAGGCCTGTGTGTTGC	5982	AATG
	CA		TGG	TATATAG	TTGTCCT
			ACC	GTGTGTC	AGCAGGA
			GTT_	CGGA	
GAM1281	HSD17B8	3'	GGGGTGGCAGTGTATGGTTC	26451	G
			GAAT	TATATA	GT TCCT
			CTTG	GTATGT	CG GGGG
			_	GA_	GT
GAM1281	HSPA1L	3'	AGGATGCCTCTACATGTATTTTC	92019	A
	A		TGGAATGTAT	TAGA G	GTCCT
			ACTTTATGTA	ATCT C	TAGGA
			C	_CG	
GAM1281	HSPA1L	3'	AGGATGCCTCTACATGTATTTTC	97766	A
	A		TGGAATGTAT	TAGA G	GTCCT
			ACTTTATGTA	ATCT C	TAGGA
			C	_CG	
GAM1281	HTR2A	3'	GGATGATTTAACATTACCA	5259	_
			TGG	AATGT	AAGT TCC
			ACC	TTACA	TTTA AGG
			A	A_____	GT
GAM1281	HTR2C	3'	AACTTTTATAAATGTTTTC	6018	A
			TGGAATGT	TATAGAAGTT	
			ATTTTGTA	ATATTTTCAA	
			A		
GAM1281	IGFBP1	3'	AGGACGGTTAACTTGTATATTC	5178	TAGA
	CA		TGGAATGTATA	AG	GTCCT
			ACCTTATATGT	TT	CAGGA
			TCAA	GG	
GAM1281	IHPK1	3'	GGGACAGCTTGCCTGTTTCT	95759	TGTAT
			GGAA	ATAG	AAGTTGTCCT
			TCTT	TGTC	TTCGACAGGG
			_____	CG	
GAM1281	IRS1	5'	GGGGCGACGAGAGATGCATCTT	18665	_
	C		GGA	ATGTAT	GTTGTCCT

		CTT TACGTA CAGCGGGG	
		C GAGAG_	
GAM1281	ITPR2	3' AGGGCAATTTCTTTATTTAT 9447	T T
		ATG ATA AGAAGTTGTCCT	
		TAT TAT TCTTTAACGGGA	
		T T	
GAM1281	ITSN1	3' AGGACAACAAAGTTTACATTTT 11616	TATAGAA
	A	TGGAATGTA GTTGCCT	
		ACTTTACAT CAACAGGA	
		TTGAAA_	
GAM1281	JJAZ1	3' AGGATGTCTTTGTAATGTGTTT 31075	TG ATA T
	CA	TGGAA TAT GAAG TGCCT	
		ACTTT GTA TTTC GTAGGA	
		GT ATG T	
GAM1281	KAL1	3' AGGACAGTTATTTGCATTT 4010	T AAG
		GAATGTA ATAG TTGCCT	
		TTTACGT TATT GACAGGA	
		T _	
GAM1281	KCND2	3' GGGGTAATTTCTGTGCAC 24399	A GT
		GT TATAGAAGTT CCT	
		CA GTGTCTTTAA GGG	
		C TG	
GAM1281	KCNK10	5' GGGGCAACTATTGGTGCGCTCC 40971	A ATAGA
	A	TGGA TGTAT AGTTGCCT	
		ACCT GCGTG TCAACGGGG	
		C GTTA_	
GAM1281	KERA	3' GGGACACATTTGTGTATGTTT 22870	A T
		GAATGTATATAGA GT GTCCT	
		TTTGTATGTGTTT CA CAGGG	
		A _	
GAM1281	KLHL2	3' AGGATGAAGTAATGTGTGTTCT 23384	TG AGAAG TG
		GGAA TATAT T TCCT	
		TCTT GTGTA A AGGA	
		GT ATGA_GT	
GAM1281	LFG	3' AGGGCCAAAGTCTATGCGTTCC 76712	AT AG _
	A	TGGAATGT ATAGA TTG TCCT	
		ACCTTGCG TATCT AAC GGGA	
		_ GA C	
GAM1281	LIG4	5' GGGACGATTTCTCCGTTTT 9754	TATAT
		GGAATG AGAAGTTGCCT	



		TTTTGC TCTTTAGCAGGG		
		CC__		
GAM1281 LIPA	3'	AGGACAAAGTAATATATGTGTT 4077	TG	GAAG_
		AA TATATA TTGTCCT		
		TT GTATAT AACAGGA		
		GT AATGA		
GAM1281 LMAN1	3'	AGAATGGCTTTTATAGGTATTT 18733	TA	TG C
	T	GGAATG TATAGAAGT T CT		
		TTTTAT ATATTTTCG A GA		
		GG GT A		
GAM1281 LMO4	3'	ATGTGGCTTTTGTGATATTCTA 22250	A	TG CCT
		TGGAATGT TATAGAAGT T		
		ATCTTATA GTGTTTTCG G		
		_ GT TAG		
GAM1281 LNK	3'	GGCAAATTTTATGTATGGTTT 18466	_	_ CT
	TA	TGGAAT GTATATAGAAGTT GTC		
		ATTTTG TATGTATTTTAA CGG		
		G A		
GAM1281 MADH5	5'	AGGACCTGTGTATGACGTTTCA 19740	_	GA TT
		TGGAATGT ATATA AG GTCCT		
		ACTTTGCA TATGT TC CAGGA		
		G G_ _		
GAM1281 MAP2K1	3'	GGGGCTATTTGTGTGTAT 10859	G T	
		GTATATA AAGT GTCCT		
		TATGTGT TTTA CGGGG		
		G T		
GAM1281 MPHOSPH9	3'	AGGAATCTCTTGTATATTTTA 42943	T A TTG	
		TGGAATGTATA AGA G TCCT		
		ATTTTATATGT TCT C AGGA		
		_ _ TA_		
GAM1281 MYCN	3'	CTTTTGTATACATCC 18193	A	
		GGA TGTATATAGAAG		
		CCT ACATATGTTTTC		
		_		
GAM1281 NBS1	3'	GAAATTCTTTATACATTCTA 69498	T GTTG	
		TGGAATGTATA AGAA TC		
		ATCTTACATAT TCTT AG		
		T AA_		
GAM1281 NCAM2	3'	GGACAGGGAATGCGTTCCA 15802	ATAGAAG	
		TGGAATGTAT TTGTCC		

			ACCTTGCGTA	GACAGG	
			AGG_____		
GAM1281	NCOA4	3'	GGATAATTGGTGCATCC	18369	A ATAGAA
			GGA TGTAT GTTGTCC		
			CCT ACGTG TAATAGG		
			_ GT_____		
GAM1281	NOTCH3	3'	AGGGCAGATGTATGCATTCC	4744	GAAGT
			GGAATGTATATA TGCCT		
			CCTTACGTATGT ACGGA		
			AG_____		
GAM1281	NPTX1	3'	AGGATCTGTGTGTGCGTGTCTA	10258	_ GA TT
			TGGA ATGTATATA AG GTCCT		
			ATCT TCGTGTGT TC TAGGA		
			G G_ _		
GAM1281	NRCAM	3'	AGGACATACCCGTGTATGTT	17206	AGAAGT
			AATGTATAT TGCCT		
			TTGTATGTG ACAGGA		
			CCCAT_		
GAM1281	NVL	3'	AGGACAATTTTAAACTGC	10300	TA_
			GTA TAGAAGTTGTCCT		
			CGT ATTTTAAACAGGA		
			CAA		
GAM1281	NYX	3'	GGGGCAGCAGGGGGTGTGTTT	42602	TG ATAGAA
			GAA TAT GTTGTCT		
			TTT GTG CGACGGGG		
			GT GGGGA_		
GAM1281	OPA1	3'	AGGAGAGCTCTATTATGTTCTA	55539	T A G
			TGGAATGTA ATAGA GTT TCCT		
			ATCTTGTAT TATCT CGA AGGA		
			_ _ G		
GAM1281	OPA1	3'	AGGAGAGCTCTATTATGTTCTA	55530	T A G
			TGGAATGTA ATAGA GTT TCCT		
			ATCTTGTAT TATCT CGA AGGA		
			_ _ G		
GAM1281	OPA1	3'	AGGAGAGCTCTATTATGTTCTA	55557	T A G
			TGGAATGTA ATAGA GTT TCCT		
			ATCTTGTAT TATCT CGA AGGA		
			_ _ G		
GAM1281	OPA1	3'	AGGAGAGCTCTATTATGTTCTA	55566	T A G
			TGGAATGTA ATAGA GTT TCCT		

		ATCTTGTAT TATCT CGA AGGA	
		— — G	
GAM1281 OPA1	3'	AGGAGAGCTCTATTATGTTCTA 55548	T A G
		TGGAATGTA ATAGA GTT TCCT	
		ATCTTGTAT TATCT CGA AGGA	
		— — G	
GAM1281 OTP	5'	GGTGATCTATATATATCTA 49502 A	AGTTGT
		TGGA TGTATATAGA CC	
		ATCT ATATATATCT GG	
		— AGT—	
GAM1281 P4HA1	3'	AGGGTGGTAATATTGGCATTCT 6217	AT GAAG TG
		GGAATGT ATA T TCCT	
		TCTTACG TAT G GGGA	
		GT AAT_ GT	
GAM1281 PACE	3'	GGGGCAGGCTGACATCTGTGTT 10397	TG T AGA _
TCA		TGGAA TA AT AGT TGCCT	
		ACTTT GT TA TCG ACGGGG	
		GT C CAG G	
GAM1281 PCDH11X	3'	AGGATGGCAGTATGTAATCCA 52015	ATG GAA TG
		TGGA TATATA GT TCCT	
		ACCT ATGTAT CG AGGA	
		A_ GA_ GT	
GAM1281 PCDH11X	3'	AGGATGGCAGTATGTAATCCA 52037	ATG GAA TG
		TGGA TATATA GT TCCT	
		ACCT ATGTAT CG AGGA	
		A_ GA_ GT	
GAM1281 PCDH11Y	3'	AGGATGGCAGTATGTAATCCA 52073	ATG GAA TG
		TGGA TATATA GT TCCT	
		ACCT ATGTAT CG AGGA	
		A_ GA_ GT	
GAM1281 PCOLN3	3'	GGGGTGATTTCTGTGACTCT 10912	AT A TG
		GGA GT TATAGAAGT TCCT	
		TCT CA GTGTCTTTA GGGG	
		— — GT	
GAM1281 PCSK2	3'	GGGACAGCTTTCCCTCATTTC 10467	TATATA
		GGAATG GAAGTTGTCCT	
		TTTTAC TTTCGACAGGG	
		TCCCC_	
GAM1281 PLCG2	3'	GGGGTAATTTCTATTATTTTC 72465	T T _ GT
		GAA GTA ATAG AAGTT CCT	

CTT TAT TATC TTAA GGG  
 T \_ C TG  
 GAM1281 PMX1 5' AGGGTGACTTTTTTAATTGTA 42654 G ATAT TG  
 TG AATGT AGAAGT TCCT  
 || |||| |||| ||||  
 AT TTATA TTTTCA GGGA  
 G AT\_\_ GT  
 GAM1281 PMX1 5' AGGGTGACTTTTTTAATTGTA 22586 G ATAT TG  
 TG AATGT AGAAGT TCCT  
 || |||| |||| ||||  
 AT TTATA TTTTCA GGGA  
 G AT\_\_ GT  
 GAM1281 POLK 5' GGGATGCAGCTGTGCTGCATTC 32569 \_ AA T  
 T GGAATGTA TATAG GT GTCCT  
 ||||| |||| |||||  
 TCTTACGT GTGTC CG TAGGG  
 C GA \_  
 GAM1281 POLR2E 3' GGACAGCTTCCTCCATCCA 59919 A TATATA  
 TGGA TG GAAGTTGTCC  
 ||| || |||||  
 ACCT AC CTTCGACAGG  
 \_ CTC\_\_  
 GAM1281 PPP2R5E 3' AGGATAAACATTATTATGCATT 20722 TAGAAG\_  
 CT GGAATGTATA TTGTCCT  
 ||||| |||||  
 TCTTACGTAT AATAGGA  
 TATTACA  
 GAM1281 PPT1 3' ACTGTTTCTGATGTGTTCCA 61803 TG A TT  
 TGGAA TAT TAGAAG GT  
 |||| || ||||| ||  
 ACCTT GTA GTCTTT CA  
 GT \_ GT  
 GAM1281 PRKACA 3' GGGGCGATTCAACCTGTGTGC 10791 A\_\_  
 GTATATAG AGTTGTCCT  
 ||||| |||||  
 CGTGTGTC TTAGCGGGG  
 CAAC  
 GAM1281 PRKCN 3' GGATGACTTCCCAGTTTCA 19448 GTATATA TG  
 TGGAAT GAAGT TCC  
 |||| |||| |||  
 ACTTTG CTTCA AGG  
 ACC\_\_ GT  
 GAM1281 PROS1 5' AGGCAAACCTTTGTTTATATTT 87424 T GT  
 TA TGGAATGTA ATAGAAGTT CCT  
 ||||| ||||| |||  
 ATTTTATAT TGTTTCAA GGA  
 T AC  
 GAM1281 PTGFRN 3' AGGGTATACTTTGTGGTATGTT 67183 ATA \_GT  
 TT GGAATGTAT GAAGT T CCT  
 ||||| |||| | |||

		TTTTGTATG TTTCA A GGA	
		GTG T TG	
GAM1281 PTH	3'	GGGCAACAATACATGCT 4346 A ATAGAA	
		GG ATGTAT GTTGTCC	
		TC TACATA CAACGGG	
		G A_____	
GAM1281 PTPN7	3'	AGGATGATTTCCCTAATGCTTC 54545 T ATA_ TG	
T		GGAA GTAT GAAGT TCCT	
		TCTT CGTA CTTTA AGGA	
		_ ATCC GT	
GAM1281 PTPN7	3'	AGGATGATTTCCCTAATGCTTC 11063 T ATA_ TG	
T		GGAA GTAT GAAGT TCCT	
		TCTT CGTA CTTTA AGGA	
		_ ATCC GT	
GAM1281 PTPN7	3'	AGGATGATTTCCCTAATGCTTC 54556 T ATA_ TG	
T		GGAA GTAT GAAGT TCCT	
		TCTT CGTA CTTTA AGGA	
		_ ATCC GT	
GAM1281 PTPRC	3'	AATTTGTATATATATTTT 55168 G	
		GGAATGTATATA AAGTT	
		TTTTATATATAT TTAA	
		G	
GAM1281 PYGO2	3'	AGGGTGATTTTTTTTGATGTTT 63982 ATAT TG	
		GAATGT AGAAGT TCCT	
		TTTGTA TTTTTA GGGA	
		GTT_ GT	
GAM1281 RAB27A	3'	AGGTGGTTTTTAATATATGTTTC 15924 A TT T	
A		TGGAATGTATAT GAAG G CCT	
		ACTTTGTATATA TTTT T GGA	
		A GG_	
GAM1281 RABIF	3'	GTGAAACTTTTATATACGTATC 11209 A GTCCT	
		GG ATGTATATAGAAGTT	
		CT TGCATATATTTTCAA	
		A AGTGA	
GAM1281 RBBP9	3'	GGGACAATTTGGATTTTGTTCC 70137 TAT AG	
A		TGGAATG AT AAGTTGTCCT	
		ACCTTGT TA TTAAACAGGG	
		TT_ GG	
GAM1281 RDX	3'	TTCTGTGTACATTTTA 11281	
		TGGAATGTATATAGAA	

ATTTTACATGTGTCTT

GAM1281 RDX	3' AGGATAATGGTGAACATTTTA 11277	A AGAA
	TGGAATGT TAT GTTGTCTT	
	ATTTTACA GTG TAATAGGA	
	A G__	
GAM1281 RDX	3' GGTTTCAGTTCTGTGTACATTT 11279	G T__ T
TA	TGGAATGTATATAGAA TTG CC	
	ATTTTACATGTGTCTT GAC GG	
	_ TTT	
GAM1281 RET	3' GGGGCAGCTTTTGGGAAGTCTC 40179	GA GTATA
A	TG AT TAGAAGTTGTCCT	
	AC TG GTTTTCGACGGGG	
	TC AAGG_	
GAM1281 RET	3' GGGGCAGCTTTTGGGAAGTCTC 4371	GA GTATA
A	TG AT TAGAAGTTGTCCT	
	AC TG GTTTTCGACGGGG	
	TC AAGG_	
GAM1281 RET	3' GGGGCAGCTTTTGGGAAGTCTC 40595	GA GTATA
A	TG AT TAGAAGTTGTCCT	
	AC TG GTTTTCGACGGGG	
	TC AAGG_	
GAM1281 RFXAP	3' AGGATATAAATGTATGTGTCTC 5013	GA TG GAAGT
A	TG A TATATA TGTCCT	
	AC T GTATGT ATAGGA	
	TC GT AAAT_	
GAM1281 RNF14	3' AGGATGATTTTAATATTAATTC 15022	GT A TG
CA	TGGAAT ATAT GAAGT TCCT	
	ACCTTA TATA TTTTA AGGA	
	AT A GT	
GAM1281 RNF26	3' AGGGCAGACTGTGCACATTTCA 49309	A AAG
	TGGAATGT TATAG TTGTCCT	
	ACTTTACA GTGTC GACGGGA	
	C A__	
GAM1281 RNF28	3' GGGACGATGTGCTGTATTTC 50861	TGT AA_
	GAA ATATAG GTTGTCTT	
	CTT TATGTC TAGCAGGG	
	_ GTG	
GAM1281 RNGTT	3' TTCTATCTACATTCTA 13733	T
	TGGAATGTA ATAGAA	

			ATCTTACAT TATCTT		
			C		
GAM1281	RNTRE	3'	AGGGTGGCCATTTATACAATCC 28034	A	TAGAA TG
	A		TGGA TGTATA GT TCCT		
			ACCT ACATAT CG GGGA		
			A TTAC_ GT		
GAM1281	RORB	3'	GGGCAACAATGCCATTTCA 22609	_	ATAGAA
			TGGAATG TAT GTTGTCC		
			ACTTTAC GTA CAACGGG		
			C A_____		
GAM1281	RUNX1	3'	GGTTTTTATTTTTATATACGTT 8266		TGT__ T
	T		GAATGTATATAGAAGT CC		
			TTTGCATATATTTTTA GG		
			TTTTT		
GAM1281	SAR1	3'	GGGATTAATTTTATAGCATTCC 39324	A	GTT
	A		TGGAATGT TATAGAA GTCCT		
			ACCTTACG ATATTTT TAGGG		
			_ AAT		
GAM1281	SC5DL	3'	GGGACTAGGCTATATGCATTT 90883		AAGTT
			GAATGTATATAG GTCCT		
			TTTACGTATATC CAGGG		
			GGAT_		
GAM1281	SCML2	3'	GGGGCAAGAATGTACATTTT 20322		AGAAG
			GGAATGTATAT TTGTCCT		
			TTTTACATGTA AACGGGG		
			AG_____		
GAM1281	SCN2B	3'	GGATGACTGTGCATTCCA 15941		ATAGA TG
			TGGAATGTAT AGT TCC		
			ACCTTACGTG TCA AGG		
			_____ GT		
GAM1281	SHANK2	3'	AGGGTGGCTTCTGTTCATCT 55733	A	TAT TG
			GGA TG ATAGAAGT TCCT		
			TCT AC TGTCTTCG GGGA		
			_ _ _ _ GT		
GAM1281	SHC1	3'	GGGGTCTGTATATACATTTCA 11652		GA TTG
			TGGAATGTATATA AG TCC		
			ACTTTACATATAT TC GGG		
			G_ TG_		
GAM1281	SHMT2	3'	GGGCCTCTATATATCTTCT 18268	T	AGTT
			GGAA GTATATAGA GTCC		

			TCTT TATATATCT CGGG		
			C C__		
GAM1281	SIAH2	3'	AGGAATTGTTTTAATGCATTTT 17373	A	GTTG
	A		TGGAATGTAT TAGAA TCCT		
			ATTTTACGTA ATTTT AGGA		
			_ GTTA		
GAM1281	SIGLEC7	3'	AGGATGACTACTTTAGATTCC 26893	G	TAT A TG
			GGAAT TA AG AGT TCCT		
			CCTTA AT TC TCA AGGA		
			G T__ A GT		
GAM1281	SIGLEC7	3'	AGGATGACTACTTTAGATTCC 33303	G	TAT A TG
			GGAAT TA AG AGT TCCT		
			CCTTA AT TC TCA AGGA		
			G T__ A GT		
GAM1281	SIM2	3'	GGGTGACCATGCAATTCCA 17387	_	ATAGAA TG
			TGGAAT GTAT GT TCC		
			ACCTTA CGTA CA GGG		
			A C_____ GT		
GAM1281	SLC13A1	3'	CTTCTATGTTTATTCTA 42379	T	
			TGGAATG ATATAGAAG		
			ATCTTAT TGTATCTTC		
			T		
GAM1281	SLC19A2	3'	AGGATGACTTTTTTTCTGATTC 68976	GTATAT	TG
			GAAT AGAAGT TCCT		
			CTTA TTTTCA AGGA		
			GTCTTT GT		
GAM1281	SLC25A14	3'	AGGGTGGGTTATTGCTATATGTG 14200	TG	AAG__ TG
	TTACA		AA TATATAG T TCCT		
			TT GTATATC G GGGA		
			GT GTTATT GT		
GAM1281	SLC25A14	3'	AGGGTGGGTTATTGCTATATGTG 43021	TG	AAG__ TG
	TTACA		AA TATATAG T TCCT		
			TT GTATATC G GGGA		
			GT GTTATT GT		
GAM1281	SLC4A7	3'	AGGATGATTCTATATATTCT 13224	AT	G TG
			GGA GTATATAGAA T TCCT		
			TCT TATATATCTT A AGGA		
			_ _GT		
GAM1281	SLC4A7	3'	AGGGCTTCTCTATTTGTGTTTC 13225	TG T	A TT
	A		TGGAA TA ATAGA G GTCCT		



		ACTTT GT TATCT C CGGGA		
		GT T _ TT		
GAM1281	SLC6A3	3' AGGGCAACTTCTACTCTTCA 6446	AT	ATAT
		TGGA GT AGAAGTTGTCCT		
		ACTT CA TCTTCAACGGGA		
		CT ____		
GAM1281	SMARCC1	3' TTTCTATATATTTTCTA 11804	T	
		TGGAA GTATATAGAAG		
		ATCTT TATATATCTTT		
		T		
GAM1281	SNX5	3' AGGGCGGTGTGTTGTATGTCTT 27033	TG	AA_ TT
	T	GAA TATATAG G GTCCT		
		TTT GTATGTT T CGGGA		
		CT GTG GG		
GAM1281	SON	3' GTTTTACTTTGATGTGCATTTT 57191	A	TGTCCT
		GGAATGTATAT GAAGT		
		TTTTACGTGTA TTTCA		
		G TTTTGA		
GAM1281	SON	3' GTTTTACTTTGATGTGCATTTT 57194	A	TGTCCT
		GGAATGTATAT GAAGT		
		TTTTACGTGTA TTTCA		
		G TTTTGA		
GAM1281	SON	3' GTTTTACTTTGATGTGCATTTT 54203	A	TGTCCT
		GGAATGTATAT GAAGT		
		TTTTACGTGTA TTTCA		
		G TTTTGA		
GAM1281	SPS2	3' GCAGTCTTTATATGCATTCC 24288	AG	
		GGAATGTATATAGA TTGT		
		CCTTACGTATATTT GACG		
		CT		
GAM1281	ST7	3' AGGGTGATTTCTTATTATTATA 25542	T_____	TG
	TGTT	TGTATA AGAAGT TCCT		
		GTATAT TCTTTA GGGA		
		TATTAT GT		
GAM1281	STAC	3' GGATGGCTGCTGGTTTCA 11994	GTATA A	TG
		TGGAAT TAG AGT TCC		
		ACTTTG GTC TCG AGG		
		_____ G GT		
GAM1281	STIM1	3' GGGGTTTTCTGTGTTATTTC 60151	T	TTG
		TGGAATG ATATAGAAG TCC		

			ACTTTAT TGTGTCTTT GGG		
			— TG—		
GAM1281	SWAP70	3'	GGGATCATAGTTTATATGCATC 71353	A	AGT —
	T		GGA TGTATATAGA TG TCCT		
			TCT ACGTATATTT AC AGGG		
			— GAT T		
GAM1281	TADA2L	3'	AGGACAATATGGGTGGGCATTTC 7638	A	AGAA
	T		GGAATGT TAT GTTGCCT		
			TCTTACG GTG TAACAGGA		
			G GGTA		
GAM1281	TAF4B	3'	AGGATAGTTTTTATAGTTCC 87166	GTA	GT
			GGAAT TATAGAA TGCCT		
			CCTTG ATATTTT ATAGGA		
			— TG		
GAM1281	TAF6	5'	AGGACGGTTGGTTGTGTGTCT 18904	ATG	A_ TT
			GGA TATATAG AG GTCCT		
			TCT GTGTGTT TT CAGGA		
			— GG GG		
GAM1281	TBL1X	3'	GGGTGCAATCTGGTGTGTGTTTC 18935	TG	AGAA —
	CA		TGGAA TATAT GTTGT CCT		
			ACCTT GTGTG TAACG GGG		
			GT GTC_ T A		
GAM1281	TBL2	3'	GGATGGCTTCTGTCTCCA 52186	ATGTAT	TG
			TGGA ATAGAAGT TCC		
			ACCT TGTCTTCG AGG		
			C_ GT		
GAM1281	TBP	3'	GGACAGAATATATGTGTT 64740	TG	GAAG
			AA TATATA TTGTCC		
			TT GTATAT GACAGG		
			GT AA_		
GAM1281	TCF4	3'	GGGACGACTTTCTTTAACATAT 12151	A	A T _
	CA		TGG ATGT TA AGAA GTTGCCT		
			ACT TACA AT TCTT CAGCAGGG		
			A _ T T		
GAM1281	TCTE1L	3'	AGGAATACTATGTGCAT 70971	AAGTTG	
			ATGTATATAG TCCT		
			TACGTGTATC AGGA		
			ATA_		
GAM1281	TEX15	3'	TTCTTGCTTCTGATATGTTTCA 48392	A	TGTCCT
			TGGAATGTAT TAGAAGT		

		ACTTTGTATA GTCTTCG		
		— TTCTTA		
GAM1281 THBS1	3'	GGGGCAGCCGTGCTTATATTTT 12284	TATAGAA	
		GGAATGTA GTTGCCT		
		TTTTATAT CGACGGGG		
		TCGTGC_		
GAM1281 THPO	3'	AGGGTAATTTCTTTGCTTC 4861	T TATA GT	
		GAA GTA GAAGTT CCT		
		CTT CGT CTTTAA GGA		
		_ TTC_ TG		
GAM1281 TIMP3	3'	AGGGCGGTTTTGAGCTTTCTA 4502	T ATATA TT	
		TGGAA GT GAAG GTCCT		
		ATCTT CG TTTT CGGGA		
		T AG_ GG		
GAM1281 TLL1	3'	GGGTGATTTGTACTTTCCA 24955	T TAGA TG	
		TGGAA GTATA AGT TCC		
		ACCTT CATGT TTA GGG		
		T _ GT		
GAM1281 TNFRSF17	3'	GGATGACTGTATTTTTCA 6818	T ATAGA TG	
		TGGAA GTAT AGT TCC		
		ACTTT TATG TCA AGG		
		T _ GT		
GAM1281 TPST1	3'	AGGTTGTCTGTACATGTTCTA 13178	A AGTTGT	
		TGGAATGT TATAGA CCT		
		ATCTTGTA ATGTCT GGA		
		C GTT_		
GAM1281 TRPM7	3'	GATACTATATACGTTTT 62129	AAGT	
		GGAATGTATATAG TGTC		
		TTTTGCATATATC ATAG		
GAM1281 TRPM8	3'	ATTTTTTTTCTATGTATGTCTC 43982	GA TTGCCT	
A		TG ATGTATATAGAAG		
		AC TGTATGTATCTTT		
		TC TTTTA		
GAM1281 TRPS1	3'	AGGGTAGCACTTATTCATTCCA 26074	T T AA GT	
		TGGAATG ATA AG GTT CCT		
		ACCTTAC TAT TC CGA GGA		
		T _ A_ TG		
GAM1281 TRPV4	3'	GGGGCCATGCCTTCTGTGTGTT 60686	GT TT_	
CT		GAAT ATATAGAAG GTCCT		

		CTTG TGTGTCTTC CGGGG		
		— CGTAC		
GAM1281 TYRP1	3'	CTTTTATGTATTTTCCA 72316 T		
		TGGAA GTATATAGAAG		
		ACCTT TATGTATTTTC		
		T		
GAM1281 UBE2A	3'	GGGACAAGGCTTGTAATGTTT 12467 A AAG		
	T	GGAATGT TATAG TTGTCCT		
		TTTTGTA ATGTT AACAGGG		
		A CGG		
GAM1281 UGT2B11	3'	AGGACAACCTTCAGTTTATTCCA 6536 TATATA		
		TGGAATG GAAGTTGTCCT		
		ACCTTAT CTTCAACAGGA		
		TTGA__		
GAM1281 WBSCR1	3'	GTGGTTTTTAGTACATTCT 42231 A TG		
		GGAATGTAT TAGAAGT T		
		TCTTACATG ATTTTGT G		
		— GT		
GAM1281 WBSCR1	3'	GTGGTTTTTAGTACATTCT 49263 A TG		
		GGAATGTAT TAGAAGT T		
		TCTTACATG ATTTTGT G		
		— GT		
GAM1281 WFDC1	5'	GGGGCCCCTCTTCTGTGTGCGT 41043 A TT__		
	CT	GGA TGTATATAGAAG GTCCT		
		TCT GCGTGTGTCTTC CGGGG		
		— TCCC		
GAM1281 XPA	3'	GGACGATTTCTGTCTCCA 4598 ATGTAT		
		TGGA ATAGAAGTTGTCC		
		ACCT TGTCTTTAGCAGG		
		C__		
GAM1281 XPC	3'	AGGAGAAATGACTTTTATAACA 16129 A ____		
	TTTT	ATGT TATAGAAGTTG TCCT		
		TACA ATATTTTCAGT AGGA		
		— AAAG		
GAM1281 YWHAZ	3'	GGGACAATGTTTTCTGTATGTT 12704 T _		
	CTA	TGGAATGTATA AGAA GTTGTCTCT		
		ATCTTGTATGT TTTT TAACAGGG		
		C G		
GAM1281 ZNF236	3'	TTTCTCTGTGCATTTT 23721 T		
		GGAATGTATA AGAAG		

			TTTTACGTGT TCTTT			
			C			
GAM1281	ZNF264	3'	GGGACTGTCTGTATATATCT	12761	A	AGTT
			GGA TGTATATAGA GTCCT			
			TCT ATATATGTCT CAGGG			
			— GT—			
GAM1281	ABCA5	5'	AGGATTGGATTTATGTATGTCC	37912	A	AGTT
	A		TGGA TGTATATAGA GTCCT			
			ACCT GTATGTATTT TAGGA			
			— AGGT			
GAM1281	ADPRTL3	3'	AGGGCAGCTTTTATAGGTTCCA	18500	G	TA
			TGGAAT TATA GAAGTTGTCCT			
			ACCTTG ATAT TTTCGACGGGA			
			G —			
GAM1281	AK5	3'	AGCTTCTTATATATTCTA	23909	T	
			TGGAATGTATA AGAAGTT			
			ATCTTATATAT TCTTCGA			
			—			
GAM1281	AKAP8	3'	AGGATTTTTTTTGTATGTTTC	19600	T	TT
	A		TGGAATGTATA AGAAG GTCCT			
			ACTTTGTATGT TTTT TAGGA			
			— TT			
GAM1281	ANKT	3'	GGGATGGTTTTTACTTAAGTCC	33026	ATG	TA TT
	A		TGGA TA TAGAAG GTCCT			
			ACCT AT ATTTT TAGGG			
			GA_ TC GG			
GAM1281	ARAP3	5'	GATGGCTCTGCTTCCA	42502	T	ATAT A TG
			TGGAA GT AGA GT TC			
			ACCTT CG TCT CG AG			
			— — — — — GT			
GAM1281	ARHGAP5	3'	TCTCCACTTTTCTATGCATTCT	77082	T	TGTCCT
	A		TGGAATGTATA AGAAGT			
			ATCTTACGTAT TTTTCA			
			C CCTCTA			
GAM1281	ARHGEF10	3'	ATTCACGACTTTTATTTATATT	60419	T	CCT
	CTA		TGGAATGTA ATAGAAGTTGT			
			ATCTTATAT TATTTTCAGCA			
			T CTTAG			
GAM1281	ARP5	5'	GACTTCTTGTGTGTTCT	71571	TG	T
			GGAA TATA AGAAGTT			

			TCTT GTGT TCTTCAG		
			GT _		
GAM1281	ARPP-19	3'	AGGATGGCTTGTGATTTATTTT 21787	T A G	TG
	A		TGGAATG AT TA AAGT TCCT		
			ATTTTAT TA GT TTCG AGGA		
			T _ G GT		
GAM1281	ATIP1	3'	GGGGTAACTTCTTGGCAGTTTT 40394	___ ATAT	GT
	TCA		GAA TGT AGAAGTT CCT		
			TTT ACG TCTTCAA GGG		
			TTG GT__ TG		
GAM1281	ATP9A	3'	GGGACAGTTTTGATCCTCATTT 62047	TATATA	GT
	T		GGAATG GAA TGCCT		
			TTTTAC TTT ACAGGG		
			TCCTAG TG		
GAM1281	BDG-29	3'	GGACAAATTGTACATTTT 72355	TAGAAG	
			GGAATGTATA TTGTCC		
			TTTTACATGT AACAGG		
			TA___		
GAM1281	BRAG	5'	TTTCTGTGTGTTTCCA 29480	TGT	
			TGGAA ATATAGAAG		
			ACCTT TGTGTCTTT		
			TG_		
GAM1281	C11orf11	3'	GGGGTGGGAGGGTGTGCATGCT 93258	A	AGAAG TG
	A		TGG ATGTATAT T TCCT		
			ATC TACGTGTG G GGGG		
			G GGAG_ GT		
GAM1281	C13orf1	3'	AGGACTTTTATTTGTATGTTTT 39964	TG	_ TT
	CT		GGAA TATATAGA AG GTCCT		
			TCTT GTATGTTT TT CAGGA		
			TT A TT		
GAM1281	C1orf22	3'	AGTTAACTTTTATAGACATTTT 47253	A	TCCT
	A		TGGAATGT TATAGAAGTTG		
			ATTTTACA ATATTTTCAAT		
			G TGA		
GAM1281	C1orf24	3'	GAATTTTCTGTACATATTTCA 53717	A	TTG
			TGGAATGT TATAGAAG TC		
			ACTTTATA ATGTCTTT AG		
			C TA_		
GAM1281	C1orf9	3'	GGGATAACTTTTCTGTTATTT 32637	TATAT	
			GAATG AGAAGTTGTCCT		

		TTTAT TTTTCAATAGGG		
		TGTCT		
GAM1281	C1orf9	3' AGGACAATGGTAGACATTTTA 32634		ATATAGAA
		TGGAATGT GTTGTCT		
		ATTTTACA TAACAGGA		
		GATGG__		
GAM1281	C20orf108	3' AGGGCTTGTATATATAATCTA 55042	A	G TGT
		TGGA TGTATATA AAGT CCT		
		ATCT ATATATAT TTCG GGA		
		A G _		
GAM1281	C20orf139	5' GGGATAGCAGGGGTGCATTCT 84759		ATAGAA
		GGAATGTAT GTTGTCT		
		TCTTACGTG CGATAGGG		
		GGGA__		
GAM1281	C20orf72	3' GGGGTTTTCTATATATTTT 53498	T	TTG
		GAA GTATATAGAAG TCC		
		CTT TATATATCTTT GGG		
		_ TG_		
GAM1281	C6orf37	3' AGGATGGAAGAATATGTGTAAT 67473	A	GAAG_ TG
	CCA	TGGA TGTATATA T TCCT		
		ACCT ATGTGTAT G AGGA		
		A AAGAA GT		
GAM1281	C6orf37	3' ACATTTTATATATACATTTTA 67472		G T
		TGGAATGTATATA AAG TGT		
		ATTTTACATATAT TTT ACA		
		A T		
GAM1281	C7orf11	3' AGGATAACTTGCAACATTT 56937		ATATAG
		GAATGT AAGTTGTCCT		
		TTTACA TTCAATAGGA		
		ACG__		
GAM1281	C8orf13	3' GGACAGCGATGTTTTCTA 81575		TGTAT GAA
		TGGAA ATA GTTGTCC		
		ATCTT TGT CGACAGG		
		T__ AG_		
GAM1281	C8orf2	3' TTCTATGTATCTTTCA 23170	T	
		TGGAA GTATATAGAA		
		ACTTT TATGTATCTT		
		C		
GAM1281	C8orf4	3' AGGTTTTTTATACATTTCA 39279	T	G
		TGGAATGTATA AGAA TT		

			ACTTTACATAT TTTT GA		
			T G		
GAM1281	CAP	3'	GGACTGATGATGCATTTTA 21024	ATAGAAGTT	
			TGGAATGTAT GTCC		
			ATTTTACGTA CAGG		
			GTAGT____		
GAM1281	CARD6	5'	AGGATGATTTTCATAATATATTT 50852	ATA TG	
	C		GGAATGTAT GAAGT TCCT		
			CTTTATATA CTTTA AGGA		
			ATA GT		
GAM1281	CASPR3	3'	GACACAGGTTTTTCATATACATT 45936	_ G CCT	
	CCA		TGGAATGTATAT AGAA TTGT		
			ACCTTACATATA TTTT GACA		
			C G CAGA		
GAM1281	CBLN1	3'	GGGACAACTTTGTCCATTTT 15124	TATATA	
			GGAATG GAAGTTGTCCT		
			CTTTAC TTTCAACAGGG		
			CTG____		
GAM1281	CBX6	3'	CTTCTGTGTCATTTT 26615 T		
			GGAATG ATATAGAAG		
			TTTTAC TGTGTCTTC		
			—		
GAM1281	CDT1	3'	GGGTGACTTTTGTTCATT 77675	TAT TG	
			AATG ATAGAAGT TCC		
			TTAC TGTTTTCA GGG		
			— GT		
GAM1281	CGGBP1	3'	GGTTCATTTTGTATTTATTTT 13364	T TGT T	
	A		TGGAATG ATATAGAAGT CC		
			ACTTTAT TATGTTTTTA GG		
			T CTT		
GAM1281	CHCR	3'	GGCCTTTCTATATATATTCT 37236	TT	
			GGAATGTATATAGAAG GTC		
			TCTTATATATATCTTT CGG		
			C_		
GAM1281	CHRFAM7A	3'	GGGAAC TACTCAATATATATTT 95022	A A TG_	
	CA		TGGAATGTATAT GA GT TCCT		
			ACTTTATATATA CT CA AGGG		
			A _ TCA		
GAM1281	CKAP2	3'	ATTTCTATGTTTCATTCCA 36562	T	
			TGGAATG ATATAGAAGT		



		ACCTTAC TGTATCTTTA		
		T		
GAM1281	CKLFH1	5' GGGACAGCTTCAAACGTTTC 53798	ATATA	
		GGAAATGT GAAGTTGTCCT		
		CTTTGCA CTTGACAGGG		
		AA__		
GAM1281	CLDN7	5' GGGTCGATTTGTGTGTAGTTT 94584	G G T	
		GAAT TATATA AAGTTG CCT		
		TTTG ATGTGT TTTAGC GGG		
		_ G T		
GAM1281	CLDN7	5' GGGTCGATTTGTGTGTAGTTT 7140	G G T	
		GAAT TATATA AAGTTG CCT		
		TTTG ATGTGT TTTAGC GGG		
		_ G T		
GAM1281	CLIC4	3' CATGTTAACTTCTGTTGTGTTT 25633	TG T TCCT	
	T	GGAA TA ATAGAAGTTG		
		TTTT GT TGTCTTCAAT		
		GT _ TGTACG		
GAM1281	CLLD8	3' AGGATGGAAGTGTATATTTTA 49164	AGAAG TG	
		TGGAATGTATAT T TCCT		
		ATTTTATATGTG G AGGA		
		AA__ GT		
GAM1281	COL21A1	5' GGGCAGCCAATCCGTTTCA 48022	TATATAGAA	
		TGGAATG GTTGTCC		
		ACTTTGC CGACGGG		
		CTAAC__		
GAM1281	COP9	3' GATATACTATATACATTTT 22005	AAGT	
		GGAATGTATATAG TGTC		
		TTTTACATATATC ATAG		
		AT__		
GAM1281	CRELD1	3' AGGACAGCTTGGTTTATTTTT 31333	T T AG	
		GAA GTA AT AAGTTGTCCT		
		TTT TAT TG TTCGACAGGA		
		T T G_		
GAM1281	CRIP1	3' TTCTGTATGCACTTTTA 73807	_	
		TGGAA TGTATATAGAA		
		ATTTT ACGTATGTCTT		
		C		
GAM1281	D15Wsu75e	3' GGGACGGCTTTTTTAAATTTCC 66649	TGTATAT	
		GGAA AGAAGTTGTCCT		

			CCTT	TTTTCGGCAGGG		
			TAAAT__			
GAM1281	D2S448	3'	GGGCTCTCTGTAACATTTCA	73530	A	A TT
			TGGAATGT TATAGA G	GTCC		
			I			
			ACTTTACA ATGTCT C	CGGG		
			_ _ T_			
GAM1281	DDX34	3'	AGGACACGCATATATGTTT	27977	AGAA	T
			GAATGTATAT GT	GTCCT		
			TTTGTATATA CA	CAGGA		
			CG__ _			
GAM1281	DIS3	3'	TTTGTTACTTTTAAGTACATTT	30239	A	TGTCCT
	TA		TGGAATGTAT TAGAAGT			
			ATTTTACATG ATTTTCA			
			A TTGTTTG			
GAM1281	DKFZp434B0417	3'	TGGCGTTTTTTATATATATTTT	25383		AGT CT
			GGAATGTATATAGA TGTC			
			TTTTATATATATTT GCGG			
			TT_ TG			
GAM1281	DKFZP434I0714	3'	CTTCATATATGTATTCCA	85798		_
			TGGAATGTATATA GAAG			
			ACCTTATGTATAT CTTC			
			A			
GAM1281	DKFZP434J1813	3'	AGGGCCGGTTTATAAATATTTT	61785	A	AGTT
	A		TGGAATGT TATAGA GTCCT			
			ATTTTATA ATATTT CGGGA			
			A GGC_			
GAM1281	DKFZP434N178	3'	AGGTTTCATATTTTATATCATT	71901	T	_ T_
	TT		GGAATG ATATAGAAGT TG CCT			
			TTTTAC TATATTTTTA AC GGA			
			_ T TT			
GAM1281	DKFZP434P0721	3'	GCTGCTTTTGTGTGTGTGTCA	63717	GA TG	T
			TG A TATATAGAAGT GT			
			I			
			AC T GTGTGTTTTTCG CG			
			TG GT T			
GAM1281	DKFZp547J036	3'	AGGACATCCGTGTATATTTT	50125	TA AGT	
			GGAATGTATA GA TGTCCT			
			CTTTATATGT CT ACAGGA			
			GC _			
GAM1281	DKFZP564C196	3'	GGATATTTATTATGTGTGTTTT	70067	TG	A T T
			GGAA TATATAG AG TGTCCT			

TTTT GTGTATT TT ATAGG  
 GT A T  
 GAM1281 DKFZP586M1120 3' GCTTTTATTACATTTTA 48464 T  
 TGGAAATGTA ATAGAAGT  
 ||||| |||||  
 ATTTTACAT TATTTTCG  
  
 —  
 GAM1281 DKFZP586M1120 3' AGTACTGTTTTGTGTGCGTTCC 48450 GTT C  
 GGAATGTATATAGAA GT CT  
 ||||| || ||  
 CCTTGCGTGTGTTTT CA GA  
 GT\_ T  
 GAM1281 DKFZP586P0123 3' GGGACATGTAGATTGTGTGCAT 94839 AAGT\_\_  
 T AATGTATATAG TGCCT  
 ||||| |||||  
 TTACGTGTGTT ACAGGG  
 AGATGT  
 GAM1281 DKFZp761D112 3' GGGGCAGTTTTTGTCTGC 50192 T GT  
 GTA ATAGAA TGCCT  
 || ||||| |||||  
 CGT TGTTTT ACGGGG  
 C TG  
 GAM1281 DKFZp762A227 3' AGGATGGTTTTGTTTCATCTTCC 34285 T AT G TG  
 A TGGAA GT ATAGAA T TCCT  
 |||| || ||||| || |||||  
 ACCTT TA TGTTTT G AGGA  
 C CT \_GT  
 GAM1281 DRCTNNB1A 3' AGGAACCCTGTGTACAATTTA 50839 A AAGTTG  
 TGGA TGTATATAG TCCT  
 |||| ||||| |||||  
 ATTT ACATGTGTC AGGA  
 A CCA\_\_  
 GAM1281 EAT2 3' CTTCTATATACATTTTA 79277  
 TGGAAATGTATATAGAAG  
 ||||| |||||  
 ATTTTACATATATCTTC  
  
 GAM1281 EIF4B 3' GCCTGCTTTTATATGCATTTT 75968 TGCCT  
 GGAATGTATATAGAAGT  
 ||||| |||||  
 TTTTACGTATATTTTCG  
 TCCG  
 GAM1281 ELF2 3' GCAATTTTGTATGCATTTTA 22499 A  
 TGGAAATGTAT TAGAAGTTGT  
 ||||| |||||  
 ATTTTACGTA GTTTTAAACG  
  
 —  
 GAM1281 ENDOFIN 3' GGGACAGCTTTGGATTTGTTTT 28387 TGTATATA  
 CA TGGAA GAAGTTGTCCT  
 |||| |||||

			ACTTT TTTTCGACAGGG		
			TGTTTAGG		
GAM1281	EPLIN	3'	AGGGCACAGTTTGTATATTTT 33021	T	AGT
			GAA GTATATAGA TGTCCT		
			TTT TATATGTTT ACGGGA		
			T GAC		
GAM1281	EREG	3'	ATTTCTGGTGTATATTTTA 7493	—	
			TGGAATGTATAT AGAAGT		
			ATTTTATATGTG TCTTTA		
			G		
GAM1281	ESPL1	5'	GGGGCAGCTTTTCTCTGC 24461	TAT	
			GTA AGAAGTTGTCCT		
			CGT TTTTCGACGGGG		
			CTC		
GAM1281	FAM3C	3'	AGGACAGCTAAGTCAGTATATT 29684	ATAGA_	
	T		GAATGTAT AGTTGTCCT		
			TTTATATG TCGACAGGA		
			ACTGAA		
GAM1281	FBXO4	3'	GGGAATTCTGATGCATTCCA 53112	A GTTG	
			TGGAATGTAT TAGAA TCC		
			ACCTTACGTA GTCTT GGG		
			— AA_		
GAM1281	FENS-1	3'	GGACAATAGGGTCATTCCA 40440	T ATAGAA	
			TGGAATG AT GTTGTCC		
			ACCTTAC TG TAACAGG		
			— GGA_		
GAM1281	FHR5	3'	AGGATAACTTTGAAACTTTCT 47899	T ATATA	
			GGAA GT GAAGTTGTCCT		
			TCTT CA TTTCAATAGGA		
			T AAG_		
GAM1281	FLJ10110	3'	TTTCTAATACATTCTA 35825	A	
			TGGAATGTAT TAGAAG		
			ATCTTACATA ATCTTT		
			—		
GAM1281	FLJ10140	3'	AGGACAGTTTGCTGTGTTCTA 35844	ATGT _ GT	
			TGGA ATATAG AA TGTCCT		
			ATCT TGTGTC TT ACAGGA		
			— G TG		
GAM1281	FLJ10498	3'	TGGACACACATATGTGTATTT 36196	GAA T T	
			GAATGTATATA GT GTCC		

TTTATGTGTAT CA CAGG  
 ACA \_ TG  
 GAM1281 FLJ10498 3' AGGATAGGAGTTATATATTCT 36191 TAGAAG  
 GGAATGTATA TTGTCCT  
 ||||| |||||  
 TCTTATATAT GATAGGA  
 TGAG\_\_  
 GAM1281 FLJ10520 3' TTCTTTATACATTCCA 36217 T  
 TGGAATGTATA AGAA  
 ||||| |||||  
 ACCTTACATAT TCTT  
 T  
 GAM1281 FLJ10525 3' GGAATAATGTGCATTTCA 36224 AGAAGTTG  
 TGGAATGTATAT TCC  
 ||||| |||||  
 ACTTTACGTGTA AGG  
 ATA\_\_\_\_  
 GAM1281 FLJ10656 3' GACAACCTTTGGTTCT 36387 GTATATA  
 GGAAT GAAGTTGTC  
 |||| |  
 TCTTG TTTCAACAG  
 G\_\_\_\_  
 GAM1281 FLJ10751 3' GGGGCAGCTTCTGGAAGTTGTT 36731 TATA\_  
 TT GGAATG TAGAAGTTGTCCT  
 |||| |  
 TTTTGT GTCTTCGACGGGG  
 TGAAG  
 GAM1281 FLJ10751 3' GGGGCAGCTTCTGGAAGTTGTT 36570 TATA\_  
 TT GGAATG TAGAAGTTGTCCT  
 |||| |  
 TTTTGT GTCTTCGACGGGG  
 TGAAG  
 GAM1281 FLJ10761 3' GGGGCTGCCTTATATGTGTGTT 36583 TG G TT\_  
 T GAA TATATA AAG GTCCT  
 || ||||| |||||  
 TTT GTGTAT TTC CGGGG  
 GT A CGT  
 GAM1281 FLJ10853 3' GGGCAAGAGACTTTTATGCACA 36770 A \_\_\_\_ T  
 TTCT ATGT TATAGAAGT TGTCC  
 |||| |  
 TACA GTATTTTCA ACGGG  
 C GAGA  
 GAM1281 FLJ10898 3' AGGATTAATATCTGTGTTCCA 59418 ATGT A \_  
 TGGA ATATAGA GTTG TCCT  
 |||| |  
 ACCT TGTGTCT TAAT AGGA  
 \_\_\_\_ A T  
 GAM1281 FLJ11320 3' GGGGTGATTCTGATGTTTTT 37245 TG A TG  
 GAA TAT TAGAAGT TCCT  
 |||| |

TTT GTA GTCTTTA GGGG  
 TT \_ GT  
 GAM1281 FLJ11383 3' GGGATGACTTTCTGGTATTTCT 46283 T ATA TG  
 GGAA GTAT GAAGT TCCT  
 |||| ||| |||| ||||  
 TCTT TATG TTTCA AGGG  
 \_ GTC GT  
 GAM1281 FLJ12085 3' GGCTTTCTATAGCATTCTA 42868 A TT  
 TGGAATGT TATAGAAG GTC  
 ||||||| ||||||| |||  
 ATCTTACG ATATCTTT CGG  
  
 \_ \_  
 GAM1281 FLJ12476 3' GGGCAATTTTTTTTTTCT 42951 TGTATAT  
 GGAA AGAAGTTGTCC  
 ||| |||||||||  
 TCTT TTTTAAACGGG  
 TT\_\_\_\_  
 GAM1281 FLJ12644 3' GGGGCAGTTTTAGAGGCTTCCA 43557 T ATA G  
 TGGA GT TAGAA TTGTCCT  
 |||| || |||| ||||||  
 ACCTT CG ATTTT GACGGGG  
 \_ GAG \_  
 GAM1281 FLJ12668 3' GGGACAGTCCTCTTCTATATGT 46520 TG \_\_\_\_  
 TTT AA TATATAGAAG TTGTCCT  
 || ||||||| ||||||  
 TT GTATATCTTC GACAGGG  
 TT TCCT  
 GAM1281 FLJ12707 3' AGGGTGGCTACTGCATTCCA 41947 ATAT A TG  
 TGGAATGT AG AGT TCCT  
 |||||| || ||| ||||  
 ACCTTACG TC TCG GGGA  
 \_\_\_\_ A GT  
 GAM1281 FLJ12761 3' AGGATGGCTGGCTGGTGTTTTT 44612 TG A A\_ TG  
 CA TGGAA TAT TAG AGT TCCT  
 |||| ||| ||| ||| ||||  
 ACTTT GTG GTC TCG AGGA  
 TT \_ GG GT  
 GAM1281 FLJ12838 3' GGATTGTGTGTATATT 44968 G AGTT  
 GAATGTATATA A GTCC  
 ||||||||| | ||||  
 TTTATATGTGT T TAGG  
 G \_\_\_\_  
 GAM1281 FLJ12960 3' ACTTCTATGCTATATTT 44944 \_  
 GGAATGTA TATAGAAGT  
 ||||||| |||||||  
 TTTTATAT GTATCTTCA  
 C  
 GAM1281 FLJ13057 3' GGGAATAATTTGTATGTAT 42456 G \_  
 GTATATA AAGTTGT CCT  
 ||||||| ||||||| |||

		TATGTAT TTTAATA GGG	
		G A	
GAM1281	FLJ13188	3' TAATTTTGTGTATTTTC 41941	T
		GAA GTATATAGAAGTTG	
		CTT TATGTGTTTTTAAT	
		T	
GAM1281	FLJ13231	3' CTTTTTGTATATTCTA 43550	T
		TGGAATGTATA AGAAG	
		ATCTTATATGT TTTTC	
		T	
GAM1281	FLJ13391	3' AGGGCAACCTCGTCCATTTTA 49789	TATATA A
		TGGAATG GA GTTGCCT	
		ATTTTAC CT CAACGGGA	
		CTG__ C	
GAM1281	FLJ13920	3' ACTTTATGTATATGTTCCA 44654	_
		TGGAATGTATATA GAAGT	
		ACCTTGTATATGT TTTCA	
		A	
GAM1281	FLJ14054	3' AGGGTAGCTTTGCCATTGCCA 44658	_ TATATA GT
		TGG AATG GAAGTT CCT	
		ACC TTAC TTTCGA GGA	
		G CCG__ TG	
GAM1281	FLJ14327	3' AGGGTGACTTTGATGTCGTGTT 46128	TG_ A TG
	CT	GGAA T ATAT GAAGT TCCT	
		TCTT G TGTA TTTCA GGGA	
		GT C G GT	
GAM1281	FLJ14442	3' AGGGTGATTTAACCTGGGTTCT 51360	G TATAG TG
		GGAAT TA AAGT TCCT	
		TCTTG GT TTTA GGGA	
		G CCAA_ GT	
GAM1281	FLJ14642	3' GGGGCAGAAGTGGTTATGTATC 51506	T AAG__
	TTCT	AA GTATATAG TTGCCT	
		TT TATGTATT GACGGGG	
		C GGTGAA	
GAM1281	FLJ14743	3' ATAATTCTGTGTGATTCT 68062	G
		GGAATGTATATAGAA TTGT	
		TCTTATGTGTGTCTT AATA	
		_	
GAM1281	FLJ14751	3' TTTTATATATATTTTA 51598	
		TGGAATGTATATAGAAG	

ATTTTATATATATTTT

GAM1281 FLJ20013 3' AGGATGGCTTTACCACCATGTC 34329 GA TATATA TG  
A TG ATG GAAGT TCCT  
|| ||| |||| ||||  
AC TAC TTTCG AGGA  
TG CACCA\_ GT

GAM1281 FLJ20054 3' AGGTACTAGTTTGTATGTATGT 38781 G GT \_ \_  
TT GAATGTATATA AA T GT CCT  
||||||| || | || |||  
TTTGTATGTAT TT A CA GGA  
G TG T T

GAM1281 FLJ20060 3' AGGATAGTTTTTGTGTATGTT 34447 \_ GT  
C GAATGTATA TAGAA TGCCT  
||||||| |||| |||||  
CTTGTATGT GTTTT ATAGGA  
T TG

GAM1281 FLJ20340 3' GGGGCGATTCTATTTATATGAC 34978 \_ \_\_\_\_  
ATTCT ATGT ATATAGA AGTTGTCCT  
||| ||||| |||||  
TACA TATATTT TTAGCGGGG  
G ATC

GAM1281 FLJ20457 3' GGGATACTACTACATTTTA 35221 ATAT A  
TGGAATGT AG AGTTGTCCT  
|||||| || |||||  
ATTTTACA TC TCAATAGGG  
\_ A

GAM1281 FLJ20508 3' TAGGGTGATTTTGACAGAAAAT 35309 ATA\_\_\_\_\_ TG  
ATATTTTA GTAT GAAGT TCCT A  
||| |||| ||| |  
TATA TTTTA GGGA T  
AAAGACAG GT

GAM1281 FLJ20635 3' AGGGTGACGCGGACACATTTCA 35478 ATATAGAA TG  
TGGAATGT GT TCCT  
|||||| || ||||  
ACTTTACA CA GGGA  
CAGGCG\_ GT

GAM1281 FLJ20716 3' GACTGCTTTTGTGATGTTTCA 35605 A T  
TGGAATGT TATAGAAGT GTC  
|||||| ||||| |||  
ACTTTGTA GTGTTTTCG CAG  
\_ T

GAM1281 FLJ20793 3' AGTGACTTTTTGTGTGTGTTTT 91803 TG \_ TG CCT  
GGAA TATATAGAA GT T  
||| ||||| || |  
TTTT GTGTGTTTT CA G  
GT T GT A

GAM1281 FLJ21140 3' GTGCAATTTTGTATGTATTTT 45481 CCT  
GGAATGTATATAGAAGTTGT  
|||||||



TTTTATGTATGTTTTTAACG  
 TG  
 GAM1281 FLJ21269 3' AGGGTGGCTTTTGGTTTTTGTT 47065 TATA\_ TG  
 TC GGAATG TAGAAGT TCCT  
 ||||| ||||| ||||  
 CTTTGT GTTTTCG GGGA  
 TTTTG GT  
 GAM1281 FLJ21272 5' GACGACAACATTTTA 46738 ATATAGAA  
 TGGAATGT GTTGTC  
 ||||| |||||  
 ATTTTACA CAGCAG  
 A\_\_\_\_\_  
 GAM1281 FLJ21302 3' GCTACTTCTGTGTATGTT 43216 T  
 AATGTATATAGAAGT GT  
 ||||| ||||| ||  
 TTGTATGTGTCTTCA CG  
 T  
 GAM1281 FLJ21302 3' TATGCTATTTCTGTGTATGTT 43218 T CCT  
 GAATGTATATAGAAGT GT  
 ||||| ||||| ||  
 CTTGTATGTGTCTTTA CG  
 T TATG  
 GAM1281 FLJ21369 3' ACCATTTTTATTATACATTTCA 45633 \_ T  
 TGGAATGTATA TAGAAGT GT  
 ||||| ||||| ||  
 ACTTTACATAT ATTTTCA CA  
 T C  
 GAM1281 FLJ21432 3' GGGATAAGAGTGGTGTGGCATT 44636 \_ AGAAG  
 TTA TGGAATGT ATAT TTGTCCT  
 ||||| ||||| |||||  
 ATTTTACG TGTG AATAGGG  
 G GTGAG  
 GAM1281 FLJ21432 3' GCCCATTTCTATGTGTGTGTCT 44635 \_TG TGTCCT  
 A TGGA A TATATAGAAGT  
 ||||| ||||| |||||  
 ATCT T GTGTATCTTTA  
 G GT CCCG  
 GAM1281 FLJ21432 3' GGGATGACTCCATTATATCC 44637 A TATA A TG  
 GGA TGTA GA GT TCCT  
 ||||| ||||| |||||  
 CCT ATAT CT CA AGGG  
 \_ TAC\_ \_ GT  
 GAM1281 FLJ21877 5' AGGGCAAAGGATGAACATTCCA 41943 A AGAAG  
 TGGAATGT TAT TTGTCCT  
 ||||| ||||| |||||  
 ACCTTACA GTA AACGGGA  
 A GGA\_  
 GAM1281 FLJ22127 3' AGCTTTTGTGATATTTTA 42880 A  
 TGGAATGT TATAGAAGTT  
 ||||| ||||| |||||

ATTTTATA GTGTTTTCGA

GAM1281 FLJ22169 3' AGGGTGACCTTGGCTGTGTACG 43999 A AA\_\_ TG  
TCCCA ATGTATATAG GT TCCT  
||||||| || ||||  
TGCATGTGTC CA GGGA  
C GGTTC GT

GAM1281 FLJ22233 3' GGGATGGCTGGATGTGCTCCA 46364 AT AGA TG  
TGGA GTATAT AGT TCCT  
|||| ||||| || ||||  
ACCT CGTGTA TCG AGGG  
\_\_ GG\_ GT

GAM1281 FLJ22584 3' AGGGTGATTTCTATAAATCACC 44549 AAT A TG  
A TGG GT TATAGAAGT TCCT  
||| || ||||| ||||  
ACC TA ATATCTTTA GGGA  
AC\_ A GT

GAM1281 FLJ22833 3' AGTCTATCTTCTGTATAAGTTT 43099 G T TC  
T GGAAT TATATAGAAG TG CT  
|||| ||||| || ||  
TTTTG ATATGTCTTC AT GA  
A T CT

GAM1281 FLJ23189 3' GGATTTTTCTGTATGGTTCT 46841 G TT  
GGAAT TATATAGAAG GTCC  
|||| ||||| ||||  
TCTTG GTATGTCTTT TAGG  
\_ T\_

GAM1281 FLJ23191 3' AGGATATCAACGTGTGTATATT 44708 GAAGT\_  
AATGTATATA TGTCCT  
||||||| |||||  
TTATATGTGT ATAGGA  
GCAACT

GAM1281 FLJ23441 5' AGGACAGTGGCTTTGTACATAT 45169 \_ T AA  
TCA TGGA ATGTATA AG GTTGTCTT  
|||| ||||| || |||||  
ACTT TACATGT TC TGACAGGA  
A T GG

GAM1281 FLJ23462 3' AGGATGGTTTCTTGAAATAATT 45801 GTATAT\_ TT  
T GAAT AGAAG GTCCT  
|||| ||||| |||||  
TTTA TCTTT TAGGA  
ATAAAGT GG

GAM1281 FLJ23550 3' AGGACCAGTTTATATATTTCT 46852 T AGTT  
GGAA GTATATAGA GTCCT  
|||| ||||| |||||  
TCTT TATATATTT CAGGA  
\_ GAC\_

GAM1281 FLJ23594 3' GGTAAACTTTTATGTACGT 45507 GT T  
ATGTATATAGAAGTT CC  
||||||| || ||

		TGCATGTATTTTCAA GG	
		AT	
GAM1281	FLJ23594	3' AACTTTTATGTACATT 45505	
		AATGTATATAGAAGTT	
		TTACATGTATTTTCAA	
GAM1281	FLJ30046	3' AGGATGAAACTGTAATGTTTTA 58099	A AAG TG
		TGGAATGT TATAG T TCCT	
		ATTTTGTA ATGTC A AGGA	
		_ AA_ GT	
GAM1281	FLJ31737	3' AGGGTGACTTGCGATGATATAT 58693	ATAG__ TG
	TT	GAATGTAT AAGT TCCT	
		TTTATATA TTCA GGGA	
		GTAGCG GT	
GAM1281	FLJ32312	3' AGGATCTATATATGTGTATATT 58495	GAAGTT_
	TT	GGAATGTATATA GTCCT	
		TTTTATATGTGT TAGGA	
		ATATATC	
GAM1281	GAS2L1	3' GGGACCTCTGTTGTACATTCC 21363	TAGA TT
		GGAATGTATA AG GTCCT	
		CCTTACATGT TC CAGGG	
		TG__ TC	
GAM1281	GBTS1	3' GGACACGATCTGTGTTCCA 59058	ATGT A_ T
		TGGA ATATAGA GT GTCC	
		ACCT TGTGTCT CA CAGG	
		__ AG _	
GAM1281	GGA2	3' AGACAATGCTTCTTGTGTGTGT 56870	TG _ _ CT
	TCT	GAA TATATA GAAGT TGTC	
		CTT GTGTGT CTTCG ACAG	
		GT T TA A	
GAM1281	GGA2	3' AGACAATGCTTCTTGTGTGTGT 30457	TG _ _ CT
	TCT	GAA TATATA GAAGT TGTC	
		CTT GTGTGT CTTCG ACAG	
		GT T TA A	
GAM1281	GIT2	3' TTTTATTGTACATTCTA 54086	_
		TGGAATGTATA TAGAAG	
		ATCTTACATGT ATTTTT	
		T	
GAM1281	GIT2	3' TTTTATTGTACATTCTA 54099	_
		TGGAATGTATA TAGAAG	

		ATCTTACATGT ATTTTT	
		T	
GAM1281	GIT2	3' TTTTATTGTACATTCTA 28764	—
		TGGAATGTATA TAGAAG	
		ATCTTACATGT ATTTTT	
		T	
GAM1281	GRP3	3' GGGGCTAAAGTGTATATATTCC 31121	GAAGTT
	A	TGGAATGTATATA GTCCT	
		ACCTTATATATGT CGGGG	
		GAAAT_	
GAM1281	GS3955	5' GGGGTGATTGCAAATTATTCCA 41319	TATATAGA TG
		TGGAATG AGT TCCT	
		ACCTTAT TTA GGGG	
		TAAACG_ GT	
GAM1281	H-L(3)MBT	3' AGGTTTCTGTATATGTTCCA 31308	TTGT
		TGGAATGTATATAGAAG CCT	
		ACCTTGTATATGTCTTT GGA	
		—	
GAM1281	HBOA	3' GTTACTCCTTATATGTGTGTTT 22969	TG G TT CCT
	TA	TGGAA TATATA AAG GT	
		ATCTT GTGTAT TTC CA	
		GT A CT TTGA	
GAM1281	HBXAP	3' AGGGTGGATGAAAATGCATTCC 33417	ATAGAAG TG
		GGAATGTAT T TCCT	
		CCTTACGTA G GGGA	
		AAAGTA_ GT	
GAM1281	HEMK	3' AGGATGACTGCCTGCTTTTCT 32426	T TATAGA TG
		GGAA GTA AGT TCCT	
		TCTT CGT TCA AGGA	
		T CCG_ GT	
GAM1281	HERC1	3' AGGACAGTTTTACATGAATATT 14066	A A_ GT
	C	GAATGT TAT GAA TGTCCT	
		CTTATA GTA TTT ACAGGA	
		A CA TG	
GAM1281	HH114	3' ACTTTTGTGTACTTTTA 50683	T
		TGGAA GTATATAGAAGT	
		ATTTT CATGTGTTTCA	
		—	
GAM1281	HNRPA3	3' ACTCTTATTTCTTGTGTATATT 19253	_ TGTCCCT
	TCA	TGGAATGTATATA GAAGT	

		ACTTTATATGTGT CTTTA		
		T TTCTCA		
GAM1281	HSA250303 3'	AGGAAAAGTTTTATGTGATTTT 37408	G	G G
	A	TGGAAT TATATAGAA TT TCCT		
		ATTTTA GTGTATTTT AA AGGA		
		— G A		
GAM1281	HSN44A4A 3'	GGGGCTCCTGGGTACATTCCA 31115		ATAGA TT
		TGGAATGTAT AG GTCCT		
		ACCTTACATG TC CGGGG		
		GG___ CT		
GAM1281	HSPC128 3'	TTTCTAAATATGTTCTA 26344	A	
		TGGAATGTAT TAGAAG		
		ATCTTGTATA ATCTTT		
		A		
GAM1281	HSPC155 5'	AGGACGGAGTAATCTGTTTACA 33087	T	AG___
	TTCT	AATGTA ATAGA TTGTCCT		
		TTACAT TGTCT GGCAGGA		
		T AATGA		
GAM1281	HSU79252 5'	GATTTTTGTGTGTGTGCCA 25245	A TG	
		TGG A TATATAGAAGTT		
		ACC T GTGTGTTTTTAG		
		G GT		
GAM1281	IRF5 5'	AAATAATTTTTATGTATTTTT 97250	T	CCT
		GAA GTATATAGAAGTTGT		
		TTT TATGTATTTTTAATA		
		T AAG		
GAM1281	IRF5 3'	AAATAATTTTTATGTATTTTT 50971	T	CCT
		GAA GTATATAGAAGTTGT		
		TTT TATGTATTTTTAATA		
		T AAG		
GAM1281	KIAA0057 3'	AGGATTAGGGTCTGTGGTGTGT 24415	TG _	AGTT_
	TCT	GGAA TAT ATAGA GTCCT		
		TCTT GTG TGTCT TAGGA		
		GT G GGGAT		
GAM1281	KIAA0087 3'	GGGCTATCTATATATATTT 28700	AGTT	
		GAATGTATATAGA GTCC		
		TTTATATATATCT CGGG		
		AT___		
GAM1281	KIAA0179 3'	CTTTTAACTTTTGTATGTGTTT 64826	TG	TCCT
	TA	TGGAA TATATAGAAGTTG		

		ATTTT GTATGTTTTCAAT		
		GT TTTCT		
GAM1281	KIAA0237	3' GGGGCAGAGCCTGTGTGTTCT 28533	GT	AAG
		GGAAT ATATAG TTGTCCT		
		TCTTG TGTGTC GACGGGG		
		— CGA		
GAM1281	KIAA0240	3' GCTTTGTATACATTTT 92437	A	
		GGAATGTATATAGA GT		
		TTTTACATATGTTT CG		
		—		
GAM1281	KIAA0247	3' GGCATTTCAATGTACATTCTA 28406	A	T
		TGGAATGTATAT GAAGT GTC		
		ATCTTACATGTA CTTTA CGG		
		A —		
GAM1281	KIAA0256	3' AGGAAAGTTTTTATATATTTTT 64416	T	GT G
	T	GGAA GTATATAGAA T TCCT		
		TTTT TATATATTTT A AGGA		
		T TG A		
GAM1281	KIAA0256	3' GGTATTTTATATGATTCCA 64422	G	GTTGT
		TGGAAT TATATAGAA CC		
		ACCTTA GTATATTTT GG		
		— AT—		
GAM1281	KIAA0268	3' GGGGCGACAGATATTATTCCA 70004	T	AGAA
		TGGAATG ATAT GTTGTCTT		
		ACCTTAT TATA CAGCGGGG		
		— GA—		
GAM1281	KIAA0275	5' AGGACAGCCGCGTGCGCTTC 28672	A	ATAGAA
		GGA TGTAT GTTGTCTT		
		CTT GCGTG CGACAGGA		
		C CGC—		
GAM1281	KIAA0319	3' GCAATTGTGTATATATTCCA 29036	GA	
		TGGAATGTATATA AGTTGT		
		ACCTTATATATGT TTAACG		
		G—		
GAM1281	KIAA0326	3' GGGGCAGTTTCTGTTAGATT 64330	G T	GT
		AAT TA ATAGAA TGTCCT		
		TTA AT TGTCTT ACGGGG		
		G — TG		
GAM1281	KIAA0475	3' ACATTTTATATACATTTT 29481	—	
		GGAATGTATATAGAA GT		

TTTTACATATATTTT CA

A

GAM1281 KIAA0475 3' GGATCTAAATTTCTAATGTGTT 29499 TG A \_\_\_\_ T  
CTA GAA TAT TAGAAGTT GTCC

||| ||| ||||| |||

CTT GTA ATCTTTAA TAGG

GT \_ ATC

GAM1281 KIAA0478 3' GGGGTGGCGGGTGTGTGTTT 29553 TG AGAA TG  
GAA TATAT GT TCCT

||| |||| | |||

TTT GTGTG CG GGGG

GT GG\_ GT

GAM1281 KIAA0513 3' GGGACGACCGCATGCACTCT 28366 A ATAGAA  
GGA TGTAT GTTGCCT

||| |||| |||||

TCT ACGTA CAGCAGGG

C CGC\_

GAM1281 KIAA0515 3' AGGATACCAGGATGTGTGCACT 63802 A GAAGT\_  
CT GGA TGTATATA TGCCT

||| ||||| ||||

TCT ACGTGTGT ATAGGA

C AGGACC

GAM1281 KIAA0523 3' GGATAGCTTCGGCATCCA 67740 A ATATA  
TGGA TGT GAAGTTGTCC

||| ||| |||||

ACCT ACG CTTCGATAGG

\_ G\_

GAM1281 KIAA0530 3' AGATACCTTTTTTGTATATATT 70865 \_\_\_\_ T CT  
T GAATGTATATA GAAG TGTC

||||||| ||| |||

TTTATATATGT TTTC ATAG

TT C A

GAM1281 KIAA0543 3' AGGATGATTTTGTCTAGGTTCT 68932 G TATA TG  
GGAAT TA GAAGT TCCT

|||| | |||| |||

TCTTG AT TTTTA AGGA

G CTG\_ GT

GAM1281 KIAA0546 3' AGGGTAATTTTGTGAAGAGGCA 71305 A\_ GT  
TTCTA AATGT TATAGAAGTT CCT

|||| ||||| |||

TTACG ATGTTTTTAA GGA

GAGA TG

GAM1281 KIAA0557 3' GGGACGGCTTTTACCTTCTA 78003 T TATA  
TGGAA GTA GAAGTTGTCCT

|||| ||| |||||

ATCTT CAT TTTCGGCAGGG

C \_

GAM1281 KIAA0648 3' GGGCTCATTTTATGTTTATTT 82656 T T\_ T  
TA TGGAAATG ATATAGAAGT GTCC

||||| ||||| |||

ATTTTAT TGTATTTTTA CGGG  
 T CT  
 GAM1281 KIAA0663 3' AGGTCCCTTTTGTATATATTCT 29124 TT T  
 GGAATGTATATAGAAG G CCT  
 ||||| ||||| I |||  
 TCTTATATATGTTTTC T GGA  
 CC\_  
 GAM1281 KIAA0680 3' GGGATTTGAATGTGTGTGTTTC 28234 TG GAAGTT  
 GGAA TATATA GTCCT  
 ||| ||||| |||||  
 CTTT GTGTGT TAGGG  
 GT AAGTT\_  
 GAM1281 KIAA0779 3' GGGACGGTTTCTATCTAT 85728 T TT  
 GTA ATAGAAG GTCCT  
 ||| ||||| |||||  
 TAT TATCTTT CAGGG  
 C GG  
 GAM1281 KIAA0789 5' GGGACCAACTTATGTGTGTTCT 63685 TG GA \_  
 GGAA TATATA AGTTG TCCT  
 ||| ||||| ||||| |||||  
 TCTT GTGTAT TCAAC AGGG  
 GT \_ C  
 GAM1281 KIAA0821 3' GGGGCAGCTTCTGAGGTTGCCA 29947 AATGTATA  
 TGG TAGAAGTTGTCCT  
 ||| ||||| |||||  
 ACC GTCTTCGACGGGG  
 GTTGGA\_  
 GAM1281 KIAA0854 3' GGGCAACTTCCTTTTCCA 30099 TGTATATA  
 TGGAA GAAGTTGTCC  
 ||||| ||||| |||||  
 ACCTT CTTCAACGGG  
 TTC\_\_\_\_  
 GAM1281 KIAA0864 3' AGGACAGCATTTTGTATTTGTT 63246 T \_  
 CCA TGGAAATG ATATAGAA GTTGTCTT  
 ||||| ||||| ||||| |||||  
 ACCTTGT TATGTTTT CGACAGGA  
 T A  
 GAM1281 KIAA0905 3' GACAGCTTCTCTTCCA 30030 TGTATAT  
 TGGAA AGAAGTTGTC  
 ||||| ||||| |||||  
 ACCTT TCTTCGACAG  
 C\_\_\_\_  
 GAM1281 KIAA0918 3' AGGATGTGTTTGTATGCATTCT 73131 AGT  
 GGAATGTATATAGA TGTCTT  
 ||||| ||||| |||||  
 TCTTACGTATGTTT GTAGGA  
 GT\_  
 GAM1281 KIAA0972 3' GGATCCTGTGTGTGTTT 30013 TG AAGTT  
 GAA TATATAG GTCC  
 ||| ||||| |||



		CTT GTGTGTC TAGG		
		GT C____		
GAM1281	KIAA0982	3' AGGGTGCTTTGTATATGTTCT 25844		A T GT
		GGAATGTATATAGA G T CCT		
		TCTTGTATATGTTT C G GGA		
		__ TG		
GAM1281	KIAA0997	3' AGGATAACTTGAATATTCATTC 30186		T AG
	TA	TGGAATG ATAT AAGTTGTCCT		
		ATCTTAC TATA TTCAATAGGA		
		T AG		
GAM1281	KIAA1005	3' GATATAATGCATTTC 72280		ATAGAAGT
		TGGAATGTAT TGTC		
		ACTTTACGTA ATAG		
		AT_____		
GAM1281	KIAA1013	3' GGAACATTTTCTATCTATATTC 88889		T T _ T
	CA	TGGAATGTA ATAGAAG TGT CC		
		ACCTTATAT TATCTTT ACA GG		
		C T A		
GAM1281	KIAA1016	3' AGGACAGAAAACAACTTTT 91731		ATA AAG_
		GGAATGT TAG TTGTCCT		
		TTTTACA ATC GACAGGA		
		__ AAAA		
GAM1281	KIAA1018	3' TTTTATGTGTGTTCCA 30357		TG
		TGGAA TATATAGAA		
		ACCTT GTGTATTTT		
		GT		
GAM1281	KIAA1018	3' TTCCACAGTTTTATGTGTGTTTC 30355		TG G CCT
	CA	TGGAA TATATAGAA TTGT		
		ACCTT GTGTATTTT GACA		
		GT _ CCTTT		
GAM1281	KIAA1024	3' GGGACTGTCTTTTCTATGTTTG 69062		T TT__
	TTCT	AATG ATATAGAAG GTCCT		
		TTGT TGTATCTTT CAGGG		
		T TCTGT		
GAM1281	KIAA1025	3' GGACAGTGGGTGTGTAC 63976		GAA
		GTATATA GTTGTCC		
		CATGTGT TGACAGG		
		GGG		
GAM1281	KIAA1025	3' AGCATGCTTGTATGTATATTC 63973		G _ CCT
	A	TGGAATGTATATA AAGT TGT		

		ACTTTATATGTAT TTCG ACG		
		G T A		
GAM1281 KIAA1041	3'	AGGGTGATGTGTACATATCTA 30125	_	AGAA TG
		TGGA ATGTATAT GT TCCT		
		ATCT TACATGTG TA GGGA		
		A ____ GT		
GAM1281 KIAA1074	3'	GGGCTGTTTATGTGACATTTT 29882	_	AGTT
		GGAATGT ATATAGA GTCC		
		TTTTACA TGTATTT CGGG		
		G GT__		
GAM1281 KIAA1077	3'	GGGACATAAGTATATACAT 72908		GAAGT
		ATGTATATA TGCCT		
		TACATATAT ACAGGG		
		GAAT_		
GAM1281 KIAA1078	3'	AGGATAATTTAATAAGCATTTT 65119	A	AG
A		TGGAATGT TAT AAGTTGTCCT		
		ATTTTACG ATA TTTAATAGGA		
		A A_		
GAM1281 KIAA1102	3'	AGGATAAATTTAATGCATTTCA 69011	A	AG
		TGGAATGTAT TAGA TTGTCCT		
		ACTTTACGTA ATTT AATAGGA		
		_ A_		
GAM1281 KIAA1161	3'	GGGGCAGTTTCTCCCATAC 81757	AT_	GT
		GTAT AGAA TGCCT		
		CATA TCTT ACGGGG		
		CCC TG		
GAM1281 KIAA1170	3'	AGGATTTTTATTTGTGAATATT 69843	A	_ TT
TCA		TGGAATGT TATAGA AG GTCCT		
		ACTTTATA GTGTTT TT TAGGA		
		A A TT		
GAM1281 KIAA1219	3'	GGGGTGGATGAGTGTGGCATTTC 61371	_	AGAAG TG
C		GGAATGT ATAT T TCCT		
		CCTTACG TGTG G GGGG		
		G AGTA_ GT		
GAM1281 KIAA1223	3'	ATTTTATAACATTCC 71143	A	
		GGAATGT TATAGAAGT		
		CCTTACA ATATTTTAA		
		-		
GAM1281 KIAA1265	3'	TTACTATTTTTGTATATATTT 70795		T CCT
		GAATGTATATAGAAGT GT		

		TTTATATATGTTTTTA CA		
		T TTG		
GAM1281	KIAA1266	3' AGGGCGGTTTTGCAGACATCTC 66113	GA	ATATA TT
	A	TG ATGT GAAG GTCCT		
		AC TACA TTTT CGGGA		
		TC GACG_ GG		
GAM1281	KIAA1271	3' AGGATAAGTATATATATATT 69537	GAAG_	
	TC	GGAATGTATATA TTGTCCT		
		CTTTATATATAT AATAGGA		
		ATATG		
GAM1281	KIAA1318	3' ACTTCTCTATACATTTCA 67304	T	
		TGGAATGTATA AGAAGT		
		ACTTTACATAT TCTTCA		
		C		
GAM1281	KIAA1322	3' AGGATGGCCACTGATGTGTGTT 72731	TG	_ AA TG
	T	GAA TATAT AG GT TCCT		
		TTT GTGTA TC CG AGGA		
		GT G AC GT		
GAM1281	KIAA1328	3' AGGATGTAAATTTGTATATAAT 61641	A	AGT_
	CTA	TGGA TGTATATAGA TGTCCCT		
		ATCT ATATATGTTT GTAGGA		
		A AAAT		
GAM1281	KIAA1371	3' GGGATAATGTCATGTGTATCTA 89047	ATG	_ A
		TGGA TATATA GA GTTGTCCCT		
		ATCT ATGTGT CT TAATAGGG		
		_ A G		
GAM1281	KIAA1371	3' GGCACCTTTTATGTTTATTCCA 89046	T	T
		TGGAATG ATATAGAAGT GTC		
		ACCTTAT TGTATTTTCA CGG		
		T _		
GAM1281	KIAA1374	3' AGGTTTTATGTTATGTATATTT 61240	AAGTTGT	
	TA	TGGAATGTATATAG CCT		
		ATTTTATATGTATT GGA		
		GTATTTT		
GAM1281	KIAA1389	3' GGTTTTTCTGTGTGCTTTCA 69767	T	TTGT
		TGGAA GTATATAGAAG CC		
		ACTTT CGTGTGTCTTT GG		
		_ TT_		
GAM1281	KIAA1434	3' GGGATGGCTTATTTGCATCTA 69617	A	TATAG TG
		TGGA TGTA AAGT TCCT		

		ATCT ACGT    TTCG AGGG	
		_ TTA_    GT	
GAM1281	KIAA1443	3' AGGGCAGTGAAGGTAGGTTTCA 63825	G ATAGAA
		TGGAAT TAT    GTTGTCT	
		ACTTTG ATG    TGACGGGA	
		G GAAG_	
GAM1281	KIAA1458	3' GGGACAATTAATGCATTTT 69005	ATAGA
		GGAATGTAT    AGTTGTCT	
		TTTTACGTA    TTAACAGGG	
		A_	
GAM1281	KIAA1468	3' GGAATTGTGTGCATTCCA 91775	GAAGTTG
		TGGAATGTATATA    TCC	
		ACCTTACGTGTGT    AGG	
		TA_	
GAM1281	KIAA1495	3' AGATATCTATTTCTGTACATT 73185	T    _    CT
		TTA    GAATGTA ATAGAAGT TGTC	
		TTTACAT TGTCTTTA ATAG	
		_    TCT A	
GAM1281	KIAA1508	5' AGGATGGCTTTCTCCAGTTCTA 61875	GTATATA    TG
		TGGAAT    GAAGT TCCT	
		ATCTTG    TTTCG AGGA	
		ACCTC_    GT	
GAM1281	KIAA1546	3' TAAGATAACTTCTGTGTGCATT 67910	CT
		TT    GGAATGTATATAGAAGTTGTC	
		TTTTACGTGTGTCTTCAATAG	
		AATC	
GAM1281	KIAA1559	3' TTTCTACTTTTGTATGTGTTT 73079	TG    TGTCT
		GAA TATATAGAAGT	
		TTT GTATGTTTTCA	
		GT    TCTTTA	
GAM1281	KIAA1560	3' GGGGCAGAATATGCATGCATTT 64178	A GAAG
		T    GGAATGTAT TA    TTGTCT	
		TTTTACGTA GT    GACGGGG	
		C ATAA	
GAM1281	KIAA1582	5' AGGGCAACTTCACTGGACATAC 65365	A ATATA
		CA    TGG ATGT    GAAGTTGTCT	
		ACC TACA    CTTCAACGGGA	
		A GGTCA	
GAM1281	KIAA1600	3' GGGAACAGAACTACTGTGTACA 71444	A _ _
		TTTCA    AATGTATATAG AGT TGT CCT	

TTACATGTGTC TCA ACA GGG  
 A AG A  
 GAM1281 KIAA1649 5' GGGACCCGCCTTTCTGTGTTGT 50276 TG \_ TT\_\_\_\_  
 GTTCT A TA TATAGAAG GTCCT  
 I || ||||| ||||  
 T GT GTGTCTTT CAGGG  
 GT T CCGCC  
 GAM1281 KIAA1649 3' GGGACCCGCCTTTCTGTGTTGT 66980 TG \_ TT\_\_\_\_  
 GTTCT A TA TATAGAAG GTCCT  
 I || ||||| ||||  
 T GT GTGTCTTT CAGGG  
 GT T CCGCC  
 GAM1281 KIAA1673 3' GCTTTTATACATTTCA 70784 T  
 TGGAATGTATA AGAAGT  
 ||||| ||||  
 ACTTTACATAT TTTTCG  
 —  
 GAM1281 KIAA1674 3' CTTCTGTCATGTGTTCTA 68779 TG \_  
 TGGAA TAT ATAGAAG  
 |||| || |||||  
 ATCTT GTA TGTCTTC  
 GT C  
 GAM1281 KIAA1719 3' GGACAATGGTTTATTCCA 68167 TATAT AA  
 TGGAATG AG GTTGTCC  
 ||||| || |||||  
 ACCTTAT TT TAACAGG  
 \_\_\_\_ GG  
 GAM1281 KIAA1729 3' AGGACATGTTATATATAATCCA 89125 A AAGT  
 TGGA TGTATATAG TGTCTT  
 ||| ||||| ||||  
 ACCT ATATATATT ACAGGA  
 A GT\_\_\_\_  
 GAM1281 KIAA1755 5' GGGTGACTTCTACCTCCA 61352 ATGTATA TG  
 TGGA TAGAAGT TCC  
 ||| ||||| |||  
 ACCT ATCTTCA GGG  
 CC\_\_\_\_ GT  
 GAM1281 KIAA1789 5' AGGATAGTTTTGAGGGAACATT 67096 ATATA\_ GT  
 TCA TGGAATGT GAA TGTCTT  
 ||||| || |||||  
 ACTTTACA TTT ATAGGA  
 AGGGAG TG  
 GAM1281 KIAA1795 3' ATATTTTCTATGTGTGTTTCA 72148 TG T  
 TGGA TATATAGAAG TGT  
 |||| ||||| |||  
 ACTTT GTGTATCTTT ATA  
 GT T  
 GAM1281 KIAA1805 3' AGGACATGGTATATGCACTCT 79967 A GAAGT  
 GGA TGTATATA TGTCTT  
 || ||||| ||||

TCT ACGTATAT ACAGGA  
 C GGT\_\_  
 GAM1281 KIAA1878 3' AGGTGTTTTAGGTACATTCCA 91708 A GTTGT  
 TGG AATGTAT TAGAA CCT  
 ||||| ||| ||  
 ACCTTACATG ATTTT GGA  
 G GT\_\_  
 GAM1281 KIAA1906 3' ATTTTATATACATTT 73189  
 GAATGTATATAGAAGT  
 |||||  
 TTTACATATATTTTAA  
  
 GAM1281 KIAA1922 3' GGGATAGCTACTTGCATGCTA 73637 A TAT A  
 TGG ATGTA AG AGTTGTCCT  
 ||| ||| || |||||  
 ATC TACGT TC TCGATAGGG  
 G \_ A  
 GAM1281 KIAA1924 3' AGGACGGCTTCTTGCGGCTCT 73664 A\_ TAT  
 GGA TGTA AGAAGTTGTCCT  
 ||| ||| |||||  
 TCT GCGT TCTTCGGCAGGA  
 CG \_  
 GAM1281 KIAA1939 5' AGGACAGCTGAATCTGCTTTTT 45760 T T AGA  
 A TGGAA GTA AT AGTTGTCCT  
 |||| ||| || |||||  
 ATTTT CGT TA TCGACAGGA  
 T C AG\_  
 GAM1281 LEFTB 3' GGGACTTGACTTGTGTGTGTTT 40654 TG GA \_  
 C GGAA TATATA AGTT GTCCT  
 |||| |||| ||| ||||  
 CTTT GTGTGT TCAG CAGGG  
 GT \_ TT  
 GAM1281 LGP1 3' AGGACAATTCTGAAGTGTATTC 50650 A\_ G  
 TA TGG AATGTAT TAGAA TTGTCCT  
 ||||| |||| |||||  
 ATCTTATGTG GTCTT AACAGGA  
 AA \_  
 GAM1281 LHFP 3' ATTTCTATATTCATTTT 19335 T  
 GGAATG ATATAGAAGT  
 |||| |||||  
 TTTTAC TATATCTTTA  
 T  
 GAM1281 LHFP 3' GGCAACTTTCTGTCCA 19337 ATGTATA \_  
 TGG A TAGAA GTTGTC  
 ||| |||| |||||  
 ACCT GTCTT CAACGG  
 \_ T  
 GAM1281 LRP1B 3' AGGATTACTTTTGTATGTTCCA 37667 GT T  
 TGG AAT ATATAGAAGT GTCCT  
 |||| ||||| |||||

			ACCTTG TATGTTTTCA TAGGA		
			— T		
GAM1281	MAP3K2	3'	AGGATGATTTCACTAGGCATTT 21733	ATATA	TG
			GAATGT GAAGT TCCT		
			TTTACG CTTTA AGGA		
			GATCA GT		
GAM1281	MBLL39	3'	AGGAGATCTGTATAATATTCTA 58603	—	AGTTG
			TGGAATGT ATATAGA TCCT		
			ATCTTATA TATGTCT AGGA		
			A AG—		
GAM1281	MDS028	3'	AGGATAGGGAATATGCATTACA 37461	G	AGAAG
			TG AATGTATAT TTGTCCT		
			AC TTACGTATA GATAGGA		
			A AGG—		
GAM1281	METAP2	3'	AGGAATGACTTATACGTTTT 60166	TAGA	TG—
			GGAATGTATA AGT T CCT		
			TTTTGCATAT TCA A GGA		
			— GT A		
GAM1281	MFN2	3'	AGGACTGTGGCTTGTGTGTGTC 29596	ATG	G —
	CA		GGA TATATA AAGTT GTCCT		
			CCT GTGTGT TTCGG CAGGA		
			— G TGT		
GAM1281	MGC10772	3'	AGGATAATAAAGGTGTGTGATC 47530	A GT	AGAA
	T		GGA T ATAT GTTGTCT		
			TCT G TGTG TAATAGGA		
			A TG GAAA		
GAM1281	MGC10960	3'	AGGACGTTGTGTGTATTTCT 51002	T	G GT
			GGAA GTATATA AA TGTCCT		
			TCTT TATGTGT TT GCAGGA		
			— G —		
GAM1281	MGC14480	3'	GGGACAATAGTGTGCATGCCA 58749	A	AGAA
			TGG ATGTATAT GTTGTCT		
			ACC TACGTGTG TAACAGGG		
			G A—		
GAM1281	MGC1842	3'	AGGATGGCTTCTCAGGGCATGC 65641	A	ATAT TG
	CA		TGG ATGT AGAAGT TCCT		
			ACC TACG TCTTCG AGGA		
			G GGAC GT		
GAM1281	MGC22014	3'	AGGACAGCTTCTGTCCTCTCT 64485	ATGTAT	
			GGA ATAGAAGTTGTCCT		

		TCT TGTCTTCGACAGGA		
		CTCC__		
GAM1281	MGC23937	3' AGGGTGGTTTCTTGCTGGATTT 58953	G TAT	TG
	CA	TGGAAT TA AGAAGT TCCT		
		ACTTTA GT TCTTTG GGGA		
		G CGT GT		
GAM1281	MGC23980	3' ATTTCTATATATATTT 58758		
		GAATGTATATAGAAGT		
		TTTATATATATCTTTA		
GAM1281	MGC26651	3' GGTCATTTTGTATGTATGTT 58306	G T T	
		AATGTATATA AAG TG CC		
		TTGTATGTAT TTT AC GG		
		G T T		
GAM1281	MGC29667	3' AGGGCAACTTCAGTGTTTTCCA 58331	TGT	A
		TGGAA ATAT GAAGTTGTCCT		
		ACCTT TGTG CTTCAACGGGA		
		T__ A		
GAM1281	MGC3113	3' GGCTAATTTTTGTATATTTT 43849	T	T
		AA GTATATAGAAGTTG CC		
		TT TATATGTTTTTAAT GG		
		T C		
GAM1281	MGC34869	3' GGGGTAAGTGCCTTGCTTCT 58095	T TATAGA	GT
		GGAA GTA AGTT CCT		
		TCTT CGT TCAA GGG		
		_ TCCG__ TG		
GAM1281	MGC34923	3' GGACAAGTTGTGTTTCT 58522	TGTAT	G G
		GGAA ATA AA TTGTCC		
		TCTT TGT TT AACAGG		
		_____ G G		
GAM1281	MGC4309	3' TGTGGCGGTTTCTGTGTACGTT 44137	TT	CT
	T	GAATGTATATAGAAG GTC		
		TTTGCATGTGTCTTT CGG		
		GG TGTG		
GAM1281	MGC4309	3' AGTTGATTTCTGTGTCTATTTT 44126	T	TCCT
	A	TGGAATG ATATAGAAGTTG		
		ACTTTAT TGTGTCTTTAGT		
		C TGA		
GAM1281	MGC4643	3' GGATGGCCAGTGCCTCCA 51155	A	ATAGAA TG
		TGGA TGTAT GT TCC		



ACCT ACGTG CG AGG  
 C AC\_\_\_ GT  
 GAM1281 MGC4796 3' TGGGATGCCCTCTTTTCTATAT 61498 T TT\_\_\_\_  
 TTATTTCA G ATATAGAAG GTCCT G  
 | ||||| ||| |  
 T TATATCTTT TAGGG T  
 T TCTCCCG  
 GAM1281 MGC4840 3' GGGACAGAAATCTGTGT 71570 AG\_  
 ATATAGA TTGTCCT  
 ||||| |||||  
 TGTGTCT GACAGGG  
 AAA  
 GAM1281 MMD 3' AGGTTTATTTTGTATATGTTT 59805 GTTGT  
 GAATGTATATAGAA CCT  
 ||||| |||  
 TTTGTATATGTTT GGA  
 ATTT\_  
 GAM1281 MPZL1 3' AGGATATGTATAAATATTCTA 14203 A GAAGT  
 TGAATGT TATA TGTCTT  
 ||||| ||| |||||  
 ATCTTATA ATAT ATAGGA  
 A GT\_\_\_  
 GAM1281 MRPL34 3' CTTCTGTAAATATTTCA 43742 A  
 TGAATGT TATAGAAG  
 ||||| |||||  
 ACTTTATA ATGTCTTC  
 A  
 GAM1281 MRPL35 3' AGGATAACAATAGAATGTTCTA 33539 ATA GAA  
 TGAATGT TA GTTGTCTT  
 ||||| || |||||  
 ATCTTGTA AT CAATAGGA  
 AG\_ AA\_  
 GAM1281 MRPS21 5' AGGATGACTTCCATGTGCTCCA 38641 AT A TG  
 TGGA GTATAT GAAGT TCCT  
 ||| ||||| ||||| |||||  
 ACCT CGTGTA CTTCA AGGA  
 \_ C GT  
 GAM1281 MSTP032 3' GTAGGCAATTCTATGTAGGTTT 47442 G G CT  
 T GGAAT TATATAGAA TTGTC  
 ||||| ||||| |||||  
 TTTTG ATGTATCTT AACGG  
 G \_ ATGG  
 GAM1281 MYO3B 3' AGGATAATTGCCTGTGTTTA 57300 T A\_  
 TG ATATAG AGTTGTCCT  
 || ||||| |||||  
 AT TGTGTC TTAATAGGA  
 T CG  
 GAM1281 N4BP2 3' CTTCTGTGTGCATTTTA 36404  
 TGAATGTATATAGAAG  
 ||||| ||||| |||||

ATTTTACGTGTGTCTTC

GAM1281	N4BP3	3'	GGGGCAGCTGCCATTCGTTCCA 66268	TATATAGA
			TGGAATG AGTTGTCCT	
			ACCTTGC TCGACGGGG	
			TTACCG__	
GAM1281	NDRG4	3'	AGGACTGCGTTGTATGCTTTCC 39981	T AA T
	A		TGGAA GTATATAG GT GTCCT	
			ACCTT CGTATGTT CG CAGGA	
			T G_ T	
GAM1281	NDRG4	3'	AGGACTGCGTTGTATGCTTTCC 43284	T AA T
	A		TGGAA GTATATAG GT GTCCT	
			ACCTT CGTATGTT CG CAGGA	
			T G_ T	
GAM1281	NEK1	3'	GGGTAACCTTTGAGTTTCA 95875	GTATATA GT
			TGGAAT GAAGTT CC	
			ACTTTG TTTCAA GG	
			AG_____ TG	
GAM1281	NEK11	3'	AGGAAGATATGTGTGTATTTC 45623	GAAGTTG
			TGGAATGTATATA TCCT	
			ACTTTATGTGTGT AGGA	
			ATAGA__	
GAM1281	NPAS3	3'	AGGGTGGTTTTTTGTTTCTGTTC 42095	TAT TG
	C		GGAATG ATAGAAGT TCCT	
			CCTTGT TGTTTTTG GGGA	
			CTT GT	
GAM1281	NT5C1B	3'	AGGATAATTAGATAGGTATTTC 71225	TA AGA
	A		TGGAATG TAT AGTTGTCCT	
			ACTTTAT ATA TTAATAGGA	
			GG GA_	
GAM1281	NUDT11	3'	ACTTTTGTATATGTTT 59994	
			GAATGTATATAGAAGT	
			TTTGTATATGTTTTCA	
GAM1281	NUP160	3'	GCTGCTTTTGTATATGATTC 87596	_ T
			GAAT GTATATAGAAGT GT	
			CTTA TATATGTTTTCG CG	
			G T	
GAM1281	NY-REN-60	3'	AGTGGATTTTTGTGTGCATTT 67106	GTCCT
			GAATGTATATAGAAGTT	

		TTTACGTGTGTTTTTAG		
		GTGA		
GAM1281	OAZ2	3' GGGCTTCTCTGTGTGCATTT 10308	A TT	
		GAATGTATATAGA G GTCC		
		TTTACGTGTGTCT C CGGG		
		_ TT		
GAM1281	OBTP	3' GGGGTGATTTTTGCTCTTGTCC 34246	ATGTATA TG	
		GGA TAGAAGT TCCT		
		CCT GTTTTGA GGGG		
		GTTCTC_ GT		
GAM1281	OCIA	3' GGTTTGACTTCTATGGTGT TTT 35210	GTA T_ T	
	A	TGGAAT TATAGAAGTTG CC		
		ATTTTG GTATCTTCAGT GG		
		TG_ TT		
GAM1281	OCLM	3' CGGATTCTGTGTGTATTCT 42348	AGTT T	
		GGAATGTATATAGA GTCC		
		TCTTATGTGTGTCT TAGG		
		_ CT		
GAM1281	OR2C3	3' TTTTGTGTGCATTTTA 75452		
		TGGAATGTATATAGAA		
		ATTTTACGTGTGTTTT		
GAM1281	OSBPL5	3' GGATGTGTCTGTGTTCCA 72687	ATGT AGT	
		TGGA ATATAGA TGTCC		
		ACCT TGTGTCT GTAGG		
		_ GT_		
GAM1281	OSBPL7	3' AGGGCGAATTGCTATGACATTC 34805	A AAG_	
	CA	TGGAATGT TATAG TTGTCCT		
		ACCTTACA GTATC AGCGGGA		
		_ GTTA		
GAM1281	P5-1	5' AGGATGTTTTGGATGCATTCTA 21914	A GT	
		TGGAATGTAT TAGAA TGTCTT		
		ATCTTACGTA GTTTT GTAGGA		
		G _		
GAM1281	PDZD2	3' TAGGACAATCAATCATTTTGTA 80879		
		TGATTTT TATATAGAA GTTGTCTT A		
		GTATGTTTT TAACAGGA T		
		ACTAAC		
GAM1281	PFDN1	3' GGGCAACGGTGTGATCCA 10513	ATG AGAA	
		TGGA TATAT GTTGTCC		

ACCT GTGTG CAACGGG  
 A\_\_ G\_\_  
 GAM1281 PIP3-E 3' GGACAGCTTGGTGTTCCTCA 66809 TGT AG  
 TGGAA ATAT AAGTTGTCC  
 |||| ||| |||||  
 ACTTT TGTG TTCGACAGG  
 \_\_ G\_  
 GAM1281 POF1B 3' AGGATGAAAATTTTACATTTC 46219 TATAGAAG TG  
 TGAATGTA T TCCT  
 ||||| | |||  
 ACTTTACAT A AGGA  
 TTTAAA\_\_GT  
 GAM1281 PRO0149 5' GGGGTGATAGATATATTCTA 26106 ATAGAA TG  
 TGAATGTAT GT TCCT  
 ||||| || |||  
 ATCTTATATA TA GGGG  
 GA\_\_GT  
 GAM1281 PRO0529 5' AGGCCATCTGTGTGTGTGTCT 25986 \_TG AGT T  
 GGA A TATATAGA TG CCT  
 ||| ||||| |||  
 TCT T GTGTGTCT AC GGA  
 G GT \_\_ C  
 GAM1281 PRO1430 3' AGGTTTTTTTATACATTTC 37748 T G  
 TGAATGTATA AGAA TT  
 ||||| ||| ||  
 ACTTTACATAT TTTT GA  
 T G  
 GAM1281 PRO2730 3' GGGATGACTTGCTGTGTTCC 47419 ATGT \_ TG  
 GGA ATATAG AAGT TCCT  
 || |||| ||| |||  
 CCT TGTGTC TTCA AGGG  
 \_\_ G GT  
 GAM1281 PRRG1 3' CTTTACTGTACGTTCTA 6284 \_  
 TGAATGTATA TAGAAG  
 ||||| |||||  
 ATCTTGCATGT ATTTTC  
 C  
 GAM1281 PSMD10 3' GATGTTTCTATGTGGATTCT 10993 G GTT  
 GGAAT TATATAGAA GTC  
 |||| ||||| |||  
 TCTTA GTGTATCTT TAG  
 G TG\_  
 GAM1281 PTRF 3' GGGATGGCACACTGATGTGTTT 63507 TG A AA\_ TG  
 GAA TAT TAG GT TCCT  
 || ||| || |||  
 TTT GTA GTC CG AGGG  
 GT \_ ACA GT  
 GAM1281 RANBP6 3' AGGATGAATGTGATGTTTATAT 61634 T GAAG\_\_TG  
 TCT GGAATGTA ATA T TCCT  
 ||||| || | |||

			TCTTATAT TGT    A AGGA		
			T AGTGTA GT		
GAM1281	RAP140	3'	GGACAATTTTCTAGTTCT    30845	GTATA    _	
			GGAAT    TAGAAG TTGTCC		
			TCTTG    ATCTTT AACAGG		
			_____ T		
GAM1281	RBM14	3'	GGGACAGTCAGTTGGTATGTAT 20910	_    ATAGAAG	
	CCA		TGGA ATGTAT    TTGTCCT		
			ACCT TGTATG    GACAGGG		
			A    GTTGA CT		
GAM1281	RC3	3'	GGGTTTTATTTTTATATACATT 30921	TGT_	
	TCA		TGGAATGTATATAGAAGT    CCT		
			ACTTTACATATATTTTTTA    GGG		
			TTTT    G		
GAM1281	RGS7	3'	TTTGTGTGTACATTCCA    11330	G	
			TGGAATGTATATA AAG		
			ACCTTACATGTGT TTT		
			G		
GAM1281	RHOBTB1	3'	GGGATAGTTACAAATGCATCCA 91441	A    ATAG G	
			TGGA TGTAT    AA TTGTCCT		
			ACCT ACGTA    TT GATAGGG		
			_    AACA    _		
GAM1281	RNF38	3'	AGCTTGACTTCTCATATGTGTT 42933	TG    _    TC	
	CT		GGAA TATAT AGAAGTTG CT		
			TCTT GTATA TCTTCAGT GA		
			GT    C    TC		
GAM1281	RNP24	3'	GGACA ACTGTTGCATGCCA    22359	A    TATAGA	
			TGG ATGTA    AGTTGTCC		
			ACC TACGT    TCAACAGG		
			G    TG_____		
GAM1281	RYK	3'	AGGGCATGATTTTCTGTGTACA 82614	T_____	
	TTT		GAATGTATATAGAAG    TGTCCT		
			TTTACATGTGTCTTT    ACGGGA		
			TAGT		
GAM1281	SAE1	3'	AGGGTGGCTGTCTTTGTTCCA    18530	GTATAT    _    TG	
			TGGAAT    AGA AGT TCCT		
			ACCTTG    TCT TCG GGGA		
			TT_____ G GT		
GAM1281	SARM	3'	GGGTGGTTCTGCATTCC    30612	ATAT    G TG	
			GGAATGT    AGAA T TCC		

			CCTTACG TCTT G GGG		
			_____GT		
GAM1281	SCGN	3'	GGGCAGCTGAGTGCATTC 22787	ATAGA	
			GAATGTAT AGTTGTCC		
			CTTACGTG TCGACGGG		
			AG__		
GAM1281	SCN12A	3'	AGCTTTCTGTTTGTGTTCCA 26222	TG T _	
			TGGAA TA ATAGAA GTT		
			ACCTT GT TGTCTT CGA		
			GT T T		
GAM1281	SDFR1	3'	AGGGTGATCTAGCCAGGTACAT 24863	ATAGAA__ TG	
			TTTA GGAATGTAT GT TCCT		
			TTTTACATG TA GGGA		
			GACCGATC GT		
GAM1281	SDFR1	3'	AGGGTGATCTAGCCAGGTACAT 33913	ATAGAA__ TG	
			TTTA GGAATGTAT GT TCCT		
			TTTTACATG TA GGGA		
			GACCGATC GT		
GAM1281	SEC14L2	3'	GGGGTAGCTTTTGGCTTTTCC 24874	TGTATA GT	
			GGAA TAGAAGTT CCT		
			CCTT GTTTTCGA GGG		
			TTCG__ TG		
GAM1281	SEC63L	3'	AGGAAGCTTTTTTTGTATTCAT 23301	T TTG__	
			TTT GGAATG ATATAGAAG TCCT		
			TTTTAC TATGTTTT AGGA		
			T TTCGA		
GAM1281	SGKL	3'	GGGGTGACTTTTCTTATATT 25144	TAT TG	
			AATGTA AGAAGT TCCT		
			TTATAT TTTTCA GGGG		
			TC_ GT		
GAM1281	SH3BGRL	3'	AGGGCAACTTTTAAAATATT 61940	ATA	
			AATGT TAGAAGTTGTCCT		
			TTATA ATTTTCAACGGGA		
			AA_		
GAM1281	SLC38A4	3'	AGGATGGTTGTGTATGTGTTT 35873	TG G G TG	
			GAA TATATA AA T TCCT		
			TTT GTATGT TT G AGGA		
			GT G _GT		
GAM1281	SLC5A6	3'	GGGATGAGTCTTGGTGTGTTCT 40832	TG AT AG TG	
			GGAA TAT AGA T TCCT		

TCTT GTG TCT A AGGG  
 GT GT G\_ GT  
 GAM1281 SLC5A7 3' GGGCTAATTTGTATGTTTCCA 41514 TGT G \_  
 TGGAA ATATA AAGTT GTCC  
 |||| |||| |||| ||||  
 ACCTT TGTAT TTTAA CGGG  
 \_ G T  
 GAM1281 SLC6A14 3' TAATTTCTATTGTGTTTCA 23357 TG T  
 TGGAA TA ATAGAAGTTG  
 |||| || |||| ||||  
 ACTTT GT TATCTTTAAT  
 GT \_  
 GAM1281 SLC7A11 3' TTTCTTTATACATTTTA 26759 T  
 TGGAATGTATA AGAAG  
 |||| |||| ||||  
 ATTTTACATAT TCTTT  
 T  
 GAM1281 SMAP1 3' AGGGCAGCTTTGCTCATATTTTC 41651 ATATA  
 GGAATGT GAAGTTGTCCT  
 |||| |||| ||||  
 CTTTATA TTTCGACGGGA  
 CTCG\_  
 GAM1281 SNRPB2 3' AACTTTTATTTGTATTCT 11856 T  
 GGAATGTA ATAGAAGTT  
 |||| |||| ||||  
 TCTTATGT TATTTTCAA  
 T  
 GAM1281 SNRPF 3' GGGATTTTTTTTTATATATATTT 60171 TT  
 C GGAATGTATATAGAAG GTCCT  
 |||| |||| ||||  
 CTTTATATATATTTT TAGGG  
 TT  
 GAM1281 STAF65(gamma) 3' AGGACAGCCTTGTGCATATTTTC 29425 A AA  
 A TGGAAATGT TATAG GTTGTCTT  
 |||| |||| ||||  
 ACTTTATA GTGTT CGACAGGA  
 C C\_  
 GAM1281 STX6 3' AGGAATACGAGCTTCTGGGTAT 19485 A TG\_\_\_\_  
 GTTTC ATGTAT TAGAAGT TCCT  
 |||| |||| ||||  
 TGTATG GTCTTCG AGGA  
 G AGCATA  
 GAM1281 SYNE-2 3' AGGGCAGCTTTTCAGATTGTGTT 30797 TG TATA\_  
 CC GGAA TA GAAGTTGTCCT  
 |||| || |||| ||||  
 CCTT GT TTTCGACGGGA  
 GT TAGAC  
 GAM1281 SYTL4 3' TTCTGTGTATAATCTA 54947 A  
 TGGA TGTATATAGAA  
 |||| |||| ||||

			ATCT ATATGTGTCTT		
			A		
GAM1281	TCF-3	3'	GCTTCTTCTGTGTGATTTC 48426	TT	
			GGAATGTATATAGAAG GT		
			CTTTATGTGTGTCTTC CG		
			TT		
GAM1281	TCF17	3'	GGTAATATTTTTATAGCATTTT 18943	A	TGT_ T
	A		TGGAATGT TATAGAAGT CC		
			ATTTTACG ATATTTTTA GG		
			TAAT		
GAM1281	TIMM22	3'	AGGACAGTTTCTGTACCACACC 78311	AA A_	GT
	A		TGG TGT TATAGAA TGTCCT		
			ACC ACA ATGTCTT ACAGGA		
			CC TG		
GAM1281	TIX1	3'	AGGACAGCTCACTGTG 61736	A_	
			TATAG AGTTGTCCT		
			GTGTC TCGACAGGA		
			AC		
GAM1281	TPD52L1	3'	AGGATGATTTACTATAAATTTC 12361	GTA _	TG
	A		TGGAAT TATAG AAGT TCCT		
			ACTTTA ATATC TTTA AGGA		
			A_ A GT		
GAM1281	TREX1	5'	AGGGTTCCAGTGTGTGTTCCA 53276	TG A_	GTTG
			TGGAA TATAT GAA TCCT		
			ACCTT GTGTG CTT GGGA		
			GT AC _		
GAM1281	TRIM6	3'	AGGATGATTTCTTCCAGCTTTT 54131	T_ ATAT	TG
	CCA		TGGAA GT AGAAGT TCCT		
			ACCTT CG TCTTTA AGGA		
			TT ACCT GT		
GAM1281	TU12B1-TY	3'	GCTTCTGTGTGTTTTT 33397	TG	
			GAA TATATAGAAGT		
			CTT GTGTGTCTTCG		
			TT		
GAM1281	URG4	3'	AGGGCAGGGACTGTACATTCT 35502	TAGAAG	
			GGAATGTATA TTGTCCT		
			TCTTACATGT GACGGGA		
			CAGG_		
GAM1281	WDR12	5'	AGGGCAACCTCGTGCTTTCT 80018	T ATA A	
			GGAA GTAT GA GTTGTCTT		



TCTT CGTG CT CAACGGGA  
 T \_\_\_\_ C  
 GAM1281 ZIM3 3' GGGATGATTTCTATAATTC 53539 GTA TG  
 GAAT TATAGAAGT TCCT  
 ||| ||||| |||  
 CTTA ATATCTTTA AGGG  
 \_\_\_\_ GT  
 GAM1281 ZNF11B 3' CTAGGATGGCTTTTGTAGGAA 73983 T\_\_\_\_ TG  
 GTGATATTCT ATAGAAGT TCCT AG  
 ||||| ||| ||  
 TGTTCG AGGA TC  
 TGAAGGAT GT  
 GAM1281 ZNF238 5' TTTCTTGTATGTTCCA 20976 T  
 TGGAATGTATA AGAAG  
 ||||| |||  
 ACCTTGTATGT TCTTT  
 -  
 GAM1281 ZNF262 3' GGGTGGCAGGTGTATTTCT 17488 T AGAA TG  
 GGAA GTATAT GT TCC  
 ||| ||||| || |||  
 TCTT TATGTG CG GGG  
 - GA\_\_ GT  
 GAM1281 ZNF286 3' AGGACCAATTCTGTATGCATCT 40294 A GTT  
 A TGGA TGTATATAGAA GTCCT  
 ||| ||||| |||  
 ATCT ACGTATGTCTT CAGGA  
 - AAC  
 GAM1281 ZNF31 3' AGGACTCAATGTATATATCT 64981 A GAAGTT  
 GGA TGTATATA GTCCT  
 ||| ||||| |||  
 TCT ATATATGT CAGGA  
 - AACT\_\_  
 GAM1281 ZNF33A 3' CTAGGACAGCTTTTGTAGGAA 91347 T\_\_\_\_  
 GTGATATTCTA ATAGAAGTTGTCCT AG  
 ||||| ||| ||  
 TGTTCGACAGGA TC  
 TGAAGGAT  
 GAM1281 ZNF33A 3' GGGTACATATGTGAACATTCCA 91352 A GAAGT \_  
 TGGAATGT TATA TGT CCT  
 ||||| ||| ||| |||  
 ACCTTACA GTGT ACA GGG  
 A AT\_\_ T  
 GAM1281 ZW10 3' GGGAGCTATATACATTGTA 16368 G AAGTTG  
 TG AATGTATATAG TCC  
 || ||||| |||  
 AT TTACATATATC GGG  
 G GA\_\_\_\_  
 GAM1281 LOC114932 3' GGAAGATGGTTTTGTATATATT 72714 \_\_ G T  
 TT GGAATGTATATAGAA GTT TCC  
 ||||| ||| |||

	TTTTATATATGTTTT TAG AGG	
	GG A	
GAM1281 LOC115294 3'	GGGTTGCTGTATATATATTCC 73016	GA TG
	GGAATGTATATA AGT TCC	
	CCTTATATATAT TCG GGG	
	G_ TT	
GAM1281 LOC120105 3'	GGCAACATTGTTCCA 75514	GTATATA A
	TGGAAT GA GTTGTC	
	ACCTTG TT CAACGG	
	_____ A	
GAM1281 LOC120892 3'	GGACAAC TAGTACATTT 74035	ATAGA
	GAATGTAT AGTTGTCC	
	TTTACATG TCAACAGG	
	A_____	
GAM1281 LOC122553 3'	AGGATTT CATATATACATTGTA 74130	G _ GTT
	TG AATGTATATA GAA GTCCT	
	AT TTACATATAT CTT TAGGA	
	G A _____	
GAM1281 LOC128272 3'	GGGACCTATATGTATATTT 74728	GA TT
	GAATGTATATA AG GTCCT	
	TTTATATGTAT TC CAGGG	
	A_ _____	
GAM1281 LOC128344 3'	AGGAGCCAATTTTATATATTCT 74734	TAG _____
A	TGGAATGTATA AAGTTG TCCT	
	ATCTTATATAT TTAAAC AGGA	
	_____ CG	
GAM1281 LOC129450 3'	GGGGTGTTTGTGTGGATTCTA 74874	G AGT GT
	TGGAAT TATATAGA T CCT	
	ATCTTA GTGTGTTT G GGG	
	G _____ TG	
GAM1281 LOC130507 3'	CTTGCTATTTTATATACATTT 74950	T CCT
C	GGAATGTATATAGAAGT GT	
	CTTTACATATATTTTTA CG	
	T TTCG	
GAM1281 LOC132235 5'	GGAACTGTGTGCATTCTA 76158	AAGTTG
	TGGAATGTATATAG TCC	
	ATCTTACGTGTGTC AGG	
	AA_____	
GAM1281 LOC132332 3'	GACAACTAACATTTTA 76162	ATATAGA
	TGGAATGT AGTTGTC	

	ATTTTACA	TCAACAG	
	A_____		
GAM1281 LOC132948 5'	GGGATAGCTTTACGGCTTCT	59174	T ATATA
	GGAA GT GAAGTTGTCCT		
	TCTT CG TTTCGATAGGG		
	_ GCA_		
GAM1281 LOC133452 5'	GGGACGGCGGCTGGTGT	75924	TG ATA AA
	GGAA T TAG GTTGCCT		
	TTTT G GTC CGGCAGGG		
	GT__ GG		
GAM1281 LOC142927 3'	GGGGTGATTTCAGCTTGTCCA	76430	AT_ ATATA TG
	TGGA GT GAAGT TCCT		
	ACCT CG CTTTA GGGG		
	GTT A__ GT		
GAM1281 LOC142955 5'	GGGGCAGCAATGGCTGTGCATT	76447	TAGAA_
TT	GGAATGTATA GTTGCCT		
	TTTTACGTGT CGACGGGG		
	CGGTAA		
GAM1281 LOC143154 3'	AAATAATTTTTGTGTATGTT	76474	CCT
	AATGTATATAGAAGTTGT		
	TTGTATGTGTTTTTAATA		
	AA		
GAM1281 LOC144231 5'	AATTTCTATGTCTGTTTCA	83010	GT
	TGGAAT ATATAGAAGTT		
	ACTTTG TGTATCTTTAA		
	TC		
GAM1281 LOC144509 5'	AGGACACCACGTGTACATCT	76859	A AGAAGT
	GGA TGTATAT TGTCT		
	TCT ACATGTG ACAGGA		
	_ CACC_		
GAM1281 LOC144558 3'	AGGGCAGCCGTGTATATTTT	83145	AGAA
	GGAATGTATAT GTTGCCT		
	TTTTATATGTG CGACGGGA		
	C__		
GAM1281 LOC144563 5'	TTCTGTGTCACATTCCA	76891	_
	TGGAATGT ATATAGAA		
	ACCTTACA TGTGTCTT		
	C		
GAM1281 LOC145355 3'	GGCATTCTATGTAATTCT	77098	G T
	GGAAT TATATAGAAGT GTC		

TCTTA ATGTATCTTTA CGG

GAM1281 LOC145717 3' GGATAACCGTGTGTATTG 66830 T GAA  
A GTATATA GTTGTCC  
| ||||| |||||  
G TATGTGT CAATAGG  
T GC\_

GAM1281 LOC145815 5' TTTCTCTGTGTGTTCCA 83526 TG T  
TGGAA TATA AGAAG  
|||| ||| |||||  
ACCTT GTGT TCTTT  
GT C

GAM1281 LOC145837 5' GGGGTGGCTTAAAGGCACTCTA 83545 A ATATAG TG  
TGGA TGT AAGT TCCT  
|||| ||| ||| |||||  
ATCT ACG TTCG GGGG  
C GAAA\_ GT

GAM1281 LOC145900 5' GGGCAGTGGTGGCATTCT 77565 ATA GAAG  
GGAATGT TA TTGTCC  
||||| || |||||  
TCTTACG GT GACGGG  
GTG \_

GAM1281 LOC146272 3' GGATAGCAGGTATTTTCA 77791 T ATAGAA  
TGGAA GTAT GTTGTCC  
|||| ||| |||||  
ACTTT TATG CGATAGG  
T GA\_

GAM1281 LOC146435 3' GGATAAACATACATTTCA 77898 ATAGAAG  
TGGAATGTAT TTGTCC  
||||||| |||||  
ACTTTACATA AATAGG  
CA\_

GAM1281 LOC146565 5' GGAACCTATATACATCCA 60501 A AAGTTG  
TGGA TGTATATAG TCC  
||| ||||| |||  
ACCT ACATATATC AGG  
\_ CA\_

GAM1281 LOC146611 3' TAGGACAATTTTATATG 78030  
TATATAGAAGTTGTCCT A  
||||||| ||||| |  
GTATATTTTAAACAGGA T

GAM1281 LOC146795 3' GGAAGTGTGTGTGTTCT 78134 TG AAGTTG  
GGAA TATATAG TCC  
||| ||||| |||  
TCTT GTGTGTC AGG  
GT A\_

GAM1281 LOC147947 5' GATGAGTGACATTCCA 78582 A AGAAG TG  
TGGAATGT TAT T TC  
||||||| ||| | ||

	ACCTTACA GTG A AG	
	— ——— GT	
GAM1281 LOC148418 3'	AGAATATTTTTATATATATTCC 78847	TG CT
	GGAATGTATATAGAAGT TC	
	CCTTATATATATTTTTA AG	
	TA A	
GAM1281 LOC148604 5'	AGGATAATCTTTGACATTTT 78917	ATA AG
	GGAATGT TAGA TTGTCCT	
	TTTTACA GTTT AATAGGA	
	—— CT	
GAM1281 LOC149127 3'	GGGGCAGCTCCTGCTGTCTTCC 84349	TG TA A
A	TGGAA TA TAG AGTTGTCCT	
	ACCTT GT GTC TCGACGGGG	
	CT C_ C	
GAM1281 LOC149134 5'	GGGCATCTCTATATTTATTTT 84362	T A T
	GGAATG ATATAGA G TGTCC	
	TTTTAT TATATCT C ACGGG	
	T _ T	
GAM1281 LOC149351 3'	GGGATAAATTTTTATATGCAT 79309	—
	ATGTATATAGAAGTT GTCCT	
	TACGTATATTTTAA TAGGG	
	A	
GAM1281 LOC150115 5'	AGGACACACTGTGTATTTCCA 79570	T AAGT
	TGGAA GTATATAG TGTCTT	
	ACCTT TATGTGTC ACAGGA	
	— AC_	
GAM1281 LOC150245 3'	GGCTTTCCATATACATTTTA 84937	A TT
	TGGAATGTATAT GAAG GTC	
	ATTTTACATATA CTTT CGG	
	C _	
GAM1281 LOC150378 3'	AGGGTGACTTCAGTGACATTCC 79738	A A TG
	GGAATGT TAT GAAGT TCCT	
	CCTTACA GTG CTTCA GGGA	
	_ A GT	
GAM1281 LOC150605 5'	GGACAGCTTAATGTAT 85084	AG
	GTATAT AAGTTGTCC	
	TATGTA TTCGACAGG	
	A_	
GAM1281 LOC151273 3'	GCAATTTTTGATGCATTTTA 67017	A
	TGGAATGTAT TAGAAGTTGT	

ATTTTACGTA GTTTTAAACG

GAM1281 LOC151473 3' GACTACATACATTCTA 80257 ATAGAA T  
TGAATGTAT GT GTC  
||||||| |||||  
ATCTTACATA CA CAG  
\_\_\_\_\_ T

GAM1281 LOC151477 5' GGGTTATAGACTCATGTGTGTT 80263 TG A A GT\_\_\_\_  
CT GAA TATAT GA GTT CCT  
||| ||||| ||||| |||||  
CTT GTGTA CT CAG GGG  
GT \_ \_ ATATT A

GAM1281 LOC151632 5' TTCTGTGTCACATTCCA 85473 \_  
TGGAATGT ATATAGAA  
||||||| |||||  
ACCTTACA TGTGTCTT  
C

GAM1281 LOC151996 3' GGGAATTGGGCTGTATGTATAT 85537 GA TG\_\_\_\_  
T AATGTATATA AGT TCCT  
||||||| ||||| |||||  
TTATATGTAT TCG AGGG  
G\_ GGTTA

GAM1281 LOC152059 3' GGAATATGATGCATTTTA 80448 ATAGAAGTT  
TGGAATGTAT GTCC  
||||||| |||||  
ATTTTACGTA CAGG  
GTAT\_\_\_\_\_

GAM1281 LOC152084 3' GGACGTGTCTGCATTTTA 85554 ATAT AGT  
TGGAATGT AGA TGTCC  
||||||| ||||| |||||  
ATTTTACG TCT GCAGG  
\_\_\_\_\_ GT\_

GAM1281 LOC152220 3' GGAAATAAATTTCTGTATATGT 85585 G G\_\_\_\_ T  
TGCA AATGTATATAGAAGTT TCC  
||||||| ||||| |||||  
TTGTATATGTCTTTAA AGG  
G ATAA

GAM1281 LOC152328 3' GGGGTGACTCTACTGTGC 80526 \_ A TG  
GTATA TAGA GT TCCT  
||||| ||||| ||||| |||||  
CGTGT ATCT CA GGGG  
C \_ GT

GAM1281 LOC153196 3' GGAACTGGATGCGTTTAA 85964 ATAGA G  
TGGAATGTAT AGTT TCC  
||||||| ||||| |||||  
ATTTTGCGTA TCAA AGG  
GG\_\_\_\_ \_

GAM1281 LOC153222 3' AGGAAATTTTAAATATATTTCA 80782 A GTTG  
TGGAATGTAT TAGAA TCCT  
||||||| ||||| |||||

ACTTTATATA ATTTT AGGA  
 \_ AA\_  
 GAM1281 LOC153232 5' GGGATGACTTCTGCACTTTGCC 85986 AAT\_ ATA TG  
 GG GT TAGAAGT TCCT  
 || || ||||| ||||  
 CC CA GTCTTCA AGGG  
 GTTT C\_ GT  
 GAM1281 LOC153338 3' GGGCAGCAATGAGTTCCA 85998 G ATAGAA  
 TGGAAT TAT GTTGTCC  
 ||||| ||| |||||  
 ACCTTG GTA CGACGGG  
 A A\_  
 GAM1281 LOC153516 3' TGGGCAGTTTCTGTGGCATTTC 56712 A GT T  
 A TGGAATGT TATAGAA TGTCC  
 ||||| ||||| ||||  
 ATTTTACG GTGTCTT ACGGG  
 \_ TG TA  
 GAM1281 LOC154739 3' GGACAGTGGTGCATGCCA 86236 A ATAGAAG  
 TGG ATGTAT TTGTCC  
 ||| ||||| |||||  
 ACC TACGTG GACAGG  
 G GT\_  
 GAM1281 LOC154813 5' AGGGTAACTTTCCGGACGTTCC 81161 ATATA GT  
 GGAATGT GAAGTT CCT  
 ||||| ||||| |||  
 CCTTGCA TTTCAA GGA  
 GGCC\_ TG  
 GAM1281 LOC155081 3' AGGACATGAGCTGTGTGTTTTC 81288 TG AAGT  
 GAA TATATAG TGCCT  
 ||| ||||| |||||  
 CTT GTGTGTC ACAGGA  
 TT GAGT  
 GAM1281 LOC157278 3' AGGACAGCCGTGTATATTTT 86421 AGAA  
 GGAATGTATAT GTTGTCTT  
 ||||| |||||  
 TTTTATATGTG CGACAGGA  
 C\_  
 GAM1281 LOC157567 5' TTTTGTAAACGTTCCA 81487 A  
 TGGAATGT TATAGAAG  
 ||||| |||||  
 ACCTTGCA ATGTTTTT  
 \_  
 GAM1281 LOC157623 3' GGCTAATTTTGTATATTTT 81500 T T  
 GAA GTATATAGAAGTTG CC  
 ||| ||||| ||||| ||  
 TTT TATATGTTTTTAAT GG  
 T C  
 GAM1281 LOC157627 3' GGGGCGGCTTTTGTGAATGT 81506 A  
 ATGT TATAGAAGTTGTCCT  
 ||| ||||| |||||

		TGTA GTGTTTTCGGCGGGG		
		A		
GAM1281	LOC157798 5'	ACTTTAGTATGTGTTCT	86546	TG A
		GGAA TATAT GAAGT		
		TCTT GTATG TTTCA		
		GT A		
GAM1281	LOC158014 5'	GGGATTTTCGTTATGTTATATTC	81654	_ AAGTT
	T	GGAATGTA TATAG GTCCT		
		TCTTATAT GTATT TAGGG		
		T GCTT_		
GAM1281	LOC158014 5'	GGACGTAATATGCATT	81653	AGAAGT
		AATGTATAT TGTCC		
		TTACGTATA GCAGG		
		AT____		
GAM1281	LOC158301 3'	GGGCGACTTTCCTTTTCC	81870	TGTATATA
		GGAA GAAGTTGTCC		
		CCTT TTTCAGCGGG		
		TTCC____		
GAM1281	LOC158527 3'	TTTCTGTGTGGATTTTA	81948	G
		TGGAAT TATATAGAAG		
		ATTTTA GTGTGTCTTT		
		G		
GAM1281	LOC158696 3'	GTTTAATTTCTGTGTAGTATTC	81975	_ TCCT
	CA	TGGAATG TATATAGAAGTTG		
		ACCTTAT ATGTGTCTTTAAT		
		G TTG		
GAM1281	LOC158696 3'	AGGAATAAGCATGTGTATATTC	81970	GAAGTTG
	CA	TGGAATGTATATA TCCT		
		ACCTTATATGTGT AGGA		
		ACGAATA		
GAM1281	LOC159371 5'	AGTGCGTTTCGATGTGTGTTCC	82191	TG A AGT TC
	A	TGGAA TATAT GA TG CT		
		ACCTT GTGTA CT GC GA		
		GT G TT_ GT		
GAM1281	LOC161416 5'	GGGAAGTACTCTGTGAGTGTTT	87087	TG A A TG_
	TA	TGGAA T TATAGA GT TCCT		
		ATTTT G GTGTCT CA AGGG		
		GT A _ TCA		
GAM1281	LOC164832 3'	AGGATATATATATATATTT	82453	GAAGT
		GAATGTATATA TGTCTT		



		TTTATATATAT	ATAGGA		
		ATAT_			
GAM1281	LOC169611 3'	GGGGCAAGCAGCATTGCATTCT	82772	TATAGAAG	
		GGAATGTA	TTGTCCT		
		TCTTACGT	AACGGGG		
		TACGACG_			
GAM1281	LOC170395 3'	GGGATGTTCTTGTGTATTTTTC	76377	T _ GT	
	A	TGGAA GTATATA GAA	TGTCCT		
		ACTTT TATGTGT CTT	GTAGGG		
		T T _			
GAM1281	LOC196424 3'	AGGGTGACTTTTATAAGCAT	87701	A TG	
		ATGT TATAGAAGT	TCCT		
		TACG ATATTTTCA	GGA		
		A GT			
GAM1281	LOC196812 3'	GGGACATGGGTATATGTGTTAC	89571	G TG GAAGT	
	A	TG AA TATATA	TGTCCT		
		AC TT GTATAT	ACAGGG		
		A GT GGGT_			
GAM1281	LOC199684 3'	GACGGCAGGCGTTTCA	88296	ATATAGAA	
		TGGAATGT	GTTGTC		
		ACTTTGCG	CGGCAG		
		GA_____			
GAM1281	LOC200169 3'	GGGCACTTTTCTGTGTGTAT	89955	T_ T	
		ATGTATATAGAAG	TGTCC		
		TATGTGTGTCTTT	ACGGG		
		TC			
GAM1281	LOC200420 3'	AGGACAAATATTGTATAGTTTC	59248	G AAG	
	A	TGGAAT TATATAG	TTGTCCT		
		ACTTTG ATATGTT	AACAGGA		
		_ ATA			
GAM1281	LOC200609 5'	GATGATTCTGTGTATATCT	90100	A G TG	
		GGA TGTATATAGAA	T TC		
		TCT ATATGTGTCTT	A AG		
		_ _GT			
GAM1281	LOC200904 5'	TTCTGTGTCACATTCCA	90190	_	
		TGGAATGT	ATATAGAA		
		ACCTTACA	TGTGTCTT		
		C			
GAM1281	LOC200982 3'	GGATGGCTTGGTGTGTCT	90222	ATG AG TG	
		GGA TATAT	AAGT TCC		

	TCT GTGTG TTCG AGG		
	___ G_ GT		
GAM1281 LOC201102 3'	AGGGCAGTTCAGATTCATTCT 88089	T ATA G	
	GGAATG AT GAA TTGTCCT		
	TCTTAC TA CTT GACGGGA		
	T GA_ _		
GAM1281 LOC201484 5'	ACTTTTATTACGTTCCA 89786	T	
	TGGAATGTA ATAGAAGT		
	ACCTTGCAT TATTTTCA		
	—		
GAM1281 LOC202018 3'	GGGCAGGGTGTGTGTTCT 89143	TG AGAAGT	
	GGAA TATAT TGTCC		
	TCTT GTGTG ACGGG		
	GT GG___		
GAM1281 LOC202025 3'	GGATAGCATCTGCATTCT 90294	ATAT A	
	GGAATGT AGA GTTGTCC		
	TCTTACG TCT CGATAGG		
	___ A		
GAM1281 LOC202451 3'	TTTTGTGTACATTTTA 90357		
	TGGAATGTATATAGAA		
	ATTTTACATGTGTTTT		
GAM1281 LOC202802 3'	AGGACATGAGCTGTGTGTTTTC 89202	TG AAGT	
	GAA TATATAG TGCCT		
	CTT GTGTGTC ACAGGA		
	TT GAGT		
GAM1281 LOC203276 3'	GGACAGTGGTGCATGCCA 90486	A ATAGAAG	
	TGG ATGTAT TTGTCC		
	ACC TACGTG GACAGG		
	G GT___		
GAM1281 LOC203305 3'	GGACAGTGGTGCATGCCA 90530	A ATAGAAG	
	TGG ATGTAT TTGTCC		
	ACC TACGTG GACAGG		
	G GT___		
GAM1281 LOC203611 3'	AGGTTACTTTAGTGTATGTTCT 60363	A TGT	
A	TGGAATGTATAT GAAGT CCT		
	ATCTTGTATGTG TTTCA GGA		
	A TT_		
GAM1281 LOC204084 5'	AGGGCAGCAAGTGTATTTCC 89444	T AGAA	
	GGAA GTATAT GTTGTCT		

		CCTT TATGTG CGACGGGA		
		— AA—		
GAM1281	LOC204970 3'	GGACGTGGTGTGTGTTCT	89414	TG AGAAGT
		GGAA TATAT TGTCC		
		TCTT GTGTG GCAGG		
		GT GT—		
GAM1281	LOC219294 3'	AAATAATTTTTGTGTATGTT	93000	CCT
		AATGTATATAGAAGTTGT		
		TTGTATGTGTTTTTAATA		
		AA		
GAM1281	LOC219376 3'	GGTATAACTTCATGTGTATTTT	93900	A _ T
	A	TGGAATGTATAT GAAGTTGT CC		
		ACTTTATGTGTA CTTCAATA GG		
		— T		
GAM1281	LOC219445 5'	GGGATAATTTTTGTATTTTTT	91577	TGT
		GAA ATATAGAAGTTGTCCT		
		TTT TATGTTTTTAATAGGG		
		TT_		
GAM1281	LOC219541 3'	AGGATGGCTTTTCCTGCTGTAC	91567	_ _ _ TG
		GTATA TAG AAGT TCCT		
		CATGT GTC TTCG AGGA		
		C CTT GT		
GAM1281	LOC219562 3'	AGGATAACTACCTTCACGTTTT	90767	ATAT A_
		GGAATGT AG AGTTGTCCT		
		TTTTGCA TC TCAATAGGA		
		CT_ CA		
GAM1281	LOC219919 5'	TTCTGTGTCACATTCCA	93296	_
		TGGAATGT ATATAGAA		
		ACCTTACA TGTGTCTT		
		C		
GAM1281	LOC219940 3'	GGGGCGGCTTTTGTGTTCTCC	93356	ATGT
		GGA ATATAGAAGTTGTCCT		
		CCT TGTGTTTTCGGCGGGG		
		CT_		
GAM1281	LOC220758 3'	AGGACAAATGTTTACATTTT	90781	T GAAG
		GGAATGTA ATA TTGTCCT		
		TTTTACAT TGT AACAGGA		
		T A_		
GAM1281	LOC220883 3'	GTTACTCCTTATATGTGTGTTT	91264	TG G TT CCT
	TA	TGGAA TATATA AAG GT		

	ATCTT GTGTAT TTC CA		
	GT A CT TTGA		
GAM1281 LOC220988 3'	ATTTCTTGTGTATATTTCA 90845	—	
	TGGAATGTATATA GAAGT		
	ACTTTATATGTGT CTTTA		
	T		
GAM1281 LOC221490 3'	GGGCGGTTTCACATTT 93666	ATATA TT	
	GAATGT GAAG GTCC		
	TTTACA CTTT CGGG		
	GG		
GAM1281 LOC221576 3'	AGGACAAAAAGTGTATGTTTTA 93703	AGAAG	
	TGGAATGTATAT TTGCCT		
	ATTTTGTATGTG AACAGGA		
	AAA_		
GAM1281 LOC221641 5'	AGGATAATTTCTAAACATTTT 93724	ATA	
	GGAATGT TAGAAGTTGTCCT		
	TTTTACA ATCTTTAATAGGA		
	A_		
GAM1281 LOC221773 3'	GGGTGGCTTTCGATTTT 91051	ATATA TG	
	GGAATGT GAAGT TCC		
	CTTTACG TTTCG GGG		
	GT		
GAM1281 LOC221795 5'	TTCTGTGTCACATTCCA 92481	—	
	TGGAATGT ATATAGAA		
	ACCTTACA TGTGTCTT		
	C		
GAM1281 LOC221810 3'	AGGACAAACTATATGTTTTGC 93931	G TG AAG	
	G AA TATATAG TTGCCT		
	C TT GTATATC AACAGGA		
	G TT A_		
GAM1281 LOC221889 3'	GTGGTTTTTAGTACATTCT 92529	A TG	
	GGAATGTAT TAGAAGT T		
	TCTTACATG ATTTTG G		
	GT		
GAM1281 LOC222008 3'	GGATAATATTTTATATACTTC 94012	T _ T	
TA	TGGAA GTATATAGAA GTTGTCC		
	ATCTT CATATATTTT TAATAGG		
	TA		
GAM1281 LOC222166 3'	GGGAGTCTTGTATATCTTCCA 94096	T _ AGTTG	
	TGGAA GTATATA GA TCC		

ACCTT TATATGT CT GGG  
 C T GA\_\_\_\_  
 GAM1281 LOC222174 5' AGGTACATTTATGTGCGTCCA 94114 A AGT \_  
 TGA TGTATATAGA TGT CCT  
 |||| ||||| ||||  
 ACCT GCGTGTATTT ACA GGA  
 \_ \_ T  
 GAM1281 LOC222228 3' AGGACATGAGCTGTGTGTTTTC 94292 TG AAGT  
 GAA TATATAG TGCCT  
 ||| ||||| |||||  
 CTT GTGTGTC ACAGGA  
 TT GAGT  
 GAM1281 LOC222233 3' AGGACATGAGCTGTGTGTTTTC 94249 TG AAGT  
 GAA TATATAG TGCCT  
 ||| ||||| |||||  
 CTT GTGTGTC ACAGGA  
 TT GAGT  
 GAM1281 LOC253017 3' AGGATAGTTAACTATTATACTC 95840 A T AAG\_  
 CA TGA TGTA ATAG TTGCCT  
 |||| ||||| |||||  
 ACCT ATAT TATC GATAGGA  
 C \_ AATT  
 GAM1281 LOC253019 3' AGGTCCTTTTGTATATATTCT 95364 TT T  
 GGAATGTATATAGAAG G CCT  
 ||||| ||||| |||||  
 TCTTATATATGTTTTC T GGA  
 CC\_  
 GAM1281 LOC253955 3' AGGACAGTTTTTGTATGGTTT 94420 GTAT GT  
 GAAT ATAGAA TGCCT  
 |||| ||||| |||||  
 TTTG TGT TTT ACAGGA  
 GTAT TG  
 GAM1281 LOC253981 3' GGGAATATTTTATATATTTT 95831 T TG  
 AA GTATATAGAAGT TCCT  
 || ||||| |||||  
 TT TATATATTTTTA AGGG  
 T TA  
 GAM1281 LOC254243 3' GGACAGTGGTGCATGCCA 97415 A ATAGAAG  
 TGG ATGTAT TTGTCC  
 ||| ||||| |||||  
 ACC TACGTG GACAGG  
 G GT\_\_\_\_  
 GAM1281 LOC254431 3' GGGACCACAGCTGTGATGTTCT 96851 A AA T  
 GGAATGT TATAG GT GTCCT  
 ||||| ||||| |||||  
 TCTTGTA GTGTC CA CAGGG  
 \_ GA C  
 GAM1281 LOC254892 5' GGGCAATTTGCATATTTT 95529 ATATAG  
 GGAATGT AAGTTGTCC  
 ||||| ||||| |||||

	CTTTATA	TTTAACGGG	
	CG_____		
GAM1281 LOC254936 5'	GGGCAGTGGTGGCATTCT	94972	ATA GAAG
	GGAATGT TA TTGTCC		
	TCTTACG GT GACGGG		
	GTG _____		
GAM1281 LOC255043 3'	AGGACGATTTGCGGAATTCCA	95327	GTATATAG
	TGGAAT AAGTTGTCCT		
	ACCTTA TTTAGCAGGA		
	AGGCG_____		
GAM1281 LOC255193 5'	GGGCAGCACATACTTCCA	95355	T ATAGAA
	TGGAA GTAT GTTGTCC		
	ACCTT CATA CGACGGG		
	_ CA_____		
GAM1281 LOC255461 5'	AGGACAGCCGTGTATATTTT	97314	AGAA
	GGAATGTATAT GTTGCCT		
	TTTTATATGTG CGACAGGA		
	C_____		
GAM1281 LOC255516 5'	AGGACAGCCGTGTATATTTT	97327	AGAA
	GGAATGTATAT GTTGCCT		
	TTTTATATGTG CGACAGGA		
	C_____		
GAM1281 LOC255981 3'	AGGGCAGTTTTTTAGTGTTCATT	97131	TATA GT
	AATG TAGAA TGTCCCT		
	TTAC ATTTT ACGGGA		
	TGTG TG		
GAM1281 LOC255995 5'	CTTTTATTTGTGTTCCA	96974	TG T
	TGGAA TA ATAGAAG		
	ACCTT GT TATTTTC		
	GT T		
GAM1281 LOC256158 5'	AGGGCAACCCCATCCATTCTA	97645	TATATAGAA
	TGGAATG GTTGCCT		
	ATCTTAC CAACGGGA		
	CTACCCC_____		
GAM1281 LOC256306 3'	AGGACAATTTCTCCTAGTTACC	96678	_ GTATAT
A	TGG AAT AGAAGTTGTCCT		
	ACC TTG TCTTTAACAGGA		
	A ATCC_____		
GAM1281 LOC256515 5'	TTCTGTGTCACATTCCA	96467	_
	TGGAATGT ATATAGAA		

	ACCTTACA TGTGTCTT	
	C	
GAM1281 LOC256530 5'	GGATTCTGGGTACATTTT 96815	A AGTT
	GGAATGTAT TAGA GTCC	
	TTTTACATG GTCT TAGG	
	G ____	
GAM1281 LOC256594 5'	TTCTGTGTCACATTCTA 97082	_
	TGGAATGT ATATAGAA	
	ATCTTACA TGTGTCTT	
	C	
GAM1281 LOC257159 5'	GGGGCAATGCGTACATATGTGG 97180	G GAA____
	TTTC AT TATATA GTTGCCT	
	TG GTGTAT TAACGGGG	
	_ ACATGCG	
GAM1281 LOC257169 3'	GGCAGCAACGTTTCA 96149	ATATAGAA
	TGGAATGT GTTGTC	
	ACTTTGCA CGACGG	
	A_____	
GAM1281 LOC257181 3'	AGGATAACTACCTTCACGTTTT 94590	ATAT A_
	GGAATGT AG AGTTGCCT	
	TTTTGCA TC TCAATAGGA	
	CT_ CA	
GAM1281 LOC257443 3'	GGGACAATTAATGCATTTT 95849	ATAGA
	GGAATGTAT AGTTGCCT	
	TTTTACGTA TTAACAGGG	
	A_____	
GAM1281 LOC257451 3'	AGGGTGATTTTTTTTGATGTTT 95552	ATAT TG
	GAATGT AGAAGT TCCT	
	TTTGTA TTTTA GGGA	
	GTT_ GT	
GAM1281 LOC257476 3'	GGGACAGCTTGCCTGTTTCT 61254	TGTAT _
	GGAA ATAG AAGTTGCCT	
	TCTT TGTC TTCGACAGGG	
	_____ CG	
GAM1281 LOC257515 3'	AGGACAAAAAGTGTATGTTTTA 97783	AGAAG
	TGGAATGTATAT TTGCCT	
	ATTTTGTATGTG AACAGGA	
	AAA_	
GAM1281 LOC257572 3'	AGGACAAAAAGTGTATGTTTTA 97912	AGAAG
	TGGAATGTATAT TTGCCT	

	ATTTTGTATGTG AACAGGA		
	AAA__		
GAM1281 LOC257618 3'	AGGATGCCTCTACATGTATTTTC 97853	A	A TT
A	TGGAATGTAT TAGA G GTCCT		
	ACTTTATGTA ATCT C TAGGA		
	C _CG		
GAM1281 LOC51000 3'	GATTGTTTTATATTCATTCCA 31976	T	GTT
	TGGAATG ATATAGAA GTC		
	ACCTTAC TATATTTT TAG		
	T GT_		
GAM1281 LOC51027 3'	GGGCAGCCCGGATGTTCCA 59366	ATATAGAA	
	TGGAATGT GTTGTCC		
	ACCTTGTA CGACGGG		
	GGCC__		
GAM1281 LOC51028 3'	ACATTATTTATATATATTCTA 32178	AGT	
	TGGAATGTATATAGA TGT		
	ATCTTATATATATTT ACA		
	ATT		
GAM1281 LOC51667 3'	GGCTTTATATATATTC 32275	A	
	GAATGTATATAGA GTT		
	CTTATATATATTT CGG		
	-		
GAM1281 LOC54103 5'	GGGCATGTGTGTGTGTGTTTCA 94215	TG	GAAGT
	TGGAA TATATA TGTCC		
	ACTTT GTGTGT ACGGG		
	GT GTGT_		
GAM1281 LOC57105 3'	AGGGTGGAGGTGATATGGCATT 39816	_	AGAAG TG
CT	GGAATGT ATAT T TCCT		
	TCTTACG TATA G GGGA		
	G GTGGA GT		
GAM1281 LOC63928 3'	GGGATGGTTTTGGGATGATTC 42037	G	ATA TT
	GAAT TAT GAAG GTCCT		
	CTTA GTA TTTT TAGGG		
	_ GGG GG		
GAM1281 LOC63928 3'	GGGATGATTCAAGTGCATTACA 42036	G	ATA G TG
	TG AATGTAT GAA T TCCT		
	AC TTACGTG CTT A AGGG		
	A AA_ _GT		
GAM1281 LOC64182 5'	GGGCAGCTGAGTGTGTCT 42297	ATG	AGA
	GGA TATAT AGTTGTCC		



			TCT GTGTG TCGACGGG		
			___ AG_		
GAM1281	LOC81034	3'	AGGACAAATCCAGTATATCT 47844	A	ATA G
			GGA TGTAT GAA TTGTCCT		
			TCT ATATG CTT AACAGGA		
			_ AC_ _		
GAM1281	LOC83693	3'	AGGAAAAATCTGTGTGTATTGT 48829	G	AGTTG
	A		TG AATGTATATAGA TCCT		
			AT TTATGTGTGTCT AGGA		
			G AAAA_		
GAM1281	LOC85439	5'	GGCTGATCTGTCTACATTCT 52402	T	AGTT
			GGAATGTA ATAGA GTC		
			TCTTACAT TGTCT CGG		
			C AGT_		
GAM1281	LOC90038	3'	GGACAGTGGTGCATGCCA 61158	A	ATAGAAG
			TGG ATGTAT TTGTCC		
			ACC TACGTG GACAGG		
			G GT_____		
GAM1281	LOC90110	3'	GGGGTGACTTAGCACCAGGTTT 61511		GTATATAG TG
	CA		TGGAAT AAGT TCCT		
			ACCTTG TTCA GGGG		
			GACCACGA GT		
GAM1281	LOC90190	3'	GGGTAATTTCTGGGTTGCA 61780	TA_	GT
			TGTA TAGAAGTT CC		
			ACGT GTCTTTAA GG		
			TGG TG		
GAM1281	LOC90317	3'	TGTAAGAATTTGTATATATATT 62258	G	GTCCT
	CCA		TGGAATGTATATA AAGTT		
			ACCTTATATATAT TTAA		
			G GAATGTG		
GAM1281	LOC90355	3'	CTTTTGTAACGTTCCA 52623	A	
			TGGAATGT TATAGAAG		
			ACCTTGCA ATGTTTTTC		
			A		
GAM1281	LOC91351	3'	GGGACAGCTTTTAAAGTGTTT 65707	TG	ATA
			GAA T TAGAAGTTGTCCT		
			TTT G ATTTTCGACAGGG		
			GT AA_		
GAM1281	LOC91650	5'	AGCTTCTTTATACATTTTA 66861	T	
			TGGAATGTATA AGAAGTT		

ATTTTACATAT TCTTCGA  
 T  
 GAM1281 LOC92370 3' AGGGCCAGATTGTAAATATTTTC 69132 A AAGTT  
 A TGGAAATGT TATAG GTCCT  
 ||||| |||| ||||  
 ACTTTATA ATGTT CGGGA  
 A AGAC\_  
 GAM1281 LOC92421 3' GGGCAATGGATGCATTTTC 69214 ATAGAA  
 GGAATGTAT GTTGTCC  
 ||||| |||||  
 CTTTACGTA TAACGGG  
 GG\_\_\_\_  
 GAM1281 LOC92578 3' GGACAGCCGTATGTGC 69829 GAA  
 GTATATA GTTGTCC  
 ||||| |||||  
 CGTGTAT CGACAGG  
 GC\_  
 GAM1281 LOC92689 3' AGGACAGAAAATACTGATGTGT 70215 TG \_ AAG\_\_\_\_  
 GTTTTA A TATAT AG TTGTCCT  
 | |||| | |||||  
 T GTGTA TC GACAGGA  
 GT G ATAAAA  
 GAM1281 LOC92703 3' AGGGTGGCTGGATTGTATATCT 56426 GA TAGA TG  
 C G ATGTATA AGT TCCT  
 | ||||| || ||||  
 C TATATGT TCG GGGA  
 TC TAGG GT  
 GAM1281 LOC92912 3' GGGTAACTTTCCCTATATTG 70845 T TA GT  
 A GTATA GAAGTT CC  
 | |||| ||||| ||  
 G TATAT TTTCAA GG  
 T CC TG  
 GAM1281 LOC93624 5' AGGACAACAGGCTGGCGTTTTT 72724 ATA AA\_  
 GGAATGT TAG GTTGCCT  
 ||||| || |||||  
 TTTTGCG GTC CAACAGGA  
 \_\_\_\_ GGA  
 GAM1282 PTP4A2 3' TCTAAATATTACGTA CT 12987  
 GAGTATGTAATATTTAGA  
 ||||| |||||  
 CTCATGCATTATAAATCT  
 GAM1282 C8orf17 3' CTCCGGTAAATTACATAACCCA 39597 C AG AT\_ TA  
 TC GA GG TATGTAAT T GAG  
 || || ||||| | |||  
 CT CC ATACATTA G CTC  
 A CA AAT GC  
 GAM1282 CBLN1 3' CTGATATATTACACACCCC 15123 A A \_  
 GG GT TGTAATAT TTAG  
 || || ||||| |||

			CC CA ACATTATA AGTC		
			C C T		
GAM1282	FLJ11618	3'	CTCTAAATCTCAGACTCC	42394	A TAAT
			GGAGT TG ATTTAGAG		
			CCTCA AC TAAATCTC		
			G TC__		
GAM1282	MGC2731	3'	CTAATCTCATACTCCCTC	43950	C TAATAT
			GA GGAGTATG TTAG		
			CT CCTCATAC AATC		
			C TCT__		
GAM1282	REG-IV	3'	CTCTAAATGTTTGCCCCG	49403	A TGT
			CGG GTA AATATTTAGAG		
			GCC CGT TTGTAAATCTC		
			C __		
GAM1282	LOC150960	3'	CTAAACTAATGTACTCC	80059	AATA
			GGAGTATGT TTTAG		
			CCTCATGTA AAATC		
			ATC_		
GAM1283	ADH1B	3'	CTTAGACATAAAGTAAAAT	72644	C CAC
			ATTT ACTTT TGTCTGAG		
			TAAA TGAAA ACAGATTC		
			A T__		
GAM1283	AHR	3'	ATCTCAGATGTTAAATAAATG	7875	CAC C T
			CATTT TTT AC GTCTGAGAT		
			GTAAA AAA TG TAGACTCTA		
			TA_ T _		
GAM1283	FDFT1	3'	TAGGAAAGTGAAATG	15518	A
			CATTTCACTTTC CTG		
			GTAAAGTGAAAG GAT		
			-		
GAM1283	JTB	3'	ATCTCAGACAGTGAAAGTGAAA	21959	
	TG		CATTTCACTTTCAGTGTCTGAGAT		
			GTAAAGTGAAAGTGACAGACTCTA		
GAM1283	KLF4	3'	TCCCAGACAGTGGATATG	14891	CT A
			CA TTCAGTGTCTG GA		
			GT AGGTGACAGAC CT		
			AT C		
GAM1283	PHYH	3'	ACAGTAAAAGTGAAAT	20608	C
			ATTTCACTTT ACTGT		

			TAAAGTGAAA TGACA		
			A		
GAM1283	PKD2	3'	TCCAGGTTGAAAAGTGAAA 60096	CTG	A
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T__ _		
GAM1283	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1283	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA	CTG
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1283	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT	CT
			TTCAC TTTCA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1283	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G	T_
			CTTTCACT TC GAGAT		
			GAAAGTGA AG TTCTA		
			G TC		
GAM1283	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT 45802	ACTTTCACT	
	G		CATTTT GTCTGAGAT		
			GTAAAG CAGACTCTA		
			AAACATTT_		
GAM1283	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281	CTT	
			CATTTCA TCACTGTCTGAGAT		
			GTAAAGT AGTGACAGACTCTA		
			C_		
GAM1283	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C	TC
			TTCA TTTCACTG TGAG		
			AAGT AAAGTGAC GTTT		
			A CT		
GAM1283	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A	_
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1283	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T	
			ATT CACTTTCACTGT		

		TAA GTGAAAGTGACG		
		C		
GAM1283	PORIMIN	3' ATCTCAGAGGGCCAAAGTGAA	53598	CA G
		TTCACTTT CT TCTGAGAT		
		AAGTGAAA GG AGACTCTA		
		CC G		
GAM1283	PP35	3' ATCTCAGACTGAAA	22814 CT	
		TTTCA GTCTGAGAT		
		AAAGT CAGACTCTA		
		—		
GAM1283	PRTD-NY3	3' CTCATTGCAATAAGTGAAATG	48148	TCAC C_
		CATTTCACTT TGT TGAG		
		GTAAAGTGAA ACG ACTC		
		TA__ TT		
GAM1283	SEP15	3' TCCTACAGTAAGAGTGAAA	14934	C CT
		TTTCACTTT ACTGT GA		
		AAAGTGAGA TGACA CT		
		A TC		
GAM1283	SFXN2	3' CTCAGGGGAAAAAAGTGAAA	73941	CACTG
		TTTCACTTT TCTGAG		
		AAAGTGAAA GGA CTC		
		AAAGG		
GAM1283	LOC149703	3' ATCTCAGACAGCCGTTTGAAAA	84647	ACTTTCA
		TTTC CTGTCTGAGAT		
		AAAG GACAGACTCTA		
		GTTTGCC		
GAM1283	LOC154007	3' ATCTCAAACCCTTTAGTGAAA	81015	TTCACT C
		TTTCACT GT TGAGAT		
		AAAGTGA CA ACTCTA		
		TTTCC_ A		
GAM1283	LOC155004	3' TCATTTAAGTGAAAGGAAA	81226	A GTC_
		TTTC CTTTCACT TGA		
		AAAG GAAAGTGA ACT		
		_ ATTT		
GAM1283	LOC222134	5' ACAGTGAAGTGAAATG	94136	T
		CATTTCACTT CACTGT		
		GTAAAGTGAA GTGACA		
		—		
GAM1284	APM1	3' GCATGAGCCACCATGCCCAGT	16592	C T C
		ACTGGGCA GGTGG CTCA GC		

			TGACCCGT CCACC GAGT CG		
			A _ A		
GAM1284	CDH1	3'	GCATGAGCTGCTGTGCCCAG 15145	TG T	C
			CTGGGCACGG G CTCA GC		
			GACCCGTGTC C GAGT CG		
			GT _ A		
GAM1284	COX15	3'	GCATGGGCCACCACGCCAG 54314	AC	T C
			CTGGGC GGTGGTC CA GC		
			GACCCG CCACCGG GT CG		
			CA _ A		
GAM1284	CYP2B6	3'	GCGTGAGTCACCGTGCCCAG 5731	T	
			CTGGGCACGGTGG CTCACGC		
			GACCCGTGCCACT GAGTGCG		
			—		
GAM1284	CYP3A4	3'	ACCACCCCCAGTTA 33924	CAC	
			TAACTGGG GGTGGT		
			ATTGACCC CCACCA		
			—		
GAM1284	CYP8B1	3'	GCATGAGCCACTGTGCCAGT 15263	T	C
			ACTGGGCACGGTGG CTCA GC		
			TGACCCGTGTCACC GAGT CG		
			_ A		
GAM1284	DPP6	3'	GCATGAGACCCGCCCA 55449	ACGGT	C
			TGGGC GGTCTCA GC		
			ACCCG CCAGAGT CG		
			C _ A		
GAM1284	EDG8	3'	GCATGCACCACCATGCCAGTT 78479	C	CT C
	A		TAACTGGGCA GGTGGT CA GC		
			ATTGACCCGT CCACCA GT CG		
			A C _ A		
GAM1284	FANCF	3'	AGGCCACCATGCCCGG 42668	C	
			CTGGGCA GGTGGTCT		
			GGCCCGT CCACCGGA		
			A		
GAM1284	HSD17B1	5'	GCATGAGCCACCGTGCCCAG 4686	T	C
			CTGGGCACGGTGG CTCA GC		
			GACCCGTGCCACC GAGT CG		
			_ A		
GAM1284	NCOA6IP	3'	GCGTGAGCTACTGTGCCAG 45738	T	
			CTGGGCACGGTGG CTCACGC		

GACCCGTGTCATC GAGTGCG

GAM1284 PRKR 3' GCATGTGCCACCCACCCA 10881 CAC CT C  
TGGG GGTGGT CA GC  
|||| ||||| ||  
ACCC CCACCG GT CG  
AC\_ T\_ A

GAM1284 RPH3AL 3' GCCACCACACCCAGTTA 22747 CAC  
TAACTGGG GGTGGT  
||||||| |||||  
ATTGACCC CCACCG  
ACA

GAM1284 SEDL 3' GCATGAACCACCGTGCCCGG 27336 C C  
CTGGGCACGGTGGT TCA GC  
||||||| |||||  
GGCCCGTGCCACCA AGT CG  
\_ A

GAM1284 SEDL 3' GCGTGAGCCACCGTGCCCA 27339 T  
TGGGCACGGTGG CTCACGC  
||||||| |||||  
ACCCGTGCCACC GAGTGCG

GAM1284 SEPN1 3' GCGTGAGCAATCGTGCCCA 66370 G T  
CTGGGCACGGT G CTCACGC  
||||||| | |||||  
GACCCGTGCTA C GAGTGCG  
A\_

GAM1284 C1orf21 5' GCGCGCCGCGCTCAGTTA 47961 A \_  
TAACTGGGC CGGTG GT  
||||||| |||||  
ATTGACTCG GCCGC CG  
C G

GAM1284 C20orf142 3' ACCACCATTCCCAGTTA 74764 CAC  
TAACTGGG GGTGGT  
||||||| |||||  
ATTGACCC CCACCA  
TTA

GAM1284 C20orf35 3' TGAGACCACAGGCCAG 37483 ACG  
CTGGGC GTGGTCTCA  
||||| |||||  
GACCCG CACCAGAGT  
GA\_

GAM1284 CYP3A7 3' ACCACCCCCAGTTA 5715 CAC  
TAACTGGG GGTGGT  
||||||| |||||  
ATTGACCC CCACCA

GAM1284 DKFZP434D146 3' GCATGAGCCACCGTGCCCA 31523 T C  
CTGGGCACGGTGG CTCA GC  
||||||| |||||

			GACCCGTGCCACC GAGT CG	
			— A	
GAM1284	FLJ10560	3'	GCGTGAGCCACCGTGCCCAG 36278	T
			CTGGGCACGGTGG CTCACGC	
			GACCCGTGCCACC GAGTGCG	
			—	
GAM1284	KIAA0469	3'	GCATGAGCCACCATGCCCAG 29334	C T C
			CTGGGCA GGTGG CTCA GC	
			GACCCGT CCACC GAGT CG	
			A — A	
GAM1284	KIAA0475	3'	GCGCCCGCCATCGTGCCCAG 29494	CTCA
			CTGGGCACGGTGGT CGC	
			GACCCGTGCTACCG GCG	
			CCC_	
GAM1284	KIAA1443	3'	GCATGAGCCACCGTGCCCGG 63830	T C
			CTGGGCACGGTGG CTCA GC	
			GGCCCGTGCCACC GAGT CG	
			— A	
GAM1284	KIAA1615	3'	GCATGAGCCACCGCACCCAG 68715	CA T C
			CTGGG CGGTGG CTCA GC	
			GACCC GCCACC GAGT CG	
			AC — A	
GAM1284	KIAA1924	3'	GCATGAGCCACTGTGCCCAG 73675	T C
			CTGGGCACGGTGG CTCA GC	
			GACCCGTGTCACC GAGT CG	
			— A	
GAM1284	MAP-1	3'	GCGTGAGACACTGCGCCCAG 42180	A G
			CTGGGC CGGTG TCTACGC	
			GACCCG GTCAC AGAGTGCG	
			C —	
GAM1284	MLZE	5'	CGTGAGCCACCGTGCCCGG 48618	T
			CTGGGCACGGTGG CTCACG	
			GGCCCGTGCCACC GAGTGC	
			—	
GAM1284	MRPL20	3'	GCGTGAGACACCGTGCCCAG 35736	G
			CTGGGCACGGTG TCTACGC	
			GACCCGTGCCAC AGAGTGCG	
			—	
GAM1284	PRO0245	5'	GCGTGAGGCACCACCCAGT 26130	CAC G
			ACTGGG GGTG TCTACGC	



			TGACCC CCAC GGAGTGCG		
			ACA _		
GAM1284	RASSF2	3'	GCGTGAGCCACTGTGCCAG 28436		T
			CTGGGCACGGTGG CTCACGC		
			GACCCGTGTCACC GAGTGCG		
			_		
GAM1284	SE70-2	5'	CGTAAGACCACCCATGCC 42089	C_ C	
			GGCA GGTGGTCT ACG		
			CCGT CCACCAGA TGC		
			AC A		
GAM1284	TU12B1-TY	3'	GCATGAGCCACCGTGCCCAG 33385		T C
			CTGGGCACGGTGG CTCA GC		
			GACCCGTGCCACC GAGT CG		
			_ A		
GAM1284	Ubc6p	3'	CGTGAGACAAGCCCAG 54151	ACGGTG	
			CTGGGC GTCTCACG		
			GACCCG CAGAGTGC		
			AA_		
GAM1284	VMP	3'	GCCACCACCCCAGTTA 54899	CAC	
			TAACTGGG GGTGGT		
			ATTGACCC CCACCG		
			CCA		
GAM1284	VPS4A	3'	GCGTGAGAACACTGAACCCAG 25103	CA G	
			CTGGG CGGTG TCTCACGC		
			GACCC GTCAC AGAGTGCG		
			AA A		
GAM1284	LOC120114	3'	GCATGAGCCACCGTGCCCAG 75528		T C
			CTGGGCACGGTGG CTCA GC		
			GACCCGTGCCACC GAGT CG		
			_ A		
GAM1284	LOC128989	3'	GCGTGTGCCACCATGCCCAG 74812	C CT	
			CTGGGCA GGTGGT CACGC		
			GACCCGT CCACCG GTGCG		
			A T_		
GAM1284	LOC147841	3'	GCGTGAGCCATCGTGCCCAG 78527		T
			CTGGGCACGGTGG CTCACGC		
			GACCCGTGCTACC GAGTGCG		
			_		
GAM1284	LOC149506	3'	GCATGAGCCACTGTGCCAG 84467		T C
			CTGGGCACGGTGG CTCA GC		

			GACCCGTGTCACC GAGT CG		
			— A		
GAM1284	LOC151701 3'	ACCACCACACTCAGTTA	85482	CAC	
		TAAGTGGG GGTGGT			
		ATTGACTC CCACCA			
		ACA			
GAM1284	LOC153688 3'	GCGTGAGCCACTGTGCCCAG	86110	T	
		CTGGGCACGGTGG CTCACGC			
		GACCCGTGTCACC GAGTGCG			
		—			
GAM1284	LOC199775 5'	GCGTGAGCCACCGTGCCCAG	88356	T	
		CTGGGCACGGTGG CTCACGC			
		GACCCGTGCCACC GAGTGCG			
		—			
GAM1284	LOC220575 3'	GCATGGGCCACCACCCCAG	76312	CAC	T C
		CTGGG GGTGGTC CA GC			
		GACCC CCACCGG GT CG			
		ACA — A			
GAM1284	LOC221060 3'	GCATGAGCTACTGTGCCCAG	93211	T	C
		CTGGGCACGGTGG CTCA GC			
		GACCCGTGTCATC GAGT CG			
		— A			
GAM1284	LOC221060 3'	GGGCCACCAGCCCAG	93214	AC	
		CTGGGC GGTGGTCT			
		GACCCG CCACCGGG			
		A_			
GAM1284	LOC222070 5'	GCGTGAGCCCCCGTGCCCAG	94154	T	T
		CTGGGCACGG GG CTCACGC			
		GACCCGTGCC CC GAGTGCG			
		— C			
GAM1284	LOC51161 3'	CTGTCCCGTGCCCAG	32511	T	TCT C
		CTGGGCACGG GG CA G			
		GACCCGTGCC CT GT C			
		— — A			
GAM1285	ARF3 3'	GCTTTCTGCTTCCTGA	8004	T	
		TCA GAAGCAGAAAGC			
		AGT CTTCGTCTTTTCG			
		C			
GAM1285	EFG2 5'	CTCGCGCCTCCTGCTTCAAGA	50475	A	AAA ACTA
		TC TGAAGCAG GC CGAG			

			AG ACTTCGTC CG GCTC		
			A CTC C__		
GAM1285	FGFR2	3'	GCCTTCTGCTTCTGA 43359	T	A
			TCA GAAGCAGAA GC		
			AGT CTTCGTCTT CG		
			— C		
GAM1285	FGFR2	3'	GCCTTCTGCTTCTGA 43371	T	A
			TCA GAAGCAGAA GC		
			AGT CTTCGTCTT CG		
			— C		
GAM1285	FGFR2	3'	GCCTTCTGCTTCTGA 43482	T	A
			TCA GAAGCAGAA GC		
			AGT CTTCGTCTT CG		
			— C		
GAM1285	FGFR2	3'	GCCTTCTGCTTCTGA 43492	T	A
			TCA GAAGCAGAA GC		
			AGT CTTCGTCTT CG		
			— C		
GAM1285	FGFR2	3'	GCCTTCTGCTTCTGA 43502	T	A
			TCA GAAGCAGAA GC		
			AGT CTTCGTCTT CG		
			— C		
GAM1285	FGFR2	3'	GCCTTCTGCTTCTGA 3763	T	A
			TCA GAAGCAGAA GC		
			AGT CTTCGTCTT CG		
			— C		
GAM1285	FZD4	3'	CTCATACCTGTCTGCTTCA 24135		A CAC C
			TGAAGCAGA AG TA GAG		
			ACTTCGTCT TC AT CTC		
			G C__ A		
GAM1285	HR	3'	GCTTCCCTCCTTCATGA 17642		C A_
			TCATGAAG AG AAGC		
			AGTACTTC TC TTCG		
			C CC		
GAM1285	PPARA	5'	GTGCTTCCTGCTTCAT 17276		A
			ATGAAGCAG AAGCAC		
			TACTTCGTC TTCGTG		
			C		
GAM1285	TBL1X	3'	CTAGTTGCTTCAGA 18930	A	GAAAGC C
			TC TGAAGCA ACTA G		

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AG ACTTCGT  TGAT C
_      _      A
GAM1285 TCF8  3' GTGAAC TTTCTGCTTCATG 47729  _
CATGAAGCAGAAAG CAC
||||| |||
GTACTTCGTCTTTC GTG
AA
GAM1285 UGT1A1 3' CTCATCTCTGCTCTGCTTCAT 4875  AAA CTAC_
ATGAAGCAG GCA GAG
||||| ||| |||
TACTTCGTC TGT CTC
C_ CTCTA
GAM1285 UGT1A4 3' CTCATCTCTGCTCTGCTTCAT 23060  AAA CTAC_
ATGAAGCAG GCA GAG
||||| ||| |||
TACTTCGTC TGT CTC
C_ CTCTA
GAM1285 UGT1A9 3' CTCATCTCTGCTCTGCTTCAT 40711  AAA CTAC_
ATGAAGCAG GCA GAG
||||| ||| |||
TACTTCGTC TGT CTC
C_ CTCTA
GAM1285 C20orf177 3' CTTGTTTACTTTCTGCCTCAGA 62147  A A CACT
TC TGA GCAGAAAG ACGAG
|| ||| ||| |||
AG ACT CGTCTTTC TGTTC
_ C ATT_
GAM1285 FLJ12121 3' TGGTGCTTCCACTCCATGA 46460  A CA A
TCATG AG GAA GCACTA
|||| || ||| |||
AGTAC TC CTT CGTGGT
C AC _
GAM1285 FLJ13910 3' TAGTGACTTTTGCCTCATGA 42930  AA AG
TCATG GCAGAA CACTA
|||| ||| |||
AGTAC CGTTTT GTGAT
CC CA
GAM1285 MGC14376 3' CTCCAGGCTTTCTGCCTC 51847  A A AC
GA GCAGAAAGC CT GAG
|| ||| ||| |||
CT CGTCTTTCG GA CTC
C _ C_
GAM1285 MGC20460 5' TCGGCTTCTGCTTCATGG 53849  A ACTA
TCATGAAGCAGAA GC CGA
||||| || |||
GGTACTTCGTCTT CG GCT
_ _ _
GAM1285 REM 5' GGGACTTTCTGCCCCAAGA 25810  A AA CA
TC TG GCAGAAAG CT
|| ||| ||| ||

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	AG AC CGTCTTTC GG	
	A CC AG	
GAM1285 SCYE1	5' CGTGGTCCTCCGCTTCATGA 16469	A AA C
	TCATGAAGC GA G ACTACG	
	AGTACTTCG CT C TGGTGC	
	C _ C	
GAM1285 SLC12A8	3' CTCACTGCAACCTCTGCTTC 44898	AA_ CTAC
	GAAGCAGA GCA GAG	
	CTTCGTCT CGT CTC	
	CCAA CA_	
GAM1285 LOC151647	3' AGCCCTCTCTGCTTCGTGA 80329	A CA
	TCATGAAGCAGA AG CT	
	AGTGCTTCGTCT TC GA	
	C CC	
GAM1285 LOC256950	3' CGAGAACTCCTGCTTCACGG 95426	A AA CA A
	TC TGAAGCAG AG CT CG	
	GG ACTTCGTC TC GA GC	
	C C_ AA _	
GAM1285 LOC90288	3' CTCGATCTCCTGACTTCATGA 62092	_ AA CACTA
	TCATGAAG CAG AG CGAG	
	AGTACTTC GTC TC GCTC	
	A C_ TA_	
GAM1285 LOC90470	3' TGTTTCTGTTCATGA 62971	G G
	TCATGAA CAGAAA CA	
	AGTACTT GTCTTT GT	
	- -	
GAM1286 A1BG	3' CCTCCCAAAGTGCTGGGATTA 55415	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	-	
GAM1286 ACADSB	3' CCTCCCAAAGTGCTGGGATTA 7844	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	-	
GAM1286 ADAMTS4	3' CCTCCCAAAGTGCTGGGATTA 17504	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	-	
GAM1286 ADAMTS4	3' TCCCAAAGTGCTGGGATTA 17520	A
	TAATCTCAGCACTTTG GGA	

ATTAGGGTCGTGAAAC CCT

GAM1286	ADCY6	5'	CCTCACAAAGTGCTGGGATTA 30925	AG
			TAATCTCAGCACTTTG GAGG	
			ATTAGGGTCGTGAAAC CTCC	
			A_	
GAM1286	ADRA1A	3'	CCTCCCAAAGTGCTGGGATTA 52786	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			-	
GAM1286	AIM1	3'	CCTCCCAAATGCTGGGATTA 91820	C A
			TAATCTCAGCA TTTG GGAGG	
			ATTAGGGTCGT AAAC CCTCC	
			A _	
GAM1286	ALDH1B1	3'	CCTCCCAAAGTGCTGGGATTA 5493	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			-	
GAM1286	APAF1	3'	CCTCCCAAAGTGCTGAGATTA 6727	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGAGTCGTGAAAC CCTCC	
			-	
GAM1286	APAF1	3'	CCTCCCAAAGTGCTGAGATTA 25036	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGAGTCGTGAAAC CCTCC	
			-	
GAM1286	APM1	3'	CCTCCCAAAGTGCTGGGATTA 16586	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			-	
GAM1286	APM1	3'	CCTCCCAAAGTGCTGGGATTA 16587	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			-	
GAM1286	APOL1	3'	CCTCCCAAAGTGCTGGGATTA 13344	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			-	
GAM1286	APPL	3'	CCTCCCAAAGTGCTGGGATTA 23924	A
			TAATCTCAGCACTTTG GGAGG	

			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	AQP6	3'	CCTCCCAAAGTGCTGGGATTA 7945	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	AQP6	3'	CCTCCCAAAGTGCTGGGATTA 53919	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	ARSF	5'	CCTCCCAAAGTGCTGGGATTA 64597	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	ATP7A	3'	CCTCCCAAAGTGCTGGGATTA 3521	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	ATP8B2	3'	CCTCCCAAAGTGCTGAGATTA 65221	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGAGTCGTGAAAC CCTCC	
			—	
GAM1286	AXL	3'	CCTCCCAAAGTGCTGAGATTA 41593	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGAGTCGTGAAAC CCTCC	
			—	
GAM1286	AXL	3'	CCTCCCAAAGTGCTGAGATTA 8096	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGAGTCGTGAAAC CCTCC	
			—	
GAM1286	B4GALT5	3'	CTTCCCAAAGTGCTGGGATTA 16500	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTTC	
			—	
GAM1286	BAZ2B	5'	CCTCCCAAAGTGCTGGGATTA 25619	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	BCL10	3'	CCTCCCAAAGTGCTGGGATTA 14057	A
			TAATCTCAGCACTTTG GGAGG	

			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	CAMLG	3'	CCTCCCAAAGTGCTGGGATTA 8236	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	CASP8	3'	CCTCCCAAAGTGCTGGGATTA 6914	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	CASP8	3'	CCTCCCAAAGTGCTGGGATTA 52920	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	CASP8	3'	CCTCCCAAAGTGCTGGGATTA 52931	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	CASP8	3'	CCTCCCAAAGTGCTGGGATTA 52944	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	CBFA2T2	3'	CCTCCCAAAGTGCCAGGATTA 17461	CA	A
			TAATCT GCACTTTG GGAGG		
			ATTAGG CGTGAAAC CCTCC		
			AC		
			—		
GAM1286	CCNF	3'	TCCCAAAGTGCTGGGATTA 8328	A	
			TAATCTCAGCACTTTG GGA		
			ATTAGGGTCGTGAAAC CCT		
			—		
GAM1286	CHRNA4	3'	CCTCCCAAAGTGCTGGGATTA 5630	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	CLECSF11	5'	CCTCCCAAAGTGCTGAGATTA 55275	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGAGTCGTGAAAC CCTCC		
			—		
GAM1286	CLECSF12	3'	CCTCCCAAAGTGCTGGGATTA 76685	A	
			TAATCTCAGCACTTTG GGAGG		



ATTAGGGTCGTGAAAC CCTCC

GAM1286	CNN2	3'	CCTCCCAAGCGCTGAGATTA	15175	A	T	A
			TAATCTCAGC CTT G GGAGG				
			ATTAGAGTCG GAA C CCTCC				
			C _ C				
GAM1286	COX15	3'	CTTCCCAAAGTGCTGAGATTA	54311	A		
			TAATCTCAGCACTTTG GGAGG				
			ATTAGAGTCGTGAAAC CCTTC				
GAM1286	CR1	3'	CCTCCCAAGTGCTGCGATTA	5132	T	A	
			TAATC CAGCACTTTG GGAGG				
			ATTAG GTCGTGAAAC CCTCC				
			C _				
GAM1286	CXCL16	3'	CCTCCCAAGTGCTGGGATTA	41917	A		
			TAATCTCAGCACTTTG GGAGG				
			ATTAGGGTCGTGAAAC CCTCC				
GAM1286	CYP1A2	3'	CCTCCCAAGTGCTGGGATTA	5686	A		
			TAATCTCAGCACTTTG GGAGG				
			ATTAGGGTCGTGAAAC CCTCC				
GAM1286	CYP1A2	3'	CCTCCCAAGTGCTGGGATTA	69106	A		
			TAATCTCAGCACTTTG GGAGG				
			ATTAGGGTCGTGAAAC CCTCC				
GAM1286	CYP2B6	3'	CCTCCCAAGTGCTGGGATTA	5727	A		
			TAATCTCAGCACTTTG GGAGG				
			ATTAGGGTCGTGAAAC CCTCC				
GAM1286	CYP2B6	3'	TTCCAAAGTGCTGATATTA	5747	C	A	
			TAAT TCAGCACTTTG GGA				
			ATTA AGTCGTGAAAC CTT				
			T _				
GAM1286	CYP4F3	3'	CCTCCCAAGTGCTGGGATTA	6114	A		
			TAATCTCAGCACTTTG GGAGG				
			ATTAGGGTCGTGAAAC CCTCC				
GAM1286	CYP51	3'	CCTCCCAAGTGCTGGGATTA	5782	A		
			TAATCTCAGCACTTTG GGAGG				

ATTAGGGTCGTGAAAC CCTCC

GAM1286	DFFB	3'	TCCCAAAGTGCTGGGATTA	87398	A
			TAATCTCAGCACTTTG	GGA	
			ATTAGGGTCGTGAAAC	CCT	
GAM1286	DHFR	3'	CCTCCCAAAGTGCTGGGATTA	5801	A
			TAATCTCAGCACTTTG	GGAGG	
			ATTAGGGTCGTGAAAC	CCTCC	
GAM1286	DISC1	3'	CTTCCCAAAGTGCTGAGATTA	37878	A
			TAATCTCAGCACTTTG	GGAGG	
			ATTAGAGTCGTGAAAC	CCTTC	
GAM1286	DNASE1L1	5'	CCTCCCAAAGTGCTGGGATTA	22074	A
			TAATCTCAGCACTTTG	GGAGG	
			ATTAGGGTCGTGAAAC	CCTCC	
GAM1286	DSC3	3'	CCTCCCAAAGTGCTGGGATTA	44339	A
			TAATCTCAGCACTTTG	GGAGG	
			ATTAGGGTCGTGAAAC	CCTCC	
GAM1286	DSC3	3'	CCTCCCAAAGTGCTGGGATTA	8674	A
			TAATCTCAGCACTTTG	GGAGG	
			ATTAGGGTCGTGAAAC	CCTCC	
GAM1286	DSCR3	3'	CCTCCCAAAGTGCTGAGATTA	20175	A
			TAATCTCAGCACTTTG	GGAGG	
			ATTAGAGTCGTGAAAC	CCTCC	
GAM1286	DSCR3	3'	CCTCCCAAAGTGCTGGGATTA	20176	A
			TAATCTCAGCACTTTG	GGAGG	
			ATTAGGGTCGTGAAAC	CCTCC	
GAM1286	EIF2S3	3'	CCTCACAAAGTGCTGGGATTA	7416	AG
			TAATCTCAGCACTTTG	GAGG	
			ATTAGGGTCGTGAAAC	CTCC	
GAM1286	EPB72	3'	CCTCCCAAAGTGCTGGATTA	14601	T
			TAATC CAGCACTTT	GGAGG	GA

ATTAG GTCGTGAAA CCTCC

GAM1286	EVC	3'	CCTCCCCAAAGTGCTGAGATTA 27293	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGAGTCGTGAAAC CCTCC	
			C	
GAM1286	F2RL2	3'	CCTCCCCAAAGTGCTGGATTA 14621	T A
			TAATC CAGCACTTTG GGAGG	
			ATTAG GTCGTGAAAC CCTCC	
GAM1286	FANCF	3'	CCTCCCCAAAGTGCTGGGATTA 42672	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
GAM1286	FCAR	3'	CCTCCCCAAAGTGCTGAGATTA 55746	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGAGTCGTGAAAC CCTCC	
GAM1286	FCAR	3'	CCTCCCCAAAGTGCTGAGATTA 55757	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGAGTCGTGAAAC CCTCC	
GAM1286	FCAR	3'	CCTCCCCAAAGTGCTGAGATTA 55768	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGAGTCGTGAAAC CCTCC	
GAM1286	FCAR	3'	CCTCCCCAAAGTGCTGAGATTA 55779	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGAGTCGTGAAAC CCTCC	
GAM1286	FCAR	3'	CCTCCCCAAAGTGCTGGGATTA 55792	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
GAM1286	FCAR	3'	CCTCCCCAAAGTGCTGAGATTA 8851	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGAGTCGTGAAAC CCTCC	
GAM1286	FEZ1	3'	CCTCCCCAAAGTGCTGGGATTA 42570	A
			TAATCTCAGCACTTTG GGAGG	

			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	FGF5	3'	CCTCCCCAAAGTGCTGGGATTA 52482	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			C		
GAM1286	FGF5	3'	CCTCCCCAAAGTGCTGGGATTA 15536	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			C		
GAM1286	FUT1	3'	CCTCCCCAAAGTGCTGGGATTA 3787	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	FZD4	3'	CCTCCCCAAAGTGCTGGGATTA 24133	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	GHR	3'	CCTCCCCAAAGTGCTGGGATTA 3880	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	GLTSCR1	5'	CCTCCCCAAAGTGCTGAGATTA 31670	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGAGTCGTGAAAC CCTCC		
			—		
GAM1286	GPR4	3'	CCTCCCCAAAGTGCTCAGATTA 59903	C	A
			TAATCT AGCACTTTG GGAGG		
			ATTAGA TCGTGAAAC CCTCC		
			C		
			—		
GAM1286	HCS	3'	CCTCCCCAAAGTGCTGGGATTA 38464	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	HLCS	5'	CCTCCCCAAAGTGCTGGGATTA 4662	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	HSD17B1	5'	CCTCCCCAAAGTGCTGGGATTA 4684	A	
			TAATCTCAGCACTTTG GGAGG		

ATTAGGGTCGTGAAAC CCTCC

GAM1286	HTR1D	3'	GCATCCCAAAGTGCTGGGATTA 5996	A	GG
			TAATCTCAGCACTTTG GGA GC		
			ATTAGGGTCGTGAAAC CCT CG		
GAM1286	HTR1E	5'	CCTCCCAAAGTGCTGGAATTA 6013	CT	A
			TAAT CAGCACTTTG GGAGG		
			ATTA GTCGTGAAAC CCTCC		
			AG		
GAM1286	HUNK	3'	CCTCCCAAAGTGCTGAGATTA 27447	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGAGTCGTGAAAC CCTCC		
GAM1286	IL11	3'	CCTCCCAAAGTGCTGGGATTA 5326	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	IMPA2	5'	CCTTGCAAAGTGCTGGGATTA 95238	AG	
			TAATCTCAGCACTTTG GAGG		
			ATTAGGGTCGTGAAAC TTCC		
			G_		
GAM1286	INMT	3'	CCTCCCAAAGTGCTGGGATTA 22267	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	LNK	3'	CCTCCCAAAGTGCTGGGATTA 18462	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	LTB4R	5'	CCTCCCAAAGTGCTGGGATTA 5645	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	LYZ	3'	CCTCCCAAAGTGCTGGGATTA 4097	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	LZTS1	3'	CCTCCCAAAGTGCTGAGATTG 40688	A	
			TAATCTCAGCACTTTG GGAGG		

			GTTAGAGTCGTGAAAC CCTCC	
			—	
GAM1286	MATN3	3'	CCTCCCAAAGTGCTGGGATTA 9936	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	MDM2	3'	CCTCCCAAAGTGCTGGGATTA 9971	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	MDM2	3'	CCTCCCAAAGTGCTGGGATTA 22517	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	MDM2	3'	CCTCCCAAAGTGCTGGGATTA 22521	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	MDM2	3'	CCTCCCAAAGTGCTGGGATTA 22509	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	MDM2	3'	CCTCCCAAAGTGCTGGGATTA 22513	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	MEFV	3'	CCTCCCAAAGTGCTGGGATTA 4131	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	MHC2TA	3'	CCTCCCAAAGTGCTGGGATTA 4168	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	MHC2TA	3'	CCTCCCAAAGTGCTGGGATTA 4169	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	MICB	3'	GCATCCCAAAGTGCTGGGATTA 19826	A GG
			TAATCTCAGCACTTTG GGA GC	

			ATTAGGGTCGTGAAAC CCT CG		
			— A —		
GAM1286	MLANA	3'	CCTCCCAAAGTGCTGGAATTA 18583	CT	A
			TAAT CAGCACTTTG GGAGG		
			ATTA GTCGTGAAAC CCTCC		
			AG —		
GAM1286	MLF2	5'	CCCCCTGGAGCTGAGAT 18374	ACT G	A
			ATCTCAGC TT AGG GGG		
			TAGAGTCG AG TCC CCC		
			— G —		
GAM1286	MPL	3'	CCTCCCAAAGTGCTGGGATTA 18137		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	MTR	3'	CCTCCCAAATGCTGGGATTA 4210	C	A
			TAATCTCAGCA TTTG GGAGG		
			ATTAGGGTCGT AAAC CCTCC		
			A —		
GAM1286	NCOA6IP	3'	CCCTCCCCAAGTGCTGGAATTA 45736	CT	T A
			TAAT CAGCACTT G GGAGGG		
			ATTA GTCGTGAA C CCTCCC		
			AG — C		
GAM1286	NDRG3	3'	CCTCCCAAAGTGCTGGGATTA 49295		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	NEU3	5'	GCCTTCCAAAGCGCTGAGATTG 21850	A	GA
			TAATCTCAGC CTTT GGAGGGC		
			GTTAGAGTCG GAAA CCTTCCG		
			C —		
GAM1286	NFRKB	5'	CCTCCCAAAGTACTGAGATTA 20496	C	A
			TAATCTCAG ACTTTG GGAGG		
			ATTAGAGTC TGAAAC CCTCC		
			A —		
GAM1286	NONO	3'	CCTCCCAAATGCTGGGATTA 82016	C	A
			TAATCTCAGCA TTTG GGAGG		
			ATTAGGGTCGT AAAC CCTCC		
			A —		
GAM1286	NQO1	3'	CCTCCCAAAGTGCTGGGATTA 6155		A
			TAATCTCAGCACTTTG GGAGG		

ATTAGGGTCGTGAAAC CCTCC

GAM1286	PCDHA9	3'	CCTCCCAAATGCTGGGATTA	25759	C	A
			TAATCTCAGCA TTTG GGAGG			
			ATTAGGGTCGT AAAC CCTCC			
			A _			
GAM1286	PCDHA9	3'	CCTCCCAAAGTGCTGGGATTA	25760		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
			_			
GAM1286	PCDHB11	3'	CCTCCCAAAGTGCTGGGATTA	38414		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
			_			
GAM1286	PCDHB11	3'	CCTCCCAAAGTGCTGTGATTA	38415	T	A
			TAATC CAGCACTTTG GGAGG			
			ATTAG GTCGTGAAAC CCTCC			
			T _			
GAM1286	PER2	3'	CCTCCCAAAGTGCTGGGATTA	43030		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
			_			
GAM1286	PIGR	3'	CCTCCCAAAGTGCTGGGATTA	72594		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
			_			
GAM1286	PIGR	3'	CTTCTCAAAGTACTGGGATTA	72601	C	
			TAATCTCAG ACTTTGAGGAG			
			ATTAGGGTC TGAACTCTTC			
			A			
GAM1286	PIK3C2B	3'	CCTCCCAAAGTGCTGGGATTA	10563		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
			_			
GAM1286	PIK3CD	3'	CCTCCCAAAGTGCTGGGATTA	17242		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
			_			
GAM1286	PMCHL1	3'	CTTCCCAAAGTGCTGGGATTA	49071		A
			TAATCTCAGCACTTTG GGAGG			



			ATTAGGGTCGTGAAAC CCTTC		
			—		
GAM1286	PPEF2	3'	CCTCCCAAAGTGCTGGGATTA 20667	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	PPID	3'	CCTCCCAAAGTGCTGGGATTA 87429	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	PRKR	3'	CCTCCCAAAGTGCTGGGATTA 10878	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	PSG6	3'	TCCCAAAGTGCTAGGATTA 10940	TC	A
			TAATC AGCACTTTG GGA		
			ATTAG TCGTGAAAC CCT		
			GA		
			—		
GAM1286	PTGIS	3'	CCTCCCAAAGTGCTAGGATTA 6330	TC	A
			TAATC AGCACTTTG GGAGG		
			ATTAG TCGTGAAAC CCTCC		
			GA		
			—		
GAM1286	PTGIS	3'	CCTCCCAAAGTGCTGGGATTA 6331	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	PTPN18	3'	CCTCCCAAAGTGCTGAGATTA 26863	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGAGTCGTGAAAC CCTCC		
			—		
GAM1286	PVR	3'	CCTCCCAAAGTGCTGAATTA 21476	C	A
			TAAT TCAGCACTTTG GGAGG		
			ATTA AGTCGTGAAAC CCTCC		
			—		
			—		
GAM1286	RAB36	3'	CCTCCCAAAGTGCTGGGATTA 16953	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	RAB36	3'	CCTCCCAAAGTGCTGGGATTA 16954	A	
			TAATCTCAGCACTTTG GGAGG		

			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	RABL2A	3'	CCTCCCAAAGTGCTGGGATTA 25501	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	RABL2B	3'	CCTCCCAAAGTGCTGGGATTA 23000	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	RAD1	5'	CCTCCCAAAGCGCTGGGATTA 55912	A	A
			TAATCTCAGC CTTTG GGAGG		
			ATTAGGGTCG GAAAC CCTCC		
			C —		
GAM1286	RGS9	5'	CCTCCCAAAGTGCTGGGATTA 13833	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	RHD	3'	CCTCCCAAAGTGCTGGA 32301 T	A	
			TC CAGCACTTTG GGAGG		
			AG GTCGTGAAAC CCTCC		
			— —		
GAM1286	RHD	3'	CCTCCCAAAGTGCTGGGATTA 32302	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	RHD	3'	CCTCCCAAAGTGCTGGA 32610 T	A	
			TC CAGCACTTTG GGAGG		
			AG GTCGTGAAAC CCTCC		
			— —		
GAM1286	RHD	3'	CCTCCCAAAGTGCTGGGATTA 32611	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	RPH3AL	3'	CCTCCCAAAGTGCTGGGATTA 22743	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	RPP30	3'	CCTCCCAAAGTGCTGGGATTA 21163	A	
			TAATCTCAGCACTTTG GGAGG		

ATTAGGGTCGTGAAAC CCTCC

GAM1286	SCML2	3'	CCTTGCAAAATGCTGGGATTA	20314	C	AG
			TAATCTCAGCA TTTG GAGG			
			ATTAGGGTCGT AAAC TTCC			
			A G_			
GAM1286	SEDL	3'	CCTCCCAAAGTACTGGGATTA	27330	C	A
			TAATCTCAG ACTTTG GGAGG			
			ATTAGGGTC TGAAAC CCTCC			
			A _			
GAM1286	SEDL	3'	CCTCCCAAAGTGCTAGGATTA	27331	TC	A
			TAATC AGCACTTTG GGAGG			
			ATTAG TCGTGAAAC CCTCC			
			GA _			
GAM1286	SEDL	3'	CCTCCCAAAGTGCTGGGATTA	27332		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
			_			
GAM1286	SEPN1	3'	CCTCCCAAAGTGCTGGGATTA	66365		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
			_			
GAM1286	SERPINB9	3'	CCTCCCAAAGTGCTAGGATTA	14751	TC	A
			TAATC AGCACTTTG GGAGG			
			ATTAG TCGTGAAAC CCTCC			
			GA _			
GAM1286	SERPINB9	3'	CCTCCCAAAGTGCTGGGATTA	14752		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
			_			
GAM1286	SH3BP2	3'	CCCTCCCATGTAGCTGGGATTA	11598	_ TT	A
			TAATCTCAGC AC TG GGAGGG			
			ATTAGGGTCG TG AC CCTCCC			
			A T_ _			
GAM1286	SH3BP2	3'	CCTCCCAAAGTGCTGGGATTA	11599		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
			_			
GAM1286	SIL	5'	CCTCCCAAATGCTGGGATTA	11687	C	A
			TAATCTCAGCA TTTG GGAGG			

			ATTAGGGTCGT AAAC CCTCC		
			A _		
GAM1286	SLA2	3'	CCTCCCAAAGTGCTGGGATTA 49897	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			-		
GAM1286	SLC15A1	3'	CAAAGTGCTGGGATTA 17397		
			TAATCTCAGCACTTTG		
			ATTAGGGTCGTGAAAC		
			-		
GAM1286	SLC17A5	3'	CCTCACAAAGTGTTGAGA 24890	AG	
			TCTCAGCACTTTG GAGG		
			AGAGTTGTGAAAC CTCC		
			A_		
GAM1286	SLC24A1	3'	CCTCCCAAAGTGCTGGGATTA 16375	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			-		
GAM1286	SNAP23	3'	CCTCCCAAAGTACTGGGATTA 13808	C	A
			TAATCTCAG ACTTTG GGAGG		
			ATTAGGGTC TGAAAC CCTCC		
			A _		
GAM1286	SNAP23	3'	CCTCCCAAAGTACTGGGATTA 55461	C	A
			TAATCTCAG ACTTTG GGAGG		
			ATTAGGGTC TGAAAC CCTCC		
			A _		
GAM1286	SNX15	3'	TCCCAAAGTGCTGAGATTA 73751	A	
			TAATCTCAGCACTTTG GGA		
			ATTAGAGTCGTGAAAC CCT		
			-		
GAM1286	SPN	3'	CCTCCCAAAGTGCTGAGATTA 11920	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGAGTCGTGAAAC CCTCC		
			-		
GAM1286	SULT2B1	5'	TCCCAAAGTGCTGGGATTA 16033	A	
			TAATCTCAGCACTTTG GGA		
			ATTAGGGTCGTGAAAC CCT		
			-		
GAM1286	TAPBP	3'	CCTCCCAAAGTGCTGGGATTA 12121	A	
			TAATCTCAGCACTTTG GGAGG		

		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	TAPBP	3' CCTCCCAAAGTGCTGGGATTA 12122	A	
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	TBXA2R	3' CCTCCCAAAGTGCTGGGAT 6486	A	
		ATCTCAGCACTTTG GGAGG		
		TAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	TERF1	3' CCTCCCAAAGTGCTGAGATTA 33970	A	
		TAATCTCAGCACTTTG GGAGG		
		ATTAGAGTCGTGAAAC CCTCC		
		—		
GAM1286	TERF2	3' CCTCCCAAAGTGCTGGGATTA 18946	A	
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	TES	3' CCTCCCAAAGTGCTGGGATTA 72002	A	
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	TIM3	3' CCTCCCAAAGCACTGGGATTA 51339	CA	A
		TAATCTCAG CTTTG GGAGG		
		ATTAGGGTC GAAAC CCTCC		
		AC —		
GAM1286	TIMM23	3' CCTCCCAAAGTGCCGAGATTG 60139	A	A
		TAATCTC GCACTTTG GGAGG		
		GTTAGAG CGTGAAAC CCTCC		
		C —		
GAM1286	TIRAP	3' CCCAAAGTGCTGGGATTA 53568	A	
		TAATCTCAGCACTTTG GG		
		ATTAGGGTCGTGAAAC CC		
		—		
GAM1286	TNFAIP1	5' GCCCCCGGGGACGCACTGAGAT 40923	CAC_	GA A
	TA	TAATCTCAG TTT GG GGGC		
		ATTAGAGTC AGG CC CCCG		
		ACGC GG _		
GAM1286	TNFRSF11A	3' CCTCCCAAAGTACTGGGATTA 13852	C	A
		TAATCTCAG ACTTTG GGAGG		

			ATTAGGGTC TGAAAC CCTCC		
			A _		
GAM1286	TNFRSF9	3'	CCTCCCAAAGTGCTGGGATTA 7787		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			-		
GAM1286	TP53BP2	5'	CCTCCCAAAGTGCTGGATTA 18301	T	A
			TAATC CAGCACTTTG GGAGG		
			ATTAG GTCGTGAAAC CCTCC		
			-		
GAM1286	TPMT	3'	CCCAAAGTGCTAGGATTA 4536	TC	A
			TAATC AGCACTTTG GG		
			ATTAG TCGTGAAAC CC		
			GA		
			-		
GAM1286	TPMT	3'	CCTCCCAAAGTGCTGGGATTA 4537		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			-		
GAM1286	TRAF5	3'	CCTCCCAAAGTGCTGAGATTA 16077		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGAGTCGTGAAAC CCTCC		
			-		
GAM1286	TRPM6	3'	CTTCCCAAAGTGCTGGGATTA 34540		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTTC		
			-		
GAM1286	TRPV1	3'	CCTCCCAAAGTGCTGGGATTA 38074		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			-		
GAM1286	TRPV1	3'	CCTCCCAAAGTGCTGGGATTA 38075		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			-		
GAM1286	TRPV1	3'	CCTCCCAAAGTGCTGGGATTA 54795		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			-		
GAM1286	TRPV1	3'	CCTCCCAAAGTGCTGGGATTA 54796		A
			TAATCTCAGCACTTTG GGAGG		

			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	TRPV1	3'	CCTCCCAAAGTGCTGGGATTA 54828		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	TRPV1	3'	CCTCCCAAAGTGCTGGGATTA 54829		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	TRPV1	3'	CCTCCCAAAGTGCTGGGATTA 54860		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	TRPV1	3'	CCTCCCAAAGTGCTGGGATTA 54861		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	TUFT1	3'	CTTCCCAAAGTGCTAGGATTA 39260	TC	A
			TAATC AGCACTTTG GGAGG		
			ATTAG TCGTGAAAC CCTTC		
			GA —		
GAM1286	UGDH	3'	CCTCCCAAAGTGCTGGGATTA 12542		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	UMPS	3'	TCTCAAAGTGCTGGGATTA 4560		
			TAATCTCAGCACTTTGAGG		
			ATTAGGGTCGTGAAACTCT		
			—		
GAM1286	VENTX2	3'	CCTCCCAAAGTGCTGGGATTA 27109		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	VHL	3'	CCCTCCTGAGCTGGGATTA 5067	ACTT G	
			TAATCTCAGC T AGGAGGG		
			ATTAGGGTCG A TCCTCCC		
			— G		
GAM1286	VIPR2	3'	CCTCCCAAAGTGCTGGGATTA 12607		A
			TAATCTCAGCACTTTG GGAGG		

			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	WHSC1	5'	CCTCCCAAAGTGCTGGGATTA 23657	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	WHSC1	5'	CCTCCCAAAGTGCTGGGATTA 29908	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	WHSC1	5'	CCTCCCAAAGTGCTGGGATTA 55826	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	WHSC1	5'	CCTCCCAAAGTGCTGGGATTA 55843	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	XRCC2	3'	CCTCCCAAAGTGCTAGGATTA 18319	TC	A
			TAATC AGCACTTTG GGAGG		
			ATTAG TCGTGAAAC CCTCC		
			GA —		
GAM1286	YES1	3'	CCTCCCAAAGTGCTGGGATTA 18351	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	ZNF133	5'	CCTCCCAAATGCTGGGATTA 12834	C	A
			TAATCTCAGCA TTTG GGAGG		
			ATTAGGGTCGT AAAC CCTCC		
			A —		
GAM1286	ZNF74	5'	CCTCCCAAAGTGCTGGGATTA 12793	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	APOL2	3'	CCTCCCAAAGTGCTGGGATTA 48045	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	ARHF	3'	CCTCCCAAAGTGCTGGGATTA 38739	A	
			TAATCTCAGCACTTTG GGAGG		



		ATTAGGGTCGTGAAAC CCTCC		
GAM1286	ARHGAP11A 3'	CCTCCCAAAGTGCTGGGATTA 28794 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC		A
GAM1286	ARHGAP5 5'	CCTCCCAAAGTGCTGCGATTA 77071 TAATC CAGCACTTTG GGAGG       ATTAG GTCGTGAAAC CCTCC C	T	A
GAM1286	ARPP-19 3'	CCTCCCAAAGTGCTGGGATTA 21793 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC		A
GAM1286	ASB16 3'	CCTCCCAAAGTGCTGGGATTA 69933 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC		A
GAM1286	BA108L7.2 3'	CCTCCCAAAGCACTGGGATTA 48260 TAATCTCAG CTTTG GGAGG       ATTAGGGTC GAAAC CCTCC AC	CA	A
GAM1286	BNIP-S 3'	CCTCCCAAAGTGCCGAGATTA 56258 TAATCTC GCACTTTG GGAGG       ATTAGAG CGTGAAAC CCTCC C	A	A
GAM1286	BTN3A1 3'	TCCCAAAGTGCTGGGATTA 22927 TAATCTCAGCACTTTG GGA       ATTAGGGTCGTGAAAC CCT		A
GAM1286	C13orf1 3'	CCTCCCAAAGTGCTGGAATTA 39966 TAAT CAGCACTTTG GGAGG       ATTA GTCGTGAAAC CCTCC AG	CT	A
GAM1286	C1orf24 3'	CTTCCCAAAGTGCTGGGATTA 53715 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTTC		A
GAM1286	C1QTNF6 3'	GCCTCTCAAATGCTGGGATTA 49146 TAATCTCAGCA TTTGAG GGGC 	C	GA

		ATTAGGGTCGT AA	CTC	TCCG	
		A	—		
GAM1286	C20orf142	3'	CCTCCCAAAGTGCTGGGATTA	74770	A
			TAATCTCAGCACTTTG	GGAGG	
			ATTAGGGTCGTGAAAC	CCTCC	
			—		
GAM1286	C22orf19	3'	CCTCCCAAAGTGCTAGGATTA	13419	TC A
			TAATC AGCACTTTG	GGAGG	
			ATTAG TCGTGAAAC	CCTCC	
			GA	—	
GAM1286	C2F	3'	TTCCCAAAGTGCTGGGATTA	20935	A
			TAATCTCAGCACTTTG	GGAG	
			ATTAGGGTCGTGAAAC	CCTT	
			—		
GAM1286	C3F	3'	CCTCCCAAAGTGCTGGGATTA	19289	A
			TAATCTCAGCACTTTG	GGAGG	
			ATTAGGGTCGTGAAAC	CCTCC	
			—		
GAM1286	C6orf5	3'	CCTCCCAAAGTGCTAGGATTA	31344	TC A
			TAATC AGCACTTTG	GGAGG	
			ATTAG TCGTGAAAC	CCTCC	
			GA	—	
GAM1286	C6orf5	3'	CCTCCCAAAGTGCTGGGATTA	31345	A
			TAATCTCAGCACTTTG	GGAGG	
			ATTAGGGTCGTGAAAC	CCTCC	
			—		
GAM1286	C9orf9	3'	CCTCCCAAAGTGCTGGGATTA	38507	A
			TAATCTCAGCACTTTG	GGAGG	
			ATTAGGGTCGTGAAAC	CCTCC	
			—		
GAM1286	C9orf9	3'	CCTCCCAAAGTGCTGGGATTA	38508	A
			TAATCTCAGCACTTTG	GGAGG	
			ATTAGGGTCGTGAAAC	CCTCC	
			—		
GAM1286	CDC14B	3'	CCTCCCAAAGTGCTGGGATTA	52847	A
			TAATCTCAGCACTTTG	GGAGG	
			ATTAGGGTCGTGAAAC	CCTCC	
			—		
GAM1286	CECR1	3'	CCTCCCAAAGCACTGGGATTA	33810	CA A
			TAATCTCAG CTTTG	GGAGG	

			ATTAGGGTC GAAAC CCTCC		
			AC _		
GAM1286	CECR1	3'	CTCCCAAAGTGCTGGAATTA 33812	CT	A
			TAAT CAGCACTTTG GGAG		
			ATTA GTCGTGAAAC CCTC		
			AG _		
GAM1286	CIP29	3'	CCTCCCAAAGTGCTGGATTA 50403	T	A
			TAATC CAGCACTTTG GGAGG		
			ATTAG GTCGTGAAAC CCTCC		
			_ _		
GAM1286	COQ7	3'	CTTCCCAAAGTGCTGGGATTA 32331		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTTC		
			_		
GAM1286	CPSF2	3'	CCTCCCAAAGTGCTGGGATTA 61576		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			_		
GAM1286	CPSF2	3'	CCTCCCAAAGTGCTGGGATTA 61577		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			_		
GAM1286	DCOHM	3'	CCTCCCAAAGTGCTGGGATTA 49594		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			_		
GAM1286	DKFZp434A2417	3'	CCTCCCAAAGTGCTGGGATTA 66099		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			_		
GAM1286	DKFZP434F0318	3'	CTTCCCAAAGTGCTGGGATTA 48010		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTTC		
			_		
GAM1286	DKFZp434F1819	5'	CAAAGTGCTGGGATTA 50005		
			TAATCTCAGCACTTTG		
			ATTAGGGTCGTGAAAC		
			_		
GAM1286	DKFZP434J037	3'	CCTCCCAAAGTGCTGGGATTA 48209		A
			TAATCTCAGCACTTTG GGAGG		

ATTAGGGTCGTGAAAC CCTCC

GAM1286 DKFZp547H025 3' CCTCCCAAAGTGCTGGGATTA 39355 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 DKFZP564K0322 3' CCTCCCAAATGCTGGGATTA 49358 C A  
TAATCTCAGCA TTTG GGAGG  
|||||  
ATTAGGGTCGT AAAC CCTCC

A  
GAM1286 DKFZP566I1024 3' CCTCCCAAAGTGCTGGGATTA 70099 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 DKFZp761J139 5' CCTCCCAAAGTGCTGGGATTA 50106 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 DKFZp761N1114 3' CCTCCCAAAGTGCTGGGATTA 79016 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 DRIM 3' CCTCCCAAAGTGCTGGGATTA 27177 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 DSCR6 3' CCTCCCAAAGTGCTGGGATTA 38544 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 EVI5 3' CCTCCCAAAGTGCTGGGATTA 18993 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 EVI5 3' CCTCCCAAAGTGCTGGGATTA 18994 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 FBP17 3' CCTCCCAAAGTGCTGAGATTA 72785 A  
TAATCTCAGCACTTTG GGAGG  
|||||

		ATTAGAGTCGTGAAAC CCTCC	
		—	
GAM1286	FER1L4	3' CCTCCCAAAGTGCTGGGATTA 47337	A
		TAATCTCAGCACTTTG GGAGG	
		ATTAGGGTCGTGAAAC CCTCC	
		—	
GAM1286	FLB6421	3' TCCCAAAGTGCTGGGATTA 39234	A
		TAATCTCAGCACTTTG GGA	
		ATTAGGGTCGTGAAAC CCT	
		—	
GAM1286	FLJ00060	5' CCTCCCAAAGTGCTGGGATTA 61095	A
		TAATCTCAGCACTTTG GGAGG	
		ATTAGGGTCGTGAAAC CCTCC	
		—	
GAM1286	FLJ10298	3' CCTCCCAAAGTGCTGGGATTA 35986	A
		TAATCTCAGCACTTTG GGAGG	
		ATTAGGGTCGTGAAAC CCTCC	
		—	
GAM1286	FLJ10346	5' CCTCCCAAAGTGCTGGGATTA 36040	A
		TAATCTCAGCACTTTG GGAGG	
		ATTAGGGTCGTGAAAC CCTCC	
		—	
GAM1286	FLJ10535	3' CCTCCCAAAGTGCTGGGATTA 36236	A
		TAATCTCAGCACTTTG GGAGG	
		ATTAGGGTCGTGAAAC CCTCC	
		—	
GAM1286	FLJ10535	3' CCTCCCAAAGTGCTGGGATTA 36237	A
		TAATCTCAGCACTTTG GGAGG	
		ATTAGGGTCGTGAAAC CCTCC	
		—	
GAM1286	FLJ10560	3' CCTCCCAAAGTGCTGGGATTA 36276	A
		TAATCTCAGCACTTTG GGAGG	
		ATTAGGGTCGTGAAAC CCTCC	
		—	
GAM1286	FLJ10687	3' CCTCCCAAAGTGCTGAGATTA 36408	A
		TAATCTCAGCACTTTG GGAGG	
		ATTAGAGTCGTGAAAC CCTCC	
		—	
GAM1286	FLJ10713	3' CCTCCCAAATGCTGGGA 36466	C A
		TCTCAGCA TTTG GGAGG	

			AGGGTCGT AAAC CCTCC		
			A _		
GAM1286	FLJ10846	3'	CCTCCCAAAGTGCTGGAATTA 36737	CT	A
			TAAT CAGCACTTTG GGAGG		
			ATTA GTCGTGAAAC CCTCC		
			AG _		
GAM1286	FLJ10922	3'	CCCAAAGTGCTGGAATTA 36873	CT	A
			TAAT CAGCACTTTG GG		
			ATTA GTCGTGAAAC CC		
			AG _		
GAM1286	FLJ10956	3'	CCTCCCAAAGTGCTGGGATTA 36916		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			_		
GAM1286	FLJ12610	3'	CCTCCCAAAGTGCTGGGATTA 45512		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			_		
GAM1286	FLJ12644	3'	CCTCATGATGAGATTA 43556	G CTT	
			TAATCTCA CA TGAGG		
			ATTAGAGT GT ACTCC		
			A _		
GAM1286	FLJ12747	3'	CCTCCCAAAGTGCTGGGATTA 49715		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			_		
GAM1286	FLJ12975	3'	CCTCCCAAAGTGCTGAGATTA 69578		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGAGTCGTGAAAC CCTCC		
			_		
GAM1286	FLJ12975	3'	CCTCCCAAAGTGCTGGGAT 69579		A
			ATCTCAGCACTTTG GGAGG		
			TAGGGTCGTGAAAC CCTCC		
			_		
GAM1286	FLJ13072	5'	CCTCCCAAAGTGCTGGGATTA 89807		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			_		
GAM1286	FLJ13102	3'	CCCTCCCAAAGTGCTGGGATTA 46006		A
			TAATCTCAGCACTTTG GGAGGG		

ATTAGGGTCGTGAAAC CCTCCC

GAM1286 FLJ13114 3' CCTCCCAAAGTGCTGGGATTA 44595 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 FLJ13193 3' CCTCCCAAAGTGCTGGGAT 49763 A  
ATCTCAGCACTTTG GGAGG  
|||||  
TAGGGTCGTGAAAC CCTCC

GAM1286 FLJ13197 3' CCTCCCAAAGTGCTGGGATTA 44849 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 FLJ13305 5' CCCAAAGTGCTGGGATTA 90126 A  
TAATCTCAGCACTTTG GG  
|||||  
ATTAGGGTCGTGAAAC CC

GAM1286 FLJ13952 3' CTTCCCAAAGTGCTGGGATTA 45615 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTTC

GAM1286 FLJ14351 3' CCTCCCAAAGTGCTAGGATTA 45322 TC A  
TAATC AGCACTTTG GGAGG  
|||||  
ATTAG TCGTGAAAC CCTCC  
GA

GAM1286 FLJ14442 3' CCTCCCAAAGTGCTGAGATTA 51365 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGAGTCGTGAAAC CCTCC

GAM1286 FLJ14824 3' CAAAGTGCTGGATTA 51640 T  
TAATC CAGCACTTTG  
|||||  
ATTAG GTCGTGAAAC

GAM1286 FLJ14950 3' CCTCCCAAAGTGCTGGGATTA 51717 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 FLJ14957 3' CCTCCCAAAGTGCTGAGATTA 51745 A  
TAATCTCAGCACTTTG GGAGG  
|||||

	ATTAGAGTCGTGAAAC CCTCC	
	—	
GAM1286 FLJ20045 3'	CCTCCCAAAGTGCTGGGATTA 34417	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 FLJ20079 3'	CCTCCCAAAGTGCTGGGATTA 34491	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 FLJ20097 3'	CCTCCCAAAGTGCTGGGATTA 34561	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 FLJ20136 3'	CCTCCCAAAGTGCTGGGATTA 34610	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 FLJ20342 3'	CCTCCCAAAGTGCTGGGATTA 34988	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 FLJ20344 3'	CCTCCCAAAGTGCTGGGATTA 35008	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 FLJ20452 3'	GCCCTCCCAAAGTGCTGGGATT 35204	A
A	TAATCTCAGCACTTTG GGAGGGC	
	ATTAGGGTCGTGAAAC CCTCCCG	
	—	
GAM1286 FLJ20507 3'	CCTCCCAAAGTGCTGGGATTA 35279	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 FLJ20507 3'	CCTCCCAAAGTGCTGGGATTA 60214	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 FLJ20671 3'	CCTCCCAAAGTGCTGGGATTA 35520	A
	TAATCTCAGCACTTTG GGAGG	



		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	FLJ20700	3' CCTCCCAAAGTGCTGGGATTA 35572		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	FLJ21302	3' CCTCCCAAAGTGCTGGGATTA 43213		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	FLJ22002	3' CCTCCCAAAGTGCTAGGATTA 45770	TC	A
		TAATC AGCACTTTG GGAGG		
		ATTAG TCGTGAAAC CCTCC		
		GA —		
GAM1286	FLJ22316	5' CCTCCCAAAGTGCTGGGATTA 46918		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	FLJ22969	3' CCTCCCAAAGTGCTGGGATTA 68648		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	FLJ23024	3' CCTCCCAAAGTGCTGGGATTA 46268		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	FLJ23209	3' TCCCAAAGTGCTAGGATTA 46056	TC	A
		TAATC AGCACTTTG GGA		
		ATTAG TCGTGAAAC CCT		
		GA —		
GAM1286	FLJ23323	3' TCCCAAAGTGCTGGGATTA 45058		A
		TAATCTCAGCACTTTG GGA		
		ATTAGGGTCGTGAAAC CCT		
		—		
GAM1286	FLJ23356	3' CCTCCCAAAGTGCTGGGATTA 49937		GA
		TAATCTCAGCACTTT GGAGG		
		ATTAGGGTCGTGAAA CCTCC		
		—		
GAM1286	FLJ23392	3' CCTCCCAAAGTGCTGGGATTA 45530		A
		TAATCTCAGCACTTTG GGAGG		

			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	FLJ23392	3'	GCCTTAAAAAGTGCTGGGATTA 45535		GAGG
			TAATCTCAGCACTTT AGGGC		
			ATTAGGGTCGTGAAA TTCCG		
			AA__		
GAM1286	FLJ23556	3'	CCTCCCAAAGTGCTGGGATTA 45945		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	FLJ31101	3'	CCTCCCAAAGTGCTGGGATTA 35708		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	FLJ31153	3'	CCTCCCAAAGCGCTGGGATTA 58120	A	A
			TAATCTCAGC CTTTG GGAGG		
			ATTAGGGTCG GAAAC CCTCC		
			C —		
GAM1286	FLJ32334	3'	CCTCCCAAAGTGCTGGGATTA 57982		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	FLJ32865	3'	CCTCCCAAAGTGCTGGGATTA 58171		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	FLJ32894	3'	CCTCCCAAAGTGCTGGGATTA 58338		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	GMPPB	5'	CTTCCCAAAGTGCTGGGATTA 95737		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTTC		
			—		
GAM1286	GNG4	3'	CCTCCCAAAGCGCTGGGATTA 15612	A	A
			TAATCTCAGC CTTTG GGAGG		
			ATTAGGGTCG GAAAC CCTCC		
			C —		
GAM1286	GOLGA3	3'	CCTCCCAAAGTGCTGGAATTA 19714	CT	A
			TAAT CAGCACTTTG GGAGG		

			ATTA GTCGTGAAAC CCTCC		
			AG —		
GAM1286	GP5	3'	CCTCCCAAAGTGCTGGGATTA 15642	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	GREB1	3'	CCTCCCAAAGTGCTGGGATTA 27867	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	GTPBG3	3'	CCTCCCAAAGTGCTGGGAT 50896	A	
			ATCTCAGCACTTTG GGAGG		
			TAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	HARS2	3'	CCTCCCAAAGTGCTGGGATTA 55032	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	HRH4	3'	CCTCCCAAAGTGCTGGGATTA 41250	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	HSNOV1	3'	CCTCCCAAAGTGCTGGGATTA 34006	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	HSPC065	3'	GCCCTCTCAAAGTGCTGGGATT 26304	G	
	A		TAATCTCAGCACTTTGAG AGGGC		
			ATTAGGGTCGTGAAACTC TCCCG		
			—		
GAM1286	ICK	3'	CCTCCCAAAGTACTGGGATTA 29925	C	A
			TAATCTCAG ACTTTG GGAGG		
			ATTAGGGTC TGAAAC CCTCC		
			A —		
GAM1286	JM11	3'	CCTCCCAAAGTGCTGGGATTA 53255	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			—		
GAM1286	KIAA0022	3'	TCCCAAAGTGCTGGGATTA 29672	A	
			TAATCTCAGCACTTTG GGA		

ATTAGGGTCGTGAAAC CCT

GAM1286 KIAA0063 3' CCTCCCAAAGTGCTGGGATTA 29620 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 KIAA0087 3' CCTCCCAAATGCTGGGATTA 28696 C A  
TAATCTCAGCA TTTG GGAGG  
|||||  
ATTAGGGTCGT AAAC CCTCC

A  
GAM1286 KIAA0090 3' CCTCCCAAAGTGCCGGGATTA 88440 A A  
TAATCTC GCACTTTG GGAGG  
|||||  
ATTAGGG CGTGAAAC CCTCC

C  
GAM1286 KIAA0161 3' CTTCCCAAAGTGCTGGAATTA 28505 CT A  
TAAT CAGCACTTTG GGAGG  
||| |||||  
ATTA GTCGTGAAAC CCTTC  
AG

GAM1286 KIAA0186 3' CTTCTCAAAGTGTTGAGAT 40749  
ATCTCAGCACTTTGAGGAG  
|||||  
TAGAGTTGTGAAACTCTTC

GAM1286 KIAA0210 5' CCTCCCAAAGTGCTGGGATTA 28474 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 KIAA0391 3' CCTCCCAAAGTGCTGGGATTA 27910 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 KIAA0459 3' CCTCCCAAAGTGCTAGGATTA 60987 TC A  
TAATC AGCACTTTG GGAGG  
||| |||||  
ATTAG TCGTGAAAC CCTCC  
GA

GAM1286 KIAA0469 3' CCTCCCAAAGTGCTAGGATTA 29325 TC A  
TAATC AGCACTTTG GGAGG  
||| |||||  
ATTAG TCGTGAAAC CCTCC  
GA

GAM1286 KIAA0469 3' CCTCCCAAAGTGCTGGGATTA 29326 A  
TAATCTCAGCACTTTG GGAGG  
|||||

		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	KIAA0472	5' CCTCCCAAAGTGCTGGGATTA 71862		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	KIAA0478	3' CCTCCCAAAGTGCTAGGATTA 29545	TC	A
		TAATC AGCACTTTG GGAGG		
		ATTAG TCGTGAAAC CCTCC		
		GA		
		—		
GAM1286	KIAA0495	3' CCTCCCAAAGTGCTGGGATTA 62578		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	KIAA0513	3' CCTCCCAAAGTGCTGGGATTA 28350		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	KIAA0544	3' CCTCCCAGAGTGCTGAGATTA 70901		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGAGTCGTGAGAC CCTCC		
		—		
GAM1286	KIAA0555	3' CCTCCCAAAGTGCTAGGATTA 28881	TC	A
		TAATC AGCACTTTG GGAGG		
		ATTAG TCGTGAAAC CCTCC		
		GA		
		—		
GAM1286	KIAA0557	3' CCTCCCAAAGTGCTGGGATTA 77994		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	KIAA0561	3' CCTCCCAAAGTGCTGGGATTA 65878		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	KIAA0562	3' CCTCCCAAAGTGCTGGAATTA 28150	CT	A
		TAAT CAGCACTTTG GGAGG		
		ATTA GTCGTGAAAC CCTCC		
		AG		
		—		
GAM1286	KIAA0594	3' CCTCCCAAAGTGCTGGGATTA 64893		A
		TAATCTCAGCACTTTG GGAGG		

		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	KIAA0599	3' CCTCCCAAAGTGCTGGGATTA 77174		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	KIAA0682	3' TCCCAAAGTGCTGAGATTA 29372		A
		TAATCTCAGCACTTTG GGA		
		ATTAGAGTCGTGAAAC CCT		
		—		
GAM1286	KIAA0737	3' CCTCCCAAAGTGCTGGGATTA 29133		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	KIAA0798	3' CCTCCCAAAGTGCTGGGATTA 27721		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	KIAA0831	5' CCTCCCAAAGTGCTGCGATTA 29969	T	A
		TAATC CAGCACTTTG GGAGG		
		ATTAG GTCGTGAAAC CCTCC		
		C —		
GAM1286	KIAA0841	3' CCTCCCAAAGTGCTGGGATTA 71380		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	KIAA0861	3' CCTCCCAAAGTGCTGGGATTA 88921		A
		TAATCTCAGCACTTTG GGAGG		
		ATTAGGGTCGTGAAAC CCTCC		
		—		
GAM1286	KIAA0931	3' CCTCCCAAAGTGCTGTGATTA 67417	T	A
		TAATC CAGCACTTTG GGAGG		
		ATTAG GTCGTGAAAC CCTCC		
		T —		
GAM1286	KIAA1010	3' CCCGCCTCCCTGCTGAGATTA 72071	CTTT	A
		TAATCTCAGCA GAGG GGG		
		ATTAGAGTCGT CTCC CCC		
		CC__ G		
GAM1286	KIAA1026	3' TCCCAAAGTGCTGGGATTA 71210		A
		TAATCTCAGCACTTTG GGA		

ATTAGGGTCGTGAAAC CCT

GAM1286	KIAA1040	3'	CCTCCCAAAGTGCTGACATTA 72224	C	A
			TAAT TCAGCACTTTG GGAGG		
			ATTA AGTCGTGAAAC CCTCC		
			C		
GAM1286	KIAA1054	3'	CCTCCCAAATGCTGGGATTA 68432	C	A
			TAATCTCAGCA TTTG GGAGG		
			ATTAGGGTCGT AAAC CCTCC		
			A		
GAM1286	KIAA1143	3'	CCTCCCAAAGTGCTGGGATTA 68674		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	KIAA1155	3'	CCTCCCAAAGTGCTGGGATTA 62230		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	KIAA1185	3'	CCCCTCAAAGTGCTGGGATTA 62603		A
			TAATCTCAGCACTTTGAGG GG		
			ATTAGGGTCGTGAAACTCC CC		
GAM1286	KIAA1185	3'	CCTCCCAAAGTGCTGGGATTA 62604		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	KIAA1193	3'	CCTCCCAAAGTGCTGGGATTA 67636		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	KIAA1198	3'	CCCAAAGTGCTGGGATTA 63296		A
			TAATCTCAGCACTTTG GG		
			ATTAGGGTCGTGAAAC CC		
GAM1286	KIAA1198	3'	CCTCCCAAAGTGCTGGGATTA 63298		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	KIAA1198	3'	CCTCCCAAAGTGCTGGGATTA 63299		A
			TAATCTCAGCACTTTG GGAGG		

	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 KIAA1198 3'	CCTCCCAAAGTGCTGGGATTA 63300	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 KIAA1200 3'	CCTCCCAAAGTGCTGGGATTA 62370	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 KIAA1254 3'	CCTCCCAAAGTGCTGGGATTA 70017	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 KIAA1257 3'	CCTCCCAAAGTGCTGGGATTA 62734	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 KIAA1287 3'	CCTCCCAAAGTGCTGGGATTA 78326	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 KIAA1320 5'	CCTCCCAAAGTGCTGGGATTA 69300	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 KIAA1328 5'	CCTCCCAAAGTGCTGGGATTA 61643	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGGGTCGTGAAAC CCTCC	
	—	
GAM1286 KIAA1349 5'	CCTCCCAAAGTGCTGAGATTA 70755	A
	TAATCTCAGCACTTTG GGAGG	
	ATTAGAGTCGTGAAAC CCTCC	
	—	
GAM1286 KIAA1373 3'	CCTCTCAAAGTGCTGGGATTA 70934	G
	TAATCTCAGCACTTTGAG AGG	
	ATTAGGGTCGTGAAACTC TCC	
	—	
GAM1286 KIAA1373 3'	CTTCCCAAAGTGCTGAGATTA 70936	A
	TAATCTCAGCACTTTG GGAGG	



ATTAGAGTCGTGAAAC CCTTC

GAM1286 KIAA1432 5' TTCTCAAACACTGAAATTG 66754 C CAC  
TAAT TCAG TTTGAGGA  
||||| |||||  
GTTA AGTC AAACCTCTT  
A ACA

GAM1286 KIAA1443 3' CCTCCCAAAGTGCTGGGATTA 63827 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 KIAA1456 3' GCCCCCCACAGTGCTGGGATTA 66997 T A A  
TAATCTCAGCACT TG GG GGGC  
||||| || || ||||  
ATTAGGGTCGTGA AC CC CCCG  
C \_ \_

GAM1286 KIAA1467 3' CCTCCCAAAGTGCTGGGATTA 71604 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 KIAA1493 3' CCTCCCAAAGTGCTGGGATTA 64158 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 KIAA1508 3' CAAAGTGCTGGGATTA 61878  
TAATCTCAGCACTTTG  
|||||  
ATTAGGGTCGTGAAAC

GAM1286 KIAA1571 3' CCTCCCAAAGTGCTGGGATTA 60953 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 KIAA1615 3' CCTCCCAAAGTGCTGGGATTA 68703 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 KIAA1615 3' CCTCCCAAAGTGCTGGGATTA 68704 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 KIAA1655 3' CCTCCCAAAGTGCTGGGATTA 66603 A  
TAATCTCAGCACTTTG GGAGG  
|||||

	ATTAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 KIAA1668	3' CCTCCCAAAGTGCTGGGATTA 66470	A	
	TAATCTCAGCACTTTG GGAGG		
	ATTAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 KIAA1671	3' CCTCCCAAAGTGCTGGGATTA 65670	A	
	TAATCTCAGCACTTTG GGAGG		
	ATTAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 KIAA1727	3' CCTCCCAAAGTGCTGGGATTA 64055	A	
	TAATCTCAGCACTTTG GGAGG		
	ATTAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 KIAA1755	3' CCTCCCAAAGTGCTGGGATTA 61341	A	
	TAATCTCAGCACTTTG GGAGG		
	ATTAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 KIAA1784	3' CCTCCCAAAGTGCTGGGAT 65146	A	
	ATCTCAGCACTTTG GGAGG		
	TAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 KIAA1821	3' CAAAGCACTGGGATTA 71777	CA	
	TAATCTCAG CTTTG		
	ATTAGGGTC GAAAC		
	AC		
GAM1286 KIAA1829	3' CTCCCAAAGTGCTGGGATTA 61947	A	
	TAATCTCAGCACTTTG GGAG		
	ATTAGGGTCGTGAAAC CCTC		
	—		
GAM1286 KIAA1829	3' CTTCCCAAAGTGCTGAGATTA 61948	A	
	TAATCTCAGCACTTTG GGAGG		
	ATTAGAGTCGTGAAAC CCTTC		
	—		
GAM1286 KIAA1922	5' CCTCCCAAATGCTGAGATTA 73621	C A	
	TAATCTCAGCA TTTG GGAGG		
	ATTAGAGTCGT AAAC CCTCC		
	A —		
GAM1286 KIAA1924	3' CCTCCCAAAGTGCTGGGAT 73668	A	
	ATCTCAGCACTTTG GGAGG		

GAM1286	KIAA1971	3'	CTCCCAAAGTGCTGGGATTA	74215		A
			TAATCTCAGCACTTTG GGAG			
			ATTAGGGTCGTGAAAC CCTC			
GAM1286	KIAA1975	5'	CCTCCCAAAGTGCTAGGATTA	73970	TC	A
			TAATC AGCACTTTG GGAGG			
			ATTAG TCGTGAAC CCTCC			
			GA			
GAM1286	KLK7	3'	CCTCCCAAAGTGCTGGGATTA	57730		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
GAM1286	KLK7	3'	CCTCCCAAAGTGCTGGGATTA	17290		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
GAM1286	LAMP3	3'	CCTCCCAAAGTGCTGGGATTA	59488		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
GAM1286	LY75	3'	CCTCCCAAAGTGCTGGGATTA	9836		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
GAM1286	MAIL	3'	TCCCAAATGCTGGGATTA	48654	C A	
			TAATCTCAGCA TTTG GGA			
			ATTAGGGTCGT AAAC CCT			
			A			
GAM1286	MCLC	3'	CCTCCCAAAGTGCTGGGATTA	30679		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
GAM1286	MGC10200	3'	CCTCCCAAAGTGCTGGGATTA	58983		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
GAM1286	MGC11386	3'	CCTCAAAGTATTGAGATTA	51949	C	
			TAATCTCAG ACTTTGAGG			

	ATTAGAGTT TGAAACTCC		
	A		
GAM1286 MGC12518 3'	CCTCCCAAAGTGCTGGGATTA 64079	A	
	TAATCTCAGCACTTTG GGAGG		
	ATTAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 MGC21675 3'	CTCCCAAAGTGCTGAGATTA 53481	A	
	TAATCTCAGCACTTTG GGAG		
	ATTAGAGTCGTGAAAC CCTC		
	—		
GAM1286 MGC21738 3'	CCTCCCAAAGTGCTGGGATTA 58916	A	
	TAATCTCAGCACTTTG GGAGG		
	ATTAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 MGC2474 3'	CCTCCCAAAGTGCTGGGATTA 43718	A	
	TAATCTCAGCACTTTG GGAGG		
	ATTAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 MGC2474 3'	CCTCCCAAAGTGCTGGGATTA 43719	A	
	TAATCTCAGCACTTTG GGAGG		
	ATTAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 MGC2477 5'	CCTCCCAAAGTGCTGGGATTA 44061	A	
	TAATCTCAGCACTTTG GGAGG		
	ATTAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 MGC2603 3'	CCTCCCAAAGTGCTGAGATTA 43858	A	
	TAATCTCAGCACTTTG GGAGG		
	ATTAGAGTCGTGAAAC CCTCC		
	—		
GAM1286 MGC29898 3'	CTTCCAAAGTGCTGGGATTA 58927	A	
	TAATCTCAGCACTTTG GGAG		
	ATTAGGGTCGTGAAAC CTTC		
	—		
GAM1286 MGC4766 5'	CCTCCCAAAGTGCTGGGATTA 48775	A	
	TAATCTCAGCACTTTG GGAGG		
	ATTAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 MGC5149 3'	TCCCAAAGCGCTGGGATTA 72301	A	A
	TAATCTCAGC CTTTG GGA		

			ATTAGGGTCG GAAAC CCT		
			C _		
GAM1286	MKRN4	3'	CCTTCCAAAGTGCTGGGATTA 47740	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CTTCC		
GAM1286	MLZE	5'	CCTCCCAAAGTGCTGGGATTA 48617	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	moblak	3'	CCTCCCAAAGTGCTGGA 55493 T	A	
			TC CAGCACTTTG GGAGG		
			AG GTCGTGAAAC CCTCC		
GAM1286	moblak	3'	CCTCCCAAAGTGCTGGGATTA 55494	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	MRPL20	3'	GCCCTCCCAAAGTGCTGGGATT 35735	A	
	A		TAATCTCAGCACTTTG GGAGGGC		
			ATTAGGGTCGTGAAAC CCTCCCG		
GAM1286	MRPL44	3'	CCTCCCAAAGTGCTGGGATTA 43315	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	MtFMT	3'	CCTCCCAAAGTGCTATGATTA 57652	TC	A
			TAATC AGCACTTTG GGAGG		
			ATTAG TCGTGAAAC CCTCC		
			TA		
GAM1286	MYO5C	3'	CCTCCCAAAGTGCTAGGATTA 38106	TC	A
			TAATC AGCACTTTG GGAGG		
			ATTAG TCGTGAAAC CCTCC		
			GA		
GAM1286	NDP52	3'	GCCGTCCAAAGTGCTGGGATTA 19531	GA	G
			TAATCTCAGCACTTT GGA GGC		
			ATTAGGGTCGTGAAA CCT CCG		
GAM1286	NINJ2	3'	CCTCCCAAAGTGCTGGGATTA 33280	A	
			TAATCTCAGCACTTTG GGAGG		

ATTAGGGTCGTGAAAC CCTCC

GAM1286	Nup43	3'	CCTCCAAAGTGCTGTGATTA	44996	T	GA
			TAATC CAGCACTTT GGAGG			
			ATTAG GTCGTGAAA CCTCC			
			T			
GAM1286	Nup43	3'	CCTCCCAAATGCTGGGATTA	44997	C	A
			TAATCTCAGCA TTTG GGAGG			
			ATTAGGGTCGT AAAC CCTCC			
			A			
GAM1286	NXN	3'	CCTCCCAAAGTGCTGGGATTA	42417		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
GAM1286	OSBPL2	3'	CCTCCCAAAGTGCTGGGATTA	29209		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
GAM1286	OSBPL2	3'	CCTCCCAAAGTGCTGGGATTA	57860		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
GAM1286	PASK	5'	TCCCAAAGTGCTGGGATTA	30727		A
			TAATCTCAGCACTTTG GGA			
			ATTAGGGTCGTGAAAC CCT			
GAM1286	PCDH16	3'	GCCCCCTCAGAGTACTAGGA	13607	TC C	A
			TC AG ACTTTGAGG GGGC			
			AG TC TGAGACTCC CCCG			
			GA A			
GAM1286	PDE10A	3'	CCTAAAGGGCTGAGAT	21861	A	G
			ATCTCAGC CTTT AGG			
			TAGAGTCG GGAA TCC			
GAM1286	PELI1	5'	CCTCCCAAAGTGCTGGGATTA	40259		A
			TAATCTCAGCACTTTG GGAGG			
			ATTAGGGTCGTGAAAC CCTCC			
GAM1286	PELI1	5'	CTTCCCAAAGTGCTGGAATTA	40266	CT	A
			TAAT CAGCACTTTG GGAGG			

			ATTA GTCGTGAAAC CCTTC		
			AG _		
GAM1286	PRO0245	5'	CCTCCCAAAGTGCTGAGATTA 26127	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGAGTCGTGAAAC CCTCC		
GAM1286	PRO0365	5'	CCTCCCAAAGTGCTGGGATTA 26155	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	PRO1992	3'	CCTCCCAAAGTGCTGGGATTA 26055	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	PRO2955	3'	CCTCCCAAAGTGCTGGGATTA 37634	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	PSPH	3'	CCTCCCAAAGTGCTGGGATTA 15913	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	PSTPIP2	3'	CCTCCCAAAGTGCTGGGATTA 44386	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	RAB14	3'	CCCTTTTCAGTGTAAGAT 32872 CA TT		
			ATCT GCACT GAGGAGGG		
			TAGA TGTGA CTTTCCC		
			A_ _		
GAM1286	RAB21	3'	CCTCCCAAAGTGCTGGGATTA 30384	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	RAB33B	3'	CTTCCCAAAGTGCTGGGATTA 48493	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTTC		
GAM1286	RAB39	3'	CCTCCCAAAGTGCTGGAATTA 76631 CT GA		
			TAAT CAGCACTTT GGAGG		

			ATTA GTCGTGAAA CCTCC	
			AG     —	
GAM1286	RAP140	3'	CCTCCCAAAGTGCTGGGATTA 30842	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	RNF8	3'	CCTCCCAAAGTGCTGAGATTA 14221	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGAGTCGTGAAAC CCTCC	
			—	
GAM1286	RNO2	5'	CCTCCCAAAGTGCTGGGATTA 52767	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	SC4MOL	3'	CCTCCCAAAGTGCTGGGATTA 22154	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	SCYA22	3'	CCTCCCAAAGTGCTGGGATTA 90940	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	SCYA22	3'	CCTCCCAAAGTGCTGGGATTA 90941	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	SCYA22	3'	CTCCCAAAGTGCTGAGATTA 90944	A
			TAATCTCAGCACTTTG GGAG	
			ATTAGAGTCGTGAAAC CCTC	
			—	
GAM1286	SEC22C	5'	GCCCTCCCGGTCGGCTAAGATT 14852	C ACT A
	G		TAATCT AGC TTG GGAGGGC	
			GTTAGA TCG GGC CCTCCCG	
			A GCT —	
GAM1286	SEC22C	5'	GCCCTCCCGGTCGGCTAAGATT 52057	C ACT A
	G		TAATCT AGC TTG GGAGGGC	
			GTTAGA TCG GGC CCTCCCG	
			A GCT —	
GAM1286	SERF1B	3'	CCTCCCAAAGTGCTGGGATTA 43414	A
			TAATCTCAGCACTTTG GGAGG	



ATTAGGGTCGTGAAAC CCTCC

GAM1286 SIRPB1 3' CCTCCCAAAGTGCTGGGATTA 20247 A  
TAATCTCAGCACTTTG GGAGG  
|||||  
ATTAGGGTCGTGAAAC CCTCC

GAM1286 SLC12A8 3' CCTCCCAAAGTACTGGGATTA 44897 C A  
TAATCTCAG ACTTTG GGAGG  
|||||  
ATTAGGGTC TGAAAC CCTCC

A  
GAM1286 SLC19A3 3' CCTCCCAAAGAGCTGAGATTA 47483 A A  
TAATCTCAGC CTTTG GGAGG  
|||||  
ATTAGAGTCG GAAAC CCTCC

A  
GAM1286 SLC5A7 3' GCCCTGTTCAAAGTACT 41513 C G  
AG ACTTTGAG AGGGC  
|| |||||  
TC TGAAACTT TCCCG  
A G

GAM1286 SLC6A14 3' CCTCCTAAAGTGCTGAGATTA 23349 G  
TAATCTCAGCACTTT AGGAGG  
|||||  
ATTAGAGTCGTGAAA TCCTCC

GAM1286 SNAPC1 3' CCTCCCAAAGTACTGGGATTA 11840 C A  
TAATCTCAG ACTTTG GGAGG  
|||||  
ATTAGGGTC TGAAAC CCTCC

A  
GAM1286 SQV7L 5' CCTCCCAAAGTGCTGTGATTA 70573 T A  
TAATC CAGCACTTTG GGAGG  
|||||  
ATTAG GTCGTGAAAC CCTCC  
T

GAM1286 STAF65(gamma) 3' CTCCCAAAGTGCTGGGATTA 29433 A  
TAATCTCAGCACTTTG GGAG  
|||||  
ATTAGGGTCGTGAAAC CCTC

GAM1286 SYT13 3' CCTCCCAAAGTACTGGGATTA 93453 C A  
TAATCTCAG ACTTTG GGAGG  
|||||  
ATTAGGGTC TGAAAC CCTCC

A  
GAM1286 SYTL4 5' CCTCCCAAAGTGCTGGGATTA 54940 A  
TAATCTCAGCACTTTG GGAGG  
|||||

ATTAGGGTCGTGAAAC CCTCC

GAM1286	TADA3L	3'	CCTCCCAAAGTGCCGGGATTA 55990	A	A
			TAATCTC GCACTTTG GGAGG		
			ATTAGGG CGTGAAAC CCTCC		
			C		
GAM1286	TCL6	5'	CCTCCCAAAGTGCTGGGATTA 40080	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	TCL6	5'	CCTCCCAAAGTGCTGGGATTA 40096	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	TCL6	5'	CTTCTCAAAGTGCTGGGATTA 40132		
			TAATCTCAGCACTTTGAGGAG		
			ATTAGGGTCGTGAAACTCTTC		
GAM1286	TCL6	5'	CTTCTCAAAGTGCTGGGATTA 40157		
			TAATCTCAGCACTTTGAGGAG		
			ATTAGGGTCGTGAAACTCTTC		
GAM1286	TCL6	5'	CCTCCCAAAGTGCTGGGATTA 26992	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	TCL6	3'	CCTCCCAAAGTGCTGGGATTA 26993	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	TCL6	5'	CCTCCCAAAGTGCTGGGATTA 24976	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	TCL6	3'	CCTCCCAAAGTGCTGGGATTA 24977	A	
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	THEA	3'	TCCCAAAGTGCTGGGATTA 66299	A	
			TAATCTCAGCACTTTG GGA		

			ATTAGGGTCGTGAAAC CCT	
			—	
GAM1286	TRIM16	3'	CCTCCCAAAGTGCTGGGATTA 21336	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	TRIM5	3'	CCTCCCAAAGTGCTGGGATTA 52296	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	TRIM5	3'	CCTCCCAAAGTGCTGGGATTA 52365	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	TRIM6	3'	TCCCAAAGTGCTGGGATTA 54147	A
			TAATCTCAGCACTTTG GGA	
			ATTAGGGTCGTGAAAC CCT	
			—	
GAM1286	TUCAN	3'	CCTCCCAAAGTGCTGGGATTA 30273	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	TUSP	3'	CCTCCCAAAGTGCTGGGATTA 39629	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	UBF-fl	3'	CTCCCAAAGTGCTGAAATTA 51563	C A
			TAAT TCAGCACTTTG GGAG	
			ATTA AGTCGTGAAAC CCTC	
			A —	
GAM1286	USP22	3'	TCCCAAAGTGCTGGGATTA 68027	A
			TAATCTCAGCACTTTG GGA	
			ATTAGGGTCGTGAAAC CCT	
			—	
GAM1286	VDU1	3'	CCTCCCAAAGTGCTGGGATTA 30416	A
			TAATCTCAGCACTTTG GGAGG	
			ATTAGGGTCGTGAAAC CCTCC	
			—	
GAM1286	WBSCR23	3'	CTTCCCAAAGTACTGGGATTA 46761	C A
			TAATCTCAG ACTTTG GGAGG	

			ATTAGGGTC TGAAAC CCTTC		
			A _		
GAM1286	YAP	5'	CCTCCCAAAGTGCTGGAATTA 36786	CT	A
			TAAT CAGCACTTTG GGAGG		
			ATTA GTCGTGAAAC CCTCC		
			AG _		
GAM1286	ZNF17	3'	CCTCCCAAAGTGCTGGGATTA 82388		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			_		
GAM1286	ZNF338	3'	CCTCCCAAAGTGCTGGGATTA 42010		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			_		
GAM1286	ZTL1	3'	CCTCACAAAGTGCTAGGATTA 43913	TC	AG
			TAATC AGCACTTTG GAGG		
			ATTAG TCGTGAAAC CTCC		
			GA A_		
GAM1286	LOC112687	3'	CCTCCCAAAGTGCTGGGATTA 72857		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			_		
GAM1286	LOC112817	3'	CCTCCCAAAGTGCTGGGATTA 56508		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
			_		
GAM1286	LOC113026	3'	GCATTCCAAAGTGCTGGGATTA 55903		A GG
			TAATCTCAGCACTTTG GGA GC		
			ATTAGGGTCGTGAAAC CTT CG		
			_ A_		
GAM1286	LOC113523	5'	CTCCCAAAGTGCTGGGATTA 73044		A
			TAATCTCAGCACTTTG GGAG		
			ATTAGGGTCGTGAAAC CCTC		
			_		
GAM1286	LOC115548	3'	CTTCCCAAAGTGCTGGGATTA 73461		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTTC		
			_		
GAM1286	LOC116411	5'	CCTCCCAAAGTGCCGAGATTG 73857	A	A
			TAATCTC GCACTTTG GGAGG		

			GTTAGAG CGTGAAAC CCTCC		
			C _		
GAM1286	LOC120114 3'		CCTCCCAAAGTGCTGGGATTA 75523		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	LOC120224 5'		GCCCTCCCAAAGTGCTGGGATT 57099		A
	A		TAATCTCAGCACTTTG GGAGGGC		
			ATTAGGGTCGTGAAAC CCTCCCG		
GAM1286	LOC120939 3'		CCTCCCAAAGTGCTGGAATTA 76251	CT	A
			TAAT CAGCACTTTG GGAGG		
			ATTA GTCGTGAAAC CCTCC		
			AG _		
GAM1286	LOC124216 3'		CCTCCCAAAGTGCTGGGATTA 74261		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	LOC124871 3'		CTTCTCAAAGTACCAGGATTA 74346	CAGC	
			TAATCT ACTTTGAGGAG		
			ATTAGG TGAACTCTTC		
			ACCA		
GAM1286	LOC125194 5'		CCTCCCAAAGTGCTGGGATTA 74396		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	LOC126272 3'		CCTCCCAAAGTGCTGGGATTA 76088		A
			TAATCTCAGCACTTTG GGAGG		
			ATTAGGGTCGTGAAAC CCTCC		
GAM1286	LOC126661 3'		GCCCTCCCAAAGTGCTGGGATT 74552		A
	A		TAATCTCAGCACTTTG GGAGGGC		
			ATTAGGGTCGTGAAAC CCTCCCG		
GAM1286	LOC127534 5'		CAAAGTGCAAGATTA 75436	CA	
			TAATCT GCACTTTG		
			ATTAGA CGTGAAAC		
			A_		
GAM1286	LOC128077 3'		CCTCCCAAAGTGCTGGGATTA 74710		A
			TAATCTCAGCACTTTG GGAGG		

	ATTAGGGTCGTGAAAC CCTCC		
GAM1286 LOC128989 3'	CCTCCCAAAGTGCTGGGATTA 74808 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC130813 3'	CCTCCCAAAGCACTGGGATTA 75768 TAATCTCAG CTTTG GGAGG            ATTAGGGTC GAAAC CCTCC AC	CA	A
GAM1286 LOC130813 3'	CCTCCCAAAGTGCTGGGATTA 75769 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC132625 3'	CCTCCCAAAGTGCTGGGATTA 75903 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC142820 5'	CTTCCCAAAGTGCTGGGATTA 76398 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTTC	A	
GAM1286 LOC142927 5'	CCTCCCAAAGTGCTGGGATTA 76423 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC143153 3'	TCCCAAAGTGCTGGGATTA 76470 TAATCTCAGCACTTTG GGA       ATTAGGGTCGTGAAAC CCT	A	
GAM1286 LOC143154 3'	TCCCAAAGTGCTGGGATTA 76487 TAATCTCAGCACTTTG GGA       ATTAGGGTCGTGAAAC CCT	A	
GAM1286 LOC144317 5'	CCTCCCAAAGTGCTGGGATTA 76786 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC144524 5'	CCTCCCAAAGTGCTGGGATTA 83124 TAATCTCAGCACTTTG GGAGG 	A	

	ATTAGGGTCGTGAAAC CCTCC		
GAM1286 LOC145009 3'	CCTCCCAAAGTGCTGGGATTA 60347 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC		A
GAM1286 LOC145082 5'	CCCCTCAAAGTGCTGGGATTA 83237 TAATCTCAGCACTTTGAGG GG       ATTAGGGTCGTGAAACTCC CC		A
GAM1286 LOC145622 3'	CCTCCCAAAGTGCTGGGATTA 77297 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC		A
GAM1286 LOC145873 5'	CCTCCCAAAGTGCTAGGATTA 77553 TAATC AGCACTTTG GGAGG            ATTAG TCGTGAAAC CCTCC GA	TC	A
GAM1286 LOC146050 3'	CCTCCCAAAGTGCTGGGATTA 77634 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC		A
GAM1286 LOC146050 3'	TCCCAAAGTGCTGGGATTA 77651 TAATCTCAGCACTTTG GGA       ATTAGGGTCGTGAAAC CCT		A
GAM1286 LOC146229 3'	CCCTCCCGAGTCACTGGGATTA 77735 TAATCTCAG TTTG GGAGGG           ATTAGGGTC GAGC CCTCCC ACT	CAC	A
GAM1286 LOC146229 3'	CCTCCCAAAGTGCTGGGATTA 77736 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC		A
GAM1286 LOC146229 3'	CCTCCCAAAGTGCTGGGATTA 77737 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC		A
GAM1286 LOC146429 5'	CCTCCCAAAGTGCTGGGATTA 83670 TAATCTCAGCACTTTG GGAGG 		A

	ATTAGGGTCGTGAAAC CCTCC		
GAM1286 LOC146443 5'	CCTCCCAAAGTGCTGGGATTA 77882 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC146455 3'	CCTCCCAAATGCTGGGATTA 77903 TAATCTCAGCA TTTG GGAGG       ATTAGGGTCGT AAAC CCTCC	C	A
GAM1286 LOC146599 5'	CCTCCCAAAGTGCTAGGATTA 78023 TAATC AGCACTTTG GGAGG            ATTAG TCGTGAAAC CCTCC GA	TC	A
GAM1286 LOC146784 5'	CCTCCCAAAGTGCTGGGATTA 78106 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC146909 3'	CCTCCCAAAGTGCTGGGATTA 78169 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC146909 3'	CTTCCCAAAGTGCTGAGATTA 78171 TAATCTCAGCACTTTG GGAGG       ATTAGAGTCGTGAAAC CCTTC	A	
GAM1286 LOC147080 5'	CCTCCCAAAGTGCTGGGATTA 83932 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC147160 5'	CCTCCCAAAGTGCTGGGATTA 83963 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC147166 3'	CCTCCCAAAGTGCTGGGATTA 78285 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC147429 3'	CCTCCCAAAGTGCTGGGATTA 78356 TAATCTCAGCACTTTG GGAGG 	A	



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GAM1286 LOC147817 3' CCTCCAAAATGCTGGGATTA 78494 C GA  
TAATCTCAGCA TTT GGAGG  
||||||| ||| ||||  
ATTAGGGTCGT AAA CCTCC

— A —  
GAM1286 LOC147817 3' CCTCCCAAAGTGCTGGGATTA 78495 A  
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||||||| ||||  
ATTAGGGTCGTGAAAC CCTCC

—  
GAM1286 LOC147990 3' CCTCCCAAAGTGCTGGGATTA 84091 A  
TAATCTCAGCACTTTG GGAGG  
||||||| ||||  
ATTAGGGTCGTGAAAC CCTCC

—  
GAM1286 LOC148147 3' CCCAAAGTGCTGGGATTA 78677 A  
TAATCTCAGCACTTTG GG  
||||||| ||  
ATTAGGGTCGTGAAAC CC

—  
GAM1286 LOC148189 5' TCCCAAAGTGCTGGGATTA 78724 A  
TAATCTCAGCACTTTG GGA  
||||||| |||  
ATTAGGGTCGTGAAAC CCT

—  
GAM1286 LOC148195 3' GCCTGGCAAATGCTGGGATTA 84130 C AGGA  
TAATCTCAGCA TTTG GGGC  
||||||| ||| ||||  
ATTAGGGTCGT AAAC TCCG  
A GG\_\_

GAM1286 LOC148443 3' GCCTCTCAAATGCTGGGATTA 78857 C GA  
TAATCTCAGCA TTTGAG GGGC  
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ATTAGGGTCGT AAATC TCCG  
A —

GAM1286 LOC148887 5' CCTCCCAAAGTGCTGGGATTA 84234 A  
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||||||| ||||  
ATTAGGGTCGTGAAAC CCTCC

—  
GAM1286 LOC149171 5' CCTCCAAAGTGCTGGAATTA 79217 CT GA  
TAAT CAGCACTTT GGAGG  
||| ||||| ||||  
ATTA GTCGTGAAA CCTCC  
AG —

GAM1286 LOC149421 3' CCTCCCAAAGTGCTGGGATTA 79357 A  
TAATCTCAGCACTTTG GGAGG  
||||||| ||||

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GAM1286 LOC149478 3'	CCTCCCAAAGTGCTGGGATTA 79375 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC149577 3'	CCTCCCAAATGCTGGGATTA 84505 TAATCTCAGCA TTTG GGAGG       ATTAGGGTCGT AAAC CCTCC A	C	A
GAM1286 LOC149577 3'	CCTCCCAAAGTGCTGGGATTA 84506 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC149684 5'	TCCCAAAGTGCTGGGATTA 84619 TAATCTCAGCACTTTG GGA       ATTAGGGTCGTGAAAC CCT	A	
GAM1286 LOC149692 3'	CCTCCCGAAGTGCTAAGATTA 84581 TAATCT AGCACTTTG GGAGG       ATTAGA TCGTGAAGC CCTCC A	C	A
GAM1286 LOC149703 5'	CCTCCCAAAGTGCTGGGATTA 84651 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC149821 5'	CCTCCCAAAGTGCTGGGATTA 84762 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC150054 5'	CCTCCCAAAGTGCTGGGATTA 84827 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC150166 5'	TCCCAAAGTGCTGGGATTA 84891 TAATCTCAGCACTTTG GGA       ATTAGGGTCGTGAAAC CCT	A	
GAM1286 LOC150212 5'	CCTCCCAAAGTGCTGGAATTA 79706 TAAT CAGCACTTTG GGAGG 	CT	A

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	AG —		
GAM1286 LOC150225 3'	CCTCCCAAAGTGCTGGGATTA 84987		A
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	—		
GAM1286 LOC150397 3'	TCCCAAAGTGCTGGGATTA 79853		A
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	ATTAGGGTCGTGAAAC CCT		
	—		
GAM1286 LOC150407 3'	CCTCCCAAAGTACTGGGATTA 79820	C	A
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	ATTAGGGTC TGAAAC CCTCC		
	A —		
GAM1286 LOC150407 3'	CCTCCCAAAGTGCTGGGATTA 79821		A
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	ATTAGGGTCGTGAAAC CCTCC		
	—		
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	ATTAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 LOC150960 3'	CCTCCCAAAGTGCTGTAATTA 80056	CT	A
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	ATTA GTCGTGAAAC CCTCC		
	AT —		
GAM1286 LOC151201 3'	CCTCCCAAAGTGCTGGGATTA 85275		A
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	ATTAGGGTCGTGAAAC CCTCC		
	C		
GAM1286 LOC151475 5'	CCTCCCAAAGTGCTGGGATTA 85399		A
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	ATTAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 LOC151826 3'	CCTCCCAAAGTGCTGGGATTA 80356		A
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	ATTAGGGTCGTGAAAC CCTCC		
	—		
GAM1286 LOC151979 5'	CCTCCCAAAGTGCTGGGATTA 80422		A
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GAM1286 LOC152343 3' TCCCAAAGTGCTGGGATTA 80572 A  
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GAM1286 LOC152348 3' CCTCCCAAAGTGCTGGGATTA 85692 A  
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GAM1286 LOC152445 3' CCTCCCAAAGTGCTGGGATTA 85750 A  
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GAM1286 LOC152620 3' CCTCCCAAAGTGCTGAGATTA 60080 A  
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GAM1286 LOC152851 3' CCTCCCAAAGTGCTGGGATTA 80706 A  
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GAM1286 LOC153606 5' CTCCCAAAGTGCTGGGATTA 86072 A  
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GAM1286 LOC153688 3' CCTCCCAAAGTGCTAGGATTA 86100 TC A  
TAATC AGCACTTTG GGAGG  
|||| |||||  
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GA

GAM1286 LOC153811 3' TCTCAAAGTGCTGGGATTA 80959  
TAATCTCAGCACTTTGAGG  
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GAM1286 LOC154141 5' CCTCCCAAAGTGCTGGGATTA 86168 A  
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GAM1286 LOC154282 5' CCTCCCAAAGTGCTGGGATTA 86194 A  
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GAM1286 LOC154726 5'	CCTCCCAAAGTGCTGGGATTA 81104 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC		A
GAM1286 LOC154877 3'	CCTCCCAAAGTGCTGGATTA 86287 TAATC CAGCACTTTG GGAGG            ATTAG GTCGTGAAAC CCTCC	T	A
GAM1286 LOC154877 3'	CCTCCCAAAGTGCTGGGATTA 86288 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC		A
GAM1286 LOC155372 3'	CCTCCCAAAGTGCTGAGATTA 81342 TAATCTCAGCACTTTG GGAGG       ATTAGAGTCGTGAAAC CCTCC		A
GAM1286 LOC157247 5'	CCTCCCAAAGTGCTGGGATTA 81363 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC		A
GAM1286 LOC157506 3'	CCTCCCAAAGTGCTGGGATTA 81439 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC		A
GAM1286 LOC157507 5'	CCTCCCAAAGTGCTGGGATTA 81455 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC		A
GAM1286 LOC157681 5'	CCTCCCAAAGTGCTGGGA 81542 TCTCAGCACTTTG GGAGG       AGGGTCGTGAAAC CCTCC		A
GAM1286 LOC158310 5'	CCTCCCAAAGTGCTGGGATTA 86751 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC		A
GAM1286 LOC158402 5'	CCTCCCAAAGTGCTGGAATTA 86802 TAAT CAGCACTTTG GGAGG 	CT	A

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	AG —		
GAM1286 LOC158476 3'	CCTCCCAAAGTGCTGGGATTA 86842		A
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	ATTAGGGTCGTGAAAC CCTCC		
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GAM1286 LOC158668 3'	CCTCCCAAAGTGCTGAGATTA 69367		A
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	ATTAGAGTCGTGAAAC CCTCC		
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GAM1286 LOC158709 3'	CCTCCCAAAGTGCTGGGATTA 81979		A
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	—		
GAM1286 LOC160646 3'	CCTCCCAAAGTGCTGGGATTA 82225		A
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	ATTAGGGTCGTGAAAC CCTCC		
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GAM1286 LOC161829 3'	CTTCCAAAGTGCTGGGATTA 82313		A
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	ATTAGGGTCGTGAAAC CTTC		
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GAM1286 LOC163590 5'	CCTCCCAAAGTGCTGGGATTA 58859		A
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	ATTAGGGTCGTGAAAC CCTCC		
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GAM1286 LOC170082 5'	CCTCCCAAAGTGCTGGGATTA 82559		A
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	—		
GAM1286 LOC170409 5'	CCTCCCAAAGTGCTGGGATTA 82860		A
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	ATTAGGGTCGTGAAAC CCTCC		
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GAM1286 LOC196047 5'	CCTCCCAAAGTGCTGCGATTA 89596	T	A
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	ATTAG GTCGTGAAAC CCTCC		
	C —		
GAM1286 LOC197358 3'	CCTCCCAAAGTACTGGGATTA 88028	C	A
	TAATCTCAG ACTTTG GGAGG		

	ATTAGGGTC TGAAAC CCTCC		
	A _		
GAM1286 LOC197358 3'	CCTCCCAAAGTGCTGGGATTA 88029	A	
	TAATCTCAGCACTTTG GGAGG		
	ATTAGGGTCGTGAAAC CCTCC		
	-		
GAM1286 LOC199699 3'	CCTCCCAAAGTGCTGGGAT 88301	A	
	ATCTCAGCACTTTG GGAGG		
	TAGGGTCGTGAAAC CCTCC		
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GAM1286 LOC199725 5'	CCTCCCAAAGTGCTGGGATTA 89836	A	
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	-		
GAM1286 LOC199775 5'	CCTCCCAAAGTGCTGGGATTA 88355	A	
	TAATCTCAGCACTTTG GGAGG		
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	-		
GAM1286 LOC199786 3'	CAAAGTGCTGGGATTA 88367		
	TAATCTCAGCACTTTG		
	ATTAGGGTCGTGAAAC		
	-		
GAM1286 LOC199786 3'	CCTCCCAAAGTGCTAGGATTA 88374	TC	A
	TAATC AGCACTTTG GGAGG		
	ATTAG TCGTGAAAC CCTCC		
	GA		
	-		
GAM1286 LOC199786 3'	CCTCCCAAAGTGCTGGGATTA 88375	A	
	TAATCTCAGCACTTTG GGAGG		
	ATTAGGGTCGTGAAAC CCTCC		
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GAM1286 LOC200014 3'	CCTCCCAAAGTGCTGGGATTA 88522	A	
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	ATTAGGGTCGTGAAAC CCTCC		
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GAM1286 LOC200169 5'	CCTCCCAAAGTGCTGGGATTA 89946	A	
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GAM1286 LOC200301 5'	CCTCCCAAAGTGCTGGGATTA 88741	A	
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GAM1286 LOC200310 3'	CCTCCCAAAGTGCTAGGATTA 65731 TAATC AGCACTTTG GGAGG                  ATTAG TCGTGAAAC CCTCC GA	TC	A
GAM1286 LOC200314 3'	CCTCCCAAAGTGCTGGGATTA 90006 TAATCTCAGCACTTTG GGAGG                 ATTAGGGTCGTGAAAC CCTCC		A
GAM1286 LOC200316 5'	CCTCCCAAAGTGCTGGGATTA 88767 TAATCTCAGCACTTTG GGAGG                 ATTAGGGTCGTGAAAC CCTCC		A
GAM1286 LOC200316 3'	TCCCAAAGTGCTGGGATTA 88776 TAATCTCAGCACTTTG GGA                ATTAGGGTCGTGAAAC CCT		A
GAM1286 LOC200845 5'	CCTCCCAAAGTGCTGGGATTA 88897 TAATCTCAGCACTTTG GGAGG                 ATTAGGGTCGTGAAAC CCTCC		A
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GAM1286 LOC201411 3'	CCTCCCAAAGTGCTGGGATTA 62954 TAATCTCAGCACTTTG GGAGG                 ATTAGGGTCGTGAAAC CCTCC		A
GAM1286 LOC201627 3'	CCTCCCAAAGTGCTGGGATTA 89007 TAATCTCAGCACTTTG GGAGG 		A



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GAM1286 LOC201705 5' TCCCAAAGTGCTGGGATTA 90256 A  
TAATCTCAGCACTTTG GGA  
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GAM1286 LOC202460 5' TCCCAAAGTGCTGGGATTA 89189 A  
TAATCTCAGCACTTTG GGA  
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GAM1286 LOC203197 3' CTCCCAAAGTGCTGGGATTA 89287 A  
TAATCTCAGCACTTTG GGAG  
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GAM1286 LOC203232 3' CCCTCCTCATCAGCAAGAT 71411 CA ACTT  
ATCT GC TGAGGAGGG  
||| || |||||  
TAGA CG ACTCCTCCC  
A\_ ACT\_

GAM1286 LOC203369 3' CCTCCCAAAGTGCTGGGATTA 89337 A  
TAATCTCAGCACTTTG GGAGG  
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GAM1286 LOC203378 3' CCTCCCAAAGTGCTGGGATTA 90598 A  
TAATCTCAGCACTTTG GGAGG  
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ATTAGGGTCGTGAAAC CCTCC

GAM1286 LOC205251 5' CCTCCCAAAGTGCTGGGATTA 90668 A  
TAATCTCAGCACTTTG GGAGG  
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GAM1286 LOC219294 3' TCCCAAAGTGCTGGGATTA 93012 A  
TAATCTCAGCACTTTG GGA  
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GAM1286 LOC219295 3' TCCCAAAGTGCTGGGATTA 92997 A  
TAATCTCAGCACTTTG GGA  
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ATTAGGGTCGTGAAAC CCT

GAM1286 LOC219673 5' CCTCCCAAAGTGCTAGGATTA 93023 TC A  
TAATC AGCACTTTG GGAGG  
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	GA _		
GAM1286 LOC219894 3'	CCTCCCAAAGTGCTGGGATTA 93280		A
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	ATTAGGGTCGTGAAAC CCTCC		
	_		
GAM1286 LOC220074 3'	CCTCCCAAAGTGCTAGGATTA 59268	TC	A
	TAATC AGCACTTTG GGAGG		
	ATTAG TCGTGAAAC CCTCC		
	GA _		
GAM1286 LOC220074 3'	CCTCCCAAAGTGCTGGGATTA 59269		A
	TAATCTCAGCACTTTG GGAGG		
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	_		
GAM1286 LOC221271 3'	CCTCCCAAAGTGTTGAGATTA 91852		A
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	ATTAGAGTTGTGAAAC CCTCC		
	_		
GAM1286 LOC221540 3'	CCTCCCAAATGCTGAGATTA 93835	C	A
	TAATCTCAGCA TTTG GGAGG		
	ATTAGAGTCGT AAAC CCTCC		
	A _		
GAM1286 LOC221663 5'	CCTCCCAAAGTGCCGGGATTA 93812	A	A
	TAATCTC GCACTTTG GGAGG		
	ATTAGGG CGTGAAAC CCTCC		
	C _		
GAM1286 LOC221964 3'	GCATCCCAAAGTGCTGGGATTA 93981		A GG
	TAATCTCAGCACTTTG GGA GC		
	ATTAGGGTCGTGAAAC CCT CG		
	_ A_		
GAM1286 LOC222070 5'	CCTCCCAAAGTGCTGGGATTA 94153		A
	TAATCTCAGCACTTTG GGAGG		
	ATTAGGGTCGTGAAAC CCTCC		
	_		
GAM1286 LOC253842 5'	CCTCCCAAAGTGCTGGGATTA 97384		A
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	ATTAGGGTCGTGAAAC CCTCC		
	_		
GAM1286 LOC254100 3'	CCTCCCAAAGTGCTGGGATTA 96413		A
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	ATTAGGGTCGTGAAAC CCTCC		
GAM1286 LOC254295 5'	CCTCCAAAGTGCTGGGATTA 96174 TAATCTCAGCACTTT GGAGG       ATTAGGGTCGTGAAA CCTCC	GA	
GAM1286 LOC254672 3'	CTTCCCAAAGTGCTGGGATTA 94644 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTTC	A	
GAM1286 LOC255196 5'	CCTCCCTAAGTGCTGAGATTA 97165 TAATCTCAGCACTT GGAGG       ATTAGAGTCGTGAA CCTCC TC_	TGA	
GAM1286 LOC255308 3'	CCTCACAAAGTGCCGGGATTA 94534 TAATCTC GCACTTTG GAGG       ATTAGGG CGTGAAAC CTCC C A_	A	AG
GAM1286 LOC255338 5'	TCCCAAAGTGCTGGGATTA 95934 TAATCTCAGCACTTTG GGA       ATTAGGGTCGTGAAAC CCT	A	
GAM1286 LOC255465 3'	TCTCAAAGTGCTGGGATTA 97304 TAATCTCAGCACTTTGAGG       ATTAGGGTCGTGAAACTCT		
GAM1286 LOC255707 3'	CCTCCCAAAGTGCTGGGATTA 96957 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC256221 3'	CCTCCCAAAGTGCTGGGATTA 95209 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC256360 5'	TCCCAAAGTGCTGAGATTA 96553 TAATCTCAGCACTTTG GGA       ATTAGAGTCGTGAAAC CCT	A	
GAM1286 LOC256364 5'	CCTCCCAAAGTGCTGGGATTA 94797 TAATCTCAGCACTTTG GGAGG 	A	

	ATTAGGGTCGTGAAAC CCTCC	
GAM1286 LOC257128 5'	GCATCCCAAAATGCTGGGATTA 96087 TAATCTCAGCA TTTG GGA GC              ATTAGGGTCGT AAAC CCT CG A _ A_	C A GG
GAM1286 LOC257463 3'	CCTCCCAAAGTGCTGGGATTA 71068 TAATCTCAGCACTTTG GGAGG            ATTAGGGTCGTGAAAC CCTCC	A
GAM1286 LOC257465 3'	CCTCCCAAAGTGCTGGGATTA 81591 TAATCTCAGCACTTTG GGAGG            ATTAGGGTCGTGAAAC CCTCC	A
GAM1286 LOC257545 3'	CCTCCCAAAATGCTGAGATTA 97803 TAATCTCAGCA TTTG GGAGG                ATTAGAGTCGT AAAC CCTCC A _	C A
GAM1286 LOC257598 3'	CCTCCCAAAATGCTGAGATTA 97918 TAATCTCAGCA TTTG GGAGG                ATTAGAGTCGT AAAC CCTCC A _	C A
GAM1286 LOC51008 5'	CCTCCCAAAGTGCTGGGATTA 31961 TAATCTCAGCACTTTG GGAGG            ATTAGGGTCGTGAAAC CCTCC	A
GAM1286 LOC51193 5'	CCTCCCAAAGTGCTGGGATTA 32904 TAATCTCAGCACTTTG GGAGG            ATTAGGGTCGTGAAAC CCTCC	A
GAM1286 LOC51219 5'	CCTCCCAAAGTGCTGGGATTA 33115 TAATCTCAGCACTTTG GGAGG            ATTAGGGTCGTGAAAC CCTCC	A
GAM1286 LOC51275 5'	CCTCCCAAAGTACTGGGATTA 33290 TAATCTCAG ACTTTG GGAGG            ATTAGGGTC TGAAAC CCTCC A _	C A
GAM1286 LOC51696 3'	CCTCCCAAAGTGCTGGGATTA 32545 TAATCTCAGCACTTTG GGAGG 	A

	ATTAGGGTCGTGAAAC CCTCC		
GAM1286 LOC56181 5'	CCTCCCAAAGTGCTGGGATTA 95533 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC56920 3'	CCAGAAGCACTGAGATTA 39383 TAATCTCAG CTTT GG          ATTAGAGTC GAAG CC AC A_	CA	GA
GAM1286 LOC57107 3'	CCTCCCAAAGTGCTGGGATTA 39832 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC57146 3'	CCTCCCAAAGTGCTGGGATTA 39916 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC81034 3'	CCTCCCAAAGTGCTGGGATTA 47848 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC89231 3'	CCTCCCAAAGTGCTGGGATTA 92730 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC89932 3'	CCTCCCAAATGCTGGGATTA 60794 TAATCTCAGCA TTTG GGAGG       ATTAGGGTCGT AAAC CCTCC A _	C	A
GAM1286 LOC89932 3'	CCTCCCAAAGTGCTGGGATTA 60795 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC90110 5'	CCTCCCAAAGTGCTGGGATTA 61508 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC90288 3'	CCTCCCAAAGTGCTGGGATTA 62086 TAATCTCAGCACTTTG GGAGG 	A	

	ATTAGGGTCGTGAAAC CCTCC		
GAM1286 LOC90333 3'	CCTCCCAAAGTGCTGAGATTA 62287 TAATCTCAGCACTTTG GGAGG       ATTAGAGTCGTGAAAC CCTCC	A	
GAM1286 LOC90408 5'	CCTCCCAAAGTACTGGGATTA 62659 TAATCTCAG ACTTTG GGAGG             ATTAGGGTC TGAAAC CCTCC	C	A
GAM1286 LOC90485 3'	A CCTCCCAAAGTGCTGGGATTA 63010 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC90485 3'	GCATCCCAAAGTGCTGGGA 63017 TCTCAGCACTTTG GGA GC          AGGGTCGTGAAAC CCT CG	A	GG
GAM1286 LOC90591 3'	A TCCCAAAGTGCTGGGATTA 63445 TAATCTCAGCACTTTG GGA       ATTAGGGTCGTGAAAC CCT	A	
GAM1286 LOC90918 3'	CCTCCCAAAGTGCCGGGATTA 64354 TAATCTC GCACTTTG GGAGG             ATTAGGG CGTGAAAC CCTCC	A	A
GAM1286 LOC91115 3'	C CCTCCCAAAGTGCTGGGATTA 64929 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC91250 5'	CCTCCCAAAGTGCTGGGATTA 65322 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC91308 3'	CCTCCCAAAGTGCTGGGATTA 65557 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC91373 3'	CCTCCCAAAGTGCTGGGATTA 65837 TAATCTCAGCACTTTG GGAGG 	A	

	ATTAGGGTCGTGAAAC CCTCC		
GAM1286 LOC91893 3'	CCTCCCAAAGTGCTGGGATTA 67460 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC92303 3'	CCTCCCAAAGTGCTGGGATTA 68822 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC92661 5'	CCTCCCAAAGTGCTGGGATTA 70080 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC92689 3'	CCTCCCAAAGTGCTGGGATTA 70222 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC92841 3'	CCTCCCAAAGTGCTGGGATTA 70707 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC93356 3'	CCTCCCAAATGCTGGGATTA 72076 TAATCTCAGCA TTTG GGAGG       ATTAGGGTCGT AAAC CCTCC	C	A
GAM1286 LOC93408 5'	CCTCCCAAAGTGCTGGGATTA 56476 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1286 LOC93496 3'	CCTCCCAAAGTGCTGGGATTA 72432 TAATCTCAGCACTTTG GGAGG       ATTAGGGTCGTGAAAC CCTCC	A	
GAM1287 FBXL11 3'	TTCAACAGGAAACCGATCTTCC 24578 C GGAAGAT GGT CT TGAA             CCCTTCTA CCA GG ACTT G AA ACA_	_	GG ATAC
GAM1287 GRINL1A 3'	GTTCAGTATGTGAAACCACCAT 69517 TTCCC GGA GATGGTGG TATACTGAAC 	A	C_____

			CCT TTACCACC	GTATGACTTG		
			— AAAGT			
GAM1287 HD	3'	TCAACATAGAGTTTGTCTTCCT 9191		TG TGG	AC	
		GGGAAGA G CTAT TGA				
		TCCTTCT T GATA ACT				
		GT TGA CA				
GAM1287 IL8	3'	TAGCCACCATCTTACC 94480 G				
		GG AAGATGGTGGCTA				
		CC TTCTACCACCGAT				
		A				
GAM1287 LASS1	3'	TCCCTGCGGCCACCACCTCCT 41200		A A	TA CT	
		GGGA G TGGTGGC TA GA				
		TCCT C ACCACCG GT CT				
		— C GC CC				
GAM1287 PNU TL1	3'	TCAGCACCACCCCTCCC 10675		A AT	CTATA	
		GGGA G GGTGG CTGA				
		CCCT C CCACC GACT				
		— CC AC—				
GAM1287 SUFU	3'	GTTCAGCACATCACACCCATC 32413		AA	GCTATA—	
CCC		GGG GATGGTG CTGAAC				
		CCC CTACCAC GACTTG				
		— ACACTACAC				
GAM1287 UBE4A	3'	TTCAATATTTATCATCCTCCT 16567		A	C AC	
		GGGA GATGGTGG TAT TGAA				
		TCCT CTACTATT ATA ACTT				
		C T —				
GAM1287 VARS2	5'	AGTCTGACCATCTCCC 20848		A	—	
		GGGA GATGGT GGCT				
		CCCT CTACCA CTGA				
		— GT				
GAM1287 XK	3'	GGAGTAGCCACCAGCCTCCC 40801		AGA	A	
		GGGA TGGTGGCTAT CT				
		CCCT ACCACCGATG GG				
		CCG A				
GAM1287 APM2	3'	CGGGCAGCCACCACCTCCT 22406		A A	ATA	
		GGGA G TGGTGGCT CTG				
		TCCT C ACCACCGA GGC				
		— C CG—				
GAM1287 ARPP-19	3'	TCAGCACACACTGCCAGTCTTC 21803		—	TG CTATA—	
CC		GGGAAGA TGG G CTGA				



			CCCTTCT ACC C GACT		
			G GT ACACAC		
GAM1287	DEPP	3'	TCAGTGCTACCATCCCC	22824	AA TAT
			GGG GATGGTGGC ACTGA		
			CCC CTACCATCG TGACT		
			— —		
GAM1287	FLJ00058	5'	CAGACCCCATCTCCC	78763	A CTATA
			GGGA GATGGTGG CTG		
			CCCT CTACCACC GAC		
			— CCA—		
GAM1287	FLJ14810	3'	AGCACGCTGTCATCCC	51620	A _
			GGGA GATGGTG GCT		
			CCCT CTGTGCGC CGA		
			A A		
GAM1287	GPS1	3'	CAGTGGCACCATTTCCC	14678	A G AT
			GGGA GATGGTG CT ACTG		
			CCCT TTACCAC GG TGAC		
			— — —		
GAM1287	GTPBP1	3'	TAGAACCCCATCTTCCC	15017	T _
			GGGAAGATGG GG CTA		
			CCCTTCTACC CC GAT		
			— AA		
GAM1287	GTPBP1	3'	TAGAACCCCATCTTCCC	15018	T _
			GGGAAGATGG GG CTA		
			CCCTTCTACC CC GAT		
			— AA		
GAM1287	KIAA0552	3'	AGCACATCATCTTCCT	28306	_
			GGGAAGATGGTG GCT		
			TCCTTCTACTAC CGA		
			A		
GAM1287	KIAA1344	3'	TTCAGCATTCTGCCATCTCCT	72453	A TG CT A
			GGGA GATGG G AT CTGAA		
			TCCT CTACC C TA GACTT		
			— GT T_ C		
GAM1287	KIAA1464	3'	TTCAGTGAACATCTCCC	68277	A GTGGCTA
			GGGA GATG TACTGAA		
			CCCT CTAC GTGACTT		
			— AA—		
GAM1287	MGC2452	5'	TAGCCACCACTTCCC	50989	A
			GGGAAG TGGTGGCTA		

CCCTTC ACCACCGAT

GAM1287 NCBP2 3' CAGTATAATTTTCCC 23746 GGTGGC  
GGGAAGAT TATACTG  
||||| |||||  
CCCTTTTA ATATGAC

GAM1287 PLSCR3 3' TATAGCCACCGCCCCC 39794 AAGA  
GGG TGGTGGCTATA  
||| |||||  
CCC GCCACCGATAT  
CCC\_

GAM1287 PLSCR3 3' TATAGCCACCGCCCCC 90761 AAGA  
GGG TGGTGGCTATA  
||| |||||  
CCC GCCACCGATAT  
CCC\_

GAM1287 POLR2D 3' ATAACACCACCTTCCC 16654 A GC  
GGGAAG TGGTG TAT  
||||| ||||| |||  
CCCTTC ACCAC ATA  
C A\_

GAM1287 RPH3A 3' TTCAGTAACACACCCTCCC 30247 AGAT GCTA  
GGGA GGTG TACTGAA  
||| ||| |||||  
CCCT CCAC ATGACTT  
C\_ ACA\_

GAM1287 SLC5A6 3' TTCAACATAGCCATAGTCCT 40835 AGATG AC  
GGGA GTGGCTAT TGAA  
||| ||||| |||  
TCCT TACCGATA ACTT  
GA\_ CA

GAM1287 LOC132946 5' CAGTGTGGCACCCACCC 75073 AAGA TG  
GGG TGG GCTATACTG  
||| ||| |||||  
CCC ACC CGGTGTGAC  
\_ CA

GAM1287 LOC139422 5' TCAGTATAGCCTAGAACTCCT 75847 AGATGGT  
GGGA GGCTATACTGA  
||| |||||  
TCCT CCGATATGACT  
CAAGAT\_

GAM1287 LOC146822 3' TCTCCATGCCACCACCTGCCC 78154 A A TATACT  
GGG AG TGGTGGC GA  
||| ||| ||||| ||  
CCC TC ACCACCG CT  
G C TACCT\_

GAM1287 LOC151816 5' GTCCAGCCACCATCTTCCT 85499 AT  
GGGAAGATGGTGGCT AC  
||||| ||| ||

TCCTTCTACCACCGA TG  
 CC  
 GAM1287 LOC221712 5' GTTCAGGGGCCACCATCCCC 93626 AA ATA  
 GGG GATGGTGGCT CTGAAC  
 ||| ||||| |||||  
 CCC CTACCACCGG GACTTG  
 C\_ G\_  
 GAM1287 LOC253430 5' CAGAGCCACCATCCCCC 96236 AA ATA  
 GGG GATGGTGGCT CTG  
 ||| ||||| |||  
 CCC CTACCACCGA GAC  
 CC \_  
 GAM1287 LOC253715 3' TTCAGTATCCAACCATCCTCTC 96928 A \_ CT  
 GGGA GATGGT GG ATACTGAA  
 ||| ||||| || |||||  
 CTCT CTACCA CC TATGACTT  
 C A \_  
 GAM1287 LOC90190 3' CAGTCCATCCCACCATCACCCC 61775 AA CTAT\_  
 GGG GATGGTGG ACTG  
 ||| ||||| |||  
 CCC CTACCACC TGAC  
 CA CTACC  
 GAM1288 TSLP 3' ATAATGCAGGGGAAGTACTACT 52309 A GT\_ G  
 AGTA TAC TT TGCATTAT  
 |||| || || |||||  
 TCAT ATG GG ACGTAATA  
 C AAG G  
 GAM1288 TSLP 3' ATAATGCAGGGGAAGTACTACT 56720 A GT\_ G  
 AGTA TAC TT TGCATTAT  
 |||| || || |||||  
 TCAT ATG GG ACGTAATA  
 C AAG G  
 GAM1288 CTSO 3' ATAATGCAATGTAACATAGTAC 7189 A C TG\_  
 TTCA TGAAGTA TA GTT TGCATTAT  
 ||||| || ||| |||||  
 ACTTCAT AT CAA ACGTAATA  
 G A TGTA  
 GAM1288 FLJ23598 3' AATGCATGTATTAC 45518 GTTT  
 GTAATAC GTGCATT  
 ||||| |||||  
 CATTATG TACGTAA  
 \_  
 GAM1288 MGC11386 3' CACAAATGCATTACCTCA 51948 A A  
 TGA GTAAT CGTTTGTG  
 ||| |||| |||||  
 ACT CATTA GTAAACAC  
 C C  
 GAM1288 OAZ2 3' GTATAAACATATTATTCA 10309 G C  
 TGAA TAATA GTTTGTGC  
 |||| |||| |||||

ACTT ATTAT CAAATATG  
 \_ A  
 GAM1289 BAT3 3' CTTCACAGTATTTAAGA 16161 G GTTT  
 TC TAAA CTGTGAAG  
 || ||| |||||  
 AG ATTT GACACTTC  
 A AT\_\_  
 GAM1289 BAT3 3' CTTCACAGTATTTAAGA 54781 G GTTT  
 TC TAAA CTGTGAAG  
 || ||| |||||  
 AG ATTT GACACTTC  
 A AT\_\_  
 GAM1289 BAT3 3' CTTCACAGTATTTAAGA 54784 G GTTT  
 TC TAAA CTGTGAAG  
 || ||| |||||  
 AG ATTT GACACTTC  
 A AT\_\_  
 GAM1289 CEACAM5 5' TCTCCACAGAGGAGGACAGAG 15162 \_ AAAG A  
 CTC GT TTTCTGTG AGA  
 ||| || ||||| |||  
 GAG CA GGAGACAC TCT  
 A GGA\_ C  
 GAM1289 ILF1 3' TCACAGGACCCACCAGG 15720 C AAA T  
 CCT GT GTT CTGTGA  
 ||| || ||| |||||  
 GGA CA CAG GACACT  
 C CC\_ \_  
 GAM1289 RYR2 3' CTTCACAGAGACACGTGG 6414 T AAA  
 CC CGT GTTTCTGTGAAG  
 || ||| ||||| |||||  
 GG GCA CAGAGACACTTC  
 T \_  
 GAM1289 C20orf38 3' TCTCAGCAGAAACCCTAC 37066 AA GA  
 GTA GTTTCTGT AGA  
 ||| ||||| |||  
 CAT CAAAGACG TCT  
 CC AC  
 GAM1289 ENDO180 3' CACAGGAACCAGAGGTA 20141 GTAAA  
 TACCTC GTTTCTGTG  
 ||||| |||||  
 ATGGAG CAAGGACAC  
 AC\_\_  
 GAM1289 KIAA0855 3' TCCTCACAAACTTCTTTACGA 30406 TTTC\_ A  
 TCGTAAAG TGTGA GA  
 ||||| ||| ||  
 AGCATTTC ACACT CT  
 TTCAA C  
 GAM1289 MGC10940 3' TCTAACAAAACTTTAC 50218 C GA  
 GTAAAGTTT TGT AGA  
 ||||| ||| |||

CATTTCAAA ACA TCT  
 A A\_  
 GAM1289 MGC3251 3' TCACAGAAAGTCATCGAGG 49314 TAAAG  
 CCTCG TTTCTGTGA  
 |||| |||||  
 GGAGC AAAGACACT  
 TACTG  
 GAM1289 MGC34869 3' TCCTCAGGACTTCACGGGTA 58096 T A T T\_  
 TACC CGT AAGTT CTG GA  
 ||| ||| |||| ||| ||  
 ATGG GCA TTCAG GAC CT  
 \_ C \_ TC  
 GAM1289 PCDH10 3' TAGAAACTTTAGAGG 51996 G  
 CCTC TAAAGTTTCTG  
 ||| |||||  
 GGAG ATTTCAAAGAT  
 \_  
 GAM1289 PLCL1 3' TCTTCAGTCAGAAAACCTTTA 20637 \_ \_  
 TAAAGTTT CTG TGAAGA  
 ||||| ||| |||||  
 ATTTCAAA GAC ACTTCT  
 A TG  
 GAM1289 PRO2949 3' TCTAACCAAAACTTTATGAGGT 37626 CT GA  
 A TACCTCGTAAAGTTT GT AGA  
 ||||| ||||| || |||  
 ATGGAGTATTTCAAA CA TCT  
 AC A\_  
 GAM1289 SEC15B 3' TCTTCACAGAAACCTTG 66689 A  
 TAA GTTTCTGTGAAGA  
 ||| |||||  
 GTT CAAAGACACTTCT  
 C  
 GAM1289 ZNF31 3' TCTTCACAACGGCCCCAGGAG 64990 GTAAA TC  
 CTC GTT TGTGAAGA  
 ||| ||| |||||  
 GAG CGG ACACTTCT  
 GACCC CA  
 GAM1289 LOC145988 3' TCCTCACAAACTTCTTTACGA 77614 TTTC\_ A  
 TCGTAAAG TGTGA GA  
 ||||| ||||| ||  
 AGCATTTC ACACT CT  
 TTCAA C  
 GAM1289 LOC146452 3' TCACAGCTGAAACTTTA 77916 \_  
 TAAAGTTTC TGTGA  
 ||||| |||||  
 ATTTCAAAG ACACT  
 TCG  
 GAM1289 LOC147669 5' TCACAAGATCCTCGAGGTA 84066 TAA TT \_  
 TACCTCG AG TCT GTGA  
 ||||| || ||| ||||

		ATGGAGC TC AGA CACT		
		___ CT A		
GAM1289	LOC157663 3'	AGAAACTTTAAAAGGTA	81534	CG
		TACCT TAAAGTTTCT		
		ATGGA ATTTCAAAGA		
		AA		
GAM1289	LOC221250 5'	TCTCCACAGAAACCAGAC	91835	AAA A
		GT GTTTCTGTG AGA		
		CA CAAAGACAC TCT		
		GAC C		
GAM1289	LOC255019 3'	TCACAGCTGAAACTTTA	95081	___
		TAAAGTTTC TGTGA		
		ATTTCAAAG ACACT		
		TCG		
GAM1290	ABCA1 3'	TCTTTGTAGAACCCTGTGGTA	18552	T TAAA T TG
		TACC CG GTT CTG AAGA		
		ATGG GT CAA GAT TTCT		
		T CC__ _ GT		
GAM1290	ADAR 3'	CTTCAAACCTCTGTGAGGTA	31750	A TCTG
		TACCTCGTA AGTT TGAAG		
		ATGGAGTGT TCAA ACTTC		
		C ____		
GAM1290	ADAR 3'	CTTCAAACCTCTGTGAGGTA	31760	A TCTG
		TACCTCGTA AGTT TGAAG		
		ATGGAGTGT TCAA ACTTC		
		C ____		
GAM1290	ADAR 3'	CTTCAAACCTCTGTGAGGTA	6625	A TCTG
		TACCTCGTA AGTT TGAAG		
		ATGGAGTGT TCAA ACTTC		
		C ____		
GAM1290	ADRA2B 3'	ATGGGGGCTTATGGGGTG	5460	A TT
		TACCTCGTAA GT CTGT		
		GTGGGGTATT CG GGTA		
		_ GG		
GAM1290	AIM1 3'	TTTTGTAGAGATGGGGT	91833	GTAAA TG
		ACCTC GTTTCTG AAG		
		TGGGG TAGAGAT TTT		
		____ GT		
GAM1290	APC 3'	TCACATGGAACCTTTAGAGGTA	3479	G _
		TACCTC TAAAGTTTC TGTGA		

			ATGGAG ATTTCAAGG ACACT		
			— T		
GAM1290 ATM	3'	TTTTGTAGAGGTGGGGT	56310	TAAAG	TG
		ACCTCG TTTCTG AAG			
		TGGGGT GGAGAT TTT			
		— GT			
GAM1290 ATP7A	3'	TCTTTACAGGAGAAAGAGGTG	3532	GTAAAG	
		TACCTC TTTCTGTGAAGA			
		GTGGAG GAGGACATTTCT			
		AAA—			
GAM1290 BACE	3'	ACAGAAGCTTGTGGGGTA	23973	GTA	
		TACCTC AAGTTTCTGT			
		ATGGGG TTCGAAGACA			
		TG—			
GAM1290 BACE	3'	ACAGAAGCTTGTGGGGTA	57283	GTA	
		TACCTC AAGTTTCTGT			
		ATGGGG TTCGAAGACA			
		TG—			
GAM1290 BCL11B	3'	AGAGATTTTGTGGGTA	43183	CG	
		TACCT TAAAGTTTCT			
		ATGGG GTTTTAGAGA			
		TT			
GAM1290 BCL6	3'	TTTTCACGGAAGTTTCAATGA	8129	— GT	
		TCGT AAA TTCTGTGAAGA			
		AGTA TTT AAGGCACTTTT			
		AC TG			
GAM1290 BCL6	3'	TTTTCACGGAAGTTTCAATGA	57225	— GT	
		TCGT AAA TTCTGTGAAGA			
		AGTA TTT AAGGCACTTTT			
		AC TG			
GAM1290 BSG	3'	TTTTATGTTTAATTTATGAGG	67800	TC_ A	
		CCTCGTAAAGTT TGTGAAG			
		GGAGTATTTTAA GTATTTT			
		TTT			
GAM1290 BSG	3'	TTTTATGTTTAATTTATGAGG	8183	TC_ A	
		CCTCGTAAAGTT TGTGAAG			
		GGAGTATTTTAA GTATTTT			
		TTT			
GAM1290 CASP10	3'	TTTTGTGGAGATGGGGT	52112	GTAAA	TG
		ACCTC GTTTCTG AAG			

			TGGGG	TAGAGGT	TTT		
			_____	GT			
GAM1290	CASP10	3'	TTTTGTGGAGATGGGGT	52128	GTAAA	TG	
			ACCTC	GTTTCTG	AAG		
			TGGGG	TAGAGGT	TTT		
			_____	GT			
GAM1290	CAV3	3'	TCTTCACAGGGGCTGCTGGCG	52894	AA__	TT	
			CGT	AGT	CTGTGAAGA		
			GCG	TCG	GACACTTCT		
			GTCG	GG			
GAM1290	CDK8	3'	TTCACAGATTGGGGTA	7001	TAAAGTT		
			TACCTCG	TCTGTGAA			
			ATGGGGT	AGACACTT			
			T_____				
GAM1290	CIS4	3'	TCTTGAGGTTTTAGAGGTG	14878	G	TT	TGT
			TACCTC	TAAAG	TC	GA	
			GTGGAG	ATTTT	AG	CT	
			_	GG	TT_		
GAM1290	CLECSF12	3'	TTTTGTAGAGACTGGGT	76704	CGTAA	TG	
			ACCT	AGTTTCTG	AAG		
			TGGG	TCAGAGAT	TTT		
			_____	GT			
GAM1290	CNGA3	3'	TTTTTATGGAATCTGCAAGGTG	7112	C	AAGT	
			TACCT	GTA	TTCTGTGAAGA		
			GTGGA	CGT	AAGGTATTTT		
			A	CT_			
GAM1290	COL9A1	5'	TCTTCATAGGGACTGTTGGC	8485	AA__	TT	
			GT	AGT	CTGTGAAGA		
			CG	TCA	GATACTTCT		
			GTTG	GG			
GAM1290	CTF1	3'	TTTTGTAGAGACGAGGT	7183	AAAGT	TG	
			ACCTCGT	TTCTG	AAG		
			TGGAGCA	GAGAT	TTT		
			_____	GT			
GAM1290	CXCL13	3'	TTTTTGTGGGGGCGGGGCCGGG	21199	_AAA	TT	TG
		G	CCTCG	T	GT	CTG	AAGA
			GGGGC	G	CG	GGT	TTTT
			C	GGG	GG	GT	
GAM1290	D1S155E	3'	TTTCGTGGGTTGGGGGGTA	23125	G	AGTT	TG
			TACCTC	TAA	TC	TGAAG	



		ATGGGG GTT GG GCTTT	
		G ____ GT	
GAM1290 DPP4	3'	TTTTTATGGAGGCTTTGC 8659	
		GTAAAGTTTCTGTGAAGA	
		CGTTTCGGAGGTATTTTT	
GAM1290 DPYSL2	3'	CAGAAGCTTTAGAGGTA 7291	G
		TACCTC TAAAGTTTCTG	
		ATGGAG ATTTCGAAGAC	
GAM1290 ELK1	3'	TCTTCCTATATTTGGTGGGGTG 17846	TA TTCTGT
		TACCTCG AAGT GAAGA	
		GTGGGGT TTTA CTTCT	
		GG TATC__	
GAM1290 ENTPD6	3'	CTTCATAGACGGCAGGTG 6970	C AAAGTT
		TACCT GT TCTGTGAAG	
		GTGGA CG AGATACTTC	
		_ GC__	
GAM1290 FOXD2	5'	TCTTTGCAGGAGCCTGGGTG 15571	CGTAAA TG
		TACCT GTTTCTG AAGA	
		GTGGG CGAGGAC TTCT	
		TC__ GT	
GAM1290 FUT1	3'	TTTTGTAGAGACGAGGT 3800	AAAGT TG
		ACCTCGT TTCTG AAG	
		TGGAGCA GAGAT TTT	
		____ GT	
GAM1290 GAB2	3'	TTTACAGAGGAGGAGG 24510	GTAAAG
		CCTC TTTCTGTGAAG	
		GGAG GGAGACATTTT	
		GA__	
GAM1290 GAB2	3'	TTTACAGAGGAGGAGG 54467	GTAAAG
		CCTC TTTCTGTGAAG	
		GGAG GGAGACATTTT	
		GA__	
GAM1290 GFAP	3'	TCTTTTGGTTTTTATGAGGTG 9019	TTTCTGT
		TACCTCGTAAAG GAAGA	
		GTGGAGTATTTT TTTCT	
		TGGT__	
GAM1290 GRB2	3'	TTTGGTTGGAACTTTAGGGGGT 9131	G TG G A
G		TACCTC TAAAGTTTC T AAG	

GTGGGG ATTTCAAGG G TTT  
 G TT G  
 GAM1290 GRIN2A 3' TCTTCCACTCAAGGAATCTTGT 5899 AG \_\_\_\_ \_  
 GAGGTG TCGTAA TTTCT GTG AAGA  
 ||||| |||| || ||||  
 AGTGTT AAGGA CAC TTCT  
 CT ACT C  
 GAM1290 GRM6 3' TTTTGTAGAGACGAGGT 5941 AAAGT TG  
 ACCTCGT TTCTG AAG  
 ||||| |||| ||  
 TGGAGCA GAGAT TTT  
 \_\_\_\_ GT  
 GAM1290 HSPA4 3' TTCATGGAGGCCAGG 89173 CGTAAA  
 CCT GTTTCTGTGAA  
 || |||||  
 GGA CGGAGGTACTT  
 C\_\_\_\_  
 GAM1290 ICMT 3' GAAGCTTTAAGAGGTG 24813 G  
 TACCTC TAAAGTTTC  
 ||||| |||||  
 GTGGAG ATTTCAAG  
 A  
 GAM1290 ID1 3' TCACCAGAGACTTTAGGGGGTG 70033 G \_  
 TACCTC TAAAGTTTCTG TGA  
 ||||| ||||| ||  
 GTGGGG ATTTCAAGAGAC ACT  
 G C  
 GAM1290 IFRD1 5' TCTTCACGGGGATTCTGC 60124 \_ TT  
 GTA AAGT CTGTGAAGA  
 || |||| |||||  
 CGT TTTA GGCACTTCT  
 C GG  
 GAM1290 IL20RA 3' CTTTAATACTTTATGAG 27046 TTCTG  
 CTCGTAAAGT TGAAG  
 ||||| ||||  
 GAGTATTTCA ATTTC  
 TA\_\_\_\_  
 GAM1290 KCNA6 3' TCTTGCCATAACTTTACAGGGT 9518 TC TC TG  
 A TACC GTAAAGTT TG AAGA  
 |||| ||||| || ||||  
 ATGG CATTTCAA AC TTCT  
 GA T\_ CG  
 GAM1290 KCNE2 3' TTTTCATGGAGATTATGTGGT 17624 T AA  
 ACC CGTA GTTTCTGTGAAGA  
 || |||| |||||  
 TGG GTAT TAGAGGTACTTTT  
 T \_\_\_\_  
 GAM1290 KRT1 3' ATGGGTGTTTTGTGAGGTA 20387 TT  
 TACCTCGTAAAG TCTGT  
 ||||| ||||

		ATGGAGTGT TTTT GGGTA	
		GT	
GAM1290 LFG	3'	CTTTGCAGAGCTGGGG 76719 GTAA T TG	
		CCTC AGTT CTG AAG	
		GGGG TCGA GAC TTC	
		____ _ GT	
GAM1290 LHCGR	3'	TTTTTATAGAAATTTTGACACA 4075 CTCG_	
GTA		TAC TAAAGTTTCTGTGAAGA	
		ATG GTTTTAAAGATATTTTT	
		ACACA	
GAM1290 LHX3	5'	GGGGCTATTGCGGGGTG 27376 _ TT	
		TACCTCGTAA AGT C	
		GTGGGGCGTT TCG G	
		A GG	
GAM1290 LZTR1	3'	TTTCACAGGGGCTGAAGG 22247 CGTAA TT	
		CCT AGT CTGTGAAG	
		GGA TCG GACACTTT	
		AG__ GG	
GAM1290 MICB	3'	TTTTGTAGAGACGGGGT 19838 AAAGT TG	
		ACCTCGT TTCTG AAG	
		TGGGGCA GAGAT TTT	
		____ GT	
GAM1290 MYO1E	3'	TCTTCATAGGAACCAGGAGG 17190 GTAAA	
		CCTC GTTTCTGTGAAGA	
		GGAG CAAGGATACTTCT	
		GAC__	
GAM1290 NCOA6	5'	TCATAGGGTTTTGTGAGG 25977 AGT	
		CCTCGTAA TTCTGTGA	
		GGAGTGTT GGGATACT	
		TT_	
GAM1290 NCOA6	5'	TTTTGTAGAGGCGGGGT 25985 AAAGT TG	
		ACCTCGT TTCTG AAG	
		TGGGGCG GAGAT TTT	
		____ GT	
GAM1290 NCOA6IP	3'	TTTTGTAGAGACGAGGT 45740 AAAGT TG	
		ACCTCGT TTCTG AAG	
		TGGAGCA GAGAT TTT	
		____ GT	
GAM1290 NID	3'	TTTTCACGGAGACCTATCTGAG 10233 TAAA_	
GT		ACCTCG GTTTCTGTGAAGA	

			TGGAGT CAGAGGCACTTTT		
			CTATC		
GAM1290 NRF1	3'	TTTTTACACGTTTGCAGAGGTG 60121		_	GTTTC
		TACCTC GTAAA TGTGAAGA			
		GTGGAG CGTTT ACATTTTT			
		A GC__			
GAM1290 PAX5	3'	TCTTTAGTATCTTTACGAGG 33637			TTT GT
		CCTCGTAAAG CT GAAGA			
		GGAGCATTTC GA TTTCT			
		TAT __			
GAM1290 PCDHGA7	3'	TTTAAAAAACTTTATAGAGGTA 49448		_	CTG
		TACCTC GTAAAGTTT TGAA			
		ATGGAG TATTTCAAA ATTT			
		A AA_			
GAM1290 PMX1	3'	TCTTTATAGAAGCTCTAGGAG 42664			G A
		CTC TA AGTTTCTGTGAAGA			
		GAG AT TCGAAGATATTTCT			
		G C			
GAM1290 PMX1	3'	TCTTTATAGAAGCTCTAGGAG 22597			G A
		CTC TA AGTTTCTGTGAAGA			
		GAG AT TCGAAGATATTTCT			
		G C			
GAM1290 PRIM2A	3'	TTTTTG TAGAGGTGGGGGGT 6277		G AAG	TG
		ACCTC TA TTTCTG AAGA			
		TGGGG GT GGAGAT TTTT			
		G __ GT			
GAM1290 RAI14	3'	TTTTTG TAGGATGCCTGACGAG 31483		AAA _	TG
	GTG	TACCTCGT GT TTCTG AAGA			
		GTGGAGCA CG AGGAT TTTT			
		GTC T GT			
GAM1290 RANBP7	3'	TCAGCGGGATTTTGGGGGTG 21115		G	TT TG
		TACCTC TAAAGT C TGA			
		GTGGGG GTTTTA G ACT			
		_ GG CG			
GAM1290 RBM8A	3'	TTTTGTAGAGATGGGGT 17551		GTAAA	TG
		ACCTC GTTTCTG AAG			
		TGGGG TAGAGAT TTT			
		__ GT			
GAM1290 RNTRE	3'	TTTCATAGGAGTCTAGG 28043		CGTAA _	
		CCT AG TTTCTGTGAAG			

GGA TC GAGGATACTTT  
 \_\_\_\_\_ T  
 GAM1290 RXRA 3' TCTTCTCCTTGCTCTGCGGGGT 11419 A TTCTGT  
 G TACCTCGTA AGT GAAGA  
 ||||| || ||||  
 GTGGGGCGT TCG CTTCT  
 C TTCCT\_  
 GAM1290 SERPINE1 3' TTTTATAGGAATAGAGG 5198 GTAAA  
 CCTC GTTTCTGTGAAG  
 ||| |||||  
 GGAG TAAGGATATTTT  
 A\_\_\_\_\_  
 GAM1290 SLC19A1 5' CCTGTGCCAGAAGCTTTGTAGG 11756 C TGA\_ A  
 TG TACCT GTAAAGTTTCTG AG  
 |||| ||||| ||  
 GTGGA TGTTTCGAAGAC TC  
 \_ CGTG CT  
 GAM1290 VDR 3' TTTTATGCGGCTGAACGGGG 4578 AA TT T  
 CCTCGT AGT C GTGAAGA  
 |||| ||| | |||||  
 GGGGCA TCG G TATTTT  
 AG GG\_  
 GAM1290 VRK1 3' TTTTCCTGTGAGTCTTGCGAGG 12622 AG CT T  
 TG TACCTCGTAA TTT G GAAGA  
 ||||| ||| | ||||  
 GTGGAGCGTT GAG T CTTT  
 CT TG C  
 GAM1290 WRB 3' CTGTGAAGATCTTGGACTTTAT 16126 T\_\_\_\_\_ GTGA  
 GAG TCGTAAAGT TCT AG  
 ||||| ||| ||  
 AGTATTCA AGA TC  
 GGTCT AGTG  
 GAM1290 ZNF236 3' TTTTACTTGAATCTTTGTGGGG 23722 T T\_ A  
 TA TACCTCGTAAAG TTC GTGAAG  
 ||||| ||| |||||  
 ATGGGGTGTTTC AAG CATTTT  
 T TT  
 GAM1290 ZNF264 3' TTTTACAGAAATTGAG 12770 TAAA  
 CTCG GTTTCTGTGAAG  
 ||| |||||  
 GAGT TAAAGACATTTT  
 \_\_\_\_\_  
 GAM1290 ZNF9 3' TTTACAGAAATCAAGATG 12774 AAA\_  
 CGT GTTTCTGTGAAG  
 ||| |||||  
 GTA TAAAGACACTTT  
 GAAC  
 GAM1290 ADAM9 3' TTTTCATAGAAATTAGGCTGG 13773 TC AA  
 CC GT AGTTTCTGTGAAGA  
 || || |||||

GG CG TTAAAGATACTTTT  
T\_ GA  
GAM1290 ALDH9 5' TCTTCCCGCCTGGAGACTGTGT 5515 A \_ \_  
GGGGTA TCGTA AGTTTCT GT GAAGA  
||||| |||  
GGTGT TCAGAGG CG CTTCT  
G TC CC  
GAM1290 AP3M1 3' TTTTCACTTAGGAAGATTTTGG 23920 G \_ \_  
AGGTG TC TAAAGTTT CT GTGAAGA  
|| ||||| || |||||  
AG GTTTTAGA GG CACTTTT  
\_ A ATT  
GAM1290 C1orf8 3' TTTTGTAGTAATTTAAGAGGT 16834 GTA T TG  
G TACCTC AAGTT CTG AAGA  
||||| ||||| ||| |||  
GTGGAG TTAA GAT TTTT  
AA\_ T GT  
GAM1290 C2orf6 3' TTTTACAGGGACTTTAT 36647 TT  
GTAAAGT CTGTGAAGA  
||||| |||||  
TATTTCA GACATTTT  
GG  
GAM1290 CGI-57 3' CTGGGTGGGAGCTTATGGGGTG 73879 A TG GA A  
TACCTCGTAA GTTTC T AG  
||||||| ||||| | ||  
GTGGGGTATT CGAGG G TC  
\_ GT GG C  
GAM1290 DDX33 3' CTTTCGTAGGGACTTGGG 39373 CGTA TT  
CCT AAGT CTGTGAAG  
||| ||||| |||||  
GGG TTCA GATGCTTC  
\_ GG  
GAM1290 DKFZP434B044 3' TTTTATTTTGTTCATTGCGGGG 48932 AGTTTCT  
TA TACCTCGTAA GTGAAGA  
||||||| |||||  
ATGGGGCGTT TATTTT  
ACTGTTT  
GAM1290 DKFZP434D193 3' CTTTGCAGCCTACGTGGTA 88878 T AAGTTT TG  
TACC CGTA CTG AAG  
||||| ||| |||  
ATGG GCAT GAC TTC  
T CC\_ GT  
GAM1290 DKFZp434M0331 3' TCTCCAAAGATCTTTGTGAGGT 34237 TT G A  
G TACCTCGTAAAG TCT TG AGA  
||||||| ||| |||  
GTGGAGTGTTC AGA AC TCT  
T\_ A C  
GAM1290 DUSP9 3' TCTTTGCGGGATGGGGGTGGGG 7344 AAAGT TG  
CCTCGT TTCTG AAGA  
||||| ||||| |||

GGGGTG AGGGC TTCT  
GGGGT GT  
GAM1290 ECE2 3' TTTTACAGAAAAGAGG 28071 GTAAAG  
CCTC TTTCTGTGAAG  
|||| ||||||||  
GGAG AAAGACATTTT  
A\_\_\_\_  
GAM1290 ENDO180 3' CTTTGCAGAGCCCGAGG 20143 TAAA T TG  
CCTCG GTT CTG AAG  
|||| ||| ||| |||  
GGAGC CGA GAC TTC  
C\_\_ \_ GT  
GAM1290 EREG 3' TTTTATAGGGGCTTTGC 7515 TT  
GTAAAGT CTGTGAAGA  
||||| |||||||  
CGTTTCG GATATTTTT  
GG  
GAM1290 FKBP9 5' TTGAAGATCTGATTTTGTGAGG 94073 T\_\_\_\_\_ GTGA  
TA ACCTCGTAAAGT TCT A  
||||||||| ||| |  
TGGAGTGTTTTA AGA T  
GTCT AGTG  
GAM1290 FLJ10922 3' TTTTGTAGAGACGGGGT 36881 AAAGT TG  
ACCTCGT TTCTG AAG  
||||| |||| |||  
TGGGGCA GAGAT TTT  
\_\_\_\_\_ GT  
GAM1290 FLJ12577 3' TCTTGGAAGACTTTGGAGGTG 48159 G \_ GTG  
TACCTC TAAAGTTT CT AAGA  
||||| ||||||| || |||  
GTGGAG GTTTCAGA GG TTCT  
\_ A G\_  
GAM1290 FLJ13449 3' TCTTCGTGGAACTATGCATGG 44619 TC A TG  
TA TACC GTA AGTTTC TGAAGA  
|||| ||| |||||| |||||||  
ATGG CGT TCAAAG GCTTCT  
TA A GT  
GAM1290 FLJ14351 3' TTTTATAGAAACCAGGT 45333 CGTAAA  
ACCT GTTTCTGTGAAG  
|||| |||||||||||  
TGGA CAAAGATATTTT  
C\_\_\_\_  
GAM1290 FLJ14594 3' TTTTGCAGGGCGCAGGTG 51455 \_ AAAGTT TG  
TACCT CGT TCTG AAG  
||||| ||| ||| |||  
GTGGA GCG GGAC TTT  
C \_\_\_\_\_ GT  
GAM1290 FLJ20311 3' TTTTGTGGGAATGTGGGAAGG 34925 \_ G AA TG  
TG TACCT C TA GTTTCTG AAGA  
||||| || ||||||| |||

			GTGGA G GT TAAGGGT TTTT		
			A G G_ GT		
GAM1290	FLJ20485	3'	TTTTGTAGAGACGGGGGT 38768	GTAAA	TG
			ACCTC GTTTCTG AAG		
			TGGGG CAGAGAT TTT		
			G_____ GT		
GAM1290	FLJ20519	3'	TCTTTACAGAGGTACCTGAGG 35347	TAAA	TT
			CCTCG G TCTGTGAAGA		
			GGAGT T AGACATTTCT		
			CCA_ GG		
GAM1290	FLJ21047	5'	TTTTTACAGAGAAAAGGGG 44693	GTAAAG	
			CCTC TTTCTGTGAAGA		
			GGGG AGAGACATTTTT		
			AAA_____		
GAM1290	FLJ22415	3'	CTTCATGATGTTATGAGG 91490	AGTT	T
			CCTCGTAA TC GTGAAG		
			GGAGTATT AG TACTTC		
			GT_ _		
GAM1290	FLJ22457	3'	TTTTTGACAGAGGTGACACAGG 46085	C AAA	TT TG
	A		TACCT GT G TCTG AAGA		
			ATGGA CA T AGAC TTTT		
			_ CAG GG GT		
GAM1290	FLJ22795	3'	TCTGAAGATCTTTGTGAGGTG 46946	TT	GTGA
			TACCTCGTAAAG TCT AGA		
			GTGGAGTGTTTC AGA TCT		
			T_ AG_		
GAM1290	FLJ31951	3'	TTTTTATGGGAATTTTGATATG 58557	_____	
	A		TCGTA AAGTTTCTGTGAAGA		
			AGTAT TTAAAGGTATTTTT		
			AGT		
GAM1290	FOXP1	3'	TCTTAAAGAGATTTTATGGGG 51071	GTG	
			CCTCGTAAAGTTTCT AAGA		
			GGGGTATTTTAGAGA TTCT		
			AA_		
GAM1290	FREQ	3'	TCTTCACGGAGGCTTCCAGCGG 26588	TCGTA	
	TG		TACC AAGTTTCTGTGAAGA		
			GTGG TTCGGAGGCACTTCT		
			CGACC		
GAM1290	FREQ	3'	TTTTTGTGGGGAAAGTGAGGT 26595	TAAAG	TT TG
			ACCTCG T CTG AAGA		



			TGGAGT	A	GGT	TTTT		
			GAA__	GG	GT			
GAM1290	GABARAPL1	3'	TTTTCACTTTTGGGATTTTGTG	48605		TT	T__	
			GGGTG		CTCGTAAAGT	C	GTGAAGA	
			GGGTGTTTTA	G	CACTTTT			
			GG	TTTT				
GAM1290	GABARAPL3	3'	ACTTATAGGATTTTGTGGGGTG	50797		T	AGA	
			TACCTCGTAAAGTT	CTGTGA				
			GTGGGGTGTTTTAG	GATATT				
				CAC				
GAM1290	GPS2	3'	CTTCATGTTAATGGGGTG	87159		A	GTTTC	
			TACCTCGT	AA	TGTGAAG			
			GTGGGGTA	TT	GTA	CTTC		
			A	_____				
GAM1290	GPS2	5'	CTTCATGTTAATGGGGTG	15665		A	GTTTC	
			TACCTCGT	AA	TGTGAAG			
			GTGGGGTA	TT	GTA	CTTC		
			A	_____				
GAM1290	GPT2	3'	TTTTCATGGGGGAGGCGGGGT	55963		AAAG	TT	
			ACCTCGT	T	CTGTGAAGA			
			TGGGGCG	G	GGTACTTTT			
			GA__	GG				
GAM1290	HERPUD1	3'	GGGAACTTTGCGGAGGTG	28019		_		
			TACCTC	GTAAAGTTTCT				
			GTGGAG	CGTTTCAAGGG				
			G					
GAM1290	HNRPU	3'	TTTTTTAGAAGCTTTGTGGGT	15695		T	T	A
			ACC	CGTAAAGTTTCTG	GAAG			
			TGG	GTGTTTCGAAGAT	TTTT			
			_	T				
GAM1290	HNRPU	3'	TTTTTTAGAAGCTTTGTGGGT	48991		T	T	A
			ACC	CGTAAAGTTTCTG	GAAG			
			TGG	GTGTTTCGAAGAT	TTTT			
			_	T				
GAM1290	HSNOV1	3'	TTTTTGTAGAGAGATGGGGT	34018		AAAG	TG	
			ACCTCGT	TTTCTG	AAGA			
			TGGGGTA	AGAGAT	TTTT			
			G__	GT				
GAM1290	HSPC232	3'	TTTTGTAGAGATGGGGT	33234		GTAAA	TG	
			ACCTC	GTTTCTG	AAG			

TGGGG TAGAGAT TTT  
 \_\_\_\_\_ GT  
 GAM1290 HSPCAL3 3' TTCACAGATTGGGGTA 76559 TAAAGTT  
 TACCTCG TCTGTGAA  
 ||||| |||||  
 ATGGGGT AGACACTT  
 T\_\_\_\_\_

GAM1290 HSU24186 5' TTTTATAGAGATGTTGGGA 25325 G A  
 TC TAA GTTCTGTGAAGA  
 || ||| |||||  
 AG GTT TAGAGATATTTTT  
 G G

GAM1290 INSM2 3' TTTTGCTGCTTTTGGGGTG 50871 T TTCT TG  
 TACCTCG AAAGT G AAG  
 ||||| |||| | |||  
 GTGGGGT TTTCG C TTT  
 \_ T\_\_\_ GT

GAM1290 KIAA0089 3' TTTTCATGGGAATTTTA 69968  
 TAAAGTTTCTGTGAAGA  
 |||||  
 ATTTTAAGGGTACTTTT

GAM1290 KIAA0100 3' TCCAGGGACTTGTGGGGTG 27972 GTA TT T  
 TACCTC AAGT CTG GA  
 ||||| ||| ||| ||  
 GTGGGG TTCA GAC CT  
 TG\_ GG \_

GAM1290 KIAA0186 3' TTTTGTGGAGATGGGGT 40769 GTAAA TG  
 ACCTC GTTCTG AAG  
 |||| ||||| |||  
 TGGGG TAGAGGT TTT  
 \_\_\_\_\_ GT

GAM1290 KIAA0478 3' TCTTTACTCATTTATTTTATGG 29561 T TTCT\_\_  
 GTA ACC CGTAAAGT GTGAAGA  
 ||| ||||| |||||  
 TGG GTATTTTA CATTTCT  
 \_ TTTACT

GAM1290 KIAA0562 3' TTTTGTTTTGTTTTGCAGGGG 28162 TTTCT TG  
 CCTCGTAAAG G AAGA  
 ||||| ||| |||  
 GGGGCGTTTT T TTTT  
 GTTTT GT

GAM1290 KIAA0633 3' TTTTCAAAGGTGGCTTTGTTAG 94055 CG \_ G  
 GTA TACCT TAAAGTT TCT TGAAGA  
 |||| ||||| ||| |||||  
 ATGGA GTTTCGG GGA ACTTTT  
 TT T A

GAM1290 KIAA0748 3' CTTTATAGAAAAAGAG 28939 GTAAAG  
 CTC TTTCTGTGAAG  
 ||| |||||

GAG AAAGATATTTTC  
 AA\_\_\_\_  
 GAM1290 KIAA0819 3' TCTTCATGGGGACATAAAGG 63581 CGTAAA TT  
 CCT GT CTGTGAAGA  
 ||| || |||||  
 GGA CA GGTACTTCT  
 AATA\_\_ GG  
 GAM1290 KIAA1032 3' CAGATGGGGAGGCTTTCCGAGG 66152 T GTGAAGA  
 TG TACCTCG AAAGTTTCT  
 ||||| |||||  
 GTGGAGC TTTCGGAGG  
 C GGTAGACT  
 GAM1290 KIAA1107 3' TCTTTCCAATTTAATGAGGTA 63995 A TTC TG  
 TACCTCGT AAGT TG AAGA  
 ||||| ||| || |||  
 ATGGAGTA TTTA AC TTCT  
 A \_\_\_\_ CT  
 GAM1290 KIAA1128 3' TGAGGAAGAAATTTTATGGGGT 68487 GTGAAGA  
 ACCTCGTAAAGTTTCT  
 ||||| |||||  
 TGGGGTATTTTAAAGA  
 AGGAGT  
 GAM1290 KIAA1128 3' TTGCACAAAACCTTTGATGGGGT 68490 \_ C AAGA  
 A TACCTCGT AAAGTTT TGTG  
 ||||| ||||| |||  
 ATGGGGTA TTTCAAA ACAC  
 G \_ GTTT  
 GAM1290 KIAA1193 3' TTTTGTAGAGATGGGGT 67656 GTAAA TG  
 ACCTC GTTTCTG AAG  
 |||| ||||| |||  
 TGGGG TAGAGAT TTT  
 \_\_\_\_ GT  
 GAM1290 KIAA1233 3' TTTTCAACAGTTTTATAAGGTA 63084 CG TTT \_  
 TACCT TAAAG CTGT GAAGA  
 |||| |||| ||| |||||  
 ATGGA ATTTT GACA CTTTT  
 AT \_\_\_\_ A  
 GAM1290 KIAA1254 3' TTTTATAGGAAAGGAGG 70028 GTAAAG  
 CCTC TTTCTGTGAAG  
 |||| |||||  
 GGAG AAGGATATTTT  
 GA\_\_\_\_  
 GAM1290 KIAA1257 3' TTTTGTAGAGATGGGGT 62765 GTAAA TG  
 ACCTC GTTTCTG AAG  
 |||| ||||| |||  
 TGGGG TAGAGAT TTT  
 \_\_\_\_ GT  
 GAM1290 KIAA1423 3' TTTTACAGAGATTTTCAGA 61730 GTA  
 TC AAGTTTCTGTGAAGA  
 || ||||| |||||

AG TTTAGAGACATTTTT  
 AC\_  
 GAM1290 KIAA1431 3' TTGAAGATTTTAATTTTATGAG 63000 T\_\_\_\_\_ GTGA  
 G CCTCGTAAAGT TCT A  
 ||||| ||| |  
 GGAGTATTTTA AGA T  
 ATTTT AGTG  
 GAM1290 KIAA1530 3' TTTTGTAGAGATGAGGT 67964 GTAAA TG  
 ACCTC GTTTCTG AAG  
 |||| ||||| ||  
 TGGAG TAGAGAT TTT  
 \_\_\_\_\_ GT  
 GAM1290 KIAA1560 3' CTTTATAGGAATTGATGTA 64177 C TAAA  
 TAC TCG GTTTCTGTGAAG  
 ||| ||| ||||| |||||  
 ATG AGT TAAGGATATTTC  
 T \_\_\_\_\_  
 GAM1290 KIAA1649 3' TTTTGTAGAGATGAGGT 50282 GTAAA TG  
 ACCTC GTTTCTG AAG  
 |||| ||||| ||  
 TGGAG TAGAGAT TTT  
 \_\_\_\_\_ GT  
 GAM1290 KIAA1671 3' TTTTGTAGAGACAAGGGT 65701 CGTAAA TG  
 ACCT GTTTCTG AAG  
 |||| ||||| ||  
 TGGG CAGAGAT TTT  
 AA\_\_\_\_\_ GT  
 GAM1290 KIAA1913 5' TCTTCGGGGCTTTATGGCGTG 73888 C TT TGT  
 TAC TCGTAAAGT C GAAGA  
 ||| ||||| | ||||  
 GTG GGTATTTTCG G CTTCT  
 C GG \_\_\_\_\_  
 GAM1290 LEAP-2 5' TTGAAGATTTGGGCTTTGGAGG 53745 G T\_\_\_\_\_ GTGA  
 TA CCTC TAAAGT TCT A  
 ||||| ||| |  
 GGAG GTTTCG AGA T  
 \_ GGTTC AGTG  
 GAM1290 LEPROTL1 3' TTTTCACAGAGACTTGCTGAAG 31065 \_ TA  
 G CCT CG AAGTTTCTGTGAAGA  
 ||| ||| ||||| |||||  
 GGA GT TTCAGAGACACTTTT  
 A CG  
 GAM1290 MCM10 3' TTTTGTAGAGATGGGGT 37578 GTAAA TG  
 ACCTC GTTTCTG AAG  
 |||| ||||| ||  
 TGGGG TAGAGAT TTT  
 \_\_\_\_\_ GT  
 GAM1290 MGC1136 3' TCTTTGTGGGAGGGGACGGGG 43805 AAAG TG  
 CCTCGT TTTCTG AAGA  
 ||||| ||||| ||||

GGGGCA GAGGGT TTCT  
GGG\_ GT  
GAM1290 MGC1203 3' TTTTACAGACTCGGGCGGGTG 44156 T AAAGTT  
TACC CGT TCTGTGAAGA  
||||| |||  
GTGG GCG AGACATTTT  
\_ GGCTC\_  
GAM1290 MGC2474 3' TTTTGCAGAGATGGGGT 43734 GTAAA TG  
ACCTC GTTTCTG AAG  
||||| |||  
TGGGG TAGAGAC TTT  
\_\_\_\_\_ GT  
GAM1290 MGC3123 3' TCTTTGTGGTGCTGTTGGGTG 44100 T TAA TT TG  
TACC CG AGT CTG AAGA  
||||| |||  
GTGG GT TCG GGT TTCT  
\_ TG\_ T\_ GT  
GAM1290 MGC3200 3' TCTTTGTGGAGATAATTAGGGG 50224 GTAAA TG  
TG TACCTC GTTTCTG AAGA  
||||| |||  
GTGGGG TAGAGGT TTCT  
ATTAA GT  
GAM1290 MGC33177 3' TTTTCGTGGGAGGGGTGGGGTG 58011 AAAG TG  
TACCTCGT TTTC TGAAGA  
||||| |||  
GTGGGGTG GAGG GCTTTT  
GG\_ GT  
GAM1290 MGC4365 3' TGAGAGAGGAAGTCTGTGGGGT 44273 A GTGAAGA  
G TACCTCGTA AGTTTCT  
||||| |||  
GTGGGGTG TCAAGGA  
C GAGAGT  
GAM1290 MGC9084 5' TCCGGAGGAGGCGTTGTGAGGT 53043 A G\_ AAGA  
G TACCTCGTAA GTTTCT TG  
||||| |||  
GTGGAGTGTT CGGAGG GC  
G AG CT  
GAM1290 MRPL34 3' TTTTGCAGGGAGCTGGGG 43743 GTAA \_ TG  
CCTC AGTTTC TG AAGA  
||||| |||  
GGGG TCGAGG AC TTTT  
\_\_\_\_\_ G GT  
GAM1290 MRS2L 3' TTTTATAGATGTGATATGAGG 40333 AA TT  
CCTCGTA G TCTGTGAAGA  
||||| |  
GGAGTAT T AGATATTTT  
AG GT  
GAM1290 OR51E2 3' TCTTCGTAACTTTATGGAGTA 47800 CT TCTG  
TAC CGTAAAGTT TGAAGA  
||| |||

		ATG GTATTTCAA GCTTCT		
		AG T__		
GAM1290	PEG10	3' TCTTTATGGAGGGGAGACGAG 30532	AAAG_	
	G	CCTCGT TTTCTGTGAAGA		
		GGAGCA GGAGGTATTTCT		
		GAGGG		
GAM1290	PRKWNK2	3' TCTTCGCAGAGGACACAGG 90540	C AAAG	
		CCT GT TTTCTGTGAAGA		
		GGA CA GGAGACGCTTCT		
		_ CA_		
GAM1290	PRO1257	5' TTGAAGATTTGGTTTTATGGGG 37712	T_____ GTGA	
	TA	ACCTCGTAAAGT TCT A		
		TGGGGTATTTTG AGA T		
		GTTT AGTG		
GAM1290	PRO2000	5' TTTTGCAGGCTTTGGAGGTA 26066	G TT TG	
		TACCTC TAAAGT CTG AAG		
		ATGGAG GTTTCG GAC TTT		
		_ _ GT		
GAM1290	PRO2949	3' TCTAACCAAACTTTATGAGGT 37626	CT GA	
	A	TACCTCGTAAAGTTT GT AGA		
		ATGGAGTATTTCAAA CA TCT		
		AC A_		
GAM1290	PTPN9	3' TTTCTAGGATTTTATGGGG 11083	T T	
		CCTCGTAAAGTT CTG GAAG		
		GGGGTATTTTAG GAT CTTT		
		_ C		
GAM1290	SC4MOL	3' TTTTGTAGAGATGGGGT 22167	GTAAA TG	
		ACCTC GTTTCTG AAG		
		TGGGG TAGAGAT TTT		
		_ GT		
GAM1290	SCYA16	3' TTTTGCAGAGACTTTGCTAG 15970	C TG	
		CT GTAAAGTTTCTG AAGA		
		GA CGTTTCAGAGAC TTTT		
		T GT		
GAM1290	SCYA22	3' TTTTGTAGAGACGGGGT 90964	AAAGT TG	
		ACCTCGT TTCTG AAG		
		TGGGGCA GAGAT TTT		
		_ GT		
GAM1290	SEMA4B	3' TCTTCGTGGAACACGACCGTGG 69039	T TAAA _ TG	
	TG	TACC CG GT TTC TGAAGA		

GTGG GC CA AAG GCTTCT  
 T CAG\_ C GT  
 GAM1290 SLC5A7 3' TCTTTGTAGAAGAGCACTGGG 41516 C AAAG TG  
 CCT GT TTTCTG AAGA  
 ||| || ||||| ||||  
 GGG CA GAAGAT TTCT  
 T CGA\_ GT  
 GAM1290 SLC7A10 3' TTTTTGTAGAGACTGAAGC 39068 AA\_ TG  
 GT AGTTTCTG AAGA  
 || ||||| ||||  
 CG TCAGAGAT TTTT  
 AAG GT  
 GAM1290 SPIN 3' TCTTTGTGGATTAGGATGGGG 59586 AAAGTT TG  
 CCTCGT TCTG AAGA  
 ||||| ||| ||||  
 GGGGTA AGGT TTCT  
 GGATT\_ GT  
 GAM1290 SYT6 3' AGAGCCTTTGTGAGGTG 78771 T  
 TACCTCGTAAAG TTCT  
 ||||| ||||  
 GTGGAGTGTTC GAGA  
 C  
 GAM1290 TP53INP1 3' TTTTTATAGAAATTTT 72962  
 AAAGTTTCTGTGAAGA  
 ||||| |||||  
 TTTTAAAGATATTTT  
  
 GAM1290 TP53INP1 3' TTTTTATAGAAATTTT 52735  
 AAAGTTTCTGTGAAGA  
 ||||| |||||  
 TTTTAAAGATATTTT  
  
 GAM1290 TReP-132 3' TTTTTGTGGGGGGTGGGGGG 37297 G AG TT TG  
 CCTC TAA T CTG AAGA  
 ||| ||| | ||| ||||  
 GGGG GTT G GGT TTTT  
 G G\_ GG GT  
 GAM1290 UCH37 3' TTTTCATGGAAACCATTATG 32023 A\_  
 CGTAA GTTTCTGTGAAGA  
 |||| ||||| |||||  
 GTATT CAAAGGTACTTTT  
 AC  
 GAM1290 USP20 3' TCTTTGTAGAAGCAGGTGGTGG 21928 \_ AAA TG  
 TG TACC TCGT GTTTCTG AAGA  
 ||| ||| ||||| ||||  
 GTGG GGTG CGAAGAT TTCT  
 T GA\_ GT  
 GAM1290 YAP1 3' TTTTACAGGAAGAGATGATGT 20361 C AAAG  
 A TAC TCGT TTTCTGTGAAGA  
 ||| ||| ||||| |||||

		ATG AGTA AAGGACATTTTT		
		T GAG_		
GAM1290 ZNF304	3'	GGAGGCTTTCATGAGGTG	40316	_
		TACCTCGT AAAGTTTCT		
		GTGGAGTA TTTCGGAGG		
		C		
GAM1290 ZNF339	3'	TTTTGTAGAGATGGGGT	41127	GTAAA TG
		ACCTC GTTTCTG AAG		
		TGGGG TAGAGAT TTT		
		_____ GT		
GAM1290 LOC113828	3'	TCTTTAAACCTTTATGGGGTG	56588	TTTCTG
		TACCTCGTAAAG TGAAGA		
		GTGGGGTATTTTCT ATTTCT		
		CAA_____		
GAM1290 LOC121441	5'	TCCCGGAGCCTTGTGGGGTG	74067	GTA T T
		TACCTC AAG TTCTG GA		
		GTGGGG TTC GAGGC CT		
		TG_ C C		
GAM1290 LOC126133	5'	TCTTCGCGGAAAGCGTTCGGGG	74446	TAAA _
	TA	TACCTCG GTTT CTGTGAAGA		
		ATGGGGC CGAA GGCGCTTCT		
		TTG_ A		
GAM1290 LOC126964	3'	ATGGAATTTTGAGGGGTG	74613	G
		TACCTC TAAAGTTTCTGT		
		GTGGGG GTTTTAAAGGTA		
		A		
GAM1290 LOC132321	3'	GGAAATTTTCCGGGGTG	75059	T
		TACCTCG AAAGTTTCT		
		GTGGGGC TTTTAAAGG		
		C		
GAM1290 LOC136442	3'	TTTCATCCTTTGCAGGTA	54288	C TTTCT
		TACCT GTAAAG GTGAAG		
		ATGGA CGTTTC TACTTT		
		_ C_____		
GAM1290 LOC143153	3'	TTTTGTAGAGGCAGAGGT	76473	GTAAA TG
		ACCTC GTTTCTG AAG		
		TGGAG CGGAGAT TTT		
		A_____ GT		
GAM1290 LOC143154	3'	TTTTGTAGAGGCAGAGGT	76489	GTAAA TG
		ACCTC GTTTCTG AAG		



	TGGAG CGGAGAT TTT	
	A_____ GT	
GAM1290 LOC144667 3'	TTTTGTAGAGATGGGGT 83175	GTAAA TG
	ACCTC GTTTCTG AAG	
	TGGGG TAGAGAT TTT	
	_____ GT	
GAM1290 LOC145231 5'	TCTTCACAGTCTCCTATGAG 83295	AAGTTT
	CTCGTA CTGTGAAGA	
	GAGTAT GACACTTCT	
	CCTCT_	
GAM1290 LOC145717 3'	TCTGAAGATCTTTGTGAGGTG 66835	TT GTGA
	TACCTCGTAAAG TCT AGA	
	GTGGAGTGTTC AGA TCT	
	T_ AG_	
GAM1290 LOC146226 5'	GAAGCTTTGGAGGTG 83623	G
	TACCTC TAAAGTTTC	
	GTGGAG GTTTCGAAG	
	—	
GAM1290 LOC146506 3'	TCTTTGTGGAGCACAGTTGAGG 77936	TAAA _ TG
	CCTCG GT TTCTG AAGA	
	GGAGT CA GAGGT TTCT	
	TGA_ C GT	
GAM1290 LOC146712 3'	GCAGGAGCTTTGTGAG 83718	
	CTCGTAAAGTTTCTGT	
	GAGTGTTTCGAGGACG	
GAM1290 LOC146895 5'	TCTTTGCTACTTTGTGAGG 83827	TTCT TG
	CCTCGTAAAGT G AAGA	
	GGAGTGTTCA C TTCT	
	T___ GT	
GAM1290 LOC147080 3'	TTTTATAGAGCTCTGTGAGGTG 83940	A T
	TACCTCGTA AGTT CTGTGAAG	
	GTGGAGTGT TCGA GATATTTT	
	C _	
GAM1290 LOC147622 5'	TCTTTATGGAAACCAAATGGTA 84055	TCGTAAA
	TACC GTTTCTGTGAAGA	
	ATGG CAAAGGTATTTCT	
	TAAAC_	
GAM1290 LOC148078 3'	TTTTCGCAGAACATTCAGGTA 84113	CGTAAAGT
	TACCT TTCTGTGAAGA	

	ATGGA	AAGACGCTTTT		
	CTTAC	_____		
GAM1290 LOC148147 3'	TTTTGTAGAGATGAGGT	78688	GTAAA	TG
	ACCTC	GTTTCTG AAG		
	TGGAG	TAGAGAT TTT		
	_____	GT		
GAM1290 LOC149570 3'	TCCTTGGGGCCTTTATG	GGGTA 84502	_____	TT TGT
	TACCTCGTAAAG T C	GA		
	ATGGGGTATTTC G G	CT		
	C GG	TTC		
GAM1290 LOC149619 5'	TTTTTGCAGAGGTGACACAGGT	84530	C AAA TT	TG
A	TACCT GT	G TCTG AAGA		
	ATGGA CA	T AGAC TTTT		
	_____	CAG GG GT		
GAM1290 LOC150587 3'	TTTTGTAGAGATGGGGGT	85068	GTAAA	TG
	ACCTC	GTTTCTG AAG		
	TGGGG	TAGAGAT TTT		
	G_____	GT		
GAM1290 LOC150696 3'	TTTTGTAGAGACGGGGT	58492	AAAGT	TG
	ACCTCGT	TTCTG AAG		
	TGGGGCA	GAGAT TTT		
	_____	GT		
GAM1290 LOC151040 3'	TCCGGGGACTGTTGTGGGGTG	80104	_____	TT T
	TACCTCGTAA AGT	CTG GA		
	GTGGGGTGTT TCA	GGC CT		
	G GG	_____		
GAM1290 LOC151201 3'	TTTTGTAGAGACGAGGT	85302	AAAGT	TG
	ACCTCGT	TTCTG AAG		
	TGGAGCA	GAGAT TTT		
	_____	GT		
GAM1290 LOC151584 3'	TTGTAAAGGGGATGTTGCGGGG	85452	A TT	GTGAAGA
TG	TACCTCGTAA GT	CT		
	GTGGGGCGTT TA	GG		
	G GG	AAATGTTT		
GAM1290 LOC151877 3'	TTTTGTAGAGATGGGGT	85513	GTAAA	TG
	ACCTC	GTTTCTG AAG		
	TGGGG	TAGAGAT TTT		
	_____	GT		
GAM1290 LOC151904 5'	TCAGAGGTAGAGGCTTTGTGGG	80394	_____	AGA
G	CTCGTAAAGTTTCTG	TGA		

	GGGTGTTTCGGAGAT	ACT	
	GGAG	A	
GAM1290 LOC152794 5'	TTTTGTGGAGATGGGGT	80687	GTAAA TG
	ACCTC GTTTCTG	AAG	
	TGGGG TAGAGGT	TTT	
	_____ GT		
GAM1290 LOC153222 5'	CTTCACGGAAGAGAGGTA	80785	GTAAAGT
	TACCTC TTCTGTGAAG		
	ATGGAG AAGGCACTTC		
	AG_____		
GAM1290 LOC154726 3'	TCCGTGAAGTTTTGCCAGGTA	81110	C GT _ T
	TACCT GTAAA TTC TG GA		
	ATGGA CGTTT AAG GC CT		
	C TG T _		
GAM1290 LOC154761 3'	TCTTTGTGATGCTTTGTGATGT	81127	C T T TG
G	TAC TCGTAAAGT TC G AAGA		
	GTG AGTGTTTCG AG T TTCT		
	T T _ GT		
GAM1290 LOC157653 5'	TTTTTGTGGGAATGTGGGAGG	81533	G AA TG
	CCTC TA GTTTCTG AAGA		
	GGAG GT TAAGGGT TTTT		
	G G_ GT		
GAM1290 LOC158287 5'	CTTCGTGGACATGTGAGG	86722	TAAA T TG
	CCTCG GT TC TGAAG		
	GGAGT TA AG GCTTC		
	G_ C GT		
GAM1290 LOC158709 5'	TCTTGCATAACTTTGTGAG	81988	TC G
	CTCGTAAAGTT TGT AAGA		
	GAGTGTTTCAA ACG TTCT		
	T_ _		
GAM1290 LOC196707 3'	TCCTGGGGGCTTTCTGGGGTG	87532	T TT T
	TACCTCG AAAGT CTG GA		
	GTGGGGT TTTCG GGT CT		
	C GG C		
GAM1290 LOC196758 3'	TCTTTATGGAGAAAGAGCAGGT	87513	C AAAG
G	TACCT GT TTTCTGTGAAGA		
	GTGGA CG AGAGGTATTTCT		
	_ AGAA		
GAM1290 LOC197044 3'	TCTCCGAAGATCTTTGTGAGGT	87876	TT G A
G	TACCTCGTAAAG TCT TG AGA		

GTGGAGTGTTC AGA GC TCT  
 T\_ A C  
 GAM1290 LOC201617 5' TCTGTGCTGGGCTTGTGGGGTG 90237 GTA CT A  
 TACCTC AAGTTT GTG AGA  
 ||||| ||||| |||||  
 GTGGGG TTCGGG CGT TCT  
 TG\_ T\_ G  
 GAM1290 LOC202908 5' TTTTGTAGAGATGAGGT 89248 GTAAA TG  
 ACCTC GTTTCTG AAG  
 ||||| ||||| |||||  
 TGGAG TAGAGAT TTT  
 \_\_\_\_\_ GT  
 GAM1290 LOC219294 3' TTTTGTAGAGGCAGAGGT 93015 GTAAA TG  
 ACCTC GTTTCTG AAG  
 ||||| ||||| |||||  
 TGGAG CGGAGAT TTT  
 A\_\_\_\_\_ GT  
 GAM1290 LOC219295 3' TTTTGTAGAGGCAGAGGT 92999 GTAAA TG  
 ACCTC GTTTCTG AAG  
 ||||| ||||| |||||  
 TGGAG CGGAGAT TTT  
 A\_\_\_\_\_ GT  
 GAM1290 LOC219673 5' TTTTGTAGAGATGAGGT 93048 GTAAA TG  
 ACCTC GTTTCTG AAG  
 ||||| ||||| |||||  
 TGGAG TAGAGAT TTT  
 \_\_\_\_\_ GT  
 GAM1290 LOC220537 3' TCTGAAGATCTTTGTGAGGTG 90732 TT GTGA  
 TACCTCGTAAAG TCT AGA  
 ||||| ||||| |||||  
 GTGGAGTGTTC AGA TCT  
 T\_ AG\_  
 GAM1290 LOC221914 3' AGGGACTTTGCAGGTG 93949 C TT  
 TACCT GTAAAGT CT  
 ||||| ||||| |||||  
 GTGGA CGTTTCA GA  
 \_\_\_\_\_ GG  
 GAM1290 LOC222252 3' TCCGGGGACTGTTGTGGGGTA 94309 \_ TT T  
 TACCTCGTAA AGT CTG GA  
 ||||| ||||| |||||  
 ATGGGGTGTT TCA GGC CT  
 G GG \_  
 GAM1290 LOC253017 5' TAATACAGGGATTTTGTAGGTA 95842 T TT AAGA  
 TACCTCG AAAGT CTGTG  
 ||||| ||||| |||||  
 ATGGAGT TTTTA GACAT  
 \_\_\_\_\_ GG AATT  
 GAM1290 LOC254100 3' TTTTGTAGAGATGGGGT 96423 GTAAA TG  
 ACCTC GTTTCTG AAG  
 ||||| ||||| |||||

TGGGG TAGAGAT TTT  
 \_\_\_\_\_ GT  
 GAM1290 LOC254532 5' TCTTTGCAGAAAAGGGAGG 96647 GTAAAG TG  
 CCTC TTTCTG AAGA  
 |||| ||||| ||||  
 GGAG AAAGAC TTCT  
 GGA\_\_\_\_ GT  
 GAM1290 LOC256446 5' TCTTCACGGAGTGAAGAACAGG 97206 C AAAGT\_  
 TG TACCT GT TTCTGTGAAGA  
 ||||| || |||||  
 GTGGA CA GAGGCACTTCT  
 \_ AGAAGT  
 GAM1290 LOC51026 3' TCTTTACAGGAGTTTAAACGT 32172 CTCG G  
 A TAC TAAA TTTCTGTGAAGA  
 ||| |||||  
 ATG ATTT GAGGACATTTCT  
 CAAA \_  
 GAM1290 LOC51171 5' TCACGGGGCTTTGGAGGTG 32697 G TT T  
 TACCTC TAAAGT C GTGA  
 ||||| ||||| | ||||  
 GTGGAG GTTTCTG G CACT  
 \_ GG\_  
 GAM1290 LOC57117 5' CTTTGCAGAAAGTGGGG 39864 TAAAG TG  
 CCTCG TTTCTG AAG  
 ||||| ||||| |||  
 GGGGT AAAGAC TTC  
 G\_\_\_\_ GT  
 GAM1290 LOC63923 3' TTTTGTCCCGTCTTTATGAGG 67125 TTTCT TG  
 CCTCGTAAAG G AAGA  
 ||||| ||||| | ||||  
 GGAGTATTTT C TTTT  
 TGCC\_ GT  
 GAM1290 LOC90120 5' CTTCGTGGACATGTGAGG 61534 TAAA T TG  
 CCTCG GT TC TGAAG  
 ||||| ||||| |||||  
 GGAGT TA AG GCTTC  
 G\_\_\_\_ C GT  
 GAM1290 LOC90161 3' ATTTTTGCAGAGGTATCAGTTT 61700 \_\_\_\_\_ TT TG  
 ATGAGG GTAAA G TCTG AAGA T  
 ||||| | ||||| ||||| |  
 TATTT T AGAC TTTT A  
 GACTA GG GT  
 GAM1290 LOC90625 3' CGGGGGAGCTTTATGAG 63610 G  
 CTCGTAAAGTTTCT TG  
 ||||| ||||| ||||| ||||| ||||| ||  
 GAGTATTTCTGAGGG GC  
 G  
 GAM1290 LOC90806 3' TTTTATAGAGACAAGGC 57988 AAA  
 GT GTTTCTGTGAAG  
 || ||||| |||||

			CG CAGAGATATTTT		
			GAA		
GAM1290	LOC91963	3'	TTTTGTAGAGGTGAGGT 67703	TAAAG	TG
			ACCTCG TTTCTG AAG		
			TGGAGT GGAGAT TTT		
			_____ GT		
GAM1290	LOC92482	3'	TTTTGTAGAGATGAGGT 69493	GTAAA	TG
			ACCTC GTTTCTG AAG		
			TGGAG TAGAGAT TTT		
			_____ GT		
GAM1290	LOC92568	3'	TCTGGGGACTGTTGTGGGGTG 69777	_ TT T	
			TACCTCGTAA AGT CTG GA		
			GTGGGGTGTT TCA GGT CT		
			G GG _		
GAM1290	LOC92609	3'	TTTTGTAGAGATGGGGT 72852	GTAAA	TG
			ACCTC GTTTCTG AAG		
			TGGGG TAGAGAT TTT		
			_____ GT		
GAM1291	ACADS	3'	ACCACTGTGCCTCAAGTTCC 3406	AAGACA	
			GGAG GGGCACAGTGGT		
			CCTT TCCGTGTCACCA		
			GAAC__		
GAM1291	AIPL1	3'	ACCCCTCCCTGTCTCCCA 59849	A A	CAC T
			TGG GA GACAGGG AG GGT		
			ACC CT CTGTCCC TC CCA		
			C _ _ C		
GAM1291	B3GAT1	5'	TGCTCTGTCCTCTCCA 53979	A	
			TGGAGA GACAGGGCA		
			ACCTCT CTGTCTCGT		
			C		
GAM1291	COG5	3'	TGTACCCTGCTTCCCC 20954	A A C	
			GG GAAG CAGGG ACA		
			CC CTTC GTCCC TGT		
			C _ A		
GAM1291	CRTAP	3'	ACCTTCATCCCTGTCTTCCTCA 21028	GA	CACAGT
			TG GAAGACAGGG GGT		
			AC CTTCTGTCCC CCA		
			TC TACTT_		
GAM1291	EPB72	3'	ACCACAACCAGCTTCTCCA 14594	ACA GCACA	
			TGGAGAAG GG GTGGT		

			ACCTCTTC CC CACCA		
			GA_ AA__		
GAM1291	GAB2	3'	TACCACTGTCTCTGCCCCCA 54459	AGAAGA	C
			TGG CAGGG ACAGTGGTA		
			ACC GTCTC TGTCACCAT		
			CCC__ C		
GAM1291	GAB2	3'	TACCACTGTCTCTGCCCCCA 24502	AGAAGA	C
			TGG CAGGG ACAGTGGTA		
			ACC GTCTC TGTCACCAT		
			CCC__ C		
GAM1291	GPD1	3'	TGCCCTGTCCCTCTCCA 59672	A_	
			TGGAGA GACAGGGCA		
			ACCTCT CTGTCCCGT		
			CC		
GAM1291	GSTT1	3'	ACCATCCCCACCCTGTCTTCCA 73457	GA	CACA_
	CA		TG GAAGACAGGG GTGGT		
			AC CTTCTGTCCC TACCA		
			AC ACCCC		
GAM1291	MATN1	3'	ACCACTGTGGCCTCTCCA 9916	AGACA	G
			TGGAGA GG CACAGTGGT		
			ACCTCT CC GTGTCACCA		
			_____ G		
GAM1291	MAZ	3'	TGCCCTGTCTTCCCA 73390	A	
			TGG GAAGACAGGGCA		
			ACC CTTCTGTCCCGT		
			—		
GAM1291	NR1D1	3'	ACCACTCTGTCTCCCCCA 41361	AGA	GGCAC
			TGG AGACAG AGTGGT		
			ACC TCTGTC TCACCA		
			CCC _____		
GAM1291	OTOF	3'	CACACCCTGTCTTCCCA 16639	A	CACA
			TGG GAAGACAGGG GTG		
			ACC CTTCTGTCCC CAC		
			— A__		
GAM1291	PCTP	3'	ACCACTGTTTACGCTTCCCC 41094	A	ACAG C
			GG GAAG GG ACAGTGGT		
			CC CTTC CT TGTCACCA		
			C CGA_ _		
GAM1291	PPP2R1A	3'	CACCTCCCGTCTCCCCCA 26442	A A A	CACA
			TGG GA GAC GGG GTG		

			ACC CT CTG CCC CAC			
			C C _ TC__			
GAM1291	PPP2R4	3'	TGTGCCTGCCTTCCCCA	60563	A	ACA
			TGG GAAG GGGCACA			
			ACC CTTC TCCGTGT			
			C CG_			
GAM1291	SH3BP2	3'	CACGCCCTGTTCCCTCCA	11595	AA	ACA
			TGGAG GACAGGGC GTG			
			ACCTC TTGTCCCG CAC			
			CC ____			
GAM1291	SMAC	3'	CACTGCCCTGTCTCCCCA	39111	A A	CA
			TGG GA GACAGGGCA GTG			
			ACC CT CTGTCCCGT CAC			
			C _ ____			
GAM1291	SMAC	3'	CACTGCCCTGTCTCCCCA	57195	A A	CA
			TGG GA GACAGGGCA GTG			
			ACC CT CTGTCCCGT CAC			
			C _ ____			
GAM1291	SMAC	3'	CACTGCCCTGTCTCCCCA	57205	A A	CA
			TGG GA GACAGGGCA GTG			
			ACC CT CTGTCCCGT CAC			
			C _ ____			
GAM1291	UVRAG	3'	TACTGTCGCCCCATCTTCTCC	12562	CA	_
			GGAGAAGA GGGC ACAGTG			
			CCTCTTCT CCCG TGTCAT			
			AC C			
GAM1291	XPA	3'	ACCACTGTACCCAGGTTCT	4596	GACA	C
			AGAA GGG ACAGTGGT			
			TCTT CCC TGTCACCA			
			GGAC A			
GAM1291	ZNF261	3'	CCATTCCCTGCCTTCTCTA	17493	A	CAC
			TGGAGAAG CAGGG AGTGG			
			ATCTCTTC GTCCC TTACC			
			C ____			
GAM1291	B3GNT7	3'	ACCGCACCTGCTTCTCCA	71123	A	CACA
			TGGAGAAG CAGGG GTGGT			
			ACCTCTTC GTCCC CGCCA			
			_ A__			
GAM1291	CBCIP2	3'	CACCTTTCCCCTCTTCTCCA	51589	CA	CACA
			TGGAGAAGA GGG GTG			



ACCTCTTCT CCC CAC  
 C\_ TTTC  
 GAM1291 DKFZP434P1750 3' GCCCTCCCTGTCTCCCCCA 31377 AGA CAC T  
 TGG AGACAGGG AG GGT  
 ||| ||||| |||||  
 ACC TCTGTCCC TC CCG  
 CCC \_\_\_\_ \_  
 GAM1291 DKFZp547I094 5' ACCCCTGTTGCCCTGCCTTCTT 49629 A \_ T  
 CA TGGAGAAG CAGGGCA CAG GGT  
 ||||| ||||| ||| |||  
 ACTTCTTC GTCCCGT GTC CCA  
 C T C  
 GAM1291 DKFZp564I1922 3' ACCACTGTTATATTACCTTCTC 31232 AC GGC\_  
 CA TGGAGAAG AG ACAGTGGT  
 ||||| || |||||  
 ACCTCTTC TT TGTCACCA  
 CA ATAT  
 GAM1291 DUSP9 3' CACCTCCCTGTTTCTCCA 7341 A CACA  
 TGGAGA GACAGGG GTG  
 ||||| ||||| |||  
 ACCTCT TTGTCCC CAC  
 \_ TC\_  
 GAM1291 FLJ14708 3' ACCACTGTGGGCCCTCCTTC 51538 AC \_  
 GAAG AGGGC ACAGTGGT  
 ||| ||| |||||  
 CTTC TCCCG TGTCACCA  
 C\_ GG  
 GAM1291 FLJ23120 3' ACCACTGCACCACTGTACTCCA 85143 AAG \_ CA  
 TGGAG ACAG GG CAGTGGT  
 |||| ||| |||||  
 ACCTC TGTC CC GTCACCA  
 A\_ A AC  
 GAM1291 IMAGE:4907098 3' ACCACTGTGGTCCCCTCCA 91656 AA AGGG  
 TGGAG GAC CACAGTGGT  
 |||| ||| |||||  
 ACCTC CTG GTGTCACCA  
 CC \_\_\_\_  
 GAM1291 KIAA0416 3' ACCACTACCACTCCA 31462 AAGACA CAC  
 TGGAG GGG AGTGGT  
 |||| ||| |||||  
 ACCTC CCC TCACCA  
 A\_ A\_  
 GAM1291 KIAA0545 3' CCACGCTGTTCTCCA 63144 AAGACA CA  
 TGGAG GGGCA GTGG  
 |||| ||| |||  
 ACCTC CTTGT CACC  
 \_\_\_\_ CG  
 GAM1291 KIAA0924 3' TGCCCTGTCCTCTGCA 29724 G A  
 TG AGA GACAGGGCA  
 || ||| |||||

AC TCT CTGTCCCGT  
 G C  
 GAM1291 KIAA1111 3' CATCCTGCCTGCCTTCTCCA 96206 ACA CA  
 TGGAGAAG GGGCA GTG  
 ||||| ||| ||  
 ACCTCTTC TCCGT TAC  
 CG\_ CC  
 GAM1291 KIAA1184 3' TGTGCCCCCTCCCCTCCA 42620 AA CA  
 TGGAG GA GGGCACA  
 |||| || |||||  
 ACCTC CT CCCGTGT  
 CC C\_  
 GAM1291 MGC13138 3' TACCACCATGCCTGGCTTC 53022 ACA CA  
 GAAG GGGCA GTGGTA  
 ||| |||| |||||  
 CTTC TCCGT CACCAT  
 GG\_ AC  
 GAM1291 MGC5590 5' TACCACTGTCAGCACTCTCCA 43927 AGACAGG \_  
 TGGAGA GC ACAGTGGTA  
 |||| || |||||  
 ACCTCT CG TGTCACCAT  
 CA\_\_\_\_\_ AC  
 GAM1291 moblak 3' CCACACCTCTGTCTCCCCCA 55490 AGA CACA  
 TGG AGACAGGG GTGG  
 ||| ||||| |||  
 ACC TCTGTCTC CACC  
 CCC CA\_  
 GAM1291 NR6A1 3' ACCACTGCGAACTTTCCA 52866 AAGAC GGCA  
 TGGAG AG CAGTGGT  
 |||| || |||||  
 ACCTT TC GTCACCA  
 \_\_\_\_\_ AAGC  
 GAM1291 NR6A1 3' ACCACTGCGAACTTTCCA 52878 AAGAC GGCA  
 TGGAG AG CAGTGGT  
 |||| || |||||  
 ACCTT TC GTCACCA  
 \_\_\_\_\_ AAGC  
 GAM1291 NR6A1 3' ACCACTGCGAACTTTCCA 7641 AAGAC GGCA  
 TGGAG AG CAGTGGT  
 |||| || |||||  
 ACCTT TC GTCACCA  
 \_\_\_\_\_ AAGC  
 GAM1291 PEG10 3' TACCACTGCCGGATGTATTCTC 30530 G G\_ CA  
 CA TGGAGAA ACA GGCA GTGGTA  
 ||||| ||| ||| |||||  
 ACCTCTT TGT CCGT CACCAT  
 A AGG \_  
 GAM1291 STMN3 3' TACCACTGCAGCATCCCCCACT 31902 ACA CA\_\_\_\_  
 TCTCCA GGAGAAG GGG CAGTGGTA  
 ||||| ||| |||||

	CCTCTTC CCC GTCACCAT		
	ACC TACGAC		
GAM1291 LOC126964 3'	ACCACTGTGTGCGCCTCCA 74610	AAGACAGG	
	TGGAG GCACAGTGGT		
	ACCTC TGTGTCACCA		
	CGCG____		
GAM1291 LOC145837 5'	CATCTGCCCTGTCTCTCCA 83543	A CA	
	TGGAGA GACAGGGCA GTG		
	ACCTCT CTGTCCCGT TAC		
	- C_		
GAM1291 LOC148930 3'	GCTTTGCCCTGTGTTCTCCA 79097	G C	
	TGGAGAA ACAGGGCA AGT		
	ACCTCTT TGTCCCGT TCG		
	G T		
GAM1291 LOC150372 3'	TACCACTGTGCCCTGGCCCA 79808	AGAAGA	
	TGG CAGGGCACAGTGGTA		
	ACC GTCCCGTGTCAACCAT		
	CG____		
GAM1291 LOC151162 5'	GCCACCCCATTTCTCCA 85244	ACA CACA	
	TGGAGAAG GGG GTGGT		
	ACCTCTTT CCC CACCG		
	A_ ____		
GAM1291 LOC154761 3'	ACCACACCCACTTCTCCA 81120	ACA CACA	
	TGGAGAAG GGG GTGGT		
	ACCTCTTC CCC CACCA		
	A_ A_		
GAM1291 LOC199964 3'	TGCCGTGCCTTCTCCA 89891	A G	
	TGGAGAAG CA GGCA		
	ACCTCTTC GT CCGT		
	C G		
GAM1291 LOC203377 5'	GCCACCCCATTTCTCCA 90582	ACA CACA	
	TGGAGAAG GGG GTGGT		
	ACCTCTTT CCC CACCG		
	A_ ____		
GAM1291 LOC203504 5'	ACCCCTCCCCAGTCTTCTCCA 90635	A CAC T	
	TGGAGAAGAC GGG AG GGT		
	ACCTCTTCTG CCC TC CCA		
	A C_ C		
GAM1291 LOC219654 3'	CGTTGTTCCCGTCTTCTCCA 91302	A C	
	TGGAGAAGAC GGG ACAGTG		

	ACCTCTTCTG CCC TGTTCG	
	C T	
GAM1291 LOC221416 3'	TGGCACCCTATCTTCTCCA 93772	C CA_
	TGGAGAAGA AGGG CA	
	ACCTCTTCT TCCC GT	
	A ACG	
GAM1291 LOC221491 5'	ACCACTGTGCCCAATGCCCCC 92010	AGAAGACA
A	TGG GGGCACAGTGGT	
	ACC CCCGTGTCACCA	
	CCCCGTAA	
GAM1291 LOC222001 3'	ACCACTAATTAAGTTTTCTCCA 92903	AGGGCAC
	TGGAGAAGAC AGTGGT	
	ACCTCTTTTG TCACCA	
	AATTAA_	
GAM1291 LOC255975 5'	TACCACCCGGCAGCCTCTCCA 95897	AGACAGG ACA
	TGGAGA GC GTGGTA	
	ACCTCT CG CACCAT	
	CCGA__ GCC	
GAM1291 LOC256901 3'	ACCACTTCCCCCTTCTCCA 96619	ACA CAC
	TGGAGAAG GGG AGTGGT	
	ACCTCTTC CCC TCACCA	
	C__ T__	
GAM1291 LOC54550 3'	ACCACTGTGCCCAGGCGCCA 77688	AGAAGACA
	TGG GGGCACAGTGGT	
	ACC CCCGTGTCACCA	
	GCGGA__	
GAM1291 LOC93097 3'	ACCACCAGCATTTCTCCA 71357	AA CAGG ACA
	TGGAG GA GC GTGGT	
	ACCTC CT CG CACCA	
	__ TTA_ AC_	
GAM1291 LOC96652 3'	ACCACCTGCACCAGCTTCTCCA 65462	ACA _ CA
	TGGAGAAG GG GCA GTGGT	
	ACCTCTTC CC CGT CACCA	
	GA_ A C_	
GAM1292 ABCC3 3'	AGTCCTGTACTCTGGGGTG 13692	A CAGC
	CACC CAGA TGCAGGACT	
	GTGG GTCT ATGTCCTGA	
	G C__	
GAM1292 ABCC3 3'	AGTCCTGTACTCTGGGGTG 39139	A CAGC
	CACC CAGA TGCAGGACT	

			GTGG GTCT ATGTCCTGA		
			G C__		
GAM1292	ABCC3	3'	AGTCCTGTACTCTGGGGTG 39151	A	CAGC
			CACC CAGA TGCAGGACT		
			GTGG GTCT ATGTCCTGA		
			G C__		
GAM1292	ARVCF	3'	AGCCCTGCAGTCACGTGAGG 8026	A	GACA A
			CC CA GCTGCAGG CT		
			GG GT TGACGTCC GA		
			A GCAC C		
GAM1292	CCS	3'	AGCTGCTGTGGTGTT 17609	A	
			AACACCACAG CAGCT		
			TTGTGGTGTGTC GTCGA		
			-		
GAM1292	CELSR1	3'	TTTGTACTTCTGCGGTG 26492	A	C C
			CACC CAGA AG TGCAGG		
			GTGG GTCT TC ATGTTT		
			C _ _		
GAM1292	CELSR3	3'	GCAAAAGTTGTCTGTGGTG 7401		_____
			CACCACAGACAGCT GC		
			GTGGTGTCTGTTGA CG		
			AAA		
GAM1292	COL19A1	3'	AGCCACCAAGCTGTCTTTGGT 8506	C	GCA_ A
			ACCA AGACAGCT GG CT		
			TGGT TCTGTCTGA CC GA		
			T ACCA _		
GAM1292	DDC	3'	CTCAGCTGTCTGTGG 5797	C	
			CCACAGACAGCTG AG		
			GGTGTCTGTCTGAC TC		
			-		
GAM1292	DLEC1	3'	AGTCCTGCACCCTGCGG 23685	A	ACAGC
			CC CAG TGCAGGACT		
			GG GTC ACGTCCTGA		
			C CC__		
GAM1292	DLEC1	3'	AGTCCTGCACCCTGCGG 23696	A	ACAGC
			CC CAG TGCAGGACT		
			GG GTC ACGTCCTGA		
			C CC__		
GAM1292	DUSP2	3'	GCCCTGTCTGTGGGT 15347	A	CT
			AAC CCACAGACAG GC		

			TTG GGTGTCTGTC CG		
			— C—		
GAM1292	ERN2	5'	AGCCGTGCAGCTGCCCAGG 52701	ACAGA	— A
			CC CAGCTGCA GG CT		
			GG GTCGACGT CC GA		
			ACCC— G —		
GAM1292	EZH1	3'	TCTGCTTTCCTGTCTGTAGTG 8830	C	CT—
			CAC ACAGACAG GCAGG		
			GTG TGTCTGTC CGTCT		
			A CTTT		
GAM1292	FUT4	3'	AGTCCTGCAGGAGTGCTG 8961	— AG	
			CAG AC CTGCAGGACT		
			GTC TG GACGTCCTGA		
			G AG		
GAM1292	GGA3	3'	AGCCCTGGGAATGTCTGTGG 56825	GCTG	A
			CCACAGACA CAGG CT		
			GGTGTCTGT GTCC GA		
			AAGG C		
GAM1292	GGA3	3'	AGCCCTGGGAATGTCTGTGG 25741	GCTG	A
			CCACAGACA CAGG CT		
			GGTGTCTGT GTCC GA		
			AAGG C		
GAM1292	GPC1	3'	AGCCCCGCACGGGCTGTCTGGG 9098	A	— A A
	TGT		ACACC CAGACAGCT GC GG CT		
			TGTGG GTCTGTCGG CG CC GA		
			— GCA C C		
GAM1292	HMG3	3'	AGTCCTGTGCATACTGTGGTGT 14902	ACA	T
	T		AACACCACAG GC GCAGGACT		
			TTGTGGTGTGTC CG TGTCTGA		
			ATA —		
GAM1292	HPS1	3'	AGCCTCCTGTCTGCAGTG 3964	CA	CTGC A
			CAC CAGACAG AGG CT		
			GTG GTCTGTC TCC GA		
			AC C— —		
GAM1292	IGFBP1	3'	TCAAAGCTACCTGTGGTG 5180	AC	GCAG
			CACCACAG AGCT GA		
			GTGGTGTGTC TCGA CT		
			CA AA—		
GAM1292	IGFBP3	3'	AGCTCACAGCCTTCTGTGGTGT 5185	CA	CA A
			ACACCACAGA GCTG GG CT		

			TGTGGTGTCT CGAC TC GA		
			TC AC _		
GAM1292	IGFBP4	3'	AGTCCTGTCTCTGCCTGCGG 7758	A A CT	
			CC CAG CAG GCAGGACT		
			GG GTC GTC TGTCCTGA		
			C C TC		
GAM1292	IL19	3'	GTCCATGTCTGTGATGT 25360	C GCTGCA	
			ACA CACAGACA GGAC		
			TGT GTGTCTGT CCTG		
			A A _		
GAM1292	INPP5B	5'	AGTCCCGTGCGCCCTGTGGTG 95521	ACA T A	
			CACCACAG GC GC GGA		
			GTGGTGTC CG TG CCTGA		
			CCG _ C		
GAM1292	ISLR	3'	CTCACTGTCTGCGGTG 18669	A C C	
			CACC CAGACAG TG AG		
			GTGG GTCTGTC AC TC		
			C _ _		
GAM1292	KAI1	3'	AGCCCTGGCTGTTCTGTGGT 9495	_ TG A	
			ACCACAGA CAGC CAGG CT		
			TGGTGTCT GTCG GTCC GA		
			T _ C		
GAM1292	KDR	3'	TGAAGCTGTGTGTGGTGT 9596	G G	
			ACACCACA ACAGCT CA		
			TGTGGTGT TGTCGA GT		
			G A		
GAM1292	MLLT4	3'	AGTTATGGGCTCTCTGCAGTGT 72482	CA C G G	
	T		AACAC CAGA AGCT CA GACT		
			TTGTG GTCT TCGG GT TTGA		
			AC C _ A		
GAM1292	MPO	3'	TCCTGGCTCTGTGG 4204	CA TG	
			CCACAGA GC CAGGA		
			GGTGTCT CG GTCCT		
			_ _		
GAM1292	PACSIN1	3'	AGTCCTGCAGCACCAGGTG 92253	ACAGACA	
			CACC GCTGCAGGACT		
			GTGG CGACGTCCTGA		
			ACCA _		
GAM1292	PCLO	3'	CAGTGTCTGTGATGTT 94224	C G	
			AACA CACAGACA CTG		

		TTGT GTGTCTGT GAC		
		A _		
GAM1292	PLOD3	5' TCCTCGCCTTGTCTGTGG 6558	CT _	
		CCACAGACAG GC AGGA		
		GGTGTCTGTT CG TCCT		
		C_ C		
GAM1292	PPP1R8	5' AGCCCCGCATCCCTCTGTGGT 10722	CAGC A A	
		ACCACAGA TGC GG CT		
		TGGTGTCT ACG CC GA		
		CCCT C C		
GAM1292	PPP2R2B	3' TGAGGTTGTCTGTAGT 15909	C G	
		AC ACAGACAGCT CA		
		TG TGTCTGTTGG GT		
		A A		
GAM1292	RAX	3' AGCCCTGCAGCTGGAGGG 25536	ACAGA A	
		CC CAGCTGCAGG CT		
		GG GTCGACGTCC GA		
		GAG_ C		
GAM1292	REGL	3' AGTCCTGCAGCCAGGAGGGT 21485	ACAGACA	
		ACC GCTGCAGGACT		
		TGG CGACGTCCTGA		
		GAGGAC_		
GAM1292	RFC1	3' GTCCTGTCCTGTGATGG 11302	CAG CT	
		CCA ACAG GCAGGAC		
		GGT TGTC TGTCCTG		
		AG_ C_		
GAM1292	RRM2	3' AGTCCTGTCTGTTTATAGTG 6407	CAC CT	
		CAC AGACAG GCAGGACT		
		GTG TTTGTC TGTCCTGA		
		ATA _		
GAM1292	RU2	5' AGTCCTGCAAGCTCCTAGTG 33020	_ AC _	
		CAC AG AGCT GCAGGACT		
		GTG TC TCGA CGTCCTGA		
		A C_ A		
GAM1292	RXRA	3' CCTGCAGCCATCTGTG 11407	CA	
		CACAGA GCTGCAGG		
		GTGTCT CGACGTCC		
		AC		
GAM1292	SH3BP2	3' AGCCCTGCAGCTACAGCTG 11589	AC_ A	
		CAG AGCTGCAGG CT		



			GTC TCGACGTCC GA		
			GACA C		
GAM1292	SLC1A4	3'	TTGTATGTCTGTGGT 11721	GC	
			ACCACAGACA TGCAG		
			TGGTGTCTGT ATGTT		
			—		
GAM1292	TBXA2R	5'	AGCCTGCCCTGTCTG 6478	CT A	
			CAGACAG GCAGG CT		
			GTCTGTC CGTCC GA		
			C_ _		
GAM1292	TEM7	3'	AGCCCCAGCTTCTGT 39880	C CA A	
			ACAGA AGCTG GG CT		
			TGTCT TCGAC CC GA		
			_ C_ _		
GAM1292	UNC13	3'	AGTCCTGCTCATCTGTGG 21055	CAGCT	
			CCACAGA GCAGGACT		
			GGTGTCT CGTCCTGA		
			ACT_		
GAM1292	WASF3	3'	AGCCCTGCAGCTGTAGTACAGT 21823	CACAG_ A	
	G		CAC ACAGCTGCAGG CT		
			GTG TGTCGACGTCC GA		
			ACATGA C		
GAM1292	ZNF138	5'	AGGCCCAGCCTCTGTGG 81184	CA CA A	
			CCACAGA GCTG GG CT		
			GGTGTCT CGAC CC GA		
			C_ _ G		
GAM1292	ABCA9	3'	AGTCCATGTTTTGTCTGTTGTG 54409	C CT _	
			CAC ACAGACAG GCA GGACT		
			GTG TGTCTGTT TGT CCTGA		
			T T_ A		
GAM1292	APCL	5'	G TTCAGCTGTCTGT 19684	CAG	
			ACAGACAGCTG GAC		
			TGTCTGTCGAC TTG		
			—		
GAM1292	BRD1	5'	AGTCCTGCAACTGTGG 27413	ACAGC	
			CCACAG TGCAGGACT		
			GGTGTC ACGTCCTGA		
			A_		
GAM1292	C16orf5	3'	AGTCCCCAGGCCTGTGG 25445	ACA GCA	
			CCACAG GCT GGACT		

GGTGTC CGG CCTGA  
 \_\_\_\_ ACC

GAM1292 C1orf24 3' AGTCTCTGCTTTCTGCAGTG 53707 CA CAGCT \_  
 CAC CAGA GCAG GACT  
 ||| |||| |||| ||||  
 GTG GTCT CGTC CTGA  
 AC TT\_\_ T

GAM1292 C1orf34 3' AGTCCCGGTCTGCTGTGGTGTT 60661 A \_ CA  
 AACACCACAG CAG CTG GGACT  
 ||||| ||| ||| ||||  
 TTGTGGTGTC GTC GGC CCTGA  
 \_ T \_

GAM1292 C20orf82 5' AGTCTCTGGTCTGTCTG 84711 CTG \_  
 CAGACAG CAG GACT  
 ||||| ||| ||||  
 GTCTGTC GTC CTGA  
 TG\_ T

GAM1292 DKFZP434C171 3' AGTCCTGATAGTCTGTGG 31551 AGCTG  
 CCACAGAC CAGGACT  
 ||||| |||||  
 GGTGTCTG GTCCTGA  
 ATA\_\_

GAM1292 DKFZP434P211 3' AGTCCTGCGATGCTAAGTG 27260 CAC A GC  
 CAC AG CA TGCAGGACT  
 ||| ||| |||||  
 GTG TC GT GCGTCCTGA  
 AA\_ \_ A\_

GAM1292 DMWD 3' AGCCCCAGGTCTGCAGTGT 60876 CA AG CA A  
 ACAC CAGAC CTG GG CT  
 ||| |||| ||| |||  
 TGTG GTCTG GAC CC GA  
 AC \_ C\_ \_

GAM1292 DOCK3 3' AGTCCTGCATGTTTCAGG 66495 ACA GC  
 CC GACA TGCAGGACT  
 || |||| |||||  
 GG TTGT ACGTCCTGA  
 AC\_ \_

GAM1292 FLJ10094 3' AGTTATATCTGTGGCGTT 35807 A C\_\_  
 AAC CCACAGA AGCT  
 ||| ||||| |||  
 TTG GGTGTCT TTGA  
 C ATA

GAM1292 FLJ10178 3' AGCCCTATAGTTCTGTG 35869 CA C A  
 CACAGA GCTG AGG CT  
 ||||| ||| ||| ||  
 GTGTCT TGAT TCC GA  
 \_ A C

GAM1292 FLJ10637 5' AGTCCCCTGTCTGTGG 68586 CTGCA  
 CCACAGACAG GGACT  
 ||||| ||||

GGTGTCTGTC CCTGA  
C\_\_\_\_

GAM1292 FLJ12891 5' AGTCCTGCAGCCTCGCTGG 46336 CA CA  
CCA GA GCTGCAGGACT  
||| || |||||  
GGT CT CGACGTCCTGA  
CG C\_

GAM1292 FLJ12903 3' GTGCTATTGTGGTGT 42778 AC T  
ACACCACAG AGC GC  
||||| ||| ||  
TGTGGTGT TCG TG  
A\_ \_

GAM1292 FLJ13902 3' AGCCCTGTAGCATCTGTG 45038 CA A  
CACAGA GCTGCAGG CT  
||||| ||||| ||  
GTGTCT CGATGTCC GA  
A\_ C

GAM1292 FLJ20033 3' TTTTGCTAGCTGTGGTGT 34351 ACAGCT  
AACACCACAG GCAGGA  
||||| |||||  
TTGTGGTGTG CGTTTT  
GAT\_\_\_\_

GAM1292 FLJ20315 3' CCAGCTGCTGCCTGTGGCGT 34933 A A T A  
AC CCACAG CAGC GC GG  
|| ||||| ||| ||  
TG GGTGTC GTCG CG CC  
C C T A

GAM1292 FLJ20374 3' AGCCCTGCAGCTGGCTGGAGT 35077 CA A A  
AC CAG CAGCTGCAGG CT  
|| ||| ||||| ||  
TG GTC GTCGACGTCC GA  
AG G C

GAM1292 FLJ22127 3' AGTCCTGTGGCTGGCCCGTGAT 42881 C AGA\_ TG  
G CA CAC CAGC CAGGACT  
|| ||| ||| |||||  
GT GTG GTCG GTCCTGA  
A CCCG GT

GAM1292 FLJ23185 5' GTCCTGCAGTATGGCGT 46833 A CAGACA  
AC CCA GCTGCAGGAC  
|| ||| |||||  
TG GGT TGACGTCCTG  
C A\_\_\_\_\_

GAM1292 FLJ31762 5' AGTCCTGCAGATGTGCGTG 58139 \_ GACAG  
CAC CACA CTGCAGGACT  
||| ||| |||||  
GTG GTGT GACGTCCTGA  
C A\_\_\_\_\_

GAM1292 GIOT-2 3' CCTTCAGTTATCTGCAGT 32749 CA C C  
AC CAGA AGCTG AGG  
|| ||| ||||| |||

		TG GTCT TTGAC TCC	
		AC A T	
GAM1292 HRH3	3'	AGCCCCGCCGTGTCTGTGG 23364	GT A A
		CCACAGACA C GC GG CT	
		GGTGTCTGT G CG CC GA	
		_ C C C	
GAM1292 HYA22	3'	TCCTACGTGTTGGTCTGTGGT 19429	_ _ C
		ACCACAGAC AGC TG AGGA	
		TGGTGTCTG TTG GC TCCT	
		G T A	
GAM1292 KCNB2	5'	TCCCACAGCCCTTTGTGGTG 96102	CA CA
		CACCACAGA GCTG GGA	
		GTGGTGTTT CGAC CCT	
		CC AC	
GAM1292 KCNT1	3'	AGTCCTGCAGATCCCTCTGTGG 61826	CAG__
T		ACCACAGA CTGCAGGACT	
		TGGTGTCT GACGTCCTGA	
		CCCTA	
GAM1292 KIAA0218	3'	GTCCCTCGTCTGTGGT 28623	_ CTGCA
		ACCACAGAC AG GGAC	
		TGGTGTCTG TC CCTG	
		C _ _ _ _	
GAM1292 KIAA0828	3'	TCCTGTGCCTGTAGTGTT 81199	C ACA T
		AACAC ACAG GC GCAGGA	
		TTGTG TGTC CG TGCCT	
		A _ _ _	
GAM1292 KIAA0953	3'	AGTCCTGCATGTAGTTGGTG 66780	CAG GC
		CACCA ACA TGCAGGACT	
		GTGGT TGT ACGTCCTGA	
		TGA _	
GAM1292 KIAA1157	3'	AGTCCGTCCATGCTCTGTGG 72239	_ GCT A
		CCACAGA CA GC GGA	
		GGTGTCT GT TG CCTGA	
		C ACC _	
GAM1292 KIAA1183	3'	GCAGCCTGTGGTGTT 62535	ACA
		AACACCACAG GCTGC	
		TTGTGGTGTC CGACG	
		_ _ _ _	
GAM1292 KIAA1280	5'	AGCCTGACTGTCCGTGGTG 69710	A CTG A
		CACCAC GACAG CAGG CT	

		GTGGTG CTGTC GTCC GA	
		C A__ _	
GAM1292 KIAA1336	3'	TCCTGGGTTTTGTAATGTT 72325	CC CA G
		AACA ACAGA GCT CAGGA	
		TTGT TGTTT TGG GTCCT	
		AA __ _	
GAM1292 KIAA1505	5'	AGTCCCACCCATCTGTGGT 94185	CAGC CA
		ACCACAGA TG GGA CT	
		TGGTGTCT AC CCTGA	
		ACCC __	
GAM1292 KIAA1786	3'	AGTCCTTCCTTATCTGTGGT 66022	CAGCTGC
		ACCACAGA AGGA CT	
		TGGTGTCT TCCTGA	
		ATTCCT_	
GAM1292 MAD4	3'	CCTGTACCGGTCTGTGG 21271	AGC
		CCACAGAC TGCAGG	
		GGTGTCTG ATGTCC	
		GCC	
GAM1292 MGC10940	3'	AGCCCCCAATCTGTGGT 50214	CAGC CA A
		ACCACAGA TG GG CT	
		TGGTGTCT AC CC GA	
		A__ CC C	
GAM1292 MGC2654	5'	AGCTTGACCTGTCTGCAGT 44103	CA CTG A
		AC CAGACAG CAGG CT	
		TG GTCTGTC GTTC GA	
		AC CAG _	
GAM1292 MVD	3'	AGTCCTGCGGCCGCCCAGGTGT 10138	ACAGACA
		ACACC GCTGCAGGA CT	
		TGTGG CGGCGTCCTGA	
		ACCCGC_	
GAM1292 NIN283	3'	AGCCCTCTGCCGGCTGTGGTGT 50065	ACA TGC A
		ACACCACAG GC AGG CT	
		TGTGGTGTC CG TCC GA	
		GGC TC_ C	
GAM1292 NTT5	3'	AGTCCTGCTACTTCTGGGGTG 25880	A C CT
		CACC CAGA AG GCAGGA CT	
		GTGG GTCT TC CGTCCTGA	
		G _ AT	
GAM1292 P2RX1	3'	TCCTGGGCTCCCTGCCTGTGG 67172	A ____ G
		CCACAG CA GCT CAGGA	

			GGTGTC GT CGG GTCCT		
			C CCCT _		
GAM1292	PMAIP1	5'	TGCAGCTGTCCGAGGTG 40892	ACA	
			CACC GACAGCTGCA		
			GTGG CTGTCGACGT		
			AGC		
GAM1292	PMVK	3'	AGTCCCCTCAGCCTGTGGTG 21610	ACA	CA_
			CACCACAG GCTG GGA		
			GTGGTGTC CGAC CCTGA		
			____ TCC		
GAM1292	PMVK	3'	AGTCCCCTCAGCCTGTGGTG 94612	ACA	CA_
			CACCACAG GCTG GGA		
			GTGGTGTC CGAC CCTGA		
			____ TCC		
GAM1292	POLD3	3'	TCTGAGCTGTCTGCAAGG 91646	A__	G
			CC CAGACAGCT CAGG		
			GG GTCTGTCTGA GTCT		
			AAC _		
GAM1292	PRO2958	3'	AGTCCTAAACTGGCATCTGT 37651	CA	C__
			ACAGA GCTG AGGACT		
			TGTCT CGGT TCCTGA		
			A_ CAAA		
GAM1292	RAN	3'	GCAGCTGTCCTGTGATGT 20907	C	_
			ACA CACAG ACAGCTGC		
			TGT GTGTC TGTCGACG		
			A C		
GAM1292	RMP	3'	AGTTTTGTGCCAGCTGTG 13707	ACA	T
			CACAG GC GCAGGACT		
			GTGTC CG TGTTTTGA		
			GAC _		
GAM1292	RMP	3'	AGTTTTGTGCCAGCTGTG 56242	ACA	T
			CACAG GC GCAGGACT		
			GTGTC CG TGTTTTGA		
			GAC _		
GAM1292	SCYD1	3'	AGTCACCCCGGCCACCTGCGGT 90924	A	ACA CAG_
	G		CACC CAG GCTG GACT		
			GTGG GTC CGGC CTGA		
			C CAC CCCA		
GAM1292	SHAPY	5'	AGTCCCGCCTGTCTGT 57108	CT	A
			ACAGACAG GC GGA		

TGTCTGTC CG CCTGA  
 \_ C  
 GAM1292 SMOC1 3' AGTCCTGCAATTGTACTGCGG 42147 A \_ C  
 CC CAG ACAG TGCAGGACT  
 || ||| ||| |||||  
 GG GTC TGTT ACGTCCTGA  
 C A A  
 GAM1292 SRPUL 3' TCCTGCAGTGTTTCCAGG 27101 AC\_ G  
 CC AGACA CTGCAGGA  
 || ||||| |||||  
 GG TTTGT GACGTCCT  
 ACC \_  
 GAM1292 SSH-3 3' AGCCCTGCACACTCACCTGTGG 35339 AC\_ C\_ A  
 CCACAG AG TGCAGG CT  
 ||||| || ||||| ||  
 GGTGTC TC ACGTCC GA  
 CAC AC C  
 GAM1292 TOSO 3' CCCAGGCTCGGACTGTGGTG 18389 AC\_\_ GCA  
 CACCACAG AGCT GG  
 ||||| ||| ||  
 GTGGTGTC TCGG CC  
 AGGC AC\_  
 GAM1292 TPC2 3' CCTGCAGCTTCCGTGGTG 57446 A C  
 CACCAC GA AGCTGCAGG  
 ||||| || |||||  
 GTGGTG CT TCGACGTCC  
 C \_  
 GAM1292 TRIM11 3' CCATGCCTGTCTGTG 72831 CT \_  
 CACAGACAG GCA GG  
 ||||| ||| ||  
 GTGTCTGTC CGT CC  
 \_ A  
 GAM1292 UGT2B10 3' AGCCCCAGTAATGCTCTGTGG 6540 \_ \_ CA A  
 CCACAGA CA GCTG GG CT  
 ||||| || ||| |||  
 GGTGTCT GT TGAC CC GA  
 C AA C\_ \_  
 GAM1292 LOC113386 3' AGTCCTGCATGTGTTGATG 57077 CA GC  
 CA GACA TGCAGGACT  
 || ||| |||||  
 GT TTGT ACGTCCTGA  
 AG GT  
 GAM1292 LOC130814 3' AGTGCTCAGACATCTGCAGTGT 74984 CA CAG C G  
 T AACAC CAGA CTG AG ACT  
 |||| ||| ||| |||  
 TTGTG GTCT GAC TC TGA  
 AC ACA \_ G  
 GAM1292 LOC131870 3' AGTCCTGCAGCCTCATATGG 75013 CAGACA  
 CCA GCTGCAGGACT  
 || |||||

GGT CGACGTCCTGA  
ATACTC  
GAM1292 LOC133491 5' GTCTGGCGCCTGTGGCGT 75096 A ACA T A  
AC CCACAG GC GC GGAC  
|| ||||| || |||||  
TG GGTGTC CG CG TCTG  
C \_ \_ G  
GAM1292 LOC139065 3' TCCTTTTGATTTGTGG 75817 \_ CTGC  
CCACAGA CAG AGGA  
||||| ||| |||||  
GGTGTTT GTT TCCT  
A T \_  
GAM1292 LOC145622 5' AGTCCTGCAAAGGTGATGGTGG 77291 AGA G \_  
T ACCAC CA CT GCAGGACT  
|||| ||| |||||  
TGGTG GT GA CGTCCTGA  
GTA G AA  
GAM1292 LOC145676 5' AGTCCTGTCCAGGGTCT 77333 AG \_  
AGAC CTG CAGGACT  
||| ||| |||||  
TCTG GAC GTCCTGA  
G\_ CT  
GAM1292 LOC145955 5' AGCCCTGAGATGTCCATGGT 83586 CA G G A  
ACCA GACA CT CAGG CT  
|||| ||| ||| ||| |||  
TGGT CTGT GA GTCC GA  
AC A \_ C  
GAM1292 LOC145957 5' CTGCTGTTGTCTGCGGT 56794 A T  
ACC CAGACAGC GCAG  
||| ||||| |||  
TGG GTCTGTTG CGTC  
C T  
GAM1292 LOC146287 5' TTGCAGCTGCCTCGGT 83654 AC A  
ACC AG CAGCTGCAG  
||| ||| |||||  
TGG TC GTCGACGTT  
C\_ C  
GAM1292 LOC146669 3' AGCCCTGCAGCCTGGG 78049 A ACA A  
CC CAG GCTGCAGG CT  
|| ||| ||||| |||  
GG GTC CGACGTCC GA  
\_ \_ C  
GAM1292 LOC147040 3' CAGTGTCTGTGATGT 78230 C G  
ACA CACAGACA CTG  
||| ||||| |||  
TGT GTGTCTGT GAC  
A \_  
GAM1292 LOC147160 5' AGCCCTGCAGTGCGTGTACAGG 83956 ACAG \_ A  
CC ACA GCTGCAGG CT  
|| ||| ||||| |||



	GG TGT TGACGTCC GA	
	ACA_ GCG C	
GAM1292 LOC149111 3'	CCTGCGTGTCTGTG 79181	GC
	CACAGACA TGCAGG	
	GTGTCTGT GCGTCC	
	—	
GAM1292 LOC150174 3'	AGTCCTGCGATGCTAAGTG 79604	CAC A GC
	CAC AG CA TGCAGGACT	
	GTG TC GT GCGTCCTGA	
	AA_ _ A_	
GAM1292 LOC150213 3'	AGTCCTGCGATGCTAAGTG 74851	CAC A GC
	CAC AG CA TGCAGGACT	
	GTG TC GT GCGTCCTGA	
	AA_ _ A_	
GAM1292 LOC150236 3'	AGTCCTGCGATGCTAAGTG 79683	CAC A GC
	CAC AG CA TGCAGGACT	
	GTG TC GT GCGTCCTGA	
	AA_ _ A_	
GAM1292 LOC154559 3'	GCAGCTGTCCTGTGATGT 81096	C _
	ACA CACAG ACAGCTGC	
	TGT GTGTC TGTCGACG	
	A C	
GAM1292 LOC158117 3'	CCTGGTCTGTTCTGTATTGTT 81703	CC _ CTG
	AACA ACAGA CAG CAGG	
	TTGT TGTCT GTC GTCC	
	TA T TG_	
GAM1292 LOC160897 3'	CCAGCTATTGTCTGTTGTGTT 82245	C CT A
	AACAC ACAGACAG GC GG	
	TTGTG TGTCTGTT CG CC	
	T AT A	
GAM1292 LOC161482 3'	GCACTTACCTGTGGTGTT 87089	AC_ C
	AACACCACAG AG TGC	
	TTGTGGTGTC TC ACG	
	CAT _	
GAM1292 LOC164382 3'	AGTCTCCCTGTCTGTGGT 87203	CTGCA
	ACCACAGACAG GGA CT	
	TGGTGTCTGTC TCTGA	
	CC__	
GAM1292 LOC200301 5'	AGCCTGTCTGTGTGTT 88736	C _
	AACAC ACAGACAG CT	

	TTGTG TGTCTGTC GA	
	— C	
GAM1292 LOC203275 3'	CCTGGTCTGTTCTGTATTGTT 89319	CC _ CTG
	AACA ACAGA CAG CAGG	
	TTGT TGTCT GTC GTCC	
	TA T TG_	
GAM1292 LOC219920 5'	TTGGGCACTGCCTGTGG 93323	A C AG
	CCACAG CAG TGC GA	
	GGTGTC GTC ACG TT	
	C _ GG	
GAM1292 LOC220932 3'	AGTCCTGTTCTCTGTTAATGT 93135	_ CT_
	ACA GACAG GCAGGACT	
	TGT TTGTC TGTCCTGA	
	AA TCT	
GAM1292 LOC221466 5'	GTCCTGTGTCCAGGGTG 93693	ACA AGCT
	CACC GAC GCAGGAC	
	GTGG CTG TGTCCTG	
	GAC _	
GAM1292 LOC221547 3'	GCAGCTGTCCTGTGATGT 91007	C _
	ACA CACAG ACAGCTGC	
	TGT GTGTC TGTCGACG	
	A C	
GAM1292 LOC221935 3'	AGCCGTCACCTGTCTGTG 92615	CT A A
	CACAGACAG GC GG CT	
	GTGTCTGTC TG CC GA	
	AC _ _	
GAM1292 LOC253681 3'	CAGTGTCTGTGATGT 95127	C G
	ACA CACAGACA CTG	
	TGT GTGTCTGT GAC	
	A _	
GAM1292 LOC257115 3'	AGTCCTGCAAGGTGAAGGCGTT 96523	A ACAGA G _
	AAC CC CA CT GCAGGACT	
	TTG GG GT GA CGTCCTGA	
	C AA_ G A	
GAM1292 LOC257577 3'	GCAGCTGTCCTGTGATGT 97838	C _
	ACA CACAG ACAGCTGC	
	TGT GTGTC TGTCGACG	
	A C	
GAM1292 LOC51112 5'	AGTCCTGCGGGCCGTGG 32082	AGACAG
	CCAC CTGCAGGACT	

			GGTG	GGCGTCCTGA			
			CCG	_____			
GAM1292	LOC51236	3'	TCCTGCAGCTGTCTGCAGG	33205	A_		
			CC CAGACAGCTGCAGGA				
			GG GTCTGTCGACGTCCT				
			AC				
GAM1292	LOC51713	3'	TTTGTACTGTCTGCGG	32762	A	C	
			CC CAGACAG TGCAGG				
			GG GTCTGTC ATGTTT				
			C				
GAM1292	LOC56920	3'	AGCCTTCCAGCCTGCGGTG	39379	A	ACA	C_ A
			CACC CAG GCTG AGG CT				
			GTGG GTC CGAC TCC GA				
			C ____ CT _				
GAM1292	LOC90408	3'	AGTCCTGTGGTCCTGTG	62655	ACA	TG	
			CACAG GC CAGGACT				
			GTGTC TG GTCCTGA				
			C__ GT				
GAM1292	LOC91397	5'	GCAGTATCTGTGGTG	65910	CA		
			CACCACAGA GCTGC				
			GTGGTGTCT TGACG				
			A_				
GAM1293	ABCC1	3'	TGATGTGGGGTAAATATTAAGG	17183	CA	AAA	C
	A		TCC AATATTTAC GC ATCA				
			AGG TTATAAATG TG TAGT				
			AA GGG _				
GAM1293	ABCC1	3'	TGATGTGGGGTAAATATTAAGG	39128	CA	AAA	C
	A		TCC AATATTTAC GC ATCA				
			AGG TTATAAATG TG TAGT				
			AA GGG _				
GAM1293	ABCC1	3'	TGATGTGGGGTAAATATTAAGG	39136	CA	AAA	C
	A		TCC AATATTTAC GC ATCA				
			AGG TTATAAATG TG TAGT				
			AA GGG _				
GAM1293	ASIC4	3'	TTTGTAATATTTAGGG	37924	_		
			CCC AAATATTTACAAA				
			GGG TTTATAAATGTTT				
			A				
GAM1293	CREBBP	3'	GATAACTTTGTGATGTTTCGGG	15207	_	T	CC
	A		TCCC AAATATT ACAAAG ATC				

AGGG TTTGTAG TGTTC TAG  
 C \_ AA  
 GAM1293 CTSS 3' TGATGGCTTAAAAATA 14545 ACA  
 TATTT AAGCCATCA  
 |||| |||||  
 ATAAA TTCGGTAGT  
 AA\_  
 GAM1293 EYA1 5' GATGGCTCCGAGTTTGGGG 4954 ATTTACAA  
 TCCCAAAT AGCCATC  
 ||||| |||||  
 GGGGTTTG TCGGTAG  
 AGCC\_\_\_\_  
 GAM1293 FBXW1B 3' TGACAGCTTTGTACTGTGG 24527 AATATT CA  
 CCA TACAAAGC TCA  
 || ||||| ||  
 GGT ATGTTTCG AGT  
 GTC\_\_\_\_ AC  
 GAM1293 FBXW1B 3' TGACAGCTTTGTACTGTGG 53331 AATATT CA  
 CCA TACAAAGC TCA  
 || ||||| ||  
 GGT ATGTTTCG AGT  
 GTC\_\_\_\_ AC  
 GAM1293 FBXW1B 3' TGACAGCTTTGTACTGTGG 53342 AATATT CA  
 CCA TACAAAGC TCA  
 || ||||| ||  
 GGT ATGTTTCG AGT  
 GTC\_\_\_\_ AC  
 GAM1293 GCN5L2 3' TGATGGCTTCAGGGGTTGG 59841 ATA ACA  
 CCAA TTT AAGCCATCA  
 ||| || |||||  
 GGTT GGA TTCGGTAGT  
 GG\_ C\_  
 GAM1293 GSPT1 3' GCTTTGTAAGTGATGTGG 9143 AA\_  
 CCA TATTTACAAAGC  
 || |||||  
 GGT GTGAATGTTTCG  
 GTA  
 GAM1293 PTPN11 3' TGATGAGAAGAAATGATTTGGG 11085 \_ ACAAAGC  
 A TCCCAAAT ATTT CATCA  
 ||||| ||| ||||  
 AGGGTTTA TAAA GTAGT  
 G GAAGA\_  
 GAM1293 RNMT 3' TGATAGCTTTGTAGGTACAGGA 13725 CAAA C  
 TCC TATTTACAAAGC ATCA  
 || ||||| ||||  
 AGG ATGGATGTTTCG TAGT  
 AC\_\_ A  
 GAM1293 ROR2 3' TGACAGCTTTGTATTTGGTGA 15855 \_ TATT CA  
 TC CAAA TACAAAGC TCA  
 || |||| ||||| ||

			AG GGT TT	ATGTTTCG	AGT	
			T	_____	AC	
GAM1293	STAM	3'	TTGTAATTATTTGGGA	12964	T	
			TCCCAAATA TTACAA			
			AGGGTTTAT AATGTT			
			T			
GAM1293	TGFBR2	3'	CTTTATAAATATTTGG	12267	C	
			CCAAATATTTA AAAG			
			GGTTTATAAAT TTTC			
			A			
GAM1293	ZNF14	3'	TGTAAGACATTTGGGA	40718	A_	
			TCCCAAAT TTTACA			
			AGGGTTTA GAATGT			
			CA			
GAM1293	DKFZP434L1123	5'	TGGTTTGTAATATTTG	49585	G	
			CAAATATTTACAAA CCA			
			GTTTATAAATGTTT GGT			
			—			
GAM1293	DKFZP434O047	5'	TGATGGCTCCACATCTTGGGG	31517	ATATTTACAA	
			TCCCAA AGCCATCA			
			GGGGTT TCGGTAGT			
			CTACACC_			
GAM1293	DKFZP564G092	5'	TGGACAGTAAATATTTG	31539	AAAG	
			CAAATATTTAC CCA			
			GTTTATAAATG GGT			
			ACA_			
GAM1293	DKFZP564O0823	3'	ATGGCTGTAAAATGTTT	59519	ACAA	
			AAATATTT AGCCAT			
			TTTGTAAG TCGGTA			
			ATG_			
GAM1293	FLJ10036	3'	GCTTTGTAAATATTTTACA	94950	CC	
			TC AAATATTTACAAAGC			
			AG TTTATAAATGTTTCG			
			AC			
GAM1293	FLJ11267	5'	TGATGGCTCTAGAATGTCTAGG	39007	CAA ACAA	
	A		TCC ATATTT AGCCATCA			
			AGG TGTAAG TCGGTAGT			
			ATC ATC_			
GAM1293	FLJ11730	3'	TGGAGGCTGTAAATATCTGG	42798	A AA AT	
			CCA ATATTTACA GCC CA			

			GGT TATAAATGT CGG GT		
			C    _ AG		
GAM1293	FLJ13194	3'	TGATAACTTTGTAAAGATGGGA 47131	AATA	CC
			TCCCA TTTACAAAG ATCA		
			AGGGT GAATGTTTC TAGT		
			A_    AA		
GAM1293	FLJ14564	3'	ATGGGGAAAAATATTTGGGA 76499	ACAAAG	
			TCCCAAATATTT CCAT		
			AGGGTTTATAAA GGTA		
			AGG_		
GAM1293	FLJ22596	5'	TGATGGCTTGATGGTATCTGG 46964	A	TACA
			CCA ATATT AAGCCATCA		
			GGT TATGG TTCGGTAGT		
			C TAG_		
GAM1293	FLJ25200	5'	TGATGGCTTCATTAATCTCTG 58514	A	T CA_
			G CCA ATA TTA AAGCCATCA		
			GGT TAT AAT TTCGGTAGT		
			C C TAC		
GAM1293	FRAT1	3'	TGAGGGCCAAAATATTTGG 18496	ACAAA	A
			CCAAATATTT GCC TCA		
			GGTTTATAAA CGG AGT		
			AC_ G		
GAM1293	GLUC	3'	ATGGCCTTTATTTGTATTTGG 40586	TTAC	_
			CCAAATAT AAAG CCAT		
			GGTTTATG TTTC GGTA		
			TTTA C		
GAM1293	GPR	3'	GGATTGTAAATTCTTGG 23336	AT	AG
			CCAA ATTTACAA CC		
			GGTT TAAATGTT GG		
			CT A_		
GAM1293	GSPT2	3'	GCTTTGTAAGTGATGTGG 36120	AA_	
			CCA TATTTACAAAGC		
			GGT GTGAATGTTTCG		
			GTA		
GAM1293	KIAA0453	3'	GTGTGTTTGTAATATATAGGA 69051	CAA	GC
			TCC ATATTTACAAA CAT		
			AGG TATAAATGTTT GTG		
			ATA GT		
GAM1293	KIAA0746	3'	GCTTTGTAAATTGG 69454	AAT	
			CCA ATTTACAAAGC		

GGT TAAATGTTTCG

GAM1293 KIAA0884 3' TGATTATTGTAAATATTTTGGGA 70207 C AGCC  
TCC AAATATTTACAA ATCA  
||| ||||| |||  
AGG TTTATAAATGTT TAGT  
T AT\_

GAM1293 KIAA0930 3' TGATGGCTTTGCCCTGGGCTGG 70554 AATATTTA  
GA TCCCA CAAAGCCATCA  
|||| |||||  
AGGGT GTTTCGGTAGT  
CGGGTCCC

GAM1293 KIAA1052 3' TGATGGCTTTTATCCTCCTGGG 30252 AATATT C  
A TCCCA TA AAAGCCATCA  
|||| || |||||  
AGGGT AT TTTTCGGTAGT  
CCTCCT \_

GAM1293 KIAA1557 3' TTGTAAATATTTGTGA 61140 C  
TC CAAATATTTACAA  
|| |||||  
AG GTTTATAAATGTT  
T

GAM1293 KIAA1587 3' TGATAGCTCTATAAAATGTTTT 40512 C ACAA\_ C  
GGA TCC AAATATTT AGC ATCA  
||| ||||| ||| |||  
AGG TTTGTAAA TCG TAGT  
T ATATC A

GAM1293 LIPI 3' ATGACTTTGTAAATATTT 79564 C  
AAATATTTACAAAG CAT  
||||||| |||  
TTTATAAATGTTTC GTA  
A

GAM1293 MARCKS 3' GTTTTGTAAATACTGGAGA 9870 \_ AA  
TC CCA TATTTACAAAGC  
|| ||| |||||  
AG GGT ATAAATGTTTTG  
A C\_

GAM1293 MED6 3' TGATGGCTTTGTTGCAGCTGAG 18439 C AATATTT  
A TC CA ACAAAGCCATCA  
|| || |||||  
AG GT TGTTTCGGTAGT  
A CGACGT\_

GAM1293 MGC17330 3' GTTTTTAAAATATTTGGGA 53531 AC  
TCCCAAATATTT AAAGC  
||||||| |||  
AGGGTTTATAAA TTTTG  
AT

GAM1293 OR51E2 3' ATGGCTTTGTACTTGTGATG 47790 A\_ TT  
CA ATA TACAAAGCCAT  
|| ||| |||||

		GT TGT ATGTTTCGGTA	
		AG TC	
GAM1293	PSTPIP2	3' CTTTCACAAATATTTGGG 44389	AC_
		CCCAAATATTT AAAG	
		GGGTTTATAAA TTTC	
		CAC	
GAM1293	PURG	3' ATGGCTTTGCTATGG 25336 AATATT _	
		CCA TA CAAAGCCAT	
		GGT AT GTTTCGGTA	
		_____ C	
GAM1293	VDU1	3' TGATGGCTTTGTTTGGTTTGG 30431	ATTT
	GG	TCCCAAAT ACAAAGCCATCA	
		GGGGTTTG TGTTCGGTAGT	
		GTTT	
GAM1293	ZNF294	3' GCTTTGTAAATGTTTGG 70828	
		CCAAATATTTACAAAGC	
		GGTTTGTAAATGTTTCG	
GAM1293	LOC127162	3' TGATGGCTACATATACTAGGGA 74638	AAA TTACAA
		TCCC TAT AGCCATCA	
		AGGG ATA TCGGTAGT	
		ATC TACA_	
GAM1293	LOC148936	5' TGATGGCTCTATAAGGGGGA 84303	AAA TTACAA
		TCCC TAT AGCCATCA	
		AGGG ATA TCGGTAGT	
		GGA TC_	
GAM1293	LOC148938	5' TGATGGCTCTATAAGGGGGA 84284	AAA TTACAA
		TCCC TAT AGCCATCA	
		AGGG ATA TCGGTAGT	
		GGA TC_	
GAM1293	LOC152084	5' GATGGCTTTCCTCAGCCTGGGA 85553	AATATTTAC
		TCCA AAAGCCATC	
		AGGGT TTTCGGTAG	
		CCGACTCC_	
GAM1293	LOC152573	3' GATGACTATATATTTGGG 80618	TTACAA C
		CCCAAATAT AG CATC	
		GGGTTTATA TC GTAG	
		TA_ A	
GAM1293	LOC152627	5' ATGGCTTCTAAGTATTCAGG 80627	CA CA
		CC AATATTTA AAGCCAT	



GG TTATGAAT TTCGGTA  
AC C\_  
GAM1293 LOC200301 3' GCTTGTTATTTGGGG 88748 TTT A  
TCCCAAATA ACAA GC  
||||||| ||| ||  
GGGGTTTAT TGTT CG  
  
GAM1294 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
GTA GGAT GGGTTGTTT  
||| ||| |||||||  
CGT CCTA CCCAACAAA  
C CGTG\_  
GAM1294 LCT 3' AACCGTAAAAATCCTT 9697 G  
AAGGATTTTTTA GGTT  
||||||||| |||  
TTCCTAAAAAT CCAA  
G  
GAM1294 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
GTAAGGATTTTTAGGGTTGTTT  
|||||||||||||||  
CATTCCTAAAAATCCCAACAAA  
  
GAM1294 FBXO30 3' AACTAAAAAAATCCTGAC 49573 A AG  
GT AGGATTTTTT GGTT  
|| ||||||| |||  
CA TCCTAAAAA TCAA  
G AA  
GAM1294 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTTT  
GTAAG AGGGTTGTT  
||||| |||||||  
CATTC TCCCAACAA  
AT\_\_\_\_  
GAM1294 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
TAAG TTTT GGGTTGTTT  
||| ||| |||||||  
GTTT AAAA CCCAACAAA  
C  
GAM1294 SMT3H2 3' AACCAACATAAAAAATCCTTGC 22670 GG  
GTAAGGATTTTTTA GTTGTT  
||||||||| |||  
CGTTCCTAAAAAT CAACAA  
A\_  
GAM1294 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
GTAAGGATTTTTT GGGTT  
||||||||| |||  
CGTTCCTAAAAA TCCAA  
GTA  
GAM1294 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
GGAT TT GGGTTGTTT  
||| || |||||||

CCTG AA CCCAACAAA  
 T\_ C  
 GAM1294 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
 C GTA GGATTTTT TTGTTT  
 ||| ||||| |||||  
 CGT CCTAAAAA AACAAA  
 C GATAA  
 GAM1294 LOC148089 3' GGCCCTAAAAATTCCTAC 78637 A  
 GTA GGATTTTTAGGGTT  
 ||| |||||  
 CAT CTTAAAAATCCCGG  
 C  
 GAM1294 LOC154547 3' AACAAACATAAAAAATCCTTGC 76050 GG  
 GTAAGGATTTTTA GTTGTT  
 ||||| |||||  
 CGTTCCTAAAAAT CAACAA  
 A\_  
 GAM1294 LOC158104 3' ACAGCCAAAAATCCTTA 60313 AG  
 TAAGGATTTTT GTTGT  
 ||||| |||||  
 ATTCCTAAAAA CCGACA  
 —  
 GAM1294 LOC205880 5' AAACAACCATCATCCTGAC 90709 A TTTTAG  
 GT AGGAT GGTGTTT  
 || ||||| |||||  
 CA TCCTA CCAACAAA  
 G CTA\_\_\_\_  
 GAM1294 LOC221561 3' AACAAACATAAAAAATCCTTGC 92130 GG  
 GTAAGGATTTTTA GTTGTT  
 ||||| |||||  
 CGTTCCTAAAAAT CAACAA  
 A\_  
 GAM1294 LOC257591 3' AACAAACATAAAAAATCCTTGC 97840 GG  
 GTAAGGATTTTTA GTTGTT  
 ||||| |||||  
 CGTTCCTAAAAAT CAACAA  
 A\_  
 GAM1294 LOC51145 3' AGCTAAAATCCTTAC 32393 TAG  
 GTAAGGATTTT GTT  
 ||||| |||||  
 CATTCCTAAAA TCGA  
 —  
 GAM1295 ACK1 3' GGAGGACCCGCTGCTCCT 19344 G CAC G \_  
 AGGAGCAG C GT CC CC  
 ||||| | |||||  
 TCCTCGTC G CA GG GG  
 \_CC\_ \_ A  
 GAM1295 ADAM19 3' GGGCACGCAAGAGAGCTTCCC 52709 A AGGCCA\_  
 GG GGAGC CGTGCCC  
 || ||||| |||||

			CC CTTCG	GCACGGG		
			—	AGAGAAC		
GAM1295	ADCY8	5'	CGTGACCCCTCCTCCT	6653	CA	C
			AGGAGGAG	GG CACG		
			TCCTCCTC	CC GTGC		
			CC	A		
GAM1295	AGPAT2	3'	GGGAATCGGGGCCTGCTGCTCC	21156	G	A TG_
	T		AGGAG	AGCAGGCC CG CCC		
			TCCTC	TCGTCCGG GC GGG		
			G	G TAA		
GAM1295	AGPAT2	3'	GGGAATCGGGGCCTGCTGCTCC	65823	G	A TG_
	T		AGGAG	AGCAGGCC CG CCC		
			TCCTC	TCGTCCGG GC GGG		
			G	G TAA		
GAM1295	AMT	5'	GGGGCTGCCCACGCCCCCT	4905	A A A__	CACGT
			AGG GG GC	GGC GCCC		
			TCC CC CG	CCG CGGGG		
			— _	CAC T__		
GAM1295	ATP4A	3'	GGGCACGTGGGACCCTCT	5531	AGCAGG	
			GGAGG	CCACGTGCCC		
			TCTCC	GGTGACGGG		
			CAG__			
GAM1295	ATRN	3'	TGGGACAGTCCCCTGCTCCTCT	57806	CC G C	
			GGAGGAGCAGG	AC TG CCCA		
			TCTCCTCGTCC	TG AC GGGT		
			CC _	A		
GAM1295	BAALC	3'	TGAAGCAGTCATACCTGCTCCT	45666	CC__ G	CC
	C		GAGGAGCAGG	AC TGC CA		
			CTCCTCGTCC	TG ACG GT		
			ATAC _	AA		
GAM1295	BGN	3'	GTTTCATGGCCTGTCCCTCC	8144	AG	CGT
			GGAGG	CAGGCCA GC		
			CCTCC	GTCCGGT TG		
			CT	ACT		
GAM1295	C1orf6	5'	GCTGCGGCCCGCCCGCC	39283	A A A	A T
			GG GG GC	GGCC CG GC		
			CC CC CG	CCGG GT CG		
			G _	C _		
GAM1295	C1orf6	5'	GGCCCGCCCGCCCTCCT	39285	A A	CAC T
			AGGAGG	GC GGC G GCC		

			TCCTCC CG CCG C CCG		
			C C _ C		
GAM1295	CACNG7	3'	GGAGCTCCCCCTGCCTCCTCCT 49096	_	CCACGT C
			AGGAGGAG CAGG GC CC		
			TCCTCCTC GTCC CG GG		
			C CCCT_ A		
GAM1295	CBFA2T3	5'	GCTGGCCCAGCCCCTCCT 17757	A A_	C
			AGGAGG GC GGCCA GT		
			TCCTCC CG CCGGT CG		
			C AC _		
GAM1295	CD244	5'	GGCAGTTCTGCTCCCC 33062	A	CC G
			GG GGAGCAGG AC TGCC		
			CC CCTCGTCT TG ACGG		
			_ _ _		
GAM1295	CDC42	3'	TGGAGCCCATCTTGCCCCTCCT 8372	A	CCACGT C
			AGGAGG GCAGG GC CCA		
			TCCTCC CGTTC CG GGT		
			C TACC_ A		
GAM1295	CLDN14	3'	CACAGCCTGCTTCTCC 24031		CAC
			GGAGGAGCAGGC GTG		
			CCTCTTCGTCCG CAC		
			A_		
GAM1295	CLDN14	3'	CACAGCCTGCTTCTCC 57837		CAC
			GGAGGAGCAGGC GTG		
			CCTCTTCGTCCG CAC		
			A_		
GAM1295	CRB1	5'	GGGCACCCGCTCCTCT 23867	A CCAC	C
			GGAGGAGC GG GTGCC C		
			TCTCCTCG CC CACGG G		
			_ _ _ A		
GAM1295	CRSP8	3'	ATGTGTACAGCTGCTCCTCC 80962		GC_
			GGAGGAGCAG CACGT		
			CCTCCTCGTC GTGTA		
			GACAT		
GAM1295	DAG1	3'	GGCAGCCTGCTCCCCT 15280	A	CACG
			AGG GGAGCAGGC TGCC		
			TCC CCTCGTCCG ACGG		
			_ _ _		
GAM1295	DAZ	5'	CACTGCCTCTGTTCCCTCCT 14548	_ C C	
			AGGAGGAGCAG G CA GTG		

			TCCTCCTTGTC C GT CAC		
			T C _		
GAM1295 DCN	5'	GCACCTACCCCCTCCTCCT	8618	CA CCAC	
		AGGAGGAG GG GTGC			
		TCCTCCTC CC CACG			
		CC ATC_			
GAM1295 DYRK1B	3'	GGGGAGATGGCCTTGCTCCTCC	16329	_ CGTG	
T		AGGAGGAGCA GGCCA CCCC			
		TCCTCCTCGT CCGGT GGGG			
		T AGA_			
GAM1295 EIF4EBP1	3'	GGGCACCTGCCCCCTCCT	14585	A_ CCACG	
		AGGAGG GCAGG TGCCC			
		TCCTCC CGTCC ACGGG			
		CC _ _ _			
GAM1295 EMD	3'	GTAGTGCTTGCTCCCCCT	3685	A C G	
		AGG GGAGCAGGC AC TGC			
		TCC CCTCGTTCG TG ATG			
		C _ _			
GAM1295 GAB2	3'	GCTGCACCTCTCCTCCT	24496	C CCA T	
		AGGAGGAG AGG CG GC			
		TCCTCCTC TCC GT CG			
		_ AC_ _			
GAM1295 GAB2	3'	GCTGCACCTCTCCTCCT	54453	C CCA T	
		AGGAGGAG AGG CG GC			
		TCCTCCTC TCC GT CG			
		_ AC_ _			
GAM1295 GDF2	5'	GGGAGATGCCGGCCCGCTCCTT	32493	A A_ GC	
C		GGAGGAGC GGCC CGT CCC			
		CTTCCTCG CCGG GTA GGG			
		C CC GA			
GAM1295 HD	3'	GCAGCCCCTCCTCCT	9185	CA CACG	
		AGGAGGAG GGC TGC			
		TCCTCCTC CCG ACG			
		C_ _ _			
GAM1295 HDAC5	3'	GGGTCTCTCAGCCTTGCCCCCTC	57611	A _ CACGT_	
CT		AGGAGG GCA GGC GCCC			
		TCCTCC CGT CCG TGGG			
		C T ACTCTC			
GAM1295 IL1F5	5'	GGGAATCCTGCTCCTCCT	24382	CCAC GC	
		AGGAGGAGCAGG GT CCC			

TCCTCCTCGTCC TA GGG  
 \_\_\_\_\_ A\_  
 GAM1295 IMMP2L 5' GGAGCTGGCCCGCTCCTCC 50730 A CGT C  
 GGAGGAGC GGCCA GC CC  
 ||||| ||| ||  
 CCTCCTCG CCGGT CG GG  
 C \_\_\_\_ A  
 GAM1295 ITPKB 3' CGGAGGCCTGCTGCCCC 9428 A \_ A\_  
 GG GG AGCAGGCC CG  
 || || ||||| ||  
 CC CC TCGTCCGG GC  
 \_ G AG  
 GAM1295 LAPTM5 3' CGCTGGCCTGCTCCTCCT 22203 C  
 AGGAGGAGCAGGCCA GTG  
 ||||| |||  
 TCCTCCTCGTCCGGT CGC  
 -  
 GAM1295 LOH11CR2A 5' TGTGGCCTACTCACCT 27543 AG C  
 AGG GAG AGGCCACG  
 ||| || |||||  
 TCC CTC TCCGGTGT  
 CA A  
 GAM1295 LY9 3' GGATGTGGCCCCTCCCCCT 71684 A CA G  
 AGG GGAG GGCCACGT CC  
 ||| ||| ||||| ||  
 TCC CCTC CCGGTGTA GG  
 C C\_ \_  
 GAM1295 LZTR1 3' TGGGGAAGTGACCTGCTCTCCT 22246 G C GTG  
 AGGAG AGCAGG CAC CCCCCA  
 |||| ||||| || ||||  
 TCCTC TCGTCC GTG GGGGT  
 \_ A AA\_  
 GAM1295 MBD3 3' GGGCTCGAGGCCAGCTCCTCC 14096 A A T  
 GGAGGAGC GGCC CG GCCC  
 ||||| ||| || |||  
 CCTCCTCG CCGG GC CGGG  
 A A T  
 GAM1295 MCC 3' GGTGCCCCGCTCTTCC 9959 A CACGT  
 GGAGGAGC GGC GCC  
 ||||| ||| |||  
 CCTTCTCG CCG TGG  
 C \_\_\_\_\_  
 GAM1295 MGAT1 3' GGGCACGAGCCCTCCT 10010 CA CA  
 AGGAG GGC CGTGCCC  
 |||| ||| |||||  
 TCCTC CCG GCACGGG  
 \_ A\_  
 GAM1295 MYO1C 3' GGACACCTCTCCTCCT 61208 C CCAC G  
 AGGAGGAG AGG GT CC  
 ||||| ||| |||

			TCCTCCTC TCC CA GG		
			— A —		
GAM1295 NCF4	3'	GGCTCGTGGCCTCCCCTCC	25510	AGC	T
		GGAGG AGGCCACG GCC			
		CCTCC TCCGGTGC CGG			
		CC_ T			
GAM1295 OGT	5'	CACACAACCTCCTCCTCCT	13200	C	CCAC
		AGGAGGAG AGG GTG			
		TCCTCCTC TCC CAC			
		C AACA			
GAM1295 OIP2	5'	GGGAGACCCGCTCCTTCT	76984	A	CCAC GC
		AGGAGGAGC GG GT CCC			
		TCTTCCTCG CC CA GGG			
		— GA			
GAM1295 PCDH11X	3'	GGCACATGACTGCTTCT	52026	GC	C
		AGGAGCAG CA GTGCC			
		TCTTCGTC GT CACGG			
		A_ A			
GAM1295 PCDH11X	3'	GGCACATGACTGCTTCT	52048	GC	C
		AGGAGCAG CA GTGCC			
		TCTTCGTC GT CACGG			
		A_ A			
GAM1295 PCDH11Y	3'	GGCACATGACTGCTTCT	52082	GC	C
		AGGAGCAG CA GTGCC			
		TCTTCGTC GT CACGG			
		A_ A			
GAM1295 PDGFRB	5'	GGCGGCTCTGCTCCTCC	65979	_	ACGT
		GGAGGAGCAG GCC GCC			
		CCTCCTCGTC CGG CGG			
		T _			
GAM1295 PFKL	3'	CACTGTGACCTGCTCCTGCC	10515	_	C _
		GG AGGAGCAGG CAC GTG			
		CC TCCTCGTCC GTG CAC			
		G A T			
GAM1295 PIK4CB	3'	TGGGGCTTCCCTGCCCTCCT	10595	A	CCACGT
		AGGAGG GCAGG GCCCA			
		TCCTCC CGTCC CGGGGT			
		C CTT_			
GAM1295 PK428	5'	GGAAGCACCCCTCCTCCT	13212	CA	CCAC C_
		AGGAGGAG GG GTGC CC			

		TCCTCCTC CC CACG GG	
		— — — — AA	
GAM1295 PMX1	5'	CACCCTCTCCTCCT 22590	C CCAC
		AGGAGGAG AGG GTG	
		TCCTCCTC TCC CAC	
		— — — —	
GAM1295 PMX1	5'	CACCCTCTCCTCCT 42658	C CCAC
		AGGAGGAG AGG GTG	
		TCCTCCTC TCC CAC	
		— — — —	
GAM1295 PROX1	5'	GCGCTCCGCTCCTCC 10894	A CCAC
		GGAGGAGC GG GTGC	
		CCTCCTCG CC CGCG	
		— T — —	
GAM1295 PRX T	3'	TGGAGCCCCGGCCCGCTGCTCC 40542	G A ACGT C
		AGGAG AGC GGCC GC CCA	
		TCCTC TCG CCGG CG GGT	
		G C CCC_ A	
GAM1295 PTPRK	5'	GGCCCGGCCCGCTCCTCC 11124	A ACGT
		GGAGGAGC GGCC GCC	
		CCTCCTCG CCGG CGG	
		C CC_	
GAM1295 RHO	3'	GGGATGTGTGCCCTCCTCCT 5020	CA _ G
		AGGAGGAG GGC CACGT CCC	
		TCCTCCTC CCG GTGTA GGG	
		C_ T _	
GAM1295 ROR2	3'	GGCCCTGCTCCTCT 15854	CCACGT C
		GGAGGAGCAGG GC C	
		TCTCCTCGTCC CG G	
		_____ A	
GAM1295 RPH3AL	3'	GGGCACGTGGCTCCCTC 22752	AGCA
		GAGG GGCCACGTGCC	
		CTCC TCGGTGCACGGG	
		C_	
GAM1295 SELPLG T	3'	TGAGGCTGTTTCCTGCTGCTCC 59691	G CC T C
		AGGAG AGCAGG ACG GCC CA	
		TCCTC TCGTCC TGT CGG GT	
		G TT _ A	
GAM1295 SERPINB9	3'	CACTGCAACCTCCTCCTCCT 14750	C C_ C
		AGGAGGAG AGG CA GTG	



			TCCTCCTC TCC GT CAC		
			C AAC _		
GAM1295 SH2D2A	3'	TGCGGAGCCTGCTCCCTCC	14275	_	CA
		GGAGG AGCAGGC CGTG			
		CCTCC TCGTCCG GCGT			
		C AG			
GAM1295 SLC2A2	5'	GGGTAGCCCAACTCCTCC	4421	CA_	CACG
		GGAGGAG GGC TGCCC			
		CCTCCTC CCG ATGGG			
		AAC _			
GAM1295 SLC9A1	3'	TGAGGCCGGCCCTGCCCTCC	70413	A	CCA T C
		GGAGG GCAGG CG GCC CA			
		CCTCC CGTCC GC CGG GT			
		C CG_ _ A			
GAM1295 SNTB1	3'	GGACATTTTTTACCTACTCCTCC	40704	C	CCAC_ _
T		AGGAGGAG AGG GTG CC			
		TCCTCCTC TCC TAC GG			
		A ATTTT A			
GAM1295 SOX12	3'	CGGAGGACCCGCCCTCCT	22695	A_ A _ A_	
		AGGAGG GC GG CC CG			
		TCCTCC CG CC GG GC			
		CC C A AG			
GAM1295 TARBP2	5'	GGAGGGCCCGCTCCTCC	56159	A	ACGTG
		GGAGGAGC GGCC CC			
		CCTCCTCG CCGG GG			
		C GA_			
GAM1295 TARBP2	5'	GGAGGGCCCGCTCCTCC	56167	A	ACGTG
		GGAGGAGC GGCC CC			
		CCTCCTCG CCGG GG			
		C GA_			
GAM1295 TCP10	3'	GCCTGGCCTGCTCCCCT	16044	A	C
		AGG GGAGCAGGCCA GT			
		TCC CCTCGTCCGGT CG			
		_ C			
GAM1295 TMEPAI	3'	CGTGTGGCCCTCCCCTCC	39445	AGCA	
		GGAGG GGCCACGTG			
		CCTCC CCGGTGTGC			
		CCTC			
GAM1295 TMSB4Y	3'	TGGAGGCCACGCCTGCTTCTCC	14845	CAC	_ _
		GGAGGAGCAGGC GTG CC CCA			

			CCTCTTCGTCCG CAC GG GGT		
			___ C A		
GAM1295	TNFSF4	3'	TGGGTGCACCTGGCCTGCTCTT 12447	C	_
	CC		GGAGGAGCAGGCCA GTGC CCCA		
			CCTTCTCGTCCGGT CACG GGGT		
			C T		
GAM1295	TRPV2	5'	GCAGCCTCCTCCTCCT 32267	C	CACG
			AGGAGGAG AGGC TGC		
			TCCTCCTC TCCG ACG		
			C ____		
GAM1295	ZFP103	5'	GGCGGCCGCTCCTCC 19024	A	ACGT
			GGAGGAGC GGCC GCC		
			CCTCCTCG CCGG CGG		
			- ____		
GAM1295	ZNF131	5'	GCCTGGGCCGCTCCTCCT 70159	A	A T
			AGGAGGAGC GGCC CG GC		
			TCCTCCTCG CCGG GT CG		
			- _ C		
GAM1295	A4GALT	3'	TGGGGCACTGGGCCGCCCTTCC 33841	A A	AC
			GGAGG GC GGCC GTGCCCA		
			CCTTC CG CCGG CACGGGGT		
			C _ GT		
GAM1295	BIRC5	3'	GGGGCACATGCTGGCCGCTCCT 6750	A	C__
	CC		GGAGGAGC GGCCA GTGCCCC		
			CCTCCTCG CCGGT CACGGGG		
			- CGTA		
GAM1295	BRD1	5'	GGGCCGGACCCCTCCTCCT 27416	CA	CCA T
			AGGAGGAG GG CG GCCC		
			TCCTCCTC CC GC CGGG		
			C_ AG_ _		
GAM1295	C12orf22	5'	GGGACTCGCTCGCTCCTCC 47980	AG	CAC G
			GGAGGAGC GC GT CCC		
			CCTCCTCG CG CA GGG		
			CT CT_ _		
GAM1295	C17orf31	3'	GGGGGACCTGCTCCTC 34126	CCACG	G
			GAGGAGCAGG T CCCC		
			CTCCTCGTCC A GGGG		
			____ G		
GAM1295	C20orf100	3'	CGGAGCACTGCTCTCCT 51810	G	_ CA
			AGGAG AGCAG GC CG		

		TCCTC TCGTC CG GC	
		_ A AG	
GAM1295	C20orf39	3' GCCCGGGACCTGCCCTCTT 46044	A _ A T
		AGGAGG GCAGG CC CG GC	
		TTCTCC CGTCC GG GC CG	
		C A _ C	
GAM1295	CAMKK1	3' GGAACCCAGCCTCTCCTCCT 50174	C CAC G
		AGGAGGAG AGGC GT CC	
		TCCTCCTC TCCG CA GG	
		_ ACC A	
GAM1295	CAMTA2	3' GGAGCCCTGCCTGCCCTGCT 61221	G A CACGT C
		AG AGG GCAGGC GC CC	
		TC TCC CGTCCG CG GG	
		G C TCC_ A	
GAM1295	CARD9	5' GGCGTCCGGCGTGCTCCTCC 53375	G ACG
		GGAGGAGCA GCC TGCC	
		CCTCCTCGT CGG GCGG	
		G CCT	
GAM1295	CARD9	5' GGCGTCCGGCGTGCTCCTCC 53381	G ACG
		GGAGGAGCA GCC TGCC	
		CCTCCTCGT CGG GCGG	
		G CCT	
GAM1295	CARD9	5' GGCGTCCGGCGTGCTCCTCC 42288	G ACG
		GGAGGAGCA GCC TGCC	
		CCTCCTCGT CGG GCGG	
		G CCT	
GAM1295	CIC	3' GGAATGAGGCCTGCTCCTCTT 30675	A G
		AGGAGGAGCAGGCC CGT CC	
		TTCTCCTCGTCCGG GTA GG	
		A A	
GAM1295	DAZ2	5' CACTGCCTCTGTTTCCTCCT 39798	_ C C
		AGGAGGAGCAG G CA GTG	
		TCCTCCTTGTC C GT CAC	
		T C _	
GAM1295	DAZ3	5' CACTGCCTCTGTTTCCTCCT 39801	_ C C
		AGGAGGAGCAG G CA GTG	
		TCCTCCTTGTC C GT CAC	
		T C _	
GAM1295	DAZ3	5' CACTGCCTCTGTTTCCTCCT 60532	_ C C
		AGGAGGAGCAG G CA GTG	

TCCTCCTTGTC C GT CAC  
T C \_  
GAM1295 DCAMKL1 3' GGCGCAGCCAGCTCCTCC 16414 A CAC  
GGAGGAGC GGC GTGCC  
||||||| ||| |||||  
CCTCCTCG CCG CGCGG  
A A\_\_  
GAM1295 DKFZP434B103 3' CGAGGCTCCTGCTCTCCT 31590 G \_ A  
AGGAG AGCAG GCC CG  
||||| ||||| ||| ||  
TCCTC TCGTC CGG GC  
\_ CT A  
GAM1295 DKFZp434I1930 3' TGGGGCACCCCTCTGCCTCCCC 50034 A \_ CCAC  
C GG GGAG CAGG GTGCCCA  
|| ||||| |||||  
CC CCTC GTCT CACGGGGT  
C C CCC\_  
GAM1295 DKFZP434N178 3' GGGAGGCCTGCTCCCTCT 71907 GA ACGTGC  
AG GGAGCAGGCC CCC  
|| ||||| |||  
TC CCTCGTCCGG GGG  
TC A\_\_\_\_  
GAM1295 DKFZP434O047 5' GGAACAAGCCCCTCCTCCT 31515 CA CAC G  
AGGAGGAG GGC GT CC  
||||||| ||| |||  
TCCTCCTC CCG CA GG  
C\_ AA\_ A  
GAM1295 DKFZP564J157 3' GGAACCTTACCTCTCCTCCT 37456 C CCAC G  
AGGAGGAG AGG GT CC  
||||||| ||| |||  
TCCTCCTC TCC CA GG  
\_ ATTC A  
GAM1295 DKFZP586J1624 3' GGGTGGGGCCTGCTCCTC 31396 ACGT  
GAGGAGCAGGCC GCCC  
||||||| |||  
CTCCTCGTCCGG TGGG  
GG\_  
GAM1295 DKFZP586M1120 3' GGGACGCGCCGGGCCTGCTCCT 48467 A\_\_ C  
CC GGAGGAGCAGGCC CGTG CCC  
||||||| ||| |||  
CCTCCTCGTCCGG GCGC GGG  
GCC A  
GAM1295 DKFZp762K222 5' GCCGTGGCCTCCCCTCC 71118 AGC T  
GGAGG AGGCCACG GC  
||||| ||||| ||  
CCTCC TCCGGTGC CG  
CC\_ \_  
GAM1295 DNAJC5 3' CACGACCCCTCCTCCT 61448 CA CCA  
AGGAGGAG GG CGTG  
||||||| || |||

			TCCTCCTC CC GCAC		
			C_ A__		
GAM1295	DOC-1R	3'	GCACCCGCTTCTCC	19580	A CCAC
			GGAGGAGC GG GTGC		
			CCTCTTCG CC CACG		
			— ———		
GAM1295	DPYSL4	3'	GGGCACTCGCCCCCTCCT	21217	AGCA CAC
			AGGAGG GGC GTGCCC		
			TCCTCC CCG CACGGG		
			CC__ CT_		
GAM1295	DRIL2	3'	GGGCAGCTCTGTCCCCTCCT	21327	A_ _ CACG
			AGGAGG GCAG GC TGCCC		
			TCCTCC TGTC CG ACGGG		
			CC T _____		
GAM1295	EFS2	3'	GGCACAGCTCTGCTCCTCC	19624	_ CAC
			GGAGGAGCAG GC GTGCC		
			CCTCCTCGTC CG CACGG		
			T A__		
GAM1295	EFS2	5'	GGCCCGCCCGCTCCTCCT	19625	A CCA T
			AGGAGGAGC GG CG GCC		
			TCCTCCTCG CC GC CGG		
			C C__ C		
GAM1295	EIF4B	3'	GGAGGCTGCCAGCCCCTCCT	75969	A A CACGT _
			AGGAGG GC GGC GCC CC		
			TCCTCC CG CCG CGG GG		
			C A T____ A		
GAM1295	EPI64	3'	TGGGGCCTCCTTCAGCCCCCTC	49196	CA CACGT____
			CTCCT AGGAGGAG GGC GCCCA		
			TCCTCCTC CCG CGGGGT		
			CC ACTTCCTC		
GAM1295	EPS8R1	5'	GGCAGCCTGTCTCCT	57602	G CACG
			AGGAGGA CAGGC TGCC		
			TCCTCCT GTCCG ACGG		
			— ———		
GAM1295	EVI5	3'	TGGGGCACACCCATGCTCACCC	19019	AG _ CCAC
			T AGG GAGCA GG GTGCCCCA		
			TCC CTCGT CC CACGGGGT		
			CA A CA__		
GAM1295	FATE	3'	TGGAGCCCTCCCTGCTTCCCCT	52361	A CCACGT C
			AGG GGAGCAGG GC CCA		

TCC CTTCGTCC CG GGT  
 C CTCC\_\_ A  
 GAM1295 FBP17 3' ATGGGACACACGCCCTACCTG 72779 CCA\_\_ C\_\_ III  
 CTCCTTC AGCAGG CGTG CCCA T  
 ||||| ||| ||| I  
 TCGTCC GCAC GGGT A  
 ATCCCC ACA III  
 GAM1295 FER1L4 3' ATGTGCCTGCTCCACC 47333 A C  
 GG GGAGCAGGC ACGT  
 || ||||| |||  
 CC CCTCGTCCG TGTA  
 A \_  
 GAM1295 FLJ10008 3' GTGGACTTGCTCCCCCT 35730 A \_  
 AGG GGAGCAGG CCAC  
 ||| ||||| |||  
 TCC CCTCGTTC GGTG  
 C A  
 GAM1295 FLJ10803 5' GGTGCCTGCTTCCCCT 36670 A CACGT  
 AGG GGAGCAGGC GCC  
 ||| ||||| |||  
 TCC CTTCGTCCG TGG  
 C \_  
 GAM1295 FLJ11280 3' GGCTGGCCTGCCCTTCT 37210 A CGT  
 AGGAGG GCAGGCCA GCC  
 ||||| ||||| |||  
 TCTTCC CGTCCGGT CGG  
 C \_  
 GAM1295 FLJ11301 3' ATGTGCCTGCTTCTCCT 37225 C  
 AGGAGGAGCAGGC ACGT  
 ||||| ||||| |||  
 TCCTCTTCGTCCG TGTA  
 \_  
 GAM1295 FLJ11383 3' CACATGGACTCCCTCTTCCT 46282 CA \_ C  
 AGGAGGAG GG CCA GTG  
 ||||| || ||| |||  
 TCCTTCTCTC GGT CAC  
 CC A A  
 GAM1295 FLJ12057 3' TGCAGAGCCCCTCCTCCT 45442 CA CA  
 AGGAGGAG GGC CGTG  
 ||||| || |||  
 TCCTCCTC CCG GCGT  
 C\_ A\_  
 GAM1295 FLJ12387 3' GGGACCTTCTCGCGCTCCTCCT 43068 A\_ CCAC G  
 AGGAGGAGC GG GT CCC  
 ||||| || |||  
 TCCTCCTCG CT CA GGG  
 CG CTTC \_  
 GAM1295 FLJ13052 3' TGGAGCACGTGGATGCTGCCTA 43474 \_ \_ GG C  
 CC GG AGG AGCA CCACGTGC CCA  
 || ||| ||| ||||| |||

			CC TCC TCGT GGTGCACG GGT		
			A G A_ A		
GAM1295	FLJ13310	3'	GGTGCCTGCTTCTCCT 47084	CACGT	
			AGGAGGAGCAGGC GCC		
			TCCTCTTCGTCCG TGG		
			_____		
GAM1295	FLJ13848	3'	GGTATCAGCTGCTCCTCCT 45471	G CAC	
			AGGAGGAGCAG C GTGCC		
			TCCTCCTCGTC G TATGG		
			_AC_		
GAM1295	FLJ20397	3'	GTCGCAGCCGCTCCTCC 35123	A CA T	
			GGAGGAGC GGC CG GC		
			CCTCCTCG CCG GC TG		
			_ AC _		
GAM1295	FLJ21019	3'	GGGAGAGAGCCAGCTCCTCCT 46245	A CACGTG	
			AGGAGGAGC GGC CCC		
			TCCTCCTCG CCG GGG		
			A AGAGA_		
GAM1295	FLJ22671	3'	GTGTGTGGCCCTCCCCCT 45867	A CA TG	
			AGG GGAG GGCCACG C		
			TCC CCTC CCGGTGT G		
			C C_ GT		
GAM1295	FOXH1	3'	ACAGGGGCCGCTCCTCC 14069	A AC_	
			GGAGGAGC GGCC GT		
			CCTCCTCG CCGG CA		
			_ GGA		
GAM1295	GNG3	3'	TGAGGCACCCTTTGCTCCACC 24192	A CCAC C	
			GG GGAGCAGG GTGCC CA		
			CC CCTCGTTT CACGG GT		
			A CC_ A		
GAM1295	HAND2	3'	GGGCATCTGCTCCCC 41749	A GCCAC C	
			GG GGAGCAG GTGCC C		
			CC CCTCGTC TACGG G		
			_ _____ A		
GAM1295	HCC-4	3'	TGGGACAGGTTGCTGGCCCTCC 56820	A A C G C	
			GGAGG GC GGC AC TG CCCA		
			CCTCC CG TCG TG AC GGGT		
			_ G T G A		
GAM1295	HS6ST	3'	GGAAGCCTGCTCCCCT 62029	A CACGTG	
			AGG GGAGCAGGC CC		

			TCC CCTCGTCCG	GG		
			— AA—			
GAM1295	HS6ST1	3'	GGAAGCCTGCTCCCCT	16660	A	CACGTG
			AGG GGAGCAGGC	CC		
			TCC CCTCGTCCG	GG		
			— AA—			
GAM1295	HSA243666	3'	CACCTGGTCTGCCCT	34146	A	C
			AGG GCAGGCCA	GTG		
			TCC CGTCTGGT	CAC		
			C	C		
GAM1295	HSJ1	3'	GGAGCCTCCTGCTCTCCT	22134	G	CCACGT C
			AGGAG AGCAGG	GC CC		
			TCCTC TCGTCC	CG GG		
			— TC—	A		
GAM1295	HSPC065	3'	GCTGCAACCTCCTCCTCCT	26313		C CCA T
			AGGAGGAG AGG	CG GC		
			TCCTCCTC TCC	GT CG		
			C	AAC —		
GAM1295	IKKE	3'	GGGGCACATGAGGCATCCT	25749	—	AGGC C
			AGGA GC	CA GTGCCCC		
			TCCT CG	GT CACGGGG		
			A	GA— A		
GAM1295	IL18BP	3'	GGAACCAGGGCCTACTCCTCTT	19109		C AC_ G
			AGGAGGAG AGGCC	GT CC		
			TTCTCCTC TCCGG	CA GG		
			A	GAC A		
GAM1295	KHDRBS3	5'	GCCCGCGCCCGCTCCTCCT	21619		A CA T
			AGGAGGAGC GGC	CG GC		
			TCCTCCTCG CCG	GC CG		
			C	C_ C		
GAM1295	KIAA0016	5'	TGAGGGTTCGTGGCCACCGCT	28647	A—	T —
	CCT		AGGAGC	GGCCACG GCCC CA		
			TCCTCG	CCGGTGC TGGG GT		
			CCAC	T A		
GAM1295	KIAA0056	3'	TGGAACACGAGAGCTCCTCCT	91555		AGGCCA CC
			AGGAGGAGC	CGTG CCA		
			TCCTCCTCG	GCAC GGT		
			AGA—	AA		
GAM1295	KIAA0133	3'	GGGCTCCTGCCTGCTCCTCCT	28769		CACGT
			AGGAGGAGCAGGC	GCCC		



		TCCTCCTCGTCCG	CGGG	
		TCCT_		
GAM1295	KIAA0285	3'	GGAACAGGCTGCTCCTTCT	29019 G AC G
			AGGAGGAGCAG CC GT CC	
			TCTTCCTCGTC GG CA GG	
			_ A_ A	
GAM1295	KIAA0322	5'	GGGGCACGTGCGCCCCC	92753 A AGCA _
			GG GG GGC CACGTGCCCC	
			CC CC CCG GTGCACGGGG	
			_ _ _ C	
GAM1295	KIAA0450	5'	GGCCGCCTCACCTGCTCCCCCT	27642 A CCA_ T
			AGG GGAGCAGG CG GCC	
			TCC CCTCGTCC GC CGG	
			C ACTCC _	
GAM1295	KIAA0513	3'	GGGCACTGCTCTCCTCCT	28367 CA CAC
			AGGAGGAG GGC GTGCCC	
			TCCTCCTC TCG CACGGG	
			_ T_	
GAM1295	KIAA0632	3'	TGGGGCACTGCTCGTGCTCC	31428 G AG CAC
			GGAG AGC GC GTGCCCCA	
			CCTC TCG CG CACGGGGT	
			G CT T_	
GAM1295	KIAA0978	3'	GCCATGCCTGCTCCTGCC	70481 _ CACGT
			GG AGGAGCAGGC GC	
			CC TCCTCGTCCG CG	
			G TAC_	
GAM1295	KIAA1028	3'	GCACACTTGGCTACTCTTCCT	91939 CA C_
			AGGAGGAG GGCCA GTGC	
			TCCTTCTCTCGGT CACG	
			A_ TCA	
GAM1295	KIAA1037	3'	TGGAGCACCCCTCGCTCCTCT	30437 _ CCAC C
			GGAGGAGC AGG GTGC CCA	
			TCTCCTCG TCC CACG GGT	
			C _ _ A	
GAM1295	KIAA1055	3'	GGGACGGAGCCAACTCCTCCT	66065 CA CA G
			AGGAGGAG GGC CGT CCC	
			TCCTCCTC CCG GCA GGG	
			AA AG _	
GAM1295	KIAA1171	3'	CACCATTGCCTGCTCCTCC	87978 CAC_
			GGAGGAGCAGGC GTG	

			CCTCCTCGTCCG	CAC		
			TTAC			
GAM1295	KIAA1388	5'	GCAGCCGCTCCTCT	93579	A	CACG
			GGAGGAGC GGC	TGC		
			TCTCCTCG CCG	ACG		
			— ———			
GAM1295	KIAA1538	3'	ATGTCTAACCTGCTCCCCT	71530	A	CC__
			AGG GGAGCAGG	ACGT		
			TCC CCTCGTCC	TGTA		
			— AATC			
GAM1295	KIAA1655	5'	GGGCTCCAACTCCTCCT	66621	CA	CCACGT
			AGGAGGAG GG	GCCC		
			TCCTCCTC CC	CGGG		
			AA T_____			
GAM1295	KIAA1753	3'	GGGCAGGCCCTGCTCCCCCT	64886	A	_ ACG
			AGG GGAGCAGG CC	TGCCC		
			TCC CCTCGTCC GG	ACGGG		
			C C _____			
GAM1295	KIAA1813	5'	TGGAGCCTCCACTTGCCCCTCC	70313	A	CCACGT C
		T	AGGAGG GCAGG	GC CCA		
			TCCTCC CGTTC	CG GGT		
			C ACCTC_ A			
GAM1295	KIAA1862	3'	GGGAGCCTCTCCTCCT	68929	C	CACGTG
			AGGAGGAG AGGC	CCC		
			TCCTCCTC TCCG	GGG		
			— A_____			
GAM1295	KIAA1904	3'	GGATGGTCTGGGCCTGCTCCTC	73493	A	T _
		CT	AGGAGGAGCAGGCC	CG GCC CC		
			TCCTCCTCGTCCGG	GT TGG GG		
			_ C TA			
GAM1295	KIAA1958	3'	GGTGTGGCCTGCCCTCC	81910	A	GT
			GGAGG GCAGGCCAC	GCC		
			CCTCC CGTCCGGTG	TGG		
			— ———			
GAM1295	KRTHB5	3'	GCAGCCCCCTCCTCCT	9654	CA	CACG
			AGGAGGAG GGC	TGC		
			TCCTCCTC CCG	ACG		
			CC _____			
GAM1295	LANCL2	5'	GCGCGCGGCCTCGCTCCTCCT	37999	_	A
			AGGAGGAGC AGGCC	CGTGC		

			TCCTCCTCG TCCGG GCGCG		
			C C		
GAM1295	LASP1	3'	TAGGTGGCCGCTCCTCC 20461	A	G
			GGAGGAGC GGCCAC TG		
			CCTCCTCG CCGGTG AT		
			- G		
GAM1295	MGC10902	3'	ACGTGCCTGCTTCCCCT 47546	A	C
			AGG GGAGCAGGC ACGT		
			TCC CTTCGTCCG TGCA		
			C -		
GAM1295	MGC11257	3'	TGGGGCATGCTGGCTCCTCC 50374	A	CAC
			GGAGGAGC GGC GTGCCCCA		
			CCTCCTCG TCG TACGGGGT		
			G -		
GAM1295	MGC15827	3'	GGGGCCTCCTCTCCTCCT 51806	C	CCACGT
			AGGAGGAG AGG GCCCC		
			TCCTCCTC TCC CGGGG		
			- TC -		
GAM1295	MGC16703	5'	GGGCACGTAGCCCTCT 73103	CA	C
			GGAG GGC ACGTGCCC		
			TCTC CCG TGCACGGG		
			- A		
GAM1295	MGC16703	5'	GGGGCCAGGCCCGTCTCCTCC 73104	- A	ACGT
			GGAGGAG C GGCC GCCCC		
			CCTCCTC G CCGG CGGGG		
			T C AC -		
GAM1295	MGC2605	3'	TGGGGCACACGGGGCCTCCC 50221	AGC	AC -
			GG AGGCC GTGCCCCA		
			CC TCCGG CACGGGGT		
			C - GGCA		
GAM1295	MGC3047	3'	GGAGTCCCACTCCTCCT 50361	CA	CCACGT C
			AGGAGGAG GG GC CC		
			TCCTCCTC CC TG GG		
			AC - A		
GAM1295	MGC5457	3'	GTGTAAACCCTCTCCTCCT 50947	C	C -
			AGGAGGAG AGG CAC		
			TCCTCCTC TCC GTG		
			- CAAAT		
GAM1295	MIG-6	5'	GGGGCAGCCGCCGCTCCTCC 38489	A	CACG
			GGAGGAGC GGC TGCCCC		

			CCTCCTCG CCG ACGGGG		
			_ CCG_		
GAM1295 MRPL24	3'	TGGGGCAGAGCAGCTCCTCC	73510	AG	CACG
		GGAGGAGC GC TGCCCCA			
		CCTCCTCG CG ACGGGGT			
		A_ AG_			
GAM1295 MYLE	3'	GGAGCGCACCTGCTTCCCC	25816	A	CCAC C
		GG GGAGCAGG GTGC CC			
		CC CTTCGTCC CGCG GG			
		C A_ A			
GAM1295 MYLE	3'	GGCCTACCTGCTCCCCT	25817	A	CCACGT
		AGG GGAGCAGG GCC			
		TCC CCTCGTCC CGG			
		_ ATC_			
GAM1295 NECL1	3'	CGCAGGGCCGCCCTCC	41025	A A	AC
		GGAGG GC GGCC GTG			
		CCTCC CG CCGG CGC			
		C _ GA			
GAM1295 NECL1	3'	GTGGCTGCCCTCCT	41026	A	G
		AGGAGG GCAG CCAC			
		TCCTCC CGTC GGTG			
		C _			
GAM1295 NRM	3'	GGGGCTCCCTGCTCTCCC	92026	AG	CCACGT
		GG GAGCAGG GCCCC			
		CC CTCGTCC CGGGG			
		CT CT_			
GAM1295 NRM	3'	GGGGCTCCCTGCTCTCCC	97765	AG	CCACGT
		GG GAGCAGG GCCCC			
		CC CTCGTCC CGGGG			
		CT CT_			
GAM1295 NRM	3'	GGGGCTCCCTGCTCTCCC	97891	AG	CCACGT
		GG GAGCAGG GCCCC			
		CC CTCGTCC CGGGG			
		CT CT_			
GAM1295 NXN	3'	ACTCAGCCTTCTCCTCCT	42415	C	CAC
		AGGAGGAG AGGC GT			
		TCCTCCTC TCCG CA			
		T ACT			
GAM1295 OBTP	3'	CGGGCCGCGCTCCTCC	34245	A_	A
		GGAGGAGC GGCC CG			

			CCTCCTCG CCGG GC		
			CG _		
GAM1295	PAK6	3'	GGACTTGCCTGCCTCCTCCT 39409	_	CAC G
			AGGAGGAG CAGGC GT CC		
			TCCTCCTC GTCCG CA GG		
			C TT_ _		
GAM1295	PDE4DIP	3'	GGAAAGGTTGGCCTGTCCCCCT 95439	A AG	CGT _
			AGG GG CAGGCCA GCC CC		
			TCC CC GTCCGGT TGG GG		
			_ CT _ _ AAA		
GAM1295	PDZ-GEF1	3'	CACCTCATCTGCTCCTTC 26494	CCAC	
			GGAGGAGCAGG GTG		
			CTTCCTCGTCT CAC		
			ACTC		
GAM1295	PP1665	3'	TGAAGCAACTCTGCTCTTCCT 47922	CCACG CC	
			AGGAGGAGCAGG TGC CA		
			TCCTTCTCGTCT ACG GT		
			CA_ _ AA		
GAM1295	PPFIA4	3'	GGGCTTAAAGCCCGCTGCTCCT 70328	G A	CACGT
			AGGAG AGC GGC GCCC		
			TCCTC TCG CCG CGGG		
			G C AAATT		
GAM1295	PPM1A	5'	GGACGCAGCCCGGCTCCTCC 40659	A_ CA	G
			GGAGGAGC GGC CGT CC		
			CCTCCTCG CCG GCA GG		
			GC AC _		
GAM1295	PRO1866	5'	ACGTTACTTGCTCCTCCT 37550	CC	
			AGGAGGAGCAGG ACGT		
			TCCTCCTCGTTC TGCA		
			AT		
GAM1295	PTPRU	3'	TGGGGGCACACTGACTGTCCTCC 55692	G	GCCAC
			GGAGGA CAG GTGCCCCA		
			CCTCCT GTC CACGGGGT		
			_ AGTCA		
GAM1295	PTPRU	3'	TGGGGGCACACTGACTGTCCTCC 55698	G	GCCAC
			GGAGGA CAG GTGCCCCA		
			CCTCCT GTC CACGGGGT		
			_ AGTCA		
GAM1295	PTPRU	3'	TGGGGGCACACTGACTGTCCTCC 19119	G	GCCAC
			GGAGGA CAG GTGCCCCA		

			CCTCCT GTC CACGGGGT		
			_ AGTCA		
GAM1295	RAB10	5'	CCCCGAGCCGCTCCTCC 85175	A CA T	
			GGAGGAGC GGC CG GC		
			CCTCCTCG CCG GC CG		
			_ A_ C		
GAM1295	RNPC1	3'	GGGCACGTGGGCGGCTTCCT 33991	A_ AGG	
			AGGAGG GC CCACGTGCCC		
			TCCTTC CG GGTGCACGGG		
			GG _		
GAM1295	SEMA4B	5'	GGGACACCGTCGCTCCTGCT 69038	G A CAC C	
			AG AGGAGC GGC GTG CCC		
			TC TCCTCG CTG CAC GGG		
			G _ C_ A		
GAM1295	STK25	3'	GGGCAGCTCTGCCTCCTCCT 21052	_ _ CACG	
			AGGAGGAG CAG GC TGCCC		
			TCCTCCTC GTC CG ACGGG		
			C T _		
GAM1295	T1A-2	5'	GGGGCTCCTGCTCCCACC 21356	A_ CCACGT	
			GG GGAGCAGG GCCCC		
			CC CCTCGTCC CGGGG		
			AC T_		
GAM1295	TNFRSF19L	3'	CATGTGCCTGCCCTCC 51773	A C	
			GGAGG GCAGGC ACGTG		
			CCTCC CGTCCG TGTAC		
			C _		
GAM1295	TOMM34	3'	TGTGGCTGCTCCTCCT 22337	G	
			AGGAGGAGCAG CCACG		
			TCCTCCTCGTC GGTGT		
			-		
GAM1295	TRIP3	3'	GGAACCTGCCTGCTCCCTCT 78219	GA CAC G	
			AG GGAGCAGGC GT CC		
			TC CCTCGTCCG CA GG		
			TC TC_ A		
GAM1295	TTY14	3'	GGCCTCGAGCCTGCTCCGCCT 49189	A CA T_	
			AGG GGAGCAGGC CG GCC		
			TCC CCTCGTCCG GC CGG		
			G A_ TC		
GAM1295	VPS4A	3'	ATGGGGCACACAGTGGACACTG 25101	G_ _	
			CTCTTCCT AGCAG CCAC GTGCCCA T		

		TCGTC GGTG CACGGGGT A		
		ACA ACA III		
GAM1295	WBSCR20A 5'	GGGGTGGCCTGCCCCTCC 49654	A	ACGT
		GGAGG GCAGGCC GCCC		
		CCTCC CGTCCGG TGGGG		
		C ____		
GAM1295	ZFP100 5'	GGGACTTGTCCTCCTCCTCCT 70056	C C C G	
		AGGAGGAG AGG CA GT CCC		
		TCCTCCTC TCC GT CA GGG		
		C T T _		
GAM1295	ZNF282 3'	GGGAAGCTGCTGGCCTGGCCCT 89216	AG	C _ _
	CCT	AGGAGG CAGGCCA GT GC CCC		
		TCCTCC GTCCGGT CG CG GGG		
		CG _ T AA		
GAM1295	LOC112885 3'	TGGGGCACACAGTCTCCCCC 56532	A AGC	CAC
		GG GG AGGC GTGCCCCA		
		CC CC TCTG CACGGGGT		
		_ CC_ ACA		
GAM1295	LOC115051 3'	GGAAGCCTGCTCCCCT 60040	A	CACGTG
		AGG GGAGCAGGC CC		
		TCC CCTCGTCCG GG		
		_ AA ____		
GAM1295	LOC115399 3'	GGGCGGCCCGTCCCCTCCT 73435	A_ A	ACGT
		AGGAGG GC GGCC GCCC		
		TCCTCC TG CCGG CGGG		
		CC C ____		
GAM1295	LOC115757 3'	GGGGCAGTCCGCTCCTCC 73577	A	CACG
		GGAGGAGC GGC TGCCCC		
		CCTCCTCG CTG ACGGGG		
		C ____		
GAM1295	LOC116071 3'	CACCACCCTCTGCTCCTCCT 56623		CCAC_
		AGGAGGAGCAGG GTG		
		TCCTCCTCGTCT CAC		
		CCCAC		
GAM1295	LOC118472 3'	GGACGGCCTGTCTCCTCCT 73916	_	AC G
		AGGAGGAG CAGGCC GT CC		
		TCCTCCTC GTCCGG CA GG		
		T _ _		
GAM1295	LOC121457 5'	GGCGGCCACGTCTGCTCCCC 74071	A	CC _ _
	T	AGG GGAGCAGG ACGTG CC CC		

		TCC CCTCGTCC TGCAC GG GG		
		C _ C C		
GAM1295	LOC124930 3'	GGCACGGCCTGGTCCCCCT 74359	A G	AC
		AGG GGA CAGGCC GTGCC		
		TCC CCT GTCCGG CACGG		
		C G _		
GAM1295	LOC130355 5'	GGGCGGGACCCGCTCCTCC 74931	A _	ACG
		GGAGGAGC GG CC TGCCC		
		CCTCCTCG CC GG GCGGG		
		C A _		
GAM1295	LOC136319 5'	GGCAGCCTAACCCTCCT 75259	AGC	CACG
		AGGAGG AGGC TGCC		
		TCCTCC TCCG ACGG		
		CAA _		
GAM1295	LOC138399 5'	GGAAGTGCCTGCTCCCACT 75329	GA	C GTG
		AG GGAGCAGGC AC CC		
		TC CCTCGTCCG TG GG		
		AC _ AA_		
GAM1295	LOC139673 3'	GGAGGCTGCCAGCCCCTCCT 75977	A A	CACGT _
		AGGAGG GC GGC GCC CC		
		TCCTCC CG CCG CGG GG		
		C A T _ A		
GAM1295	LOC139770 3'	GGACACATGACCTAGTTTCTTC 75389	_ C C _	
	T	AGGAGGAGC AGG CA GTG CC		
		TCTTCTTTG TCC GT CAC GG		
		A A A A		
GAM1295	LOC144519 5'	ACATGCCTGCTCCCCCT 76863	A	CAC
		AGG GGAGCAGGC GT		
		TCC CCTCGTCCG CA		
		C TA_		
GAM1295	LOC144866 5'	TGGGGAGGAGCCTGGCCCCTCC 83207	A _	CACGTG
	T	AGGAGG GC AGGC CCCCA		
		TCCTCC CG TCCG GGGGT		
		C G AGGA_		
GAM1295	LOC145195 3'	GCCTGGCCTGCTCCTCTT 83272	C	
		AGGAGGAGCAGGCCA GT		
		TTCTCCTCGTCCGGT CG		
		C		
GAM1295	LOC145919 3'	TGAGGCAGCAAGACCAGCCCCT 77572	A A	CCACG_ C
	CCT	AGGAGG GC GG TGCC CA		



	TCCTCC CG CC	ACGG GT	
	C A AGAACG	A	
GAM1295 LOC147004 3'	GGACCTCACTCCCAGCTCCTCC	83902	A CCAC CC__
T	AGGAGGAGC GG GTG CC		
	TCCTCCTCG CC CAC GG		
	A CT__ TCCA		
GAM1295 LOC147229 5'	TGTGGCCTGCTCCCC	78324	A
	GG GGAGCAGGCCACG		
	CC CCTCGTCCGGTGT		
	—		
GAM1295 LOC148697 3'	GTGCAGCCTGCTCCCTCC	78931	_ CAC TG
	GGAGG AGCAGGC G C		
	CCTCC TCGTCCG C G		
	C A__ GT		
GAM1295 LOC149372 5'	GGGGCAGGCCACCCTCCT	79327	AGCA ACG
	AGGAGG GGCC TGCCCC		
	TCCTCC CCGG ACGGGG		
	CAC_ _		
GAM1295 LOC149386 5'	GCTGGCCCCTCCTCCT	84406	CA C
	AGGAGGAG GGCCA GT		
	TCCTCCTC CCGGT CG		
	C_ _		
GAM1295 LOC150378 5'	CAGTGTGGCCCAGTCCTCC	79741	GCA _
	GGAGGA GGCCACG TG		
	CCTCCT CCGGTGT AC		
	GAC G		
GAM1295 LOC151736 5'	TGAAGCTTGTTCCTCTCCTCC	82606	C CC T CC
T	AGGAGGAG AGG ACG GC CA		
	TCCTCCTC TCC TGT CG GT		
	_ CT T AA		
GAM1295 LOC152426 5'	GGACAGCCATCCTCCT	85717	GCA CACG C
	AGGAGGA GGC TG CC		
	TCCTCCT CCG AC GG		
	A_ _ A		
GAM1295 LOC152765 5'	GGCCTTCAGCCTGCTCTCCT	80660	G CACGT
	AGGAG AGCAGGC GCC		
	TCCTC TCGTCCG CGG		
	_ ACTTC		
GAM1295 LOC157254 5'	GGAGCCTTTGCCTGCTCCTCCT	81387	CACGT C
	AGGAGGAGCAGGC GC CC		

	TCCTCCTCGTCCG CG GG	
	TTTC_ A	
GAM1295 LOC158377 5'	CGAGGCCAGCTCCTCCT 86793	A_ A
	AGGAGGAGC GGCC CG	
	TCCTCCTCG CCGG GC	
	AC A	
GAM1295 LOC158972 3'	GGTCTCGTCCCGCCCCTCCT 86955	A A CC T_
	AGGAGG GC GG ACG GCC	
	TCCTCC CG CC TGC TGG	
	C C _ TC	
GAM1295 LOC159199 5'	GTGCCTGCTCCTCCT 82185	C
	AGGAGGAGCAGGC AC	
	TCCTCCTCGTCCG TG	
	-	
GAM1295 LOC161753 3'	TGGGGCACTCACTGCCCTC 82297	A GCCAC
	GAGG GCAG GTGCCCCA	
	CTCC CGTC CACGGGGT	
	C ACT_	
GAM1295 LOC163782 5'	GGAGCCACCGGCCTCCTCCTCC 82158	C AC _ C
T	AGGAGGAG AGGCC GTG C CC	
	TCCTCCTC TCCGG CAC G GG	
	C C_ CA	
GAM1295 LOC166316 5'	GGCACACTTTCTGCTCCTCTT 87260	CCAC
	AGGAGGAGCAGG GTGCC	
	TTCTCCTCGTCT CACGG	
	TTCA	
GAM1295 LOC196746 3'	GGGCTGGGCCTGCTCCCCC 87512	A A T
	GG GGAGCAGGCC CG GCCC	
	CC CCTCGTCCGG GT CGGG	
	C _ _	
GAM1295 LOC196812 3'	GTGGCCACTCCTCCT 89575	CA
	AGGAGGAG GGCCAC	
	TCCTCCTC CCGGTG	
	A_	
GAM1295 LOC196890 3'	TGGGGCACCCCTGACCCTCC 89652	AG CCAC
	GGAGG CAGG GTGCCCA	
	CCTCC GTCC CACGGGGT	
	CA C_	
GAM1295 LOC200531 3'	GGCGCCCTGCTCTTCC 88823	CCAC
	GGAGGAGCAGG GTGCC	

CCTTCTCGTCC CGCGG

GAM1295 LOC200734 3' ACATGGCCTGCTCCCC 88856 A C  
GG GGAGCAGGCCA GT  
|| ||||| ||  
CC CCTCGTCCGGT CA

— A  
GAM1295 LOC200734 3' ACATGGCCTGCTCCCC 88857 A C  
GG GGAGCAGGCCA GT  
|| ||||| ||  
CC CCTCGTCCGGT CA

— A  
GAM1295 LOC200779 5' ACCTGCCTGCTCGCTCCT 88872 — CAC  
AGGAG GAGCAGGC GT  
|||| ||||| ||  
TCCTC CTCGTCCG CA  
G TC\_

GAM1295 LOC200782 5' GGGACTCTGGCCTGCCCTACC 89508 \_ A C\_ G  
GG AGG GCAGGCCA GT CCC  
|| || ||||| || |||  
CC TCC CGTCCGGT CA GGG  
A C CT \_

GAM1295 LOC201242 3' GTACCCTGCTCCCCCT 87361 A CCAC  
AGG GGAGCAGG GTGC  
|| ||||| |||  
TCC CCTCGTCC CATG  
C —

GAM1295 LOC202126 3' GGGGCCTCCTGTTCCCTCCT 90316 CCACGT  
AGGAGGAGCAGG GCCCC  
||||||| |||||  
TCCTCCTTGTCC CGGGG  
TC\_

GAM1295 LOC202518 5' TGGCCCGGCTCCTCCT 87487 A\_  
AGGAGGAGC GGCCA  
||||||| |||||  
TCCTCCTCG CCGGT  
GC

GAM1295 LOC203339 3' GTACAGCCCTCTCCTCCT 90548 CA CAC  
AGGAGGAG GGC GTGC  
||||||| || |||||  
TCCTCCTC CCG CATG  
TC A\_

GAM1295 LOC206372 5' GGAGGTGCGGGGCTGCTCCCG 89531 A\_ A TG \_  
CC GG GGAGCAGGCC CG CC CC  
|| ||||| || |||  
CC CCTCGTCCGG GC GG GG  
GC G GT A

GAM1295 LOC219513 3' GGAGAACAGCCTGCTCCACCT 94332 A CAC GCC  
AGG GGAGCAGGC GT CC  
|| ||||| || ||

	TCC CCTCGTCCG CA GG	
	A A__ AGA	
GAM1295 LOC220370 3'	CACACCTGCTCCTCC 92825	CCAC
	GGAGGAGCAGG GTG	
	CCTCCTCGTCC CAC	
	A__	
GAM1295 LOC221119 3'	TGGGGGACACCCCTCCTCCT 93443	CA CCAC G
	AGGAGGAG GG GT CCCC	
	TCCTCCTC CC CA GGGGT	
	CC A__ G	
GAM1295 LOC221596 5'	GGCATGCCTGCTTCCCCT 91979	A CAC
	AGG GGAGCAGGC GTGCC	
	TCC CTTCGTCCG TACGG	
	C ____	
GAM1295 LOC221882 3'	GGCCCTGTTCTCCTC 92500	CCACGT C
	GGAGGAGCAGG GC C	
	CCTCCTTGTC CG G	
	____ A	
GAM1295 LOC222031 3'	GGCTGGCCCCCTCCTCCT 94026	CA CGT
	AGGAGGAG GGCCA GCC	
	TCCTCCTC CCGGT CGG	
	CC ____	
GAM1295 LOC222166 5'	GGGGTGCCGGCCGCTCCTCCT 94097	A AC TG
	GGAGGAGC GGCC G CCCC	
	CCTCCTCG CCGG C GGGG	
	_ C_ GT	
GAM1295 LOC253148 3'	GGGAGGCCCGGCTCCTCCT 96879	A_ ACGTG
	AGGAGGAGC GGCC CCC	
	TCCTCCTCG CCGG GGG	
	GC A__	
GAM1295 LOC254911 5'	GGAGACGCCGGCTGCTCCTCCT 97054	G A_ GC
	GGAGGAGCAG CC CGT CC	
	CCTCCTCGTC GG GCA GG	
	_ CC GA	
GAM1295 LOC255187 5'	ACTGGCCTGCCACCCCT 97181	A A_ C
	AGG GG GCAGGCCA GT	
	TCC CC CGTCCGGT CA	
	_ AC _	
GAM1295 LOC255520 5'	GGCAGCTCCTGCTCCCCCT 95861	A CCACG
	AGG GGAGCAGG TGCC	

		TCC CCTCGTCC	ACGG		
		C	TCG__		
GAM1295	LOC256789	3'	GGCGCCAGCCTGCTCCACC	97449	A CAC
			GG GGAGCAGGC GTGCC		
			CC CCTCGTCCG CGCGG		
			A AC_		
GAM1295	LOC256815	5'	GGCAGCCTGCTCTCCT	94709	G CACG
			AGGAG AGCAGGC TGCC		
			TCCTC TCGTCCG ACGG		
			— —		
GAM1295	LOC256980	3'	GGCCTGGCCTGCCCTCC	95221	A CGT
			GGAGG GCAGGCCA GCC		
			CCTCC CGTCCGGT CGG		
			— C_		
GAM1295	LOC257619	5'	TGGCCCGGCTCCTCCT	97812	A_
			AGGAGGAGC GGCCA		
			TCCTCCTCG CCGGT		
			GC		
GAM1295	LOC51087	3'	GTACCCTGCTCCCCCT	32014	A CCAC
			AGG GGAGCAGG GTGC		
			TCC CCTCGTCC CATG		
			C —		
GAM1295	LOC51117	3'	GGGGCCTGGCCTACCTCC	32093	AGC CGT
			GGAGG AGGCCA GCCCC		
			CCTCC TCCGGT CGGGG		
			A_ C_		
GAM1295	LOC51279	3'	CACAGACCGCTCCTCCT	33308	A CCAC
			AGGAGGAGC GG GTG		
			TCCTCCTCG CC CAC		
			— AGA_		
GAM1295	LOC51619	3'	CACTACCGCCGCTCCTCC	32016	A CAC_
			GGAGGAGC GGC GTG		
			CCTCCTCG CCG CAC		
			C CCAT		
GAM1295	LOC59346	5'	CGCGCGGCCCGCCCTCC	41275	A A A
			GGAGG GC GGCC CGTG		
			CCTCC CG CCGG GCGC		
			— C C		
GAM1295	LOC90381	3'	TGGAACAGCGTCCGCTCCTCCT	62547	A CC GCC_
			AGGAGGAGC GG ACGT CCA		

TCCTCCTCG CC TGCG GGT  
 \_ \_ ACAA  
 GAM1295 LOC91464 3' TGGAGGACAGGGCCTGCTCCCC 66146 A AC G \_  
 T AGG GGAGCAGGCC GT CC CCA  
 ||| ||||| || |||  
 TCC CCTCGTCCGG CA GG GGT  
 \_ GA \_ A  
 GAM1295 LOC93268 3' TACAGCCTGCTCCCC 71886 A CAC  
 GG GGAGCAGGC GTG  
 || ||||| |||  
 CC CCTCGTCCG CAT  
 \_ A \_  
 GAM1296 CSNK1G2 3' GGCCCAGCCCTGCAGGT 7170 AAC ACTT  
 ACCTGTAG CTG GGCC  
 ||||| ||| |||  
 TGGACGTC GAC CCGG  
 CC\_ \_  
 GAM1296 PCDH11X 3' CAATCATATTCTACAG 27238 CC C  
 CTGTAGAA TGA TTG  
 ||||| ||| |||  
 GACATCTT ACT AAC  
 AT \_  
 GAM1296 SFTPA2 3' GGTCAGGCTCTCCAGGTG 22650 T A  
 CACCTG AGA CCTGACT  
 ||||| ||| |||||  
 GTGGAC TCT GGACTGG  
 C C  
 GAM1296 TBX5 5' CCAAGTCCTATAGGTG 3956 AACCT  
 CACCTGTAG GACTTGG  
 ||||| |||||  
 GTGGATATC CTGAACC  
 \_  
 GAM1296 TBX5 5' CCAAGTCCTATAGGTG 54888 AACCT  
 CACCTGTAG GACTTGG  
 ||||| |||||  
 GTGGATATC CTGAACC  
 \_  
 GAM1296 ZNF132 3' GCCAAGTCAAACCTTCATGCAG 12826 \_ CC\_  
 CTGTA GAA TGACTTGGC  
 ||||| ||| |||||  
 GACGT CTT ACTGAACCG  
 A CAA  
 GAM1296 C9orf14 5' GCCAAGTCCATCTAAAGTG 86676 CTG ACCT  
 CAC TAGA GACTTGGC  
 ||| ||| |||||  
 GTG ATCT CTGAACCG  
 AA\_ AC\_  
 GAM1296 DKFZP434J037 3' GCCCGGTCAAGGCTCTCAG 48213 T A T  
 CTG AGA CCTGACT GGC  
 ||| ||| ||||| |||

			GAC TCT GGA	CTG CCG		
			_ C C			
GAM1296	ELOVL2	3'	GCCTAGGTTATACAG	34959	G	ACTT
			CTGTA AACCTG	GGC		
			GACAT TTGGAT	CCG		
			A			
GAM1296	FLJ11996	3'	TTAGGTGCCTACAGGT	46447	A_	
			ACCTGTAG ACCTGA			
			TGGACATC TGGATT			
			CG			
GAM1296	FLJ13265	3'	GCCAGAACTTTACAGGTG	45926		ACCTGAC
			CACCTGTAGA	TTGGC		
			GTGGACATTT	GACCG		
			CAA			
GAM1296	FLJ20038	5'	CCAAGTCAGAACTGCG	34402	AAC	
			TGTAG CTGACTTGG			
			GCGTC GACTGAACC			
			AA			
GAM1296	FLJ20972	3'	GCCAAGTCAGTTCCTGGTG	46725	TGTA	C
			CACC GAAC TGACTTGGC			
			GTGG CTTG ACTGAACCG			
			TC			
GAM1296	KIAA0061	3'	GCCAAGTTCTACATGTG	68292	C	ACCTG
			CAC TGTAGA	ACTTGGC		
			GTG ACATCT	TGAACCG		
			T			
GAM1296	KIAA0141	3'	CGGGAGTTCAGGTTCCCAAG	28732	GTA	_ GG
			CT GAACCTGA CTT CCG			
			GA CTTGGACT GAG GGC			
			ACC T			
GAM1296	KIAA1260	3'	GTCAGGTTGCACAGGTG	60029	AG	
			CACCTGT AACCTGAC			
			GTGGACA TTGGA	CTG		
			CG			
GAM1296	KIAA1301	3'	GCCTATGGGTTTACAGG	66342	A	ACTT
			CCTGTAGA CCTG	GGC		
			GGACATTT GGGT	CCG		
			_ AT			
GAM1296	KIAA1485	3'	GGCTGCCAGGCTCTGCAGG	89262	A	ACT
			CCTGTAGA CCTG	TGGCC		

GGACGTCT GGAC GTCGG  
C C\_\_  
GAM1296 KIAA1546 3' CAGGCAAACACCTACAGGT 67904 AACC\_ A  
ACCTGTAG TG CTTG  
||||||| || ||||  
TGGACATC AC GGAC  
CACAA \_  
GAM1296 KIAA1643 3' CACCTCAGGTTCCCAGGTG 64548 TA CT  
CACCTG GAACCTGA TG  
||||| ||||| ||  
GTGGAC CTTGGACT AC  
C\_ CC  
GAM1296 MGC10981 3' CTGAGTCGATCCCACAGGTG 51017 A\_ ACC TG  
CACCTGT GA TGA CT G  
||||| || |||| |  
GTGGACA CT GCTGA C  
CC A\_ GT  
GAM1296 MGC11324 3' AGGCAGAACCTACAGGTG 51164 AAC A  
CACCTGTAG CTG CTT  
||||||| ||| |||  
GTGGACATC GAC GGA  
CAA \_  
GAM1296 MOST2 5' CGGCCAAGCCTGTGCCTACGGT 39682 T A\_ CTGA  
G CACC GTAG AC CTTGGCCG  
|||| ||| || |||||  
GTGG CATC TG GAACCGGC  
\_ CG TCC\_  
GAM1296 PADI3 3' CGGCCAAGCTCCTGC 32657 AACCT \_  
GTAG GA CTTGGCCG  
|||| || |||||  
CGTC CT GAACCGGC  
\_\_\_\_\_ C  
GAM1296 phospho1 5' CAGAGTCCCTACAGGTG 82367 A\_ \_  
CACCTGTAG AC CTG  
||||||| || |||  
GTGGACATC TG GAC  
CC A  
GAM1296 RAB3D 3' TGGCTGCCAGGTTCCCTCAGG 15010 TA ACT  
CCTG GAACCTG TGGCCG  
|||| ||||| |||||  
GGAC CTTGGAC GTCGGT  
TC C\_  
GAM1296 LOC122955 5' GCTGTCAAGTTCTACAG 75585 C TT  
CTGTAGAAC TGAC GGC  
||||||| ||| |||  
GACATCTTG ACTG TCG  
\_ \_  
GAM1296 LOC149386 5' CAAGTCAGGTCCACA 84404 A A  
TGT GA CCTGACTTG  
||| || |||||



ACA CT GGACTGAAC  
 C \_  
 GAM1296 LOC150197 5' GCCAGGTCCTACGG 79598 AACCT  
 CTGTAG GACTTGGC  
 ||||| |||||  
 GGCATC CTGGACCG  
 \_\_\_\_\_  
 GAM1296 LOC151878 5' CTAGTTCAGACTCTAAGG 80374 G AC C  
 CCT TAGA CTGA TTGG  
 ||| ||| ||| |||  
 GGA ATCT GACT GATC  
 \_ CA T  
 GAM1296 LOC153146 5' GCCAGAGCCTACAGGT 85929 AAC GAC  
 ACCTGTAG CT TTGGC  
 ||||| || |||||  
 TGGACATC GA GACCG  
 C\_ \_  
 GAM1296 LOC221931 3' AAGTTGCAGGTTCTTCAG 93992 T \_  
 CTG AGAACCTG ACTT  
 ||| ||||| |||  
 GAC TCTTGGAC TGAA  
 T GT  
 GAM1296 LOC254848 5' CGGCAGGCACAGGTTCTCCA 97090 T A\_ G  
 TG AGAACCTG CTTG CCG  
 || ||||| ||| |||  
 AC TCTTGGAC GGAC GGC  
 C AC \_  
 GAM1297 RCN1 3' ATTGAAATTTACCTTGTA 11270 ATAT  
 TACAAG AATTTAGT  
 ||||| |||||  
 ATGTTC TTAAAGTTA  
 CACT  
 GAM1297 RCN1 3' ATTGAAATTTACCTTGTA 59629 ATAT  
 TACAAG AATTTAGT  
 ||||| |||||  
 ATGTTC TTAAAGTTA  
 CACT  
 GAM1297 C20orf36 3' CATTTACTTGCTGATATTTTGT 36795 AATTTC  
 A TACAAGATAT AGTAAATG  
 ||||| |||||  
 ATGTTTATA TCATTTAC  
 GTCGT\_  
 GAM1297 PARVA 3' TTA CTTAATGTTATATCTTG 36656 TTC\_  
 CAAGATATAAT AGTAA  
 ||||| |||  
 GTTCTATATTG TCATT  
 TAAT  
 GAM1297 STAF65(gamma) 3' CTGATGCAAAATATATCTTGTA 29435 ATT\_\_\_\_  
 TACAAGATATA TCAG  
 ||||| |||

ATGTTCTATAT AGTC  
 AAAACGT  
 GAM1297 LOC158230 3' TGCTGAAGTCTCTTGTA 81802 TATA  
 TACAAGA ATTTTCAGTA  
 ||||| |||||  
 ATGTTCT TGAAGTCGT  
 C\_\_  
 GAM1297 LOC221773 3' CATTTACTGAAATGCGCTCTTT 91040 C TATA  
 A AAGA ATTTTCAGTAAATG  
 |||| |||||  
 A TTCT TAAAGTCATTTAC  
 T CGCG  
 GAM1298 ADH1B 3' CTTAGACATAAAGTAAAAT 72644 C CAC  
 ATTT ACTTT TGTCTGAG  
 ||| |||| |||||  
 TAAA TGAAA ACAGATTC  
 A T\_\_  
 GAM1298 AHR 3' ATCTCAGATGTTAAATAAATG 7875 CAC C T  
 CATTT TTT AC GTCTGAGAT  
 |||| ||| |||||  
 GTAAA AAA TG TAGACTCTA  
 TA\_ T \_  
 GAM1298 FDFT1 3' TAGGAAAGTGAAATG 15518 A  
 CATTTCACTTTC CTG  
 ||||| |||||  
 GTAAAGTGAAAG GAT  
 -  
 GAM1298 JTB 3' ATCTCAGACAGTGAAAGTGAAA 21959  
 TG CATTTCACTTTCACTGTCTGAGAT  
 ||||| ||||| |||||  
 GTAAAGTGAAAGTGACAGACTCTA  
 GAM1298 KLF4 3' TCCCAGACAGTGGATATG 14891 CT A  
 CA TTCAGTGTCTG GA  
 || ||||| ||  
 GT AGGTGACAGAC CT  
 AT C  
 GAM1298 PHYH 3' ACAGTAAAAGTGAAAT 20608 C  
 ATTTCACTTT ACTGT  
 ||||| |||||  
 TAAAGTGAAA TGACA  
 A  
 GAM1298 PKD2 3' TCCAGGTTGAAAGTGAAA 60096 CTG A  
 TTTCAGTTTCA TCTG GA  
 ||||| |||||  
 AAAGTGAAAGT GGAC CT  
 T\_\_ \_  
 GAM1298 WRN 3' GGGCAGTGAAAATGAAA 5098 C  
 TTTCA TTTCAGTGTCT  
 |||| |||||

			AAAGT AAAGTGACGGG		
			A		
GAM1298	ZNF216	3'	ATCTGCACAGCAAAGTGAAA	20017	CA CTG
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1298	CG012	5'	CTCACTCTGAAAGTGAA	83218	CT CT
			TTCACCTTCA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1298	EIF2C2	3'	ATCTTCTGAGAGTGAAAG	71946	G T_
			CTTTCACCT TC GAGAT		
			GAAAGTGA AG TTCTA		
			G TC		
GAM1298	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT	45802	ACTTTCACCT
	G		CATTTTC GTCTGAGAT		
			GTAAAG CAGACTCTA		
			AAACATTT_		
GAM1298	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG	45281	CTT
			CATTTCA TCACTGTCTGAGAT		
			GTAAAGT AGTGACAGACTCTA		
			C_		
GAM1298	KIAA0984	3'	TTTGTCCAGTGAAAATGAA	65534	C TC
			TTCA TTTCACTG TGAG		
			AAGT AAAGTGAC GTTT		
			A CT		
GAM1298	KLHL6	3'	ATCTCAGAGCAGGAAA	55299	A _
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1298	NIR3	3'	GCAGTGAAAGTGCAAT	66242	T
			ATT CACTTTCACTGT		
			TAA GTGAAAGTGACG		
			C		
GAM1298	PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA	53598	CA G
			TTCACCTT CT TCTGAGAT		
			AAGTGAAA GG AGACTCTA		
			CC G		
GAM1298	PP35	3'	ATCTCAGACTGAAA	22814	CT
			TTTCA GTCTGAGAT		

AAAGT CAGACTCTA

GAM1298 PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148 TCAC C\_  
CATTTCACCTT TGT TGAG  
||||||| ||| |||  
GTAAAGTGAA ACG ACTC  
TA\_\_ TT

GAM1298 SEP15 3' TCCTACAGTAAGAGTGAAA 14934 C CT  
TTTCACTTT ACTGT GA  
||||||| ||||| ||  
AAAGTGAGA TGACA CT  
A TC

GAM1298 SFXN2 3' CTCAGGGGAAAAAAGTGAAA 73941 CACTG  
TTTCACTTT TCTGAG  
||||||| |||||  
AAAGTGAAA GGA CTC  
AAAGG

GAM1298 LOC149703 3' ATCTCAGACAGCCGTTTGAAA 84647 ACTTTCA  
TTTC CTGTCTGAGAT  
||| |||||  
AAAG GACAGACTCTA  
GTTTGCC

GAM1298 LOC154007 3' ATCTCAAACCCTTTAGTGAAA 81015 TTCACT C  
TTTCACT GT TGAGAT  
||||| || |||||  
AAAGTGA CA ACTCTA  
TTTCC\_ A

GAM1298 LOC155004 3' TCATTTAAGTGAAAGGAAA 81226 A GTC\_  
TTTC CTTTCACT TGA  
||| ||||| |||  
AAAG GAAAGTGA ACT  
\_ ATTT

GAM1298 LOC222134 5' ACAGTGAAGTGAAATG 94136 T  
CATTTCACCTT CACTGT  
||||||| |||||  
GTAAAGTGAA GTGACA

GAM1299 ABCD2 3' CTCTCTGGTTTAGTGCTCTTTT 17699 \_ CTTC  
GTTA GACGGAAGAG ATTGAGCTA  
||||||| |||||  
TTGTTTTCTC TGATTTGGT  
G CTCTCA

GAM1299 ABCG5 3' GAAGTGGTTTATAGTCC 42358 AGAGAT  
GGA TGAGCTACTTC  
||| |||||  
CCT ATTTGGTGAAG  
GAT\_\_

GAM1299 ADD1 3' AGCTCAGTTTCTTTTCA 26376 C  
TGA GGAAGAGATTGAGCT  
||| |||||

ACT TTTTCTTTGACTCGA

GAM1299 ADD1 3' AGCTCAGTTTCTTTTCA 26372 C  
TGA GGAAGAGATTGAGCT  
||| |||||  
ACT TTTTCTTTGACTCGA

GAM1299 AKAP2 3' GCTTTAATCTTTCTGTCA 23263 A \_  
TGACGGA GAGATTGA GC  
||||| ||||| ||  
ACTGTCT TTCTAATT CG

GAM1299 AKAP2 3' GGAGTGGAGTGAGAATTTCTTT 23264 GAG\_\_  
T GGAAGAGATT CTACTTC  
||||| |||||  
TTTTCTTTAA GGTGAGG  
GAGTGA

GAM1299 ARHGEF7 3' GACGTCCTCAGTTCTTTCTGTT 14004 AG CTACTTC  
GACGGAAG ATTGAG  
||||| |||||  
TTGTCTTT TGA CTC  
CT CTGCAGG

GAM1299 ASH1 3' AGCTTAGGTTTTCTGTCA 37498 A  
TGACGGAAGAG TTGAGCT  
||||| |||||  
ACTGTCTTTT GATTCTG  
G

GAM1299 ASPH 3' GGGGTAGCTCTTGATTTTGTTA 50619 GAGATT  
TGACGGAA GAGCTACTTC  
||||| |||||  
ATTGTTTT CTCGATGGGG  
AGTT\_\_

GAM1299 ASPH 3' GGGGTAGCTCTTGATTTTGTTA 50631 GAGATT  
TGACGGAA GAGCTACTTC  
||||| |||||  
ATTGTTTT CTCGATGGGG  
AGTT\_\_

GAM1299 ATP2B1 3' ATTGATAGTTTAATTTCTGCTG 8063 A CTTC  
TT GACGG AGAGATTGAGCTA  
||||| |||||  
TTGTC TCTTTAATTTGAT  
G AGTTAA

GAM1299 BAT1 5' GTTTAGCTCTTCTGTGA 16163 A  
TGACGGAAGAG TTGAGC  
||||| |||||  
ATTGTCTTCTC GATTTG

GAM1299 BDP1 3' AGACAGTCTTGTCTGTT 37362 \_ AG  
GACGGAA GAGATTG CT  
||||| ||||| ||

		TTGTCTT TTCTGAC GA		
		G A_		
GAM1299 BPAG1	3'	GTATAATTTTTTTGTCA 31431	A	
		TGACGGAAGAGATTG GC		
		ACTGTTTTTTTAAT TG		
		A		
GAM1299 C1orf6	3'	GCATTCGGTTCTTCTGTCA 39282	G	_
		TGACGGAAGA ATTGA GC		
		ACTGTCTTCT TGGCT CG		
		_ TA		
GAM1299 CA3	3'	GGCACCAGTTTTTCTGTTA 17737	A	A_
		TGACGGA GAGATTG GCT		
		ATTGTCT TTTTGAC CGG		
		_ CA		
GAM1299 CARD4	3'	GGGCAGTCTTTTGTGTCA 20332	G	AG
		TGACG AAGAGATTG CT		
		ACTGT TTTTCTGAC GG		
		G G_		
GAM1299 CASP10	3'	AGATAGTCTCATTCTGTCA 52096	_	AG
		TGACGGAA GAGATTG CT		
		ACTGTCTT CTCTGAT GA		
		A A_		
GAM1299 CASP10	3'	AGATAGTCTCATTCTGTCA 52114	_	AG
		TGACGGAA GAGATTG CT		
		ACTGTCTT CTCTGAT GA		
		A A_		
GAM1299 CAST	3'	CTTAATTTTTTTTGTTA 8255		
		TGACGGAAGAGATTGAG		
		ATTGTTTTTTTAATTC		
GAM1299 CDH17	3'	TTGTAGTCAGTTTTGTTTGTTA 14510	A	G TTC
		TGACGGA GAGATTGA CTAC		
		ATTGTTT TTTTGA CT GATG		
		G _ TTG		
GAM1299 CDKN2D	3'	GGTTCAGTTTCTTCTGCG 54381	A	
		TG CGGAAGAGATTGAGCT		
		GC GTCTTCTTTGACTTGG		
		_		
GAM1299 CDKN2D	3'	GGTTCAGTTTCTTCTGCG 8398	A	
		TG CGGAAGAGATTGAGCT		

GC GTCTTCTTTGACTTGG

GAM1299 CEBPA 3' GAGTGGTTTGGGGTCGCCG 15164 AA GA TG  
CGG GA T AGCTACTT  
||| || | |||||  
GCC CT G TTGGTGAG  
G\_ GG GT

GAM1299 CIS4 3' AGTTGAATTTTCTGTT 14876 A G  
GACGGA GAGATT AGCT  
||||| ||||| |||  
TTGTCT TTTTAA TTGA  
G

GAM1299 CKTSF1B1 3' GAGGTAGTTTAGAACTCTCTGC 25368 A A A\_  
A TG CGGA GAG TTGAGCTACTTC  
|| ||| || |||||  
AC GTCT CTC GATTTGATGGAG  
\_ \_ AA

GAM1299 CLCN4 3' TTCGGTCTTTTCTGCG 8446 A  
TG CGGAAGAGATTGAG  
|| |||||  
GC GTCTTTTCTGGCTT

GAM1299 CLN5 3' GGAGTGTTTTGTTTCTGTT 21429 AGATT T  
GACGGAAG GAGC ACTTC  
||||| ||| |||||  
TTGTCTTT TTTG TGAGG  
GTT\_\_ \_

GAM1299 COG3 5' GAAGTGCCCCAGGTCTCTCTGT 48697 A GA\_  
C GACGGA GAGATT GCTACTTC  
||||| ||||| |||||  
CTGTCT CTCTGG CGGTGAAG  
ACC

GAM1299 CRH 3' GAAGTCACTCAATTGTTTTGT 5663 A CT  
T GACGGAAG GATTGAG ACTTC  
||||| ||||| |||||  
TTGTTTTT TTAAGTCT TGAAG  
G AC

GAM1299 CXorf6 3' CTTAATCTCTTTTGCG 18514 A  
TG CGGAAGAGATTGAG  
|| |||||  
GC GTTTTCTCTAATTC

GAM1299 DGKB 3' GAAGTGTTTAAACAGTTTTTGT 92532 AGA  
TA TGACGGAAG TTGAGCTACTTC  
||||| |||||  
ATTGTTTTT AATTTGGTGAAG  
GAC

GAM1299 DMC1 5' GAAGTGATTATTTTCTGTT 22973 AT GC  
GACGGAAGAG TGA TACTTC  
||||| ||| |||||

			TTGTCTTTTT ATT GTGAAG	
			__ A_	
GAM1299 DUSP4	5'	GGAGTCTGGATTTGTTTGT	54056	G G CT
		GACGGAA AGATT AG ACTTC		
		TTGTTTT TTTAG TC TGAGG		
		G G _		
GAM1299 DYRK2	3'	GAGTAGCTCAGACCTGTT	13127	AAGAGA
		GACGG TTGAGCTACTT		
		TTGTC GACTCGATGAG		
		CA__		
GAM1299 DYRK2	3'	GAGTAGCTCAGACCTGTT	21391	AAGAGA
		GACGG TTGAGCTACTT		
		TTGTC GACTCGATGAG		
		CA__		
GAM1299 ECM2	3'	GGGGTAGCTTTCATTTCTTCC	7331	T_
		GGAAGAGAT GAGCTACTTC		
		CCTTCTTTA TTCGATGGGG		
		CT		
GAM1299 EDN1	3'	GCTTTGGTCTCTTCTTCA	8729	C TG_
		TGA GGAAGAGAT A GC		
		ACT TCTTCTCTG T CG		
		T GT T		
GAM1299 EN2	3'	GAGTGGCTGCTTCTG	7464	AGATTG
		CGGAAG AGCTACTT		
		GTCTTC TCGGTGAG		
		G__		
GAM1299 FCAR	3'	GTTTAATTTCTTCCTTCA	8857	C
		TGA GGAAGAGATTGAGC		
		ACT CCTTCTTTAATTTG		
		T		
GAM1299 FCAR	3'	GTTTAATTTCTTCCTTCA	55752	C
		TGA GGAAGAGATTGAGC		
		ACT CCTTCTTTAATTTG		
		T		
GAM1299 FCAR	3'	GTTTAATTTCTTCCTTCA	55763	C
		TGA GGAAGAGATTGAGC		
		ACT CCTTCTTTAATTTG		
		T		
GAM1299 FCAR	3'	GTTTAATTTCTTCCTTCA	55774	C
		TGA GGAAGAGATTGAGC		



		ACT CCTTCTTTAATTTG		
		T		
GAM1299 FCAR	3'	GTTTAATTTCTTCCTTCA 55785	C	
		TGA GGAAGAGATTGAGC		
		ACT CCTTCTTTAATTTG		
		T		
GAM1299 FE65L2	3'	GGGGTGTCTTCTCTTTTCTTG 55679	C	TT C
		A GGAAGAGA GAG TACTTC		
		G TCTTTTCT TTC GTGGGG		
		T C_ T		
GAM1299 FE65L2	3'	GGGGTGTCTTCTCTTTTCTTG 55684	C	TT C
		A GGAAGAGA GAG TACTTC		
		G TCTTTTCT TTC GTGGGG		
		T C_ T		
GAM1299 FOG2	3'	GAAGATGGCAATTTTTTTC 23876		GA _
		GGAAGAGATT GCTA CTTC		
		CTTTTTTTAA CGGT GAAG		
		_ A		
GAM1299 FOXF1	3'	GCTTCAGCCTCTTCTGTTA 7569		AT _
		TGACGGAAGAG TGA GC		
		ATTGTCTTCTC ACT CG		
		CG T		
GAM1299 GALNT7	3'	GTTTACATCTTTTTTGTGTT 33802		_
		GACGGAAGAGAT TGAGC		
		TTGTTTTTCTA ATTTG		
		C		
GAM1299 GARS	5'	GGGGTGGCTTGACGCACTTCTG 8988		AGA_ TG
	T	ACGGAAG T AGCTACTTC		
		TGTCTTC A TCGGTGGGG		
		ACGC GT		
GAM1299 GCLM	3'	GGCAGATATTCTTTCGTCA 9025		_ GA
		TGACGGAAGAG ATT GCT		
		ACTGCTTCTT TAG CGG		
		A A_		
GAM1299 GNS	3'	CGGAGTGGCTGTCTCTGGTCTC 9083		_____
	TTCC	AAGAGATTG AGCTACTTC	G	
		TTCTCTGGT TCGGTGAGG	C	
		CTCTG		
GAM1299 GOCAP1	3'	GAGGTACATCTTTTTTCC 42701		TT GC
		GGAAGAGA GA TACTTC		

			CCTTTTTT CT ATGGAG		
			T_ AC		
GAM1299	GPR30	3'	GGGGTGGTTCAGTCACTGCTTG 7696	A_ A	
	TT		GACGG AG GATTGAGCTACTTC		
			TTGTT TC CTGACTTGGTGGGG		
			CG A		
GAM1299	GRINL1A	3'	TCGCTCATTTCATATTTTTCTG 69519	_____	TACTTC
	TT		CGGAAGAGAT TGAGC		
			GTCTTTTTTA ACTCG		
			TACTT CTT		
GAM1299	GRM1	3'	GAAGTGGTTTGAAAATTTGTTA 5914	AGAGA TG	
			TGACGGA T AGCTACTTC		
			ATTGTTT A TTGGTGAAG		
			AAA_ GT		
GAM1299	GRP58	3'	GGGGTATTTTCTAATTTTTTTT 17999	_ C_	
	GT		ACGGAAGAGATT GAG TACTTC		
			TGTTTTTTTTAA CTT ATGGGG		
			T TT		
GAM1299	HADHB	3'	GGTTGTTTTTGGTCTCTGTTGT 3940	A TG__ T TC	
	CA		TGACGG AGAGAT A GC ACT		
			ACTGTT TCTCTG T TG TGG		
			G GT TT T		
GAM1299	HIRA	3'	GGGGTGGGCGATTTCTTTTGT 12440	AG	
			ACGGAAGAGATTG CTACTTC		
			TGTTTCTTTAGC GGTGGGG		
			G_		
GAM1299	HUS1	3'	AGACGGTCTCATTCTGTCA 91099	_ AG	
			TGACGGAA GAGATTG CT		
			ACTGTCTT CTCTGGC GA		
			A A_		
GAM1299	ITCH	3'	GGAGTAGTGTTTTTTCTTTTA 48948	C TTGA	
			TGA GGAAGAGA GCTACTTC		
			ATT TCTTTTTT TGATGAGG		
			T TG__		
GAM1299	ITGAL	3'	AGTCCAGTCTCTCTG 9385	AG	
			CGGAAGAGATTG CT		
			GTCTTCTCTGAC GA		
			CT		
GAM1299	ITSN2	3'	GGAGTGGTTTGGTGACGCTGT 38973	AAGAG TG	
			ACGG AT AGCTACTTC		

			TGTC	TG	TTGGTGAGG		
			GCAG_	GT			
GAM1299	KCNJ10	3'	GAAGTGGCTTAGAAGGCCTCA	9536	C	AAGAGA	
			TGA GG	TTGAGCTACTTC			
			ACT CC	GATTCGGTGAAG			
			_	GGAA_			
GAM1299	KNSL2	3'	TAGTTTGGTTTTTTTT	73852	TG		
			GGAAGAGAT	AGCTA			
			TTTTTTTTG	TTGAT			
			GT				
GAM1299	LAMC1	3'	GGGGTGGTTTGGTTTGGTTTCC	9676	_	TG	
			GGAAG	AGAT AGCTACTTC			
			CCTTT	TTTG TTGGTGGGG			
			GG	GT			
GAM1299	LIMD1	3'	GTCTGTTTAATTTTTTTAGTT	26465	G	T_	
			GAC	GAAGAGATTGAGC AC			
			TTG	TTTTTTTAATTTG TG			
			A	TC			
GAM1299	LPP	5'	GAGGGAAGATCTTTTTCCTCA	18748	C	GAGCTA	
			TGA	GGAAGAGATT CTTC			
			ACT	CTTTTCTAG GGAG			
			C	AAG_			
GAM1299	LRP4	3'	GGGTGGCTCAGGCTGTTT	64443	G	A	
			GAA	AG TTGAGCTACTT			
			CTT	TC GACTCGGTGGG			
			G	G			
GAM1299	MAP3K1	3'	AGCTGATCTTTTTTTTCA	67813	C	G	
			TGA	GGAAGAGATT AGCT			
			ACT	TTTTTCTAG TCGA			
			-	-			
GAM1299	MBTPS1	3'	GAAGCAAAGCTATTTTTTTTGT	13703	TG	A_	
	CA		TGACGGAAGAGAT	AGCT CTTC			
			ACTGTTTTTTT	TA TCGA GAAG			
			_	AAC			
GAM1299	MFAP3	3'	TTCAGTTTTTCCGTCA	19809	A		
			TGACGGA	GAGATTGAG			
			ACTGCCT	TTTTGACTT			
			-				
GAM1299	MMP25	3'	GGCTGTTAACCTTTTCCGTT	42444	A	_	
			GACGGAAGAG	TTG AGCT			

		TTGCCTTTTC AAT TCGG	
		C TG	
GAM1299 MX2	3'	GGCCAAACTCTTCTGTCA 10149	A A
		TGACGGAAGAG TTG GCT	
		ACTGTCTTCTC AAC CGG	
		A _	
GAM1299 MYOG	3'	GGTGATTCTTTTGTTA 59347	GA
		TGACGGAAGAGATT GCT	
		ATTGTTTTCTTTAG TGG	
		—	
GAM1299 NAV2	3'	GGGTTTGT TTT TTTTGTCA 60160	T G
		TGACGGAAGAGAT GA CT	
		ACTGTTTTTTTG TT GG	
		T G	
GAM1299 NCALD	3'	GACGCCTTCAGCCTCTTTTGTC 49373	AT _ TACTTC
		GACGGAAGAG TGA GC	
		CTGTTTTCTC ACT CG	
		CG TC CAG	
GAM1299 NEURL	3'	GGGGTGGCTGCTGCTTCC 14861	AGATTG
		GGAAG AGCTACTTC	
		CCTTC TCGGTGGGG	
		GTCG_	
GAM1299 NFRKB	5'	AAGTCACTTCTTCTGTT 20491	GATTG CT
		GACGGAAGA AG ACTT	
		TTGTCTTCT TC TGAA	
		_____ AC	
GAM1299 NOTCH2	3'	AGGTGGTTTAGGGATTTTG 44312	GAGA
		CGGAA TTGAGCTACTT	
		GTTTT GATTGTTGGA	
		AGG_	
GAM1299 NOVA1	3'	AAGTGAAGTTTTTCTGTTA 21407	ATTGAGC
		TGACGGAAGAG TACTT	
		ATTGTCTTTT GTGAA	
		GAA_	
GAM1299 NOVA1	3'	AAGTGAAGTTTTTCTGTTA 10245	ATTGAGC
		TGACGGAAGAG TACTT	
		ATTGTCTTTT GTGAA	
		GAA_	
GAM1299 NPY1R	3'	GAAGTGGTTTGAGGTTTCTGTT 6179	AGA TG
		GACGGAAG T AGCTACTTC	

		TTGTCTTT A TTGGTGAAG		
		GG_ GT		
GAM1299 NR2F2	3'	GTTTGCTTAATTCCTTCTGTT 40665	_	T_ TTC
A		TGACGGAAG AGATTGAGC AC		
		ATTGTCTTC TTTAATTCG TG		
		C TT		
GAM1299 NR3C2	3'	GGGGCATTAAATTTCTTTTGTT 6133	_	_ ACTTC
A		TGACGGAAGAG ATTGA GCT		
		ATTGTTTTCTT TAATT CGG		
		A A GG		
GAM1299 NRAS	3'	GAAGTGGTTTGTAGACTCC 10272	AGAGAT	
		GGA TGAGCTACTTC		
		CCT GTTTGGTGAAG		
		CAGAT_		
GAM1299 NXT1	3'	GGTTGAACTCTTTTTTGTT 25115	_	G
		GACGGAAGAGA TT AGCT		
		TTGTTTTTCT AA TTGG		
		C G		
GAM1299 OPCML	3'	CGGGCTTCTTTTTGTTTTTTC 10344	TT_____	ACTTC
TGTTA		GAAGAGA GAGCT		
		CTTTTTT TTCGG		
		TGTTTTTC G CT		
GAM1299 PACE4	3'	GAAGAGATTAGTCTTCTGT 56350	G A	
		ACGGAAGAGATTGA CT CTTC		
		TGTCTTCTCTGATT GA GAAG		
		A _		
GAM1299 PAFAH1B1	3'	GAAGGAAAATCACTTCCGTTA 4727	A	GAGCTA
		TGACGGAAG GATT CTTC		
		ATTGCCTTC CTAA GAAG		
		A AAG_		
GAM1299 PATE	3'	GAAGTGGCTCAAGTCTTCTTG 56313	C	GA
		A GGAAGA TTGAGCTACTTC		
		G TCTTCT AACTCGGTGAAG		
		T G_		
GAM1299 PCDH11X	3'	CATTAGTTTTCTTCTGTT 52019	TTGA	CTTC
		GACGGAAGAGA GCTA		
		TTGTCTTCTTT TGAT		
		_____ TACA		
GAM1299 PCDH11X	3'	CATTAGTTTTCTTCTGTT 52041	TTGA	CTTC
		GACGGAAGAGA GCTA		

		TTGTCTTCTTT	TGAT		
		_____	TACA		
GAM1299	PCDH15	3'	GTAATTTTAATCTCTTTT	52337	C_
			GGAAGAGATTGAG	TAC	
			TTTTCTCTAATTT	ATG	
			TA		
GAM1299	PCMT1	3'	GGAGTGGTTTTTCTTTCTTG	18223	C TT
			A GGAAGAGA	GAGCTACTTC	
			G TCTTTTCT	TTGGTGAGG	
			T T_		
GAM1299	PCSK1	3'	AGTGGTTGTTTTGTCA	4770	G GATTGA
			TGACGGAA A	GCTACT	
			ACTGTTTT T	TGGTGA	
			G _____		
GAM1299	PER2	3'	GTCCTGTTTGGTTTTCTTCCGT	43039	_TG TACTTC
	T		GACGGAAGAGA T	AGC	
			TTGCCTTCTTT G	TTG	
			T GT TCCTG		
GAM1299	PIK3CG	3'	TTCAATTCTTTTGTCA	10590	A
			TGACGGAAGAG	TTGAG	
			ACTGTTTTCTT	AACTT	
			_____		
GAM1299	PLA2G1B	5'	GGTCATCTCAGTTTCTTTTCTC	6249	CG CT_ TC
	A		TGA GAAGAGATTGAG	ACT	
			ACT TTTCTTTGACTC	TGG	
			CT TAC		
GAM1299	PLDN	5'	GGGTGCGACAATCTCTTCTGTC	24745	A_ T C
			GACGGAAGAGATTG	GC ACTT	
			CTGTCTTCTCTAAC	CG TGGG	
			AG _		
GAM1299	PLS1	5'	AGATAGTCTTTTCTGTC	10656	AG
			GACGGAAGAGATTG	CT	
			CTGTCTTTTCTGAT	GA	
			A_		
GAM1299	PODXL	3'	TTTTTGCTTGATTTTTTTTTT	18247	CG TG TACTTC
	A		TGA GAAGAGAT	AGC	
			ATT TTTTTTA	TCG	
			TT GT TTTTG		
GAM1299	POLH	5'	TCCCTTCTCGGTTTCTCCGTC	21467	A CTACTTC
			GACGGA	GAGATTGAG	

			CTGCCT CTTTGGCTC		
			— TTCCCTA		
GAM1299	PRCP	3'	ATTGTTTTCAATTTCTTCTTTT 17277	C	CTACTTC
	A		TGA GGAAGAGATTGAG		
			ATT TCTTCTTTAACTT		
			T TTGTTAG		
GAM1299	PRCP	3'	GAAGTGAGAGCCATTTCTTTTG 17278	T A	—
	T		ACGGAAGAGAT G GCT ACTTC		
			TGTTTTCTTTA C CGA TGAAG		
			— GAG		
GAM1299	PTHR2	3'	GGAGTAGTTTATTACCTTCTAT 17306	CG	AGAT
	T		GA GAAG TGAGCTACTTC		
			TT CTTC ATTTGATGAGG		
			AT CATT		
GAM1299	PTPRK	5'	AGGTAGTTTGGCGACCGCG 11120	A	AAGAGA TG
			TG CGG T AGCTACTT		
			GC GCC G TTGATGGA		
			— AGC— GT		
GAM1299	PUM1	3'	AAAAATAGCTTGGTTTTATTTG 27957	A	TG CTTC
	TCA		TGACGGA GAGAT AGCTA		
			ACTGTTT TTTTG TCGAT		
			A GT AAAAAA		
GAM1299	PUM1	3'	GAAGTAAATTTTTTCTTTTG 27960	TT	GC
			CGGAAGAGA GA TACTTC		
			GTTTTCTTT TT ATGAAG		
			TT AA		
GAM1299	RANBP2	3'	GGGGTTTTGTTTCAAACCTTTTC 20766	A	CT—
	TGTCA		CGGAAGAG TTGAG ACTTC		
			GTCTTTTC AACTT TGGGG		
			A TGTTT		
GAM1299	RENT1	3'	TCGGTCAATTTAAGTTCTTTTG 11293	—	GCTACTTC
	TCA		CGGAAGA GATTGA		
			GTTTTCT TTAAC		
			TGAAT GG CTT		
GAM1299	RTN3	3'	GGCAAGTTTTTTTCTTCA 73902	C	GA
			TGA GGAAGAGATT GCT		
			ACT CTTTTTTTGA CGG		
			T A—		
GAM1299	SDPR	3'	AAAGTGATTCATTCTTTTTTG 16221	T	C C
	CA		TGACGGAAGAGA TGAG TACTT		

			ACTGTTTTTCT ACTT GTGAA		
			T A AA		
GAM1299	SEDL	3'	AAGTGTGTTGCTTCTGTCA 27310	AG TGA T	
			TGACGGAAG AT GC ACTT		
			ACTGTCTTC TG TG TGAA		
			GT ____ _		
GAM1299	SEDL	5'	GGCGCGGGTCTCTTCCGCG 27352	A GA_	
			TG CGGAAGAGATT GCT		
			GC GCCTTCTCTGG CGG		
			____ GCG		
GAM1299	SET7	3'	GAATGGCTTTGGTTTTTTTC 47636	TG_ CTTC	
			GGAAGAGAT A GCTA		
			CTTTTTTTG T CGGT		
			GT T AAG		
GAM1299	SFPQ	3'	GAAGTAGTTTGATGATTTGTT 17371	AGAG TG	
			GACGGA AT AGCTACTTC		
			TTGTTT TA TTGATGAAG		
			AG__ GT		
GAM1299	SLC13A2	5'	TTTGGTCCTTCTGTTA 14318	A TG	
			TGACGGAAG GAT AG		
			ATTGTCTTC CTG TT		
			____ GT		
GAM1299	SLC22A2	5'	GGGGTGGCTTACGCACTTCCTC 59537	C AGAT	
	A		TGA GGAAG TGAGCTACTTC		
			ACT CCTTC ATTCGGTGGGG		
			____ ACGC		
GAM1299	SMARCA2	3'	TGGCTTCTTTTGTCA 11784	GATTG	
			TGACGGAAGA AGCTA		
			ACTGTTTTCT TCGGT		
			_____		
GAM1299	SNCAIP	3'	AGTGTTTTTTCTGTCA 95919	TGA	
			TGACGGAAGAGAT GCT		
			ACTGTCTTTTTTG TGA		
			_____		
GAM1299	STAC	3'	GTCAGTTTGATTTATTTTGTTA 11995	G TG _	
			TGACGGAA AGAT AGCT AC		
			ATTGTTTT TTTA TTGA TG		
			A GT C		
GAM1299	STE	5'	GAAGTGGTCTCATCTTTTTTT 18295	AC T_	
	GCA		TG GGAAGAGAT GAGCTACTTC		



			AC TTTTCTA CTTGGTGAAG		
			GT CT		
GAM1299	TLL1	3'	GAAGTAGCTTTGTGTCTGTTA 24953	AGAGATT	
			TGACGGA GAGCTACTTC		
			ATTGTCT TTCGATGAAG		
			GTGT__		
GAM1299	TM7SF3	3'	GGAGTGGTTCAACAGTCTCTGG 59667	GA	__
	TG		CG AGAGAT TGAGCTACTTC		
			GT TCTCTG ACTTGGTGAGG		
			GG ACA		
GAM1299	TNFAIP1	3'	GTCTCAGTCTTTTTTGCCG 40924	A	_
			TG CGGAAGAGATTGAG C		
			GC GTTTTTCTGACTC G		
			C T		
GAM1299	TNFRSF10B	3'	GGAGTTTTTGGTCTTTTCTGTC 13875	TG CT	
			GACGGAAGAGAT AG ACTTC		
			CTGTCTTTTCTG TT TGAGG		
			GT T_		
GAM1299	TNFSF9	3'	AGATGGTCTTGTCTGTCA 13752	_	GAG
			TGACGGAA GAGATT CT		
			ACTGTCTT TTCTGG GA		
			G TA_		
GAM1299	TRPM1	3'	GGCTTAGTTTTTTCAGTT 10060	G	
			GAC GAAGAGATTGAGCT		
			TTG CTTTTTGATTCCG		
			A		
GAM1299	TRPM7	3'	AGCCAGTTTTTTTTTTTA 62125	CG	A
			TGA GAAGAGATTG GCT		
			ATT TTTTTTGAC CGA		
			TT _		
GAM1299	UBE2A	3'	GCTTCAGTTTTTCTGTT 12466	A	_
			GACGGA GAGATTGA GC		
			TTGTCT TTTTGA CT		
			_ T		
GAM1299	UBE2B	3'	TTAATCTTTTTCATCA 12478	C	
			TGA GGAAGAGATTGA		
			ACT CTTTTCTAATT		
			A		
GAM1299	WSX1	5'	GGGGTGGTTCGGCTTCCCGTT 16738	AA	A
			GACGG GAG TTGAGCTACTTC		

			TTGCC TTC GGCTTGGTGGGG		
			C_ _		
GAM1299	ABLM	3'	GGGGTAGTTTTCTATCTGTCA 9774	AG	TT
			TGACGGA AGA GAGCTACTTC		
			ACTGTCT TCT TTTGATGGGG		
			A_ _		
GAM1299	ABLM	3'	GGGGTAGTTTTCTATCTGTCA 22035	AG	TT
			TGACGGA AGA GAGCTACTTC		
			ACTGTCT TCT TTTGATGGGG		
			A_ _		
GAM1299	AK000009	3'	GCATTCAATTATTTCTGTTA 76999	A	_
			TGACGGAAG GATTGA GC		
			ATTGTCTTT TTAAC T CG		
			A TA		
GAM1299	AKAP10	3'	AGGTGGTTTGCTTTGTCC 23252	_	ATT
			GGA AGAG GAGCTACTT		
			CCT TTTC TTTGGTGGA		
			G G_		
GAM1299	AMSH	5'	GGTGGTTCCTTTCTT 21319	TT	
			AAGAGA GAGCTACT		
			TTCTTT CTTGGTGG		
			C_		
GAM1299	ARHE	3'	CTTGGTCTCTGTTGTTA 17713	A	TG
			TGACGG AGAGAT AG		
			ATTGTT TCTCTG TC		
			G GT		
GAM1299	ARL8	3'	GGCTGGCTCAATTTTCTTCTGT 93197	_	CTTC
	CA		TGACGGAAGAGA TTGAGCTA		
			ACTGTCTTCTTT AACTCGGT		
			T CGG		
GAM1299	B1	3'	AAGTAGTTGCCTTTGGTCA 27080	G	AGATTG
			TGAC GAAG AGCTACTT		
			ACTG TTTC TTGATGAA		
			G CG_		
GAM1299	BAL	5'	GAAGTAGCTCTCCAGCTTCCTT 48803	C	AGATT
	C		GA GGAAG GAGCTACTTC		
			CT CCTTC CTCGATGAAG		
			T GACCT		
GAM1299	BLP2	3'	GAAGTGGGAGTGTTTCTGTT 47117	AGA	GAG
			GACGGAAG TT CTACTTC		

TTGTCTTT AG GGTGAAG  
 GTG \_\_\_\_  
 GAM1299 BLP2 3' GAAGTGGGAGTGTTTCTGTT 54335 AGA GAG  
 GACGGAAG TT CTACTTC  
 ||||| || |||||  
 TTGTCTTT AG GGTGAAG  
 GTG \_\_\_\_  
 GAM1299 C11orf25 3' TTTAGTTTCTTTTTTCA 48648 CG  
 TGA GAAGAGATTGAG  
 || |||||  
 ACT TTTCTTTGATTT  
 TT  
 GAM1299 C1QTNF2 3' GAGGTGGAAATTTGTTTCTTTT 49127 CG TGAG\_\_  
 TTTA GA GAAGAGAT CTACTTC  
 || ||||| |||||  
 TT TTTCTTTG GGTGGAG  
 TT TTTAAA  
 GAM1299 C20orf100 3' GGCTGAGTCTCTTCCTCA 51814 C G  
 TGA GGAAGAGATT AGCT  
 || ||||| |||||  
 ACT CCTTCTCTGA TCGG  
 \_ G  
 GAM1299 C20orf64 3' GCCTCAGTTTCTTTTCTTA 53223 CG \_  
 TGA GAAGAGATTGAG C  
 || ||||| ||  
 ATT TTTCTTTGACTC G  
 CT C  
 GAM1299 C2orf7 3' GGAGTGTTTAAAGAGCTG 50301 AAGAGA  
 CGG TTGAGCTACTTC  
 || |||||  
 GTC AATTGGTGAGG  
 GAGA\_\_  
 GAM1299 C8orf17 5' GCTTCAATTTTTTCCCTTA 39603 C \_  
 TGA GGAAGAGATTGA GC  
 || ||||| ||  
 ATT CCTTTTTTAACT CG  
 C T  
 GAM1299 CDH24 3' GGCTTTTTGTTTTTTCTGTT 94931 TT\_\_  
 GACGGAAGAGA GAGCT  
 ||||| |||||  
 TTGTCTTTTTT TTCGG  
 TGTTT  
 GAM1299 CITED2 3' CTTGGTCTTTTTCGTT 20295 TG  
 GACGGAAGAGAT AG  
 ||||| ||  
 TTGCTTTTTCTG TC  
 GT  
 GAM1299 CLIC4 3' GAGGTAGCTTGCCATCTCTC 25635 A \_  
 GA GAGAT TGAGCTACTTC  
 || ||||| |||||

CT CTCTA GTTCGATGGAG  
 \_ CC  
 GAM1299 DCAMKL1 3' GAGGTCAGAGTGTCTTTCTGT 16409 TGAG \_  
 C GACGGAAGAGAT CT ACTTC  
 ||||| |||||  
 CTGTCTTTTGT GA TGGAG  
 TGA\_ C  
 GAM1299 DGKD 3' GGGTGGTTTGACCTCTTC 59408 A TG  
 GAAGAG T AGCTACTT  
 ||||| | |||||  
 CTTCTC A TTGGTGGG  
 C GT  
 GAM1299 DIS3 3' AACCTGTTTAATTTCTTTTGT 30224 TACTTC  
 ACGGAAGAGATTGAGC  
 |||||  
 TGTTTCTTTAATTTG  
 TCCAAA  
 GAM1299 DKFZP434O047 5' AGGAAGTCTCTTCTTCA 31501 C GAG  
 TGA GGAAGAGATT CT  
 || ||||| ||  
 ACT TCTTCTCTGA GA  
 \_ AG\_  
 GAM1299 DKFZP564D0462 3' GAGGTAGTGGGTTTTT 70497 GA  
 AAGAGATT GCTACTTC  
 ||||| |||||  
 TTTTTTGG TGATGGAG  
 G\_  
 GAM1299 DKFZP566J091 3' GGGGTGGTTTATTATTTTGCT 48126 A \_  
 G CGG AGAGAT TGAGCTACTTC  
 || ||||| |||||  
 GTC TTTTTA ATTTGGTGGGG  
 G TT  
 GAM1299 DKFZP586F1524 3' GGGGTGGTATAACTTTTCTTCA 31492 C A A  
 TGA GGAAGAG TTG GCTACTTC  
 || ||||| || |||||  
 ACT TCTTTTC AAT TGGTGGGG  
 \_ \_ A  
 GAM1299 DKFZp586G0123 5' GGCTGTTGATCTTTTCTGCA 95417 A TG \_  
 TG CGGAAGAGAT A GCT  
 || ||||| | |||  
 AC GTCTTTTCTA T CGG  
 \_ GT GT  
 GAM1299 DNAJA4 3' AGCGGGACCTCTTTGTCA 37752 A GA  
 TGACGGAAGAG TT GCT  
 ||||| || |||  
 ACTGTTTCTC AG CGA  
 C GG  
 GAM1299 EDR2 3' GGTTAACTCTTCCGTT 60496 ATTG  
 GACGGAAGAG AGCT  
 ||||| |||

		TTGCCTTCTC TTGG	
		AA__	
GAM1299 EML4	5'	GAAGTGGTTCGGGCGGCCGCG 38810	A AAGAGA
		TG CGG TTGAGCTACTTC	
		GC GCC GGCTTGGTGAAG	
		_ GGCG__	
GAM1299 FACTP140	3'	AATAAACTGGGTTTTTTTGT 23234	G CTACTTC
		GACGGAAGAGATT AG	
		TTGTTTTTTTGG TC	
		G AAATAAG	
GAM1299 FENS-1	3'	GTGTTTGATTTTTTTG 40442	TG T
		CGGAAGAGAT AGC AC	
		GTTTTTTTGA TTG TG	
		GT _	
GAM1299 FKBP9	3'	AGCTGATCTTTTCTG 94060	G
		CGGAAGAGATT AGCT	
		GTCTTTTCTAG TCGA	
		-	
GAM1299 FLJ10120	3'	AGCAAAGCAGTCTCTTT 35830	A__
		GGAAGAGATTG GCT	
		TTTTCTCTGAC CGA	
		GAAA	
GAM1299 FLJ10139	3'	GAGGTAGAGATTTTTTTC 35840	GAG
		GGAAGAGATT CTACTTC	
		CTTTTTTTAG GATGGAG	
		A__	
GAM1299 FLJ10154	3'	GAAGTGGTTTTTTGTTTTGT 35854	AGATT
		GACGGAAG GAGCTACTTC	
		TTGTTTT TTTGGTGAAG	
		GTTT_	
GAM1299 FLJ10350	3'	GGGTGGGTCCTCTCTGTT 95509	A ATT G
		GACGGA GAG GA CTACTT	
		TTGTCT CTC CT GGTGGG	
		- _ _ G	
GAM1299 FLJ10560	3'	GGCAGAGTCTTGTTCTGTC 36282	_ GA
		GACGGAA GAGATT GCT	
		CTGTCTT TTCTGA CGG	
		G GA	
GAM1299 FLJ10702	3'	TTTTGTTTCTTTTGTTA 36445	T
		TGACGGAAGAGAT GAG	

	ATTGTTTTCTTTG TTT	
	T	
GAM1299 FLJ11011 3'	GCAATCTTGTCTTTTGTTA 36976	T_ _
	TGACGGAAGAGAT GA GC	
	ATTGTTTTCTTTG CT CG	
	TT AA	
GAM1299 FLJ11222 5'	AAGGGGTATTTTCGTCA 37170	GATTGA TA
	TGACGGAAGA GC CTT	
	ACTGCTTTTT TG GAA	
	A_ _ GG	
GAM1299 FLJ11996 3'	GGGTAGCTCTATTTCTT 46441	T
	AAGAGAT GAGCTACTT	
	TTCTTTA CTCGATGGG	
	T	
GAM1299 FLJ12577 3'	GAGGTGCCTATTTTTCTG 48157	TGA T
	CGGAAGAGAT GC ACTTC	
	GTCTTTTTTA CG TGGAG	
	TC_ _	
GAM1299 FLJ13448 3'	GAGGTAGTTTGGCTGCTCTTTC 47137	A_ TG
	GGAAGAG T AGCTACTTC	
	CTTTCTC G TTGATGGAG	
	GTC GT	
GAM1299 FLJ14642 3'	GAAGTGGTTATGTATCTTCTG 51500	GATTG
	CGGAAGA AGCTACTTC	
	GTCTTCT TTGGTGAAG	
	ATGTA	
GAM1299 FLJ20170 3'	TTAATTTCTTCTTTCA 34673	C
	TGA GGAAGAGATTGA	
	ACT TCTTCTTAATT	
	T	
GAM1299 FLJ20190 3'	GGAGTTTGTGAGTTTTTTTC 34705	GCT
	GGAAGAGATTGA ACTTC	
	CTTTTTTTGACT TGAGG	
	GTT	
GAM1299 FLJ20272 5'	TTCACTTCTTTTGTT 34813	T
	GACGGAAGAGA TGAG	
	TTGTTTTCTTT ACTT	
	C	
GAM1299 FLJ20507 3'	TCGCCCATTAGGTCTCTTTTG 35302	_ A TACTTC
TT	CGGAAGAGAT TG GC	

		GTTTTCTCTG	AC CG		
		GATTT C	CTT		
GAM1299	FLJ20507	3'	TCGCCCATTAGGTCTCTTTTG	60237	_____ A TACTTC
		TT	CGGAAGAGAT	TG GC	
		GTTTTCTCTG	AC CG		
		GATTT C	CTT		
GAM1299	FLJ20984	3'	GAAGTGGCTGCTTTCTTTTG	44909	TTG
			CGGAAGAGA	AGCTACTTC	
		GTTTTCTTT	TCGGTGAAG		
		CG_			
GAM1299	FLJ21791	3'	GGTACAATTCTTTTGTTA	61440	A A
			TGACGGAAGAG	TTG GCT	
		ATTGTTTTCTT	AAC TGG		
		_ A			
GAM1299	FLJ22002	3'	GAAGTAGTAACTCTTCTATTA	45772	CG A GA
			TGA GAAGAG	TT GCTACTTC	
		ATT	CTTCTC	AA TGATGAAG	
		AT	_ A_		
GAM1299	FLJ22029	3'	GGTGTTTGGTTTTTTTG	46332	TG T
			CGGAAGAGAT	AGC ACT	
		GTTTTTTTG	TTG TGG		
		GT	_		
GAM1299	FLJ22055	3'	AGTAATCTCTTCCCTTA	45491	C GA
			TGA GGAAGAGATT	GCT	
		ATT	CCTTCTCTAA	TGA	
		C	_		
GAM1299	FLJ22202	3'	GGGGTAGTCTCAATTTCTGTCA	45991	AGA _
			TGACGGA	GATTGAG CTACTTC	
		ACTGTCT	TTAACTC	GATGGGG	
		_	T		
GAM1299	FLJ22393	3'	GGTAGCTCGGCTGCCG	47061	AAG A
			CGG	AG TTGAGCTACT	
		GCC	TC GGCTCGATGG		
		G_ _			
GAM1299	FLJ22833	5'	GGAGTGGTTCGCCTTTTTTTC	43106	T_
			GGAAGAGA	TGAGCTACTTC	
		CTTTTTT	GCTTGGTGAGG		
		CC			
GAM1299	FLJ23027	3'	GCAAAATGTTTGGTTTTTCTC	49931	C TG TACTTC
		TTA	TGA GGAAGAGAT	AGC	

		ATT TCTTTTTTG TTG	
		C GT TAAACGG	
GAM1299 FLJ23590	3'	GAGGCTTTAGCTCTCTTTTGTC 45020	TT__ ACTTC
	A	TGACGGAAGAGA GAGCT	
		ACTGTTTTCTCT TTCGG	
		CGAT AG	
GAM1299 FLJ30058	3'	GGGGATGCTTGGTCTCTTG 58640	TG TA
		CGGAAGAGAT AGC CTTC	
		GTCTTCTCTG TCG GGGG	
		GT TA	
GAM1299 FLJ31952	5'	TCAGTTGCTTTTGTTA 58389	AG
		TGACGGAAG ATTGA	
		ATTGTTTTC TGACT	
		GT	
GAM1299 GK001	3'	GGGGTGGTGGGTATTTTTGTT 39497	G GA
		GACGGAAGA ATT GCTACTTC	
		TTGTTTTTT TGG TGGTGGGG	
		A G_	
GAM1299 GMEB2	5'	AGTAGCCCTTCTGTT 24727	AGATTGA
		GACGGAAG GCTACT	
		TTGTCTTC CGATGA	
		C_____	
GAM1299 GREB1	3'	GAAGTAGCTCATTTTCTCTT 27871	T__
		AAGAGA TGAGCTACTTC	
		TTCTCT ACTCGATGAAG	
		TTT	
GAM1299 GTF2H3	3'	AACCACTGTCAGGCTCTTTTG 7701	A GCTACTTC
	CA	TGACGGAAGAG TTGA	
		ACTGTTTTCTC GACT	
		G GTCACCAAG	
GAM1299 HNRPA0	3'	GGGTAGTTTACTTTGTTGT 22322	A AT
		ACGG AGAG TGAGCTACTT	
		TGTT TTTC ATTTGATGGG	
		G _	
GAM1299 HSA250839	3'	TGGCCTTTTTTGTC 37261	ATTGA
		TGACGGAAGAG GCTA	
		ACTGTTTTTTC CGGT	
		_____	
GAM1299 HSPC067	3'	GGGTGGTTTTTTCTTT 26335	TT
		GAAGAGA GAGCTACTT	



TTTCTTT TTTGGTGGG  
 T\_  
 GAM1299 HSU53209 3' GAAGTAGTTCAGTCATGTCA 25239 GAAGA  
 TGACG GATTGAGCTACTTC  
 |||| |||||  
 ACTGT CTGACTTGATGAAG  
 A\_\_\_\_  
 GAM1299 IL17D 3' GGTCCCTTGATCTTTTCT 56282 TG CT  
 GGAAGAGAT AG ACT  
 ||||| || ||  
 TCTTTTCTA TC TGG  
 GT C\_  
 GAM1299 KDELR2 3' CTTAACTCTTTTGTT 22452 A  
 GACGGAAGAG TTGAG  
 ||||| ||||  
 TTGTTTCTC AATTC  
 -  
 GAM1299 KIAA0026 3' GTTCTTAGTCTTTTTC 24409 CT  
 GGAAGAGATTGAG AC  
 ||||| ||  
 CTTTTTCTGATTC TG  
 T\_  
 GAM1299 KIAA0063 3' GGGGTGGCTTGTTTCTTC 29637 TG  
 GAAGAGAT AGCTACTTC  
 ||||| |||||  
 CTTCTTTG TCGGTGGGG  
 GT  
 GAM1299 KIAA0121 3' AATTAGTTTATTTTGTCA 72652 AGAT C  
 TGACGGAAG TGAGCTA TT  
 ||||| ||||| ||  
 ACTGTTTT ATTTGAT AA  
 T  
 GAM1299 KIAA0286 3' CTTAGTCTTTTGTGTT 68325 G  
 GACG AAGAGATTGAG  
 ||| |||||  
 TTGT TTTTCTGATTC  
 -  
 GAM1299 KIAA0356 3' GGGTTTGCTGGTCTCTCTGTC 66195 A G T\_  
 GACGGA GAGATT AGC ACTT  
 |||| |||| || ||||  
 CTGTCT CTCTGG TCG TGGG  
 - - TT  
 GAM1299 KIAA0377 3' AGCCAGCAACCTTTTCTGTT 27793 A A\_  
 GACGGAAGAG TTG GCT  
 ||||| || ||  
 TTGTCTTTTC AAC CGA  
 C GAC  
 GAM1299 KIAA0418 3' GAAGTGGTTCATTATTTT 27555 GAT  
 GGAAGA TGAGCTACTTC  
 |||| |||||

		TTTTTT ACTTGGTGAAG		
		ATT		
GAM1299	KIAA0469	3' GTTTTCTCAGTCTTTTTTGCG 29346	A	CT_
		TG CGGAAGAGATTGAG AC		
		GC GTTTTTTCTGACTC TG		
		— TTT		
GAM1299	KIAA0532	3' GGAGAGAGGGTCTCATTCTGTC 70775	—	GAG A
	A	TGACGGAA GAGATT CT CTTC		
		ACTGTCTT CTCTGG GA GAGG		
		A GA_ _		
GAM1299	KIAA0537	3' AGGTGGGCTCTTCTGCCA 29242	A	ATTGAG
		TG CGGAAGAG CTACTT		
		AC GTCTTCTC GGTGGA		
		C G_ _ _		
GAM1299	KIAA0546	3' GTTTTTCTGTCTCTTTTGTT 71312	T	CT
		GACGGAAGAGAT GAG AC		
		TTGTTTTCTCTG CTT TG		
		T TT		
GAM1299	KIAA0553	3' GAAGGGTATATTTTCTTCTGTT 69891	T	A A
		GACGGAAGAGA TG GCT CTTC		
		TTGTCTTCTTT AT TGG GAAG		
		T A _		
GAM1299	KIAA0560	3' GAAGGAACTGTTTCTTCTGTT 61503	T	CTA
	A	TGACGGAAGAGAT GAG CTTC		
		ATTGTCTTCTTTG TTC GAAG		
		_ AAG		
GAM1299	KIAA0625	3' GTCATCTTCAGTATTTTCTGTC 30480	G	CTACTTC
	A	TGACGGAAGA ATTGAG		
		ACTGTCTTTT TGA CTT		
		A CTACTGG		
GAM1299	KIAA0682	3' GCCTTGGTCTTTTTTGTC 29367	TG	_
		GACGGAAGAGAT AG C		
		CTGTTTTTCTG TC G		
		GT C		
GAM1299	KIAA0841	3' AGATGCAGTCTCATTCTGTT 71371	_	AG_
		GACGGAA GAGATTG CT		
		TTGTCTT CTCTGAC GA		
		A GTA		
GAM1299	KIAA0894	3' GGGGTGGAATTTTTTTCCTT 29706	C	TTGAG
	CA	TGA GGAAGAGA CTACTTC		

		ACT CCTTTTTT	GGTGGGG		
		T	TTTAA		
GAM1299	KIAA0914	3'	GAGGTAGCAGCTCTCTTCTGTC	29679	TTGA
	A		TGACGGAAGAGA	GCTACTTC	
			ACTGTCTTCTCT	CGATGGAG	
			CGA_		
GAM1299	KIAA0924	3'	GGCAGAGTCTTGTCTGTT	29720	_ GA
			GACGGAA	GAGATT GCT	
			TTGTCTT	TTCTGA CGG	
			G	GA	
GAM1299	KIAA0930	3'	AGCTGGGTCTCTTTGTT	70538	G G
			GACG	AAGAGATT AGCT	
			TTGT	TTCTCTGG TCGA	
			_	G	
GAM1299	KIAA0939	3'	GGGGTGGTTTAATTCATC	62018	A A
			GA	GAG TTGAGCTACTTC	
			CT	CTT AATTTGGTGGGG	
			A	_	
GAM1299	KIAA0997	3'	GAAGTGGCACCATCTTTTCTGT	30190	TGA
	C		GACGGAAGAGAT	GCTACTTC	
			CTGTCTTTTCTA	CGGTGAAG	
			CCA		
GAM1299	KIAA1013	3'	TTGATCTTTTTTGTCA	88892	TG
			TGACGGAAGAGAT	A	
			ACTGTTTTTCTA	T	
			GT		
GAM1299	KIAA1025	3'	GAAGTTCTGAATTTCTTTTGT	63975	G CT
			GACGGAAGAGATT	AG ACTTC	
			TTGTTTCTTTAA	TC TGAAG	
			G	T_	
GAM1299	KIAA1102	3'	CAAGTAGATGTTTTTCTGT	69012	ATTGAG C
			TGACGGAAGAG	CTACTT	
			ATTGTCTTTT	GATGAA	
			GTA__	CT	
GAM1299	KIAA1143	3'	GGAGTAGCCTCTGATCCTTTTG	68684	A _ _
	TTA		GACGGAAG	GATT GAG CTACTTC	
			TTGTTTTC	CTAG CTC GATGAGG	
			_	T C	
GAM1299	KIAA1181	3'	GGAGAGCTGCAGTCTCTCCCT	68375	C _ A
	CA		TGA	GGAAGAGATTG AGCT CTTC	

ACT CCTTCTCTGAC TCGA GAGG  
 C G \_  
 GAM1299 KIAA1202 3' GAAGTGCTTTCAATCTTCTTTG 72019 AG \_ T  
 TTA GACGGA AGATTGA GC ACTTC  
 ||||| ||||| || |||||  
 TTGTTT TCTAACT CG TGAAG  
 CT TT \_  
 GAM1299 KIAA1233 3' AGCACACGGTCTCTTTTGTT 63079 A\_  
 GACGGAAGAGATTG GCT  
 ||||| ||||| ||  
 TTGTTTCTCTGGC CGA  
 ACA  
 GAM1299 KIAA1239 3' GGTGTGGTCTTTTTGTCA 71334 G A  
 TGACG AAGAGATTG GCT  
 ||||| ||||| ||  
 ACTGT TTTTCTGGT TGG  
 \_ G  
 GAM1299 KIAA1492 3' GGAGTAGTGCATGTTTTCTTCT 64506 T\_ A  
 GTTA GACGGAAGAGA TG GCTACTTC  
 ||||| || |||||  
 TTGTCTTCTTT AC TGATGAGG  
 TGT G  
 GAM1299 KIAA1509 3' AGTCACTCTCTTCTGTC 61614 T G  
 GACGGAAGAGA TGA CT  
 ||||| || ||  
 CTGTCTTCTCT ACT GA  
 C \_  
 GAM1299 KIAA1695 3' AGCAAATCACTTCTGTCA 47104 A GA  
 TGACGGAAG GATT GCT  
 ||||| || ||  
 ACTGTCTTC CTAA CGA  
 A A\_  
 GAM1299 KIAA1710 3' GGAGTGAGGAATATCTTTTCTT 62518 C TGAG \_  
 TT GA GGAAGAGAT CT ACTTC  
 || ||||| || |||||  
 TT TCTTTTCTA GA TGAGG  
 T TAAG G  
 GAM1299 KIAA1750 3' GGAGATTGGTAGTCTCTTTTG 68249 AGCTA  
 CGGAAGAGATTG CTTC  
 ||||| || ||  
 GTTTCTCTGAT GAGG  
 GGTTA  
 GAM1299 KIAA1765 3' AAGTGGCTCCTGTTCTTT 70607 ATT  
 GAAGAG GAGCTACTT  
 ||||| |||||  
 TTTCTT CTCGGTGAA  
 GTC  
 GAM1299 KIAA1786 3' GAGGTAGTGAGTTCTTTGGTT 66030 G ATTGA  
 GAC GAAGAG GCTACTTC  
 || ||||| |||||

		TTG TTTCTT TGATGGAG		
		G GAG__		
GAM1299	KIAA1795	3' GAGGTGTTGGGTTTTTTTTT 72152	G	T
		GGAAGAGATT AGC ACTTC		
		TTTTTTTTGG TTG TGGAG		
		G _		
GAM1299	KIAA1804	3' GCCTTGGTTCCTTATGTTA 69790	G	TG _
		TGACG AAGAGAT AG C		
		ATTGT TTCTTTG TC G		
		A GT C		
GAM1299	KIAA1866	3' TTCGGTCTCATTTGTCA 60937	A	
		TGACGGA GAGATTGAG		
		ACTGTTT CTCTGGCTT		
		A		
GAM1299	KIAA1906	3' GAAGAAATTTCACTTTTTCC 73193		CTA_
		GGAAGAGATTGAG CTTC		
		CCTTTTCTGACTT GAAG		
		TAAA		
GAM1299	KIAA1913	3' AGCATGATCTCTTTTATTA 73883	CG	A
		TGA GAAGAGATTG GCT		
		ATT TTTCTCTAGT CGA		
		AT A		
GAM1299	KIAA1956	3' GAAGTAAACCTTGGTTGTCTTT 78435	_	TG C__
	CGTT	CGGAAGA GAT AG TACTTC		
		GCTTTCT TTG TC ATGAAG		
		G GT CAA		
GAM1299	KIAA1958	3' GAGGTTGTAATCTTTCTGTT 81903	A	AGCT
		GACGGA GAGATTG ACTTC		
		TTGTCT TTCTAAT TGGAG		
		_ GT__		
GAM1299	KIAA1979	3' GATGAGTTTGATTCTTTTG 88281	TG	ACTTC
		CGGAAGAGAT AGCT		
		GTTTTCTTTA TTGA		
		GT GTAGG		
GAM1299	KPNA6	3' GGCAGAATCTTTTTTCA 24611	C	GA
		TGA GGAAGAGATT GCT		
		ACT TTTTTTCTAA CGG		
		_ GA		
GAM1299	LIN-28	3' GGAGTAAGCATTGTTTTTTTTT 45149	C	TGA _
	CA	TGA GGAAGAGAT GCT ACTTC		

		ACT TTTTTTTTG CGA TGAGG	
		— TTA A	
GAM1299	LIPG	3' AGCAAATCTCTTCTGTT 20094	GA
		GACGGAAGAGATT GCT	
		TTGTCTTCTCTAA CGA	
		A_	
GAM1299	LIPG	5' AGGTGGTTTTTGT TTTT 20095	T_
		AAGAGAT GAGCTACTT	
		TTTTTTG TTTGGTGGA	
		TT	
GAM1299	MAP4K3	3' GAAGTGGTTCAAATTTCTCTT 13241	—
		AAGAGA TTGAGCTACTTC	
		TTCTCT AACTTGGTGAAG	
		TTA	
GAM1299	MAWBP	3' GAATGTAATTTCAATCTTTTTC 42107	C_ _
		GGAAGAGATTGAG TAC TTC	
		CTTTTCTAACTT ATG AAG	
		TA T	
GAM1299	MGC10924	3' AAGTAGCTTGGAACTTTTG 47549	AGA TG
		CGGAAG T AGCTACTT	
		GTTTTC G TCGATGAA	
		AA_ GT	
GAM1299	MGC14697	5' AGGTGGTTACATTCGTT 51247	AGAGAT _
		GACGGA TG AGCTACTT	
		TTGCTT AC TTGGTGGA	
		_____ A	
GAM1299	MGC20496	3' AGGTGGCTTTGTTCCGT 53430	G GATT
		ACGGAA A GAGCTACTT	
		TGCCTT T TTCGGTGGA	
		G_	
GAM1299	MGC2776	3' GGCCTCAGTTTTTCCCTCA 47521	C _
		TGA GGAAGAGATTGA GCT	
		ACT CCTTTTTTGA CT CGG	
		C G	
GAM1299	MGC29891	5' GGGGTGCATCATCTTCTGTTA 58214	A T _ T
		TGACGGA GAGAT GA GC ACTTC	
		ATTGTCT TTCTA CT CG TGGGG	
		_ _ A _	
GAM1299	MGC5338	3' GTTCTTAGTTTTTGCCGTTA 43941	A CT
		TGACGG AGAGATTGAG AC	

		ATTGCC TTTTGGATTC TG		
		G T_		
GAM1299 MOT8	3'	GGGGTGGGAATCTCTTCCG 38120	GAG	
		CGGAAGAGATT CTACTTC		
		GCCTTCTCTAA GGTGGGG		
		G_		
GAM1299 NCK1	3'	GGAGAGTGTTAATCTTTTCTGT 20472	_ A	
		ACGGAAGAGATTGA GCT CTTC		
		TGTCTTTTCTAATT TGA GAGG		
		G _		
GAM1299 NDRG4	3'	GGTTGTCTCTTTGGTCA 39988	G TG	
		TGAC GAAGAGAT AGCT		
		ACTG TTTCTCTG TTGG		
		G _		
GAM1299 NDRG4	3'	GGTTGTCTCTTTGGTCA 43291	G TG	
		TGAC GAAGAGAT AGCT		
		ACTG TTTCTCTG TTGG		
		G _		
GAM1299 NUDT11	3'	GTTTGTGTGATTTTTTCTTTTA 59996	C TG T_	
		TGA GGAAGAGAT AGC AC		
		ATT TCTTTTTTA TTG TG		
		T GT TT		
GAM1299 NUDT12	3'	TTTAGTCCTTTTGTTA 48722	A	
		TGACGGAAG GATTGAG		
		ATTGTTTTTC CTGATTT		
		-		
GAM1299 P15-2	3'	AAGTGGAGTTTTTTTGTTA 38004	G ATTGAG	
		TGAC GAAGAG CTACTT		
		ATTG TTTTTT GGTGAA		
		G GA_		
GAM1299 PAK7	3'	GCAAGACGTTTGGTTTCATTTG 69647	A TG TA C	
TCA		TGACGGA GAGAT AGC CTT		
		ACTGTTT CTTTG TTG GAA		
		A GT CA CGG		
GAM1299 PEGASUS	3'	TTTTGTGGTTTGGTTTTTTTG 42434	TG TTC	
TT		GACGGAAGAGAT AGCTAC		
		TTGTTTTTTTTG TTGGTG		
		GT TTTTT		
GAM1299 PFTK1	3'	GGAGAAGTCTGTTTTGTTA 24759	G GAG	
		TGACGGAA AGATT CT		

		ATTGTTTT TCTGA GG	
		G AGA	
GAM1299 PLEKHA3	3'	GAGTAGTTTTTCCCTT 38861	A TT
		AAG GA GAGCTACTT	
		TTC CT TTTGATGAG	
		C TT	
GAM1299 PORIMIN	3'	AAGTAGTTTAGTTATGTCT 53596	AGA
		GGA GATTGAGCTACTT	
		TCT TTGATTTGATGAA	
		GTA	
GAM1299 PP3501	5'	TGGTTTAATTTCTTTC 41374	
		GGAAGAGATTGAGCTA	
		CTTCTTTAATTTGGT	
GAM1299 PPP1R15B	3'	GATCTAGTTTAATTTTTTTTTT 51595	CG CT
	T	GA GAAGAGATTGAGCTA TC	
		TT TTTTTTAATTTGAT AG	
		TT CT G	
GAM1299 PRO0767	5'	GTTACTGGGTTTTTTTGTCA 26024	G CT
		TGACGGAAGAGATT AG AC	
		ACTGTTTTTTTGG TC TG	
		G AT	
GAM1299 PRO2325	3'	GAGTGGCCTGTTCCGTT 96302	G ATTGA
		GACGGAA AG GCTACTT	
		TTGCCTT TC CGGTGAG	
		G ____	
GAM1299 PRO2831	5'	AGGTGGTGA CTCTTTTGT 37599	ATTGA
		ACGGAAGAG GCTACTT	
		TGTTTCTC TGGTGGA	
		AG__	
GAM1299 PTBP2	3'	ACCAGAGTTTGATTTTTTTTGT 41030	TG A TC
	T	GACGGAAGAGAT AGCT CT	
		TTGTTTTTTTA TTGA GA	
		GT _ CCAG	
GAM1299 PTPRU	3'	GCTTTTTTGTTTCTTTTGTTA 55691	T__
		TGACGGAAGAGAT GAGC	
		ATTGTTTCTTTG TTCG	
		TTTT	
GAM1299 PTPRU	3'	GCTTTTTTGTTTCTTTTGTTA 55697	T__
		TGACGGAAGAGAT GAGC	



		ATTGTTTTCTTTG	TTCG		
		TTTT			
GAM1299	PTPRU	3' GCTTTTTTGTTC	TTTTGTTA	19118	T__
		TGACGGAAGAGAT	GAGC		
		ATTGTTTTCTTTG	TTCG		
		TTTT			
GAM1299	RAB10	5' GGGTGGCTCGGTTTCCTG	85177	AA	
		CGG GAGATTGAGCTACTT			
		GTC CTTTGGCTCGGTGGG			
		—			
GAM1299	RBBP4	3' TTTCCTCTTGTTTCTTCAGTT	18827	G	TG CTA
	A	TGAC GAAGAGAT	AG		
		ATTG CTTCTTTG	TC		
		A	GT TCCTTG		
GAM1299	RBBP7	3' GGGGTGGCTTATGGCTTCT	60001	AGAT	
		GGAAG TGAGCTACTTC			
		TCTTC ATTCGGTGGGG			
		GGT_			
GAM1299	RFX3	3' GGGGTAGTTTATACCTTGTC	11315	A	AT_
		GA GAG TGAGCTACTTC			
		CT TTC ATTTGATGGGG			
		G	CAT		
GAM1299	RHOBTB1	3' GGGGTGGGGCTCATTCTGTT	91442	GAGAT	—
		GACGGAA TGAGCT	ACTTC		
		TTGTCTT	ACTCGG TGGGG		
		—	GG		
GAM1299	RINZF	3' AAGTAACTTTCTTCTG	43695	GATT	C
		CGGAAGA GAG TACTT			
		GTCTTCT	TTC ATGAA		
		—	A		
GAM1299	RNPS1	3' GGGGTGGTTTGACCCTGCTT	54580	_	A_TG
		AAG AG T AGCTACTTC			
		TTC TC A TTGGTGGGG			
		G	CC GT		
GAM1299	RNPS1	3' GGGGTGGTTTGACCCTGCTT	22008	_	A_TG
		AAG AG T AGCTACTTC			
		TTC TC A TTGGTGGGG			
		G	CC GT		
GAM1299	RRN3	3' AGACTGGGTTTTTTTGT	37352	G	_
		GACGGAAGAGATT	AG CT		

		TTGTTTTTTTTTGG TC GA	
		G A	
GAM1299 SDS3	3'	GAGGACTTAATATTTTCTTTTG 69230	___ _ ACTTC
	TCA	CGGAAGAGA TTGAG CT	
		GTTTTCTTT AATTC GG	
		TAT A AG C	
GAM1299 SKIL	5'	GAGGTGTGCCTCTTTTCT 18281	TTGA _
		GGAAGAGA GC TACTTC	
		TCTTTTCT CG GTGGAG	
		C___ T	
GAM1299 SLC6A14	3'	GGGGTCAGAGTCTTGTTCTGTT 23355	_ _ G ACTTC
		GACGGAA GAGAT TGA CT	
		TTGTCTT TTCTG ACT GG	
		G AG G G C	
GAM1299 SMBP	3'	GGATCAATTTCTTTTTTCA 72160	C G
		TGA GGAAGAGATTGA CT	
		ACT TTTTCTTTAACT GG	
		_ A	
GAM1299 SPUVE	3'	GGCCAAATTGTTTTTTGTCA 23155	_ GA
		TGACGGAAGA GATT GCT	
		ACTGTTTTTT TTAA CGG	
		G AC	
GAM1299 SRPK1	3'	GGGGTGGGATGGCACTTTTTTTT 11966	T AG___
	TGTT	CGGAAGAGA TG CTACTTC	
		GTTTTTTTTT AC GGTGGGG	
		C GGTAG	
GAM1299 SSH2	3'	GAGGCTTGCAGATTTGCTTTTCG 62207	_ _ _ ACTTC
	TT	CGGAAG AGATT GAGCT	
		GCTTTC TTTAG TTCGG	
		G ACG AG C	
GAM1299 STAT2	3'	GAAGTAGACCTCTTTTTTCTT 18294	TT _
		AAGAGA GAG CTACTTC	
		TTCTTT CTC GATGAAG	
		TT CA	
GAM1299 STI2	3'	AGCTTCTGGTTTCTTCTGCA 88964	A _
		TG CGGAAGAGATT GAGCT	
		AC GTCTTCTTTGG TTCGA	
		_ TC	
GAM1299 TDPGD	3'	GAAGTGCACTCTTTTCTTTTG 59726	TT C_
		CGGAAGAGA GAG TACTTC	

			GTTCCTTC CTC GTGAAG		
			T_ AC		
GAM1299	TNFAIP3	3'	AGGAAATCTCTTCTGTT 20821	_	GAG
			GACGGAA GAGATT CT		
			TTGTCTT CTCTAA GA		
			T AG_		
GAM1299	TRIM36	3'	GGATATCTAATTTATTTCTGTC 38014	_	AGCTACTTC
	A		TGACGGAAG AGATTG		
			ACTGTCTTT TTTAAT		
			A CTATAGG		
GAM1299	TRIM6	3'	GTTCTCAATTCTTTTGTT 54142	A	CT
			GACGGAAGAG TTGAG AC		
			TTGTTTCTT AACTC TG		
			_ T_		
GAM1299	UBE2N	3'	GAGGTAGTTTAATTTT 12512		
			GAGATTGAGCTACTTC		
			TTTAATTTGATGGAG		
GAM1299	UBE2N	3'	GAGGTAGTTTAATTTT 94542		
			GAGATTGAGCTACTTC		
			TTTAATTTGATGGAG		
GAM1299	UBE2V2	3'	TTATCTAGTTTAATTTCTTCT 12526		CTTC
			GGAAGAGATTGAGCTA		
			TCTTCTTTAATTTGAT		
			CTATTA		
GAM1299	USP8	3'	GGCAAAGCAATTTTCTGTT 17666	A	A__
			GACGGA GAGATTG GCT		
			TTGTCT TTTAAC CGG		
			_ GAAA		
GAM1299	X123	5'	GAAGGCAAGATTTGCTTCTGTT 69924	_	GA ACTTC
			GACGGAAG AGATT GCT		
			TTGTCTTC TTTAG CGG		
			G AA AAG		
GAM1299	ZNF262	3'	GGGGTGGCAGGTGTATTTCTTT 17487		TGA__
	T		GGAAGAGAT GCTACTTC		
			TTTTCTTTA CGGTGGGG		
			TGTGGA		
GAM1299	LOC113179	3'	GGCCTCGATTTCTTCCGCA 56548	A	_
			TG CGGAAGAGATTGAG CT		

AC GCCTTCTTTAGCTC GG  
 — C  
 GAM1299 LOC120856 3' AGTTCTGTTTTGTTTCGTT 74025 A T  
 GACGGA GAGAT GAGCT  
 ||||| ||||| |||||  
 TTGCTT TTTTG CTTGA  
 G T  
 GAM1299 LOC121536 3' GAAGTAATCTGCAATCTCTTTT 74086 \_ C\_  
 GTT GACGGAAGAGATTG AG TACTTC  
 ||||| ||||| || |||||  
 TTGTTTCTCTAAC TC ATGAAG  
 G TA  
 GAM1299 LOC121838 5' GGTATTTCTTCTGTC 76003 TGA  
 GACGGAAGAGAT GCT  
 ||||| ||||| |||||  
 CTGTCTTCTTTA TGG  
 —  
 GAM1299 LOC126603 5' GAGGTGGTGAGCCTCTTTGTCA 75394 G ATTGA  
 TGACG AAGAG GCTACTTC  
 ||||| ||||| ||||| |||||  
 ACTGT TTCTC TGGTGGAG  
 \_ CGAG\_  
 GAM1299 LOC126964 3' GGGGTAGTTTAAATCCGTT 74620 AGAGA  
 GACGGA TTGAGCTACTTC  
 ||||| ||||| ||||| |||||  
 TTGCCT AATTTGATGGGG  
 A\_\_\_\_  
 GAM1299 LOC129644 3' AGGTACGCTTTTTTTCCTCA 74881 C GATT \_  
 TGA GGAAGA GAGC TACTT  
 ||||| ||||| ||||| |||||  
 ACT CCTTTT TTCG ATGGA  
 — — C  
 GAM1299 LOC131870 3' AGTTTGAATCTCTTCT 75014 \_  
 GGAAGAGATT GAGCT  
 ||||| ||||| ||||| |||||  
 TCTTCTCTAA TTTGA  
 G  
 GAM1299 LOC133088 5' GGGGGCTTGGTTTTTTTC 75078 TG TA  
 GGAAGAGAT AGC CT  
 ||||| ||||| ||||| |||||  
 CTTTTTTTG TCG GG  
 GT GG  
 GAM1299 LOC138241 5' GGGGTGGCTTTGATTTC 75311 TG\_  
 GAGAT A GCTACTTC  
 ||||| ||||| ||||| |||||  
 CTTTA TCGGTGGGG  
 GT T  
 GAM1299 LOC138639 3' GAAGTGGTTGGGATTTTTTG 75363 GA G  
 CGGAAGA TT AGCTACTTC  
 ||||| ||||| ||||| |||||

GTTTTTT GG TTGGTGAAG  
 A\_ G  
 GAM1299 LOC139221 3' GTTCAATTTCTGCTGTT 75826 A  
 GACGG AGAGATTGAGC  
 ||||| |||||  
 TTGTC TCTTTAACTTG  
 G  
 GAM1299 LOC144195 3' CTTGATTTCTTTCTCA 60356 C TG  
 TGA GGAAGAGAT AG  
 ||| ||||| ||  
 ACT CTTTCTTTA TC  
 \_ GT  
 GAM1299 LOC144509 3' AGCTGGCTTTTCTGTC 76858 ATTG  
 GACGGAAGAG AGCT  
 ||||| |||  
 CTGTCTTTTC TCGA  
 GG\_  
 GAM1299 LOC144600 3' AGCTGGGTCTCTTTGTT 83160 G G  
 GACG AAGAGATT AGCT  
 ||| ||||| |||  
 TTGT TTCTCTGG TCGA  
 \_ G  
 GAM1299 LOC145815 5' GGTTTGTTCTTTTCGTTA 83522 G TT  
 TGACG AAGAGA GAGCT  
 ||||| ||||| |||||  
 ATTGC TTTTCT TTTGG  
 \_ TG  
 GAM1299 LOC145942 3' GATTTGCTTCAGTTTTTTCCTC 77575 C \_ TACTTC  
 A TGA GGAAGAGATTGA GC  
 ||| ||||| ||||| ||  
 ACT CCTTTTTTGA CT  
 \_ T TTTAG  
 GAM1299 LOC145945 3' GAAGTAGTGGAATTCTTTCATCA 83575 C A GA  
 TGA GGAAGAG TT GCTACTTC  
 ||| ||||| || |||||  
 ACT CTTTCTT AG TGATGAAG  
 A \_ G\_  
 GAM1299 LOC146901 3' GGGTTGCTTGGTTTTTGTTGTT 83845 A TG T C  
 GACGG AGAGAT AGC ACTT  
 ||||| ||||| ||| |||||  
 TTGTT TTTTGT TCG TGGG  
 G GT T  
 GAM1299 LOC147341 3' GGTAATTTTCTGT 83996 GA  
 ACGGAAGAGATT GCT  
 ||||| ||||| |||  
 TGTCTTTTAA TGG  
 \_  
 GAM1299 LOC147515 3' GAAGTGATGCTGGGACTCTTCT 84022 A G \_  
 GTT GACGGAAGAG TT AGC TACTTC  
 ||||| || ||| |||||

		TTGTCTTCTC GG TCG GTGAAG		
		A G TA		
GAM1299	LOC149103 3'	GAGGTGGTTTAAATTCCTTT 79197	AG	_
		GAAG ATTGAG CTA		
		TTTC TAATTT GGTGGAG		
		CT T		
GAM1299	LOC149448 3'	AGACTGAATTTCTTCTGCCA 84418	A	G _
		TG CGGAAGAGATT AG CT		
		AC GTCTTCTTTAA TC GA		
		C G A		
GAM1299	LOC149995 3'	GAAGTGATGCTGGGACTCTTCT 84844	A G	_
	GTT	GACGGAAGAG TT AGC TACTTC		
		TTGTCTTCTC GG TCG GTGAAG		
		A G TA		
GAM1299	LOC150159 3'	AGCATAGTCTTTTCCTCA 57537	C	A
		TGA GGAAGAGATTG GCT		
		ACT CCTTTTCTGAT CGA		
		_ A		
GAM1299	LOC150225 3'	GAAGGCATTGGTTTTTTTTTTC 84994	CG	TG _ ACTTC
	A	TGA GAAGAGAT A GCT		
		ACT TTTTTTTG T CGG		
		TT GT A AAG		
GAM1299	LOC150280 3'	GCTCAATTTTTTTTGTCA 79712		
		TGACGGAAGAGATTGAGC		
		ACTGTTTTTTTAACTCG		
GAM1299	LOC151174 5'	GAGGGCCTCGATCTTTTCTG 85250		CTA
		CGGAAGAGATTGAG CTTC		
		GTCTTTTCTAGCTC GGAG		
		CG_		
GAM1299	LOC152220 3'	GTTTTTGTCTTTTCTGTT 85587	T_	
		GACGGAAGAGAT GAGC		
		TTGTCTTTTCTG TTTG		
		TT		
GAM1299	LOC152313 3'	GACAGTGTTAATCTCTTCTTTC 85661	C	_ ACTTC
	A	TGA GGAAGAGATTGA GCT		
		ACT TCTTCTCTAATT TGA		
		T G CAG		
GAM1299	LOC152447 5'	GGGGTAGGAAGCTTTCTGTT 80589	A	ATTGAG
		GACGGA GAG CTA		

		TTGTCT TTC	GATGGGG		
		— GAAG—			
GAM1299	LOC152453 3'	TTTGATCTTTTGTCA	80605	G	TG
		TGACG AAGAGAT AG			
		ACTGT TTTTCTA TT			
		— GT			
GAM1299	LOC152905 3'	GGCAAGTTTTTTCTTCA	60478	C	GA
		TGA GGAAGAGATT GCT			
		ACT CTTTTTTTGA CGG			
		T A—			
GAM1299	LOC153020 3'	AGCCACGTTTCTTTTGTTA	80762		— A
		TGACGGAAGAGAT TG GCT			
		ATTGTTTCTTTG AC CGA			
		C C			
GAM1299	LOC153027 3'	GGGGTGGTTTGACCCTGCTT	67434		— A— TG
		AAG AG T AGCTACTTC			
		TTC TC A TTGGTGGGG			
		G CC GT			
GAM1299	LOC153396 3'	GGCTAAAGTCTCTTCTGTT	80820		G—
		GACGGAAGAGATT AGCT			
		TTGTCTTCTCTGA TCGG			
		AA			
GAM1299	LOC153432 5'	GGATTAATCTCCTCTGTCA	87271	A	G
		TGACGGA GAGATTGA CT			
		ACTGTCT CTCTAATT GG			
		C A			
GAM1299	LOC153525 5'	AAGTAGCTTGGAACCTTTTG	86042		AGA TG
		CGGAAG T AGCTACTT			
		GTTTTC G TCGATGAA			
		AA— GT			
GAM1299	LOC153525 5'	GGGTCAATTTTTTTCTTCA	86046	C	G
		TGA GGAAGAGATTGA CT			
		ACT CTTTTTTTAACT GG			
		T G			
GAM1299	LOC153688 3'	AGGTATATTTTTTCTGTT	86094		TGAGC
		GACGGAAGAGAT TACTT			
		TTGTCTTTTTTA ATGGA			
		T—			
GAM1299	LOC153711 3'	GAAGTGGCTCAGTACTGTTA	86135		AAGAG
		TGACGG ATTGAGCTACTTC			

	ATTGTC TGACTCGGTGAAG	
	A_____	
GAM1299 LOC153914 5'	GTACTTGGTGCTTTTTTGTGTT 80991	_ TG C
	GACGGAAGAG AT AG TAC	
	TTGTTTTTTC TG TC ATG	
	G GT _	
GAM1299 LOC154789 5'	GAAGTAGGAAAATTGTTTCTGT 81135	A GAG
CA	TGACGGAAG GATT CTACTTC	
	ACTGTCTTT TTAA GATGAAG	
	G AAG	
GAM1299 LOC155036 3'	GCTCCAGTCTCTTCCGT 86344	_
	ACGGAAGAGATTG AGC	
	TGCCTTCTCTGAC TCG	
	C	
GAM1299 LOC155255 3'	AGCTGATCTTTTCTG 81327	G
	CGGAAGAGATT AGCT	
	GTCTTTTCTAG TCGA	
	-	
GAM1299 LOC158187 3'	TCAGTCTTTGCTGTCA 86696	A
	TGACGG AGAGATTGA	
	ACTGTC TTTCTGACT	
	G	
GAM1299 LOC158828 3'	GAGGTGGCTTGTGTGTTTGTCA 82029	AGAGAT
	TGACGGA TGAGCTACTTC	
	ACTGTT GTTCGGTGGAG	
	GTGT__	
GAM1299 LOC159989 5'	AGTTTATTTCTTTTTC 82203	T_
	GGAAGAGA TGAGCT	
	CTTTTCT ATTTGA	
	TT	
GAM1299 LOC162891 5'	AAGGGATTTTTTCTGTTA 87172	TTGAG A
	TGACGGAAGAGA CT CTT	
	ATTGTCTTTTTT GG GAA	
	TA__ _	
GAM1299 LOC199232 3'	GTGTGGTTTTGTTTTTTTGTGTT 88973	T TTC
	GACGGAAGAGAT GAGCTAC	
	TTGTTTTTTTG TTTGGTG	
	T TG	
GAM1299 LOC199678 3'	GAAGTGTGAATATTTTTGTCA 89791	G GA T
	TGACGGAAGA ATT GC ACTTC	



	ACTGTTTTTT TAA TG TGAAG		
	A G_ _		
GAM1299 LOC199678 3'	GAGAAGCCTTTTCCGTT 89792	ATTGA A	
	GACGGAAGAG GCT CTT		
	TTGCCTTTTC CGA GAG		
	_____ A		
GAM1299 LOC199729 5'	GGGGTAGTTTGAGCCATTTCTG 73033	A AGA_ TG	
CG	TG CGGAAG T AGCTACTTC		
	GC GTCTTT A TTGATGGGG		
	_ ACCG GT		
GAM1299 LOC200982 3'	AACAAGATCGGTCTTTTTTG 90214	G ACTTC	
	CGGAAGAGATTGA CT		
	GTTTTTCTGGCT GA		
	A ACAAG		
GAM1299 LOC201705 5'	GGTGTCAGTCTTTTCTGTC 90254	_	
	GACGGAAGAGATTGA GCT		
	CTGTCTTTTCTGACT TGG		
	G		
GAM1299 LOC203428 3'	GGGTGGTTTTTTTCTTT 89361	TT	
	GAAGAGA GAGCTACTT		
	TTTCTTT TTTGGTGGG		
	T_		
GAM1299 LOC204804 3'	GGTTAATTTTTTCTGTC 89482	TTG	
	GACGGAAGAGA AGCT		
	CTGTCTTTTTT TTGG		
	TAA		
GAM1299 LOC219347 3'	GAGCTGCTGGTCTCTTCTG 92983	G TA	
	CGGAAGAGATT AGC CTT		
	GTCTTCTCTGG TCG GAG		
	_ TC		
GAM1299 LOC219673 5'	AGATGATCTCATTCTGTT 93019	_ GAG	
	GACGGAA GAGATT CT		
	TTGTCTT CTCTAG GA		
	A TA_		
GAM1299 LOC221312 3'	ATTGTATTTTAATCCCTTTTGT 91906	A C TTC	
TA	TGACGGAAG GATTGAG TAC		
	ATTGTTTTT CTAATTT ATG		
	C T TTAG		
GAM1299 LOC221437 5'	GAGGTGGCAGCCATCTCTTCCT 92840	C TGA_	
C	GA GGAAGAGAT GCTACTTC		

		CT CCTTCTCTA	CGGTGGAG		
		—	CCGA		
GAM1299	LOC221711 3'	GGAGTGGTGTGCTTTTTTTTT	92209	CG	ATTGA
	A	TGA GAAGAG	GCTACTTC		
		ATT TTTTC	TGGTGAGG		
		TT	GTTG_		
GAM1299	LOC221715 3'	GTCTTAATTTCTTTGTCA	93753	G	—
		TGACG AAGAGATTGAG	C		
		ACTGT TTCTTTAATTC	G		
		—	T		
GAM1299	LOC221935 3'	AGGTGGCTCACTCT	92617	AT	
		AGAG TGAGCTACTT			
		TCTC	ACTCGGTGGA		
		—			
GAM1299	LOC222237 5'	GGGGTGGTTTGGAATTCTTC	94290	A_	TG
		GAAGAG T	AGCTACTTC		
		CTTCTT G	TTGGTGGGG		
		AA	GT		
GAM1299	LOC222933 5'	GGAGTAAGGACTCTTTTCCTTC	94360	C	TTGAGC
	A	TGA GGAAGAGA	TACTTC		
		ACT CCTTTTCT	ATGAGG		
		T	CAGGA_		
GAM1299	LOC253264 3'	AGACTTAGTTTCTTCTGTCA	94689		—
		TGACGGAAGAGATTGAG	CT		
		ACTGTCTTCTTTGATTC	GA		
		A			
GAM1299	LOC253992 3'	GGCCACAACCTTCTTCTGTC	96623	A	A_
		GACGGAAGAG TTG	GCT		
		CTGTCTTCTT AAC	CGG		
		C	AC		
GAM1299	LOC254302 5'	AGCGGTTTCTCCCGTCA	96184	A	GA
		TGACGG AGAGATT	GCT		
		ACTGCC TCTTTGG	CGA		
		C	—		
GAM1299	LOC254874 5'	GGAGCGGTTTCTCCCGTCA	96181	A	AG
		TGACGG AGAGATTG	CT		
		ACTGCC TCTTTGGC	GG		
		C	GA		
GAM1299	LOC51107 3'	CTTGGTCTTTTCTCA	32061	C	TG
		TGA GGAAGAGAT	AG		

		ACT CTTTTTCTG TC		
		— GT		
GAM1299	LOC51193	3' AGATGGTCTCGTTCTGTT 32901	—	GAG
		GACGGAA GAGATT CT		
		TTGTCTT CTCTGG GA		
		G TA_		
GAM1299	LOC84524	3' GGAGTAGTTTACAAGATTCCTC 50671	C	GAGAT
	A	TGA GGAA TGAGCTACTTC		
		ACT CCTT ATTTGATGAGG		
		— AGAAC		
GAM1299	LOC85414	3' GGCCTGTTGGTCCTTCTGTT 52399	A	TG ____
		GACGGAAG GAT A GCT		
		TTGTCTTC CTG T CGG		
		— GT GTC		
GAM1299	LOC91660	5' TGGCTTAGTTTCTCTGTTA 66871	A	
		TGACGGA GAGATTGAGCTA		
		ATTGTCT CTTTGATTGCGT		
		—		
GAM1299	LOC92218	3' GACAATTCAATTATTTTCTGTT 68506	—	CTACTTC
	A	TGACGGAAGA GATTGAG		
		ATTGTCTTTT TTAAGTT		
		A AACAG		
GAM1299	LOC92703	3' GGAGTGGCCCTGTTTTCTGT 56429		GATTGA
		ACGGAAGA GCTACTTC		
		TGTCTTTT CGGTGAGG		
		GTCC_		
GAM1299	LOC93097	3' GGAGTGTGATTTTCTTTTTTCA 71363	CG	TTGA T
		TGA GAAGAGA GC ACTTC		
		ACT TTTCTTT TG TGAGG		
		TT TAG_ _		
GAM1300	TNFAIP1	3' CATCAGCTGAGGACAGCAAAC 40917	AG	G
	CC	GGA TTGCTG CTTGAGCTGATG		
		CCT AACGAC GGAGTCGACTAC		
		CA A		
GAM1300	C1orf2	3' CAGCTGGTTGGGACCAGCAGCC 21681	AA	— ____
	CCC	GG GTTGCTGG CT TCAGCTG		
		CC CGACGACC GG GGTCGAC		
		CC A GTT		
GAM1300	C1orf2	3' CAGCTGGTTGGGACCAGCAGCC 94622	AA	— ____
	CCC	GG GTTGCTGG CT TCAGCTG		

CC CGACGACC GG GGTCGAC  
 CC A GTT  
 GAM1300 C20orf59 3' CATCCCTAGCCAGCAGCTCC 41992 A TC CT  
 GGA GTTGCTGGCT AG GATG  
 ||| ||||| || ||||  
 CCT CGACGACCGA TC CTAC  
 \_ \_ C\_  
 GAM1300 FLJ20079 3' CATTCTGGTAAACCAGCAGCCT 34490 A CT\_\_ CT  
 CC GGA GTTGCTGG TCAG GATG  
 ||| ||||| ||| ||||  
 CCT CGACGACC GGTC TTAC  
 C AAAT \_  
 GAM1300 SSAT2 3' CATCAGCTGAAGCACTCTTC 56041 TTGCTG  
 GAAG GCTTCAGCTGATG  
 ||| ||||| |||||  
 CTTC CGAAGTCGACTAC  
 TCA\_  
 GAM1300 SYNJ2 3' ATCAGCTTAAGCAATTCC 61763 GTTGCTG C  
 GGAA GCTT AGCTGAT  
 ||| ||| |||||  
 CCTT CGAA TCGACTA  
 AA\_\_\_\_\_ T  
 GAM1300 LOC162333 5' CTGAAGCCAGCAATTCC 87131 G  
 GGAA TTGCTGGCTTCAG  
 ||| ||||| |||||  
 CCTT AACGACCGAAGTC  
 \_  
 GAM1300 LOC222060 5' CACCTCCCACCAGCAACCCCC 94104 AA CTTC C  
 GG GTTGCTGG AG TG  
 || ||||| || ||  
 CC CAACGACC TC AC  
 CC ACCC C  
 GAM1300 LOC255650 3' CATCAGCCCCAGGCAACTTCC 96711 \_ CTTCA  
 GGAAGTTGC TGG GCTGATG  
 ||||| || |||||  
 CCTTCAACG ACC CGACTAC  
 G C\_  
 GAM1301 EPB41 5' CATGAAGACTTGACCAAGA 15430 C \_ CCT  
 TC TGGT AGG TCTTCATG  
 || ||| || |||||  
 AG ACCA TTC AGAAGTAC  
 A G \_  
 GAM1301 LILRB5 3' AAGACCACCAGGACA 22421 A C  
 TGTCTGGT GG CTT  
 ||||| || |||  
 ACAGGACCA CC GAA  
 \_ A  
 GAM1301 PWP2H 3' CATGTAGCCCATCAGGACA 17308 A CTTCTT  
 TGTCTGGT GGC CATG  
 ||||| || |||

ACAGGACTA CCG GTAC  
 C AT\_\_\_\_  
 GAM1301 DKFZP434P211 3' AAGGCCTTCCAGGACA 27257 T  
 TGTCTGG AGGCCTT  
 ||||| |||||  
 ACAGGACC TCCGGAA  
 T  
 GAM1301 FLJ20464 3' GCATGAAGAAAGTTCCCTGGAC 35233 T TA C  
 A TGTCC GG GGC TTCTTCATGC  
 |||| | || |||||  
 ACAGG CC TTG AAGAAGTACG  
 T C\_ A  
 GAM1301 KIAA1911 5' GCATTCACGCCTACCAGGACA 73507 CTTCTTC  
 TGTCTGGTAGGC ATGC  
 ||||| |||||  
 ACAGGACCATCCG TACG  
 CACT\_\_\_\_  
 GAM1301 NY-REN-60 3' CATAAAGAACTTTCTCAGGAC 67108 GT CC\_ C  
 A TGTCTG AGG TTCTT ATG  
 ||||| || |||||  
 ACAGGAC TCC AAGAA TAC  
 \_ TTTC A  
 GAM1301 LOC130471 3' CATGAAGAACTCAGACA 74940 CT AGGCC  
 TGTC GGT TTCTTCATG  
 ||| || |||||  
 ACAG TCA AAGAAGTAC  
 AC \_\_\_\_  
 GAM1301 LOC144147 3' AAGACCTACCAGCACA 71728 C C  
 TGT CTGGTAGG CTT  
 || ||||| |||  
 ACA GACCATCC GAA  
 C A  
 GAM1301 LOC147976 5' CATAAAGAAGAAGCTAGGA 78587 AGGC C  
 TCCTGGT CTTCTT ATG  
 ||||| ||||| |||  
 AGGATCG GAAGAA TAC  
 AA\_ A  
 GAM1301 LOC164295 5' GCACTTTGGCCACCAGAACA 82510 C A TTCTTCA  
 TGT CTGGT GGCC TGC  
 || |||| |||| |||  
 ACA GACCA CCGG ACG  
 A C TTTC\_\_\_\_  
 GAM1301 LOC200860 3' AGAAAGCCTCCAGGACA 90158 T C  
 TGTCTGG AGGC TTCT  
 ||||| ||||| |||||  
 ACAGGACC TCCG AAGA  
 \_ A  
 GAM1301 LOC201626 5' CACGAAGAAGGTGACTGAGGAC 88987 \_ AG A  
 GTCCT GGT GCCTTCTTC TG  
 ||||| || ||||| ||

CAGGA TCA TGGAAGAAG AC  
 G G\_ C  
 GAM1301 LOC257464 3' GTGTTGGCTACCAGGACA 89673 G TTCTT  
 TGTCTGGTAG CC CAT  
 ||||| || ||  
 ACAGGACCATC GG GTG  
 \_ TT\_  
 GAM1302 TFAP2C 3' AATCCTTCTCCACCGCA 12229 T TTGTA  
 TCGGTGG AGG GATT  
 ||||| || ||  
 ACGCCACC TCT CTAA  
 \_ TC\_  
 GAM1302 KIAA1918 3' AAGAATCTACAACCTGGAGC 73158 GG  
 GT TAGGTTGTAGATTCTT  
 || |||||  
 CG GTCCAACATCTAAGAA  
 AG  
 GAM1302 LOC133308 5' AAGAATCCTATCTTCCCACCGC 75084 T\_ TGTA  
 A TCGGTGG AGGT GATTCTT  
 ||||| || |||||  
 ACGCCACC TCTA CTAAGAA  
 CT TC\_  
 GAM1303 ADH1B 3' CTTAGACATAAAGTAAAAT 72644 C CAC  
 ATTT ACTTT TGTCTGAG  
 ||| |||| |||||  
 TAAA TGAAA ACAGATTC  
 A T\_  
 GAM1303 AHR 3' ATCTCAGATGTTAAAATAAATG 7875 CAC C T  
 CATTT TTT AC GTCTGAGAT  
 |||| || |||||  
 GTAAA AAA TG TAGACTCTA  
 TA\_ T\_  
 GAM1303 FDFT1 3' TAGGAAAGTGAAATG 15518 A  
 CATTTCACTTTC CTG  
 ||||| |||||  
 GTAAAGTGAAAG GAT  
 \_  
 GAM1303 JTB 3' ATCTCAGACAGTGAAAGTGAAA 21959  
 TG CATTTCACTTTCACTGTCTGAGAT  
 |||||  
 GTAAAGTGAAAGTGACAGACTCTA  
 GAM1303 KLF4 3' TCCCAGACAGTGGATATG 14891 CT A  
 CA TTCACTGTCTG GA  
 || ||||| ||  
 GT AGGTGACAGAC CT  
 AT C  
 GAM1303 PHYH 3' ACAGTAAAAGTGAAAT 20608 C  
 ATTTCACTTT ACTGT  
 ||||| |||||

			TAAAGTGAAA TGACA		
			A		
GAM1303	PKD2	3'	TCCAGGTTGAAAAGTGAAA 60096	CTG	A
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T__ _		
GAM1303	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1303	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA	CTG
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1303	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT	CT
			TTCAC TTTCA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1303	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G	T_
			CTTTCACT TC GAGAT		
			GAAAGTGA AG TTCTA		
			G TC		
GAM1303	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT 45802	ACTTTCACT	
	G		CATTTT GTCTGAGAT		
			GTAAAG CAGACTCTA		
			AAACATTT_		
GAM1303	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281	CTT	
			CATTTCA TCACTGTCTGAGAT		
			GTAAAGT AGTGACAGACTCTA		
			C_		
GAM1303	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C	TC
			TTCA TTTCACTG TGAG		
			AAGT AAAGTGAC GTTT		
			A CT		
GAM1303	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A	_
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1303	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T	
			ATT CACTTTCACTGT		

		TAA GTGAAAGTGACG		
		C		
GAM1303	PORIMIN	3' ATCTCAGAGGGCCAAAGTGAA	53598	CA G
		TTCACTTT CT TCTGAGAT		
		AAGTGAAA GG AGACTCTA		
		CC G		
GAM1303	PP35	3' ATCTCAGACTGAAA	22814 CT	
		TTTCA GTCTGAGAT		
		AAAGT CAGACTCTA		
		—		
GAM1303	PRTD-NY3	3' CTCATTGCAATAAGTGAAATG	48148	TCAC C_
		CATTTCACTT TGT TGAG		
		GTAAAGTGAA ACG ACTC		
		TA__ TT		
GAM1303	SEP15	3' TCCTACAGTAAGAGTGAAA	14934	C CT
		TTTCACTTT ACTGT GA		
		AAAGTGAGA TGACA CT		
		A TC		
GAM1303	SFXN2	3' CTCAGGGGAAAAAAGTGAAA	73941	CACTG
		TTTCACTTT TCTGAG		
		AAAGTGAAA GGA CTC		
		AAAGG		
GAM1303	LOC149703	3' ATCTCAGACAGCCGTTTGAAAA	84647	ACTTTCA
		TTTC CTGTCTGAGAT		
		AAAG GACAGACTCTA		
		GTTTGCC		
GAM1303	LOC154007	3' ATCTCAAACCCTTTAGTGAAA	81015	TTCACT C
		TTTCACT GT TGAGAT		
		AAAGTGA CA ACTCTA		
		TTTCC_ A		
GAM1303	LOC155004	3' TCATTTAAGTGAAAGGAAA	81226	A GTC_
		TTTC CTTTCACT TGA		
		AAAG GAAAGTGA ACT		
		_ ATTT		
GAM1303	LOC222134	5' ACAGTGAAGTGAAATG	94136	T
		CATTTCACTT CACTGT		
		GTAAAGTGAA GTGACA		
		—		
GAM1304	ACVR1	3' GGAAACTCAAGGAGGTGGTGAA	6610	GGGTA_ C
		TTCATCACT AGT TCC		



			AAGTGGTGG	TCA AGG		
			AGGAAC	A		
GAM1304	CDH1	3'	GAGACTGGT	TAGTGATG	15144	G A
			CATCACTGG	TA GTCTC		
			GTAGTGATT	GT CAGAG		
			G	_		
GAM1304	CHST5	5'	GCTCCCAGT	GAGGAA	24027	A TA
			TTC TCACTGGG	AGT		
			AAG AGTGACCC	TCG		
			G	_		
GAM1304	CLN5	5'	GAAACTTCTTTCCAGTGA	21427	T_ C	
			TCACTGGG	AAGT TC		
			AGTGACCT	TTCA AG		
			TTC	A		
GAM1304	CRACC	3'	GGAGACCTCCCTACCAAGTGAT	41007	G A_	
	GAA		TTCATCACT	GGTA GTCTCC		
			AAGTAGTGA	CCAT CAGAGG		
			A	CCCTC		
GAM1304	CYP4F3	3'	GGAGACTTAATAATGAT	6120	C GG	
			ATCA TG	TAAGTCTCC		
			TAGT AT	ATTCAGAGG		
			A	A_		
GAM1304	DTR	3'	GAGACTTGTGCTCAAGGA	8690	AC _	
			TC TGGGTA	AGTCTC		
			AG ACTCGT	TCAGAG		
			GA	GT		
GAM1304	EDG8	3'	GGAGATGATTCCAGTGA	78480	TAA	
			TCACTGGG	GTCTCC		
			AGTGACCT	TAGAGG		
			TAG			
GAM1304	FASN	3'	GGAGACTCCTGGTCTGTGAA	14634	C_ TG TA	
			TTCAT AC	GG AGTCTCC		
			AAGTG TG	CC TCAGAGG		
			TC	GT _		
GAM1304	FLT1	3'	GGAGACTTGTAATAATGA	8919	C GG_	
			TCA TG	TAAGTCTCC		
			AGT AT	G TTCAGAGG		
			A	AAT		
GAM1304	IL1RAP	3'	AGACTTGTTCAATGCGAA	9309	AT C GG	
			TTC CA	TG TAAGTCT		

		AAG GT AC GTTCAGA		
		C_ A TT		
GAM1304	KLRG1	3' GAGAAGGTACAGTGATGAA	19437	GG AAG
		TTCATCACTG T TCTC		
		AAGTAGTGAC G AGAG		
		AT GA_		
GAM1304	LIFR	3' AGAAATGTTTCAGTAATGAA	9743	C GG AG
		TTCAT ACTG TA TCT		
		AAGTA TGAC GT AGA		
		A TT AA		
GAM1304	SHC1	3' GAGACCTGAGGCAGATGAA	11648	A__ G TAA
		TTCATC CT GG GTCTC		
		AAGTAG GA TC CAGAG		
		ACG G ____		
GAM1304	SHC1	3' GAGACCTGAGGCAGATGAA	11649	A__ G TAA
		TTCATC CT GG GTCTC		
		AAGTAG GA TC CAGAG		
		ACG G ____		
GAM1304	SLC16A7	5' GGAAACTTATGTCTTGGTGA	16404	TG ____ C
		TCAC GG TAAGT TCC		
		AGTG TC ATTCA AGG		
		GT TGT A		
GAM1304	SPRR1B	3' GAGACTTAAGATGAA	87405	ACTGGG
		TTCATC TAAGTCTC		
		AAGTAG ATTCAGAG		
		A_____		
GAM1304	SVIL	5' GGATTTGCCCAGTAATGGA	41410	C
		TTCAT ACTGGGTAAGTCT		
		AGGTA TGACCCGTTTAGG		
		A		
GAM1304	UQCRFS1	3' GGAGACTTATTTGAGAGGAA	20006	A AC GG
		TTC TC T GTAAGTCTCC		
		AAG AG G TATTCAGAGG		
		G A_ TT		
GAM1304	WHSC1L1	3' GGAAACATTTCAGTGA	35032	AA C
		TCACTGGGT GT TCC		
		AGTGACTTA CA AGG		
		__ A		
GAM1304	C1GALT1	3' GGAATCCCAGTGAGGAA	39344	A TAAG
		TTC TCACTGGG TCT		

AAG AGTGACCC AGG  
 G TA\_\_  
 GAM1304 DKFZp434K114 3' AGAAGCCCAGTGATGAG 60732 AAG  
 TTCATCACTGGGT TCT  
 ||||| |||  
 GAGTAGTGACCCG AGA  
 A\_\_  
 GAM1304 DKFZP434O047 5' GAAGACCCAGTGAGAA 31512 A AAG  
 TTC TCACTGGGT TC  
 ||| ||||| ||  
 AAG AGTGACCCA AG  
 \_ GA\_  
 GAM1304 DKFZp761H079 5' GGATTCCAGTGATGAA 58733 TAA  
 TTCATCACTGGG GTCT  
 ||||| |||  
 AAGTAGTGACCT TAGG  
 \_\_\_\_\_  
 GAM1304 FASTK 5' GGAGACTTAGAGAGACGAA 46991 A A GGG  
 TTC TC CT TAAGTCTCC  
 ||| || |||||  
 AAG AG GA ATTCAGAGG  
 C A G\_\_  
 GAM1304 FLJ12085 3' AGATTGTTACCCAGTAATGAA 42867 C \_  
 TTCAT ACTGGGTAA GTCT  
 |||| ||||| |||  
 AAGTA TGACCCATT TAGA  
 A GT  
 GAM1304 FLJ13441 3' GGAGACCCACCCGGTGG 43666 AA  
 TCACTGGGT GTCTCC  
 ||||| |||||  
 GGTGGCCCA CAGAGG  
 CC  
 GAM1304 FLJ20069 3' AGATGTATACCCAGTGTGAA 34467 T A\_\_  
 TTCA CACTGGGTA GTCT  
 ||| ||||| |||  
 AAGT GTGACCCAT TAGA  
 \_ ATG  
 GAM1304 FLJ20127 3' GGAGATGTACAATGATG 34592 CTGG A  
 CATCA GTA GTCTCC  
 |||| ||| |||||  
 GTAGT CAT TAGAGG  
 AA\_\_ G  
 GAM1304 FLJ21007 3' GAAACGAGCCAGTGACTGAA 47925 \_ GTAA C  
 TTCA TCACTGG GT TC  
 ||| ||||| |||  
 AAGT AGTGACC CA AG  
 C GAG\_ A  
 GAM1304 FLJ22167 5' GCTCCCAGTGAGGAA 44578 A TA  
 TTC TCACTGGG AGT  
 ||| ||||| |||

			AAG AGTGACCC TCG		
			G _		
GAM1304	FLJ23506	3'	GGAGACTTACCTGTGTTGA	45745	T T
			TCA CAC GGGTAAGTCTCC		
			AGT GTG TCCATTCAGAGG		
			T _		
GAM1304	FLJ23584	3'	GAGCCTCCCAGTGAGAA	44739	A TA T
			TTC TCACTGGG AG CTC		
			AAG AGTGACCC TC GAG		
			_ _ C		
GAM1304	FLJ32954	5'	GAGACTTACTTTGGAT	58511	ACT
			ATC GGGTAAGTCTC		
			TAG TTCATTCAGAG		
			GT_		
GAM1304	GFR	3'	GAGAGTACCAGTGATGA	24472	G AG
			TCATCACTGG TA TCTC		
			AGTAGTGACC AT AGAG		
			_ G_		
GAM1304	IMP-1	3'	AGATGTTCCAGTGAGGAA	21564	A TAA
			TTC TCACTGGG GTCT		
			AAG AGTGACCT TAGA		
			G TG_		
GAM1304	KIAA0020	5'	AGACAACTCAGTGAT	29650	AA
			ATCACTGGGT GTCT		
			TAGTGA CTCA CAGA		
			A_		
GAM1304	KIAA0062	3'	GAAAATTTCACTGATGGA	70239	TAAG
			TTCATCACTGGG TC		
			AGGTAGTGACTT AG		
			TAAA		
GAM1304	KIAA1013	3'	GAGAGGACTCAGTGTGAA	88888	T AAG
			TTCA CACTGGGT TCTC		
			AAGT GTGACTCA AGAG		
			_ GG_		
GAM1304	KIAA1274	3'	GGAGACTTCAGGAATGA	91366	CA GTA
			TCAT CTGG AGTCTCC		
			AGTA GACT TCAGAGG		
			AG _		
GAM1304	MAP2K4	3'	GAAGGACACAGTGATGAA	11549	G AAG
			TTCATCACTG GT TC		

AAGTAGTGAC CA AG  
 A GGA  
 GAM1304 MGC16075 5' GGAAACTTACTCAGGGTGAA 51287 A C  
 TTCATC CTGGGTAAGT TCC  
 ||||| ||||| |||  
 AAGTGG GACTCATTCA AGG  
 \_ A  
 GAM1304 MRPS21 3' GGACACCCAGTGCGAA 49116 AT AA  
 TTC CACTGGGT GTCT  
 ||| ||||| |||  
 AAG GTGACCCA CAGG  
 C\_ \_  
 GAM1304 MRPS21 3' GGACACCCAGTGCGAA 38642 AT AA  
 TTC CACTGGGT GTCT  
 ||| ||||| |||  
 AAG GTGACCCA CAGG  
 C\_ \_  
 GAM1304 MY014 5' AGATCCCAGTGACGA 48138 A TAA  
 TC TCACTGGG GTCT  
 || ||||| |||  
 AG AGTGACCC TAGA  
 C \_  
 GAM1304 OSBPL10 3' GGAGACTTCTTTTGTGATGAA 35048 T\_ T  
 TTCATCAC GGG AAGTCTCC  
 ||||| ||| |||||  
 AAGTAGTG TTC TTCAGAGG  
 TT \_  
 GAM1304 PAFAH2 5' GATTCACCCGGTGATGAA 4765 A  
 TTCATCACTGGGT AGTC  
 ||||| ||||| |||  
 AAGTAGTGGCCCA TTAG  
 C  
 GAM1304 PIP3-E 3' GGAGCCCCCAGTGATGAA 66810 TAA T  
 TTCATCACTGGG G CTCC  
 ||||| ||| |||  
 AAGTAGTGACCC C GAGG  
 C\_ \_  
 GAM1304 SYTL2 3' GGAGACAGACATCAGTGATGA 50472 \_ AA  
 TCATCACTGG GT GTCTCC  
 ||||| || |||||  
 AGTAGTGA CT CA CAGAGG  
 A GA  
 GAM1304 SYTL2 3' GGAGACAGACATCAGTGATGA 51961 \_ AA  
 TCATCACTGG GT GTCTCC  
 ||||| || |||||  
 AGTAGTGA CT CA CAGAGG  
 A GA  
 GAM1304 TUSP 5' AGACTTGCGTATGAGAA 39623 A C G  
 TTC TCA TG GTAAGTCT  
 ||| ||| || |||||

			AAG AGT AT CGTTCAGA		
			— _ G		
GAM1304	ZNF302	3'	GGAGACTTTTAGCAATGA	37418	CA GT
			TCAT CTGG AAGTCTCC		
			AGTA GATT TTCAGAGG		
			AC —		
GAM1304	ZNF302	3'	GGAGACTTTTAGCAATGA	37927	CA GT
			TCAT CTGG AAGTCTCC		
			AGTA GATT TTCAGAGG		
			AC —		
GAM1304	LOC115400	5'	GGAGACTTACAATGATGA	73444	CTGG
			TCATCA GTAAGTCTCC		
			AGTAGT CATTGAGAGG		
			AA—		
GAM1304	LOC150351	3'	GGAGACTTATTTGAGAGGAA	60248	A AC GG
			TTC TC T GTAAGTCTCC		
			AAG AG G TATTGAGAGG		
			G A_ TT		
GAM1304	LOC158801	3'	AGACTCCAGTGATGAA	86892	GTA
			TTCATCACTGG AGTCT		
			AAGTAGTGACC TCAGA		
			—		
GAM1304	LOC161635	5'	GAGACTTAGAGGGATGA	96571	A GGG
			TCATC CT TAAGTCTC		
			AGTAG GG ATTCAGAG		
			_ AG_		
GAM1304	LOC161734	3'	GGGTATCAGTGATGGA	87102	GTAAGT
			TTCATCACTGG CTC		
			AGGTAGTGACT GGG		
			AT—		
GAM1304	LOC197259	3'	GGAACCTTACCCAGCCATGAA	87962	CA TC
			TTCAT CTGGGTAAG TCC		
			AAGTA GACCCATTC AGG		
			CC CA		
GAM1304	LOC199699	3'	GAGACACAGTGATGA	88305	GGTAA
			TCATCACTG GTCTC		
			AGTAGTGAC CAGAG		
			A—		
GAM1304	LOC203080	5'	GACTCTTTACCCAGGGACGAA	89267	A A —
			TTC TC CTGGGTA AGTC		

		AAG AG GACCCAT TCAG		
		C G TTC		
GAM1304	LOC90190	3' GGAAACAGATTCAGTGA 61779	AA	C
		TCACTGGGT GT TCC		
		AGTGACTTA CA AGG		
		GA A		
GAM1304	LOC91960	3' GAGACCTGGCCTAGTGA 67662	AA	_
		TCACTGGGT GTCTC		
		AGTGATCCG CAGAG		
		GTC		
GAM1304	LOC92379	3' ACTTAGATCTGAGTGATGGA 69145	G	___
		TTCATCACT GG TAAGT		
		AGGTAGTGA TC ATTCA		
		G TAG		
GAM1305	CA11	5' AGGAAGATCAGGAGCTAGAGG 6870	TCC	G
		CCTCTAGCTCCT AT TTCCT		
		GGAGATCGAGGA TA AAGGA		
		C__ G		
GAM1305	CALU	3' GATGTGGAAAGAGCTAAAG 6888	C	C
		CT TAGCTC TTCCATGTT		
		GA ATCGAG AAGGTGTAG		
		A A		
GAM1305	DXS1283E	3' AGGAACATGGAAAATGGAGG 70835	GCTCC	
		CCTCTA TTCCATGTTCT		
		GGAGGT AAGGTACAAGGA		
		AA__		
GAM1305	FKBP1B	3' GGCAGGAAGGAACTCAAGGT 54010	CT C	A
		ACCT AG TCCTTCC TGTT		
		TGGA TC AGGAAGG ACGG		
		AC A _		
GAM1305	FKBP1B	3' GGCAGGAAGGAACTCAAGGT 14649	CT C	A
		ACCT AG TCCTTCC TGTT		
		TGGA TC AGGAAGG ACGG		
		AC A _		
GAM1305	FLG	3' AGAAATATCGAAGGAGC 70875	C	C
		GCTCCTTC ATGTT CT		
		CGAGGAAG TATAA GA		
		C A		
GAM1305	FNTB	3' GGAAAAGAGCTGGAGGT 8954	C	_
		ACCTCTAGCTC TTCC		

			TGGAGGTCGAG AAGG		
			AA		
GAM1305	GNB3	5'	GGAACCGGAGCTGGA 9079	TTCCAT	
			TCTAGCTCC GTTCC		
			AGGTCGAGG CAAGG		
			C_____		
GAM1305	HCFC1	5'	GAAAGGGAAGAGCCAAAGG 70994	CTA C ATG	
			CCT GCTC TTCC TTC		
			GGA CGAG AAGG AAG		
			AAC _ GA_		
GAM1305	HOXD4	5'	AGGAACATGAGGTGCAAAGGT 27520	CTA T TC	
			ACCT GC CCT CATGTTCT		
			TGGA CG GGA GTACAAGGA		
			AA_ T _		
GAM1305	MOCS2	5'	TGTGGAAGGAGATAGA 15770	G	
			TCTA CTCCTTCCATG		
			AGAT GAGGAAGGTGT		
			A		
GAM1305	MSX1	3'	GAACAGAGCTAGAGG 10129	CTTCCA	
			CCTCTAGCTC TGTTT		
			GGAGATCGAG ACAAG		
			_____		
GAM1305	NR4A1	3'	GGAAGAAAGAGCTTGAGGT 9239	T _	
			ACCTC AGCTC CTTCC		
			TGGAG TCGAG GAAGG		
			T AAA		
GAM1305	PLD2	3'	TGAAGGGAAGCTAGAGGT 10627	C C	
			ACCTCTAG TCCTT CA		
			TGGAGATC AGGGA GT		
			A A		
GAM1305	PRX	5'	AGGAGGCCCAAGGAGCTGGAGG 40517	CCATG	
	T		ACCTCTAGCTCCTT TTCCT		
			TGGAGGTCGAGGAA GAGGA		
			CCCG_		
GAM1305	SIM1	3'	AATATGGAAAGGCCAGAGG 17376	A CC	
			CCTCT GCT TTCCATGTT		
			GGAGA CGG AAGGTATAA		
			C A_		
GAM1305	SP3	3'	CATAGAAGAACTAGAGGT 82495	CTC C	
			ACCTCTAG CTTC ATG		



			TGGAGATC GAAG TAC			
			AA_ A			
GAM1305	TIRAP	3'	AGGCCATGAGGAAGCCAGA 53566	A _ TC TT		
			TCT GCT CCT CATG CCT			
			AGA CGA GGA GTAC GGA			
			C A _ C_			
GAM1305	WHSC1	3'	AGGCTCATGGAGGAAGCCAAAG 23653	A_ C TT		
	A		TCT GCT CTTCCATG CCT			
			AGA CGA GGAGGTAC GGA			
			AAC A TC			
GAM1305	XRCC2	3'	GAACAAAGCTGGAGG 18322	CCTTCCA		
			CCTCTAGCT TGTTC			
			GGAGGTCGA ACAAG			
			A_____			
GAM1305	C1orf34	3'	GGCTTGGAAGGAACTAAAG 60678	C C T		
			CT TAG TCCTTCCA GTT			
			GA ATC AGGAAGGT CGG			
			A A T			
GAM1305	C2orf7	3'	AACAAAAGGAGCTGAAGG 50300	C CCA		
			CCT TAGCTCCTT TGTT			
			GGA GTCGAGGAA ACAA			
			A A_			
GAM1305	CDW92	3'	AGAAACATGGAACATAAAGC 54503	CC_ C		
			GCT TTCCATGTT CT			
			CGA AAGGTACAA GA			
			AATAC A			
GAM1305	FLJ10210	5'	ATGGAAGAAAGCTAGAG 35900	C_		
			CTCTAGCT CTTCCAT			
			GAGATCGA GAAGGTA			
			AA			
GAM1305	FLJ14107	3'	AGGGAGGAAGGGAGCCAAAGG 46688	CTA _ ATG		
			CCT GCTCC TTCC TTCCT			
			GGA CGAGG AAGG AGGGA			
			AAC G _			
GAM1305	GREB1	3'	GCTGGAAGAGCTAGA 27879	C T		
			TCTAGCTC TTCCA GT			
			AGATCGAG AAGGT CG			
			A _			
GAM1305	HPCAL4	3'	GAATCAGAAAGAGCTAGA 32736	C CAT		
			TCTAGCTC TTC GTTC			

AGATCGAG AAG TAAG  
 A AC\_  
 GAM1305 KIAA0433 3' AGGAACATAAAAGCCCAGCAGG 30833 CTA C\_\_ CC  
 CCT GCT CTT ATGTTCT  
 ||| ||| ||| |||||  
 GGA CGA GAA TACAAGGA  
 \_\_ CCC AA  
 GAM1305 KIAA0494 3' AGCTCAGAAGTAGCTAGAGG 28737 C CAT  
 CCTCTAGCT CTTC GTT  
 ||||| ||| |||  
 GGAGATCGA GAAG CGA  
 T ACT  
 GAM1305 KIAA0555 3' ATTGAAGGAGCTGAGG 60114 T C  
 CCTC AGCTCCTTC AT  
 ||| ||||| ||  
 GGAG TCGAGGAAG TA  
 \_ T  
 GAM1305 KIAA0836 3' AATTTGGAAAGGAGCTAGTAG 64559 \_ \_ T  
 CT CTAGCTCCTT CCA GTT  
 || ||||| ||| |||  
 GA GATCGAGGAA GGT TAA  
 T A T  
 GAM1305 KIAA1032 3' AACAGAAGGAGACCAGA 66147 AG\_ CA  
 TCT CTCCTTC TGTT  
 ||| ||||| |||  
 AGA GAGGAAG ACAA  
 CCA \_  
 GAM1305 MGC32104 3' AACATGGATGCAGAGG 58400 A TCCT  
 CCTCT GC TCCATGTT  
 |||| || |||||  
 GGAGA CG AGGTACAA  
 \_ T\_\_  
 GAM1305 PCAF 5' AGGAACATGTCCGCAGCCAGGG 13944 A CCTTC  
 CTCT GCT CATGTTCT  
 ||| ||| |||||  
 GGA CGA GTACAAGGA  
 C CGCCT  
 GAM1305 POF1B 3' AGGAGTCATGGATGGAAGTAGA 46218 C T \_  
 GGT ACCTCTAG TCC TCCATG TTCCT  
 ||||| ||| ||||| |||||  
 TGGAGATC AGG AGGTAC GAGGA  
 A T T  
 GAM1305 RPL41 3' AGAAACATGGAATGCCAGA 40854 A TCC C  
 TCT GC TTCCATGTT CT  
 ||| || ||||| ||  
 AGA CG AAGGTACAA GA  
 C T\_\_ A  
 GAM1305 SNTG1 3' AGGGACATAAAAGAGTTA 38573 C CC  
 TAGCTC TT ATGTTCT  
 ||||| || |||||

ATTGAG AA TACAGGGA  
 \_ AA  
 GAM1305 TNRC3 3' AACACAAAGAGGCTAGAG 19654 TC CCA  
 CTCTAGC CTT TGTT  
 ||||| ||| ||||  
 GAGATCG GAA ACAA  
 GA AC\_  
 GAM1305 TRIM15 5' AGGGACCAGAAGGAGCCAGGAG 52652 CT A CAT  
 T AC CT GCTCCTTC GTTCCT  
 || || ||||| |||||  
 TG GA CGAGGAAG CAGGGA  
 AG C AC\_  
 GAM1305 LOC126520 5' GAACATGGAGGTGAAGA 74523 AGC \_  
 TCT TC CTTCCATGTTT  
 ||| || |||||  
 AGA AG GGAGGTACAAG  
 \_ T  
 GAM1305 LOC131000 3' GAAACGGAGGAGCAGA 75854 A CATG  
 TCT GCTCCTTC TTC  
 ||| ||||| |||  
 AGA CGAGGAGG AAG  
 \_ CA\_  
 GAM1305 LOC131873 5' GGGCTGAAGGGAGCTAGAGG 75881 C T  
 CCTCTAGCTCCTT CA GTTC  
 ||||| || ||||  
 GGAGATCGAGGGA GT CGGG  
 A \_  
 GAM1305 LOC133584 3' AGGAACATGTGTTACCGAGGT 75098 \_ TCCTTC  
 ACCTC TAGC CATGTTCT  
 |||| ||| |||||  
 TGGAG ATTG GTACAAGGA  
 CC T\_\_\_\_  
 GAM1305 LOC142941 5' GACTTGGGGAAGGAGCTAAGA 82883 \_ AT\_  
 TCT AGCTCCTTCC GTT  
 ||| ||||| |||  
 AGA TCGAGGAAGG CAG  
 A GGTT  
 GAM1305 LOC143970 3' ACATGGAAAGACTAGA 82999 C C  
 TCTAG TC TTCCATGT  
 |||| || |||||  
 AGATC AG AAGGTACA  
 \_ A  
 GAM1305 LOC144559 5' AACTGAGAAAGGAGCTAAAG 76877 C \_ T  
 CT TAGCTCCTT C CA GTT  
 || ||||| || |||  
 GA ATCGAGGAA G GT CAA  
 A A A \_  
 GAM1305 LOC144715 5' AACGTGGATGGAAGTAGAGGT 76928 C T  
 ACCTCTAG TCC TCCATGTT  
 ||||| || |||||

		TGGAGATC AGG AGGTGCAA		
		A T		
GAM1305	LOC145900 5'	AGCCGAAAGGGAGCTAGAGGT 77562		CCAT
		ACCTCTAGCTCCTT GTT		
		TGGAGATCGAGGGA CGA		
		AAGC		
GAM1305	LOC146712 5'	AGGAACATGCCCAGAGCCAGAG 83713	A	CTTC
	G	CCTCT GCTC CATGTTCT		
		GGAGA CGAG GTACAAGGA		
		C ACCC		
GAM1305	LOC146952 5'	AGGAAATCAGGAGTTAGAG 83858		TCCATG
		CTCTAGCTCCT TTCCT		
		GAGATTGAGGA AAGGA		
		CTA__		
GAM1305	LOC148523 5'	GACGGCGAAGGAGCTGGA 58451		CA
		TCTAGCTCCTTC TGTT		
		AGGTCGAGGAAG GCAG		
		CG		
GAM1305	LOC149684 5'	GGAAGAAGGGGCCAGA 84614	A	CATG
		TCT GCTCCTTC TTCC		
		AGA CGGGGAAG AAGG		
		C ____		
GAM1305	LOC151162 5'	AGGAACATTTTGTAGCTAGA 85239		CTTCC
		TCTAGCTC ATGTTCT		
		AGATCGAG TACAAGGA		
		TTTT_		
GAM1305	LOC155179 3'	AGCCAGTGAGGAGCTAAAG 81308	C	CCAT
		CT TAGCTCCTT GTT		
		GA ATCGAGGAG CGA		
		A TGAC		
GAM1305	LOC160414 3'	AGGAACATGAAAGAATGC 87065	TC_	C
		GC CTT CATGTTCT		
		CG GAA GTACAAGGA		
		TAA A		
GAM1305	LOC160717 5'	GGAACCGGGGAGCCAGGG 82237	A	CCAT
		CTCT GCTCCTT GTTCC		
		GGGA CGAGGGG CAAGG		
		C C__		
GAM1305	LOC161527 5'	GGAAGGAGCTAGAGAGT 82277	_	
		AC CTCTAGCTCCTTCC		

		TG GAGATCGAGGAAGG		
		A		
GAM1305	LOC196205 3'	AGGAATTGGAAGGAGGTAGA	87587	G T
		TCTA CTCCTTCCA GTTCCT		
		AGAT GAGGAAGGT TAAGGA		
		G _		
GAM1305	LOC203377 5'	AGGAACATTTTGTAGCTAGA	90577	CTTCC
		TCTAGCTC ATGTTCT		
		AGATCGAG TACAAGGA		
		TTTT_		
GAM1305	LOC203530 3'	GGAGGAAAGAGCTAGA	89378	C ATGT
		TCTAGCTC TTCC TCC		
		AGATCGAG AAGG AGG		
		A _		
GAM1305	LOC219918 5'	AACTGAGAAAGGAGCTAAAG	91537	C _ _ T
		CT TAGCTCCTT C CA GTT		
		GA ATCGAGGAA G GT CAA		
		A A A _		
GAM1305	LOC220071 5'	AACTGAGAAAGGAGCTAAAG	93432	C _ _ T
		CT TAGCTCCTT C CA GTT		
		GA ATCGAGGAA G GT CAA		
		A A A _		
GAM1305	LOC221296 3'	GAACAAAAGGCTAGAGG	91963	CCTTCCA
		CCTCTAGCT TGTTC		
		GGAGATCGG ACAAG		
		AAA_		
GAM1305	LOC221300 3'	AACATGGATGGAAGTAGAGGT	91925	C T
		ACCTCTAG TCC TCCATGTT		
		TGGAGATC AGG AGGTACAA		
		A T		
GAM1305	LOC221501 5'	GAAAGACGGAAGGAGCCAAGAG	93793	A_ ATG_
		CTCT GCTCCTTCC TTC		
		GAGA CGAGGAAGG AAG		
		AC CAGA		
GAM1305	LOC222252 5'	GAACAAAGCTGGAGG	94308	CCTTCCA
		CCTCTAGCT TGTTC		
		GGAGGTCGA ACAAG		
		A_		
GAM1305	LOC222488 5'	GGAAAGGCTAGAGGT	94346	CC
		ACCTCTAGCT TTCC		

TGGAGATCGG AAGG  
 A\_  
 GAM1305 LOC253256 5' GGTGTGGAAGGAGCCAGGT 96244 T A TG  
 ACC CT GCTCCTTCCA TT  
 ||| || ||||| ||  
 TGG GA CGAGGAAGGT GG  
 \_ C GT  
 GAM1305 LOC254936 5' AGCCGAAAGGGAGCTAGAGGT 94970 CCAT  
 ACCTCTAGCTCCTT GTT  
 ||||| |||  
 TGGAGATCGAGGGA CGA  
 AAGC  
 GAM1305 LOC254947 5' GGAAGGAGCTAGAGAGT 96578 \_  
 AC CTCTAGCTCCTTCC  
 || |||||  
 TG GAGATCGAGGAAGG  
 A  
 GAM1305 LOC256283 5' AGCAAAGGAGCTAGA 97037 CCA  
 TCTAGCTCCTT TGTT  
 ||||| |||  
 AGATCGAGGAA ACGA  
 —  
 GAM1305 LOC256309 3' ATGGAAGGAGCTGAG 95844 T  
 CTC AGCTCCTTCCAT  
 ||| |||||  
 GAG TCGAGGAAGGTA  
 —  
 GAM1305 LOC257471 3' CATAGAAGAACTAGAGGT 95686 CTC C  
 ACCTCTAG CTTC ATG  
 ||||| ||| |||  
 TGGAGATC GAAG TAC  
 AA\_ A  
 GAM1305 LOC58489 3' AACAAAAAGAACTAGGGGT 72524 CTC CCA  
 ACCTCTAG CTT TGTT  
 ||||| ||| |||  
 TGGGGATC GAA ACAA  
 AAA AA\_  
 GAM1305 LOC63875 3' GAACTGGAGCTAGAG 41937 TTCCAT  
 CTCTAGCTCC GTTC  
 ||||| |||  
 GAGATCGAGG CAAG  
 T\_\_\_\_  
 GAM1305 LOC90625 3' AGGTAGGAGGGAGCCAAAGA 63608 A\_\_ ATGTT  
 TCT GCTCCTTCC CCT  
 ||| ||||| |||  
 AGA CGAGGGAGG GGA  
 AAC AT\_\_\_\_  
 GAM1305 LOC91050 3' TATGGGAAGAGCTAGA 64751 C  
 TCTAGCTC TTCCATG  
 ||||| |||||

			AGATCGAG AGGGTAT		
			A		
GAM1305	LOC91531	5'	AGAAACTTGCAGAGCTAGA	66337	CTTC T C
			TCTAGCTC CA GTT CT		
			AGATCGAG GT CAA GA		
			AC__ T A		
GAM1306	ATRN	3'	TTAATGGGTGCAGCACAC	57809	C TT
			GTGTGCTGT TT TTAA		
			CACACGACG GG AATT		
			T GT		
GAM1306	ATRN	3'	TTAATGGGTGCAGCACAC	23833	C TT
			GTGTGCTGT TT TTAA		
			CACACGACG GG AATT		
			T GT		
GAM1306	BHLHB3	3'	TTAAAAAAGACATAATGGATG	47769	GTGTGC
			CATCCA TGTCTTTTTTAA		
			GTAGGT ACAGAAAAAATT		
			AAT__		
GAM1306	MLLT2	3'	TAAAAAAGAAGCACACGAGAT	19851	CA _ G
	G		CATC GTG TGCT TCTTTTTTA		
			GTAG CAC ACGA AGAAAAAAT		
			AG C _		
GAM1306	MTMR2	3'	AAAGAACACACTGCATG	32379	C CTG
			CAT CAGTGTG TCTTT		
			GTA GTCACAC AGAAA		
			C A__		
GAM1306	SCN3A	3'	AAGGAAACACACTGGAT	22627	CTG
			ATCCAGTGTG TCTTT		
			TAGGTCACAC AGGAA		
			AA_		
GAM1306	SOX9	3'	TAAAAAAGACAGCAAAC	4440	G
			AGT TGCTGTCTTTTTTA		
			TCA ACGACAGAAAAAAT		
			A		
GAM1306	CNOT7	3'	TAAAAAAGACAAGAAAC	25333	GTG _
			AGT CT GTCTTTTTTA		
			TCA GA CAGAAAAAAT		
			AA_ A		
GAM1306	DKFZp762K2015	3'	AAAAAAGAAGCCAC	72472	T G
			GTG GCT TCTTTTTT		

CAC CGA AGAAAAAA

GAM1306 FUBP3 3' TTAAAAAAGACAATTGGA 63735 GTGC  
TCCAGT TGTCTTTTTTAA  
||||| |||||  
AGGTTA ACAGAAAAAATT

GAM1306 GOLPH3 3' TTAAATTGAAACAGCACA 42116 C T\_  
TGTGCTGT TT TTAA  
||||| || |||||  
ACACGACA AG AAATT  
A TT

GAM1306 KIAA1001 3' AAAAAAGACTTTGCCTGG 30286 T CT  
CCAG GTG GTCTTTTTT  
||| ||| |||||  
GGTC CGT CAGAAAAAA  
\_ TT

GAM1306 KIAA1466 3' AAAAAAGACATAGAC 71912 G C  
GT TG TGTCTTTTTT  
|| || |||||  
CA AT ACAGAAAAAA  
G \_

GAM1306 KIAA1468 3' TAAAAAAGACATTGGCTG 91776 GTGC  
CAGT TGTCTTTTTTA  
||| |||||  
GTCG ACAGAAAAAAT  
GTT\_

GAM1306 KIAA1883 3' TAAAAAAGACAAAAACA 73420 GC\_  
TGT TGTCTTTTTTA  
||| |||||  
ACA ACAGAAAAAAT  
AAA

GAM1306 MEGF10 3' TTAAAAAAGAAAATCTGGA 50587 TGTGCTG  
TCCAG TCTTTTTTAA  
||||| |||||  
AGGTC AGAAAAAATT  
TAAA\_

GAM1306 MOST2 5' TAAAAAAGACAGGAGGA 39690 AGTGTG  
TCC CTGTCTTTTTTA  
||| |||||  
AGG GACAGAAAAAAT  
AG\_

GAM1306 PPP1R16B 3' TTAAAAAAAACAGTCGCT 61394 T C  
AGTG GCTGT TTTTTTAA  
||| ||| |||||  
TCGC TGACA AAAAAATT

GAM1306 SLC11A2 3' AAAAGCGCAGACTGGATG 5230 G T T  
CATCCAGT TGC G CTTT  
||||| ||| | |||||



	GTAGGTCA ACG C GAAAA	
	G _ _	
GAM1306 LOC124783 5'	AAAGAGCACACTGGA 74334	TG
	TCCAGTGTGC TCTTT	
	AGGTCACACG AGAAA	
	—	
GAM1306 LOC144248 5'	TAAAAAAGACAAACA 76743	GC
	TGT TGTCTTTTTTA	
	ACA ACAGAAAAAAT	
	A_	
GAM1306 LOC146712 5'	AAGGCCAGCACACAGGA 83712	A _
	TCC GTGTGCTG TCTT	
	AGG CACACGAC GGAA	
	A C	
GAM1306 LOC146723 3'	AAAAAAGACACTTGTACAC 78081	—
	GTGTGC TGTCTTTTTT	
	CACATG ACAGAAAAAA	
	TTC	
GAM1306 LOC151040 3'	TTAATGGGTGCAGCACAC 80105	C TT
	GTGTGCTGT TT TTAA	
	CACACGACG GG AATT	
	T GT	
GAM1306 LOC153606 5'	TTAAAACAAAACAAACTGGA 86077	GC C _
	TCCAGTGT TGT TT TTTTAA	
	AGGTCACA ACA AA AAAATT	
	A_ A C	
GAM1306 LOC157697 5'	GACAGCACACAGATG 81549	CA
	CATC GTGTGCTGTC	
	GTAG CACACGACAG	
	A_	
GAM1306 LOC220906 3'	AAAAAGACCCACACCGGA 91395	A CT
	TCC GTGTG GTCTTTTT	
	AGG CACAC CAGAAAAA	
	C C_	
GAM1306 LOC222252 3'	TTAATGGGTGCAGCACAC 94310	C TT
	GTGTGCTGT TT TTAA	
	CACACGACG GG AATT	
	T GT	
GAM1306 LOC222697 3'	TAAAAAAACACACTGGA 94354	CTGTC
	TCCAGTGTG TTTTTTA	

		AGGTCACAC	AAAAAAT		
		A_____			
GAM1306	LOC90317	5'	AAAGGAGTCACACTGGA	62248	_ G
			TCCAGTGTG CT TCTTT		
			AGGTCACAC GA GGAAA		
			T _		
GAM1306	LOC90829	3'	TTAATGGGTGCAGCACAC	64101	C TT
			GTGTGCTGT TT TTAA		
			CACACGACG GG AATT		
			T GT		
GAM1306	LOC92876	3'	TTAATGGGTGCAGCACAC	70806	C TT
			GTGTGCTGT TT TTAA		
			CACACGACG GG AATT		
			T GT		
GAM1307	ABCF1	3'	ATTCAGGCACATGAAGGTGGAG	6566	C_ AT
	TG		CATTTCACTTTCA TGTCTGAG		
			GTGAGGTGGAAGT ACGGACTT		
			AC A		
GAM1307	ACVRL1	5'	GCGGTGGAGGGGAGGTG	3418	A
			CATTTTCTTTCACTGT		
			GTGGAG GGAGGTGGCG		
			G		
GAM1307	ADRA1A	3'	TCTTGATGGAAGTGAGG	5448	CTG T
			TTTCACTTTCA TC GAGA		
			GGAGTGAAGGT AG TTCT		
			_____		
GAM1307	AGT	3'	ATTTTAGAGAATGGGGGTGGGG	3453	TT TT CTG
			T CACT CA TCTGAGAT		
			G GTGG GT AGATTTTA		
			GG GG AAG		
GAM1307	AIM1	3'	ATCTCAGGCTGGAGTGCAGTG	91816	T CACT
			CATT CACTTT GTCTGAGAT		
			GTGA GTGAGG CGGACTCTA		
			C T_____		
GAM1307	AKAP13	3'	GTTTTGGGCATGGATAAAGTGA	58580	___ C TG
	AG		TTTCACT TTCA TGTC AGAT		
			GAAGTGA AGGT ACGG TTTG		
			AAT _ GT		
GAM1307	AKAP13	3'	GTTTTGGGCATGGATAAAGTGA	22144	___ C TG
	AG		TTTCACT TTCA TGTC AGAT		

		GAAGTGA AGGT ACGG TTTG	
		AAT _ GT	
GAM1307 AKAP13	3'	GTTTTGGGCATGGATAAAGTGA 23248	___ C TG
	AG	TTTCACT TTCA TGTC AGAT	
		GAAGTGA AGGT ACGG TTTG	
		AAT _ GT	
GAM1307 ATP11B	3'	ATTCAGGTGTGGCTGTGGAAT 80315	TT TGT
	G	CATTTAC TCAC CTGAGAT	
		GTAAGGTG GGTG GACTTTA	
		TC TG_	
GAM1307 B4GALT4	3'	TAGCAGGAGGGTGGAGTG 13674	A T
		CATTTCACTTTC CTG CTG	
		GTGAGGTGGGAG GAC GAT	
		- -	
GAM1307 BLAME	3'	ATCTGGGAGTGAGGGTGGAG 39239	TG G
		TTTCACTTTCAC TCT AGAT	
		GAGGTGGGAGTG AGG TCTA	
		_ G	
GAM1307 C20orf1	5'	ATTCAGAAAAGGGGTGAAA 23999	CACTG
		TTTCACTTT TCTGAGAT	
		AAAGTGGGG AGACTTTA	
		AAA_	
GAM1307 C21orf5	3'	TTTCAGGCTAGGTGCGGTG 17614	TT _
		CACT CACT GTCTGAGA	
		GTGG GTGG CGGACTTT	
		C_ AT	
GAM1307 CAPN10	3'	GTCTCAGAACCGAGTGAGGTG 43604	TCACTG
		CATTTCACTT TCTGAGAT	
		GTGGAGTGAG AGACTCTG	
		CCA_	
GAM1307 CARPX	3'	ATTCAGATAGTGCCTAGGA 39415	A TT_
		TC CT CACTGTCTGAGAT	
		AG GA GTGATAGACTTTA	
		_ TCCT	
GAM1307 CARPX	5'	TCGGGTGGGAGTGCGAGTG 39426	_ TT TGT
		CATTT CACT CAC CTGA	
		GTGAG GTGA GTG GGCT	
		C GG _	
GAM1307 CASP10	3'	TTTTGGACTGGGTGCGGTG 52111	TT _ TG
		CACT CACT GTC AGA	

			GTGG GTGG CAG TTT			
			C_ GT GT			
GAM1307	CASP10	3'	TTTTGGACTGGGTGCGGTG 52127	TT	__	TG
			CACT CACT GTC AGA			
			GTGG GTGG CAG TTT			
			C_ GT GT			
GAM1307	CCND1	3'	GTGGTGGCAGTGGAGGTGGGGT 53891	TT		TGAGAT
	G		CAT CACTTTCACTGTC			
			GTG GTGGAGGTGACGG			
			GG TGGTG			
GAM1307	CDK4	5'	GTCACATGGTGAGGGTGGGG 53763	TT		C GAT
			T CACTTTCACTGT TGA			
			G GTGGGAGTGGTA ACT			
			GG C G			
GAM1307	CDK4	5'	GTCACATGGTGAGGGTGGGG 3573	TT		C GAT
			T CACTTTCACTGT TGA			
			G GTGGGAGTGGTA ACT			
			GG C G			
GAM1307	CDKN2A	5'	GTCCGGGTGGGAGTGGGGGTGG 54229	TT	TT	G__ A
	GGTG		T CACT CACT TCTG GAT			
			G GTGG GTGA GGGC CTG			
			GG GG GGGT _			
GAM1307	CDKN2A	5'	TATCTTGAGAGTCCGGGTGGGA 54230	TT	G_____	TG
	GTGGGG		ACT CACT TC AGAT A			
			TGA GTGG AG TCTA T			
			GG GCCTGG GT			
GAM1307	CDKN2B	3'	AGGTGGTGGAGTGGAGTG 54353	T		TG
			CATTTCATT CAC TCT			
			GTGAGGTGAG GTG GGA			
			_ GT			
GAM1307	CERD4	3'	ATCTCAGAGCAGAGGAGGTGGG 23849	TT	A _	
	G		T CACTTTC CTG TCTGAGAT			
			G GTGGAGG GAC AGACTCTA			
			GG A G			
GAM1307	CHRM1	3'	TTTTCTGGGAGTGGGAGTCAA 94794	C	TT	G T_ T
	GTG		CATTT ACT CACT TC GAGA			
			GTGAA TGA GTGA GG CTTT			
			C GG G TC TA			
GAM1307	CLASP1	3'	GGGGGTGGGGTGGGGTG 65305	TT	T	G
			CAT CACTT CACT TC			

GTG GTGGG GTGG GG  
 GG \_ G  
 GAM1307 CMAR 5' ATTTTGGACGGTGCTCTGA 17772 CTTT TG  
 TCA CACTGTC AGAT  
 ||| ||||| |||  
 AGT GTGGCAG TTTA  
 CTC\_ GT  
 GAM1307 COL1A1 3' ATCTATGTGATGGGTGGGGTG 3601 TT \_ TGTCTG  
 CAT CACTT TCAC AGAT  
 ||| ||||| ||| |||  
 GTG GTGGG AGTG TCTA  
 GG T TA\_\_\_\_  
 GAM1307 COL4A4 5' CAGGCGGGGAAGTGGGGTG 3626 TT A  
 CAT CACTTTC CTGTCTG  
 ||| ||||| |||||  
 GTG GTGAAGG GGCGGAC  
 GG \_  
 GAM1307 COL4A6 3' GTCTTAGGCAGGCAAGAGAATT 8473 \_\_\_\_ CA\_  
 GAAATG TCA CTTT CTGTCTGAGAT  
 ||| ||| |||||  
 AGT GAGA GACGGATTCTG  
 TAA ACG  
 GAM1307 CPT1B 3' GCCCAGGTGGTGGAGGTGGGGT 15199 TT TG AGAT  
 AT CACTTTCAC TCTG  
 || ||||| |||  
 TG GTGGAGGTG GGAC  
 GG GT CCG  
 GAM1307 D10S170 3' GTTTTGTACTTTGGTAGTGAAG 18367 T CT CT  
 TG CATTTCACT TCA GT GAGAT  
 ||||| ||| || |||||  
 GTGAAGTGA GGT CA TTTTG  
 T TT TG  
 GAM1307 DDEF2 3' ATTTTAGGCGGCCAGTGAAGTGA 13952 T TTCA  
 CA TTCACT CTGTCTGAGAT  
 || ||||| |||||  
 GT AAGTGA GGCGGATTTTA  
 C CC\_  
 GAM1307 DES 3' TCTCAGGCTGGTGGGAG 72132 TT \_  
 CT CACT GTCTGAGA  
 || ||| |||||  
 GA GTGG CGGACTCT  
 GG T  
 GAM1307 DLEC1 3' TAGAGAGAGTGAGGTG 23706 A  
 CATTTCACTTTC CTG  
 ||||| |||  
 GTGGAGTGAGAG GAT  
 A  
 GAM1307 DPYSL3 3' ATCTCAGCTTATATGAAAGTCA 7311 C C \_\_\_\_  
 AGTG TTT ACTTTC TGT CTGAGAT  
 ||| ||||| ||| |||||

GAA TGAAAGT ATA GACTCTA  
 C \_ TTC  
 GAM1307 DRIL1 3' GTTTTGGACATTCAGAGAGATG 17831 A TTCAC TG  
 CATTTC CT TGTC AGAT  
 ||||| || ||| ||||  
 GTAGAG GA ACAG TTTG  
 A CTT\_ GT  
 GAM1307 DXS1283E 3' GTTTTAGATAGTTTTTGATGGA 70836 CTTTC\_  
 A TTTCA ACTGTCTGAGAT  
 |||| | ||||| |||||  
 AAGGT TGATAGATTTTG  
 AGTTTT  
 GAM1307 EHF 3' GTCTCAGATGGTTAGGACAAAG 24063 \_ \_  
 TGGA CACTT TC ACTGTCTGAGAT  
 |||| | ||||| |||||  
 GTGAA AG TGGTAGACTCTG  
 AC GAT  
 GAM1307 EIF2B1 5' CTGCGGAAGTGGAGTG 59658 T G \_  
 CACTT CACT TCTG AG  
 |||| ||| ||| ||  
 GTGAG GTGA AGGC TC  
 \_ \_ G  
 GAM1307 EPHA1 3' GTTTTAAAAGGGAGGTGGGG 17861 TT A GTC  
 T CACTTTC CT TGAGAT  
 | ||||| || |||||  
 G GTGGAGG GA ATTTTG  
 GG \_ AA\_  
 GAM1307 ESRRA 3' ATCTCAGGGAGGGAAGGGGATG 15479 TT A A G  
 CAT C CTTTC CT TCTGAGAT  
 || | |||| | |||||  
 GTA G GAAGG GA GGA CTCTA  
 GG \_ \_ G  
 GAM1307 FCAR 3' GCACTGAGAGTGAAGTG 55798 C  
 CATTTCAC TTTCA TGT  
 ||||| ||||| |||  
 GTGAAGTGAGAGT ACG  
 C  
 GAM1307 FCAR 3' GCACTGAGAGTGAAGTG 55814 C  
 CATTTCAC TTTCA TGT  
 ||||| ||||| |||  
 GTGAAGTGAGAGT ACG  
 C  
 GAM1307 FGF2 3' GTCTCAGATACTTGGGAGGCTG 8873 \_ AC\_  
 AGGTG TTCA CTTTC TGTCTGAGAT  
 ||| |||| | |||||  
 GAGT GGAGG ATAGACTCTG  
 C GTTC  
 GAM1307 FRAT2 3' GGCTGGTGAAGGTGGGA 23881 TT \_  
 T CACTTTC ACT GTC  
 | ||||| |||

		A GTGGAAGTGG CGG	
		GG T	
GAM1307 GCKR	3'	ATTTTCAGAAATAAAATGAAATG 7635	C CACTG
		CATTTCA TTT TCTGAGAT	
		GTAAAGT AAA AGACTTTA	
		A TAA__	
GAM1307 GNPI	3'	GTCTTAGGCCTTCATGGAGTGG 18448	CACT__
A		TTCACTTT GTCTGAGAT	
		AGGTGAGG CGGATTCTG	
		TACTTC	
GAM1307 GPR61	3'	TGGGCTGGTGGGAGTGGGAT 78914	TT TT _
		AT CACT CACT GTCTG	
		TA GTGA GTGG CGGGT	
		GG GG T	
GAM1307 GUCY1B3	3'	ATCTTGATTATGGGGTGAAG 5963	T CT TG
		TTTCACTT CA GTC AGAT	
		GAAGTGGG GT TAG TCTA	
		_ AT GT	
GAM1307 GYG2	3'	ATTTTCAGGTGAGTCAGGGTTGG 14047	TC C _GT
ATG		CATT ACTTT AC T CTGAGAT	
		GTAG TGGGA TG G GACTTTA	
		GT C A TG	
GAM1307 HHEX	3'	ATTTTCAGGCAGCCTTGGAGT 10784	CA__
		ACTTT CTGTCTGAGAT	
		TGAGG GACGGACTTTA	
		TTCC	
GAM1307 HMGA2	3'	TCTGGGGTGGGGTGGGGTG 13004	TT TTCA TG G
		CAT CACT C TCT AGA	
		GTG GTGG G GGG TCT	
		GG ____GT G	
GAM1307 HOXD4	5'	TTTTGGGGTACTAGGGAGTGAG 27534	TT AC_ GT G T
GT		ATTTCACT C T CT AGA	
		TGGAGTGA G A GG TTT	
		GG ATC TG G TG	
GAM1307 HPCAL1	3'	TTATGTATGGTGAAGTGGAGTG 9272	T CTGAGAT
		CATTTCACTT CACTGT	
		GTGAGGTGAA GTGGTA	
		_ TGTATTA	
GAM1307 HPCAL1	5'	GTGGTGACAGGTGAAATG 56190	_ TG
		CATTTCACTT TCAC T	

			GTAAGGTGGA AGTG G				
			C GT				
GAM1307 HPCAL1	3'	TTATGTATGGTGAAGTGGAGTG 56191	T CTGAGAT				
		CATTTCACCT CACTGT					
		GTGAGGTGAA GTGGTA					
		_ TGTATTA					
GAM1307 IGF1R	3'	TTCTCTCAGTGAAGGTGGGG 6049 TT TCT T					
		T CACTTTCAC TGAGA					
		G GTGGAAGTGAC CTCT					
		GG T__ TT					
GAM1307 IL11	3'	AT TTCAGGAGCAGGGGTGGGA 5324 TT CA G					
		T CACTTT CT TCTGAGAT					
		A GTGGGG GA GGACTTTA					
		GG AC _					
GAM1307 IL13RA1 G	3'	TTAGGGGCAGTGGAGGTAGAAT 7782 TC GAGAT					
		CATT ACTTTCACCTGTCT					
		GTAA TGGAGGTGACGGG					
		GA GATTG					
GAM1307 IL1F5	3'	ATTTCTGTGGGGGTGGGGTG 24377 TT TT TGTCT					
		CAT CACT CAC GAGAT					
		GTG GTGG GTG CTTTA					
		GG GG T____					
GAM1307 IL1RN	3'	GATGGTGAAAAGTAAGTG 5143 C					
		CATTT ACTTTCACCTGTC					
		GTGAA TGAAAGTGGTAG					
		-					
GAM1307 IL24	3'	TTGGGGTGGGGGTAAGGTG 22447 C TT GT TG					
		CATTT ACT CACT C A					
		GTGGA TGG GTGG G T					
		A GG __GT					
GAM1307 IRS1 G	3'	ATCTTTTTTTTGGATGTGGGAT 18662 TT T CTGTCT					
		CAT CAC TTCA GAGAT					
		GTA GTG AGGT TTCTA					
		GG T TTTT_					
GAM1307 IRS2	3'	TCTCAATGGAAGTGAAAT 59723 CTGTC					
		ATTTCACTTTCA TGAGA					
		TAAAGTGAAGGT ACTCT					
		A_____					
GAM1307 JTB AATG	3'	CTATCTCAGACAGTGAAAGTGA 21961 CATTTCACTTTCACTGTCTGAGAT					



			GTAAAGTGAAAGTGACAGACTCTA		
			TCC		
GAM1307 KCNA7	3'	TCTCAGAGCAGGGGAGTG	49061	TT A _	
		CACT C CTG TCTGAGA			
		GTGA G GAC AGACTCT			
		GG _ G			
GAM1307 KCNK6	3'	ATGGAGGAGGTGAGGTG	16690	A	
		CATTTCACTTTC CTGT			
		GTGGAGTGGAGG GGTA			
		A			
GAM1307 KCNK6	3'	TTTCAGGCTGAGTGTGGTG	16699	TT _	
		CACT CACT GTCTGAGA			
		GTGG GTGA CGGACTTT			
		T _ GT			
GAM1307 LAMC1	3'	GTCTCAGGCCACAATGGGGTG	9677	TT CTTTCACT	
		CAT CA GTCTGAGAT			
		GTG GT CGGACTCTG			
		GG AACAC__			
GAM1307 MALT1	3'	ATTTTAGATGCCTGTGAAAT	22291	TTTCACT	
		ATTTCAC GTCTGAGAT			
		TAAAGTG TAGATTTTA			
		TCCG__			
GAM1307 MAPK14	3'	TCCTCCATGGTGGAAGGGGGTG	7161	TT A CT AT	
		CAT C CTTTCACTGT GAG			
		GTG G GAAGGTGGTA CTC			
		GG _ C _ CTT			
GAM1307 MAPK14	3'	TCCTCCATGGTGGAAGGGGGTG	57335	TT A CT AT	
		CAT C CTTTCACTGT GAG			
		GTG G GAAGGTGGTA CTC			
		GG _ C _ CTT			
GAM1307 MAPK14	3'	TCCTCCATGGTGGAAGGGGGTG	57346	TT A CT AT	
		CAT C CTTTCACTGT GAG			
		GTG G GAAGGTGGTA CTC			
		GG _ C _ CTT			
GAM1307 MAPRE1	3'	ATTTTTTGGGGAAGTGAGGTG	24661	A GTCT	
		CATTTCACTTTC CT GAGAT			
		GTGGAGTGAAGG GG TTTTA			
		_ TT _			
GAM1307 MBP	5'	TTTTGGAAGGTGGAGTG	89783	T G TG	
		CACTT CACT TC AGA			

			GTGAG GTGG AG TTT			
			— A GT			
GAM1307	MGAT5	5'	TGCCTCATGGTGGGAGTGAAA 10030	TT	TC	AT
			TTTCACT CACTG TGAG			
			AAAGTGA GTGGT ACTC			
			GG — CGTT			
GAM1307	MGEA5	3'	GTTTCAGAAGTGTGAGGGTGGA 24218	—	G	
	GTG		ATTTCACTTT CACT TCTGAGAT			
			TGAGGTGGGA GTGA AGACTTTG			
			CT —			
GAM1307	MMP19	3'	TCAATGGTGGAGGGAGATG 10086	A	C	
			CATTTC CTTTCACTGT TGA			
			GTAGAG GGAGGTGGTA ACT			
			— —			
GAM1307	MMP19	3'	TCAATGGTGGAGGGAGATG 42975	A	C	
			CATTTC CTTTCACTGT TGA			
			GTAGAG GGAGGTGGTA ACT			
			— —			
GAM1307	MMP19	3'	TCAATGGTGGAGGGAGATG 42981	A	C	
			CATTTC CTTTCACTGT TGA			
			GTAGAG GGAGGTGGTA ACT			
			— —			
GAM1307	MMP19	3'	TCAATGGTGGAGGGAGATG 42985	A	C	
			CATTTC CTTTCACTGT TGA			
			GTAGAG GGAGGTGGTA ACT			
			— —			
GAM1307	MOG	3'	TCTTGGCAGGGGTGGAG 10107	TCA	T TG	
			TTTCACTT CTG C AGA			
			GAGGTGGG GAC G TCT			
			— — GT			
GAM1307	MPP4	5'	TATCGGGAGCAGTGAGGTG 52347	T	— GAT	
			CACTT CACTGT CTGA			
			GTGGA GTGACG GGCT			
			— AG ATT			
GAM1307	MS4A1	3'	ATTTTGGGGAGACAAAGGGAAA 3748	A	CA G TG	
	TG		CATTTC CTTT CT TC AGAT			
			GTAAAG GAAA GA GG TTTA			
			G CA G GT			
GAM1307	MTNR1A	3'	ACAATGAAAGTGGGGTG 19887	TT	C	
			CAT CACTTTCA TGT			

			GTG GTGAAAGT ACA		
			GG A		
GAM1307 MYOZ1	5'	ATCTCAGGCTCTAGGTGCAATG 41149	T TCACT		
		CATT CACTT GTCTGAGAT			
		GTAA GTGGA CGGACTCTA			
		C TCT__			
GAM1307 NAV2	3'	TTTCATTAGGGGTGGGGTG 60162	TT TCA TC		
		CAT CACTT CTG TGAGA			
		GTG GTGGG GAT ACTTT			
		GG __ T_			
GAM1307 NDST2	3'	ATCTTGGGAGGTGGGGAGGAAT 13296	AC TT GT TG		
G		CATTTT C T CACT C AGAT			
		GTAAGG G GTGG G TCTA			
		A_ GG AG GT			
GAM1307 NEBL	3'	TTTTTGTGGTAGGGAAGTGGGA 21126	TT A GT_ T		
TG		CAT CACTTTC CT C TGAGA			
		GTA GTGAAGG GA G GTTTT			
		GG _ TG T TA			
GAM1307 NEU1	3'	GTCTTGGGCAGGTCTAGTGAGC 4742	T TTCA TG		
TG		CA TTCACT CTGTC AGAT			
		GT GAGTGA GACGG TCTG			
		C TCTG GT			
GAM1307 NEUROD2	3'	ATTTTGGCGGGAGGGGAAGTG 20478	A A T TG		
		CATTTT CTTTC CTG C AGAT			
		GTGAAG GGGAG GGC G TTTA			
		_ _ _GT			
GAM1307 NFE2L1	3'	TGTCTGCCCCAGACAAGTGGGA 12177	TT _ _		
GTGAAATG		ACT CACT GTCTG AGAT G			
		TGA GTGA CAGAC TCTG T			
		GG A CCG			
GAM1307 NFRKB	5'	GTCTTAAGGGAAGTGAAAGAGG 20497	A G_ _		
AGTG		ATTTC CTTTCACT TCT GAGAT			
		TGAGG GAAAGTGA GGA TTCTG			
		A AG A			
GAM1307 NGB	3'	GTTTTGGTGGCAGAGGTGGGAT 41188	TT CA T TG		
G		CAT CACTTT CTG C AGAT			
		GTA GTGGAG GGT G TTTG			
		GG AC _GT			
GAM1307 NLGN1	3'	CCTTTTGGTAAGGTGAAGTG 30024	C GTCT AT		
		CATTTCACTTT ACT GAG			

			GTGAAGTGGAA TGG TTC	
			_ TT_ CT	
GAM1307 NPC2	3'	GTCTTAGGTGGTTTCATTAAAT 21223	CACTTTC TG	
G		CATTT AC TCTGAGAT		
		GTAAA TG GGATTCTG		
		TTACTT_ GT		
GAM1307 OCRL	3'	GTTTCTTGGTGGGGGTGGGG 7830	TT TT GTCT	
		T CACT CACT GAGAT		
		G GTGG GTGG CTTTG		
		GG GG TT_		
GAM1307 OCRL	3'	GTTTCTTGGTGGGGGTGGGG 4264	TT TT GTCT	
		T CACT CACT GAGAT		
		G GTGG GTGG CTTTG		
		GG GG TT_		
GAM1307 PER2	3'	TTTTTGATGGAGGTGAAAT 43051	CTG T	
		ATTTCACTTTCA TC GAGA		
		TAAAGTGGAGGT AG TTTT		
		_ T		
GAM1307 PGAM1	3'	TTTCATGGCAGTGAAA 76276	_	
		TTTCACTGTC TGAGA		
		AAAGTGACGG ACTTT		
		T		
GAM1307 PIGN	5'	GTCTCAGTCCTGTGCAAAGTGA 24672	_ TGT_	
GATG		ATTTCACTTT CAC CTGAGAT		
		TAGAGTGAAA GTG GACTCTG		
		C TCCT		
GAM1307 PKP4	3'	GAAATGTGAAAGTGAAGTG 13266	TG_	
		CATTTCACTTTTCA C TC		
		GTGAAGTGAAAGTG AG		
		TAA		
GAM1307 PRDM2	3'	GTCTCGGAGAAACGGGTGAGCT 24250	T TCACTG	
G		CA TTCACTT TCTGAGAT		
		GT GAGTGGG AGGCTCTG		
		C CAAAG_		
GAM1307 PSEN1	5'	ATAGTGAGGCTGGGATG 23621	TT _	
		CAT CA CTTTCACTGT		
		GTA GT GGAGGTGATA		
		GG C		
GAM1307 RALB	3'	GTTTTGGAGGAGGGAGTGGAGT 11245	TT A G TG	
		ATTTCACT C CT TC AGAT		

				TGAGGTGA G GG AG TTTG		
				GG A _ GT		
GAM1307	RAMP3	3'	CGGTGAGATGGAGTG	19589	C	
			CATTTCA TTTCACTG			
			GTGAGGT AGAGTGGC			
GAM1307	RANBP7	3'	ATTTTGGGGGTGGGGGGGA	21113	A TT	G TG
			TTC CT CACT TC AGAT			
			AGG GG GTGG GG TTTA			
			_ GG _ GT			
GAM1307	RGS19IP1	3'	GATGGTGAGGGGAGGTG	62509	A	
			CATTTTCTTTCACTGTC			
			GTGGAG GGGAGTGGTAG			
GAM1307	RNASE1	3'	ATTTTGGGGGTGAAGAGTGGGT	63875	T	_ G TG
	TG		CA TTCACCTTT CACT TC AGAT			
			GT GGGTGAGA GTGG GG TTTA			
			T A _ GT			
GAM1307	RNGTT	3'	ATTTTGGACATTGTGAAGGAAA	13729	A T	_ TG
	TG		CATTTTCTT CAC TGTC AGAT			
			GTAAAG GAA GTG ACAG TTTA			
			_ _ TT GT			
GAM1307	RXRB	3'	CAGTGGTGGAGGTGGG	41758	T	
			TTCACCTTTCACTG CTG			
			GGGTGGAGGTGGT GAC			
GAM1307	SED1	3'	ATTCTGCAGTTGGGAGTGAAAT	27322	TT _	CT AT
	G		CATTTCACT CA CTGT GAG			
			GTAAAGTGA GT GACG CTT			
			GG T T_ A			
GAM1307	SH3BP4	3'	CAGTAGAGTGAGGTG	27232	C	
			CATTTCACTTT ACTG			
			GTGGAGTGAGA TGAC			
GAM1307	SIGLEC6	3'	ATTTTAAGACTGAAAGTGAAAT	59926	CT	_
			ATTTCACTTTCA GTCT GAGAT			
			TAAAGTGAAAGT CAGA TTTTA			
			_ A			
GAM1307	SLC17A2	5'	TTTAATGGTGAAGGTAAGTG	19546	C	C
			CATTT ACTTTCACTGT TGAG			

GTGAA TGGAAGTGGTA ATTT

GAM1307 SLC19A1 5' GTCTCGGGGCCCTGGGGTGAG 11758 T CT \_  
TTCACTT CA GTCT GAGAT  
||||| || ||| ||||  
GAGTGGG GT CGGG CTCTG  
\_ CC G

GAM1307 SLC38A2 3' TCTCGGGTTAAGGGAAGTG 38593 A G\_  
CACTTTC CT TCTGAGA  
||||| || |||||  
GTGAAGG GA GGGCTCT  
\_ ATT

GAM1307 SLC6A4 3' TTTTGGACGTGTGAGGATG 6452 CT \_ TG  
CA TTCAC TGTC AGA  
|| |||| ||| |||  
GT GAGTG GCAG TTT  
AG T GT

GAM1307 SLC7A8 3' GTCTTGGGGCAGGGTGAAA 24282 TTCA \_ TG  
TTTCACT CTGT C AGAT  
||||| ||| | |||  
AAAGTGG GACG G TCTG  
\_ G GT

GAM1307 SMARCB1 3' TCGGGTGGGGGTGGAGTG 65586 TT TGT  
CATTTCACT CAC CTGA  
||||||| ||| |||  
GTGAGGTGG GTG GGCT  
GG \_

GAM1307 SNCA 3' TTAATTATTGAAAGTGGGGTG 4433 TT C TC  
CAT CACTTTCA TG TGA  
||| ||||| || |||  
GTG GTGAAAGT AT ATT  
GG T TA

GAM1307 SRRM2 3' TTTGGGGTGGGAGGGAATG 32918 A TT GT TG  
CATTTC CT CACT C AG  
||||| || ||| | ||  
GTAAGG GA GTGG G TT  
\_ GG \_ GT

GAM1307 SSPN 3' GTCTTAGAAGAAAGTGGAAT 17445 ACTG  
ATTTCACTTTC TCTGAGAT  
||||||| |||||  
TAAGGTGAAAG AGATTCTG  
A\_

GAM1307 STAR 3' ATCTCCATCTGGTGACAGTGGG 4443 TT T GTCT\_  
ATG CAT CACT TCACT GAGAT  
||| ||| |||| |||||  
GTA GTGA AGTGG CTCTA  
GG C TCTAC

GAM1307 T 3' GTCTCAGGTTAAGAAGGAAATG 12077 A CACTG  
CATTTC CTTT TCTGAGAT  
||||| ||| |||||

		GTAAAG GAAG GGACTCTG		
		_ AATT_		
GAM1307 TAF1C	3'	TGGTGAGGGTGGAGTG 19060		
		CATTTCACTTTCACTG		
		GTGAGGTGGGAGTGGT		
GAM1307 TIMP3	3'	GTTTTAGTGTCAAAAGTGAGAT 4517		CACTGT
G		CATTTCACTTT CTGAGAT		
		GTAGAGTGAAA GATTTTG		
		ACTGT_		
GAM1307 TMOD4	5'	TACCACACAGTGGGAGGGGGTG 25331	TT A TT	C AGAT
		CAT C CT CACTGT TG		
		GTG G GA GTGACA AC		
		GG_ GG C CATG		
GAM1307 TNFRSF4	3'	ATCTTGCCAGGGTGGAGTG 12451		TTCA T TG
		CATTTCACT CTG C AGAT		
		GTGAGGTGG GAC G TCTA		
		___ C GT		
GAM1307 TRH	3'	CAGCCAGTGAGGGTGGGGTG 23051	TT	T
		CAT CACTTTCACTG CTG		
		GTG GTGGGAGTGAC GAC		
		GG C		
GAM1307 TRHDE	3'	TTTTGGGCAATGTGAGAG 25393	___	TG
		CTTTCAC TGTC AGA		
		GAGAGTG ACGG TTT		
		TA GT		
GAM1307 TRIM9	3'	GTTTCAAATGGGTGGTGGGGTG 53761	TT TTCA	C
		CAT CACT CTGT TGAGAT		
		GTG GTGG GGTA ACTTTG		
		GG TG_ A		
GAM1307 TSG	3'	ATTCCTACTGTGAGTGGAGTG 40231	TT T CT	
		CATTCAC TCAC GT GAGAT		
		GTGAGGTG AGTG CA CTTTA		
		___ T TC		
GAM1307 TSLP	5'	TTTAGTGTGAAACTGGGGTG 52310	TT C	TGT
		CAT CA TTTTAC CTGAG		
		GTG GT AAAGTG GATTT		
		GG C T_		
GAM1307 VDAC1	3'	TTTGGGGTGGAGAAGGTGGA 12583	A TG G T	
		TTCACTTTC C TCT AGA		

AGGTGGAAG G GGG TTT  
 A G T G T  
 GAM1307 VDR 3' TCTTTGTGAGAGTGAGCTG 4571 T TGTCT  
 CA TTCAC TTT CAC GAGA  
 || ||||| ||||  
 GT GAGTGAGAGTG TTCT  
 C T\_\_\_\_  
 GAM1307 WNT10B 3' GGGTGGTGGGGGTCAGGTG 12675 C TT TG  
 CATTT ACT CAC TCT  
 ||||| ||| ||| |||  
 GTGGA TGG GTG GGG  
 C GG GT  
 GAM1307 ZNF239 5' GTCAGGATAATGGTGGGAATGG 19042 TT C TT \_\_\_\_ GAT  
 GGTG CAT CACTGT CTGA  
 || ||||| ||||  
 GT A GTGGTA GACT  
 GG A GG ATAG G  
 GAM1307 AKAP6 5' GTTTTGGAAAGAAGTGAGGT 14996 CACTG TG  
 ATTTCACTTT TC AGAT  
 ||||| || ||||  
 TGGAGTGAAG AG TTTG  
 AA\_\_\_\_ GT  
 GAM1307 APXL2 3' TAGGTGGAGAGGGTGGGGTG 75196 TT A TG  
 CAT CACTTTC C TCTG  
 ||| ||||| | ||||  
 GTG GTGGGAG G GGAT  
 GG A GT  
 GAM1307 ARFGAP3 3' ATCTCAGGCGGCAGTGAAGT 27385 TTCA  
 ATTTCACT CTGTCTGAGAT  
 ||||| |||||  
 TGAAGTGA GGC G GACTCTA  
 C\_\_\_\_  
 GAM1307 ARHGEF9 3' TTTTAGGTACTGTGAAGG 30827 \_\_\_\_GT  
 CTTTCAC T CTGAGA  
 ||||| | |||||  
 GGAAGTG A GATTTT  
 TC TG  
 GAM1307 ARHGEF9 3' TTTTGGGGAAGTGAAAT 30829 ACTGT TG  
 ATTTCACTTTC C AGA  
 ||||| ||| |||  
 TAAAGTGAAGG G TTT  
 \_\_\_\_GT  
 GAM1307 BCL2L1 3' GTCTGTGTGAAGGTGAAA 56807 TGTCTG  
 TTTCAC TTT CAC AGAT  
 ||||| ||||  
 AAAGTGGAAGTG TCTG  
 TG\_\_\_\_  
 GAM1307 C19orf7 3' AGACAGTGAGAGTGAAA 61124  
 TTTCAC TTTCACTGTCT  
 ||||| |||||



AAAGTGAGAGTGACAGA

GAM1307 C1orf17 3' TTTCAGAGTGGGGAAGTG 68219 A \_  
 CACTTTC CTG TCTGAGA  
 ||||| ||| |||||  
 GTGAAGG GGT AGACTTT  
 \_ G

GAM1307 C1orf34 3' GCAGTGAGGGTGAGCTG 60673 T  
 CA TTCACTTTCACTGT  
 || |||||  
 GT GAGTGGGAGTGACG  
 C

GAM1307 C20orf151 3' TCTGGCAGTGAGGGTGGAG 88703 T  
 TTTCACCTTTCACTGTC GA  
 ||||| ||||| ||  
 GAGGTGGGAGTGACGG CT  
 T

GAM1307 C20orf21 3' TCTCAGGACAAGTGGAAG 35117 \_ \_  
 CTTTCACT GTC TGAGA  
 ||||| ||| |||||  
 GAAGGTGA CAG ACTCT  
 A G

GAM1307 C20orf29 3' GTCTCAGACTCCCCTGAGGGTG 37129 CT\_\_  
 GAG TTTCACTTTCA GTCTGAGAT  
 ||||| |||||  
 GAGGTGGGAGT CAGACTCTG  
 CCCCT

GAM1307 C20orf60 3' TAGGGGTGGGGGTGGGATG 53738 TT TT G  
 CAT CACT CACT TCTG  
 ||| ||| ||| |||  
 GTA GTGG GTGG GGAT  
 GG GG \_

GAM1307 C22orf5 5' GACAGTGAGGGGGGATG 24342 TT A  
 CAT C CTTTCACTGTC  
 ||| | |||||  
 GTA G GGGAGTGACAG  
 GG \_

GAM1307 C8orf2 3' ATAGTGAAAGTAAGATG 23157 C  
 CATTT ACTTTCACTGT  
 |||| |||||  
 GTAGA TGAAAGTGATA  
 A

GAM1307 CCR5 3' ATTCAGACTGAATGGGGGTGG 5147 TT TT CT\_\_  
 GG T CACT CA GTCTGAGAT  
 | ||| || |||||  
 G GTGG GT CAGACTTTA  
 GG GG AAGT

GAM1307 CCR6 3' TCTCTTCAGGGTGGGGTG 15173 TT TTCA TCT  
 CAT CACT CTG GAGA  
 ||| ||| ||| |||

			GTG GTGG GAC CTCT		
			GG ____ TT_		
GAM1307 CCR6	3'	TCTCTTCAGGGTGGGGTG	48589	TT TTCA TCT	
		CAT CACT CTG GAGA			
		GTG GTGG GAC CTCT			
		GG ____ TT_			
GAM1307 CECR7	5'	ATAGTGGGAATGAAATG	79615	C TT	
		CATTTCA T CACTGT			
		GTAAAGT A GTGATA			
		A GG			
GAM1307 CENTA2	3'	TCTCAGATGGCTGAAATGT	37269	_ _	
		AC TTTCA CTGTCTGAGA			
		TG AAAGT GGTAGACTCT			
		T C			
GAM1307 CEP3	3'	ATCTTGGCCAAAAAAGGAAGTG	21247	A CAC T TG	
		CATTTTCTTT TG C AGAT			
		GTGAAG GAAA AC G TCTA			
		_ AAA _ GT			
GAM1307 CHSY1	3'	TTGGGGACAAAAGTGAAATG	29905	CAC GA T	
		CATTTCACTTT TGTCT GA			
		GTAAAGTGAAA ACAGG TT			
		____ GG T			
GAM1307 CNNM2	3'	GGACAGTGAGGGAGGAATG	34461	A	
		CATTTTCTTTCACTGTCT			
		GTAAGG GGGAGTGACAGG			
		A			
GAM1307 COLEC10	3'	TTTCAGACCATGTGGAATG	21230	TTTCACT	
		CATTTTCACT GTCTGAGA			
		GTAAGGTG CAGACTTT			
		TAC____			
GAM1307 CRR9	3'	ATTTTCAGGTGGTTTTCTAAGTG	47878	TC____ TG	
		CACTT AC TCTGAGAT			
		GTGAA TG GGACTTTA			
		TCTTT GT			
GAM1307 CYYR1	3'	ATTTTAGGTGGGTGTGAAGTG	53670	TTTCA TG	
		CATTTTCACT C TCTGAGAT			
		GTGAAGTG G GGATTTTA			
		TG____ GT			
GAM1307 DAPK3	3'	GTCGTGGGACGGGGAGGGTG	7211	TT A GA_	
ATG		CAT CACTTTC CTGTCT GAT			

GTA GTGGGAG GGCAGG CTG  
 GG G GTG  
 GAM1307 DDX8 3' GGATGGGAAGGTGGAGTG 17053 A  
 CATTTCACCTTC CTGTCT  
 ||||| ||||  
 GTGAGGTGGAAG GGTAGG  
 —  
 GAM1307 DKFZp434B217 3' GGGTTTGGGCGGGAGTGGGCTG 70701 T TCA TG AT  
 CA TTCACCTT CTGTC AG  
 || ||||| |||| ||  
 GT GGGTGAG GCGG TT  
 C — GT GGGT  
 GAM1307 DKFZP434K028 3' CTTACAGTGGAGGTAAAGTG 93231 C CT  
 CATT ACTTTCACCTGT GAG  
 |||| ||||| |||| ||  
 GTGAA TGGAGGTGACA TTC  
 A —  
 GAM1307 DKFZp434O0320 3' GGTGGCAGGTGGAGTG 83696 —  
 CATTTCACCTT TCACT  
 ||||| ||||  
 GTGAGGTGGA GGTGG  
 C  
 GAM1307 DKFZP434O047 5' ATTTTGGACAAGGTGCTGAAGT 31503 CTTT — TG  
 G CATTTC CACT GTC AGAT  
 ||||| |||| ||||  
 GTGAAGT GTGG CAG TTTA  
 C — AA GT  
 GAM1307 DKFZp547F072 5' TCCATGGGCGGGGGTGGGGTG 50094 TT TTA GTC A T  
 CAT CACT C CT TG GA  
 || |||| | || ||||  
 GTG GTGG G GG AC CT  
 GG GG C GT \_ \_ T  
 GAM1307 DKFZP564C103 3' TCTTAGATAAGTAAGGTG 31612 C \_  
 CACTTT ACT GTCTGAGA  
 ||||| ||||| |||||  
 GTGGAA TGA TAGATTCT  
 \_ A  
 GAM1307 DKFZP564I052 3' GTTTTAGGTGGTGATCTTAAAT 66718 CACTT TG  
 G CATTTC TCAC TCTGAGAT  
 |||| |||| |||||  
 GTAAA AGTG GGATTTTG  
 TTCT \_ GT  
 GAM1307 DKFZP564I052 3' GTTTTGAGAGGGGAGTAGAAGT 66719 \_ TT A G T  
 G CATTTC ACT C CT TC GAGAT  
 ||||| |||| | || |||||  
 GTGAAG TGA G GA AG TTTTG  
 A GG \_ G \_  
 GAM1307 DKFZP566G1424 3' ATTTTGGACTCAGTGAAAGTG 84773 \_ TG  
 CACTTTCACCT GTC AGAT  
 ||||| |||| ||||

GTGAAAGTGA CAG TTTA  
 CT GT  
 GAM1307 DKFZp761N1114 3' GTTTCAGAAAGCTGGGTGGTGG 79022 \_ \_ G  
 TCACT TTCA CT TCTGAGAT  
 |||| ||| || |||||  
 GGTGG GGGT GA AGACTTTG  
 T C A  
 GAM1307 DKFZp762P2111 3' GTCTCAGGTGTTCTGGGGATG 86361 TT ACTTT TGT  
 CAT C CAC CTGAGAT  
 || | || |||||  
 GTA G GTG GACTCTG  
 GG GTCTT \_  
 GAM1307 DKFZp762P2111 3' TGAGAAACAGTGGAGTGGAGTG 86365 T CTGAGAT  
 CATTTCACTT CACTGT  
 ||||| |||||  
 GTGAGGTGAG GTGACA  
 \_ AAGAGTA  
 GAM1307 DMRTA2 3' GTTTTGTTTAGGAGGGTGGG 60660 A TC  
 TTCAC TTTC CTG TGAGAT  
 ||||| || |||||  
 GGGTGGGAG GAT GTTTTG  
 \_ TT  
 GAM1307 DRIL2 3' ATCGTGGGGGCGGGGAGGTGGA 21322 A GA\_  
 GTG ATTTCACTTTC CTGTCT GAT  
 ||||| ||||| |||  
 TGAGGTGGAGG GGCGGG CTA  
 \_ GGTG  
 GAM1307 EAT2 3' TCAGGTGAAGGTGAGG 79281 TGT  
 TTTCAC TTTCAC CTGA  
 ||||| |||||  
 GGAGTGGAAGTG GACT  
 \_  
 GAM1307 EPS8R1 5' TAGAACATGAAGGTGGGATG 34803 TT C \_  
 CAT CACTTTCA TGT CTG  
 || ||||| || |||  
 GTA GTGGAAGT ACA GAT  
 GG \_ A  
 GAM1307 FBXL3B 5' ATCTTCTGTATGTAGGAGGTGG 24070 \_ TGTCT\_  
 AATG ATTTCACTTTC AC GAGAT  
 ||||| || |||||  
 TAAGGTGGAGG TG TTCTA  
 A TATGTC  
 GAM1307 FHX 3' TCAAGGGTGAAAGTGATGATG 37307 \_ GTC  
 CATT TCACTTTCACT TGA  
 ||| ||||| |||  
 GTAG AGTGAAAGTGG ACT  
 T GA\_  
 GAM1307 FKSG42 3' GTCTCAGGGTGGGAAGTGGGA 49335 TT \_ GT  
 T CACTTTC ACT CTGAGAT  
 | ||||| || |||||

	A GTGAAGG TGG GACTCTG	
	GG G _	
GAM1307 FLJ00024	3' GTCTTGGGAGAAGGGTGAGG 63765	CA G TG
	TTTCACTTT CT TC AGAT	
	GGAGTGGGA GA GG TCTG	
	A _ _ GT	
GAM1307 FLJ10052	3' ATCTCAGGCTCCACAGTGAGG 35771	TTCACT
	TTTCACT GTCTGAGAT	
	GGAGTGA CGGACTCTA	
	CACCT_	
GAM1307 FLJ11506	3' TGGGTGGGGAAGTGAAATG 45115	A TG
	CATTTCACTTTC C TCTG	
	GTAAAGTGAAGG G GGGT	
	_ GT	
GAM1307 FLJ12056	3' TTTGGGGGCAGGGAGGTTGGGT 46258	TC A GA T
G	CATT ACTTTC CTGTCT GA	
	GTGG TGGAGG GACGGG TT	
	GT _ GG TT	
GAM1307 FLJ12121	3' GTTTTGGACAGTCATTTGGAAT 46458	CTTTC TG
	ATTTCA ACTGTC AGAT	
	TAAGGT TGACAG TTTG	
	TTAC_ GT	
GAM1307 FLJ12547	3' ATCTCAGCCAGAGAGAGTGAAC 46489	T A T
TG	CA TTCACTTTC CTG CTGAGAT	
	GT AAGTGAGAG GAC GACTCTA	
	C A C	
GAM1307 FLJ12581	3' TCTCATGGAGGGTGAGT 45881	ACTGTC
	ATTTCACTTTC TGAGA	
	TGAGGTGGGAG ACTCT	
	GT_____	
GAM1307 FLJ12787	3' TTTCAGGTCAGAGGAA 49756	A _
	TTTC CTG TCTGAGA	
	AAGG GAC GGACTTT	
	A T	
GAM1307 FLJ12891	3' ACTGTGGAGGTGGAGTG 46335	T
	CATTTCACTTTTAC GT	
	GTGAGGTGGAGGTG CA	
	T	
GAM1307 FLJ13072	5' GACAGTGAGAGTGAAA 89814	
	TTTCACTTTCACTGTC	

AAAGTGAGAGTGACAG

GAM1307 FLJ13852 3' TGGGCAGTGGTAGGTGGGGTG 43579 TT \_  
CAT CACTT TCACTGTCTG  
||| |||| |||||  
GTG GTGGA GGTGACGGGT  
GG T

GAM1307 FLJ14107 3' GCAGGGGAGGTGAAATG 46693 A  
CATTTCACTTTC CTGT  
||||||| |||  
GTAAAGTGGAGG GACG  
G

GAM1307 FLJ14346 3' GGCAGGGAAGTGAGATG 46714 A  
CATTTCACTTTC CTGTC  
||||||| |||  
GTAGAGTGAAGG GACGG

GAM1307 FLJ14502 3' GTTTTGGGCTTAATAAATGGGG 62717 TT C TCACT TG  
TG CAT CA TT GTC AGAT  
||| ||| ||| |||  
GTG GT AA CGG TTTG  
GG A TAATT GT

GAM1307 FLJ14641 5' CGGGGAAGTGGAATG 51483 A  
CATTTCACTTTC CTG  
||||||| |||  
GTAAGGTGAAGG GGC

GAM1307 FLJ14743 3' GCTCTGGGGTGGGGGTGGGGTG 68064 TT TT G T AT  
CAT CACT CACT TC GAG  
||| ||| ||| ||| |||  
GTG GTGG GTGG GG CTC  
GG GG \_ T GT

GAM1307 FLJ20034 3' TTTGTACGTGAGGGTGGA 34392 T CT  
TTCACTTTCAC GT GAG  
||||||| || |||  
AGGTGGGAGTG CA TTT  
\_ TG

GAM1307 FLJ20043 3' GTTTTGGGAAAGGAGTGGGAT 34406 TT CACTG TG  
AT CACTTT TC AGAT  
|| ||||| || |||  
TA GTGAGG GG TTTG  
GG AAA\_ GT

GAM1307 FLJ20306 3' GAAGGTGGAGGTGGAA 34916 G  
TTTCACTTTCAC TC  
||||||| |||  
AAGGTGGAGGTGG AG  
A

GAM1307 FLJ20340 3' TTGGAGTGGAGTGGGGTG 34980 TT T TG TG  
CAT CACTT CAC TC A  
||| ||||| ||| |||

		GTG GTGAG GTG AG T		
		GG _ _ GT		
GAM1307	FLJ20400	3' TTCTTGACTGAAGGTGAGATG 66514	CT	T T
		CATTTCACTTTCA GTC GAGA		
		GTAGAGTGGAAGT CAG TTCT		
		_ _ TT		
GAM1307	FLJ20729	3' GTCTTGGAGTGCAAGTGGTATG 35649	T	T TG TG
		CAT TCACTT CAC TC AGAT		
		GTA GGTGAA GTG AG TCTG		
		T C _ GT		
GAM1307	FLJ21125	3' GTTTGGATGCAGGAAGGTGGGA 44892	TT	A _ TG AT
	TG	CAT CACTTTC CTGT C AG		
		GTA GTGGAAG GACG G TT		
		GG _ TAGT G		
GAM1307	FLJ21162	3' TCTTGGGCTGGGTGCAGTG 45896	TT	_ TG
		CACT CACT GTC AGA		
		GTGA GTGG CGG TCT		
		C_ GT GT		
GAM1307	FLJ21324	5' ATCTGCAGGTGGAAGGAGGTG 91189	A	TGT _
		CATTTC CTTTCAC CTG AGAT		
		GTGGAG GAAGGTG GAC TCTA		
		_ _ _ G		
GAM1307	FLJ21736	3' TTTCAGATGGAAGTGAGA 46234	CTG	
		TTTCACTTTCA TCTGAGA		
		AGAGTGAAGGT AGACTTT		
		_		
GAM1307	FLJ22378	3' GTCTCGGGTCCAGGGAGTGGAG 46905	TT	ACTG
		TTTCACT C TCTGAGAT		
		GAGGTGA G GGGCTCTG		
		GG ACCT		
GAM1307	FLJ22659	5' GTGGTGAAGGTAAATG 46261	C	TG
		CATTT ACTTTCAC T		
		GTAAA TGGAAGTG G		
		T GT		
GAM1307	FLJ23059	3' ATCTCAGAACAGAAGGGTGGGA 49933	TT	CA _
		T CACTTT CTGT CTGAGAT		
		A GTGGGA GACA GACTCTA		
		GG A_ A		
GAM1307	FLJ23091	3' ACCTCATGTGGGGGTGGGGTG 46124	TT	TT TGTC AT
		CAT CACT CAC TGAG		

		GTG GTGG GTG ACTC	
		GG GG T__ CAA	
GAM1307	FLJ23185	3' TTTCAGGCAGGTGGAG 46837 CA	
		CTTT CTGTCTGAGA	
		GAGG GACGGACTTT	
		TG	
GAM1307	FLJ23309	3' ATCTTGGGTGATGGAGGAAATG 46061	A T C GT TG
		CATTTC CTT CA T C AGAT	
		GTAAAG GAG GT G G TCTA	
		_ _ A TG GT	
GAM1307	FLJ23476	3' GTCTCAGGTGGCTGCGTGTGGT 44962	TT TTT _ TG
	G	CAT CAC CA C TCTGAGAT	
		GTG GTG GT G G GACTCTG	
		GT C__ C GT	
GAM1307	FLJ23510	3' ATCTCAGACAGTGAAGTGAATG 45281	CTT
		CATTTC TCACTGTCTGAGAT	
		GTAAAGT AGTGACAGACTCTA	
		C__	
GAM1307	FLJ23556	3' GTTTAAATAAGGGAGGTGGAA 45956	A GTC
		TTTCACTTTC CT TGAGAT	
		AAGGTGGAGG GA ATTTTG	
		_ ATA	
GAM1307	FLJ31762	3' TCTTCTGGGGGTGAGATG 58145	TT CTGTCT
		CATTTCACT CA GAGA	
		GTAGAGTGG GT TTCT	
		GG C__	
GAM1307	FTSJ3	3' GTCTGAAGAACAGTGAGGTGGA 34455	T _ G_
	GTG	ATTTCACTT CACTGT CT AGAT	
		TGAGGTGGA GTGACA GA TCTG	
		_ A AG	
GAM1307	G4	5' ATCTCAGATTGTGGGGGTGTGG 90991	_ TT T
	ATG	CATTTC ACT CAC GTCTGAGAT	
		GTAGG GTGG GTG TAGACTCTA	
		T GG T	
GAM1307	GBTS1	3' ATTTTGGGGAGTGGGTGATATG 59050	T TT G TG
		CAT TCACT CACT TC AGAT	
		GTA AGTGG GTGA GG TTTA	
		T _ G GT	
GAM1307	GBTS1	3' TTAGTGAGGGAAGGTGAGATG 59064	A GT_
		CATTTCACTTTC CT CTGA	



			GTAGAGTGAAG GG GATT		
			_ AGT		
GAM1307	GK001	3'	TTTCTGGTGGGAGTGGGGTG 39503	TT TT TCT T	
			CAT CACT CACTG GAGA		
			GTG GTGA GTGGT CTTT		
			GG GG _ T		
GAM1307	GPS2	5'	GTCTTTGAGGTGAAAGTGGAA 15671	G T	
			TTTCACTTTCACT TC GAGAT		
			AAGGTGAAAGTGG AG TTCTG		
			_ T		
GAM1307	GPT2	3'	TTTCAGATCTGGAGAAATG 55962	ACT CT	
			CATTTC TTCA GTCTGAGA		
			GTAAAG AGGT TAGACTTT		
			_ C_		
GAM1307	GRSF1	3'	ATTTTAGAACAAGTAGGGGTG 9139	TC _ _	
			CACTT ACT GT CTGAGAT		
			GTGGG TGA CA GATTTTA		
			GA A A		
GAM1307	HBXAP	5'	CAGTGAAATGAAGTG 33420	C	
			CATTTCA TTTCACTG		
			GTGAAGT AAAGTGAC		
			-		
GAM1307	HIC	5'	GTTTCAGGATTGTAGGAGTGGA 67452	TC TG_	
	A		TTTCACTT AC TCTGAGAT		
			AAGGTGAG TG GGACTTTG		
			GA TTA		
GAM1307	HIF1AN	3'	ATCTATTCAAGTGGGAGTGGGGT 61968	TT TT TCTG	
			AT CACT CACTG AGAT		
			TG GTGA GTGAC TCTA		
			GG GG TTA_		
GAM1307	HSF2	3'	TCGGGGGTGGGATGGGATG 15710	TT C TT G	
			CAT CA T CACT TCTGA		
			GTA GT A GTGG GGGCT		
			GG _ GG _		
GAM1307	HSPC054	3'	TTTTACAGCTGTGGAAAGTGAA 26264	_ T T _ T	
	GTG		ATTTCACTTTC AC G CTG AGA		
			TGAAGTGAAAG TG C GAC TTT		
			G T _ A TG		
GAM1307	HXCP2	3'	ATCTCAGTTTGGGAAGTGGGAT 50832	TT ACTGT	
	G		CAT CACTTTC CTGAGAT		

		GTA GTGAAGG GACTCTA		
		GG GTTT_		
GAM1307 HYPK	3'	TCTTGGGTCAAGTAGAGTG	33080	C __ TG
		CACTTT ACT G TC AGA		
		GTGAGA TGA C GG TCT		
		_ A T GT		
GAM1307 IL18BP	3'	TCTTGGGCAGAGGAGGTG	19113	A TG
		CACTTTC CTGTC AGA		
		GTGGAGG GACGG TCT		
		A GT		
GAM1307 IL22R	3'	GTGGTGAAGATGAAATG	41192	C TG
		CATTTC A TTTCAC T		
		GTAAAGT GAAGTG G		
		A GT		
GAM1307 IMAGE3451454	3'	GTTTTAGCCAAAAGTGAAAT	53873	CAC T
		ATTTCACTTT TG CTGAGAT		
		TAAAGTGAAA AC GATTTTG		
		_ C		
GAM1307 KIAA0092	3'	ATTTTGGAATAAAGTGAGA	27967	CACTG TG
		TTTCACTTT TC AGAT		
		AGAGTGAAA AG TTTA		
		TA__ GT		
GAM1307 KIAA0174	5'	ATTTTGATGGTGAACCCTGAA	78592	CT_ TG
	GT	ATTTC A TTCACTGTC AGAT		
		TGAAGT AAGTGGTAG TTTA		
		CCC GT		
GAM1307 KIAA0212	3'	GTGAGACCGTGGTGAAAGGGGG	27940	TT A _ GAGAT
	ATG	T C CTTTCACT GTCT		
		A G GAAAGTGG CAGA		
		GG G TGC GTG		
GAM1307 KIAA0284	3'	TGGTGGGGGTGGACGTG	63119	_ TT
		CAT TTCACT CACTG		
		GTG AGGTGG GTGGT		
		C GG		
GAM1307 KIAA0285	5'	GGCAGTGGAGGTGAGA	29020	
		TTTCACTTTCACTGTC		
		AGAGTGGAGGTGACGG		
GAM1307 KIAA0419	5'	ATTTCAAGATAGTGTGTGA	28187	TTT
		TCAC CACTGTCTGAGAT		

AGTG GTGATAGACTTTA  
 T\_\_  
 GAM1307 KIAA0426 3' GTTT TAGATGGTGT TACTGAGA 28261 CTTT  
 TTTCA CACTGTCTGAGAT  
 |||| |||||  
 AGAGT GTGGTAGATTTTG  
 CATT  
 GAM1307 KIAA0453 3' GTCTTGCTGGGGGGTGGTGATG 69049 \_ TT ACT CT  
 CATT TCACT C GT GAGAT  
 ||| |||| | || ||||  
 GTAG GGTGG G CG TTCTG  
 T GG GT\_ \_  
 GAM1307 KIAA0459 3' ATTTCAGATGGGATGCAGGTG 60983 T \_  
 CACTT CA CTGTCTGAGAT  
 |||| || |||||  
 GTGGA GT GG TAGACTTTA  
 C AG  
 GAM1307 KIAA0523 3' ATCTTGGGCTCACAAGTGAGG 67728 TCACT TG  
 TTTCACTT GTC AGAT  
 ||||| ||| |||  
 GGAGTGAA CGG TCTA  
 CACT\_ GT  
 GAM1307 KIAA0552 3' GTTTTGGGGGGCAAGGTGGAG 28320 CA G TG  
 TTTCACTTT CT TC AGAT  
 ||||| || || |||  
 GAGGTGGAA GG GG TTTG  
 C\_ G GT  
 GAM1307 KIAA0660 3' GTTTCAGGCAGGAGTGGGGT 24515 TT TCA  
 AT CACTT CTGTCTGAGAT  
 || |||| |||||  
 TG GTGAG GACGGACTTTG  
 GG \_  
 GAM1307 KIAA0759 3' GTTTCTGTTTTGAAAGTGAAAT 67329 CTGTCT  
 G CATTTCACTTTCA GAGAT  
 ||||| ||||  
 GTAAAGTGAAAGT CTTTG  
 TTTGT\_  
 GAM1307 KIAA0795 3' ATTTCAGGGAAGAGGTGGGAT 46588 TT CA GT  
 AT CACTTT CT CTGAGAT  
 || |||| || |||||  
 TA GTGGAG GG GACTTTA  
 GG AA \_  
 GAM1307 KIAA0830 3' ATTTCAGCAGTGTGAAGGTAAA 69694 CA \_ T  
 TG CATTT CTTT CACTG CTGAGAT  
 |||| ||| |||| |||||  
 GTAAA GAAG GTGAC GACTTTA  
 TG T \_  
 GAM1307 KIAA0871 3' ATTTCAGAATAGGAAGTAAATG 30299 C ACTG  
 CATTT ACTTTC TCTGAGAT  
 |||| |||| |||||

			GTAAA TGAAGG AGACTTTA		
			_ ATA_		
GAM1307	KIAA0893	3'	GTTTCAGGCTAAAAGGTAAATG 30360	C	CACT
			CATTT ACTTT GTCTGAGAT		
			GTAAA TGGAA CGGACTTTG		
			_ AAT_		
GAM1307	KIAA0918	3'	GTTTCAACGTTTAGGGTGAAGT 73134	CAC	C
	G		CATTTCACTTT TGT TGAGAT		
			GTGAAGTGGGA GCA ACTTTG		
			TTT _		
GAM1307	KIAA0931	3'	ATCTCAGACTAATGGGGTGTGA 67412	_ TT	CT_
			TCAC T CA GTCTGAGAT		
			AGTG G GT CAGACTCTA		
			T GG AAT		
GAM1307	KIAA0934	3'	GGCATGGGGGTGAAATG 64223	TT	C
			CATTTCACT CA TGTC		
			GTAAAGTGG GT ACGG		
			GG _		
GAM1307	KIAA0978	3'	CTCGACGTGAGGGTGAAATG 70480	T	T
			CATTTCACTTTTCACT GTC GAG		
			GTAAAGTGGGAGTG CAG CTC		
			_ _		
GAM1307	KIAA1036	3'	TGATGGGGGGGTGGGGGTGGGGT 29831	TT	TT G AGAT
	G		CAT CACT CACT TCTG		
			GTG GTGG GTGG GGGT		
			GG GG G AGTG		
GAM1307	KIAA1046	3'	ATCTTAGAAGAGGGGTGGG 29990	CACTG	
			TTCATTT TCTGAGAT		
			GGGTGGGG AGATTCTA		
			AGA_		
GAM1307	KIAA1046	3'	TTTCAGATGTTGGAAATG 30002	C	CT
			CA TTTCA GTCTGAGA		
			GT AAGGT TAGACTTT		
			A TG		
GAM1307	KIAA1237	3'	TTTTGGATGAAGTGAGGG 80476	_	TG
			CTTTCACT GTC AGA		
			GGGAGTGA TAG TTT		
			AG GT		
GAM1307	KIAA1257	3'	GTTGGCACGACTGAGAGTGGGA 62755	TT	CT _ A_
	TG		CAT CACTTTCA GTC TG GAT		

GTA GTGAGAGT CAG AC TTG  
 GG    \_ C GG  
 GAM1307 KIAA1456 3' GTTTTGGAGGAAGGAGGAAATG 67006    A\_ A TG TG  
 CATTTC CTTTC C TC AGAT  
 ||||| ||||| || |||||  
 GTAAAG GGAAG G AG TTTG  
 GA    \_ \_ GT  
 GAM1307 KIAA1538 3' GTTTTAGACAGGCTCCCTGAA 71556    CTTTCA  
 TTCA    CTGTCTGAGAT  
 ||||    |||||  
 AAGT    GACAGATTTTG  
 CCCTCG  
 GAM1307 KIAA1559 3' TTGGAGACAGTGAGGGAAGTG 73078    A T    GAGAT  
 CATTTC CTT CACTGTCT  
 ||||| || |||||  
 GTGAAG GGA GTGACAGA  
 \_ \_    GTTT  
 GAM1307 KIAA1560 3' TTTGGGAGAGGGAGGGA 64183    A A G G  
 TC CTTTC CT TCT AGA  
 || ||||| || |||||  
 AG GGAGG GA AGG TTT  
 \_ \_ G G  
 GAM1307 KIAA1655 5' ATCTCACCTCCAGTGGGAGGGA 66590    A TT    TC\_  
 AGTG    ATTTCT CT CACTG    TGAGAT  
 ||||| || ||||| |||||  
 TGAAG GA GTGAC    ACTCTA  
 G GG    CTCC  
 GAM1307 KIAA1655 5' TCTCACTGAGAGTGAGA 66634    CTGTC  
 TTTCACTTTCA    TGAGA  
 ||||| ||||| |||||  
 AGAGTGAGAGT    ACTCT  
 C\_  
 GAM1307 KIAA1729 3' GTCTTAGGCGATTTGTGGGGTG 89130    TT TTTCAC  
 CAT CAC    TGTCTGAGAT  
 || ||||| |||||  
 GTG GTG    GCGGATTCTG  
 GG TTTA\_  
 GAM1307 KIAA1799 5' ATCTTATTTCCGGTGGCGGTGA 74634    T    TC\_  
 GGTG    ATTTCACT TCACTG    TGAGAT  
 ||||| ||||| |||||  
 TGGAGTGG GGTGGC    ATTCTA  
 C    CTTT  
 GAM1307 KIAA1808 5' CATTGAGGGTGAGGTG 85861    C  
 CATTTCACTTTCA TG  
 ||||| ||||| |||||  
 GTGGAGTGGGAGT AC  
 T  
 GAM1307 KIAA1811 3' ATCTCTCTGCGGGGTGGGGTG 64793    TT TTCA    CT\_  
 CAT CACT    CTGT    GAGAT  
 || ||||| ||||| |||||

		GTG GTGG GCG CTCTA		
		GG ____ TCT		
GAM1307 KIAA1821	3'	GGGCAGTGAGGGTGAGG 71790		
		TTTCACTTTCACTGTCT		
		GGAGTGGGAGTGACGGG		
GAM1307 KIAA1893	3'	GTCTCGGGCAGCACGTGAGGT 73217	TTTCA	
		ATTTAC CTGTCTGAGAT		
		TGGAGTG GACGGGCTCTG		
		CAC__		
GAM1307 KPNA6	3'	GCAGAGGAGGGTGAGTG 24609	A_	
		CATTTCACTTTC CTGT		
		GTGAGGTGGGAG GACG		
		GA		
GAM1307 LMOD1	3'	ATCTTTGAGGTGAGGGTGGGGT 24038	TT	G T
G		CAT CACTTTCACT TC GAGAT		
		GTG GTGGGAGTGG AG TTCTA		
		GG _ T		
GAM1307 LY6G5B	5'	TTTCAGGCTCAGAGAAGTG 41131	CACT_	
		CACTTT GTCTGAGA		
		GTGAAG CGGACTTT		
		AGACT		
GAM1307 MAGE-E1	3'	GATTGGACGGTGGAGCTGGGAT 47945	TT C	TG GAT
G		CAT CA TTTCAGTGC A		
		GTA GT GAGGTGGCAG T		
		GG C GT AG		
GAM1307 MGC10960	3'	ATCTCCCCAGGAGGGTGAGATG 51003	A TCT	
		CATTTCACTTTC CTG GAGAT		
		GTAGAGTGGGAG GAC CTCTA		
		_ CC_		
GAM1307 MGC2628	3'	ATTTCCGGGTTAGGGTGGAATG 43968	C GT T	
		CATTTCACTTT ACT C GAGAT		
		GTAAGGTGGGA TGG G CTTTA		
		T _ C		
GAM1307 MGC27044	5'	CTTGGTGTTGAAAGTGAAATG 58673	CTGT TG	
		CATTTCACTTTCA C AG		
		GTAAAGTGAAAGT G TC		
		TGT_ GT		
GAM1307 MGC35558	3'	TCTCAGGTGGGTGAGGG 58787	_ TG	
		CTTTCA C TCTGAGA		

		GGGAGT G GGA	CT		
		G GT			
GAM1307	MGC4251	3' GTTGGCCTGGTGGGGGTGGAGT	50460	TT	__ TGAGAT
		ATTTCACT CACT GTC			
		TGAGGTGG GTGG CGG			
		GG TC TTG			
GAM1307	MLLT10	5' AGGCGGTGGAGGGGAGGTG	16166	A	
		CATTTC CTTTCACTGTCT			
		GTGGAG GGAGGTGGCGGA			
		G			
GAM1307	MOCS3	3' TCTTGGACATGTGAGATGT	27161	_	_ TG
		AC TTTCAC TGTC AGA			
		TG AGAGTG ACAG TCT			
		T T GT			
GAM1307	NR6A1	3' ATTTTGAGGGAGAGGGTGGGAT	7642	TT	A G T
	G	CAT CACTTTC CT TC GAGAT			
		GTA GTGGGAG GG AG TTTTA			
		GG A G _			
GAM1307	NR6A1	3' ATTTTGAGGGAGAGGGTGGGAT	52867	TT	A G T
	G	CAT CACTTTC CT TC GAGAT			
		GTA GTGGGAG GG AG TTTTA			
		GG A G _			
GAM1307	NR6A1	3' ATTTTGAGGGAGAGGGTGGGAT	52879	TT	A G T
	G	CAT CACTTTC CT TC GAGAT			
		GTA GTGGGAG GG AG TTTTA			
		GG A G _			
GAM1307	P450RAI-2	3' TGGTGGAGATGGAATG	39107	C	
		CATTTCAT TTTCACTG			
		GTAAGGT GAGGTGGT			
		A			
GAM1307	PALM	3' TCTCAGGCAGTTGGGGTGA	10417	TC	
		TCACTT ACTGTCTGAGA			
		AGTGGG TGACGGA			
		CTCT			
		GT			
GAM1307	PB1	3' ATTTTAGTTACTGGGGGTGGGG	36368	TT	TT C T
		T CACT CA TG CTGAGAT			
		G GTGG GT AT GATTTTA			
		GG GG C T			
GAM1307	pcnp	3' GTTTTGAAATTGGGGTGTGGGG	39789	TT	_ TT CTG T
	TG	CAT CAC T CA TC GAGAT			

		GTG GTG G GT AG TTTTG		
		GG T GG TAA _		
GAM1307	PEF	3' TCTGTGGAGAGTGGAGTG 24754	T G _	
		CACTT CACT TCTG AGA		
		GTGAG GTGA AGGT TCT		
		_ G G		
GAM1307	PGGT1B	3' ATTTTAGATTGGGAGGGTGGGG 17231	TT ACT	
		T CACTTTC GTCTGAGAT		
		G GTGGGAG TAGATTTTA		
		GG GGT		
GAM1307	PINK1	3' GTCTGTGAATGGTGAGGGTGGG 50543	TT _TG	
	A	T CACTTTCACTGT C AGAT		
		A GTGGGAGTGGTA G TCTG		
		GG A TG		
GAM1307	PP1057	5' GTTTTGTGGGGGTGGGAGTGGA 48435	TT G _	
	G	TTTCACT CACT TC TGAGAT		
		GAGGTGA GTGG GG GTTTTG		
		GG G T		
GAM1307	PRMT3	3' GTTTTAAATGTGGGGGTAGAGT 65025	TC TT TGTCT	
	G	CATT ACT CAC GAGAT		
		GTGA TGG GTG TTTTG		
		GA GG TAAT_		
GAM1307	PRMT6	3' GTTTCGCGGGGGAGTGAGG 36272	TT A CT	
		TTTCACT C CTGT GAGAT		
		GGAGTGA G GGCG CTTTG		
		GG _ _		
GAM1307	PRO2900	5' TTCAACTGAGAGTGAGGTG 37809	CT C	
		CATTTCACTTTCA GT TGAG		
		GTGGAGTGAGAGT CA ACTT		
		_ _		
GAM1307	PSMF1	3' GTCTTAGGTGTTCTATGGGAGG 22354	A TT C____GT	
	AAGTG	TC CT CA T CTGAGAT		
		AG GA GT G GATTCTG		
		_ GG ATCTT TG		
GAM1307	PXR2b	3' ATTTTAACTTGGGGGTGAAA 33338	TT CT CT	
		TTTCACT CA GT GAGAT		
		AAAGTGG GT CA TTTTA		
		GG T_ AT		
GAM1307	RAB6B	3' GTCTTTAGGAGTAGGGTGGGAT 33414	TT C G _	
	G	CAT CACTTT ACT TCTGA GAT		



GTA GTGGGA TGA GGATT CTG  
 GG \_ \_ T  
 GAM1307 RACGAP1 3' GTCTCAGGGTGGGAAGTGGGA 25200 TT \_ GT  
 T CACTTTC ACT CTGAGAT  
 | ||||| || |||||  
 A GTGAAGG TGG GACTCTG  
 GG G \_  
 GAM1307 RAD51 3' TTTCAGGCCAGTGTGGTG 56023 TT \_  
 CACT CACTG TCTGAGA  
 ||| ||| |||||  
 GTGG GTGAC GGACTTT  
 T\_ C  
 GAM1307 RAD51 3' TTTCAGGCCAGTGTGGTG 11229 TT \_  
 CACT CACTG TCTGAGA  
 ||| ||| |||||  
 GTGG GTGAC GGACTTT  
 T\_ C  
 GAM1307 RASSF2 3' GTTTCAGGTTGAAGGGAAATG 28443 A CTG  
 CATTTTCTTTCA TCTGAGAT  
 ||||| ||||| |||||  
 GTAAAG GGAAGT GGACTTTG  
 \_ T\_  
 GAM1307 RBM7 3' ATTTTAGACACTTTAGGAGGGG 32235 TT A CAC\_  
 GTG AT C CTTT TGTCTGAGAT  
 || ||| |||||  
 TG G GAGG ACAGATTTTA  
 GG\_ ATTTT  
 GAM1307 RIL 3' GGGGGTGGTGGTGGGGTG 13488 TT T G  
 CAT CACT TCACT TC  
 ||| ||| ||||| ||  
 GTG GTGG GGTGG GG  
 GG T G  
 GAM1307 RILP 5' GTCCCAGTGGAGGGTGGGGTG 48694 TT ACTGT A  
 CAT CACTTTC CTG GAT  
 ||| ||||| ||| |||  
 GTG GTGGGAG GAC CTG  
 GG GT\_ C  
 GAM1307 RNO2 5' ATTTTTTTAGTGGAGATGGGGT 52762 TT C TCT  
 G CAT CA TTTCAGT GAGAT  
 ||| ||| ||||| |||||  
 GTG GT GAGGTGAT TTTTA  
 GG A TT\_  
 GAM1307 RoXaN 3' ACAGTGGGTGTGAGATG 46627 T  
 CATTTTCACTTCACTGT  
 ||||| |||||  
 GTAGAGTG GGGTGACA  
 T  
 GAM1307 SAE1 3' TTTTGGGAGAAAGGAGATG 18537 A ACTG TG  
 CATTTTCTTTT TC AGA  
 ||||| ||||| || |||

			GTAGAG GAAAG GG TTT		
			_ A__ GT		
GAM1307	SDS3	3'	ATTTTCCATTGAAGGTGGAGT 69223	C	TCT
			ATTTCACTTTCA TG GAGAT		
			TGAGGTGGAAGT AC TTTTA		
			T CT_		
GAM1307	SEMA4C	3'	ACATATGGAGGTGGGGTG 35052	TT	C_
			CAT CACTTTCA TGT		
			GTG GTGGAGGT ACA		
			GG AT		
GAM1307	SFXN5	3'	TCTTAGGGTAGGGGAAGTG 58040	A	GT_
			CACTTTC CT C TGAGA		
			GTGAAGG GA G ATTCT		
			G TG G		
GAM1307	SGT1	3'	ATTTCAACATGGTGAACTG 21992	C	_
			CA TTTCACT GTCTGAGAT		
			GT AAAGTGG CAGACTTTA		
			C TA		
GAM1307	SH3BGRL2	3'	ATCTCAGACAGTGATCAGGA 48883	ACTT	
			TC TCACTGTCTGAGAT		
			AG AGTGACAGACTCTA		
			GA CT		
GAM1307	SMC1L1	3'	GTCTTAGGCAGTTACCTGAAA 71960	CTTTC	
			TTTCA ACTGTCTGAGAT		
			AAAGT TGACGGATTCTG		
			CCAT_		
GAM1307	SPTLC2	5'	GTTTCGGGGAGGTGGGTGGGGT 16809	TT	TCA G
	G		CAT CACTT CT TCTGAGAT		
			GTG GTGGG GA GGGCTTTG		
			GG TG_ G		
GAM1307	STK29	3'	GTCTCAGGCAGTGGGGG 87579	TT	
			CT CACTGTCTGAGAT		
			GG GTGACGGA CTCTG		
			GG		
GAM1307	TA-PP2C	3'	GTAGACGCGGTGGGGGCGGGGT 57759	TT A TT	_ AGAT
	G		CAT C CT CACT GTCTG		
			GTG G GG GTGG CAGAT		
			GG C GG CG G		
GAM1307	THEA	3'	TTT TAGGCCAGGTGTGGTG 66305	TT	_
			CACT CACT GTCTGAGA		

GTGG GTGG CGGATTTT  
 T\_ AC  
 GAM1307 TIAM2 3' ATCTTGGGCTGTATCAAGGGAG 24931 A TC\_ T TG  
 TG CATTTC CTT AC GTC AGAT  
 ||||| ||| || ||| ||||  
 GTGAGG GAA TG CGG TCTA  
 \_ CTA T GT  
 GAM1307 TP53TG3 3' ATCTTGGACATCTTGGAGATG 31102 ACTTTCAC TG  
 CATTTC TGTC AGAT  
 ||||| ||| ||||  
 GTAGAG ACAG TCTA  
 GTTCT\_\_ GT  
 GAM1307 TRIP3 3' GTTTCAGGCAGACTTGGGGT 78220 TT CTTTCA  
 AT CA CTGTCTGAGAT  
 || || |||||  
 TG GT GACGGACTTTG  
 GG TCA\_\_  
 GAM1307 VIAAT 3' GTTTTGGGGGGAGGCGGGGTG 54541 TT A A GT TG  
 CAT C CTTTC CT C AGAT  
 ||| | ||||| || | ||||  
 GTG G GGAGG GG G TTTG  
 GG C \_ \_ GT  
 GAM1307 VPS39 3' GTCTTTGATGGTGGTGAGGGTG 62849 \_ T  
 GG TTCACTTTCAC GTC GAGAT  
 ||||| ||| ||||  
 GGGTGGGAGTGG TAG TTCTG  
 TGG T  
 GAM1307 ZAP3 3' GTTTTGGGGAGGGAGGGAG 77224 A A G TG  
 TTC CTTTC CT TC AGAT  
 ||| ||||| || || ||||  
 GAG GGAGG GA GG TTTG  
 \_ \_ G GT  
 GAM1307 ZNF297B 3' ATTTCACTACTAAGGTGGTGA 25775 T ACT \_  
 TCACT TC GT CTGAGAT  
 ||||| || || |||||  
 AGTGG GG CA GACTTTA  
 T AAT T  
 GAM1307 ZNF323 5' ATCTTAAGATTGTGAAAGTGGA 48077 T \_  
 G TTCACTTTCAC GTCT GAGAT  
 ||||| ||||| ||||| |||||  
 GAGGTGAAAGTG TAGA TTCTA  
 T A  
 GAM1307 ZNF84 3' TCTTGGACTTCAGGAAATG 12817 A TTCACT TG  
 CATTTC CT GTC AGA  
 ||||| || || ||| |||  
 GTAAAG GA CAG TCT  
 \_ CTT\_\_ GT  
 GAM1307 LOC114987 3' TCTTGAGGGGAGTGGGATG 59124 TT TT A GTC  
 CAT CACT C CT TGAGA  
 ||| |||| | || |||||

		GTA GTGA G GA GTTCT	
		GG GG _ _	
GAM1307	LOC115219 5'	GGCGGTGGAGGGGAGATG 73312	A
		CATTTC CTTTCACTGTC	
		GTAGAG GGAGGTGGCGG	
		G	
GAM1307	LOC115297 3'	ATCTCAGATATCCTACGGTGAG 72884	TTCAC_
	A	TTTCACT TGTCTGAGAT	
		AGAGTGG ATAGACTCTA	
		CATCCT	
GAM1307	LOC116150 3'	TCTTACTTGAGAGTGAG 56638	CT CT
		TTCACTTTCA GT GAGA	
		GAGTGAGAGT CA TTCT	
		T_ _	
GAM1307	LOC124446 3'	TTTTAGAAAAAGTGAAG 74293	CACTG
		TTTCACTTT TCTGAGA	
		GAAGTGAAA AGATTTT	
		A_	
GAM1307	LOC126964 3'	GTTTTGGTGGGATGGGGGGAGG 74622	A TT _ GT TG
	TG	CATTTC CT CA CT C AGAT	
		GTGGAG GG GT GG G TTTG	
		_ GG A GT GT	
GAM1307	LOC128977 3'	GTCTGTGAACAGTGGGGGTGGG 74827	TT TT _ TG
	G	T CACT CACTGT C AGAT	
		G GTGG GTGACA G TCTG	
		GG GG A TG	
GAM1307	LOC130940 5'	GTCTCGGGCGCGGGAGGGGGTG 57139	TT A TT AC
		CAT C CT C TGTCTGAGAT	
		GTG G GA G GCGGGCTCTG	
		GG_ GG C_	
GAM1307	LOC131368 3'	ATTTTCAGATACTTTAAGTGAAT 75858	T TCAC
	TG	CA TTCACTT TGTCTGAGAT	
		GT AAGTGAA ATAGACTTTA	
		T TTTC	
GAM1307	LOC134288 3'	TCCACAGAGGTGAGAGTCGGGT 75178	TC G AGAT
	G	CATT ACTTTCACT TCTG	
		GTGG TGAGAGTGG AGAC	
		GC _ ACCTT	
GAM1307	LOC142948 3'	GTCTTGGCAGCATGGAAGTGAG 82891	_ T TG
	A	TTTCACTTTCA CTG C AGAT	

AGAGTGAAGGT GAC G TCTG  
 AC \_GT  
 GAM1307 LOC143279 5' GTCCTGGTGGTGGAGGTGGGG 76511 TT TG TGA  
 T CACTTTCAC TC GAT  
 | ||||| || ||  
 G GTGGAGGTG GG CTG  
 GG GT TC\_  
 GAM1307 LOC144483 3' TTTCATGGCAGTGAAA 60179 \_  
 TTTCAGTGC TGAGA  
 ||||| ||||  
 AAAGTGACGG ACTTT  
 T  
 GAM1307 LOC144486 3' TTTTGGTGTGAAGGTGAAAT 83090 TGT TG T  
 ATTTCACTTTCAC C AGA  
 ||||| || ||  
 TAAAGTGGAAGTG G TTT  
 T\_\_GT T  
 GAM1307 LOC144845 5' GTGGGGCAAGGTGGGGGTGAAG 56664 TT \_\_ GAGAT  
 TG CATTTCACT CACT GTCT  
 ||||| || ||  
 GTGAAGTGG GTGG CGGG  
 GG AA GTG  
 GAM1307 LOC144845 5' TCGCTCAGGGAGGTGGAGTG 56665 A TC  
 CATTTCACTTTC CTG TGA  
 ||||| || ||  
 GTGAGGTGGAGG GAC GCT  
 \_ TC  
 GAM1307 LOC145828 5' GTTTTGGGAAGGGAGAGGAGGTG 83538 A A G TG  
 CATTTT CTTTC CT TC AGAT  
 |||| |||| || ||  
 GTGGAG GAGAG GG AG TTTG  
 \_ \_ A GT  
 GAM1307 LOC146050 3' ATCTCAGATGATTTAGGAAGTG 77625 ACT\_\_  
 CACTTTC GTCTGAGAT  
 |||| |||||  
 GTGAAGG TAGACTCTA  
 ATTTAG  
 GAM1307 LOC146229 3' GTGGTAGAGTGGAATG 77769 C TG  
 CATTTCACTTT AC T  
 ||||| || |  
 GTAAGGTGAGA TG G  
 \_ GT  
 GAM1307 LOC146336 3' GACAGTGAGGCTGAAATG 77832 C  
 CATTTCA TTTCAGTGC  
 |||| |||||  
 GTAAAGT GGAGTGACAG  
 C  
 GAM1307 LOC146728 5' TCGGAGTGGGGTGGAGTG 83753 T TG  
 CATTTCACTT CAC TCTGA  
 ||||| || ||

GTGAGGTGGG GTG AGGCT

GAM1307 LOC146990 5' ATCTCGGGCGGCTGGAGGGGTG 83884 — —  
AGG TTCACT TTCA CTGTCTGAGAT  
||||| ||| |||||||||  
GAGTGG AGGT GGCGGGCTCTA  
GG C

GAM1307 LOC147632 5' TGGTGGAATGAGATG 56670 C  
CATTTCA TTTCAGT  
||||| |||||||  
GTAGAGT AAGGTGGT

GAM1307 LOC148413 3' GCAGTGAGGATGGAGTG 78830 CT  
CATTTCA TTCAGT  
||||| |||||||  
GTGAGGT GAGTGACG  
AG

GAM1307 LOC148479 3' GTTCCCTGCAGTGGAGGTGGAC 78879 T CT\_ AT  
TG CA TTCAGTTTCACTGT GAG  
|| ||||||||| |||  
GT AGGTGGAGGTGACG CTT  
C TCC G

GAM1307 LOC148529 5' TCTTAGGCGAGTGGGAG 84172 TT \_  
CT CACT GTCTGAGA  
|| ||| |||||||  
GA GTGA CGGATTCT  
GG G

GAM1307 LOC149076 3' ATCTTGAGGCAGGGAGGTGAG 79148 A \_  
G TTTCACTTTC CTGTCT GAGAT  
||||||| ||||| |||||  
GGAGTGGAGG GACGGA TTCTA  
GG

GAM1307 LOC149182 5' TCTTGTGCAGGGTGAGATG 84379 TTCA CT  
CATTTCACT CTGT GAGA  
||||||| ||| |||||  
GTAGAGTGG GACG TTCT  
TG

GAM1307 LOC149711 3' ATTTACCTGCTTGGAAAGTGA 84673 ACT C\_  
GATG ATTTCACTTTC GT TGAGAT  
||||||| || |||||||  
TAGAGTGAAAG CG ACTTTA  
GTT TCC

GAM1307 LOC149837 5' GTTTTGAGGGTGGAAATGAGGTG 84745 C G T  
CATTTCA TTTCAGT TC GAGAT  
||||||| ||||| || |||||  
GTGGAGT AAGGTGG AG TTTTG  
G \_

GAM1307 LOC149844 5' GGTGGTGGGGGTGGTGGTG 79519 \_ TT TG  
CATT TCACT CAC TC  
||| ||||| ||| ||

GTGG GGTGG GTG GG  
 T GG GT  
 GAM1307 LOC149844 3' TGGTGAGTGAGATG 79521 TT  
 CATTTTCACTCACTG  
 ||||| |||||  
 GTAGAGTG AGTGGT  
 —  
 GAM1307 LOC150225 3' GTCTTTTGCAGGTGAAGGTGGG 85009 TT \_ CT  
 A T CACTTTCACT TGT GAGAT  
 | ||||| || |||||  
 A GTGGAAGTG ACG TTCTG  
 GG G TT  
 GAM1307 LOC150351 5' TTTTAGATAGTACGAAGT 60249 C\_  
 ACTTT ACTGTCTGAGA  
 |||| |||||  
 TGAAG TGATAGATTTT  
 CA  
 GAM1307 LOC150358 3' TCTCAGAGAGTGAAGTGA 84928 T G  
 TCACTT CACT TCTGAGA  
 |||| || |||||  
 AGTGAA GTGA AGACTCT  
 \_ G  
 GAM1307 LOC150819 5' GTTAGGGAGCAGTGAAAGTGAG 85122 \_ GAT  
 G TTTCACTTTCACTGT CTGA  
 ||||| |||||  
 GGAGTGAAAGTGACG GATT  
 AGG G  
 GAM1307 LOC150933 3' ATTTCAAGTCACAGGAAATGGGG 85156 TT C A \_  
 TG CAT CA TTTC CTGT CTGAGAT  
 || || || || || |||||  
 GTG GT AAAG GACA GACTTTA  
 GG \_ \_ CT  
 GAM1307 LOC151056 3' ATCTTTTTTGGGAGTGAAGTGA 80106 T TT CTGTCT  
 CA TTCACT CA GAGAT  
 || |||| || |||||  
 GT AAGTGA GT TTCTA  
 C GG TTT\_  
 GAM1307 LOC151176 3' GTTTTGATAAGGGGGTGATGTG 85263 T TT AC T  
 CAT TCACT C TGTC GAGAT  
 || |||| | || |||||  
 GTG AGTGG G ATAG TTTTG  
 T GG A\_ \_  
 GAM1307 LOC151194 3' ATTTTAGATGGTGAAATTAGAA 59213 AC\_  
 GT ATTC TTTCAGTGTCTGAGAT  
 |||| |||||  
 TGAAG AAAGTGGTAGATTTTA  
 ATT  
 GAM1307 LOC151414 3' ATTTTGGCATATGGGGGTGGAG 80235 TT C \_ TG  
 TTTCAGT CA TGT C AGAT  
 ||||| || || | ||||

	GAGGTGG GT ATA G TTTA		
	GG _ C GT		
GAM1307 LOC151438 5'	TTTTCGGTGTGAAGGTGGGATG 85373	TT	TGT T
	CAT CACTTTCAC CTGAGA		
	GTA GTGGAAGTG GGCTTT		
	GG T__ TT		
GAM1307 LOC151610 3'	GGATGGTGGGAGTGAAG 80288	TT	
	TTTCACT CACTGTCT		
	GAAGTGA GTGGTAGG		
	GG		
GAM1307 LOC151658 5'	GTGGTGGAGTGGAGTG 85481	T TG	
	CATTTCACTT CAC T		
	GTGAGGTGAG GTG G		
	_ GT		
GAM1307 LOC151826 3'	TTTTAGGCTAGTGAAG 80370	_	
	TTTCACT GTCTGAGA		
	AAAGTGA CGGATTTT		
	T		
GAM1307 LOC151904 5'	CCCTGCGTGGTGGAGGGAGGTG 80387	A	TG CTGAGAT
	CATTTTCTTTTCACT T		
	GTGGAG GGAGGTG G		
	_ GT CGTCCCT		
GAM1307 LOC152274 3'	TCTTGGATTGGATGAGATG 80509	CT CT TG	
	CATTTCA TTCA GTC AGA		
	GTAGAGT AGGT TAG TCT		
	_ _ GT		
GAM1307 LOC152275 3'	GGGGGCGACAGGGAGGTGGGAT 85620	TT A TGAGAT	
G	CAT CACTTTC CTGTC		
	GTA GTGGAGG GACAG		
	GG _ CGGGGGT		
GAM1307 LOC152633 5'	GTCTTGCTGTGCTGGGGGTGGG 85817	TT TT CTGTCT_	
GTG	CAT CACT CA GAGAT		
	GTG GTGG GT TTCTG		
	GG GG CGTGTCTG		
GAM1307 LOC152805 5'	TCTCAGGATGAGTGAGG 80689	TCACTG	
	TTTCACTT TCTGAGA		
	GGAGTGAG GGA CTCT		
	TA__		
GAM1307 LOC153196 5'	GTCTTAGAGCTAGAGATGAGGT 85975	C ACTG	
G	CATTTCA TTTC TCTGAGAT		



GTGGAGT AGAG AGATTCTG  
 \_ ATCG  
 GAM1307 LOC153222 3' TTTTGGAGGAGTCAAAT 80791 CACTG TG  
 ATTTCACTTT TC AGA  
 ||||| || ||  
 TAAAGTGAGG AG TTT  
 \_\_\_\_\_ GT  
 GAM1307 LOC153339 5' GTTTTGGTGGGGTGGTGGGATG 86012 TT T A T TG  
 CAT CACT TC CTG C AGAT  
 || |||| || || || ||  
 GTA GTGG GG GGT G TTTG  
 GG T \_ \_ GT  
 GAM1307 LOC153651 3' TTTTAGATGGTGATTGT 80918 TT  
 AC TCACTGTCTGAGA  
 || ||||| |||||  
 TG AGTGGTAGATTTT  
 TT  
 GAM1307 LOC153711 3' TCGGGTGGGAGAGGGA 86138 A A TG  
 TTC CTTTC C TCTGA  
 || |||| | ||||  
 AGG GAGAG G GGGCT  
 \_ \_ GT  
 GAM1307 LOC153811 3' GCAGTGGGGGTAAGGTG 80950 C TT  
 CATTT ACT CACTGT  
 |||| || ||||  
 GTGGA TGG GTGACG  
 A GG  
 GAM1307 LOC154386 3' GTTTCAGTTCTGGAAGGTGAAA 81084 ACTGT  
 TTTCACTTTC CTGAGAT  
 ||||| |||||  
 AAAGTGGAAG GACTTTG  
 GTCTT  
 GAM1307 LOC154792 3' TTTTGGATATGTGAGAG 86250 \_ TG  
 CTTTCAC TGTC AGA  
 ||||| |||| ||  
 GAGAGTG ATAG TTT  
 T GT  
 GAM1307 LOC154877 3' GTCTTTACTGAGGGTGGCAGTG 86306 T G T\_\_\_\_  
 CACT TCACT TC GAGAT  
 |||| |||| || ||||  
 GTGA GGTGG AG TTCTG  
 C G TCAT  
 GAM1307 LOC157623 5' CAACGAGGCGGTGTGGGTGGAG 81493 TT GAGAT  
 TG CATTTCAC CACTGTCT  
 ||||| |||||  
 GTGAGGTGG GTGGCGGA  
 GT GCAACT  
 GAM1307 LOC157693 3' TCTTGGACGCAGTGAAGT 81558 TTCAC TG  
 ATTTCACT TGTC AGA  
 ||||| |||| ||

	TGAAGTGA GCAG TCT	
	C____ GT	
GAM1307 LOC157918 3'	GTCTTGGGCACAGGTGGGGT 86649	TT TCAC TG
	AT CACTT TGTC AGAT	
	TG GTGGA ACGG TCTG	
	GG C____ GT	
GAM1307 LOC157919 3'	GTTTCAGACAGTGGAA 81637	
	TTTCACTGTCTGAGAT	
	AAGGTGACAGACTTTG	
GAM1307 LOC158117 3'	GGCGTGGTGGGAATGGAATG 81709	C ____
	CATTTCATTTCACT GTC	
	GTAAGGT AAGGTGG CGG	
	____ TG	
GAM1307 LOC158382 5'	ACGGGGGAAGTGAGGTG 86782	A
	CATTTCATTTTC CTGT	
	GTGGAGTGAAGG GGCA	
	G	
GAM1307 LOC158382 5'	GTGGTGGGAAGATGAAGTG 86789	____ TG
	CATTTCATTTTCAC T	
	GTGAAGT GAAGGTG G	
	A GT	
GAM1307 LOC158954 3'	TTTTGGGTGGGGGGGAAGTG 60437	A TT TGT TG
	CATTTCCTCAC C AGA	
	GTGAAGGGGTG G TTT	
	G GG ____ GT	
GAM1307 LOC159184 5'	TCAATGGTGAAGGTGAAGT 60051	C
	ATTTCACTTTCACTGT TGA	
	TGAAGTGAAGTGGTA ACT	
GAM1307 LOC163882 3'	ATGCTGGCAGTGAGAGTGAAA 82163	TGAGAT
	TTTCACTTTCACTGTC	
	AAAGTGAGAGTGACGG	
	TCGTA	
GAM1307 LOC166983 5'	GTCTGGCCCAAGGGGAGGTGGA 87266	A ____ T GAT
	GTG TTTCACTTTCTCT GTC GA	
	GAGGTGGAGG GA CGG CT	
	G ACC T G	
GAM1307 LOC169436 5'	GGGGTAGATGTGGGGGTGGAAT 82743	TT T AGAT
	G CATTTCACTCACGTCTG	

GTAAGGTGG GTG TAGAT  
 GG \_ GGGGT  
 GAM1307 LOC196761 3' GTTTTGGGCAGTGGAG 89556 TG  
 TTTCAGTGTG AGAT  
 ||||| |||  
 GAGGTGACGG TTTG  
 GT  
 GAM1307 LOC197379 3' GATGGTGAGGGTGGGGT 89742 TT  
 AT CACTTTCAGTGTG  
 || |||||  
 TG GTGGGAGTGGTAG  
 GG  
 GAM1307 LOC197414 3' ATTTTGGGCAGGCGCTGAGTGG 88061 TT TCA\_\_ TG  
 GG T CACTT CTGTC AGAT  
 | ||| ||| |||  
 G GTGAG GACGG TTTA  
 GG TCGCG GT  
 GAM1307 LOC201203 3' ATCTCAGATTGTGAGGTAAATG 88140 C T T  
 CATTT ACTT CAC GTCTGAGAT  
 |||| ||| ||| |||||  
 GTAAA TGGA GTG TAGACTCTA  
 \_ \_ T  
 GAM1307 LOC201895 3' TCTTAGGCCAGTGCAGTG 89094 TT \_  
 CACT CACTG TCTGAGA  
 ||| ||| |||||  
 GTGA GTGAC GGATTCT  
 C\_ C  
 GAM1307 LOC202152 3' ATCTCAGATTTAAAAACGTGGG 89157 TT \_ CACT  
 ATG CAT CAC TTT GTCTGAGAT  
 ||| ||| ||| |||||  
 GTA GTG AAA TAGACTCTA  
 GG C AATT  
 GAM1307 LOC203275 3' GGC GTGGTGGGAATGGAATG 89325 C \_  
 CATTTCA TTTCAGT GTC  
 ||||| ||||| |||  
 GTAAGGT AAGGTGG CGG  
 \_ TG  
 GAM1307 LOC203317 5' GTCTTGCCAATGGAAGTTGGAG 89333 \_ C TC  
 TG CATTTCA CTTTCA TG TGAGAT  
 ||||| ||||| || |||||  
 GTGAGGT GAAGGT AC GTTCTG  
 T A C\_  
 GAM1307 LOC219333 3' GTCAGGGCAGTGGGAAGTGA 93542 GA  
 TTCACTTTCACTGTCT GAT  
 ||||| ||||| |||  
 AGGTGAAGGTGACGGG CTG  
 A\_  
 GAM1307 LOC219529 3' GTCTCAGGTGAGTGGAGG 92972 \_ GT  
 CTTTCAC T CTGAGAT  
 ||||| | |||||

	GGAGGTG G GACTCTG	
	A TG	
GAM1307 LOC220143 5'	GCGGGAGGGTGAAATG 93589	A
	CATTTCACTTTC CTGT	
	GTAAAGTGGGAG GGCG	
	—	
GAM1307 LOC220549 5'	GCGGTGAGAGAGAGGTG 92919	A
	CATTTC CTTTCACTGT	
	GTGGAG GAGAGTGGCG	
	A	
GAM1307 LOC220739 5'	ATTTCCCATGGGAGTGGAGT 92925	TT C TCT
	ATTTCACT CA TG GAGAT	
	TGAGGTGA GT AC CTTTA	
	GG _ C__	
GAM1307 LOC221400 3'	GTCTCAGGTTGATGGTGGGGTG 92299	TT T CTG
	CAT CACT TCA TCTGAGAT	
	GTG GTGG AGT GGA CTCTG	
	GG T T__	
GAM1307 LOC221405 3'	TTT TAGATTAGTGGAA 93892	—
	TTTCACTG TCTGAGA	
	AAGGTGAT AGATTTT	
	T	
GAM1307 LOC221415 3'	TTTCCTGGGGGTTGAGGTG 93878	C G T_
	CACTTT ACT TC GAGA	
	GTGGAG TGG GG CTTT	
	T G TC	
GAM1307 LOC221584 3'	TCTCGAGAGAAAGGGAGTG 93833	A A GTC
	CATTTT CTTTC CT TGAGA	
	GTGAGG GAAAG GA GCTCT	
	— A —	
GAM1307 LOC221683 5'	GTCTTAGGTTTGGTGTGA 93717	TT CT
	TCAC TCA GTCTGAGAT	
	AGTG GGT TGGATTCTG	
	T_ TT	
GAM1307 LOC221865 3'	ATTTTGGGTATATGGGGTGAAA 92486	CAC GT TG
T	ATTTCACTTT T C AGAT	
	TAAAGTGGGG A G TTTA	
	TAT TG GT	
GAM1307 LOC222134 5'	ACAGTGAAGTGAAATG 94136	T
	CATTTCACTT CACTGT	

GTAAAGTGAA GTGACA

GAM1307 LOC245728 5' TTCAGGCAATGAAGTG 91135 T C  
CACTT CA TGTCTGAG  
||||| || |||||  
GTGAA GT ACGGACTT

\_ A  
GAM1307 LOC253115 3' ATTTTATTGTGGGGTGGGATG 94494 TT T TGTCT  
CAT CACTT CAC GAGAT  
||| ||||| ||| |||||  
GTA GTGGG GTG TTTTA  
GG \_ TTAT\_

GAM1307 LOC254485 3' CTGGGAAGTGAGGTG 95013 T G G  
CACTT CACT TCT AG  
||||| ||||| ||| ||  
GTGGA GTGA AGG TC

\_ \_ G  
GAM1307 LOC254755 3' GCAGGGAGGTGGGGTG 97369 TT A  
CAT CACTTTC CTGT  
||| ||||| ||||| |||||  
GTG GTGGAGG GACG

GG \_  
GAM1307 LOC254756 3' GCAGGGAGGTGGGGTG 97363 TT A  
CAT CACTTTC CTGT  
||| ||||| ||||| |||||  
GTG GTGGAGG GACG

GG \_  
GAM1307 LOC255391 5' TCTCTGGGGGTGCGGTG 97614 TT G T  
CACT CACT TC GAGA  
||||| ||||| || |||||  
GTGG GTGG GG CTCT

C\_ G T  
GAM1307 LOC255394 3' GTTTCAGACACTGCTTAGGTGC 94886 T T\_\_ C  
AGTG ATT CACTT CA TGTCTGAGAT

||| ||||| || |||||  
TGA GTGGA GT ACAGACTTTG  
C TTC C  
GAM1307 LOC255452 5' GTCTCTATCCGAGAGGGTGGAG 97543 ACTGTCT  
TG CATTTCACTTTC GAGAT  
||||||| |||||  
GTGAGGTGGGAG CTCTG  
AGCCTAT

GAM1307 LOC255480 3' TCTTGAGGAGGTGAAGG 96521 GT \_  
CTTTCACT CT GAGA  
||||||| || |||||  
GGAAGTGG GA TTCT  
AG G

GAM1307 LOC255779 3' ATTTCCCATGCAAAGTGGGAT 96013 TT \_ C TCT  
G CAT CACTTT CA TG GAGAT  
||| ||||| ||| || |||||

	GTA GTGAAA GT AC CTTTA	
	GG C _ CC_	
GAM1307 LOC256145 5'	GTCTCGGGCATCGTGGG 96543	___
	TTCAC TGTCTGAGAT	
	GGGTG ACGGGCTCTG	
	CT	
GAM1307 LOC256405 5'	ATCTCAGGACCAGATAGTGGAG 95872	T ACTG
TG	CATTTCACT TC TCTGAGAT	
	GTGAGGTGA AG GGA CTCTA	
	T ACCA	
GAM1307 LOC256639 5'	GTCTTGCTTCAGGAAGGTGAAG 96219	A TC_
TG	CATTTCACTTTC CTG TGAGAT	
	GTGAAGTGGAAG GAC GTTCTG	
	_ TTC	
GAM1307 LOC257048 3'	TATGTAGGTAGTGGGGGGAAAT 96216	A TT GT AGAT
G	CATTTTC CT CACT CTG	
	GTAAAG GG GTGA GAT	
	_ GG TG GTATT	
GAM1307 LOC257554 5'	ATCTCAGATTGTGGGGGTGTGG 97691	_ TT T
ATG	CATTT CACT CAC GTCTGAGAT	
	GTAGG GTGG GTG TAGACTCTA	
	T GG T	
GAM1307 LOC257556 3'	ATTTTTATTGTGGGGGTGGGATG 97707	TT T TGTCT
	CAT CACTT CAC GAGAT	
	GTA GTGGG GTG TTTTA	
	GG _ TTAT_	
GAM1307 LOC257617 3'	ATTTTTATTGTGGGGGTGGGATG 97813	TT T TGTCT
	CAT CACTT CAC GAGAT	
	GTA GTGGG GTG TTTTA	
	GG _ TTAT_	
GAM1307 LOC51107 3'	TTTCTGCTGAGGGTGGAGTG 32064	CT CT
	CATTTCACTTTCA GT GAGA	
	GTGAGGTGGGAGT CG CTTT	
	_ T_	
GAM1307 LOC51152 3'	GTCTCAAAGGAGAAAGTGAGGT 32454	A GTC
G	CATTTCACTTTC CT TGAGAT	
	GTGGAGTGAAAG GG ACTCTG	
	A AA_	
GAM1307 LOC51716 3'	GCAGTGAAGGTGAGGT 32792	
	ATTTCACTTTCACTGT	

TGGAGTGGAAGTGACG

GAM1307 LOC56912 5' CTCACGAGAGTGGAAG 39336 G \_  
CTTTCAC TC TGAG  
||||||| || ||||  
GAAGGTGA AG ACTC  
G C

GAM1307 LOC56959 5' TCTTGACCGGAGGTGGAA 81927 ACT T  
TTTCACTTTC GTC GAGA  
||||||| || ||||  
AAGGTGGAGG CAG TTCT  
C \_ \_

GAM1307 LOC89135 3' TGGTGAGTGAGATG 60319 TT  
CATTTAC TCACTG  
||||||| |||||  
GTAGAGTG AGTGGT

GAM1307 LOC90170 5' GGTGGTGAGGGTTAAATG 61710 C TG  
CATTT ACTTTCAC TC  
||||| ||||| ||  
GTAAA TGGGAGTG GG  
T GT

GAM1307 LOC90826 5' GTCTTGGGTTTGAATGTGAAA 64095 \_ CTG TG  
TG CATTTAC TTTCA TC AGAT  
||||||| ||||| || ||||  
GTAAAGTG AAGGT GG TCTG  
T TT\_ GT

GAM1307 LOC91363 3' ATCTCAGAACAGAAAGGGTGGA 65776 TT CA \_  
T CACTTT CTGT CTGAGAT  
| ||||| ||||| |||||  
A GTGGGA GACA GACTCTA  
GG A\_ A

GAM1307 LOC91450 3' GTTTTGGGCAGAGGAGTG GGG 66076 TT CA TG  
T CACTTT CTGTC AGAT  
| ||||| ||||| |||||  
G GTGAGG GACGG TTTG  
GG A\_ GT

GAM1307 LOC91628 3' GCAGTGATGTGGGATG 66760 TT T  
CAT CAC TTCACTGT  
||| ||| |||||  
GTA GTG AGGTGACG  
GG T

GAM1307 LOC92305 3' GTCTCAGACTCCTGGGTAGGGG 56418 TT\_ TCACT  
TG CAT C ACTT GTCTGAGAT  
||| | ||||| |||||  
GTG G TGGG CAGACTCTG  
GG A TCCT\_

GAM1307 LOC93349 3' CTTAGGCGGATGGAGG 56457 \_  
CTTTCA CTGTCTGAG  
||||| |||||

			GGAGGT GGCGGATTC		
			A		
GAM1307	LOC93587	3'	TAGGAGAAAGTGAGGTG 72648	A_	
			CATTTCACCTTC CTG		
			GTGGAGTGAAAG GAT		
			AG		
GAM1308	ABH	3'	TAGTTACATGTTGGCTGTA 59752	--	
			TACGGTTA C TGTGATTA		
			ATGTCGGT G ACATTGAT		
			T T		
GAM1308	ACOX3	3'	TGGGATCGCGGTGATTTG 13027	C	TA
			A GGTTACTGTGAT CG		
			G TTAGTGGCGCTA GT		
			T GG		
GAM1308	ADCY6	5'	GTGGTGGCAGTGGCTGTG 30936	G	
			TACGGTTACTGT ATTAC		
			GTGTCGGTGACG TGGTG		
			G		
GAM1308	AIPL1	3'	TGGTTCGATTGACCAGGATCGT 59851	A	TGATTA
	G		TACGGTT CTG CGGACTA		
			GTGCTAG GAC GCTTGGT		
			_ CAGTTA		
GAM1308	AK3	3'	TGGTCTTGAGTGACTGTG 25499	GT_	
			TACGGTTACT GATTA		
			GTGTCAGTGA CTGGT		
			GTT		
GAM1308	AKAP2	3'	GGTTTTAGAGTGATTGTG 23266	G	TTACG
			TACGGTTACT TGA GACT		
			GTGTTAGTGA ATT TTGG		
			G _____		
GAM1308	APC	3'	TAATCATGTGGCTGTG 3478	T	
			TACGGTTAC GTGATTA		
			GTGTCGGTG TACTAAT		
			-		
GAM1308	ARHA	3'	TAGTTACCTTATAGTTACTGTG 70699	T	TTACG
			TACGGT ACTGTGA GACTA		
			GTGTCA TGATATT TTGAT		
			T CCA__		
GAM1308	ARIH1	3'	TGGTCTGTAGTACCAGAATTGT 19231	A	TG
			ACGGTT CTG ATTACGGACTA		



			TGTTAA GAC TGATGTCTGGT		
			— CA		
GAM1308	ATP11B	3'	TATGTTTGTAAATCATGGTAATT 80319	C	TA
	TA		A GGTTACTGTGATTACGGAC		
			A TTAATGGTACTAATGTTTG		
			T TATA		
GAM1308	BCL11B	3'	GTTCTTGTTACAGTAACTGTA 43193		TAC
			TACGGTTACTGTGAT GGAC		
			ATGTCAATGACATTG CTTG		
			TT_		
GAM1308	BNIP3L	3'	TGGTGTATTGTCACAGTAGCTT 15082	C	TACGG
	A		A GGTTACTGTGAT ACTA		
			A TCGATGACACTG TGGT		
			T TTATG		
GAM1308	CANX	3'	TTGTTCTGTGGTCACAGTGACC 87485		CTA
			GGTTACTGTGATTACGGA		
			CCAGTGACACTGGTGTCT		
			TGTTG		
GAM1308	CCND1	3'	TGGTTACAGTAGCGTA 53894	G	
			TACG TTA CTGTGATTA		
			ATGC GATGACATTGGT		
			—		
GAM1308	CD28	5'	TGGTGGCGGTGGTGGTGGCCGT 20443		TG G ACGG
	G		TACGGTTAC T ATT ACTA		
			GTGCCGGTG G TGG TGGT		
			GT G CGG_		
GAM1308	CIT	3'	TGGTTTCAATGGTGGTAGTTGT 69750	GG	TG G AC
	G		TAC TTAC T ATT GGACTA		
			GTG GATG G TAA TTTGGT		
			TT GT G C_		
GAM1308	CNGB3	3'	AGTTCCCAAAGTGATTGTA 38872		G ATTAC
			TACGGTTACT TG GGACT		
			ATGTTAGTGA AC CTTGA		
			A C_		
GAM1308	CNTFR	3'	TAGTCTGACTCAATGGTAACTT 8456	C	GATTA
	G		A GGTTACTGT CGGACTA		
			G TCAATGGTA GTCTGAT		
			T ACTCA		
GAM1308	CREBL2	3'	TAGTCTAGTCTAGTCATGTGTG 7146	_	C_
	ACTGTG		GTTAC TGTGATTA GGACTA		

			CAGTG GTACTGAT TCTGAT		
			T CTGA		
GAM1308	EFNB2	3'	TGGTTTGTGGACGAGAGGGCTG 14579	ACTG A	
	TG		TACGGTT TG TTACGGACTA		
			GTGTCGG GC GGTGTTTGGT		
			GAGA A		
GAM1308	EGR2	3'	GGTTTGTGACTATAGTG 4630 A		
			TACTGTG TTACGGACT		
			GTGATAT AGTGTTTGG		
			C		
GAM1308	EHD4	3'	TGGTTCTCTGCAGTGATCGT 57693	_ TTAC	
			ACGGTTACTGT GA GGACTA		
			TGCTAGTGACG CT CTTGGT		
			T ____		
GAM1308	ELAVL2	5'	TAGACCAAATGGTCATAGTTAC 15416 T	C__ A	
	TGTG		ACGGT ACTGTGATTA GG CTA		
			TGTCA TGATACTGGT CC GAT		
			T AAA A		
GAM1308	ELK4	3'	GTGGGCTTTAGTGACTGTG 8771	TGA_	
			TACGGTTACTG TTAC		
			GTGTCAGTGAT GGTG		
			TTCG		
GAM1308	ETS2	3'	TAATTATATAACTGTA 17880 C		
			TACGGTTA TGTGATTA		
			ATGTCAAT ATATTAAT		
			-		
GAM1308	EXTL3	3'	GGTCACGGTGGCAGTA 7534 G		
			TAC GTTACTGTGATT		
			ATG CGGTGGCACTGG		
			A		
GAM1308	F2RL3	3'	CCGGGTTTCGTAGTAGTCGTA 14174 GT	TTA	
			TACG TACTGTGA CGG		
			ATGC ATGATGCT GCC		
			TG TGG		
GAM1308	FAT2	3'	TGGTTTGTGGCTGTGTGTGA 7548	TGTGA__	
	CTGTG		GGTTAC TTACGGACTA		
			TCAGTG GGTGTTTGGT		
			TGTGTGTC		
GAM1308	GALNT1	3'	TGGTTTGTGGGCTGTTGGAATT 40021	A TGA__	
	GTA		ACGGTT CTG TTACGGACTA		

			TGTTAA GGT GGTGTTTGGT	
			_ TGTCG	
GAM1308	GLUL	3'	TGGTTCTTAGATGGTGATC 9049	GA C
			GGT TACTGT TTA G GACTA	
			CTAGTGGTA GAT CTTGGT	
			_ T	
GAM1308	GOT1	3'	TGGTTCTTTAGGGTGACTGTG 9097	G TTAC
			TACGGTTACT TGA G GACTA	
			GTGTCAGTGG ATT CTTGGT	
			G T__	
GAM1308	GRB10	3'	AACTGCAGTGACTGTA 17969	GA
			TACGGTTACTGT TT	
			ATGTCAGTGACG AA	
			TC	
GAM1308	GRM6	3'	GGTTGCAGTGAGCTGTG 5939	_ TG
			TACGG T TACTG ATT	
			GTGTC AGTGAC TGG	
			G GT	
GAM1308	GUCY1A3	3'	TATCAGATAATTGTAGTCAATT 63493	_ TG CG_ CTA
	GTA		ACGGTT ACTG ATTA GA	
			TGTTAA TGAT TAAT CT	
			C GT AGA AT	
GAM1308	HDAC4	3'	TGGTCTGTCCTAGGAGCTGTA 20121	A T TTA
			TACGGTT CTG GA CGGACTA	
			ATGTCGA GAT CT GTCTGGT	
			G C _	
GAM1308	HIP2	5'	TGGCGGCGGTGGCGGTGGTCGT 18070	GT G A_ GACTA
	A		TACG TACTGT ATT CG	
			ATGC GTGGCG TGG GC	
			TG G CG GGT	
GAM1308	HLCS	3'	GCTGGTGTGGTTGCAGTGACC 4670	TG GACTA
			GGT TACTG ATTACG	
			CCAGTGAC TGGTGT	
			GT GGTCGA	
GAM1308	HS2ST1	3'	TGGTTTGTACTTGCAGTGGCTG 24338	TG T
			CGGTTACTG A TACGGACTA	
			GTCGGTGAC T ATGTTTGGT	
			GT C	
GAM1308	INHBC	3'	GTCTGTGTAAGTGTG 18655	TGTGATT _
			TACGGTTAC ACGGA C	

			GTGTCAATG	TGTCT G	
			_____	T	
GAM1308	JAK2	3'	TAGTTTTTACCACAGTGGATGT	17129	G AT CG
	A		TACG TTAGTGTG TA GACTA		
			ATGT GGTGACAC AT TTGAT		
			A C_ TT		
GAM1308	LMCD1	3'	AATCGCATAGCTGTA	27425	C
			TACGGTTA TGTGATT		
			ATGTCGAT ACGCTAA		
			—		
GAM1308	M6PR	3'	AATTGGGGTGA	9861	G
			TACGGTTACT TGATT		
			ATGTCAGTGG GTTAA		
			G		
GAM1308	MBL2	3'	AGTTAGGTA	4114	G
			TACGGTTACT TGATT		
			ATGTCAATGG ATTGA		
			—		
GAM1308	MMP25	3'	TAGTCGCGGGGATTGTG	42446	TA
			TACGGT CTGTGATTA		
			GTGTTA GGCGCTGAT		
			GG		
GAM1308	MNT	3'	CCGGTTGCAGTCACTGTG	39708	T TG TA
			TACGGT ACTG AT CGG		
			GTGTCA TGAC TG GCC		
			C GT —		
GAM1308	MUT	3'	AATCATGGT	4225	G
			TACG TTAGTGTGATT		
			ATGT AGTGGTACTAA		
			—		
GAM1308	NAPB	3'	TGAAAAGAATCAAAGTAATTGT	70191	G ACGGACTA
	A		TACGGTTACT TGATT		
			ATGTTAATGA ACTAA		
			A GAAAAGT		
GAM1308	NBS1	3'	AGTCTGTGGCTTGACTGT	69495	CT GAT
			ACGGTTA GT TACGGACT		
			TGTCAGT CG GTGTCTGA		
			T_ —		
GAM1308	NEURL	3'	GGTCGCTGTGATTGTG	14862	T
			TACGGTTAC GTGATT		

		GTGTTAGTG CGCTGG	
		T	
GAM1308 NFATC1	3'	CTGTGATTGACAGTAGCTGTA 20485	—
		TACGGTTACTGT GATTACGG	
		ATGTCGATGACA TTAGTGTC	
		G	
GAM1308 NUFIP1	3'	AGTCATTGTACTAGCTGTA 24719	C TG TACG
		TACGGTTA TG AT GACT	
		ATGTCGAT AT TA CTGA	
		C GT ____	
GAM1308 ONECUT1	3'	TGGTTTGGAGCATAGTGATT 62136	ATTA
		GGTTACTGTG CGGACTA	
		TTAGTGATAC GTTTGGT	
		GAG_	
GAM1308 OSBP	5'	GGCTGATGCGGTAGCCGTG 10367	ATTA A
		TACGGTTACTGTG CGG CT	
		GTGCCGATGGCGT GTC GG	
		A____ _	
GAM1308 PAM	3'	AGTCTGTGTGGGACTGTA 6222	ACTGTGAT
		TACGGTT TACGGA CT	
		ATGTCAG GTGTCTGA	
		GGT_____	
GAM1308 PAM	3'	AGTCTGTGTGGGACTGTA 57046	ACTGTGAT
		TACGGTT TACGGA CT	
		ATGTCAG GTGTCTGA	
		GGT_____	
GAM1308 PAM	3'	AGTCTGTGTGGGACTGTA 57188	ACTGTGAT
		TACGGTT TACGGA CT	
		ATGTCAG GTGTCTGA	
		GGT_____	
GAM1308 PKIB	3'	AGTCTGGTGGTAACTGTG 50641	TG GATTA
		TACGGTTAC T CGGACT	
		GTGTCAATG G GTCTGA	
		GT _____	
GAM1308 PPM1D	3'	TCTGATACACAGTAATTGTG 13251	ATTA
		TACGGTTACTGTG CGGA	
		GTGTTAATGACAC GTCT	
		ATA_	
GAM1308 PTGER2	3'	GTTTAATCATAGTTACTGTG 6306	T CG
		TACGGT ACTGTGATTA GAC	

			GTGTCA TGATACTAAT TTG		
			T _		
GAM1308	RBM8A	3'	TAGTCTTATGTGCAGTAACT 17549	ATTAC	
			GGTACTGTG GGA		
			TCAATGACGT TCTGAT		
			GTAT_		
GAM1308	RCN1	3'	GTCTAATTACAGCAGTTGTG 11272	GG A AC	
			TAC TT CTGTGATT GGAC		
			GTG GA GACATTAA TCTG		
			TT C _		
GAM1308	RECK	3'	TGGTTTGTAGTTGAATATTG 40872	TACTG	
			CGGT TGATTACGGACTA		
			GTTA GTTGATGTTTGGT		
			TAA_		
GAM1308	RELN	3'	AGTTACAGTGGCAGTA 94302	G	
			TAC GTTACTGTGATT		
			ATG CCGTGACATTGA		
			A		
GAM1308	RET	3'	TGGTCTGTGGTGCTGTGGTC 40186	GT T G	
			G TAC GT ATTACGGACTA		
			C GTG CG TGGTGTCTGGT		
			TG T _		
GAM1308	RNF4	3'	GAGAGGTGGTGGCAGTAATTGT 11357	G GGACTA	
	G		TACGGTTACTGT ATTAC		
			GTGTTAATGACG TGGTG		
			G GAGAGT		
GAM1308	RPE	3'	TAAATGTAATTATAGCAACTGT 62186	A GACTA	
	G		TACGGTT CTGTGATTACG		
			GTGTCAA GATATTAATGT		
			C AAAT		
GAM1308	RPS6KA2	3'	GGTCTGTGGAGAACTGTG 40908	A GTGA	
			TACGGTT CT TTACGGACT		
			GTGTCAA GA GGTGTCTGG		
			A _		
GAM1308	RYR3	3'	GTA	_TG T	
			CTTGTGCTAGTGACTGTA 6417		
			TACGGTTACT G A TAC		
			ATGTCAGTGAC C T ATG		
			T GT C		
GAM1308	SCML2	3'	TCAGAATTGCAGAACTGTA 20324	A TG ACG	
			TACGGTT CTG ATT GA		

			ATGTCAA GAC TAA CT		
			_ GT GA_		
GAM1308	SERPINB8	3'	AGTTGGTGCAGTGGCTTG 10549	C	GATT G
			A GGTTACTGT AC GACT		
			I		
			G TCGGTGACG TG TTGA		
			T ____ G		
GAM1308	SERPIND1	3'	AGTCACTGTAAGTGTGTA 3943	T	
			TACGGTTAC GTGATT		
			ATGTCAATG CACTGA		
			T		
GAM1308	SLC25A1	3'	TGGTCTGTGCATTGTGGCTGT 19965	T AT	
			ACGGTTAC GTG TACGGACTA		
			TGTCGGTG TAC GTGTCTGGT		
			T _		
GAM1308	SLC4A1AP	5'	TGGTTTGTTGATTAGTGATC 36364	TGATT	
			GGTTACTG ACGGACTA		
			CTAGTGAT TGTTTGGT		
			TAGT_		
GAM1308	SLC9A1	3'	GGTTTCTACGGTGACAGTG 70410	G ATTAC	
			TAC GTTACTGTG GGACT		
			GTG CAGTGGCAT TTTGG		
			A C_		
GAM1308	SNCA	3'	GGTTCCTTAAGTGGCTGTG 4432	GTGATTAC	
			TACGGTTACT GGACT		
			GTGTCGGTGA CTTGG		
			ATTC_		
GAM1308	SNX9	3'	TGGTCCGACGGGTGAGTGGCTG 32596	GTGATTA	
	TG		TACGGTTACT CGGACTA		
			GTGTCGGTGA GCCTGGT		
			GTGGGCA		
GAM1308	SON	3'	TGGTCCATGATAGTGGCC 54205	G TAC	
			GGTTACTGT AT GGACTA		
			CCGGTGATA TA CCTGGT		
			G _		
GAM1308	SON	3'	TGGTCCATGATAGTGGCC 57192	G TAC	
			GGTTACTGT AT GGACTA		
			CCGGTGATA TA CCTGGT		
			G _		
GAM1308	STAU2	3'	GAGCTGTTGTTACAGTAGCTGT 26906	T A A	
	A		TACGGTTACTGTGAT ACGG CT		

		ATGTCGATGACATTG TGTC GA	
		T _ GG	
GAM1308 STS	5'	TAGTGAGGTTGCAGTGATTG 4454	TG TA GG
		CGGTTACTG AT C ACTA	
		GTTAGTGAC TG G TGAT	
		GT GA__	
GAM1308 SYT4	3'	TGGTTTGTAATTATTTGAT 62438	CT
		GTTA GTGATTACGGACTA	
		TAGT TATTAATGTTTGGT	
		T_	
GAM1308 TACC1	3'	CTCTTTGTGGTCATGTGATTGT 20797	T CTA
G		TACGGTTAC GTGATTACGGA	
		GTGTTAGTG TACTGGTGTTT	
		_ CTCT	
GAM1308 TAF4	3'	TGGTGTATTTTGTGAGTAATTG 12094	TGAT__ GACTA
TA		TACGGTTACTG TACG	
		ATGTTAATGAC ATGT	
		TGTTTT GGT	
GAM1308 TBL1X	3'	TGGTCGGGTTACAGTGACCG 18939	TTA G
		CGGTTACTGTGA CG ACTA	
		GCCAGTGACACT GC TGGT	
		TGG _	
GAM1308 TEX15	3'	TAGTCTTTATTACAGTAATTTA 48390	C TAC
		A GGTTACTGTGAT GGACTA	
		A TTAATGACATTA TCTGAT	
		T TT_	
GAM1308 TTC3	5'	TGATTGTGTATTGCAGTAGTTG 12421	GG TG _ ACTA
TG		TAC TTA CTG AT TACGG	
		GTG GATGAC TA GTGTT	
		TT GT T AGT	
GAM1308 USP9Y	3'	TGGTTTATTTGCAGTAATTTG 64039	C TG TTAC
		A GGTTACTG A GGACTA	
		G TTAATGAC T TTTGGT	
		T GT TA__	
GAM1308 USP9Y	5'	TGGAGATAATTCTGGTGGCTGT 64038	GT CGGACTA
G		TACGGTTACT GATTA	
		GTGTCGGTGG TTAAT	
		TC AGAGGT	
GAM1308 UVRAG	3'	TGGTTCTGTAACCCAGTAGCTG 12563	TGA _
TG		TACGGTTACTG TTACGGA CTA	



GTGTCGATGAC AATGTCT GGT  
 CC\_ T  
 GAM1308 WASF3 5' TAGTCAACGATTACATGATTGT 21828 C ACG  
 G TACGGTTA TGTGATT GACTA  
 ||||| ||||| ||||  
 GTGTTAGT ACATTAG CTGAT  
 \_ CAA  
 GAM1308 AMOT 3' GGTTTGTGTGTAGCC 55722 TGTGAT  
 GGTTAC TACGGACT  
 ||||| |||||  
 CCGATG GTGTTTGG  
 T\_\_\_\_  
 GAM1308 ARHGEF15 3' TGGTGTGTGTGTGGTGATTGTG 30264 TG AT G  
 TACGGTTAC TG TACG ACTA  
 ||||| || |||||  
 GTGTTAGTG GT GTGT TGGT  
 GT \_ G  
 GAM1308 ARHGEF9 5' TAGTCGTTTTTGCCGTGATTGT 30820 T TG TT G  
 A TACGGTTAC G A ACG ACTA  
 ||||| | | |||||  
 ATGTTAGTG C T TGC TGAT  
 C GT TT \_  
 GAM1308 B3GNT6 5' TAGTCTGTGGCCGGGTGGTCGT 22507 GT G AT  
 ACG TACT TG TACGGACTA  
 || |||| || |||||  
 TGC GTGG GC GTGTCTGAT  
 TG \_ CG  
 GAM1308 BRPF3 3' GGTTTGTGTGGAGCTGTG 92322 A TG GATT  
 TACGGTT C T ACGGACT  
 ||||| | | |||||  
 GTGTCGA G G TGTTTGG  
 \_GT\_\_\_\_  
 GAM1308 C11orf11 5' TGGTTTGTGATCCTGTCCGTG 93263 TT TGT  
 TACGG AC GATTACGGACTA  
 |||| || |||||  
 GTGCC TG CTAGTGTTTGGT  
 \_ TC\_  
 GAM1308 C11orf23 3' TGGTTTGTGTATATATAGTG 37015 AT\_\_\_\_  
 ATTATG GTTACTGTG TACGGACTA  
 ||||| |||||  
 TAGTGATAT GTGTTTGGT  
 ATATAT  
 GAM1308 C11orf25 3' TAGTTTGTAAATTGTCTGAGTCT 48646 \_ ACT TG  
 GTG TACGG TT G ATTACGGACTA  
 |||| || | |||||  
 GTGTC GA T TAATGTTTGAT  
 T GTC GT  
 GAM1308 C16orf5 3' GGTCTCGGCAGTGGCTGTA 25452 GATTA \_  
 TACGGTTACTGT CG GACT  
 ||||| || ||||

ATGTCGGTGACG GC CTGG  
 \_\_\_\_\_ T  
 GAM1308 C19orf7 3' TGGTCTCTTAATCCAGTAATTG 61132 T C\_  
 TA TACGGTTACTG GATTA G GACTA  
 ||||| |||| I ||||  
 ATGTTAATGAC CTAAT C CTGGT  
 \_ T T  
 GAM1308 C1orf22 3' TGGTTTGTGTTGTTGTAGTAG 47260 GT TG T\_\_\_\_  
 TC G TACTG AT ACGGACTA  
 I |||| II |||||  
 C ATGAT TG TGTGTTGGT  
 TG GT TTGT  
 GAM1308 C1orf28 3' TAGTCTGTAATGGAAATTGTA 44554 A GTG  
 TACGGTT CT ATTACGGACTA  
 ||||| II |||||  
 ATGTAA GG TAATGTCTGAT  
 A \_\_\_\_  
 GAM1308 C21orf100 3' AATTACAGTGATGTG 58858 G  
 TACG TTA CTGTGATT  
 ||| |||||  
 GTGT AGTGACATTAA  
 -  
 GAM1308 CAMP-GEFII 3' TGGTCTGTAATTTCTGAATGTA 22829 G CTGT  
 TACG TTA GATTACGGACTA  
 ||| ||| |||||  
 ATGT AGT TTAATGTCTGGT  
 A CT\_  
 GAM1308 CCR8 3' AATCAAGGTGATTGTG 17781 G  
 TACGGTTACT TGATT  
 ||||| ||||  
 GTGTTAGTGG ACTAA  
 A  
 GAM1308 CECR2 3' TAGTAAATCAGTCATGGTGAT 48609 C ACGG\_\_\_\_  
 TTA A GGTTACTGTGATT ACTA  
 I ||||| ||||  
 A TTAGTGGTACTGA TGAT  
 T CTA AAA  
 GAM1308 CECR6 3' CCTAATCTCAGTGA CTGTG 49083 T C  
 TACGGTTACTG GATTA GG  
 ||||| |||| II  
 GTGTCAGTGAC CTAAT CC  
 T \_  
 GAM1308 CLIC4 3' TAGTTATGGTGAGTGTG 25636 G  
 TACG TTA CTGTGATTA  
 ||| |||||  
 GTGT AGTGGTATTGAT  
 G  
 GAM1308 CUL4A 3' TAATTGCAGTATTTGTG 13155 T TG  
 TACGG TACTG ATTA  
 |||| |||| |||

		GTGTT ATGAC TAAT		
		T GT		
GAM1308	CYYR1	3' AGTTATAGTACCTGTA 53669	T	
		TACGG TACTGTGATT		
		ATGTC ATGATATTGA		
		C		
GAM1308	DAMS	3' TACCAGCTGATTGCAGTAGCCG 41822	TG C__ ACTA	
		CGGTTACTG ATTA GG		
		GCCGATGAC TAGT CC		
		GT CGA AT		
GAM1308	DKFZp434B0417	3' TAATTATGGTAATTGTG 25381		
		TACGGTTACTGTGATTA		
		GTGTTAATGGTATTAAT		
GAM1308	DKFZp434B0417	3' TAGCTAGATAATTATGGTAATT 25382	C__ A	
		GTG ACGGTTACTGTGATTA GG CTA		
		TGTTAATGGTATTAAT TC GAT		
		AGA _		
GAM1308	DKFZp434K114	3' TGGTTTCTATTACGGTGACTTG 60733	C TAC	
		A GGTTACTGTGAT GGA CTA		
		G TCAGTGGCATT TTTGGT		
		T TC_		
GAM1308	DKFZp547C176	3' TAGTTTGGGAATTATGATTGTA 67231	ACT A	
		TACGGTT GTGATT CGGACTA		
		ATGTTAG TATTAA GTTTGAT		
		_ G		
GAM1308	DKFZP564D166	3' CTGTAGCACAGTGATTGTG 47675	A	
		TACGGTTACTGTG TTACGG		
		GTGTTAGTGACAC GATGTC		
GAM1308	DKFZP564I052	3' CCAGTGGTAGTAACTGTG 66705	GTG _	
		TACGGTTACT ATTAC GG		
		GTGTCAATGA TGGTG CC		
		_ A		
GAM1308	DKFZp566H0824	5' TAGTCCGTGGGTTTGGTGATTG 34059	TGA	
		TG TACGGTTACTG TTACGACTA		
		GTGTTAGTGGT GGTGCCTGAT		
		TTG		
GAM1308	DKFZP586F1318	3' TGGCCATGTATATGGTAGCTGT 31620	AT C A	
		G TACGGTTACTGTG TA GG CTA		

			GTGTCGATGGTAT GT CC GGT		
			AT A _		
GAM1308	DKFZP727M111	5'	AGTTCAGTGGCCGTG	31405	T
			TACGGTTACTG GATT		
			GTGCCGGTGAC TTGA		
			—		
GAM1308	DNAJA2	3'	TGGAAAAAATTACATTAGCTGT	59784	C
	G		TACGGTTA TGTGATT		ACGGACTA
			GTGTCGAT ACATTAA		
			T AAAAGGT		
GAM1308	DNAJB5	5'	TGGTCCAGTGGCTGTG	24354	T
			TACGGTTACTG GATTA		
			GTGTCGGTGAC CTGGT		
			—		
GAM1308	EAT2	3'	GGTTCTGTACAGTGATGTA	79280	G
			TACG TTA CTGTG GGACT		ATTAC
			ATGT AGTGACAT CTTGG		
			— GT—		
GAM1308	FLJ10290	3'	AGTTTCCATGGTAGCTG	35970	ATTAC
			CGGTTACTGTG GGACT		
			GTCGATGGTAC TTTGA		
			C—		
GAM1308	FLJ11040	3'	AATCTTGTGATTACAGTAACTG	37001	ACTA
			CGGTTACTGTGATTACGG		
			GTCAATGACATTAGTGTT		
			CTAAT		
GAM1308	FLJ11210	3'	AAGGGAAAATTAAGTGACTGTG	59572	G
			TACGGTTACT TGATT		ACGGACTA
			GTGTCAGTGA ATTAA		
			— AAGGGAAT		
GAM1308	FLJ12443	3'	GGTTTCCATGGTGA CTG	45731	ATTAC
			CGGTTACTGTG GGACT		
			GTCAGTGGTAC TTTGG		
			C—		
GAM1308	FLJ12592	3'	GGTTACAGTAAGCTGTG	49700	—
			TACGGTT ACTGTGATT		
			GTGTCGA TGACATTGG		
			A		
GAM1308	FLJ13310	5'	GGTTACAGTCATCGTA	47085	T
			TACGGT ACTGTGATT		

ATGCTA TGACATTGG  
 C  
 GAM1308 FLJ13441 3' AGTTGCAGTGGTCTGTA 43657 \_ TG  
 TACGG TTAGTG ATT  
 ||||| ||||| ||  
 ATGTC GGTGAC TGA  
 T GT  
 GAM1308 FLJ13848 3' TGGTCTCATGGCAGTGAAGTTG 45475 C G TAC  
 A GGTTACTGT AT GGAATA  
 | ||||| || |||||  
 G TCAGTGACG TA TCTGGT  
 T G C\_\_  
 GAM1308 FLJ14009 3' AGTCTGTGGTGTAGACTG 45409 \_ TGTG  
 CGGTT AC ATTACGGACT  
 ||||| || |||||  
 GTCAG TG TGGTGTCTGA  
 A \_\_\_\_  
 GAM1308 FLJ14011 5' TGAATGCAGTAATTGTA 42066 A  
 TACGGTTACTGTG TTA  
 ||||| ||||| ||  
 ATGTTAATGACGT AGT  
 A  
 GAM1308 FLJ14082 3' TGATCATAGGGACTGTA 46676 TA  
 TACGGT CTGTGATTA  
 ||||| |||||  
 ATGTCA GATACTAGT  
 GG  
 GAM1308 FLJ14251 3' TGGGGTCACTGTGGCTGTA 45979 T TA  
 TACGGTTAC GTGAT CG  
 ||||| ||||| ||  
 ATGTCGGTG CACTG GT  
 T GG  
 GAM1308 FLJ14494 3' TGGTCCGTGAATGTAGTTAT 90872 T GT A  
 GT ACT G TTACGGACTA  
 || ||| | |||||  
 TA TGA T AGTGCCTGGT  
 T TG A  
 GAM1308 FLJ14721 5' AATCACAGTGCCTGTG 51575 T  
 TACGG TACTGTGATT  
 ||||| |||||  
 GTGTC GTGACACTAA  
 C  
 GAM1308 FLJ20070 3' TGAGTGCAGTGAAGTGTG 34478 GA  
 TACGGTTACTGT TTA  
 ||||| ||||| ||  
 GTGTCAGTGACG AGT  
 TG  
 GAM1308 FLJ20156 5' TGGTCGTTTCCATGGTAACC 34653 ATT G  
 GGTTACTGTG ACG ACTA  
 ||||| ||||| |||||

			CCAATGGTAC	TGC TGGT		
			CTT _			
GAM1308	FLJ22477	3'	AGTGACGGT	GACTGTG	45339	G
			TACGGTTACTGT	ATT		
			GTGTCAGTGGCA	TGA		
			G			
GAM1308	FLJ22649	3'	AGTCATAATAA	CTGTA	41634	C
			TACGGTTA	TGTGATT		
			ATGTCAAT	ATACTGA		
			A			
GAM1308	FLJ22843	3'	AGTCACGGTGA	AATGTG	47224	G
			TACG	TTACTGTGATT		
			GTGT	AGTGGCACTGA		
			A			
GAM1308	FLJ23563	3'	AGTTAGAGTGG	CTGTG	67586	G
			TACGGTTACT	TGATT		
			GTGT	CGGTGA ATTGA		
			G			
GAM1308	FLJ32783	3'	TATTGTAGTTGTAG	CTAATTGT	58647	
			TACGGTTA	CTG ATTACGG		
			GTGTTAAT	GAT TGATGTT		
			C GT	AT		
GAM1308	FTSJ1	3'	AAACCAGTTACAG	CAACTGTA	24388	A
			TACGGTT	CTGTGATT GG		
			ATGTCAA	GACATTGA CC		
			C _	AAAC		
GAM1308	FUSIP1	3'	TGGTTTATTGTGC	AGTGACTGT	21775	
			TACGGTTACTGTG	GGACTA		
			ATGTCAGTGACGT	TTTGGT		
			GTTA_			
GAM1308	GTF3C4	3'	TGGTCCGTGGC	ATCTGATGTA	24196	G
			TACG	TTA GTG TTACGGACTA		
			ATGT	AGT TAC GGTGCCTGGT		
			_ C_ _			
GAM1308	GTPBP2	3'	GTAATTTGTAGT	GACTGT	38870	TG_
			ACGGTTACTG	A TTAC		
			TGTCAGTGAT	T AATG		
			GT T			
GAM1308	GTSE1	3'	TAGGCTGGTCGC	AGTGGCTTA	33141	C
			A	GGTTACTGTGAT CGG CTA		

			A TCGGTGACGCTG GTC GAT		
			T        G		
GAM1308	H326	3'	AAGGAACTGATTACAGTGGCTG 31701		CGGA A
			CGGTTACTGTGATTA CT		
			GTCGGTGACATTAGT GA		
			CAAG AT		
GAM1308	HCA4	3'	GTCAGCATGGTGGTTGTG 77589	TT	ATTACG
			TACGG ACTGTG GAC		
			GTGTT TGGTAC CTG		
			GG GA		
GAM1308	HSJ1	3'	TGGTGTATGGTTACGGAGCTGT 22140	A	CGG
	G		TACGGTT CTGTGATTA ACTA		
			GTGTCGA GGCATTGGT TGGT		
			ATG		
GAM1308	HSMPP8	3'	TAGTCTGTAAGATGCGACATAG 93483	C	GA
			CTGTG GGTTA TGT TTACGGACTA		
			TCGAT GCG AATGTCTGAT		
			ACA TAG		
GAM1308	HSPB7	3'	GGTTCGTGATAAACTG 27030		ACTGTG
			CGGTT ATTACGGACT		
			GTCAA TAGTGCTTGG		
			A		
GAM1308	JAM1	5'	CTGTAGTCGCGGAGCTGTG 57953		A
			TACGGTT CTGTGATTACGG		
			GTGTCGA GGCGCTGATGTC		
GAM1308	JAM1	5'	CTGTAGTCGCGGAGCTGTG 33760		A
			TACGGTT CTGTGATTACGG		
			GTGTCGA GGCGCTGATGTC		
GAM1308	JAM1	5'	CTGTAGTCGCGGAGCTGTG 57882		A
			TACGGTT CTGTGATTACGG		
			GTGTCGA GGCGCTGATGTC		
GAM1308	JAM1	5'	CTGTAGTCGCGGAGCTGTG 57898		A
			TACGGTT CTGTGATTACGG		
			GTGTCGA GGCGCTGATGTC		
GAM1308	KDEL3	5'	TGCGATCGCGGAGCTGTG 33608		A TA
			TACGGTT CTGTGAT CG		

		GTGTCGA GGCCTA GT		
		— GC		
GAM1308	KDEL3	5' TCGATCGCGGAGCTGTG 22460	A	TA
		TACGGTT CTGTGAT CG		
		GTGTCGA GGCCTA GT		
		— GC		
GAM1308	KIAA0061	3' TGGTCTGTGTAGTTGTGGCTG 68296	TGTGAT	
		CGGTAC TACGACTA		
		GTCGGTG GTGTCTGGT		
		TTGAT_		
GAM1308	KIAA0077	3' TAGTTCTTTATTATAGTGATT 67021	TAC	
		GGTACTGTGAT GACTA		
		TTAGTGATATTA CTTGAT		
		TTT		
GAM1308	KIAA0101	3' TAATTATGGTAACTTA 28425 C		
		A GGTACTGTGATTA		
		A TCAATGGTATTAAT		
		T		
GAM1308	KIAA0217	3' AGTTATGTAATCGTG 67035 T		
		TACGGTTAC GTGATT		
		GTGCTAATG TATTGA		
		—		
GAM1308	KIAA0226	5' TGGTCTAAGTATGGTGGCTTG 63526 C	ATTAC	
		A GGTACTGTG GACTA		
		G TCGGTGGTAT TCTGGT		
		T GAA_		
GAM1308	KIAA0332	3' AATTATATGACCGTG 62697 C		
		TACGGTTA TGTGATT		
		GTGCCAGT ATATTAA		
		—		
GAM1308	KIAA0446	5' ATCATAAATGTAGTGA CTGTG 68854	_____	
		TACGGTTACT GTGAT		
		GTGTCAGTGA TACTA		
		TGTAAA		
GAM1308	KIAA0565	5' TAGTCTTGGATTATAGTAATC 66896	AC	
		GGTACTGTGATT GACTA		
		CTAATGATATTAG TCTGAT		
		GT		
GAM1308	KIAA0630	3' TGGCCTGGGTCA CAGTGACC 89398	AC A	
		GGTACTGTGATT GG CTA		



		CCAGTGACACTGG CC GGT		
		GT _		
GAM1308	KIAA0644	3' TGGTTATGGTCACAGTGGTTAT 29067	CG TT	CG
	G	TA G ACTGTGATTA GACTA		
		GT T TGACACTGGT TTGGT		
		AT GG A_		
GAM1308	KIAA0820	3' GGTTACCAGTGATTGTA 69028	_	
		TACGGT TACTG TGATT		
		ATGTTAGTGAC ATTGG		
		C		
GAM1308	KIAA0930	3' GGACCAGTCACAGTGATGTG 70546	G	AC A A
		TACG T TACTGTGATT GG CT		
		GTGT AGTGACACTGA CC GG		
		_ _ A A		
GAM1308	KIAA0970	3' GTCAAGTTACAGTGGCTTA 29965	C	TACG
		A GGTTACTGTGAT GAC		
		A TCGGTGACATTG CTG		
		T AA_		
GAM1308	KIAA0980	5' TAGTCTGTGGCCAGTGTAGCC 47205	TG AT	
		GGTTAC TG TACGGACTA		
		CCGATG AC GTGTCTGAT		
		TG CG		
GAM1308	KIAA1046	5' GTTATCACAGTGATTTA 29998	C	T
		A GGTTACTGTGAT AC		
		A TTAGTGACACTA TG		
		T T		
GAM1308	KIAA1102	3' TGGTCTGTGATCAGCAAGAACC 69017	AC _	
		GGTT TG TGATTACGGACTA		
		CCAA AC ACTAGTGTCTGGT		
		GA G		
GAM1308	KIAA1126	3' TAGCCACAATTCAGTAGTCGTA 71939	GT T AC A	
		TACG TACTG GATT GG CTA		
		ATGC ATGAC TTAA CC GAT		
		TG _ CA _		
GAM1308	KIAA1238	3' TAGTTTGTAGTTTATGAAATC 71079	ACTGT	
		GGTT GATTACGGACTA		
		CTAA TTGATGTTTGAT		
		AGTAT		
GAM1308	KIAA1257	3' GTGTGGTGGTGGCTGTG 62754	TG G T	
		TACGGTTAC T AT AC		

GTGTCGGTG G TG TG  
 GT G \_  
 GAM1308 KIAA1309 3' GATTATAGTAAATGTA 53118 G  
 TACG TTAGTGTGATT  
 |||| |||||  
 ATGT AATGATATTAG  
 A  
 GAM1308 KIAA1354 3' AATTGTAGATGACTGTG 60912 \_ TG  
 TACGGTTA CTG ATT  
 ||||| ||| |||  
 GTGTCAGT GAT TAA  
 A GT  
 GAM1308 KIAA1560 3' GTCAGTTGTAGTAGCT 64179 TG ACG  
 GGTTACTG ATT GAC  
 ||||| ||| |||  
 TCGATGAT TGA CTG  
 GT \_  
 GAM1308 KIAA1573 3' TAGTGTTTTAATTACAGTGATG 62689 G CG\_  
 TA TACG TTAGTGTGATTA G ACTA  
 |||| ||||| |||  
 ATGT AGTGACATTAAT T TGAT  
 \_ TT G  
 GAM1308 KIAA1598 3' TAGTAATAATTGCAGTAGTTGT 37079 GG TG CGG  
 A TAC TTAGTGTG ATTA ACTA  
 ||| ||||| ||| |||  
 ATG GATGAC TAAT TGAT  
 TT GT AA\_  
 GAM1308 KIAA1674 3' TAGCCGGGCGTGTTGGCTGTA 68795 TG ATTA A  
 TACGGTTAC TG CGG CTA  
 ||||| || ||| |||  
 ATGTCGGTG GC GCC GAT  
 GT GG\_ \_  
 GAM1308 KIAA1854 3' TGGTTCCTCAGTGTGTTAACCG 71748 C GT ATTAC  
 TG TACGGTTA T G GGA CTA  
 ||||| | | |||||  
 GTGCCAAT G T CTTGGT  
 T TG GACTC  
 GAM1308 KIAA1881 3' TAGTCGCTTCTCACGGTGGCC 95345 TTACG  
 GGTTACTGTGA GACTA  
 ||||| |||||  
 CCGGTGGCACT CTGAT  
 CTTG  
 GAM1308 KIAA1918 3' GTTGTCATGGTGATTG 73164 T  
 CCGTTACTGTGAT AC  
 ||||| ||| |||  
 GTTAGTGGTACTG TG  
 T  
 GAM1308 KLHL6 3' TAGTTTTTACACAGTGATTTA 55308 C AT CG  
 A GGTTACTGTG TA GACTA  
 | ||||| || |||||

A TTAGTGACAC AT TTGAT  
 T     — TT  
 GAM1308 LAMB4 3' GTCAGTCATGTGACTGTG 81175 T ACG  
 TACGGTTAC GTGATT GAC  
 ||||| ||||| ||  
 GTGTCAGTG TACTGA CTG

— —  
 GAM1308 LHX6 3' GATTATGTGGCCGTA 26857 T  
 TACGGTTAC GTGATT  
 ||||| |||||  
 ATGCCGGTG TATTAG

—  
 GAM1308 LRPPRC 3' AGCTAGGTATAGTGACCGTG 55702 ATTAC A A  
 TACGGTTACTGTG GG CT  
 ||||| ||||| ||  
 GTGCCAGTGATAT TC GA  
 GGA— \_ G

GAM1308 MDN1 3' TGGTCCCTGTTGTTGTAGTAAT 62682 C TG T —  
 TTA A GGTTACTG AT AC GGA  
 | ||||| || || |||||  
 A TTAATGAT TG TG CCTGGT  
 T GT T TC

GAM1308 MGC2721 3' GTCTGTGATTTGCCG 51222 TACTGT  
 CGGT GATTACGGAC  
 ||| |||||  
 GCCG TTAGTGTCTG  
 T—

GAM1308 MGC3079 3' TAGTCTGTGATTACTGGC 50954 CT  
 GTTA GTGATTACGGACTA  
 ||| |||||  
 CGGT CATTAGTGTCTGAT

—  
 GAM1308 MGC35558 3' AGTCGCCGGTGGCTGTG 58774 —  
 TACGGTTACTG TGATT  
 ||||| |||||  
 GTGTCGGTGGC GCTGA  
 C

GAM1308 MGC5442 3' GATTAAAGTAACTGTG 48710 G  
 TACGGTTACT TGATT  
 ||||| |||||  
 GTGTCAATGA ATTAG  
 A

GAM1308 MKRN2 3' TGGTTCGTAAGTGATC 72415 G T  
 GGTTACT TGA TACGGACTA  
 ||||| || |||||  
 CTAGTGA ACT ATGCTTGGT  
 \_ C

GAM1308 NAV3 3' TAGTTTGTGAAACATTTGTCTG 29774 TTAC\_ GA  
 TA TACGG TGT TTACGGACTA  
 |||| || |||||

			ATGTC ACA AGTGT	TTTGAT	
			TGTTT A_		
GAM1308 NESCA	5'	TAGTTCGTGGTCCTTCGCCG	26745	TACTGT	
		CGGT GATTACGGACTA			
		GCCG CTGGTGCTTGAT			
		CTTC__			
GAM1308 NPFF	5'	GGTTGGGGTGGCTGTA	13556	G	
		TACGGTTACT TGATT			
		ATGTCGGTGG GTTGG			
		G			
GAM1308 NUBP2	3'	TGGTTGGCCTGCAGTGCCGTG	64234	T GATTA G	
		TACGGT ACTGT CG ACTA			
		GTGCCG TGACG GT TGGT			
		_ TCCG_ _			
GAM1308 NUP133	3'	TAGTTATGTA	ACTGTG 36687	T	
		TACGGTTAC GTGATTA			
		GTGTCAATG TATTGAT			
		_			
GAM1308 OPRL1	3'	GGCTGTGGTGGCTGTG	6199	GTGATT A	
		TACGGTTACT ACGG CT			
		GTGTCCGTGG TGTC GG			
		_____ _			
GAM1308 P1P373C6	3'	TGGTTACAGAAATTGTG	38906	A	
		TACGGTT CTGTGATTA			
		GTGTTAA GACATTGGT			
		A			
GAM1308 P5-1	3'	GATTACAGAACTGTA	21918	A	
		TACGGTT CTGTGATT			
		ATGTCAA GACATTAG			
		_			
GAM1308 PDCD7	3'	TAGTTAGGAAGATGGCAGTGGC	72142	G ACG__	
	TGTA	ACGGTTACTGT ATT GACTA			
		TGTCGGTGACG TAG TTGAT			
		G AAGGA			
GAM1308 PDE4DIP	3'	TGGTCACTGATGGTTATAATGA	27692	C CG__	
	CTGTG	GGTTA TGTGATTA GACTA			
		TCAGT ATATTGGT CTGGT			
		A AGTCA			
GAM1308 PDE8B	3'	AATCACAGTAGCGTA	67576	G	
		TACG TTA	CTGTGATT		

ATGC GATGACACTAA

GAM1308 PELI1 5' TGATGATAGTAGTTGTG 40292 GG G

TAC TTACTGT ATTA

||| ||||| |||

GTG GATGATA TAGT

TT G

GAM1308 PJA1 3' TTCCTGTAATTGCAGTGCCGTA 42326 T TG ACTA

TACGGT ACTG ATTACGG

||||| ||| |||||

ATGCCG TGAC TAATGTC

\_ GT CTTG

GAM1308 PNMA1 3' AGTTACGGAGCTGTG 20072 A

TACGGTT CTGTGATT

||||| |||||

GTGTCGA GGCATTGA

GAM1308 POLM 3' TAGTTGCACTGCAGTAACTGT 91091 \_ GATTACG

G

TACGGTTA CTGT GACTA

||||| ||| |||

GTGTCAAT GACG TTGAT

T TCACG\_\_

GAM1308 PRDM10 3' TCTGTGGTTGTGGTGGTGGTA 39579 G TT TG

TAC G ACTG ATTACGGA

||| | ||| |||||

ATG T TGGT TGGTGTCT

G GG GT

GAM1308 PRDM12 3' TGGTCGGGCGCGGGGGTTGTG 41237 GG TA ATTA G

TAC T CTGTG CG ACTA

||| | ||| || |||

GTG G GGCGC GC TGGT

TT GG GG\_\_ \_

GAM1308 PRO0159 5' GATCACAGGACTGTG 26113 A

TACGGTT CTGTGATT

||||| |||||

GTGTCAG GACACTAG

GAM1308 PRO0456 5' TAGTGCAATCACAGTGTCGTG 26179 T TTACGG

TACGGT ACTGTGA ACTA

||||| ||||| |||

GTGCTG TGACACT TGAT

\_ TACG\_\_

GAM1308 PRO0461 3' TGGTCTGTAGCTGTAAGTGTG 48378 T GAT

TACGGTTAC GT TACGGAATA

||||| || |||||

GTGTCAATG CG ATGTCTGGT

T \_\_\_\_

GAM1308 PRO0478 3' GGTCACAGAGACCGTG 26195 A

TACGGTT CTGTGATT

||||| |||||

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GTGCCAG GACACTGG
      A
GAM1308 PSMD12  3' TGGTTCCAATCACAGTAGCTTG 11003  C      AC
      A GGTTACTGTGATT GGA CTA
      | ||||| ||||
      G TCGATGACACTAA CTTGGT
      T      C_
GAM1308 RNF38  3' GATTACAGTGGACGTG 42936  GT
      TACG TACTGTGATT
      ||| |||||
      GTGC GTGACATTAG
      AG
GAM1308 RNF38  3' TGGGATTGTTATACTAACCGTG 42940  C  TACGGA
      TACGGTTA TGTGAT  CTA
      ||||| ||||  ||
      GTGCCAAT ATATTG  GGT
      C  TTAG__
GAM1308 SDF1  3' TAGGAAGTAAATTATAGTGATG 90861  G  _ GGA
      TA      TACG TTAGTGATGATT AC  CTA
      ||| ||||| || ||
      ATGT AGTGATATTAA TG  GAT
      _      A AAG
GAM1308 SE70-2 5' TGGAAGTGATCCAGTAGTTGTA 42090  GG  T  GGA
      TAC TTAGTG GATTAC  CTA
      || ||||| |||| ||
      ATG GATGAC CTAGTG  GGT
      TT  _  AA_
GAM1308 SEC15L 3' TGGTCATGATACAGTAATTTG 72272  C      A  CG
      A GGTTACTGTG TTA GACTA
      | ||||| || ||||
      G TTAATGACAT AGT CTGGT
      T      _  A_
GAM1308 SMC2L1 3' TGGTCCAATTATTGTGGTTGTG 21240  TT T  AC
      TACGG AC GTGATT GGA CTA
      |||| ||||| ||||
      GTGTT TG TATTAA CCTGGT
      GG T  _
GAM1308 SNIP1  3' TGATCATATTAAGTGA 45216  C
      TACGGTTA TGTGATTA
      ||||| |||||
      ATGTCAAT ATACTAGT
      T
GAM1308 SSR3  3' GTCAGAGGTCACAGTAACC 23041  ACG
      GGTTACTGTGATT GAC
      ||||| ||||
      CCAATGACACTGG CTG
      AGA
GAM1308 STAF65(gamma) 3' TAGTTTCCATAAAGTGGCCGTA 29442  GTG TAC
      TACGGTTACT AT GGA CTA
      ||||| || ||||

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ATGCCGGTGA TA TTTGAT  
 AA\_ CC\_  
 GAM1308 STMN3 3' TGAGAGAGGTGGCGGTGACCGT 31903 G ACGGACTA  
 G TACGGTTACTGT ATT  
 ||||| |||  
 GTGCCAGTGGCG TGG  
 G AGAGAGT  
 GAM1308 TOLLIP 3' AGTGTGTGGTGGCCGTG 38679 GTGATT G  
 TACGGTTACT ACG ACT  
 ||||| ||| |||  
 GTGCCGGTGG TGT TGA  
 \_\_\_\_\_ G  
 GAM1308 TRIM36 3' GATCACAATGACTGTG 38012 C  
 TACGGTTA TGTGATT  
 ||||| |||||  
 GTGTCAGT AACTAG  
 A  
 GAM1308 TSPAN-2 3' TAGTTTGTACCCAGTAGTTG 19166 GG TGAT  
 C TTAGTG TACGGACTA  
 | |||| |||||  
 G GATGAC ATGTTTGAT  
 TT CCC\_  
 GAM1308 TU12B1-TY 3' TAGTTTGTAAATTGTGCTAGTGC 33403 T \_ \_  
 TG CCGT ACT GT GATTACGGACTA  
 ||| ||| || |||||  
 GTCG TGA CG TTAATGTTTGAT  
 \_ T TG  
 GAM1308 UNC5D 3' GGTCACAGGAATCGTG 55142 A  
 TACGGTT CTGTGATT  
 ||||| |||||  
 GTGCTAA GAACTGG  
 G  
 GAM1308 UQCR 3' TGGCTTGGTTACTGTGACTGTA 22410 T C A  
 TACGGTTAC GTGATTA GG CTA  
 ||||| ||||| |||  
 ATGTCAGTG CATTGGT TC GGT  
 T \_ \_ G  
 GAM1308 UST 3' GGTTGCAGTGAGCTGTG 19136 \_ TG  
 TACGG TTAGTG ATT  
 |||| ||||| |||  
 GTGTC AGTGAC TGG  
 G GT  
 GAM1308 VILL 5' GATCATGGAGGCTGTG 68414 TA  
 TACGGT CTGTGATT  
 |||| |||||  
 GTGTCG GGTACTAG  
 GA  
 GAM1308 YME1L1 5' TGTCTGTCGTTGCAGTAGCTGT 26533 TG T TA  
 A TACGGTTACTG AT ACGGAC  
 ||||| || |||||

		ATGTCGATGAC TG TGTCTG	
		GT C T	
GAM1308 YME1L1	5'	TGTCTGTCGTTGCAGTAGCTGT 57783	TG T TA
A		TACGGTACTG AT ACGGAC	
		ATGTCGATGAC TG TGTCTG	
		GT C T	
GAM1308 YME1L1	5'	TGTCTGTCGTTGCAGTAGCTGT 57787	TG T TA
A		TACGGTACTG AT ACGGAC	
		ATGTCGATGAC TG TGTCTG	
		GT C T	
GAM1308 LOC118851	5'	TGGTGGATGACTGTGGTGATCG 75506	TG GA CGG
TA		TACGGTTAC T TTA ACTA	
		ATGCTAGTG G AGT TGGT	
		GT TC AGG	
GAM1308 LOC122553	3'	CCAATCATGGTAATTG 74131	AC
		CGGTTACTGTGATT GG	
		GTTAATGGTACTAA CC	
		—	
GAM1308 LOC124801	5'	TAGTTGTGGAACCGTG 74339	A TG
		TACGGTT CTG ATTA	
		GTGCCAA GGT TGAT	
		_ GT	
GAM1308 LOC126549	5'	GGCCAGTGTTGCGGTGTTGTG 75711	GG T TG _ A A
		TAC T ACTG ATTAC GG CT	
		GTG G TGGC TGGTG CC GG	
		TT _ GT A _ G	
GAM1308 LOC127534	5'	TGACACGGTGATTGTG 75442	A
		TACGGTACTGTG TTA	
		GTGTTAGTGGCAC AGT	
		—	
GAM1308 LOC130250	5'	TAGAAGTATCATGGTGACC 74914	T GGA
		GGTACTGTGAT AC CTA	
		CCAGTGGTACTA TG GAT	
		_ AA_	
GAM1308 LOC138389	5'	GTGTCACAGTTGCCGTG 76231	T T
		TACGGT ACTGTGAT AC	
		GTGCCG TGACACTG TG	
		T _	
GAM1308 LOC143154	3'	TAATCACAGTATTGTG 76484	T
		TACGGT ACTGTGATTA	



GTGTTA TGACACTAAT

GAM1308 LOC144289 5' TAATTACAGTGA CTTG 83028 C  
A GGT TACTGTGATTA  
| |||||  
G TCAGT GACATTAAT  
T

GAM1308 LOC144321 3' TAAAGGAATCAATAGTAGTTGT 83064 GG \_ ACGGACTA  
G TAC TTACTGT GATT  
||| ||||| ||||  
GTG GATGATA CTAA  
TT A GGAAAT

GAM1308 LOC145622 5' TGGTCTCCTGCACTAGCTGTG 77319 CT ATTAC  
TACGGTTA GTG GGACTA  
||||| ||| |||||  
GTGTCGAT CAC TCTGGT  
\_ GTCC\_

GAM1308 LOC145623 3' TGGTCTGTAGTTTTCA 83402 T\_  
TG GATTACGGACTA  
|| |||||  
AC TTGATGTCTGGT  
TT

GAM1308 LOC146839 5' TGGTTTGT AATTGATCTTAACT 83816 CTG\_  
G CCGTTA TGATTACGGACTA  
||||| |||||  
GTCAAT GTTAATGTTTGGT  
TCTA

GAM1308 LOC147004 5' GGTCCGTGTGGTGATGTG 83905 G TG GATT  
TACG TTAC T ACGGACT  
||| ||| | |||||  
GTGT AGTG G TGCCTGG  
\_ GT \_

GAM1308 LOC147081 3' TAGTCATGGTTGCAGAACTGTA 78245 A TG CG  
TACGGTT CTG ATTA GACTA  
||||| ||| ||| |||||  
ATGTCAA GAC TGGT CTGAT  
\_ GT A\_

GAM1308 LOC148223 3' CGTCAGCTCACAGTGGCCGTG 78738 TTACG TA  
TACGGTTACTGTGA GAC  
||||| ||| |||  
GTGCCGGTGACACT CTG  
CGA\_ CT

GAM1308 LOC148479 3' GGTCCGTGGTAGCTGTG 78876 GTGATT  
TACGGTTACT ACGGACT  
||||| |||||  
GTGTCGATGG TGCCTGG

GAM1308 LOC149401 5' TAGTCCTCAGACGGTAATGTG 79336 G GATTAC  
TACG TTACTGT GGACTA  
||| ||||| |||||

		GTGT AATGGCA CCTGAT			
		— GACT—			
GAM1308	LOC149498 5'	CCAGTCGCTGTGACTGTG 79407	T	AC	
		TACGGTTAC GTGATT GG			
		GTGTCAGTG CGCTGA CC			
		T —			
GAM1308	LOC149684 5'	GTGTCACAGGATCGTA 84616	A	T	
		TACGGTT CTGTGAT AC			
		ATGCTAG GAACTG TG			
		— —			
GAM1308	LOC149711 5'	AATCATGGTGCTGTG 84665	T		
		TACGGT ACTGTGATT			
		GTGTCG TGGTACTAA			
		—			
GAM1308	LOC150212 5'	TGTGGCCATAGTGGCTGTG 79708		AT	
		TACGGTTACTGTG TACG			
		GTGTCGGTGATAC GTGT			
		CG			
GAM1308	LOC150759 3'	TTCTGATTACAGAACTGTA 80012	A	C	
		TACGGTT CTGTGATTA GGA			
		ATGTCAA GACATTAGT CTT			
		— —			
GAM1308	LOC151098 5'	TGGTCTTATAAACAGTAATTG 80119		GATTAC	
		CGGTTACTGT GGAATA			
		GTTAATGACA TCTGGT			
		AATAT—			
GAM1308	LOC151283 3'	AGCTGTGGTTGCAGAAACCGTG 80198	A	TG	A A
		TACGGTT CTG ATTACGG CT			
		GTGCCAA GAC TGGTGTC GA			
		A GT — A			
GAM1308	LOC151512 5'	CGTTGATCAGGTGATTGTG 85430	G	—	
		TACGGTTACT TGATTA CG			
		GTGTTAGTGG ACTAGT GC			
		— T			
GAM1308	LOC152200 3'	GAGACATTAATTGCAGGGCTGT 85575	A	TG	CGGACTA
	G	TACGGTT CTG ATTA			
		GTGTCGG GAC TAAT			
		— GT TACAGAGA			
GAM1308	LOC152348 3'	TGGTACATTGTTATAGTAGCC 85701		TACGG	
		GGTTACTGTGAT ACTA			

	CCGATGATATTG TGGT		
	TTACA		
GAM1308 LOC153642 3'	TACAAAAGGGTTAACAGTGATC 80912	_	ACGGACTA
	GTG TACGGTTACTGT GATT		
	GTGCTAGTGACA TTGG		
	A GAAAACAT		
GAM1308 LOC154141 5'	TGATCATGGCTGGCCGTG 86176	_	
	TACGGTTA CTGTGATTA		
	GTGCCGGT GGTACTAGT		
	C		
GAM1308 LOC158288 5'	GGCCCATCTGGTGGCTGTG 86719	T	TAC A
	TACGGTTACTG GAT GG CT		
	GTGTCGGTGGT CTA CC GG		
	_ C _ _		
GAM1308 LOC158328 3'	TGGATCTAGTCATGGTGATC 86779	C	A
	GGTACTGTGATTA GG CTA		
	CTAGTGGTACTGAT CT GGT		
	_ A		
GAM1308 LOC158376 5'	TGGTGCTGTTCGTGGTGACTGT 86798	TG	TT _
	G TACGGTTAC TGA ACGG ACTA		
	GTGTCAGTG GCT TGTC TGGT		
	GT _ G		
GAM1308 LOC158438 3'	TAGTTTGTGATTAAGTTATTCT 86833	TT_	G
	G CGG ACT TGATTACGGACTA		
	GTC TGA ATTAGTGTTTGAT		
	TTAT _		
GAM1308 LOC162048 5'	TGGTTTTGTCTATAGTGGTCG 82331	GT	_ TAC
	CG TACTGT GAT GGA CTA		
	GC GTGATA CTG TTTGGT		
	TG T T_		
GAM1308 LOC199675 3'	AGTCACAGTGAATGTG 88259	G	
	TACG TTA CTTGTGATT		
	GTGT AGTGACACTGA		
	A		
GAM1308 LOC199863 5'	TGGGCACTAATCACAGAACTGT 89868	A	CGGA
	A TACGGTT CTGTGATTA CTA		
	ATGTCAA GACACTAAT GGT		
	_ CACG		
GAM1308 LOC199992 5'	GTGTCACAGCTGGTTGTG 88511	TT_	T
	TACGG A CTGTGAT AC		

GTGTT T GACACTG TG  
 GG C \_  
 GAM1308 LOC200399 3' TTCTGATTACAGAACTGTA 88813 A C  
 TACGGTT CTGTGATTA GGA  
 ||||| ||||| ||  
 ATGTCAA GACATTAGT CTT

\_ \_  
 GAM1308 LOC201287 5' TAGTCTTGGATTGTAGTAATC 88183 TG AC  
 GGTTACTG ATT GGACTA  
 ||||| || |||||  
 CTAATGAT TAG TCTGAT  
 GT GT

GAM1308 LOC219294 3' TAATCACAGTATTGTG 93010 T  
 TACGGT ACTGTGATTA  
 ||||| |||||  
 GTGTTA TGACACTAAT

\_  
 GAM1308 LOC219790 3' TGGTCCAGTGTCTCATAGTAAT 91362 G T\_ \_  
 AGTA AC GTTACTGTGA TAC GGACTA  
 || ||||| || |||||  
 TG TAATGATACT GTG CCTGGT  
 A CT A

GAM1308 LOC220081 3' TGGTTTGTAAATTTGGGACC 91748 ACTGT  
 GGTT GATTACGGACTA  
 ||| |||||  
 CCAG TTAATGTTTGGT  
 GGT\_

GAM1308 LOC220143 5' GTGTCACAGTGCTGTG 93591 T T  
 TACGGT ACTGTGAT AC  
 ||||| ||||| ||  
 GTGTCG TGACACTG TG

\_ \_  
 GAM1308 LOC220143 5' GTGTCACAGTGCTGTG 93592 T T  
 TACGGT ACTGTGAT AC  
 ||||| ||||| ||  
 GTGTCG TGACACTG TG

\_ \_  
 GAM1308 LOC221271 3' ATGGTAATCATATCGTAGTTAC 91848 T \_\_\_\_\_ GGACTA  
 CGTA GT ACT GTGATTAC  
 || ||| |||||  
 CA TGA TACTAATG  
 T TGCTA GT AT

GAM1308 LOC221301 3' TAGTTCTGTTACTTAGTAGCTG 91889 TGATT \_  
 TG TACGGTTACTG ACGGA CTA  
 ||||| ||||| ||  
 GTGTCGATGAT TGTCT GAT  
 TCAT\_ T

GAM1308 LOC221399 5' CAGTATTAATCATGATAGTTGT 93846 GG CT CGG A  
 A TAC TTA GTGATTA ACT  
 ||| ||| ||||| |||

	ATG GAT TACTAAT TGA	
	TT AG TA_ CG	
GAM1308 LOC221491 5'	TGGTCGGGGTGGTGGTGGCTGT 92014	TG G TA G
G	TACGGTTAC T AT CG ACTA	
	I	
	GTGTCGGTG G TG GC TGGT	
	GT G GG _	
GAM1308 LOC254428 3'	AATCATAGAACCGTA 95452 A	
	TACGGTT CTGTGATT	
	ATGCCAA GATACTAA	
	—	
GAM1308 LOC254428 3'	AGTTACAGAACTGTG 95455 A	
	TACGGTT CTGTGATT	
	GTGTCAA GACATTGA	
	—	
GAM1308 LOC254556 3'	GAGAGGTGGTGGCAGTAATTGT 94616	G GGACTA
G	TACGGTTACTGT ATTAC	
	GTGTTAATGACG TGGTG	
	G GAGAGT	
GAM1308 LOC255328 3'	TAGCCTATTGTAGTGA CT 96563	TG TAC A
	GGT TACTG AT GG CTA	
	TCAGTGAT TA CC GAT	
	GT T__ _	
GAM1308 LOC255527 5'	TGGTCTGTGAAATAGTCTGTA 96858	TT GA
	TACGG ACTGT TTACGGACTA	
	ATGTC TGATA AGTGTCTGGT	
	_ A_	
GAM1308 LOC256107 3'	TAGTTTGTTCATGACATAACTG 96786	C G T_
TA	TACGGTTA TGT AT ACGGACTA	
	ATGTCAAT ACA TA TGTTTGAT	
	_ G CT	
GAM1308 LOC256112 5'	AGTCATCGTGGCTGTG 96361	T
	TACGGTTAC GTGATT	
	GTGTCGGTG TACTGA	
	C	
GAM1308 LOC256207 5'	TAGTCTTGGATTATAGTAATC 95175	AC
	GGT TACTGTGATT GGACTA	
	CTAATGATATTAG TCTGAT	
	GT	
GAM1308 LOC256730 3'	TGGTTCGTCTCCCTGGTAATTG 95234	GTGATT
	CGGTTACT ACGGACTA	

GTTAATGG TGCTTGGT  
 TCCCTC  
 GAM1308 LOC256946 3' TGGTTTATTGTGCAGTGA CTGT 94548 ATTAC  
 A TACGGTTACTGTG GGACTA  
 ||||| ||||  
 ATGTCAGTGACGT TTTGGT  
 GTTA\_  
 GAM1308 LOC257007 5' TGGTTTGGTGGTGGTGGCGGTG 97587 G TG G TA  
 TAC GTTAC T AT CGGACTA  
 || |||| | || |||||  
 GTG CGGTG G TG GTTTGGT  
 G GT G \_  
 GAM1308 LOC257159 3' AATTACAGTATTGTG 97178 T  
 TACGGT ACTGTGATT  
 |||| |||||  
 GTGTTA TGACATTAA  
 -  
 GAM1308 LOC257407 5' GGTCACAGTGA CTGTG 96989  
 TACGGTTACTGTGATT  
 |||||  
 GTGTCAGTGACACTGG  
 -  
 GAM1308 LOC257481 3' GAGTCAGGTAGTGCAGTGGTTG 61109 TT G G\_ A  
 TA TACGG ACTGT ATTAC GACT  
 |||| |||| |||| ||||  
 ATGTT TGACG TGATG CTGA  
 GG \_ GA GT  
 GAM1308 LOC51099 3' TAGTCTGTGATGAAGAGTAG 32054 GTG\_  
 TTACT ATTACGGACTA  
 |||| |||||  
 GATGA TAGTGTCTGAT  
 GAAG  
 GAM1308 LOC51107 3' TAATCAAGGTGATTGTG 32062 G  
 TACGGTTACT TGATTA  
 ||||| |||||  
 GTGTTAGTGG ACTAAT  
 A  
 GAM1308 LOC91250 5' AGTTATAGTGACGTG 65320 G  
 TACG TTACTGTGATT  
 ||| |||||  
 GTGC AGTGATATTGA  
 -  
 GAM1308 LOC91351 3' TAGTCTGTGGTTTTCTGT 65709 TTACTGT  
 ACGG GATTACGGACTA  
 ||| |||||  
 TGTC TTGGTGTCTGAT  
 TT\_\_\_\_  
 GAM1308 LOC91517 5' TGGGATTGCGGTGCCTGTG 66312 T TG TA  
 TACGG TACTG AT CG  
 |||| |||| || ||

		GTGTC GTGGC TA GT		
		C GT GG		
GAM1308	LOC92285 5'	TGAATGCAGTGACTGTG 68753	A	
		TACGGTTACTGTG TTA		
		GTGTCAGTGACGT AGT		
		A		
GAM1308	LOC92391 3'	TAGTTCAGCCACAAAGTAGTTG 69159	GG G ATTAC	
	TG	TAC T TACT TG GGACTA		
		GTG GATGA AC CTTGAT		
		TT A ACCGA		
GAM1308	LOC92539 5'	ACGAGGGTGGTCACGGTGGTGG 69626	G TT GGACTA	
	TA	TAC G ACTGTGATTAC		
		ATG T TGGCACTGGTG		
		G GG GGAGCAA		
GAM1308	LOC92973 5'	GGTTCCCATGGTGGCTG 71039	ATTAC	
		CGGTTACTGTG GGACT		
		GTCGGTGGTAC CTTGG		
		C_____		
GAM1308	LOC92997 3'	GGTCACAGTGACTGTG 71090		
		TACGGTTACTGTGATT		
		GTGTCAGTGACACTGG		
GAM1308	LOC96652 3'	GTACACGCGGTAAGTGTG 65472	AT	
		TACGGTTACTGTG TAC		
		GTGTCAATGGCGC ATG		
		AC		
GAM1309	ADRB3 3'	GGTGTGTGTGTGTGTGTG 3437	TC T	
		TACACA CACAC CATT		
		GTGTGT GTGTG GTGG		
		GT T		
GAM1309	AKAP2 3'	AGATGGGGTGTGTGTGGATGTG 23256	T CA	
	TG	TACACATCCACAC CATTCT		
		GTGTGTAGGTGTG GTGGGG		
		T TAGAA		
GAM1309	AKAP2 3'	GGATGTGTGTGTGTGTGTG 23265	TC T	
		TACACA CACAC CATTCT		
		GTGTGT GTGTG GTAGG		
		GT T		
GAM1309	AKAP2 3'	TGAGTAAGGGTGTGTGTGTGTG 23269	TC ATT	
		TACACA CACACTC CTCA		

			GTGTGT GTGTGGG GAGT		
			GT AAT		
GAM1309	AKAP2	3'	TGGGGTGTGTGTGGATGTGTG 23271	T	CA
			TACACATCCACAC CATTCT		
			GTGTGTAGGTGTG GTGGGG		
			T T		
GAM1309	APBA2	3'	GTGGTGTGGAGTGTGTG 18563	_	T
			TACACA TCCACAC CAT		
			GTGTGT AGGTGTG GTG		
			G _		
GAM1309	ARF3	3'	TGTATATGGGTGTGGGTGTGT 8011		TCT
			ACACATCCACACTCAT CA		
			TGTGTGGGTGTGGGTA GT		
			TAT		
GAM1309	B4GALT5	3'	GGGTGTGTGTGTGTAT 16511		TC
			GTACACA CACACTC		
			TATGTGT GTGTGGG		
			GT		
GAM1309	CARPX	5'	TGGGAGTGCAGAGTGTGCA 39427	A _	A
			TGTACAC TC CAC CTCA		
			ACGTGTG AG GTG GGGT		
			_ C A		
GAM1309	CDKN1A	3'	TGGGGGTGAGGGTCCCATGTG 54302		CC_ A
			CACAT AC CTCATTCTCA		
			GTGTA TG GAGTGGGGGT		
			CCC G		
GAM1309	CLASP1	3'	TGACGTGTGTGTGTGTGTG 65312	TC	T TC
			TACACA CACAC CAT TCA		
			GTGTGT GTGTG GTG AGT		
			GT T C_		
GAM1309	CLN6	3'	GGATTCGTGTGTGTGTGTG 35409	TC	TC
			TACACA CACAC ATTC		
			GTGTGT GTGTG TAGG		
			GT CT		
GAM1309	COL9A3	3'	TGAGAGAAGGTAGGGTGTGTAT 8492		AC CA
	A		TGTACACATCC ACT TTCTCA		
			ATATGTGTGGG TGG GAGAGT		
			A_ AA		
GAM1309	CRIM1	3'	TGAGAGTATGTATGTGTGTGTG 33180	TC	TC_____
	TGTG		CACA CACAC ATTCTCA		



			GTGT GTGTG TGAGAGT		
			GT TATGTA		
GAM1309	CRLF1	3'	ACCCCAGTGGGTGTGTGTGTGT 16451	TC	CTCA
	G		TACACA CACACTCATT		
			GTGTGT GTGTGGGTGA		
			GT CCCCAC		
GAM1309	CRLF1	3'	GGGTGTGTGTGTGTGTGTG 16454	TC	T
			TACACA CACAC CATTG		
			GTGTGT GTGTG GTGGG		
			GT T		
GAM1309	CRY2	3'	TGAGCCACAAAGTGTGTGTGTGTG 72211	TC	CATT__
	TG		TACACA CACACT CTCA		
			GTGTGT GTGTGA GAGT		
			GT AACACC		
GAM1309	CSPG3	3'	GAGGGTGCATGAGTGTAT 15232	A	CACACT
			GTACAC TC CATTCTC		
			TATGTG AG GTGGGAG		
			_ TAC__		
GAM1309	CUL4B	3'	TGAGTATGGGATGTGTG 13144	AC_	
			TACACATCC ACTCA		
			GTGTGTAGG TGAGT		
			GTA		
GAM1309	DSP	3'	GAGTGTGGATTGTATA 15340	C	
			TGTACA ATCCACACTC		
			ATATGT TAGGTGTGAG		
			-		
GAM1309	DYRK2	3'	TGGGAATGGAAACGTGTGTG 13130	CCACAC	
			TACACAT TCATTCTCA		
			GTGTGTG GGTAAGGGT		
			CAAA__		
GAM1309	DYRK2	3'	TGGGAATGGAAACGTGTGTG 21394	CCACAC	
			TACACAT TCATTCTCA		
			GTGTGTG GGTAAGGGT		
			CAAA__		
GAM1309	EGR3	3'	GTGAGTGTGTGTGTGTGC 59560	TC	
			GTACACA CACACTCAT		
			CGTGTGT GTGTGAGTG		
			GT		
GAM1309	ENDOG	3'	TGAGACTGTGGGTGTGTGCA 15423		CTCAT
			TGTACACATCCACA TCTCA		

			ACGTGTGTGGGTGT AGAGT		
			C_____		
GAM1309	EPHB3	3'	TGAGTGTGTGTGTGTGTGTG 15456	TC	T T
	C		GTACACA CACAC CAT CTCA		
			CGTGTGT GTGTG GTG GAGT		
			GT T T		
GAM1309	EPHB3	3'	TGGGATGTGTGAGTGTGTGTGT 15457	TC	_____
	GTG		ACACA CACACTCAT TCTCA		
			TGTGT GTGTGAGTG AGGGT		
			GT TGT		
GAM1309	F2RL3	3'	TGGGGGTGGACAGTGTGTGC 14195	_____	A
			GTACACA TCCAC CTCA		
			CGTGTGT AGGTG GGGT		
			GAC G		
GAM1309	FBXW1B	3'	TGGGGATCAGTGTGTGTGTAT 24528	TC	C
			GTACACA CACACT ATTCTCA		
			TATGTGT GTGTGA TAGGGGT		
			_____ C		
GAM1309	FBXW1B	3'	TGGGGATCAGTGTGTGTGTAT 53332	TC	C
			GTACACA CACACT ATTCTCA		
			TATGTGT GTGTGA TAGGGGT		
			_____ C		
GAM1309	FBXW1B	3'	TGGGGATCAGTGTGTGTGTAT 53343	TC	C
			GTACACA CACACT ATTCTCA		
			TATGTGT GTGTGA TAGGGGT		
			_____ C		
GAM1309	FGF5	3'	GGATTTGTGTGTATGTGTAT 52491	C	TC
			GTACACAT CACAC ATTC		
			TATGTGTA GTGTG TAGG		
			T TT		
GAM1309	FGF5	3'	GGATTTGTGTGTATGTGTAT 15545	C	TC
			GTACACAT CACAC ATTC		
			TATGTGTA GTGTG TAGG		
			T TT		
GAM1309	FGFR3	3'	TGGTCTGTGTGTGTGTGTGC 3778	TC	T TT CA
			GTACACA CACAC CA CT		
			CGTGTGT GTGTG GT GG		
			GT T CT T		
GAM1309	FHOD1	3'	GAGTGTGTGTGTATGTGTG 60195	C	T
			TACACAT CACAC CATTC		

			GTGTGTA GTGTG GTGAG		
			T T		
GAM1309	FREB	3'	GGGGATGGTGGGATGTGTG 51227	A T	A
			TACACATCC CAC CATTCTC		
			GTGTGTAGG GTG GTAGGGG		
			- - G		
GAM1309	FXD6	3'	GATGTGTGTGTGTGTGTG 41838	TC	T
			TACACA CACAC CATT		
			GTGTGT GTGTG GTAG		
			GT T		
GAM1309	GAS11	3'	TGAGGGCTGGGTGGGTGCA 7627	A	CA_
			TGTAC CATCCA CTCA		
			ACGTG GTGGGT GAGT		
			G CGG		
GAM1309	GLTSCR1	3'	TGACCTGTGTGTGTGTGTGTC 31679	TC	T TTCTCA
	A		TGTACACA CACAC CA		
			ACGTGTGT GTGTG GT		
			GT T CCAGT		
GAM1309	GNA11	3'	GGGCATGTGGGGTGTGTG 76105	A	TCATT
			TACACATCC CAC CTC		
			GTGTGTGGG GTG GGG		
			- TAC__		
GAM1309	GSN	3'	TGAGTGTGTGTGTGTGTGTGTG 3928	TC	T T
			TACACA CACAC CAT CTCA		
			GTGTGT GTGTG GTG GAGT		
			GT T T		
GAM1309	GSN	3'	TGCTATGAGTGTGTGTGTGTG 3929	TC	TCTCA
			TACACA CACACTCAT		
			GTGTGT GTGTGAGTA		
			GT TCGT		
GAM1309	GSTM5	3'	GGATGGGTGTGTGTGTGTG 5955	TC	
			TACACA CACACTCATTC		
			GTGTGT GTGTGGGTAGG		
			GT		
GAM1309	GSTM5	3'	GGGTGTGTGTGTGTGTGTG 5956	TC	T
			TACACA CACAC CATTC		
			GTGTGT GTGTG GTGGG		
			GT T		
GAM1309	HMGB2	3'	GATGCGTGTGGAATGTGTG 9229	-	T
			TACACAT CCACAC CATT		

			GTGTGTA GGTGTG GTAG		
			A C		
GAM1309	HMGE	3'	GAGAAATGGGTGTGGG 72730	—	
			TCCACACTCATT CTC		
			GGGTGTGGGTAA GAG		
			A		
GAM1309	HMOX2	3'	TGAGGGTGGGTGTGGGTG 65160		
			CATCCACACTCATTCTCA		
			GTGGGTGTGGGTGGGAGT		
GAM1309	HMOX2	3'	TGGGAGTGAGGGTGGGTGTG 65161	A	
			CACATCCAC CTCATTCTCA		
			GTGTGGGTG GAGTGAGGGT		
			G		
GAM1309	HOXC10	3'	TGGGAGTGTGGCTGGTGTGTG 61272	—	ATTCTCA
			TACACAT CCACACTC		
			GTGTGTG GGTGTGAG		
			GTC GGT A		
GAM1309	HSPA4	3'	GGTGTGTGTGTGTGTGTG 89172	TC	T
			TACACA CACAC CATT		
			GTGTGT GTGTG GTGG		
			GT T		
GAM1309	IL6R	3'	GAGGGTGAGTGGGTG 5121	T A	
			CA CC CACTCATTCTC		
			GT GG GTGAGTGGGAG		
GAM1309	ITGA1	3'	TGAGGTTTGTGTGTGTGTGTG 63537	TC	T T_
	G		TACACA CACAC CA TCTCA		
			GTGTGT GTGTG GT GGAGT		
			GT T TT		
GAM1309	ITGB3	3'	GGAAGTGTGGGTCTGTGTG 3996	—	CAT
			TACACA TCCACACT TCT		
			GTGTGT GGGTGTGA AGG		
			CT —		
GAM1309	ITGB3	3'	TGGGTCTGTGTGTGTGTAT 3999	TC	—
			GTACACA CAC ACTCA		
			TATGTGT GTG TGGGT		
			GT TC		
GAM1309	KCNK10	3'	TGAGCGTTGTGTGTGTGTGTG 40973	TC	T TT_
	G		TACACA CACAC CA CTCA		

			GTGTGT GTGTG GT GAGT		
			GT T TGC		
GAM1309	KCNK10	3'	TGAGCGTTGTGTGTGTGTGTGT 56341	TC	T TT_
	G		TACACA CACAC CA CTCA		
			GTGTGT GTGTG GT GAGT		
			GT T TGC		
GAM1309	KCNK10	3'	TGAGCGTTGTGTGTGTGTGTGT 56345	TC	T TT_
	G		TACACA CACAC CA CTCA		
			GTGTGT GTGTG GT GAGT		
			GT T TGC		
GAM1309	KLHL3	3'	GGAGTGTGTGTGTGTGTGTG 87460	TC	T
			TACACA CACAC CATTCT		
			GTGTGT GTGTG GTGAGG		
			GT T		
GAM1309	MATN1	3'	TGGGAGCTCGTGTGTGTATGTG 9928	C	TCA__
	TGC		GTACACAT CACAC TTCTCA		
			CGTGTGTA GTGTG GAGGGT		
			T TGCTC		
GAM1309	MEF2A	3'	TGTATGTGGGTGTGAGTGTGTG 18786	TC	TCT
			TACACA CACACTCAT CA		
			GTGTGT GTGTGGGTG GT		
			GA TAT		
GAM1309	MELK	3'	GCCGGATGAGTGTGGGTGTGAT 28893	_	TCA
	ACA		TGTA CACATCCACACTCATTC		
			ACAT GTGTGGGTGTGAGTAGG		
			A CCGT		
GAM1309	MEN1	5'	GTGGTGTGTGTGTGTG 93377	TC	T
			TACACA CACAC CAT		
			GTGTGT GTGTG GTG		
			GT _		
GAM1309	MEN1	5'	TGGTGTGTGTGTGTGTC 93384	TC	_
			GTACACA CACAC TCA		
			CGTGTGT GTGTG GGT		
			GT T		
GAM1309	MLLT2	3'	TGGGGTTGTGTGTGTATGTG 19856	C	T _
	TG		TACACAT CACAC CAT TCTCA		
			GTGTGTA GTGTG GTG GGGGT		
			T T TT		
GAM1309	MSF	3'	ATGAGTGTGAGTGTGTG 88078	TC	
			TACACA CACACTCAT		

		GTGTGT GTGTGAGTA		
		GA		
GAM1309	MUCDHL	3' TGGGGGTGGGTGCGCCGTGTG	34760	CCA_
		CACAT CACTCATTCTCA		
		GTGTG GTGGGTGGGGGT		
		CCGC		
GAM1309	NAPB	3' AGAATGAATGTATGT	70177	CC C
		ACAT ACA TCATTCT		
		TGTA TGT AGTAAGA		
		— A		
GAM1309	NCOA3	3' TGGGCTGTGTGTGTGTGTAT	21533	TC T TT
		GTACACA CACAC CA CTCA		
		TATGTGT GTGTG GT GGGT		
		GT T C_		
GAM1309	OAS3	3' GGTGTGTGTGTGTGTGTG	20542	TC T
		TACACA CACAC CATT		
		GTGTGT GTGTG GTGG		
		GT T		
GAM1309	OAS3	3' TGAGCACATGTGTGCATGTGTG	20544	C TCATT
		TACACAT CACAC CTCA		
		GTGTGTA GTGTG GAGT		
		C TACAC		
GAM1309	PABPC1	5' GAGTGCGGAGTGTGTG	10387	_ A
		TACACA TCC CACTC		
		GTGTGT AGG GTGAG		
		G C		
GAM1309	PAK4	3' GTGAGTGTGCATGTGTG	19690	C
		TACACAT CACACTCAT		
		GTGTGTA GTGTGAGTG		
		C		
GAM1309	PAX7	5' TGGGGGTAGGGAGTGTGTGTG	10438	TC A _
		CACA CAC CTC ATTCTCA		
		GTGT GTG GGG TGGGGGT		
		GT A A		
GAM1309	PAX7	5' TGGGGGTAGGGAGTGTGTGTG	25642	TC A _
		CACA CAC CTC ATTCTCA		
		GTGT GTG GGG TGGGGGT		
		GT A A		
GAM1309	PIK3C2B	3' GGGGGTGGGTGGGTGGAT	10574	_
		ATCCAC ACTCATTCTC		

			TAGGTG TGGGTGGGGG		
			GG		
GAM1309	PKD1	3'	TGACTGTGTGTGTGTGTGTGTG 4312	TC	T TC
			TACACA CACAC CAT TCA		
			GTGTGT GTGTG GTG AGT		
			GT T TC		
GAM1309	PON1	3'	TGGGAGTGATATGATGTGTA 4806	CACAC	
			TACACATC TCATTCTCA		
			ATGTGTAG AGTGAGGGT		
			TAT__		
GAM1309	PPARGC1	3'	TGATGGAGTGTGCGTGTGTGCA 25163	C	ATTC
			TGTACACAT CACACTC TCA		
			ACGTGTGTG GTGTGAG AGT		
			C GT__		
GAM1309	PPIC	3'	AGGGGTGTGTGTGTGTGTG 6267	TC	T CA
			CACA CACAC CATTCT		
			GTGT GTGTG GTGGGG		
			GT T AC		
GAM1309	PTGES	3'	TGGGGAATCCGTGTGTGTGTGT 16866	TC	TC A
	G		TACACA CACAC ATTCTC		
			GTGTGT GTGTG TAAGGG		
			GT CC GT		
GAM1309	PTGS2	3'	TGGGAATTTGGGTTGTGTAT 6362	T A	CTC
			GTACACA CC CA ATTCTCA		
			TATGTGT GG GT TAAGGGT		
			T _ T__		
GAM1309	PTP4A2	3'	GGGGGAGGGGGTGTGTGTGTGT 12984	TC	A A
	G		TACACA CACACTC TTCTC		
			GTGTGT GTGTGGG GAGGG		
			GT G GGG		
GAM1309	PTPN1	3'	AGTTTGGGTGTGTATA 11045	C	
			TGTACACATCCA ACT		
			ATATGTGTGGGT TGA		
			T		
GAM1309	RABIF	3'	TGAGAGTGACTTTGTTGTAT 11210	_	TCCACAC
			GTACA CA TCATTCTCA		
			TATGT GT AGTGAGAGT		
			T TTC__		
GAM1309	SCN4A	3'	GAACACGTGTGTGTGTGTGCA 4412	TC	TCA
			TGTACACA CACAC TTC		

			ACGTGTGT GTGTG AAG		
			GT CAC		
GAM1309	SCN4A	3'	GAGTGTGTGGATGCGTG 4413	A	TCATT
			TAC CATCCACAC CTC		
			GTG GTAGGTGTG GAG		
			C T____		
GAM1309	SERPINA4	3'	TGGGAGTGAGTAGCTCTGTGT 20614		TCCAC
			ACACA ACTCATTCTCA		
			TGTGT TGAGTGAGGGT		
			CTCGA		
GAM1309	SFN	3'	TGGAGATGGGTGTGTGTGTGTG 74562	TC	CT
			TACACA CACACTCATT CA		
			GTGTGT GTGTGGGTAG GT		
			GT AG		
GAM1309	SFN	3'	TGGGTGTGTGTGTGTGTGTGTG 74564	TC	T T
			TACACA CACAC CAT CTCA		
			GTGTGT GTGTG GTG GGGT		
			GT T T		
GAM1309	SH2D1A	3'	TGGGAATTCTGGATTGTGTAT 9852	_	CACTC
			GTACACA TCCA ATTCTCA		
			TATGTGT AGGT TAAGGGT		
			T CT____		
GAM1309	SIX3	5'	GTGTGTGTGGATGTGTG 18277	T	
			TACACATCCACAC CAT		
			GTGTGTAGGTGTG GTG		
			T		
GAM1309	SLC38A3	3'	GAGGGTGGGGCTGGTGT 22423	T	CA
			ACA CCA CTCATTCTC		
			TGT GGT GGGTGGGAG		
			_ CG		
GAM1309	SLC6A8	3'	TGAGTCTGTTGTGTGGATGTGC 18853	TA	T_ TT
	GT		G CACATCCACAC CA CTCA		
			T GTGTAGGTGTG GT GAGT		
			GC TT CT		
GAM1309	SOX9	3'	GTGTGTGTGGGTGTGTG 4439	T	
			TACACATCCACAC CAT		
			GTGTGTGGGTGTG GTG		
			T		
GAM1309	TCF15	3'	GTGAGTGTGAGTGTGTG 16041	TC	
			TACACA CACACTCAT		



			GTGTGT GTGTGAGTG		
			GA		
GAM1309	TEM6	3'	GGGTGTTGTGTGTGTGTGC 42747	TC	CT
			GTACACA CACA CATTG		
			CGTGTGT GTGT GTGGG		
			GT T_		
GAM1309	TMEM2	3'	TGAGTGTGTGTGTGTGTGTG 25428	TC	T T
			TACACA CACAC CAT CTCA		
			GTGTGT GTGTG GTG GAGT		
			GT T T		
GAM1309	TMEM2	3'	TGAGTGTGTGTGTGTG 25427	TC	
			TACACA CACACTCA		
			GTGTGT GTGTGAGT		
			GT		
GAM1309	TNFSF6	3'	GGGGTGTGTGTGTGTGTG 5319	TC	T
			CACA CACAC CATTCT		
			GTGT GTGTG GTGGGG		
			GT T		
GAM1309	TSG101	5'	GGGTGTGCGATTGTGTG 20840	--	
			TACACA TC CACACTC		
			GTGTGT AG GTGTGGG		
			T C		
GAM1309	UBE2H	3'	GGTGTGTGTGTGTGTGTA 12489	TC	T
			TACACA CACAC CATT		
			ATGTGT GTGTG GTGG		
			GT T		
GAM1309	USF2	3'	GGGGTGTGTGTGTGTG 12558	TC	T
			CACA CACAC CATTCT		
			GTGT GTGTG GTGGGG		
			_ T		
GAM1309	VAX2	3'	TGAGTGCAGTGTGAGTGTGTG 25013	TC	_ TCA
			TACACA CACACT CATTG		
			GTGTGT GTGTGA GTGAG		
			GA C T		
GAM1309	VDR	3'	TGAGAGTGAGCTGTAGGTGTGC 4572	ATCC	_
			GTACAC ACA CTCATTCTCA		
			CGTGTG TGT GAGTGAGAGT		
			GA_ C		
GAM1309	WBSCR14	3'	GTGTGTGTGGATGTGTG 51973	T	
			TACACATCCACAC CAT		

		GTGTGTAGGTGTG GTG			
		T			
GAM1309	WBSCR14	3' GTGTGTGTGGATGTGTG 51978	T		
		TACACATCCACAC CAT			
		GTGTGTAGGTGTG GTG			
		T			
GAM1309	WSX1	5' GAGAGTGTGTGTGTGTGTG 16734	TC	T	A
		CACA CACAC CATTCTC			
		GTGT GTGTG GTGAGAG			
		GT T A			
GAM1309	WT1	3' TGGTCGTGTGTGTGTGTGTGTG 4591	TC	T	TC
		TACACA CACAC CAT TCA			
		GTGTGT GTGTG GTG GGT			
		GT T CT			
GAM1309	WT1	3' TGGTCGTGTGTGTGTGTGTGTG 44356	TC	T	TC
		TACACA CACAC CAT TCA			
		GTGTGT GTGTG GTG GGT			
		GT T CT			
GAM1309	WT1	3' TGGTCGTGTGTGTGTGTGTGTG 44366	TC	T	TC
		TACACA CACAC CAT TCA			
		GTGTGT GTGTG GTG GGT			
		GT T CT			
GAM1309	WT1	3' TGGTCGTGTGTGTGTGTGTGTG 44376	TC	T	TC
		TACACA CACAC CAT TCA			
		GTGTGT GTGTG GTG GGT			
		GT T CT			
GAM1309	ZNF147	3' GAGAGTGATTGTGTTGTG 17435	TC	C	
		CACA CACA TCATTCTC			
		GTGT GTGT AGTGAGAG			
		T_ T			
GAM1309	ABCC13	3' AGAGTGTGTGTGTGTGTGTG 56989	TC	T	
		CACA CACAC CATTCT			
		GTGT GTGTG GTGAGA			
		GT T			
GAM1309	ABLM	3' TGGGGATGGAGAGGATGGTGCA 9780	A	ACAC	
		TGTAC CATCC TCATTCTCA			
		ACGTG GTAGG GGTAGGGGT			
		_ AGA_			
GAM1309	ABLM	3' TGGGGATGGAGAGGATGGTGCA 22042	A	ACAC	
		TGTAC CATCC TCATTCTCA			

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          ACGTG GTAGG  GGTAGGGGT
            _  AGA_
GAM1309 AKAP11  3' GAAAGGTGTGTGTGTGTG  32709  TC  CA
          TACACA CACACT TTC
          ||||| ||||| |||
          GTGTGT GTGTGG AAG
            GT  A_
GAM1309 ATP9A  3' GGGGGTGTGTGTGTGTGTG  62048  TC  T
          CACA CACAC CATTCTC
          ||| ||||| |||||
          GTGT GTGTG GTGGGGG
            GT  T
GAM1309 BHLHB2  3' AGGGTGTGTGTGTGTGTG  13376  TC  T
          CACA CACAC CATTCT
          ||| ||||| |||||
          GTGT GTGTG GTGGGA
            GT  T
GAM1309 C1orf17  3' TGAGTGTGTGCATGTGTGCA  68218  C__
          TGTACACAT CACACTCA
          ||||| |||||
          ACGTGTGTA GTGTGAGT
            CGT
GAM1309 C1orf34  3' TGAGGGTGAGCTGTCTGTGGGC 60682  TA  TCC  _
          A          TG CACA ACA CTCATTCTCA
          || ||| ||| |||||
          AC GTGT TGT GAGTGGGAGT
            GG  C__ C
GAM1309 CYP2D6  5' TGGGGGTGCCAGGTGTGTCCA 3658  T  CACACT
          TG ACACATC  CATTCTCA
          || ||||| |||||
          AC TGTGTGG  GTGGGGGT
            C  ACC__
GAM1309 DGS-A  3' TGAGCGAGTGGGTGTGTG  84903  A__
          TACACATCCAC CTCA
          ||||| |||
          GTGTGTGGGTG GAGT
            AGC
GAM1309 DKFZP434A043 3' TGAGAATGAATATGTCTGTGTG 31196  TC  CAC
          TACACA CA TCATTCTCA
          ||||| || |||||
          GTGTGT GT AGTAAGAGT
            CT ATA
GAM1309 DKFZP434B172 3' GAGAACTTTGTGTGTGTGTA 70036  TC  CTCA  A
          TACACA CACA TTCTC
          ||||| ||| ||||
          ATGTGT GTGT AAGAG
            GT  TTC_ G
GAM1309 DKFZP434K1772 3' TGGTGTGATGGGTGTGTGCA 67717  _  _
          TGTACACATCCA CAC TCA
          ||||| ||| |||

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ACGTGTGTGGGT GTG GGT  
 A T  
 GAM1309 DKFZP434K2235 3' TGGGGTGTGTGTGGGGATGTGT 83500    \_\_ T CA  
 G TACACATCC ACAC CATTCT  
 ||||| ||| |||||  
 GTGTGTAGG TGTG GTGGGG  
 GG T T  
 GAM1309 DKFZp547D155 3' GGGAGGTGAGGTGTGTGTG 70437 TC A \_  
 CACA CAC CTCAT TCTC  
 ||| || ||||| |||  
 GTGT GTG GAGTG AGGG  
 GT \_ G  
 GAM1309 DKFZP564O0423 3' TGAGAATGGCCAGGAGGTGTG 91701 A ACAC  
 TACAC TCC TCATTCTCA  
 ||||| ||| |||||  
 GTGTG AGG GGTAAGAGT  
 G ACC\_  
 GAM1309 DNAH8 3' TGAGGGACTCAGTGATGTGTG 7260 C ACTCA  
 TACACATC AC TTCTCA  
 ||||| || |||||  
 GTGTGTAG TG GGGAGT  
 \_ ACTCA  
 GAM1309 DUSP9 3' TGGGTGGCGGGTGTGCGTGTGT 7345 C ATT\_  
 G TACACAT CACACTC CTCA  
 ||||| ||||| |||  
 GTGTGTG GTGTGGG GGGT  
 C CGGT  
 GAM1309 EML4 3' ATGGAAGGGTGTGGGTGTGTG 38807 A CA  
 TACACATCCCACTC TTCT  
 ||||| ||||| |||  
 GTGTGTGGGTGTGGG AAGG  
 \_ TAT  
 GAM1309 EML4 3' TGGAAGGGTGTGGGTGTGTG 38814 A CA  
 TACACATCCCACTC TTCT  
 ||||| ||||| |||  
 GTGTGTGGGTGTGGG AAGG  
 \_ T  
 GAM1309 ET 3' TGAGAATGCAGAGATGTGTTG 44222 T CACA \_  
 G ACACATC CT CATTCTCA  
 | ||||| || |||||  
 G TGTGTAG GA GTAAGAGT  
 T A\_\_ C  
 GAM1309 FLJ10350 3' TGGGGTACAGTGGATGTG 95512 ACTCAT  
 CACATCCAC TCTCA  
 ||||| |||  
 GTGTAGGTG GGGGT  
 ACAT\_  
 GAM1309 FLJ10743 3' TGGGGATGAGGCATGGGT 36554 CA\_  
 ATCCA CTCATTCTCA  
 ||||| |||||

		TGGGT GAGTAGGGGT	
		ACG	
GAM1309	FLJ11171	3' TGAGGTGTGTGTATGTGTAT 37132	C TCAT
		GTACACAT CACAC TCTCA	
		TATGTGTA GTGTG GGAGT	
		T T__	
GAM1309	FLJ14100	5' GAGAACAATGGTGTGTGCA 46680	T CACTCA
		TGTACACA CCA TTCTC	
		ACGTGTGT GGT AAGAG	
		_ AAC__	
GAM1309	FLJ20043	3' TGGGGTGTGTGTGTGTGTG 34407	TC T CA
		TACACA CACAC CATTCT	
		GTGTGT GTGTG GTGGGG	
		GT T T	
GAM1309	FLJ20079	3' TGGGGGGTCACTGTGTGTGTGT 34506	TC TC__ A
		GTG TACACA CACAC ATTCTC	
		GTGTGT GTGTG TGGGGG	
		GT TCAC GT	
GAM1309	FLJ20123	5' TGAGGGTGGGGCCTGTATGTG 34588	C CA_
		CACAT CA CTCATTCTCA	
		GTGTA GT GGGTGGGAGT	
		T CCG	
GAM1309	FLJ20330	5' GAGGTGGGTGTGTGC 38619	A
		GTACACATCCAC CTC	
		CGTGTGTGGGTG GAG	
		-	
GAM1309	FLJ20337	3' GTGGGTGTGAATGTGTATA 34969	C
		TGTACACAT CACTCAT	
		ATATGTGTA GTGTGGGTG	
		A	
GAM1309	FLJ21276	3' TGGGGTGTGTGTGTGTGTG 44921	TC T CA
		CACA CACAC CATTCT	
		GTGT GTGTG GTGGGG	
		GT T TA	
GAM1309	FLJ21276	3' TGGGGTGTGTGTGTGTGTG 44922	TC T CA
		TACACA CACAC CATTCT	
		GTGTGT GTGTG GTGGGG	
		GT T T	
GAM1309	FLJ21742	3' TGAGGGTGGACGTGATGAGTGT 49849	A __ AC
		A TACAC TC CAC TCATTCTCA	

		ATGTG AG GTG GGTGGGAGT		
		_ TA CA		
GAM1309	FLJ22479	3' TGAGGCTGTGTGTGTGTGTGTG 46078	TC	T TT
		TACACA CACAC CA CTCA		
		GTGTGT GTGTG GT GAGT		
		GT T CG		
GAM1309	FLJ31121	3' GGTTCTATGGTGTGTGGATGTG 58536	_	TCTCA
	TG	TACACATCCACAC TCAT		
		GTGTGTAGGTGTG GGTA		
		T TCTTGGT		
GAM1309	FLJ31121	3' TGGTGTGTGGATGTGTG 58538	_	
		TACACATCCACAC TCA		
		GTGTGTAGGTGTG GGT		
		T		
GAM1309	FLJ32356	3' GAGTGGTGTGGGTGTG 58361	T	
		CACATCCACAC CATTG		
		GTGTGGGTGTG GTGAG		
		-		
GAM1309	GRASP1	3' TGGGGATGCTGGGTGGGTGTGT 39304	ACT_	
	G	TACACATCCAC CATTCTCA		
		GTGTGTGGGTG GTAGGGGT		
		GGTC		
GAM1309	HIF1AN	3' GAGAGGATGCGTGTGGATGTGT 61974	T	A
	G	TACACATCCACAC CATTCTC		
		GTGTGTAGGTGTG GTAGGAG		
		C AGT		
GAM1309	HIF1AN	3' GGGTGTGTGTGTGTGTGTGC 61977	TC	T
		GTACACA CACAC CATTG		
		CGTGTGT GTGTG GTGGG		
		GT T		
GAM1309	HIF1AN	3' TGGGTGTGTGTGTGTG 61981	TC	
		TACACA CAACTCA		
		GTGTGT GTGTGGGT		
		GT		
GAM1309	HSP105B	3' GTGGGTGTGGATGTTTATA 21821	C	
		TGTA ACATCCCACTCAT		
		ATAT TGTAGGTGTGGGTG		
		T		
GAM1309	HTCD37	3' TGAGGGTGTGATGTCTGTA 67681	_ _	A
		TAC ACATC CAC CTCA		

ATG TGTAG GTG GAGT  
 TC T G  
 GAM1309 IMAGE:4215339 3' TGGGGGTGGGCTGTGCGCA 72977 TA \_ A  
 TG CACA TCCAC CTCA  
 || ||| |||| |||  
 AC GTGT GGGTG GGGT  
 GC C G  
 GAM1309 KIAA0053 3' TGAGGGTGAGCAGAGATGTGTG 29676 CACA  
 TACACATC CTCATTCTCA  
 ||||| |||||  
 GTGTGTAG GAGTGGGAGT  
 AGAC  
 GAM1309 KIAA0121 3' GAGACCGGGGTGTGTGTG 72658 TC AT\_  
 CACA CACTC TCTC  
 ||| ||||| |||  
 GTGT GTGTGGG AGAG  
 \_ GCC  
 GAM1309 KIAA0212 3' TGAGGGTGAGTGAGTTAGTACA 27944 ACATCCA  
 TGTAC CACTCATTCTCA  
 |||| |||||  
 ACATG GTGAGTGGGAGT  
 ATTGA\_  
 GAM1309 KIAA0217 3' GAGAGTGAGTGTCTTG 67037 TCC  
 CA ACACTCATTCTC  
 || |||||  
 GT TGTGAGTGAGAG  
 TC\_  
 GAM1309 KIAA0232 3' GGGTGGGTGTGTGTGTGTG 72753 TC  
 TACACA CACTCATTC  
 |||| |||||  
 GTGTGT GTGTGGGTGGG  
 GT  
 GAM1309 KIAA0232 3' TGGGTGTGTGTGTGTGTGTGTG 72761 TC T T  
 C GTACACA CACAC CAT CTCA  
 ||||| |||| ||| |||  
 CGTGTGT GTGTG GTG GGGT  
 GT T T  
 GAM1309 KIAA0252 3' TGAGAGCGAGAGTGTGTATGTG 62799 C A\_  
 TG TACACAT CACTC TTCTCA  
 ||||| ||||| |||||  
 GTGTGTA GTGTGAG GAGAGT  
 T AGC  
 GAM1309 KIAA0275 3' GAGTGTGAGTGTGCA 28680 ATC  
 TGTACAC CACTC  
 ||||| |||||  
 ACGTGTG GTGTGAG  
 A\_  
 GAM1309 KIAA0319 3' GGGAGTGGGTGTTTGTA 29038 CATCC  
 TACA ACACTCATTCTC  
 ||| |||||

	ATGT TGTGGGTGAGGG	
	T____	
GAM1309 KIAA0319	5' TGAACGTGTGTGTGTGTGTGTG 29041	TC T TC
	TACACA CACAC CAT TCA	
	GTGTGT GTGTG GTG AGT	
	GT T CA	
GAM1309 KIAA0408	3' TGAGTTTGTGTGTGTGTGTGTG 28140	TC T TT
	TACACA CACAC CA CTCA	
	GTGTGT GTGTG GT GAGT	
	GT T TT	
GAM1309 KIAA0635	3' TGAAGTGTGTGTGTGTGTGTG 27699	TC T C
	TACACA CACAC CATT TCA	
	GTGTGT GTGTG GTGA AGT	
	GT T _	
GAM1309 KIAA0677	3' TGGGGATAACATGGGTGTGTGC 27834	CACTC
	GTACACATCCA ATTCTCA	
	CGTGTGTGGGT TAGGGGT	
	ACAA_	
GAM1309 KIAA0865	3' TGAGATCCCGTGTGTGTGTGTG 61251	TC T ____
	TGTG ACACA CACAC CAT TCTCA	
	TGTGT GTGTG GTG AGAGT	
	GT T CCCT	
GAM1309 KIAA1025	3' TGAGGACAGTGGGTGTGTAC 63978	ACTCA
	GTACACATCCAC TTCTCA	
	CATGTGTGGGTG AGGAGT	
	AC__	
GAM1309 KIAA1161	5' GAAGAGTGTGCGTGTGTG 81751	C A
	TACACAT CACTC TTC	
	GTGTGTG GTGTGAG AAG	
	C _	
GAM1309 KIAA1257	3' TGGGGACACTTGGCTGTGTG 62763	T CACTCA
	TACACA CCA TTCTCA	
	GTGTGT GGT AGGGGT	
	C TCAC__	
GAM1309 KIAA1260	5' TGGGACAGCTGTGGATGTG 60031	_ CAT
	CACATCCACA CT TCTCA	
	GTGTAGGTGT GA AGGGT	
	C C__	
GAM1309 KIAA1266	3' GAGGGTGGGGCCTGTGTCA 66119	T TCCACA
	TG ACACA CTCATTCTC	



		AC TGTGT	GGGTGGGAG		
		— CCG___			
GAM1309	KIAA1322	3'	TGAGGATGGCCACTGATGTGTG 72742	CACAC	
			TACACATC TCATTCTCA		
			GTGTGTAG GGTAGGAGT		
			TCACC		
GAM1309	KIAA1340	3'	GAGGTTGTGTGTGTGTGTG 69182	TC	T TT
			CACA CACAC CA CTC		
			GTGT GTGTG GT GAG		
			GT T TG		
GAM1309	KIAA1340	3'	TGGGGGTGTGTGTGTGTGTGTG 69186	TC	T
			TACACA CACAC CATTCTCA		
			GTGTGT GTGTG GTGGGGGT		
			GT T		
GAM1309	KIAA1357	3'	TGGGTGTGTATGTGTGCA 71983	C	
			TGTACACAT CACACTCA		
			ACGTGTGTA GTGTGGGT		
			T		
GAM1309	KIAA1364	3'	TGAGGGTGAGAGATGCTGTG 63598	—	CACA
			TACA CATC CTCATTCTCA		
			GTGT GTAG GAGTGGGAGT		
			C A___		
GAM1309	KIAA1374	3'	TGAGGATGGATTTGTACA 61243	C	CA
			TGTACA ATCCA CTCA		
			ACATGT TAGGT GAGT		
			T AG		
GAM1309	KIAA1484	3'	TGTAGTGTGTGTGTGTG 69981	TC	—
			TACACA CACACT CA		
			GTGTGT GTGTGA GT		
			GT T		
GAM1309	KIAA1546	3'	TGAGAGTGAAAGCATTGTGTA 67911	TCCACAC	
			TACACA TCATTCTCA		
			ATGTGT AGTGAGAGT		
			TACGAA_		
GAM1309	KIAA1804	3'	TGGCGTGTGTGTGTGTGCA 69793	TC	—
			TGTACACA CACAC TCA		
			ACGTGTGT GTGTG GGT		
			GT C		
GAM1309	KIAA1821	3'	TGGGGACTTGGGTGTGACA 71799	A	CA___
			TGT CACATCCA CTCA		

		ACA GTGTGGGT GGGT		
		_ TCAG		
GAM1309 KIAA1884	3'	GGATCTGTGTGTGTGTGTG 73338	TC	TC
		TACACA CACAC ATTC		
		GTGTGT GTGTG TAGG		
		GT TC		
GAM1309 KIAA1962	3'	GGGTGTGTGTGCATGTGTG 81919	C	T
		TACACAT CACAC CATTG		
		GTGTGTA GTGTG GTGGG		
		C T		
GAM1309 KLF5	3'	TGGGGGTGAAGGGGAGTGTGTG 8186	_	ACAC
CA		TGTACACA TCC TCATTCTCA		
		ACGTGTGT AGG AGTGGGGGT		
		G GGA_		
GAM1309 LAT1-3TM	5'	TGAGGGGGATGGTTGTGTG 68601	T	CA ATT
		TACACA CCA CTC CTCA		
		GTGTGT GGT GGG GAGT		
		T AG _		
GAM1309 LETAL	5'	TGAGGGTGAATGTGTACA 57523	C	A
		TGTACACAT CAC CTCA		
		ACATGTGTA GTG GAGT		
		A G		
GAM1309 LPAAT-delta	3'	TGAGAATGGCTGTGTGGTGAGT 39292	AT_	_
GTG		TACAC CCACAC TCATTCTCA		
		GTGTG GGTGTG GGTAAGAGT		
		AGT TC		
GAM1309 LW-1	5'	TGGGGACCGACAGTGTGGGTGT 60262	T	CA_
GTTA		ACACATCCACACT TTCTCA		
		TGTGTGGGTGTGA AGGGGT		
		T CAGCC		
GAM1309 LW-1	5'	TGGGGACCGACAGTGTGGGTGT 32371	T	CA_
GTTA		ACACATCCACACT TTCTCA		
		TGTGTGGGTGTGA AGGGGT		
		T CAGCC		
GAM1309 MGC12466	3'	TGAGTTCATGTGTGTGTGTG 79035	TC	T T_
TG		TACACA CACAC CAT CTCA		
		GTGTGT GTGTG GTA GAGT		
		GT T CTT		
GAM1309 MGC12466	3'	TGAGTTCATGTGTGTGTGTG 52631	TC	T T_
TG		TACACA CACAC CAT CTCA		

		GTGTGT GTGTG GTA GAGT	
		GT T CTT	
GAM1309	MGC17299 3'	TGGGGATGAAATGTCATTGTGT 58241	TCC C_
	AT	GTACACA ACA TCATTCTCA	
		TATGTGT TGT AGTAGGGGT	
		TAC AA	
GAM1309	MGC20496 3'	GAGCCGTGTGTGTGTGTGTG 53431	TC T T_
		CACA CACAC CAT CTC	
		GTGT GTGTG GTG GAG	
		GT T CC	
GAM1309	MGC4309 3'	TGAGGTGTGGGTGTGGC 44134 A	_
		GT CACATCCACAC TCA	
		CG GTGTGGGTGTG AGT	
		_ G	
GAM1309	MGC4309 3'	TGGGGATGGGCTGCTGTGTG 44135	CCA _
		CACAT CA CTCATTCTCA	
		GTGTG GT GGGTAGGGGT	
		TC_ C	
GAM1309	MGC4549 3'	GGTGTGAGTGAGTGTGGGTGTG 50466	T
	TG	TACACATCCACACTCATTC CA	
		GTGTGTGGGTGTGAGTGAG GT	
		T GGG	
GAM1309	MGC4549 3'	TGGGTGTGCGTGTGGGTGTG 50468	T T
		CACATCCACAC CAT CTCA	
		GTGTGGGTGTG GTG GGGT	
		C T	
GAM1309	MKRN1 3'	TGAGTGTGTGGGTGTGTG 25576	TCATT
		TACACATCCACAC CTCA	
		GTGTGTGGGTGTG GAGT	
		T_	
GAM1309	MKRN4 3'	GTGTGTGTGAGTGTGGGTGTGT 47755	TCTCA
	G	TACACATCCACACTCAT	
		GTGTGTGGGTGTGAGTG	
		TGTGTGG	
GAM1309	MKRN4 3'	TGGGTGTGTGAGTGTGGGTGTG 47758	T_
	TG	TACACATCCACACTCAT CTCA	
		GTGTGTGGGTGTGAGTG GGGT	
		TGT	
GAM1309	MOST2 5'	TGAGGATGTTGCTGTGTGTGTG 39694	TC _ CT
	C	GTACACA CA CA CATTCTCA	

			CGTGTGT GT GT GTAGGAGT		
			GT C T_		
GAM1309	MRPS10	3'	TGAGGGTGGGCCAGATGAGTAT 36299	A	CACA
			GTAC CATC CTCATTCTCA		
			TATG GTAG GGGTGGGAGT		
			A ACC_		
GAM1309	NUDT3	3'	TGAGGGTGGGGGTGGGTGTGT 21989		CA_
	A		TACACATCCA CTCATTCTCA		
			ATGTGTGGGT GGGTGGGAGT		
			TGG		
GAM1309	ODZ2	3'	TGGGGGTGATTTGTGTGTA 70859		CCACAC
			TACACAT TCATTCTCA		
			ATGTGTG AGTGGGGGT		
			TTT_		
GAM1309	PIP5K2A	3'	TGGGGGGGGGTGAGTGTGTGC 17263	TC	A A
			GTACACA CAC CTC TTCTCA		
			CGTGTGT GTG GGG GGGGGT		
			GA _ _		
GAM1309	PLCL1	3'	GGAAGAGTGTGTGTGTGTG 20634	TC	A
			TACACA CACTC TTCT		
			GTGTGT GTGTGAG AAGG		
			GT _		
GAM1309	POMT2	3'	TGGGAGTGGGTGCGCGTGTGTG 25397		CCA_
	TAT		GTACACAT CACTCATTCTCA		
			TATGTGTG GTGGGTGAGGGT		
			TGCGC		
GAM1309	PPFIA4	3'	GGGTGTGTGTGGGTGGGTG 70329	A	T
			TAC CATCCACAC CATTC		
			GTG GTGGGTGTG GTGGG		
			G T		
GAM1309	PPFIA4	3'	GTGGGTGTGAGTGTGGGTGTGT 70330		T
	AC		GTACACATCCCACTCAT CTCA		
			CATGTGTGGGTGTGAGTG GGGT		
			T GG		
GAM1309	PPFIA4	3'	TGGGTGTATGGGTGTGTG 70335		_
			TACACATCC AACTCA		
			GTGTGTGGG TGTGGGT		
			TA		
GAM1309	PPFIA4	3'	TGGGTGTGAGTGTGGGTGTGTA 70336		T
	C		GTACACATCCCACTCAT CTCA		

			CATGTGTGGGTGTGAGTG GGGT		
			T		
GAM1309	PYPAF6	3'	GATGTGTGTGTGTGTGTG 58764	TC	T
			TACACA CACAC CATT		
			GTGTGT GTGTG GTAG		
			GT T		
GAM1309	RANBP6	3'	TGAGGATGAATGTGATGTTTAT 61640	C	C C
	A		TGTA ACATC ACA TCATTCTCA		
			ATAT TGTAG TGT AGTAGGAGT		
			T _ A		
GAM1309	RAP2B	3'	TACTATGGTGTGTGTGTGTAT 95823	TC	T TCTCA
			GTACACA CACAC CAT		
			TATGTGT GTGTG GTA		
			GT _ TCATG		
GAM1309	RPS6KB2	3'	TGGGGGTGGGGTGTGAGTGCGT 14202	A TC	_
	AT		GTAC CA CACACTC ATTCTCA		
			TATG GT GTGTGGG TGGGGGT		
			C GA G		
GAM1309	SLC34A1	3'	TGAGAGTGTGCGGTGTGTGTGCA 11748	TC	ACT
			TGTACACA CAC CATTCTCA		
			ACGTGTGT GTG GTGAGAGT		
			_ GCT		
GAM1309	SMOC2	5'	TGGGTGTGCGTGTGTG 72380	C	
			TACACAT CACACTCA		
			GTGTGTG GTGTGGGT		
			C		
GAM1309	SRF	3'	TGGGGTATGTGTGTGTGGGTGT 11952	T	___
	GTGC		ACACATCCACAC CAT TCTCA		
			TGTGTGGGTGTG GTG GGGGT		
			T TAT		
GAM1309	STARD7	3'	TGGGATGTGGATGGATGTGTGC 57699	CACT	CA
	A		TGTACACATCCA CATTCT		
			ACGTGTGTAGGT GTAGGG		
			AGGT T		
GAM1309	STARD7	3'	TGGGATGTGGATGGATGTGTGC 39332	CACT	CA
	A		TGTACACATCCA CATTCT		
			ACGTGTGTAGGT GTAGGG		
			AGGT T		
GAM1309	STMN4	3'	TGAGGTCTGTGTGTGTGTG 47928	TC	TCAT
			TACACA CACAC TCTCA		

			GTGTGT GTGTG GGAGT		
			GT TCT_		
GAM1309	TBX21	3'	GGTTGTGTGTGGGTGTGTG 25328	T TT	
			TACACATCCACAC CA C		
			GTGTGTGGGTGTG GT G		
			T TG		
GAM1309	TCL6	3'	TGAGTATGTGTATGTGTAT 40118	C _	
			GTACACAT CAC ACTCA		
			TATGTGTA GTG TGAGT		
			T TA		
GAM1309	TCL6	3'	TGAGTATGTGTATGTGTAT 40150	C _	
			GTACACAT CAC ACTCA		
			TATGTGTA GTG TGAGT		
			T TA		
GAM1309	TGOLN2	3'	TGAGGGTGAGTGGAGGGGTATA 64051	ACA A_	
			TGTAC TCC CACTCATTCTCA		
			ATATG GGG GTGAGTGGGAGT		
			_ AG		
GAM1309	TOR1B	3'	TGAGCTGACCTGTGTGTGTGTG 27207	TC _ TT	
	TG		TACACA CACAC TCA CTCA		
			GTGTGT GTGTG AGT GAGT		
			GT TCC C_		
GAM1309	TTY8	3'	AGGGGTGTGTGTGTGTGTG 50850	TC T CA	
			CACA CACAC CATTCT		
			GTGT GTGTG GTGGGG		
			GT T AT		
GAM1309	VPS39	3'	AGGGTGGGTGATGGTG 62842	T _	
			CA CCA CACTCATTCT		
			GT GGT GTGGGTGGGA		
			_ A		
GAM1309	WBSCR17	3'	AGGGTGTGTGTGTGTGTG 81296	TC T	
			CACA CACAC CATTCT		
			GTGT GTGTG GTGGGA		
			GT T		
GAM1309	ZNF294	3'	TGAGAGTGAAGTACTATGTGTG 70830	CCAC _	
			TACACAT ACT CATTCTCA		
			GTGTGTA TGA GTGAGAGT		
			TCA_ A		
GAM1309	ZNF33A	3'	GAGGTGGATGTTGCA 91349	C A	
			TGTA ACATCCAC CTC		

ACGT TGTAGGTG GAG

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      - -
GAM1309 LOC113251 3' TGTTGTGGGTGTGAGTGTGTAC 53525   TC   TCTCA
      A           TGTACACA CACACTCAT
                ||||| |||||
                ACATGTGT GTGTGGGTG
                  GA   TTGT
GAM1309 LOC116150 3' TGAGAGTGAGTGTGTGTGTGTG 56639   TC
      C           GTACACA CACACTCATTCTCA
                ||||| |||||
                CGTGTGT GTGTGAGTGAGAGT
                  GT
GAM1309 LOC126037 3' TGAGTGTGTGTATGTGTGC 74435   C__
                GTACACAT CACACTCA
                ||||| |||||
                CGTGTGTA GTGTGAGT
                  TGT
GAM1309 LOC134637 3' GGTTTTGTGTGTGTGTGTGTG 75202   TC   T TT_
                TACACA CACAC CA  CT
                ||||| ||||| ||
                GTGTGT GTGTG GT  GG
                  GT   T TTT
GAM1309 LOC143098 5' TGGGAGTGACACTGGTCTGTAT 76457   CAT  CAC
                GTACA CCA TCATTCTCA
                ||||| ||| |||||
                TATGT GGT AGTGAGGGT
                  CT_ CAC
GAM1309 LOC144524 3' TGGGTGTGGAGGTGTAT 83141   A
                GTACAC TCCACACTCA
                ||||| |||||
                TATGTG AGGTGTGGGT
                  G
GAM1309 LOC144596 3' GGGGTGTGTGTGTGTG 76907   TC   T
                CACA CACAC CATTCT
                ||||| ||||| |||||
                GTGT GTGTG GTGGGG
                  _   T
GAM1309 LOC145098 5' GAGTTGGATGTGTAT 76992   C
                GTACACATCCA ACTC
                ||||| ||||| |||||
                TATGTGTAGGT TGAG
      -
GAM1309 LOC145717 5' GGGGGTGAGTCTGTGTTTG 66832   TC   _
                CA CAC ACTCATTCTC
                || ||| |||||
                GT GTG TGAGTGGGGG
                  TT TC
GAM1309 LOC145800 5' GGGGAGCTGGGTGTGTG 77503   CA  ATT
                TACACATCCA CTC CTC
                ||||| ||| |||
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		GTGTGTGGGT GAG GGG		
		C_ ____		
GAM1309	LOC146237 3'	TGAGCACACGTGTGTGTGTGTA	83636	TC TCATT
	T	GTACACA CACAC CTCA		
		TATGTGT GTGTG GAGT		
		GT CACAC		
GAM1309	LOC146667 5'	TGCAGTGTGTGTGTGTG	83710	TC _
		TACACA CACACT CA		
		GTGTGT GTGTGA GT		
		GT C		
GAM1309	LOC147040 3'	AGGGTGTGTGTGTGTGTG	78228	TC T
		CACA CACAC CATTCT		
		GTGT GTGTG GTGGGA		
		GT T		
GAM1309	LOC147341 5'	TGGGGGTGAGGGGGAGTGGGTG	83997	A_____
	TGTG	CACATCCAC CTCATTCTCA		
		GTGTGGGTG GAGTGGGGGT		
		AGGGG		
GAM1309	LOC148014 3'	GGGGTGTGTGTGTGTGTGC	78611	TC T
		GTACACA CACAC CATTCT		
		CGTGTGT GTGTG GTGGGG		
		_ T		
GAM1309	LOC148113 3'	GGGGAGCTGGTTGTGGGTGTG	78668	CT _ A
		CACATCCACA CA TTCTC		
		GTGTGGGTGT GT GAGGG		
		TG C GT		
GAM1309	LOC148932 3'	GGGGTGTGTGTGTGTGTG	79111	TC T
		CACA CACAC CATTCT		
		GTGT GTGTG GTGGGG		
		GT T		
GAM1309	LOC149182 5'	GGTGAGGATGTGTACA	84375	A
		TGTACACATCC CACT		
		ACATGTGTAGG GTGG		
		A		
GAM1309	LOC149535 5'	TGAGTCTCTGTGTGGGTCTGTG	79422	_ TCATT
	TG	TACACA TCCACAC CTCA		
		GTGTGT GGGTGTG GAGT		
		CT TCTCT		
GAM1309	LOC149684 5'	TGGGGATGTTGTGTGTGTATA	84620	TC CT
		TGTACACA CACA CATTCTCA		



	ATATGTGT GTGT GTAGGGGT		
	— T—		
GAM1309 LOC150236 3'	TGGGGGTGGGGCGTGTGT 79692	CCACA	
	ACACAT CTCATTCTCA		
	TGTGTG GGGTGGGGGT		
	CG—		
GAM1309 LOC150406 3'	ATGGGTGTGTGTGTGTG 79856	TC	
	TACACA CACACTCAT		
	GTGTGT GTGTGGGTA		
	GT		
GAM1309 LOC150406 3'	TGGGTGTGTGTGTGTGTGTGTG 79858	TC	T T
	TACACA CACAC CAT CTCA		
	GTGTGT GTGTG GTG GGGT		
	GT T T		
GAM1309 LOC151242 3'	TAGACATGAGTGTGTGTGTGTG 80179	TC	_ CA
	TACACA CACACTCAT TCT		
	GTGTGT GTGTGAGTA AGA		
	GT C T		
GAM1309 LOC151242 3'	TGAGTGTGTGTGTGTGTGTGTG 80180	TC	T T
	TACACA CACAC CAT CTCA		
	GTGTGT GTGTG GTG GAGT		
	GT T T		
GAM1309 LOC151475 3'	GAATGTGTGGGTGTGTG 85403	TC	
	TACACATCCACAC ATTC		
	GTGTGTGGGTGTG TAAG		
	—		
GAM1309 LOC152633 5'	TGAGCGTGTGTGTGTGTGTGCA 85825	TC	T T
	TGTACACA CACAC CAT CTCA		
	ACGTGTGT GTGTG GTG GAGT		
	— T C		
GAM1309 LOC152762 3'	GGAAGTGGAGTGTGC 80652	A	CACTCA
	GTACAC TCCA TTCT		
	CGTGTG AGGT AAGG		
	— C—		
GAM1309 LOC153346 3'	GGGGGTGTGTGTGTGTGTA 86025	TC	T
	TACACA CACAC CATTCTC		
	ATGTGT GTGTG GTGGGGG		
	— T		
GAM1309 LOC153346 3'	GTGGTGGGGGTGTGTG 86026	A	T
	TACACATCC CAC CAT		

		GTGTGTGGG GTG GTG	
		G _	
GAM1309	LOC155061 3'	TGGGGATGGGGTCCTGTGTGTG 81271	CC_ A
	C	GTACACAT AC CTCATTCTCA	
		CGTGTGTG TG GGGTAGGGGT	
		TCC _	
GAM1309	LOC155438 5'	GGGTGTGAATGTGTACA 86396	C
		TGTACACAT CAACTC	
		ACATGTGTA GTGTGGG	
		A	
GAM1309	LOC157653 5'	TGAGAATGTGTAGATGTGTGTC 81530	_ C TC
	A	TG TACACATC ACAC ATTCTCA	
		AC GTGTGTAG TGTG TAAGAGT	
		T A _	
GAM1309	LOC157653 5'	TGAGTCTCTGTGTGTGTGTGTG 81531	TC TCATT
		TACACA CACAC CTCA	
		GTGTGT GTGTG GAGT	
		GT TCTCT	
GAM1309	LOC157737 5'	TGGGGATGGGAAAGAAGGTGTG 86541	ATCCACA
	C	GTACAC CTCATTCTCA	
		CGTGTG GGGTAGGGGT	
		GAAGAAA	
GAM1309	LOC158014 5'	GGGGTGTGTGTGTGTGTG 81655	TC T
		CACA CACAC CATTCT	
		GTGT GTGTG GTGGGG	
		GT T	
GAM1309	LOC161528 5'	GGGGGTGAGTCTGTGTTTG 82279	TC _
		CA CAC ACTCATTCTC	
		GT GTG TGAGTGGGGG	
		TT TC	
GAM1309	LOC170082 3'	TGGGGGTTTGTGTGTATGTGTG 82568	C TC
		TACACAT CACAC ATTCTCA	
		GTGTGTA GTGTG TGGGGGT	
		T TT	
GAM1309	LOC196527 3'	TGGGGAAATTGATGGGTGTGGC 87759	A _ CTCA
	A	TGT CACATCCA CA TTCTCA	
		ACG GTGTGGGT GT AGGGGT	
		_ A TAA_	
GAM1309	LOC196988 5'	GGGGAGCTGGGTGTGTG 87857	CA ATT
		TACACATCCA CTC CTC	

	GTGTGTGGGT GAG GGG		
	C_ ____		
GAM1309 LOC197135 5'	GAGGGTGGGTGTTTATG 87892 CC		
	CAT ACACTCATTCTC		
	GTA TGTGGGTGGGAG		
	TT		
GAM1309 LOC201564 3'	TGGGATCCCGTGTGTGTGTGTG 80439 TC T ____		
	TGTG ACACA CACAC CAT TCTCA		
	TGTGT GTGTG GTG AGGGT		
	GT T CCCT		
GAM1309 LOC202025 5'	GAATGTGTGTGTGTGTGTG 90288 TC T		
	TACACA CACAC CATT		
	GTGTGT GTGTG GTAAG		
	GT T		
GAM1309 LOC202025 5'	TGAGAAGTGAATGTGTGTGTGT 90299 TC _ _		
	GTG ACACA CACAC TCATT CTCA		
	TGTGT GTGTG AGTGA GAGT		
	GT TA A		
GAM1309 LOC219940 5'	TGGGGCGACAGGTGGATGAGTG 93360 A ACTCAT		
	TAC CATCCAC TCTCA		
	GTG GTAGGTG GGGGT		
	A GACAGC		
GAM1309 LOC220846 3'	GGTGTGTGTGTGTGTGTG 90819 TC T		
	TACACA CACAC CATT		
	GTGTGT GTGTG GTGG		
	GT T		
GAM1309 LOC220963 3'	AAACGTGAGTGTGTGTGTGTG 91444 TC TCTCA		
	TACACA CACACTCAT		
	GTGTGT GTGTGAGTG		
	GT CAAAT		
GAM1309 LOC220963 3'	TGAGTGTGTGTGTGTGTGTG 91452 TC T T		
	TACACA CACAC CAT CTCA		
	GTGTGT GTGTG GTG GAGT		
	GT T T		
GAM1309 LOC221143 3'	TGGGAGTGAAATGCATGTG 93570 C CAC		
	CACAT CA TCATTCTCA		
	GTGTA GT AGTGAGGGT		
	C AA_		
GAM1309 LOC221178 3'	GGCATGTGTGGGGGTGTGTG 93535 A T T		
	TACACATCC CAC CAT CT		

	GTGTGTGGG GTG GTA GG		
	G T C		
GAM1309 LOC221178 3'	GGGTGTGTGTGTGTAT	93538	TC
	GTACACA CACTC		
	TATGTGT GTGTGGG		
	GT		
GAM1309 LOC221337 3'	TGAGGCTGTGTGTGTGTGTG	92115	TC T TT
	TACACA CACAC CA CTCA		
	GTGTGT GTGTG GT GAGT		
	GT T CG		
GAM1309 LOC221466 5'	TGAGGCTGATGTGGATGT	93695	C TT
	ACATCCACA TCA CTCA		
	TGTAGGTGT AGT GAGT		
	_ CG		
GAM1309 LOC221466 3'	TGATGTGTGGAGTGTGC	93696	A _
	GTACAC TCCACAC TCA		
	CGTGTG AGGTGTG AGT		
	_ T		
GAM1309 LOC221490 5'	TGGGTGTGTGTGTGTG	93669	TC
	TACACA CACTCA		
	GTGTGT GTGTGGGT		
	GT		
GAM1309 LOC221490 5'	TGGGTGTGTGTGTGTG	93670	TC
	TACACA CACTCA		
	GTGTGT GTGTGGGT		
	GT		
GAM1309 LOC222166 3'	TGAGAGTGAGAGATGTGTA	94100	CACA
	TACACATC CTCATTCTCA		
	ATGTGTAG GAGTGAGAGT		
	A__		
GAM1309 LOC245727 5'	GGGGGTGAGTCTGTGTTTG	91129	TC _
	CA CAC ACTCATTCTC		
	GT GTG TGAGTGGGGG		
	TT TC		
GAM1309 LOC253070 3'	TGGGTGTGGGTGTGCATGTGTG	97014	C T
	TACACAT CACTCAT CTCA		
	GTGTGTA GTGTGGGTG GGGT		
	C T		
GAM1309 LOC253681 3'	AGGGTGTGTGTGTGTGTG	95125	TC T
	CACA CACAC CATTCT		

	GTGT GTGTG GTGGGA	
	GT T	
GAM1309 LOC253816 3'	TGAGGGGATCCTGGATGTGTG 94389	CAC A
	TACACATCCA TC TTCTCA	
	GTGTGTAGGT AG GGGAGT	
	CCT _	
GAM1309 LOC254251 3'	TGAGTGTGTGTGTGTGTGTG 95912	TC T T
	TACACA CACAC CAT CTCA	
	GTGTGT GTGTG GTG GAGT	
	GT T T	
GAM1309 LOC254251 3'	TGTTTGTGAGTGTGTGTGTGTG 95913	TC TCT
	TACACA CACACTCAT CA	
	GTGTGT GTGTGAGTG GT	
	GT TTT	
GAM1309 LOC254685 3'	GGGTTGTGTGTGTGTGTG 96486	TC T TT
	CACA CACAC CA CTC	
	GTGT GTGTG GT GGG	
	GT T T_	
GAM1309 LOC256283 5'	GAGTGTGTGTGAGTGTGTG 97038	TC T
	TACACA CACAC CATTG	
	GTGTGT GTGTG GTGAG	
	GA T	
GAM1309 LOC51195 3'	TGAGGGTGGATGTTGTGTGTGC 32949	CC CT
	GTACACAT ACA CATTCTCA	
	CGTGTGTG TGT GTGGGAGT	
	T_ AG	
GAM1309 LOC51200 3'	TGGTTTGTGTGTGTGTGTGTG 33005	TC T TT CA
	TACACA CACAC CA CT	
	GTGTGT GTGTG GT GG	
	GT T TT T	
GAM1309 LOC55924 3'	TGAGCTGTGCGTGTGTGTGTG 38876	TC T T_
G	TACACA CACAC CAT CTCA	
	GTGTGT GTGTG GTG GAGT	
	GT C TC	
GAM1309 LOC64744 3'	GTGAGTGTGTGTGTGTG 61799	TC
	TACACA CACACTCAT	
	GTGTGT GTGTGAGTG	
	GT	
GAM1309 LOC64744 3'	TGAGTGTGTGTGTGTG 61802	TC
	TACACA CACACTCA	

		GTGTGT GTGTGAGT		
		GT		
GAM1309	LOC88523	5' TGGGGATGAGGTTCTGGTACA 52410	A	TCC A
		TGTAC CA AC CTCATTCTCA		
		ACATG GT TG GAGTAGGGGT		
		_ CT_ _		
GAM1309	LOC90538	3' TGGGGGGCCTGTGGCTGTGTAT 63199	T	CTCA
	A	TGTACACA CCACA TTCTCA		
		ATATGTGT GGTGT GGGGGT		
		C CCG_		
GAM1309	LOC91585	3' GAGTGTGTGTGTGTGTAT 66578	TC	T
		GTACACA CACAC CATTCTC		
		TATGTGT GTGTG GTGAG		
		GT T		
GAM1309	LOC91585	3' GTATCTGAGTGTGTGTGTGTG 66580	TC	TTCTCA
		TACACA CACACTCA		
		GTGTGT GTGTGAGT		
		GT CTATGT		
GAM1309	LOC91694	3' AGAGAGTGTGTGTGTGTGTG 66960	TC	T A
	C	GTACACA CACAC CATTCTC		
		CGTGTGT GTGTG GTGAGAG		
		GT T AG		
GAM1309	LOC91694	3' GGGGGTTGGGTAGTGTGTG 66963	TC	_ _
		CACA CAC ACTCA TTCTC		
		GTGT GTG TGGGT GGGGG		
		_ A T		
GAM1309	LOC91768	3' TGGGGCGTGTGGGTGTGTG 67119		TCAT
		TACACATCCACAC TCTCA		
		GTGTGTGGGTGTG GGGGT		
		C_		
GAM1309	LOC93626	3' GGGCATGTGGGGTGTGTG 72773	A	TCATT
		TACACATCC CAC CTC		
		GTGTGTGGG GTG GGG		
		_ TAC_		
GAM1310	ADH1B	3' CTTAGACATAAAGTAAAAT 72644	C	CAC
		ATTT ACTTT TGTCTGAG		
		TAAA TGAAA ACAGATTC		
		A T_		
GAM1310	AHR	3' ATCTCAGATGTTAAAATAAATG 7875	CAC	C T
		CATTT TTT AC GTCTGAGAT		

			GTAAA AAA TG TAGACTCTA		
			TA_ T _		
GAM1310	FDFT1	3'	TAGGAAAGTGAAATG 15518	A	
			CATTTCACTTTC CTG		
			GTAAAGTGAAAG GAT		
			-		
GAM1310	JTB	3'	ATCTCAGACAGTGAAAGTGAAA 21959		
	TG		CATTTCACTTTCACTGTCTGAGAT		
			GTAAAGTGAAAGTGACAGACTCTA		
GAM1310	KLF4	3'	TCCCAGACAGTGGATATG 14891	CT	A
			CA TTCACTGTCTG GA		
			GT AGGTGACAGAC CT		
			AT C		
GAM1310	PHYH	3'	ACAGTAAAAGTGAAAT 20608	C	
			ATTTCACTTT ACTGT		
			TAAAGTGAAA TGACA		
			A		
GAM1310	PKD2	3'	TCCAGGTTGAAAGTGAAA 60096	CTG	A
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T_ _		
GAM1310	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1310	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA	CTG
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1310	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT	CT
			TTCACCTTCA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1310	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G	T_
			CTTTCACT TC GAGAT		
			GAAAGTGA AG TTCTA		
			G TC		
GAM1310	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT 45802	ACTTTCACT	
	G		CATTTC GTCTGAGAT		

		GTAAAG	CAGACTCTA		
		AAACATTT_			
GAM1310	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281	CTT	
			CATTTCA TCACTGTCTGAGAT		
			GTAAAGT AGTGACAGACTCTA		
			C_		
GAM1310	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C	TC
			TTCA TTCACTG TGAG		
			AAGT AAAGTGAC GTTT		
			A CT		
GAM1310	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A	_
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1310	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T	
			ATT CACTTTCACTGT		
			TAA GTGAAAGTGACG		
			C		
GAM1310	PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA 53598	CA	G
			TTCACTTT CT TCTGAGAT		
			AAGTGAAA GG AGACTCTA		
			CC G		
GAM1310	PP35	3'	ATCTCAGACTGAAA 22814	CT	
			TTTCA GTCTGAGAT		
			AAAGT CAGACTCTA		
			—		
GAM1310	PRTD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148	TCAC	C_
			CATTTCACTT TGT TGAG		
			GTAAAGTGAA ACG ACTC		
			TA_ TT		
GAM1310	SEP15	3'	TCCTACAGTAAGAGTGAAA 14934	C	CT
			TTTCACTTT ACTGT GA		
			AAAGTGAGA TGACA CT		
			A TC		
GAM1310	SFXN2	3'	CTCAGGGGAAAAAAGTGAAA 73941	CACTG	
			TTTCACTTT TCTGAG		
			AAAGTGAAA GGA CTC		
			AAAGG		
GAM1310	LOC149703	3'	ATCTCAGACAGCCGTTTGAAA 84647	ACTTTCA	
			TTTC CTGTCTGAGAT		



			AAAG GACAGACTCTA		
			GTTTGCC		
GAM1310	LOC154007	3'	ATCTCAAACCCTTTAGTGAAA	81015	TTCACT C
			TTTCACT GT TGAGAT		
			AAAGTGA CA ACTCTA		
			TTTCC_ A		
GAM1310	LOC155004	3'	TCATTTAAGTGAAAAGGAAA	81226	A GTC_
			TTTC CTTTCACT TGA		
			AAAG GAAAGTGA ACT		
			_ ATTT		
GAM1310	LOC222134	5'	ACAGTGAAGTGAAATG	94136	T
			CATTTCACTT CACTGT		
			GTAAAGTGAA GTGACA		
			-		
GAM1311	ABR	3'	AGGCGGTGAACTTGAGTCT	6569	C TC
			AGAC CAGGTTTCAT CCT		
			TCTG GTTCAAGTG GGA		
			A GC		
GAM1311	ABR	3'	AGGCGGTGAACTTGAGTCT	41721	C TC
			AGAC CAGGTTTCAT CCT		
			TCTG GTTCAAGTG GGA		
			A GC		
GAM1311	ANGPT2	3'	GATGAACCCGAGGCTGA	6705	A CA_
			TCAG CC GGTTCATT		
			AGTC GG CCAAGTAG		
			_ AGC		
GAM1311	CALCRL	5'	AAGAGAAAATGTGATTTGAGTC	19385	C _ CC
	TGG		TCAGAC CAGGTT CATT CTCTT		
			GGTCTG GTTTAG GTAA GAGAA		
			A T AA		
GAM1311	CHRNA2	3'	AAGAGAGAGGCCTGGGTGTGA	5621	G TCA C
			TCA ACCCAGGT TTC CTCTT		
			AGT TGGGTCCG GAG GAGAA		
			G _ A		
GAM1311	DLX4	3'	AGGAATGGAGCAGAGCCTG	8651	A_ C_
			CAGGTTC TTCC TCTT		
			GTCCGAG GAGG AGGA		
			AC TA		
GAM1311	DLX4	3'	AGGAATGGAGCAGAGCCTG	56275	A_ C_
			CAGGTTC TTCC TCTT		

			GTCCGAG GAGG AGGA	
			AC TA	
GAM1311 DSC3	3'	AAGAGAGAGCTTCCTAGGCCTG 44335	A C TTCA C	
G		TCAG CC AGG TTC CTCTT		
		GGTC GG TCC GAG GAGAA		
		C A TTC_ A		
GAM1311 DSC3	3'	AAGAGAGAGCTTCCTAGGCCTG 8672	A C TTCA C	
G		TCAG CC AGG TTC CTCTT		
		GGTC GG TCC GAG GAGAA		
		C A TTC_ A		
GAM1311 F8	3'	AAGAAAAATGGATCCCAATCTG 3721	CCCA CCC	
A		TCAGA GGTTTCATT TCTT		
		AGTCT CTAGGTAA AGAA		
		AACC AA_		
GAM1311 IL6R	3'	AGAAAAATGAGCCTGG 5116	CCC	
		CCAGGTTTCATT TCT		
		GTCCGAGTAA AGA		
		AA_		
GAM1311 LMO4	3'	GGA CTCCATGAACCTGGGCT 22253	A _____	
		AG CCCAGGTTTCAT TCC		
		TC GGGTCCAAGTA AGG		
		_ CCTC		
GAM1311 MB	3'	AGAGAGAGCGGGGTCTGA 18113	AG ATTCC	
		TCAGACCC GTTC CTCT		
		AGTCTGGG CGAG GAGA		
		G_ A_____		
GAM1311 SLC7A6	3'	AGAGGGAATGCTAGGTT 14297	C GTT	
		GACC AG CATTCCCTCT		
		TTGG TC GTAAGGGAGA		
		A _____		
GAM1311 ZNFN2A1	3'	GGGGAATGAACCTGAATC 60740	CC	
		GA CAGGTTTCATTCCCT		
		CT GTCCAAGTAAGGGG		
		AA		
GAM1311 BRD2	5'	AAGAGGGAATCCCTG 17532	TTC	
		CAGG ATTCCCTCTT		
		GTCC TAAGGGAGAA		
		C_		
GAM1311 BTBD1	3'	AAGAGAAAAGAACTGGGTTT 47473	G A CC	
		AGACCCAG TTC TT CTCTT		

TTTGGGTC AAG AA GAGAA  
 \_ \_ AA  
 GAM1311 CAGE 5' AGGAAGAATGGACCTG 82695 \_  
 CAGGTTTCATT CCT  
 ||||| ||  
 GTCCAGGTAAG GGA  
 AA  
 GAM1311 DKFZp434J1015 3' AAGAGAAAGTGGACCGGGGCTGA 92629 A A CC  
 TCAG CCC GGTTCATT CTCTT  
 ||| || ||||| ||||  
 AGTC GGG CCAGGTGA GAGAA  
 \_ G A\_  
 GAM1311 DKFZp566H0824 5' AGAGAGAAGCTGGACCTGG 34042 \_ C  
 CCAGGTTCA TTC CTCT  
 ||||| || |||  
 GGTCCAGGT AAG GAGA  
 CG A  
 GAM1311 INA 3' AAGAGGGAATGATATGCATTTG 51185 CC GGT  
 A TCAGA CA TCATTCCCTCTT  
 |||| || |||||  
 AGTTT GT AGTAAGGGAGAA  
 AC AT\_  
 GAM1311 KCNS1 3' AAGAGGGAATCATCTGGCCTGA 9570 AC TC  
 TCAG CCAGGT ATTCCCTCTT  
 ||| |||| |||||  
 AGTC GGTCTA TAAGGGAGAA  
 C\_ C\_  
 GAM1311 KIAA1281 5' AGGAAAAGGTGGACCTGG 89150 C\_  
 CCAGGTTTCATT CCT  
 ||||| ||  
 GGTCCAGGTGG GGA  
 AAAA  
 GAM1311 KIAA1281 5' GGTGGACCTGGACTGA 89152 AC  
 TCAG CCAGGTTTCATT  
 ||| |||||  
 AGTC GGTCCAGGTGG  
 A\_  
 GAM1311 KIAA1719 5' AAGAAGGCAGCACGCTGGGCCT 68152 A \_ TCATT C  
 GA TCAG CCCAG GT CC TCTT  
 ||| |||| || |||  
 AGTC GGGTC CA GG AGAA  
 C G CGAC\_ A  
 GAM1311 KRTHB2 5' AGGGGGGAAGCTGAGCCTG 52286 \_  
 CAGGTTCA TTCCCTCTT  
 ||||| |||||  
 GTCCGAGT AAGGGGGGA  
 CG  
 GAM1311 MTO1 3' GAGAGACAGTGAACCTAAACT 56113 ACCC CC  
 GA TCAG AGGTTTCATT CTCTT  
 ||| ||||| ||||

		AGTC TCCAAGTGA GAGAG		
		AAAA CA		
GAM1311 NICE-3	3'	AGGGAATGTTTTGGCACCTGA	31275	AC_ TT
		TCAG CCAGG CATTCCCT		
		AGTC GGTTT GTAAGGGA		
		CAC T_		
GAM1311 P2RXL1	3'	AAGAGAGCTGCAGCCTGGG	18377	_ TTCC
		CCCAGGTT CA CTCTT		
		GGGTCCGA GT GAGAA		
		C CGA_		
GAM1311 LOC155036	5'	AATGATAAACCTGGGTC	86335	___
		GACCCAGGT TCATT		
		CTGGGTCCA AGTAA		
		AAT		
GAM1311 LOC157562	5'	AAGAAGGAATGGGCGGACTTGA	86475	AC AG C
		TCAG CC GTTCATTCC TCTT		
		AGTT GG CGGGTAAGG AGAA		
		CA _ A		
GAM1311 LOC196047	5'	AAGAGGGTGGACCCCAATCTGA	89584	CCCA TT
		TCAGA GGTTC A CCTCTT		
		AGTCT CCAGGT GGGAGAA		
		AACC _		
GAM1311 LOC219405	3'	AAGAGAAAGGCACCTGGGTT	90771	TCA CC
		GACCCAGGT TT CTCTT		
		TTGGGTCCA GA GAGAA		
		CG_ AA		
GAM1311 LOC219731	5'	AAGAGCCTCAACCTGGACCTGA	93087	AC CATTCC
		TCAG CCAGGTT CTCTT		
		AGTC GGTCCAA GAGAA		
		CA CTCC_		
GAM1311 LOC219855	3'	AGGGATGGGACTAGGGCTGA	91512	A A AT
		TCAG CCC GGTTT TCCCT		
		AGTC GGG TCAGG AGGGA		
		_ A GT		
GAM1311 LOC253626	3'	AAGAGGGAACACAAACTCT	97218	CCCAG TCA
		AGA GT TTCCCTCTT		
		TCT CA AAGGGAGAA		
		CAAAA C_		
GAM1311 LOC51027	3'	GAGAGGGAGGACCAGGATCCGA	59364	A C A AT
		TC GA CC GGTTT TCCCTCTT		

AG CT GG CCAGG AGGGAGAG  
 C A A \_  
 GAM1312 AARS 3' TTGCTGCAGAGAATAAAAAG 7833 CAG TATT  
 CTTT TCTT TGCAGCAA  
 |||| ||| |||||  
 GAAA AGAG ACGTCGTT  
 ATA \_  
 GAM1312 ADRA2B 3' TTGCTGCAGGGAGATGAAAAG 5466 G AT  
 CTTTCA TCTTT TTGCAGCAA  
 ||||| ||||| |||||  
 GAAAGT AGAGG GACGTCGTT  
  
 GAM1312 AGRN 3' CTGTGAAATAAAGTCTGAAA 78836 T \_  
 TTTTCA GCTTTATTT GCAG  
 ||||| ||||| |||||  
 AAAGTC GAAATAAA TGTC  
 T G  
 GAM1312 BECN1 3' TTTGCTGCAGTCTGAAAAGTGA 13650 C T\_  
 AA TTTTCA GT TTTA TTGCAGCAAA  
 ||||| ||||| |||||  
 AAAGTCA AAGT GACGTCGTTT  
 A CT  
 GAM1312 CLASP1 3' CTGCAACTGCTAGGACTGAAAAG 65302 TAT\_  
 CTTTCA GTCTT TTGCAG  
 ||||| |||||  
 GAAAGTCAGGA AACGTC  
 TCGTC  
 GAM1312 DNMT3L 5' CTGCAAACCGGCACTGAAGG 25358 \_ TTA  
 CTTTCA GT CT TTTGCAG  
 ||||| || |||||  
 GGAAGTCA GG AAACGTC  
 C CC\_  
 GAM1312 ENC1 3' TTTGCTGCACAAACATGAAA 13287 GTCTTTATT  
 TTTCA TGCAGCAAA  
 |||| |||||  
 AAAGT ACGTCGTTT  
 ACAAAC\_  
 GAM1312 FLRT3 3' CTGCAAAACACTGGAA 25216 CTTTA  
 TTTCA GT TTTGCAG  
 ||||| |||||  
 AAGGTCA AAACGTC  
 CA\_  
 GAM1312 FSTL3 3' AAATAAAGACTCAAAG 19605 C  
 CTTT AGTCTTTATTT  
 |||| |||||  
 GAAA TCAGAAATAAA  
 C  
 GAM1312 KCNK10 3' CTGTGCCATAAACAAGTGAAG 40969 C\_ TT\_  
 CTTTCA GT TTTAT GCAG  
 ||||| ||||| |||||

		GAAAGTCA AAATA TGTC		
		AC CCG		
GAM1312	KCNK10	3' CTGTGCCATAAACTGAAAG 56338	C_	TT_
		CTTTCAGT TTTAT GCAG		
		GAAAGTCA AAATA TGTC		
		AC CCG		
GAM1312	KCNK10	3' CTGTGCCATAAACTGAAAG 56343	C_	TT_
		CTTTCAGT TTTAT GCAG		
		GAAAGTCA AAATA TGTC		
		AC CCG		
GAM1312	RP2	3' TTTGATAAACTAAGACTGAAA 22622	TA	GCAG
		TTTCAGTCTT TTT CAAA		
		AAAGTCAGAA AAA GTTT		
		TC ATA_		
GAM1312	SCA1	5' TGCTGCAAGGAACTGATAG 4401	T	CTTTA
		CT TCAGT TTTGCAGCA		
		GA AGTCA GAACGTCGT		
		T AG__		
GAM1312	VSX1	3' CTGTCAAAGGCTGAAA 27466	ATTT	
		TTTCAGTCTTT GCAG		
		AAAGTCGGAAG TGTC		
		C__		
GAM1312	DKFZP586C1324	3' CTGCATTGGGTGAAGACTAAAA 69797	C	__
		TTT AGTCTTTATT TGCAG		
		AAA TCAGAAGTGG ACGTC		
		A GTT		
GAM1312	DNAH7	3' TGAAATAAATAAAGACTAAAG 38159	C	CAG
		CTTT AGTCTTTATTTG CA		
		GAAA TCAGAAATAAAT GT		
		__ AAA		
GAM1312	EDR1	3' TGCTGCAGGGACTAAAAG 15385	C	TTAT
		CTTT AGTCT TTGCAGCA		
		GAAA TCAGG GACGTCGT		
		A __		
GAM1312	FLJ10305	5' CTGCAGCCAGCACTGAAAG 68359	_	TTAT
		CTTTCAGT CT TTGCAG		
		GAAAGTCA GA GACGTC		
		C CC__		
GAM1312	FLJ10460	3' TTTGCTGCTGGTAATACTGAAA 36135	CT	TT
	G	CTTTCAGT TTAT GCAGCAAA		

		GAAAGTCA AATG CGTCGTTT		
		T_ GT		
GAM1312	FLJ20340	3' TTTGCTACAAAGGGGCTGCAAA 34981	_ TA C	
	G	CTTT CAGTCTT TTTG AGCAAA		
		GAAA GTCGGGG AAAC TCGTTT		
		C _ A		
GAM1312	FLJ22557	3' TGTTGAAAAGACTGAAAG 45256	ATTG	
		CTTTCAGTCTTT CAGCA		
		GAAAGTCAGAAA GTTGT		
		A _		
GAM1312	FLJ22940	5' TGCTGCAGACCAGAAAG 44698	A_ TTATTT	
		CTTTC GTCT GCAGCA		
		GAAAG CAGA CGTCGT		
		AC _		
GAM1312	GBTS1	3' TTGCTGTTGCAAGACTGAAGG 59066	TATTT	
		CTTTCAGTCTT GCAGCAA		
		GGAAGTCAGAA TGTCGTT		
		CGT_		
GAM1312	GT650	3' CTGCTATTCAAAAAGTGAAGAG 53455	C ATTT_	
		CTTTCAGT TTT GCAG		
		GAGAGTCA AAA CGTC		
		A CTTAT		
GAM1312	KIAA0537	3' GCTGTGACAACAGACTGAAA 29250	TTAT TG	
		TTTCAGTCT T CAGC		
		AAAGTCAGA A GTCG		
		CAAC GT		
GAM1312	KIAA1165	3' CTGCCTTAAAGATTGAAA 67406	TTT	
		TTTCAGTCTTTA GCAG		
		AAAGTTAGAAAT CGTC		
		TC_		
GAM1312	KIAA1464	3' TTGCTACAAATAAGGA 68278	C	
		TCTTTATTTG AGCAA		
		AGGAATAAAC TCGTT		
		A		
GAM1312	MAP2K4	3' TGCCACAAACCACCAGGACTGA 11553	TA_ CA	
	AAG	CTTTCAGTCTT TTTG GCA		
		GAAAGTCAGGA AAAC CGT		
		CCACC AC		
GAM1312	NYD-SP15	3' GAATAAATACTGAAAG 48110	C	
		CTTTCAGT TTTATTT		

			GAAAGTCA AAATAAG		
			T		
GAM1312	PEX11A	3'	TTTGCTGAATGAATAAAAATTG 13890	C	G__
			AAAG CTTTCAGT TTTATTT CAGCAAA		
			GAAAGTTA AAATAAG GTCGTTT		
			A TAA		
GAM1312	PIGM	5'	TGCTGCAAAGAACCGAAGG 59047	A	CTTTA
			CTTTC GT TTTGCAGCA		
			GGAAG CA AAACGTCGT		
			C AG__		
GAM1312	PPIL3	5'	GCTGTAAGACTGAGA 55656		TTATT
			TTTCAGTCT TGCAGC		
			AGAGTCAGA ATGTCG		
			_____		
GAM1312	PPIL3	5'	GCTGTAAGACTGAGA 55658		TTATT
			TTTCAGTCT TGCAGC		
			AGAGTCAGA ATGTCG		
			_____		
GAM1312	PPIL3	5'	GCTGTAAGACTGAGA 50645		TTATT
			TTTCAGTCT TGCAGC		
			AGAGTCAGA ATGTCG		
			_____		
GAM1312	SLC17A6	3'	TTGCTGTAAAAATGAAA 39749		GTCTTTA
			TTTCA TTTGCAGCAA		
			AAAGT AAATGTCGTT		
			AA_____		
GAM1312	TBLR1	3'	CTGCCAATTAAGACTAGAAG 45101	TC	T _
			CTT AGTCTTTA TTG CAG		
			GAA TCAGAAAT AAC GTC		
			GA T C		
GAM1312	ZNF304	3'	TTGCTAGGAAAGACTGAAA 40319		ATTT
			TTTCAGTCTTT GCAG		
			AAAGTCAGAAA CGTT		
			GGAT		
GAM1312	LOC113115	5'	TGCTGTAAGACAGAAAG 56547	A	TTATT
			CTTTC GTCT TGCAGCA		
			GAAAG CAGA ATGTCGT		
			A _____		
GAM1312	LOC115004	3'	TGCTGCTCAGACTGAA 73176		TTATTT
			TTCAGTCT GCAGCA		



	AAGTCAGA	CGTCGT	
	CT____		
GAM1312	LOC145845 3'	CAGATAAAGACTAAAA	83552 C
		TTT AGTCTTTATTTG	
		AAA TCAGAAATAGAC	
		A	
GAM1312	LOC160897 3'	GCAGTACCAAGACTGAAA	82246 TAT_
		TTTCAGTCTT TTGC	
		AAAGTCAGAA GACG	
		CCAT	
GAM1312	LOC162333 5'	CTCAGATAAAGACTGAA	87129 C
		TTTCAGTCTTTATTTG AG	
		AAGTCAGAAATAGAC TC	
		—	
GAM1312	LOC223073 5'	TTGCCTGAAGACTGAAA	94381 TTT
		TTTCAGTCTTTA GCAG	
		AAAGTCAGAAGT CGTT	
		C_	
GAM1312	LOC255177 3'	CTGGGATTACAGAGACTGAAA	96604 AT_ G
		TTTCAGTCTTT TT CAG	
		AAAGTCAGAGA AG GTC	
		CATT G	
GAM1312	LOC256730 3'	TTGCAGCAAGACTGAAA	95236 TTATT A
		TTTCAGTCT TGC GCAA	
		AAAGTCAGA ACG CGTT	
		_____ A	
GAM1312	LOC257469 3'	CTGCTGGTGAAGACTG	95714 TT
		CAGTCTTTAT GCAG	
		GTCAGAAGTG CGTC	
		GT	
GAM1312	LOC90529 3'	TGCCGCAGACTGAAGG	63165 TTATTT A
		CTTTCAGTCT GC GCA	
		GGAAGTCAGA CG CGT	
		_____ C	
GAM1313	ARHGEF5 3'	AACAGAATCTCACCTCA	18362 AATA
		TGAGGT ATTCTGTT	
		ACTCCA TAAGACAA	
		CTC_	
GAM1313	GATA6 3'	AACAACACTTTACTACCT	17914 A TTC
		AGGTA TAA TGTTGTT	

		TCCAT ATT ACAACAA	
		C TC_	
GAM1313	STC1	5' AACACAACAAAAAAATCCT 12030	TAATAATTC
	CA	TGAGG TGTGTGTGTT	
		ACTCC ACAACAACAA	
		TAAAAAAA	
GAM1313	TDRD1	5' AACAGAATTTACCACCTCA 48393	AAT_
		TGAGGT AATTCTGTT	
		ACTCCA TTAAGACAA	
		CCAT	
GAM1313	XRCC2	3' AACACAACGAGATACCATCTC 18315	AA A T
	A	TGAGGT TA TTC GTTGTGTGTT	
		ACTCTA AT GAG CAACAACAA	
		CC A _	
GAM1313	GBTS1	3' AACACACATGCTTATTATCTC 59049	TTC T
	A	TGAGGTAATAA TGT GTTGTGTT	
		ACTCTATTATT ACA CAACAA	
		CGT _	
GAM1313	HSA250303	3' AACACAACAAAATTAT 37407	C
		ATAATT TGTTGTTGTT	
		TATTAA ACAACAACAA	
		A	
GAM1313	KIAA1789	3' AACACAACAAAAAAGCCT 67094	AATAATTC
		AGGT TGTTGTTGTT	
		TCCG ACAACAACAA	
		AAAAA_	
GAM1313	KLHL6	3' AACACAACAAAACCTGGCTC 55296	G ATAATTC
		GAG TA TGTTGTTGTT	
		CTC GT ACAACAACAA	
		G CCAA_	
GAM1313	MGC12466	3' ACAACAACAAAACACCTC 52629	AATAATTC
		GAGGT TGTTGTTGT	
		CTCCA ACAACAACA	
		CAA_	
GAM1313	SCYA5	3' AACACAACAAAAGCTTC 11449	AATAATTC
		GAGGT TGTTGTTGTT	
		CTTCG ACAACAACAA	
		AAAA_	
GAM1313	LOC147093	5' AACACAACAAAATAAAACCCA 83941	A AATA C
		TG GGT ATT TGTTGTTGTT	

AC CCA TAA ACAACAACAA  
 \_ AAA\_ A  
 GAM1313 LOC58489 3' AACAACTTGATCTTACCTCA 72525 TA CT  
 TGAGGTAA ATT GTTGT  
 ||||| || |||||  
 ACTCCATT TAG CAACAA  
 C\_ TT  
 GAM1314 FCN2 3' CAAATATTGTCCAGACAACTT 31735 CTA GC  
 AAG TCTGGATAG TTTG  
 || ||||| ||  
 TTC AGACCTGTT AAAC  
 AAC AT  
 GAM1314 FLJ00060 3' ATCCAGATGGCCTGAA 61090 A  
 TTCA GCTATCTGGAT  
 ||| |||||  
 AAGT CGGTAGACCTA  
 C  
 GAM1314 H11 3' AAAGGCCAGATAGCCTGA 26846 A ATAGG  
 TCA GCTATCTGG CTTT  
 || ||||| ||  
 AGT CGATAGACC GAAA  
 C G\_\_\_\_  
 GAM1314 HHLA3 3' ATCCAGATGGCCTGAA 22982 A  
 TTCA GCTATCTGGAT  
 ||| |||||  
 AAGT CGGTAGACCTA  
 C  
 GAM1314 KIAA0748 3' ATCCAGATGGCCTGAA 28934 A  
 TTCA GCTATCTGGAT  
 ||| |||||  
 AAGT CGGTAGACCTA  
 C  
 GAM1314 KIAA1877 3' CAAAACCAAGGATAGCTAGAA 66166 A GGATA C  
 TTC AGCTATCT GG TTTG  
 || ||||| || |||  
 AAG TCGATAGG CC AAAC  
 A AA\_\_\_\_ A  
 GAM1314 KLK7 3' AAAGTACCAGATGGCTT 57720 ATAG  
 AAGCTATCTGG GCTTT  
 ||||| |||  
 TTCGGTAGACC TGAAA  
 A\_\_\_\_  
 GAM1314 KLK7 3' AAAGTACCAGATGGCTT 17280 ATAG  
 AAGCTATCTGG GCTTT  
 ||||| |||  
 TTCGGTAGACC TGAAA  
 A\_\_\_\_  
 GAM1314 PRO2266 3' CAAAGCCTTCCATAGCTTGA 37579 TC T  
 TCAAGCTA TGGA AGGCTTTG  
 ||||| ||| |||||

		AGTTCGAT ACCT TCCGAAAC		
		— T		
GAM1314	LOC119587 3'	TTTATCCAAATAACTTGGA 73998	C C	
		TTCAAG TAT TGGATAGG		
		AGGTTC ATA ACCTATTT		
		A A		
GAM1314	LOC139171 5'	ATCACAGAAGCCTGAA 75819	A A _	
		TTCA GCT TCTG GAT		
		AAGT CGA AGAC CTA		
		C _ A		
GAM1314	LOC151534 5'	AAAGCCCACAGAGCTT 56681	TA GATA	
		AAGC TCTG GGCTTT		
		TTCG AGAC CCGAAA		
		— AC—		
GAM1315	ARSD 3'	TTCGGACAATGCAGA 23799	CA	
		TCTGCATTGTCC GAA		
		AGACGTAACAGG CTT		
		—		
GAM1315	HTRA3 3'	AAGTCACTTCCAAGTTCTCCGG 89119	CATTGTCCCA	
	A	TCTG GAAGTGA		
		AGGC CTTCACTGAA		
		CTCTTGAAC_		
GAM1315	IL10RA 3'	GGTCCTGGGAGAATGCAGA 59645	G AAGT	
		TCTGCATT TCCCAG GACT		
		AGACGTAA AGGGTC CTGG		
		G —		
GAM1315	LAMP2 3'	TTGCTTCTAAACAATAAAGA 25722	GC CCC TG	
		TCT ATTGT AGAAG A		
		AGA TAACA TCTTC T		
		AA AAA GT		
GAM1315	MS4A2 3'	ACAAC TAGGGACAATACAGA 41694	C _ AA	
		TCTG ATTGTCCC AG GT		
		AGAC TAACAGGG TC CA		
		A A AA		
GAM1315	PDGFRA 3'	CACTTTATTGCAATGCGGA 20594	CCCA	
		TCTGCATTGT GAAGTG		
		AGGCGTAACG TTTCAC		
		TTA_		
GAM1315	ALOX15B 3'	CTCCTGGGACAACCAGA 6689	CA A	
		TCTG TTGTCCCAG AG		

AGAC AACAGGGTC TC  
 C\_ C  
 GAM1315 C6orf5 3' GCTACTAAGACAATGAAGA 31352 G CC A  
 TCT CATTGTC AG AGT  
 ||| ||||| || |||  
 AGA GTAACAG TC TCG  
 A AA A  
 GAM1315 CEP3 5' AAGCCACTTCTGAAGCCACTTG 21245 G TT\_ CC A  
 AGA TCT CA GT CAGAAGTG CTT  
 ||| || || ||||| |||  
 AGA GT CG GTCTTCAC GAA  
 \_ TCAC AA C  
 GAM1315 KIAA0102 5' AAGGTACTTCTGGAAAAATACA 28565 C GTC A  
 TG ATT CCAGAAGTG CTT  
 || ||| ||||| |||  
 AC TAA GGTCTTCAT GAA  
 A AAA G  
 GAM1315 KIAA1695 3' TCACTTCTGTCACAGT 47106 CC  
 ATTGT CAGAAGTGA  
 |||| |||||  
 TGACA GTCTTCACT  
 CT  
 GAM1315 KIAA1970 3' ACATCCCGGAACAGTGCAGA 74294 \_ CA A  
 TCTGCATTGT CC GA GT  
 ||||| || |||  
 AGACGTGACA GG CT CA  
 A CC A  
 GAM1315 NUP133 3' TCACTTCTAGGCCTCAG 36688 CATT T C  
 CTG G CC AGAAGTGA  
 || | || |||||  
 GAC C GG TCTTCACT  
 TC\_ \_ A  
 GAM1315 LOC150406 3' TTTCTACTGCAACAATGCA 79861 CC A T  
 TGCATTGT CAG AG GA  
 ||||| ||| |||  
 ACGTAACA GTC TC TT  
 AC A T  
 GAM1315 LOC157858 5' GTCATTCTACTCAGA 86599 CATT CCC  
 TCTG GT AGAAGTGAC  
 ||| || |||||  
 AGAC CA TCTTCACTG  
 T\_ \_  
 GAM1315 LOC159121 5' GTCCTGGGAAATGCAGA 86997 G AAGT  
 TCTGCATT TCCCAG GAC  
 ||||| ||||| |||  
 AGACGTAA AGGGTC CTG  
 \_ \_  
 GAM1315 LOC220021 5' AAGTCAGAGCAGGCAATGCAGA 93390 CCAGAAG  
 TCTGCATTGTC TGA CTT  
 ||||| |||||

AGACGTAACGG    ACTGAA  
                   ACGAG\_\_  
 GAM1315 LOC221935 3' AGCCACTTCTGCATGAGA    92614    G TGTCC    A  
                   TCT CAT    CAGAAGTG CT  
                   ||| |||    ||||| ||  
                   AGA GTA    GTCTTCAC GA  
                   \_ C\_\_\_\_    C  
 GAM1315 LOC255320 5' AAGTTACTTCTGGAAAAATACA 95002    C GTC  
                   TG ATT    CCAGAAAGTGACTT  
                   || |||    ||||| |||||  
                   AC TAA    GGTCTTCATTGAA  
                   A AAA  
 GAM1316 CLCN5    5' TGAAATACCTAAGCTGCTCCAA 3595    \_\_\_\_\_  
                   TTGGAGCAG    GTTTCA  
                   ||||| |||  
                   AACCTCGTC    TAAAGT  
                   GAATCCA  
 GAM1316 FLRT2    5' ATTGAAAAATGAGGTCTGC    25056    GT    CTC  
                   GCAG TTCATT CAAT  
                   ||| ||||| |||  
                   CGTC GAGTAA GTTA  
                   TG    AAA  
 GAM1316 IL17    3' TGGGGAAAATGAAACCCTCC 9333    CA    \_\_\_\_  
                   GGAG GGTTTCAT TCTCCA  
                   ||| ||||| |||||  
                   CCTC CCAAAGTA AGGGGT  
                   \_\_\_\_    AA  
 GAM1316 NLGN1    5' TGAAGATGCTGCTCCAA    30026    G\_\_\_\_  
                   TTGGAGCAG TTTCA  
                   ||||| |||  
                   AACCTCGTC GAAGT  
                   GTA  
 GAM1316 POLG    3' GTGATAAACCTGCTCCAA    10682    \_\_\_\_  
                   TTGGAGCAGGTT TCAT  
                   ||||| |||  
                   AACCTCGTCCAA AGTG  
                   AT  
 GAM1316 TPK1    3' GGAGAACCTGTCCAA    42384    G    TTCAT  
                   TTGGA CAGGT    TCTCC  
                   |||| |||    |||  
                   AACCT GTCCA    AGAGG  
                   \_\_\_\_  
 GAM1316 C1orf8    5' GAGAATGAAACCCTC    16832    CA  
                   GAG GGTTTCATTCTC  
                   || ||||| |||||  
                   CTC CCAAAGTAAGAG  
                   \_\_\_\_  
 GAM1316 CLIC6    3' TGGAGAACATGTTCCAA    82536    G TTCAT  
                   TTGGAGCA GT    TCTCCA  
                   ||||| ||    |||||

AACCTTGT CA AGAGGT  
A \_\_\_\_\_  
GAM1316 CLIPR-59 3' TGGAGAATTTCAATGCCCCGA 31374 A GGTTTC  
TTGG GCA ATTCTCCA  
||||| ||| |||||  
AGCC CGT TAAGAGGT  
C AACTT\_  
GAM1316 DKFZP547L112 3' TGGAGAACTCTTGCTCCA 66532 TTTCA  
TGGAGCAGG TTCTCCA  
||||||| |||||  
ACCTCGTTC AAGAGGT  
TC\_\_\_\_\_  
GAM1316 EPS8R3 5' GGACCACCTGCTCCAA 55701 TTCATTC  
TTGGAGCAGGT TCC  
||||||| |||  
AACCTCGTCCA AGG  
CC\_\_\_\_\_  
GAM1316 EPS8R3 5' GGACCACCTGCTCCAA 57404 TTCATTC  
TTGGAGCAGGT TCC  
||||||| |||  
AACCTCGTCCA AGG  
CC\_\_\_\_\_  
GAM1316 FLJ20552 3' AGAACAAAAGTCTGCTCCAA 35389 G CA  
TTGGAGCAG TTT TTCT  
||||||| ||| |||  
AACCTCGTC AAA AAGA  
\_ AC  
GAM1316 FLJ22865 5' TGGAGAAAACTGCTCTAA 47071 GTTTCA  
TTGGAGCAG TTCTCCA  
||||||| |||||  
AATCTCGTC AAGAGGT  
AA\_\_\_\_\_  
GAM1316 KIAA0372 5' ATTGAAATTTGTTACCTACTCC 27663 C TT TTCTC  
AA TTGGAG AGGT CA CAAT  
||||| ||| || |||  
AACCTC TCCA GT GTTA  
A TT TAAA  
GAM1316 PRO0132 5' ATGAAACCACTCCAA 26101 CA  
TTGGAG GGTTTCAT  
||||| |||||  
AACCTC CCAAAGTA  
A\_  
GAM1316 TEX27 3' AGAGTGGAACCCGCTGCAA 41658 G A  
TTG AGC GGTTTCATTCT  
||| ||| |||||  
AAC TCG CCAAGGTGAGA  
G C  
GAM1316 LOC149373 3' ATTGGGGTGATGATACCCACCC 79312 AGCA T \_  
CAA TTGG GGT TCATT CTCCAAT  
|||| ||| ||||| |||||

AACC CCA AGTAG GGGGTTA  
 CCAC T T  
 GAM1316 LOC152687 3' TTGGAGAATATTGCTCC 80643 GTTTC  
 GGAGCAG ATTCTCCAA  
 ||||| |||||  
 CCTCGTT TAAGAGGTT  
 A\_\_\_\_  
 GAM1316 LOC51202 3' ATTGGAGAATGAAACCTGCTCC 33017  
 AA TTGGAGCAGGTTTCATTCTCCAAT  
 |||||  
 AACCTCGTCCAAAGTAAGAGGTTA  
  
 GAM1317 A1BG 3' ACAGCAACCTCTACCTC 55409 C A  
 GAGG AGAGGTTGC GT  
 ||| ||||| ||  
 CTCC TCTCCAACG CA  
 A A  
 GAM1317 ACVR1 5' ACTGCAGCCTCCACCTC 6598 CA  
 GAGG GAGGTTGCAGT  
 ||| |||||  
 CTCC CTCCGACGTCA  
 AC  
 GAM1317 ADRB3 3' CAGCCTTTCCACAACCTCTACC 3432 C C\_\_ TA  
 TT GAGG AGAGGTTG AG GCTG  
 ||| ||||| || |||  
 TTCC TCTCCAAC TT CGAC  
 A ACC TC  
 GAM1317 AHR 3' ACTGCAACCTCTACCTC 7873 C  
 GAGG AGAGGTTGCAGT  
 ||| |||||  
 CTCC TCTCCAACGTCA  
 A  
 GAM1317 AIM1 3' ACTGCAGCCTCTACCTC 91812 C  
 GAGG AGAGGTTGCAGT  
 ||| |||||  
 CTCC TCTCCGACGTCA  
 A  
 GAM1317 ALDH1B1 3' ACTGCAACCTCCGCCTC 5485 A  
 GAGGC GAGGTTGCAGT  
 ||| |||||  
 CTCCG CTCCAACGTCA  
 C  
 GAM1317 APM1 3' TACTGCAACCTTTGCCTC 16601  
 GAGGCAGAGGTTGCAGTA  
 |||||  
 CTCCGTTTCCAACGTCAT  
  
 GAM1317 APOL1 3' TCAGCTCACTGCAAGCTCTGCC 13352 G \_  
 TC GAGGCAGAG TTGCAGT AGCTGA  
 ||||| ||||| |||||



			CTCCGTCTC AACGTCA TCGACT		
			G C		
GAM1317 APPBP2	3'	ACTGCAACCTCCGCCTC	21068	A	
		GAGGC GAGGTTGCAGT			
		CTCCG CTCCAACGTCA			
		C			
GAM1317 AQP6	3'	ACTGCAACCTCTACCTC	53906	C	
		GAGG AGAGGTTGCAGT			
		CTCC TCTCCAACGTCA			
		A			
GAM1317 AQP6	3'	ACTGCAACCTCTACCTC	7937	C	
		GAGG AGAGGTTGCAGT			
		CTCC TCTCCAACGTCA			
		A			
GAM1317 ARCN1	3'	TCAGCTCACTGCAACCTCCGCC	7988	A	—
TC		GAGGC GAGGTTGCAGT AGCTGA			
		CTCCG CTCCAACGTCA TCGACT			
		C C			
GAM1317 ARHG	3'	TCAGCCATCTCTAACCTCTGCC	8017	A	C TA_
CT		AG GGCAGAGGTTG AG GCTGA			
		TC CCGTCTCCAAT TC CGACT			
		— C TAC			
GAM1317 ATP7A	3'	ACTGCAACCTCTGCCT	3516		
		AGGCAGAGGTTGCAGT			
		TCCGTCTCCAACGTCA			
GAM1317 ATP8B2	3'	TCAGCTCACTGCAACCTCCACC	65237	CA	—
TC		GAGG GAGGTTGCAGT AGCTGA			
		CTCC CTCCAACGTCA TCGACT			
		AC C			
GAM1317 BAP1	3'	CAGCCACCAGCCTGTCCCT	16214	CAG	CA A
		AGG AGGTTG GT GCTG			
		TCC TCCGAC CA CGAC			
		CTG — C			
GAM1317 BAZ2A	5'	TCAGCTTACTCAACCTCTGCCT	25611	C	—
CT		AGAGGCAGAGGTTG AGTA GCTGA			
		TCTCCGTCTCCAAC TCAT CGACT			
		— T			
GAM1317 BCL10	3'	ACTGCAACTTCTGCCTC	14055		
		GAGGCAGAGGTTGCAGT			

CTCCGTCTTCAACGTCA

GAM1317 BRIP1 3' ACTGCAACCTTCACCTC 49393 CA  
GAGG GAGGTTGCAGT  
|||||  
CTCC TTCCAACGTCA  
AC

GAM1317 C7 3' CTGCAACCTCCGCCTC 5162 A  
GAGGC GAGGTTGCAG  
|||||  
CTCCG CTCCAACGTC  
C

GAM1317 CAMLG 3' ACCGCAACCTCCACCTT 8228 CA A  
GAGG GAGGTTGC GT  
|||||  
TTCC CTCCAACG CA  
AC C

GAM1317 CBFA2T2 3' ACGGTAACCTCTGCCTC 17455 A  
GAGGCAGAGGTTGC GT  
|||||  
CTCCGTCTCCAATG CA  
G

GAM1317 CCNF TC 3' TCAACTCACTGTAACCTCCGCC 8325 A \_ C  
GAGGC GAGGTTGCAGT AG TGA  
|||||  
CTCCG CTCCAATGTCA TC ACT  
C C A

GAM1317 CDH17 C 3' CAGCTCACTGCAACCTCCGCCT 14503 A \_  
GAGGC GAGGTTGCAGT AGCTG  
|||||  
CTCCG CTCCAACGTCA TCGAC  
C C

GAM1317 CDKN1A 3' AGCTACTTCCTCCTC 54291 CAG TTGC  
GAGG AGG AGTAGCT  
|||||  
CTCC TCC TCATCGA  
\_ T \_

GAM1317 CDX1 3' ACTCACACCTGCCTCT 8402 AG T C  
AGAGGCAG GT G AGT  
|||||  
TCTCCGTC CA C TCA  
CA \_ \_

GAM1317 CHAT 5' CAGGCTGCAGCCCCCACC 40622 CAGA AG  
GG GGTTCAGT CTG  
|||  
CC CCGACGTCG GAC  
ACCC \_

GAM1317 CIAS1 5' ACTGCAGCCTCCACCTC 16895 CA  
GAGG GAGGTTGCAGT  
|||||

			CTCC CTCCGACGTCA		
			AC		
GAM1317	CR1	3'	ACTGCAACGTCCGCCTC	5130	A G
			GAGGC GA GTTGCAGT		
			CTCCG CT CAACGTCA		
			C G		
GAM1317	CRTAP	3'	TCAGCTCACTGCAACCTCCGCC	21040	A
	TCT		AGAGGC GAGGTTGCAGT AGCTGA		—
			TCTCCG CTCCAACGTCA TCGACT		
			C C		
GAM1317	CSNK2A2	5'	TCAGCTCACTGCAACCTCCACC	8568	CA
	TC		GAGG GAGGTTGCAGT AGCTGA		—
			CTCC CTCCAACGTCA TCGACT		
			AC C		
GAM1317	CYP1A2	3'	TCAGCTCACTGCAACCTCCACC	5708	CA
	TC		GAGG GAGGTTGCAGT AGCTGA		—
			CTCC CTCCAACGTCA TCGACT		
			AC C		
GAM1317	CYP1A2	3'	TCAGCTCACTGCAACCTCTGCC	5709	
	TC		GAGGCAGAGGTTGCAGT AGCTGA		—
			CTCCGTCTCCAACGTCA TCGACT		
			C		
GAM1317	CYP1A2	3'	TCAGCTCACTGCAACCTCCACC	69128	CA
	TC		GAGG GAGGTTGCAGT AGCTGA		—
			CTCC CTCCAACGTCA TCGACT		
			AC C		
GAM1317	CYP1A2	3'	TCAGCTCACTGCAACCTCTGCC	69129	
	TC		GAGGCAGAGGTTGCAGT AGCTGA		—
			CTCCGTCTCCAACGTCA TCGACT		
			C		
GAM1317	CYP2B6	3'	ACTGCAACCTCTGCCTT	5721	
			GAGGCAGAGGTTGCAGT		
			TTCCGTCTCCAACGTCA		
GAM1317	CYP4F3	3'	ATTGCAACCTCCGCCTC	6107	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTTA		
			C		
GAM1317	CYP51	3'	TCAGCTCACTGCATCCTCTGCC	5787	T
	TC		GAGGCAGAGG TGCAGT AGCTGA		—

			CTCCGTCTCC ACGTCA TCGACT		
			T C		
GAM1317 CYP8B1	3'	ACTGCAACCTCTGCCTC	15252		
		GAGGCAGAGGTTGCAGT			
		CTCCGTCTCCAACGTCA			
GAM1317 CYP8B1	3'	CTGAACCCCTGCCTCT	15262	A	G
		AGAGGCAG GGTT CAG			
		TCTCCGTC CCAA GTC			
		C _			
GAM1317 CYP8B1	3'	ACTACAACCTCTGCCTC	15250		C
		GAGGCAGAGGTTG AGT			
		CTCCGTCTCCAAC TCA			
		A			
GAM1317 DFFB	3'	ACTGCAACCTCCGCCTCT	87374	A	
		AGAGGC GAGGTTGCAGT			
		TCTCCG CTCCAACGTCA			
		C			
GAM1317 DHFR	3'	TACTGCAACCTCCGCCTT	5814	A	
		GAGGC GAGGTTGCAGTA			
		TTCCG CTCCAACGTCAT			
		C			
GAM1317 DISC1	3'	ACTGCAACCTCTACCTC	37869		C
		GAGG AGAGGTTGCAGT			
		CTCC TCTCCAACGTCA			
		A			
GAM1317 DSCR3	3'	TCAGCTCACTGCAACCTCCACC	20193	CA	_
TC		GAGG GAGGTTGCAGT AGCTGA			
		CTCC CTCCAACGTCA TCGACT			
		AC C			
GAM1317 EHD2	3'	TCAGCTCACTGCAACCTCCACC	27500	CA	_
TC		GAGG GAGGTTGCAGT AGCTGA			
		CTCC CTCCAACGTCA TCGACT			
		AC C			
GAM1317 EPB72	3'	ACTGCAACCTCCGCCTC	14595	A	
		GAGGC GAGGTTGCAGT			
		CTCCG CTCCAACGTCA			
		C			
GAM1317 F2RL2	3'	ATTGCAACCTCTGCCTC	14617		
		GAGGCAGAGGTTGCAGT			

CTCCGTCTCCAACGTTA

GAM1317 FANCE 3' ACTGTAACTCTGCCTC 41610  
GAGGCAGAGGTTGCAGT  
|||||  
CTCCGTCTCCAATGTCA

GAM1317 FCAR 3' ACTGCAACCTTCGCCTC 55789 AG  
GAGGC AGGTTGCAGT  
|||| |||||  
CTCCG TCCAACGTCA  
CT

GAM1317 FCAR 3' ACTGCAACCTTCGCCTC 55808 AG  
GAGGC AGGTTGCAGT  
|||| |||||  
CTCCG TCCAACGTCA  
CT

GAM1317 FCRH1 3' ACTGCAACGCCTGCCTCT 53625 AG  
AGAGGCAG GTTGCAGT  
||||| |||||  
TCTCCGTC CAACGTCA  
CG

GAM1317 FEZ1 3' ACTGCAACCTCCACCTC 42563 CA  
GAGG GAGGTTGCAGT  
||| |||||  
CTCC CTCCAACGTCA  
AC

GAM1317 FGF5 3' ACTGCAACCTCCAACCTC 52475 GCA  
GAG GAGGTTGCAGT  
|| |||||  
CTC CTCCAACGTCA  
AAC

GAM1317 FGF5 3' ACTGCAACCTCCAACCTC 15529 GCA  
GAG GAGGTTGCAGT  
|| |||||  
CTC CTCCAACGTCA  
AAC

GAM1317 FUT1 3' ACTGCAACTTCCGCCTC 3783 A  
GAGGC GAGGTTGCAGT  
|||| |||||  
CTCCG CTTCAACGTCA  
C

GAM1317 FUT1 3' TCAGCTCACTGCAAGCTCTGCC 3796 G  
TC GAGGCAGAG TTGCAGT AGCTGA  
||||| ||||| |||||  
CTCCGTCTC AACGTCA TCGACT  
G C

GAM1317 FZD4 3' ACTGCAACCTCTGCCTC 24120  
GAGGCAGAGGTTGCAGT  
|||||

CTCCGTCTCCAACGTCA

GAM1317	G6PC	3'	ACTGCAACCTCTTCCTC	3816	C
			GAGG AGAGGTTGCAGT		
			CTCC TCTCCAACGTCA		
			T		
GAM1317	GBF1	3'	CTGCAGCCTCTGCCTC	14832	
			GAGGCAGAGGTTGCAG		
			CTCCGTCTCCGACGTC		
GAM1317	GHR	3'	ACTGCAATCTCCACCTC	3875	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCTAACGTCA		
			AC		
GAM1317	GM2A	3'	ACTGCAACCTCCGCCTC	67766	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	GPR4	3'	ACTGCAGCCTCCACCTC	59897	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCGACGTCA		
			AC		
GAM1317	GPR81	3'	ACTGCAACCTCTGCCTC	50749	
			GAGGCAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1317	GRAF	3'	ACTGCAACCTCCGCCTC	30547	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	GTF2E2	5'	TCAGCTACCGCCGCTGCC	9149	A TGCA
			GGCAG GGT GTAGCTGA		
			CCGTC CCG CATCGACT		
			G C__		
GAM1317	GYS1	5'	CAGCTACTCGGCCCGC	88399	AGA C
			GC GGTG AGTAGCTG		
			CG CCGGC TCATCGAC		
			CC_ _		
GAM1317	HCS	3'	ACCGCAACCTCCGCCTT	38452	A A
			GAGGC GAGGTTGC GT		

			TTCCG CTCCAACG CA		
			C C		
GAM1317 HCS	3'	ACTGCAACCTCCGCCTT	38456	A	
		GAGGC GAGGTTGCAGT			
		TTCCG CTCCAACGTCA			
		C			
GAM1317 HLCS	5'	ACCACAACCTCTGCCT	4657	CA	
		AGGCAGAGGTTG GT			
		TCCGTCTCCAAC CA			
		AC			
GAM1317 HOXC5	3'	AGTAGCTGATCCACAACCTCTT	38491	C	_____ TAG
CC		GG AGAGGTTG CAG CT			
		CC TCTCCAAC GTC GA			
		T ACCTIIIA GAT			
GAM1317 HTR1D	3'	TCAGCTCACTGCAACCTCCGCA	6002	G A	—
TC		GA GC GAGGTTGCAGT AGCTGA			
		CT CG CTCCAACGTCA TCGACT			
		A C C			
GAM1317 HTR1E	5'	ATTGCAACCTCCGCCTC	6008	A	
		GAGGC GAGGTTGCAGT			
		CTCCG CTCCAACGTTA			
		C			
GAM1317 IFNAR2	3'	ACTGCAACATCCGCCTC	6037	A G	
		GAGGC GA GTTGCAGT			
		CTCCG CT CAACGTCA			
		C A			
GAM1317 ITGAM	3'	ACTGCAACCTCCGCCTC	71832	A	
		GAGGC GAGGTTGCAGT			
		CTCCG CTCCAACGTCA			
		C			
GAM1317 JAK3	3'	CAGTGCAACCTCTGCTTC	4002	AGTA	
		GAGGCAGAGGTTGC GCTG			
		CTTCGTCTCCAACG TGAC			
		_____			
GAM1317 KMO	3'	ACTGCAACCTCTGCCTC	13439		
		GAGGCAGAGGTTGCAGT			
		CTCCGTCTCCAACGTCA			
GAM1317 LCP1	3'	TCAGCCACTAAGAACCCCTCT	9695	CAGA GC_ A	
		AGAGG GGTT AGT GCTGA			

			TCTCC CCAA TCA CGACT		
			_____ GAA C		
GAM1317 LILRA3	3'	ACTGCAACCTCCGCCTCT	95305	A	
		AGAGGC GAGGTTGCAGT			
		TCTCCG CTCCAACGTCA			
		C			
GAM1317 LNK	3'	ACTGCAACCTCCACCTT	18453	CA	
		GAGG GAGGTTGCAGT			
		TTCC CTCCAACGTCA			
		AC			
GAM1317 LYZ	3'	ACTGCAACCTCCACCTC	4095	CA	
		GAGG GAGGTTGCAGT			
		CTCC CTCCAACGTCA			
		AC			
GAM1317 MAK	3'	TACTGCAACCTCCACCTC	19767	CA	
		GAGG GAGGTTGCAGTA			
		CTCC CTCCAACGTCAT			
		AC			
GAM1317 MEF2A	5'	ACTGCAACCTCCGCCTC	18776	A	
		GAGGC GAGGTTGCAGT			
		CTCCG CTCCAACGTCA			
		C			
GAM1317 MEFV	3'	ACTGCAACCTCCGCCTC	4121	A	
		GAGGC GAGGTTGCAGT			
		CTCCG CTCCAACGTCA			
		C			
GAM1317 MEFV	3'	TCAGCTCACTGCAACCTCCACC	4154	CA	
TC		GAGG GAGGTTGCAGT AGCTGA			
		CTCC CTCCAACGTCA TCGACT			
		AC C			
GAM1317 MHC2TA	3'	ACTGCAACCTCCGCCTCT	4160	A	
		AGAGGC GAGGTTGCAGT			
		TCTCCG CTCCAACGTCA			
		C			
GAM1317 MICB	3'	TCAGCTCACTGCAACCTCTGCC	19834		
TC		GAGGCAGAGGTTGCAGT AGCTGA			
		CTCCGTCTCCAACGTCA TCGACT			
		C			
GAM1317 MPDU1	3'	CAGCCAAGCCTCCTCCTCT	16827	CA	GCAGTA
		AGAGG GAGGT GCTG			



TCTCC CTCCGA CGAC  
 TC AC\_\_\_\_  
 GAM1317 MPL 3' ACTGCAACCTCTGCCTC 18127  
 GAGGCAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1317 MPL 3' TCAGCTCACTGCAACCTCCACC 18156 CA  
 TC GAGG GAGGTTGCAGT AGCTGA  
 ||| |||||  
 CTCC CTCCAACGTCA TCGACT  
 AC C

GAM1317 MRPL49 3' ACTGCAACTTCCACCTCT 69564 CA  
 AGAGG GAGGTTGCAGT  
 ||| |||||  
 TCTCC CTTCAACGTCA  
 AC

GAM1317 MYCL2 3' ACTGCAACCTCTGCCTC 18170  
 GAGGCAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1317 MYO1F 3' TCACTGCTGCAGCCCCGCCCC 82427 A AGA C  
 T AG GGC GGTTCAGTAG TGA  
 || ||| ||||| |||  
 TC CCG CCGACGTCGTC ACT  
 C CCC

GAM1317 NONO 3' ACTGCAATCTCTGCCTC 82015  
 GAGGCAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCTAACGTCA

GAM1317 NQO1 3' ACTGCAACCTCTGCCTC 6148  
 GAGGCAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1317 PCDHA9 3' ACTGCAACGTCTGCCTC 25753 G  
 GAGGCAGA GTTGCAGT  
 ||||| |||||  
 CTCCGTCT CAACGTCA  
 G

GAM1317 PCDHB11 3' TCAGCTCACTGCAACCTCTGCC 38423  
 TC GAGGCAGAGGTTGCAGT AGCTGA  
 ||||| |||||  
 CTCCGTCTCCAACGTCA TCGACT  
 C

GAM1317 PCDHB16 3' ACTGCAACCTCTGCCTC 40545  
 GAGGCAGAGGTTGCAGT  
 |||||

CTCCGTCTCCAACGTCA

GAM1317 PCDHB9 3' TCAGCTCACTGCAACCTCCGCC 38949 A \_  
TC GAGGC GAGGTTGCAGT AGCTGA  
||||| ||||||| |||||  
CTCCG CTCCAACGTCA TCGACT  
C C

GAM1317 PDCL 3' ACTGCAACCTCCACCTC 18206 CA  
GAGG GAGGTTGCAGT  
||| |||||||  
CTCC CTCCAACGTCA  
AC

GAM1317 PDE6B 3' TCAGCTCACTGCAACCTCCACC 4290 CA \_  
TC GAGG GAGGTTGCAGT AGCTGA  
||| ||||||| |||||  
CTCC CTCCAACGTCA TCGACT  
AC C

GAM1317 PER2 3' ACTGCAACCTCTGCCTC 43024  
GAGGCAGAGGTTGCAGT  
||||| |||||||  
CTCCGTCTCCAACGTCA

GAM1317 PFKL 3' CAGCCCATCCCCTGCCTCT 10516 A T CAGTA  
AGAGGCAG GG TG GCTG  
||||| || || |||  
TCTCCGTC CC AC CGAC  
C T C\_\_\_\_

GAM1317 PIGR 3' ACTGCAACCTCCGCCTC 72588 A  
GAGGC GAGGTTGCAGT  
||||| |||||||  
CTCCG CTCCAACGTCA  
C

GAM1317 PIK3CD 3' ACTGTAACCTCCGCCTC 17238 A  
GAGGC GAGGTTGCAGT  
||||| |||||||  
CTCCG CTCCAATGTCA  
C

GAM1317 PK428 5' GCAAGCCTCCGCCTCT 13210 A \_  
AGAGGC GAGGTT GC  
||||| ||||| ||  
TCTCCG CTCCGA CG  
C A

GAM1317 PMCHL1 3' ACTGAAACCTCTGCCTC 49067 G  
GAGGCAGAGGTT CAGT  
||||| ||||| |||  
CTCCGTCTCCAA GTCA  
A

GAM1317 PON1 3' ACTGCAACTTCTACCTC 4797 C  
GAGG AGAGGTTGCAGT  
||| |||||||

			CTCC TCTTCAACGTCA			
			A			
GAM1317 PPID	3'	ACTGCATCCTCTGCCTC	87427	T		
		GAGGCAGAGG TGCAGT				
		CTCCGTCTCC ACGTCA				
		T				
GAM1317 PRKR	3'	ACTGCAACTTCTGCCTCT	10876			
		AGAGGCAGAGGTTGCAGT				
		TCTCCGTCTTCAACGTCA				
GAM1317 PRKWNK3	3'	TCACTGCTGCAACCTCCCCCTC	61555	CA	C	
		GAGG GAGGTTGCAGTAG TGA				
		CTCC CTCCAACGTCGTC ACT				
		CC _				
GAM1317 PSMB2	3'	ACTGCAACCTCCGCCTC	10944	A		
		GAGGC GAGGTTGCAGT				
		CTCCG CTCCAACGTCA				
		C				
GAM1317 PSMB9	3'	TTATTGAACCTCTGCCTC	10965	G		
		GAGGCAGAGGTT CAGTAG				
		CTCCGTCTCCAA GTTATT				
GAM1317 PTGES	3'	ACTGCAGCCTCCGCCTC	16857	A		
		GAGGC GAGGTTGCAGT				
		CTCCG CTCCGACGTCA				
		C				
GAM1317 PTGIS	3'	ACTGCAAGCTCTGCCTC	6323	G		
		GAGGCAGAG TTGCAGT				
		CTCCGTCTC AACGTCA				
		G				
GAM1317 PTN	5'	TCAGCGGTAGCAACCTCGCCCC	82715	A	A	AGTA
	T	AG GGC GAGGTTGC GCTGA				
		TC CCG CTCCAACG CGACT				
		C _ ATGG				
GAM1317 RABL2A	3'	GCTGCAACCTCTGACTC	25503	G		
		GAG CAGAGGTTGCAGT				
		CTC GTCTCCAACGTCG				
		A				
GAM1317 RABL2B	3'	GCTGCAACCTCTGACTC	23002	G		
		GAG CAGAGGTTGCAGT				

		CTC GTCTCCAACGTCG	
		A	
GAM1317 RAMP3	3'	CAGCTACTGTGGCCACACCC 19587	CAGA TG
		GG GGT CAGTAGCTG	
		CC CCG GTCATCGAC	
		CACA GT	
GAM1317 RHD	3'	ACTGCAACCTCCGCCTC 32290	A
		GAGGC GAGGTTGCAGT	
		CTCCG CTCCAACGTCA	
		C	
GAM1317 RHD	3'	ACTGCAACCTCTACCTC 32293	C
		GAGG AGAGGTTGCAGT	
		CTCC TCTCCAACGTCA	
		A	
GAM1317 RHD	3'	ACTGCAACCTCCGCCTC 32599	A
		GAGGC GAGGTTGCAGT	
		CTCCG CTCCAACGTCA	
		C	
GAM1317 RHD	3'	ACTGCAACCTCTACCTC 32602	C
		GAGG AGAGGTTGCAGT	
		CTCC TCTCCAACGTCA	
		A	
GAM1317 RPH3AL	3'	ACTGCAACCTCCACCTC 22739	CA
		GAGG GAGGTTGCAGT	
		CTCC CTCCAACGTCA	
		AC	
GAM1317 SAS	3'	ACCGCAACCTCTGCCTC 19946	A
		GAGGCAGAGGTTGC GT	
		CTCCGTCTCCAACG CA	
		C	
GAM1317 SCML2	3'	ACTGCAACCTCGCCTC 20309	A
		GAGGC GAGGTTGCAGT	
		CTCCG CTCCAACGTCA	
		—	
GAM1317 SEDL	3'	ACCGTAACCTCTGCCTC 27311	A
		GAGGCAGAGGTTGC GT	
		CTCCGTCTCCAATG CA	
		C	
GAM1317 SEDL	3'	ACTGCAACCTCCACCTC 27315	CA
		GAGG GAGGTTGCAGT	

			CTCC CTCCAACGTCA		
			AC		
GAM1317	SEDL	3'	ACTGCAACCTCCACCTC	27316	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	SEDL	3'	ACTGCAACCTCCGCCTC	27319	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	SEPN1	3'	ACTGCAACCTCCACCTC	66358	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	SERPINB9	3'	ACTGCAACCTCCTCCTC	14744	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			TC		
GAM1317	SHOX	3'	ACTGCAACCTCCGCCTC	22526	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	SIL	3'	TCAGATCACTGCAACCTCTGCC	11697	AG_
	TC		GAGGCAGAGGTTGCAGT	CTGA	
			CTCCGTCTCCAACGTCA	GACT	
			CTA		
GAM1317	SLA2	3'	TCAGCTCACTGCAACCTCCATC	49907	CA
	TC		GAGG GAGGTTGCAGT	AGCTGA	_
			CTCT CTCCAACGTCA	TCGACT	
			AC	C	
GAM1317	SLC14A2	5'	ACTGCAACCTCCACCTC	23128	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	SLC15A1	3'	TCAGCTCACTGCAACCTCCGCC	17408	A
	TC		GAGGC GAGGTTGCAGT	AGCTGA	_
			CTCCG CTCCAACGTCA	TCGACT	
			C	C	
GAM1317	SLC1A4	3'	CAGCCACTGTTTCTGCC	11712	GTT A
			GGCAGAG GCAGT	GCTG	

			CCGTCTT TGTCA CGAC		
			____ C		
GAM1317	SLC6A12	3'	TCAGCGGACAGCCTCTGCCTCT 11737		CAGTA
			AGAGGCAGAGGTTG GCTGA		
			TCTCCGTCTCCGAC CGACT		
			AGG__		
GAM1317	SLC7A6	5'	ACTGCAACCTCCGACTC 14296 GCA		
			GAG GAGGTTGCAGT		
			CTC CTCCAACGTCA		
			AGC		
GAM1317	SMAC	5'	ACTGCAACCTCTGCCTC 57200		
			GAGGCAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1317	SMAC	5'	TCAGCTCACTGCAACCTGTGCC 57218 G		—
	TC		GAGGCA AGGTTGCAGT AGCTGA		
			CTCCGT TCCAACGTCA TCGACT		
			G C		
GAM1317	SMURF1	3'	CAGCCATGCCCCCTGCCCT 92449 A A TT GTA		
			AG GGCAG GG GCA GCTG		
			TC CCGTC CC CGT CGAC		
			C _ C_ AC_		
GAM1317	SNAP23	3'	ACTGCAACCTCCGCCTC 55454 A		
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	SNAP23	3'	CAGTTTTGCAACCTCTGCT 55460 T		
			GGCAGAGGTTGCAG AGCTG		
			TCGTCTCCAACGTT TTGAC		
GAM1317	SNAP23	3'	ACTGCAACCTCCGCCTC 13801 A		
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	SNAP23	3'	CAGTTTTGCAACCTCTGCT 13807 T		
			GGCAGAGGTTGCAG AGCTG		
			TCGTCTCCAACGTT TTGAC		
GAM1317	SNX15	3'	ACTGCAACCTCCACCTC 73732 CA		
			GAGG GAGGTTGCAGT		

			CTCC CTCCAACGTCA		
			AC		
GAM1317	SPN	3'	TCAGTTCACTGCAACCTCTGCC 11928	—	
	TC		GAGGCAGAGGTTGCAGT AGCTGA		
			CTCCGTCTCCAACGTCA TTGACT		
			C		
GAM1317	SS18	3'	TCAGCTCACTGCAACCTCCGCC 18890	A	—
	TC		GAGGC GAGGTTGCAGT AGCTGA		
			CTCCG CTCCAACGTCA TCGACT		
			C C		
GAM1317	SSA1	3'	TCAGCCACAAACCCTGCCTCT 11977	A GCA A	
			AGAGGCAG GGTT GT GCTGA		
			TCTCCGTC CCAA CA CGACT		
			— A C		
GAM1317	ST5	3'	CAGCCCACCTCTGCCTT 57496	TGCAGTA	
			GAGGCAGAGGT GCTG		
			TTCCGTCTCCA CGAC		
			CC_____		
GAM1317	ST5	3'	CAGCCCACCTCTGCCTT 18290	TGCAGTA	
			GAGGCAGAGGT GCTG		
			TTCCGTCTCCA CGAC		
			CC_____		
GAM1317	STAU	5'	ACTGCAACCTCCACCTC 15993	CA	
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	STAU	5'	ACTGCAACCTCCACCTC 15994	CA	
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	SULT2B1	5'	ACTGCAACCTCCGCCTC 16017	A	
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	TAPBP	3'	TACTGCAACCTCCGCCTC 12134	A	
			GAGGC GAGGTTGCAGTA		
			CTCCG CTCCAACGTCAT		
			C		
GAM1317	TAT	3'	ACTGCAACCTCCACCTC 4459	CA	
			GAGG GAGGTTGCAGT		

			CTCC CTCCAACGTCA			
			AC			
GAM1317	TBXA2R	3'	ACTGCAACCTCCGCCTC	6474	A	
			GAGGC GAGGTTGCAGT			
			CTCCG CTCCAACGTCA			
			C			
GAM1317	TBXA2R	3'	TCAGCTCACTGCAACCTCCACC	6505	CA	_
	TC		GAGG GAGGTTGCAGT AGCTGA			
			CTCC CTCCAACGTCA TCGACT			
			AC C			
GAM1317	TCF7	3'	CAGCCAGAAGCCTCTGCCTC	12158		GCAGTA
			GAGGCAGAGGTT GCTG			
			CTCCGTCTCCGA CGAC			
			AGAC__			
GAM1317	TDGF1	3'	ACTGCAACCTCCGCATC	12198	G A	
			GA GC GAGGTTGCAGT			
			CT CG CTCCAACGTCA			
			A C			
GAM1317	TERF1	3'	TCAGCTCACTGAACCTCTGCCT	33979	G	_
	C		GAGGCAGAGGTT CAGT AGCTGA			
			CTCCGTCTCCAA GTCA TCGACT			
			_ C			
GAM1317	TFAP4	3'	CAGCCCCACCTCTGCCTC	12236		TGCAGTA
			GAGGCAGAGGT GCTG			
			CTCCGTCTCCA CGAC			
			CCCC__			
GAM1317	TLR5	5'	ACTGCAACCACTGCCTC	12321	A	
			GAGGCAG GGTTGCAGT			
			CTCCGTC CCAACGTCA			
			A			
GAM1317	TMC1	5'	CTGCAACCTCCGCCTC	56903	A	
			GAGGC GAGGTTGCAG			
			CTCCG CTCCAACGTC			
			C			
GAM1317	TNFAIP1	3'	TCAGCTACTAGTTCTTCCAGCC	40925	A A_ TT _	
	CT		AG GGC GAGG GC AGTAGCTGA			
			TC CCG CTTC TG TCATCGACT			
			_ AC T_ A			
GAM1317	TNS	5'	CAGCCACAGCTGCTGCCTC	42628	A	CAGTA
			GAGGCAG GGTTG GCTG			



			CTCCGTC TCGAC	CGAC	
			G	AC	_____
GAM1317	TPMT	3'	ACTGCAACCTCTGCCTC	4530	
			GAGGCAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1317	TRAF5	3'	TCAGCTCACTGCAAACCTCTGCC	16086	G
	TC		GAGGCAGAG TTGCAGT AGCTGA		—
			CTCCGTCTC AACGTCA TCGACT		
			A	C	
GAM1317	TRIM9	5'	ACTGCAACCTCCGCCTC	30744	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	TRPM6	3'	ACTGCAACCTCTGCCTC	34527	
			GAGGCAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1317	TRPV1	3'	ACTGCAACCTCTGCCTC	38068	
			GAGGCAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1317	TRPV1	3'	CTGCAACCTCCGCCTC	38081	A
			GAGGC GAGGTTGCAG		
			CTCCG CTCCAACGTC		
			C		
GAM1317	TRPV1	3'	ACTGCAACCTCTGCCTC	54787	
			GAGGCAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1317	TRPV1	3'	CTGCAACCTCCGCCTC	54802	A
			GAGGC GAGGTTGCAG		
			CTCCG CTCCAACGTC		
			C		
GAM1317	TRPV1	3'	ACTGCAACCTCTGCCTC	54822	
			GAGGCAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1317	TRPV1	3'	CTGCAACCTCCGCCTC	54835	A
			GAGGC GAGGTTGCAG		

		CTCCG CTCCAACGTC		
		C		
GAM1317 TRPV1	3'	ACTGCAACCTCTGCCTC	54854	
		GAGGCAGAGGTTGCAGT		
		CTCCGTCTCCAACGTCA		
GAM1317 TRPV1	3'	CTGCAACCTCCGCCTC	54867	A
		GAGGC GAGGTTGCAG		
		CTCCG CTCCAACGTC		
		C		
GAM1317 TUFT1	3'	TCAGTCACTGCAACCTCTGCC	39265	—
TC		GAGGCAGAGGTTGCAGT AGCTGA		
		CTCCGTCTCCAACGTCA TCGACT		
		C		
GAM1317 VENTX2	3'	ACTGCAACCTCCGCCTC	27103	A
		GAGGC GAGGTTGCAGT		
		CTCCG CTCCAACGTCA		
		C		
GAM1317 VHL	3'	ACTACAAGCTCTGCCTC	5050	G C
		GAGGCAGAG TTG AGT		
		CTCCGTCTC AAC TCA		
		G A		
GAM1317 VHL	3'	ACTGCAACCTCTGCCTC	5052	
		GAGGCAGAGGTTGCAGT		
		CTCCGTCTCCAACGTCA		
GAM1317 XRCC2	3'	GCTGCAGCCTCTGCCTCT	18326	
		AGAGGCAGAGGTTGCAGT		
		TCTCCGTCTCCGACGTCTG		
GAM1317 YES1	3'	ACTGCAAGCTCTGCCTC	18347	G
		GAGGCAGAG TTGCAGT		
		CTCCGTCTC AACGTCA		
		G		
GAM1317 ZNF133	5'	TCAACTCACTGCAACCTCCACC	12839	CA — C
		GG GAGGTTGCAGT AG TGA		
		CC CTCCAACGTCA TC ACT		
		AC C A		
GAM1317 ZNF253	3'	ACTGCAATCTCTGCCTC	40735	
		GAGGCAGAGGTTGCAGT		

CTCCGTCTCTAACGTCA

GAM1317 ZNF264 3' ACTGCAACCTCCGCCTC 12741 A  
GAGGC GAGGTTGCAGT  
||||| |||||||||  
CTCCG CTCCAACGTCA  
C

GAM1317 ZNF264 3' CTGCAACCTCTGCCTC 12754  
GAGGCAGAGGTTGCAG  
||||| |||||||||  
CTCCGTCTCCAACGTC

GAM1317 ZNF74 5' ACTGCAACCTCTGCTTC 12789  
GAGGCAGAGGTTGCAGT  
||||| |||||||||  
CTTCGTCTCCAACGTCA

GAM1317 20D7-FC4 5' ACTGCAGCCTCCACCTC 60891 CA  
GAGG GAGGTTGCAGT  
||| |||||||||  
CTCC CTCCGACGTCA  
AC

GAM1317 AP3S2 3' ACTGCAACCTCTGCTTC 19516  
GAGGCAGAGGTTGCAGT  
||||| |||||||||  
CTTCGTCTCCAACGTCA

GAM1317 ARPP-19 3' ACTGCAACCTCTGCCTC 21783  
GAGGCAGAGGTTGCAGT  
||||| |||||||||  
CTCCGTCTCCAACGTCA

GAM1317 ASB16 5' ACTGCAACCTCCGCCTC 69928 A  
GAGGC GAGGTTGCAGT  
||||| |||||||||  
CTCCG CTCCAACGTCA  
C

GAM1317 ASE-1 3' ACTGCAACCTCCGCCTC 23940 A  
GAGGC GAGGTTGCAGT  
||||| |||||||||  
CTCCG CTCCAACGTCA  
C

GAM1317 ATP1B4 3' ACTGCAACCTCCACCTC 23812 CA  
GAGG GAGGTTGCAGT  
||| |||||||||  
CTCC CTCCAACGTCA  
AC

GAM1317 BA108L7.2 3' ACTGCAACCTCTGCCTC 48249  
GAGGCAGAGGTTGCAGT  
||||| |||||||||

CTCCGTCTCCAACGTCA

GAM1317 BAG5 3' TCAGCTCACTGCAACCTCCACC 16853 CA \_  
TC GAGG GAGGTTGCAGT AGCTGA  
||||| |||||  
CTCC CTCCAACGTCA TCGACT  
AC C

GAM1317 BNIP-S 3' ACTGCAACCTCCGCCTC 56253 A  
GAGGC GAGGTTGCAGT  
||||| |||||  
CTCCG CTCCAACGTCA  
C

GAM1317 BTN3A1 3' TCAGCTCCCTGCAACCTCCACC 22925 CA T\_  
TC GAGG GAGGTTGCAG AGCTGA  
||||| |||||  
CTCC CTCCAACGTC TCGACT  
AC CC

GAM1317 C13orf1 3' ACTGCAACCTCTGCTTC 39963  
GAGGCAGAGGTTGCAGT  
||||| |||||  
CTTCGTCTCCAACGTCA

GAM1317 C1orf24 3' ACTGCAACCTCCGCCTC 53702 A  
GAGGC GAGGTTGCAGT  
||||| |||||  
CTCCG CTCCAACGTCA  
C

GAM1317 C1QTNF6 3' TCAGTTCACTGCAACCTCTGCC 49152 \_  
TC GAGGCAGAGGTTGCAGT AGCTGA  
||||| |||||  
CTCCGTCTCCAACGTCA TTGACT  
C

GAM1317 C20orf151 3' CAGCCCAGCCCTACCCCT 88697 A C A CAGTA  
AG GG AG GGTG GCTG  
|| || ||||| |||||  
TC CC TC CCGAC CGAC  
C A \_ C\_\_\_\_

GAM1317 C21orf25 3' TACTGCAACCTCCACCTC 63556 CA  
GAGG GAGGTTGCAGTA  
||||| |||||  
CTCC CTCCAACGTCAT  
AC

GAM1317 C21orf93 3' TCAGCTACCACTCTGCCTGCC 59088 \_ GT CA  
GGCAG AG TG GTAGCTGA  
||||| || |||||  
CCGTC TC AC CATCGACT  
CG TG \_

GAM1317 C3F 3' TCAGCTACCGCAACCTCCACC 19298 CA A \_  
TC GAGG GAGGTTGC GT AGCTGA  
||||| ||||| || |||||

			CTCC CTCCAACG CA TCGACT		
			AC C C		
GAM1317	C6orf5	3'	ACTGCAACCTGCGCCTC 31337	AG	
			GAGGC AGGTTGCAGT		
			CTCCG TCCAACGTCA		
			CG		
GAM1317	C9orf9	3'	ACTGCAACCTCCACCTC 38498	CA	
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	C9orf9	3'	ACTGCAACCTCCGCCTC 38500	A	
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	CARD6	3'	ACCGCAACCTCTGCTTC 50851	A	
			GAGGCAGAGGTTGC GT		
			CTTCGTCTCCAACG CA		
			C		
GAM1317	CECR1	3'	TCAGCTCAGTGCAACCTCCGCC 33819	A	GT_
			GGC GAGGTTGCA AGCTGA		
			CCG CTCCAACGT TCGACT		
			C GAC		
GAM1317	CENPH	3'	ACTGCAACCTCTGCCTC 43267		
			GAGGCAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1317	CHRA1	3'	TCAGCTCACTGCAACCTCCGCC 33879	A	—
	TC		GAGGC GAGGTTGCAGT AGCTGA		
			CTCCG CTCCAACGTCA TCGACT		
			C C		
GAM1317	CIP29	3'	TCAGCTTACTGCAACCTCTGTC 50408		—
	TC		GAGGCAGAGGTTGCAGTA GCTGA		
			CTCTGTCTCCAACGTCAT CGACT		
			T		
GAM1317	CPSF2	3'	ACCGCAACCTCTGCCTC 61566	A	
			GAGGCAGAGGTTGC GT		
			CTCCGTCTCCAACG CA		
			C		
GAM1317	CXYorf1	3'	CAGCCACTGCAGCCCCCT 82037	CAGA	A
			AGG GGTTCAGT GCTG		

			TCC CCGACGTCA CGAC		
			C_____C		
GAM1317	DBR1	3'	ACCGCAACCTCCGCCTC	32524	A A
			GAGGC GAGGTTGC GT		
			CTCCG CTCCAACG CA		
			C C		
GAM1317	DIRC2	5'	ACAGCAGCCTCCGCCTC	51608	A A
			GAGGC GAGGTTGC GT		
			CTCCG CTCCGACG CA		
			C A		
GAM1317	DKFZp434A2417	3'	ACTGCAACTTCCACCTC	66091	CA
			GAGG GAGGTTGCAGT		
			CTCC CTTCAACGTCA		
			AC		
GAM1317	DKFZP434C212	3'	ACTGCAACCTCCACCTC	68903	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	DKFZP434D146	3'	ACTGCAACCTCTGCTTC	31519	
			GAGGCAGAGGTTGCAGT		
			CTTCGTCTCCAACGTCA		
GAM1317	DKFZp434E2220	5'	ACTGCAACCTCCGCCTC	34290	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	DKFZP434F0318	3'	ACTGCAACCTCCGACTC	48003	GCA
			GAG GAGGTTGCAGT		
			CTC CTCCAACGTCA		
			AGC		
GAM1317	DKFZp547H025	3'	TCAGCTCACTGCAACCTCCACC	39366	CA
	TC		GAGG GAGGTTGCAGT AGCTGA		
			CTCC CTCCAACGTCA TCGACT		
			AC C		
GAM1317	DKFZP564O0523	3'	ACTGCAACCTCCACCTC	49510	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	DKFZP566G1424	5'	CAGCCACACCACCTCTGCCTT	84775	T CA A
			GAGGCAGAGGT G GT GCTG		

TTCCGTCTCCA C CA CGAC  
 \_ CA C  
 GAM1317 DKFZP566G1424 5' CAGCCACTGCAGCCCTCC 84776 C A A  
 GG AG GGTTGCAGT GCTG  
 || || ||||| ||||  
 CC TC CCGACGTCA CGAC  
 \_ \_ C  
 GAM1317 DKFZP566M1046 5' CAGCCTGGTATAACCTCTGGCT 49535 G \_ TA  
 C GAG CAGAGGTTG CAG GCTG  
 ||| ||||| || ||||  
 CTC GTCTCCAAT GTC CGAC  
 G ATG \_  
 GAM1317 DKFZp761J139 5' TCAGCTCACTGCAACGTCCACC 50119 CA G \_  
 TCT AGAGG GA GTTGCAGT AGCTGA  
 |||| || ||||| |||||  
 TCTCC CT CAACGTCA TCGACT  
 AC G C  
 GAM1317 DKFZp761N1114 3' ACTGCAACCTCCGCCTC 79010 A  
 GAGGC GAGGTTGCAGT  
 |||| ||||| ||||  
 CTCCG CTCCAACGTCA  
 C  
 GAM1317 DKFZp761O0113 5' ACCGCAGCCTCCGCCTC 37274 A A  
 GAGGC GAGGTTGC GT  
 |||| ||||| ||  
 CTCCG CTCCGACG CA  
 C C  
 GAM1317 DKFZp762L0311 3' ACTGCAACCTTTGCCTC 38053  
 GAGGCAGAGGTTGCAGT  
 ||||| ||||| |||||  
 CTCCGTTTCCAACGTCA  
 GAM1317 DKFZp762P2111 3' ACTGCAACCTCCGCCTCT 86349 A  
 AGAGGC GAGGTTGCAGT  
 |||| ||||| |||||  
 TCTCCG CTCCAACGTCA  
 C  
 GAM1317 DSCR6 3' ACTGCAACCTCCACTTCT 38540 CA  
 AGAGG GAGGTTGCAGT  
 |||| ||||| |||||  
 TCTTC CTCCAACGTCA  
 AC  
 GAM1317 EREG 3' ACTGCAACCTCACCTC 7488 CA  
 GAGG GAGGTTGCAGT  
 |||| ||||| |||||  
 CTCC CTCCAACGTCA  
 A\_  
 GAM1317 FER1L4 3' ACTGCAACCTCCACCTC 47325 CA  
 GAGG GAGGTTGCAGT  
 |||| ||||| |||||

			CTCC CTCCAACGTCA			
			AC			
GAM1317	FER1L4	3'	ACTGCAACCTCCACCTC	47327	CA	
			GAGG GAGGTTGCAGT			
			CTCC CTCCAACGTCA			
			AC			
GAM1317	FKBP9	3'	ACTGCAGCCTCCGCCTC	94059	A	
			GAGGC GAGGTTGCAGT			
			CTCCG CTCCGACGTCA			
			C			
GAM1317	FLJ00024	5'	ACTGCAACCTCTGCCTC	63744		
			GAGGCAGAGGTTGCAGT			
			CTCCGTCTCCAACGTCA			
GAM1317	FLJ00060	5'	ACTGCAAGCTCTGCCTC	61089	G	
			GAGGCAGAG TTGCAGT			
			CTCCGTCTC AACGTCA			
			G			
GAM1317	FLJ10232	3'	ACTGCAACCTCCGCCTC	35917	A	
			GAGGC GAGGTTGCAGT			
			CTCCG CTCCAACGTCA			
			C			
GAM1317	FLJ10298	3'	ACCGCAACCTCCGTCTC	35985	A	A
			GAGGC GAGGTTGC GT			
			CTCTG CTCCAACG CA			
			C C			
GAM1317	FLJ10535	3'	ACTGCAACCTCTGCCTC	36230		
			GAGGCAGAGGTTGCAGT			
			CTCCGTCTCCAACGTCA			
GAM1317	FLJ10560	3'	ACTGCAAGCTCTGCCTC	36274	G	
			GAGGCAGAG TTGCAGT			
			CTCCGTCTC AACGTCA			
			G			
GAM1317	FLJ10604	5'	CAGCCACAGCCCCTGCCCT	36335	A	A CAGTA
			AG GGCAG GGTG GCTG			
			TC CCGTC CCGAC CGAC			
			C C AC__			
GAM1317	FLJ10846	3'	ACTGCAAGCTCTGCCTC	36735	G	
			GAGGCAGAG TTGCAGT			



			CTCCGTCTC AACGTCA		
			G		
GAM1317	FLJ10901	3'	ACTGCAACCCCGTCTC	36816	AGA
			GAGGC GGTTCAGT		
			CTCTG CCAACGTCA		
			CCC		
GAM1317	FLJ10921	3'	CAGCTACTCCTAACCTC	36861	C_
			GAGGTTG AGTAGCTG		
			CTCCAAT TCATCGAC		
			CC		
GAM1317	FLJ10922	3'	ACTGCAACCTCCGCCTC	36864	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	FLJ11004	5'	ACTGCAACCTCTACCTC	36964	C
			GAGG AGAGGTTGCAGT		
			CTCC TCTCCAACGTCA		
			A		
GAM1317	FLJ12363	3'	TCAGCTCACTGCAACCTCCACC	49692	CA
			GAGG GAGGTTGCAGT AGCTGA		
			CTCC CTCCAACGTCA TCGACT		
			AC C		
GAM1317	FLJ12409	3'	ACTGCAACCTCCGCCTC	47040	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	FLJ12572	5'	ACTGCAACCTCTGCCTC	43242	
			GAGGCAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1317	FLJ12586	3'	ACAGCAACCTCTGCCTC	44874	A
			GAGGCAGAGGTTGC GT		
			CTCCGTCTCCAACG CA		
			A		
GAM1317	FLJ12649	3'	ACTGCAACCTCCGCCTC	44771	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	FLJ12668	3'	ACTGCAACCTCCATCTC	46510	CA
			GAGG GAGGTTGCAGT		

			CTCT CTCCAACGTCA			
			AC			
GAM1317	FLJ12687	3'	ACTGCAACCTCCGCCTC	46182	A	
			GAGGC GAGGTTGCAGT			
			CTCCG CTCCAACGTCA			
			C			
GAM1317	FLJ12747	3'	ACTGCAACCTCTGCCTC	49706		
			GAGGCAGAGGTTGCAGT			
			CTCCGTCTCCAACGTCA			
GAM1317	FLJ12787	3'	ACTGCAACCTCTGCCCT	49743	A	
			AG GGCAGAGGTTGCAGT			
			TC CCGTCTCCAACGTCA			
			—			
GAM1317	FLJ12960	3'	CTATGCAACCTCCACCTC	44949	CA	G
			GAGG GAGGTTGCA TAG			
			CTCC CTCCAACGT ATC			
			AC —			
GAM1317	FLJ12973	3'	ACCGCAACCTCCGCCTC	46098	A	A
			GAGGC GAGGTTGC GT			
			CTCCG CTCCAACG CA			
			C C			
GAM1317	FLJ12975	3'	ACTGCAATCTCTGCCTC	69575		
			GAGGCAGAGGTTGCAGT			
			CTCCGTCTCTAACGTCA			
GAM1317	FLJ13072	5'	ACTGCAACCTCTGCCTC	89798		
			GAGGCAGAGGTTGCAGT			
			CTCCGTCTCCAACGTCA			
GAM1317	FLJ13197	3'	ACTGCAACCTCTACCTC	44845	C	
			GAGG AGAGGTTGCAGT			
			CTCC TCTCCAACGTCA			
			A			
GAM1317	FLJ14260	3'	TCAGCCACCATTTTATGCTGCC	46705		AGGTTGCA_ A
			TCT AGAGGCAG GT GCTGA			
			TCTCCGTC CA CGACT			
			GTATTTTAC C			
GAM1317	FLJ14442	3'	TCAGCTCACTGCAACTTCTGCC	51375		—
			TC GAGGCAGAGGTTGCAGT AGCTGA			

			CTCCGTCTTCAACGTCA TCGACT		
			C		
GAM1317	FLJ14803	3'	ACTACAACTTCTGCCTC 51614	C	
			GAGGCAGAGGTTG AGT		
			CTCCGTCTTCAAC TCA		
			A		
GAM1317	FLJ14950	3'	ACTGCAACCTCCACCTC 51711	CA	
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	FLJ14957	3'	ACTGCAACCTCTGCCTC 51734		
			GAGGCAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1317	FLJ20004	3'	ATTGCAACCTCCGCCTC 95287	A	
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTTA		
			C		
GAM1317	FLJ20034	3'	TCAGCTCACTGCAACCTCTGCC 34386		—
	TC		GAGGCAGAGGTTGCAGT AGCTGA		
			CTCCGTCTCCAACGTCA TCGACT		
			C		
GAM1317	FLJ20045	3'	ACTGCAACCTCTGCCTC 34409		
			GAGGCAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1317	FLJ20079	3'	ACCGCAACCTCCACCTC 34484	CA	A
			GAGG GAGGTTGC GT		
			CTCC CTCCAACG CA		
			AC C		
GAM1317	FLJ20136	3'	ACTGCAATCTCTGCCTCT 34609		
			AGAGGCAGAGGTTGCAGT		
			TCTCCGTCTCTAACGTCA		
GAM1317	FLJ20342	3'	TCAGGTCACTGCAACCTCTGCC 34996		AG _
	TC		GAGGCAGAGGTTGCAGT C TGA		
			CTCCGTCTCCAACGTCA G ACT		
			CT G		
GAM1317	FLJ20344	3'	ACTGCAACCTCCGCCTCT 35004	A	
			AGAGGC GAGGTTGCAGT		

TCTCCG CTCCAACGTCA  
 C  
 GAM1317 FLJ20507 3' TCAGCTCACTGCAACCTCTGCC 35300 —  
 TC GAGGCAGAGGTTGCAGT AGCTGA  
 |||||  
 CTCCGTCTCCAACGTCA TCGACT  
 C  
 GAM1317 FLJ20507 3' TCAGCTCACTGCAACCTCTGCC 60235 —  
 TC GAGGCAGAGGTTGCAGT AGCTGA  
 |||||  
 CTCCGTCTCCAACGTCA TCGACT  
 C  
 GAM1317 FLJ20542 3' CAGCCGCCACCTCTGCCCT 49782 A T AGTA  
 AG GGCAGAGGT GC GCTG  
 || ||||| || ||||  
 TC CCGTCTCCA CG CGAC  
 — C C\_\_\_  
 GAM1317 FLJ20700 3' ACTGCAACCTCTGTCTC 35568  
 GAGGCAGAGGTTGCAGT  
 |||||  
 CTCTGTCTCCAACGTCA  
  
 GAM1317 FLJ20813 3' ACTGCAACTCCACCTC 35676 CA G  
 GAGG GAG TTGCAGT  
 ||| ||| |||||  
 CTCC CTC AACGTCA  
 AC \_  
 GAM1317 FLJ21302 3' TCAGATCACTGCAACCTCCGCC 43221 A AG\_  
 TC GAGGC GAGGTTGCAGT CTGA  
 |||| ||||| ||||  
 CTCCG CTCCAACGTCA GACT  
 C CTA  
 GAM1317 FLJ21324 5' CAGCCGCACACCTCCTGCCTCT 91192 — \_ AGTA  
 AGAGGCAG AGGT TGC GCTG  
 ||||| ||| ||| ||||  
 TCTCCGTC TCCA ACG CGAC  
 C C C\_\_\_  
 GAM1317 FLJ21415 3' TCAGAGGCAACCTCCTCCCCT 45357 A CA AGTAG  
 AG GG GAGGTTGC CTGA  
 || || ||||| ||||  
 TC CC CTCCAACG GACT  
 C TC GA\_\_\_  
 GAM1317 FLJ22002 3' TCAGCTCACTGCAACCTCCGCC 45778 A —  
 TC GAGGC GAGGTTGCAGT AGCTGA  
 |||| ||||| |||||  
 CTCCG CTCCAACGTCA TCGACT  
 C C  
 GAM1317 FLJ22167 5' TCAGCTCACTGCCACCTCTGCC 44583 T \_  
 TC GAGGCAGAGGT GCAGT AGCTGA  
 ||||| |||| |||||

		CTCCGTCTCCA CGTCA TCGACT	
		C C	
GAM1317	FLJ22332	5' TCAGCTACAGTGGCTCTGC 45303	G TG A
		GCAGAG T C GTAGCTGA	
		CGTCTC G G CATCGACT	
		_ GT A	
GAM1317	FLJ22531	5' ACTGCAACCTCCACCTC 45026	CA
		GAGG GAGGTTGCAGT	
		CTCC CTCCAACGTCA	
		AC	
GAM1317	FLJ22794	3' TCAGCTCACTGCAACTTCCACC 91613	CA _
	TC	GAGG GAGGTTGCAGT AGCTGA	
		CTCC CTTCAACGTCA TCGACT	
		AC C	
GAM1317	FLJ22965	3' ACTGCAACCTCCGCCTC 42045	A
		GAGGC GAGGTTGCAGT	
		CTCCG CTCCAACGTCA	
		C	
GAM1317	FLJ22969	3' ACTGCAACCTCTGCCTC 68641	
		GAGGCAGAGGTTGCAGT	
		CTCCGTCTCCAACGTCA	
GAM1317	FLJ23024	3' TCAGCTCACTGCAACCTCTGCC 46276	_
	TC	GAGGCAGAGGTTGCAGT AGCTGA	
		CTCCGTCTCCAACGTCA TCGACT	
		C	
GAM1317	FLJ23053	3' TACTGCAAGCTCCGCCTC 43263	A G
		GAGGC GAG TTGCAGTA	
		CTCCG CTC AACGTCAT	
		C G	
GAM1317	FLJ23356	3' ACTGCAGCCTCTGCCTC 49935	
		GAGGCAGAGGTTGCAGT	
		CTCCGTCTCCGACGTCA	
GAM1317	FLJ23392	3' TCAGCTCACTGCAACCTCTGCC 45547	_
	TC	GAGGCAGAGGTTGCAGT AGCTGA	
		CTCCGTCTCCAACGTCA TCGACT	
		C	
GAM1317	FLJ23556	3' ACTGCACCTCTGCCTC 45939	T
		GAGGCAGAGGT GCAGT	

CTCCGTCTCCA CGTCA

GAM1317 FLJ23563 3' ACTGCAACCTCTGCCTC 67582  
GAGGCAGAGGTTGCAGT  
|||||  
CTCCGTCTCCAACGTCA

GAM1317 FLJ25416 5' ACTGCAACCTCCGCATC 58802 G A  
GA GC GAGGTTGCAGT  
|| ||  
CT CG CTCCAACGTCA  
A C

GAM1317 FLJ30473 3' TCAGCCACCTGGCTCCCCTC 58464 CA GTTG TA\_  
GAGG GAG CAG GCTGA  
||| ||| ||| |||  
CTCC CTC GTC CGACT  
C\_ G\_ CAC

GAM1317 FLJ30532 3' ACTGCAGCCTCTGCCTC 58541  
GAGGCAGAGGTTGCAGT  
|||||  
CTCCGTCTCCGACGTCA

GAM1317 FLJ31101 3' TCAGCTCACTGCAACCTCTGCC 35719  
TC GAGGCAGAGGTTGCAGT AGCTGA  
|||||  
CTCCGTCTCCAACGTCA TCGACT  
C

GAM1317 FLJ31153 3' ACTGCAATCTCTGCCTC 58119  
GAGGCAGAGGTTGCAGT  
|||||  
CTCCGTCTCTAACGTCA

GAM1317 FLJ32865 3' TCAGCTCACTGCAACCTCTGCC 58184  
TC GAGGCAGAGGTTGCAGT AGCTGA  
|||||  
CTCCGTCTCCAACGTCA TCGACT  
C

GAM1317 FOXN4 3' CAGCCACTGATGACCCTGTCCC 75572 A A \_ A  
T AG GGCAG GGTTG CAGT GCTG  
|| ||| ||| ||| |||  
TC CTGTC CCAGT GTCA CGAC  
C \_ A C

GAM1317 GAL3ST-4 3' ACTGCAACCTCTGCCTC 44929  
GAGGCAGAGGTTGCAGT  
|||||  
CTCCGTCTCCAACGTCA

GAM1317 GFRA4 3' CAGCTACTCCACCCTGCCT 42155 A T C  
AGGCAG GGT G AGTAGCTG  
||||| ||| | |||

			TCCGTC CCA C TCATCGAC		
			— _ C		
GAM1317	GMPPB	5'	ACTGCAACCTCCACCTC	95719	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	GNG4	3'	TCAGCTCACTGCGACCTCCACC	15624	CA
	TC		GAGG GAGGTTGCAGT AGCTGA		—
			CTCC CTCCAGCGTCA TCGACT		
			AC C		
GAM1317	GPR88	5'	TCAGCCACCACTCCTGCTTCT	41881	AG TGCA A
			AGAGGCAG GT GT GCTGA		
			TCTTCGTC CA CA CGACT		
			CT C__ C		
GAM1317	GR6	5'	ACTGAAACCTCTGCCTC	23725	G
			GAGGCAGAGGTT CAGT		
			CTCCGTCTCCAA GTCA		
			A		
GAM1317	GREB1	3'	ACTGCAACCTCTGCCTC	27859	
			GAGGCAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1317	GRWD	3'	ACTGCAACCTCCGCCTC	48958	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	GTF2E1	3'	ACTGCAACCTCTGCCTC	18606	
			GAGGCAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1317	GTPBG3	3'	ACTGCAACCTCCATCTC	50894	CA
			GAGG GAGGTTGCAGT		
			CTCT CTCCAACGTCA		
			AC		
GAM1317	GTPBG3	3'	TACTGCAACCTCCACCTC	50907	CA
			GAGG GAGGTTGCAGTA		
			CTCC CTCCAACGTCAT		
			AC		
GAM1317	H-plk	5'	ACTGCAACCTCCACCTC	31802	CA
			GAGG GAGGTTGCAGT		

		CTCC CTCCAACGTCA	
		AC	
GAM1317 HEY2	3'	TCAGCTTAAAACCTCTGC 24320	GCAGT
		GCAGAGGTT AGCTGA	
		CGTCTCCAA TCGACT	
		AAT__	
GAM1317 HRH4	3'	ACTGCAACCTCTGCCTC 41243	
		GAGGCAGAGGTTGCAGT	
		CTCCGTCTCCAACGTCA	
GAM1317 HSJ1	3'	CAGCTGCAGACCCCCAACCCCT 22127	A CAGA_ GCA
		AG GG GGTT GTAGCTG	
		TC CC CCAG CGTCGAC	
		_ AACCC A__	
GAM1317 HSMPP8	3'	ACTGCAAGCTCTGCCTC 93472	G
		GAGGCAGAG TTGCAGT	
		CTCCGTCTC AACGTCA	
		G	
GAM1317 HSNV1	3'	TCAGCTTACTGTAACTCTGCC 34013	_
TC		GAGGCAGAGGTTGCAGTA GCTGA	
		CTCCGTCTCCAATGTCAT CGACT	
		T	
GAM1317 HSPC065	3'	ACTGCAACCTCCACCTCT 26286	CA
		AGAGG GAGGTTGCAGT	
		TCTCC CTCCAACGTCA	
		AC	
GAM1317 HSPC065	3'	GCTGCAACCTCCTCCTC 26310	CA
		GAGG GAGGTTGCAGT	
		CTCC CTCCAACGTCTG	
		TC	
GAM1317 ICK	3'	CTGCAACCTCTGCCTC 29928	
		GAGGCAGAGGTTGCAG	
		CTCCGTCTCCAACGTC	
GAM1317 JAM1	3'	ACTGTAACCTCCGCCTC 33747	A
		GAGGC GAGGTTGCAGT	
		CTCCG CTCCAATGTCA	
		C	
GAM1317 JAM1	3'	ACTGTAACCTCCGCCTC 57885	A
		GAGGC GAGGTTGCAGT	



			CTCCG CTCCAATGTCA		
			C		
GAM1317	JAM1	5'	ACTGCAACCTCCTCCTC	57909	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			TC		
GAM1317	JAM1	3'	ACTGTAACCTCCGCCTC	57912	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAATGTCA		
			C		
GAM1317	JAM1	3'	ACTGTAACCTCCGCCTC	57939	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAATGTCA		
			C		
GAM1317	JM11	3'	TCAGCTCACTGCAACCTCTGCC	53270	—
	TC		GAGGCAGAGGTTGCAGT AGCTGA		
			CTCCGTCTCCAACGTCA TCGACT		
			C		
GAM1317	KIAA0063	3'	ACTGCAACCTCCACCTC	29614	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	KIAA0161	3'	ACTGCAAGCTCTGCCTC	28496	G
			GAGGCAGAG TTGCAGT		
			CTCCGTCTC AACGTCA		
			G		
GAM1317	KIAA0210	5'	TCAGCTCACCGCAATCTCCGCC	28487	A A _
	TC		GAGGC GAGGTTGC GT AGCTGA		
			CTCCG CTCTAACG CA TCGACT		
			C C C		
GAM1317	KIAA0391	3'	TCAGTTCACTGCAACCTCTGCC	27923	—
	TC		GAGGCAGAGGTTGCAGT AGCTGA		
			CTCCGTCTCCAACGTCA TTGACT		
			C		
GAM1317	KIAA0397	3'	CAGCCACCAACCGACCCACCT	61673	CAGA__ CA A
	CT		AGAGG GGTG GT GCTG		
			TCTCC CCAAC CA CGAC		
			ACCCAG _ C		
GAM1317	KIAA0426	3'	ACTGCAACCTCCGCCTC	28251	A
			GAGGC GAGGTTGCAGT		

			CTCCG CTCCAACGTCA		
			C		
GAM1317	KIAA0450	5'	CAGCTACTTCCACCTCTGCCCT	27621	A TGC
			AG GGCAGAGGT AGTAGCTG		
			TC CCGTCTCCA TCATCGAC		
			— CCT		
GAM1317	KIAA0450	5'	TTGCAGCCTCCACCCCT	27657	A CA
			AG GG GAGGTTGCAG		
			TC CC CTCCGACGTT		
			C AC		
GAM1317	KIAA0459	3'	ACTGCAACCTCCACCTC	60981	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	KIAA0469	3'	ACTGCAGCCTCCACCTC	29317	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCGACGTCA		
			AC		
GAM1317	KIAA0471	3'	CAGTGTCTTCTGCCCT	29389	A TTGCAGTA
			AG GGCAGAGG GCTG		
			TC CCGTCTTC TGAC		
			C TG_____		
GAM1317	KIAA0475	3'	ACTGCAACCTCCGTCTC	29483	A
			GAGGC GAGGTTGCAGT		
			CTCTG CTCCAACGTCA		
			C		
GAM1317	KIAA0495	3'	ACTGCAACCTCCGTCTC	62573	A
			GAGGC GAGGTTGCAGT		
			CTCTG CTCCAACGTCA		
			C		
GAM1317	KIAA0513	3'	ACTGCAACCTCCACCTC	28330	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	KIAA0513	5'	ACTGCAGCCTCCACCTC	28333	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCGACGTCA		
			AC		
GAM1317	KIAA0527	3'	ACTGCAACCTCTGCCTC	95788	
			GAGGCAGAGGTTGCAGT		

CTCCGTCTCCAACGTCA

GAM1317 KIAA0544 3' ACTGCAACCTCCGCCTC 70883 A

GAGGC GAGGTTGCAGT

||||| |||||||||

CTCCG CTCCAACGTCA

C

GAM1317 KIAA0561 3' TCAGCTCACTGCAACCTCCGCC 65897 A

TC

GAGGC GAGGTTGCAGT AGCTGA

||||| ||||||||| |||||||

CTCCG CTCCAACGTCA TCGACT

C

C

GAM1317 KIAA0562 3' CTGCAACCTCCGCCTC 28153 A

GAGGC GAGGTTGCAG

||||| |||||||||

CTCCG CTCCAACGTC

C

GAM1317 KIAA0563 5' ACTGCAACCTCTGCCTC 29179

GAGGCAGAGGTTGCAGT

||||| |||||||||

CTCCGTCTCCAACGTCA

GAM1317 KIAA0594 3' TACTGCAACCTCCGCCTC 64901 A

GAGGC GAGGTTGCAGTA

||||| |||||||||

CTCCG CTCCAACGTCAT

C

GAM1317 KIAA0599 3' ACTGCAACCTCCGCCTC 77162 A

GAGGC GAGGTTGCAGT

||||| |||||||||

CTCCG CTCCAACGTCA

C

GAM1317 KIAA0599 3' TACTGCAACCTCCGCCTC 77189 A

GAGGC GAGGTTGCAGTA

||||| |||||||||

CTCCG CTCCAACGTCAT

C

GAM1317 KIAA0720 3' ACTGCAACCTCTGCCTC 62314

GAGGCAGAGGTTGCAGT

||||| |||||||||

CTCCGTCTCCAACGTCA

GAM1317 KIAA0737 3' TCAGCTCACTGAAACCTCTGCC 29147

TC

GAGGCAGAGGTT CAGT AGCTGA

||||| ||| |||||||

CTCCGTCTCCAA GTCA TCGACT

A C

GAM1317 KIAA0798 3' ACTGCAACCCCGCCTC 27713 AGA

GAGGC GGTTCAGT

||||| |||||||||

CTCCG CCAACGTCA  
 CC\_  
 GAM1317 KIAA0831 3' TCAACCACTGTTTTTCTACTC 29981 GC TT AGC  
 T AGAG AGAGG GCAGT TGA  
 |||| |||| |||| ||  
 TCTC TCTTT TGTCA ACT  
 A\_ TT CCA  
 GAM1317 KIAA0841 3' TCAGCTCACTGCAACCTCCGCC 71400 A \_  
 TC GAGGC GAGGTTGCAGT AGCTGA  
 |||| |||| |||| ||||  
 CTCCG CTCCAACGTCA TCGACT  
 C C  
 GAM1317 KIAA0841 3' TCAGCTCACTGCAACCTCTGCC 71401 \_  
 TC GAGGCAGAGGTTGCAGT AGCTGA  
 |||| |||| |||| ||||  
 CTCCGTCTCCAACGTCA TCGACT  
 C  
 GAM1317 KIAA0889 3' ACTGTAACCTCCGCCTC 31126 A  
 GAGGC GAGGTTGCAGT  
 |||| |||| |||| ||||  
 CTCCG CTCCAATGTCA  
 C  
 GAM1317 KIAA0961 3' ACTGCAAGCTCTGCCTC 29727 G  
 GAGGCAGAG TTGCAGT  
 |||| |||| |||| ||||  
 CTCCGTCTC AACGTCA  
 G  
 GAM1317 KIAA1040 3' ACTGCAACCTCTGCTTC 72217  
 GAGGCAGAGGTTGCAGT  
 |||| |||| |||| ||||  
 CTTCGTCTCCAACGTCA  
 GAM1317 KIAA1041 3' ACTGCAACCTCCGCCTC 30121 A  
 GAGGC GAGGTTGCAGT  
 |||| |||| |||| ||||  
 CTCCG CTCCAACGTCA  
 C  
 GAM1317 KIAA1054 3' ACTGCAACCTCCGCCTC 68424 A  
 GAGGC GAGGTTGCAGT  
 |||| |||| |||| ||||  
 CTCCG CTCCAACGTCA  
 C  
 GAM1317 KIAA1056 3' CAGCTACTGCCCAGCTCT 29692 G AGA TT  
 AGAG C GG GCAGTAGCTG  
 |||| | || |||| ||||  
 TCTC G CC CGTCATCGAC  
 \_ A \_ \_  
 GAM1317 KIAA1128 3' ACTGCAACTTCTGCCTC 68468  
 GAGGCAGAGGTTGCAGT  
 |||| |||| |||| ||||

CTCCGTCTTCAACGTCA

GAM1317 KIAA1161 5' TCAGCTCACTGCAACCCCTCCT 81762 C A \_  
C GAGG AG GGTTGCAGT AGCTGA

||||| || ||||| |||||  
CTCC TC CCAACGTCA TCGACT  
\_ C C

GAM1317 KIAA1170 3' ACTGCAACCTCCGCCTC 69840 A  
GAGGC GAGGTTGCAGT

||||| ||||| |||||  
CTCCG CTCCAACGTCA  
C

GAM1317 KIAA1193 3' ACTGCAACCTCCGCCTC 67624 A  
GAGGC GAGGTTGCAGT

||||| ||||| |||||  
CTCCG CTCCAACGTCA  
C

GAM1317 KIAA1198 3' GCGCAACCTCTGCCTC 63311 A  
GAGGCAGAGGTTGC GT

||||| ||||| || ||  
CTCCGTCTCCAACG CG

GAM1317 KIAA1198 3' ACCGCAACCTCCGCCTC 63280 A A  
GAGGC GAGGTTGC GT

||||| ||||| ||  
CTCCG CTCCAACG CA  
C C

GAM1317 KIAA1198 3' ACTGCAACCTCCACTTCT 63284 CA  
AGAGG GAGGTTGCAGT

||||| ||||| |||||  
TCTTC CTCCAACGTCA  
AC

GAM1317 KIAA1198 3' ACTGCAATCTCTGCCTC 63286  
GAGGCAGAGGTTGCAGT

||||| ||||| |||||  
CTCCGTCTCTAACGTCA

GAM1317 KIAA1209 3' ACTGCAGCCTCCACCTC 60745 CA  
GAGG GAGGTTGCAGT

||||| ||||| |||||  
CTCC CTCCGACGTCA  
AC

GAM1317 KIAA1254 3' TCAGCTCACTGCAACCTCTGTC 70024 \_  
TC GAGGCAGAGGTTGCAGT AGCTGA

||||| ||||| ||||| |||||  
CTCTGTCTCCAACGTCA TCGACT  
C

GAM1317 KIAA1257 3' TCAGCTCACCGCAACCTCCGCC 62760 A A \_  
TC GAGGC GAGGTTGC GT AGCTGA

||||| ||||| || |||||

CTCCG CTCCAACG CA TCGACT  
 C C C  
 GAM1317 KIAA1320 5' ACTGCAACCTCTGCCTC 69291  
 GAGGCAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1317 KIAA1373 3' TCAGCTCACTGCAACCTCCACC 70952 CA \_  
 TC GAGG GAGGTTGCAGT AGCTGA  
 ||| ||||| |||||  
 CTCC CTCCAACGTCA TCGACT  
 AC C

GAM1317 KIAA1464 5' CAGGGGCAACCTCCGCGTC 68262 G A AGTAG  
 GA GC GAGGTTGC CTG  
 || ||||| ||  
 CT CG CTCCAACG GAC  
 G C GG\_\_

GAM1317 KIAA1467 3' ACTGCAACCTTTCGCCTC 71602 AG  
 GAGGC AGGTTGCAGT  
 |||| |||||  
 CTCCG TCCAACGTCA  
 CT

GAM1317 KIAA1473 3' TCAGCTCACTGCAACCTCCGTC 70673 A \_  
 TC GAGGC GAGGTTGCAGT AGCTGA  
 |||| ||||| |||||  
 CTCTG CTCCAACGTCA TCGACT  
 C C

GAM1317 KIAA1497 5' ACTGCAACCTCTGCCTC 67500  
 GAGGCAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA

GAM1317 KIAA1508 3' TCAGCTCACTGCAACCTCCGCC 61893 A \_  
 TC GAGGC GAGGTTGCAGT AGCTGA  
 |||| ||||| |||||  
 CTCCG CTCCAACGTCA TCGACT  
 C C

GAM1317 KIAA1535 3' CAGCCAGCACCTCTGCCTT 79409 T AGTA  
 GAGGCAGAGGT GC GCTG  
 ||||| || |||  
 TTCCGTCTCCA CG CGAC  
 \_ AC\_\_

GAM1317 KIAA1571 3' ACCGCAACCTCCACCTC 60947 CA A  
 GAGG GAGGTTGC GT  
 ||| ||||| ||  
 CTCC CTCCAACG CA  
 AC C

GAM1317 KIAA1615 3' TCAGATCACTGCAACCTCCACC 68730 CA AG\_  
 TC GAGG GAGGTTGCAGT CTGA  
 |||| ||||| |||

CTCC CTCCAACGTCA GACT  
 AC CTA  
 GAM1317 KIAA1643 3' AGCTACCACTTCCCCT 64544 CA TGCA  
 AGG GAGGT GTAGCT  
 ||| |||| |||||  
 TCC CTTCA CATCGA  
 C\_ C\_\_  
 GAM1317 KIAA1655 3' ATTGCAACCTCCGCCTC 66593 A  
 GAGGC GAGGTTGCAGT  
 |||| |||||  
 CTCCG CTCCAACGTTA  
 C  
 GAM1317 KIAA1655 3' TCAGCTCACTGTAACCTCCACC 66627 CA \_  
 TC GAGG GAGGTTGCAGT AGCTGA  
 ||| ||||| |||||  
 CTCC CTCCAATGTCA TCGACT  
 AC C  
 GAM1317 KIAA1712 3' ACCGCAACCTCTGCCT 67530 A  
 AGGCAGAGGTTGC GT  
 ||||| ||  
 TCCGTCTCCAACG CA  
 C  
 GAM1317 KIAA1737 3' ACTGCAACCTCCGCCTC 67345 A  
 GAGGC GAGGTTGCAGT  
 |||| |||||  
 CTCCG CTCCAACGTCA  
 C  
 GAM1317 KIAA1784 3' ACTGCAACCTCCGCCTC 65140 A  
 GAGGC GAGGTTGCAGT  
 |||| |||||  
 CTCCG CTCCAACGTCA  
 C  
 GAM1317 KIAA1829 3' ACTGCAGCCTCTGCCTC 61943  
 GAGGCAGAGGTTGCAGT  
 ||||| |||||  
 CTCCGTCTCCGACGTCA  
 C  
 GAM1317 KIAA1863 3' CAGCCCGGGGCAGCCCCTGCCT 64868 A AGTA\_  
 CT AGAGGCAG GGTG GCTG  
 ||||| ||||| |||  
 TCTCCGTC CCGACG CGAC  
 C GGGCC  
 GAM1317 KIAA1922 5' TCAGCTCACTGCAACCTCCGCC 73643 A \_  
 TC GAGGC GAGGTTGCAGT AGCTGA  
 |||| ||||| |||||  
 CTCCG CTCCAACGTCA TCGACT  
 C C  
 GAM1317 KIAA1941 3' TCAGCCAAGCTGCCCTGCC 74845 A TT A\_  
 GGCAG GG GCAGT GCTGA  
 |||| || |||| |||||

		CCGTC CC CGTCG CGACT	
		— — AAC	
GAM1317 KIAA1956	3'	TCAGCTCACTGCAGCCTCCACC 78442	CA —
		TC GAGG GAGGTTGCAGT AGCTGA	
		CTCC CTCCGACGTCA TCGACT	
		AC C	
GAM1317 KIAA1971	3'	TACTGCAACCTCCACCTC 74227	CA
		GAGG GAGGTTGCAGTA	
		CTCC CTCCAACGTCAT	
		AC	
GAM1317 KIAA1987	5'	ACTGCAATCTCCGCCTC 88011	A
		GAGGC GAGGTTGCAGT	
		CTCCG CTCTAACGTCA	
		C	
GAM1317 KLK7	3'	ACTGCAACCTCCGCCTC 17281	A
		GAGGC GAGGTTGCAGT	
		CTCCG CTCCAACGTCA	
		C	
GAM1317 KLK7	3'	ACTGCAACCTCCGCCTC 57721	A
		GAGGC GAGGTTGCAGT	
		CTCCG CTCCAACGTCA	
		C	
GAM1317 KPNA6	3'	CAGCCACCACACACCTCTG 24602	— CA A
		CAGAGGT TG GT GCTG	
		GTCTCCA AC CA CGAC	
		C AC C	
GAM1317 KRT6	3'	CAGCTACAAGCCCCTCTGCC 82219	TT A_
		GGCAGAGG GC GTAGCTG	
		CCGTCTCC CG CATCGAC	
		C_ AA	
GAM1317 MCLC	3'	ACTGCAACCTCCACCTC 30677	CA
		GAGG GAGGTTGCAGT	
		CTCC CTCCAACGTCA	
		AC	
GAM1317 MEF-2	3'	ACTGCAACCTCCGCCTC 64374	A
		GAGGC GAGGTTGCAGT	
		CTCCG CTCCAACGTCA	
		C	
GAM1317 MGC10200	3'	GCTGCAAACCTCTGCCTC 58990	G
		GAGGCAGAG TTGCAGT	



		CTCCGTCTC AACGTCG	
		A	
GAM1317	MGC10818	3' TCAGCCACCTGCTACCTCTGCC 47543	T TA_
	TT	GAGGCAGAGGT GCAG GCTGA	
		TTCCGTCTCCA CGTC CGACT	
		T CAC	
GAM1317	MGC12518	3' TACTGCAACCTCTGCCCCT 64084 A	
		AG GGCAGAGGTTGCAGTA	
		TC CCGTCTCCAACGTCAT	
		C	
GAM1317	MGC13138	3' TCAGCTCACTGCAACCTCTGCC 53025	_
	TC	GAGGCAGAGGTTGCAGT AGCTGA	
		CTCCGTCTCCAACGTCA TCGACT	
		C	
GAM1317	MGC13198	5' TCAGCTCACTGCAACCTCCGTC 51097 A	_
	TCT	AGAGGC GAGGTTGCAGT AGCTGA	
		TCTCTG CTCCAACGTCA TCGACT	
		C C	
GAM1317	MGC14836	3' ACTGCAACCTCCGCCTC 53032 A	
		GAGGC GAGGTTGCAGT	
		CTCCG CTCCAACGTCA	
		C	
GAM1317	MGC21621	3' CAGCCTAGCCACCTCTGCCTCT 58794	T _ TA
		AGAGGCAGAGGT GC AG GCTG	
		TCTCCGTCTCCA CG TC CGAC	
		C A _	
GAM1317	MGC2474	3' ACTGCAACTTCCACCTC 43708 CA	
		GAGG GAGGTTGCAGT	
		CTCC CTTCAACGTCA	
		AC	
GAM1317	MGC2477	5' ACTGCAAGCTCTGCCTC 44057 G	
		GAGGCAGAG TTGCAGT	
		CTCCGTCTC AACGTCA	
		G	
GAM1317	MGC29891	3' ACTGCAACCTCCGCCTC 58194 A	
		GAGGC GAGGTTGCAGT	
		CTCCG CTCCAACGTCA	
		C	
GAM1317	MGC3113	3' ACTGCAGCCTCCACCTC 43836 CA	
		GAGG GAGGTTGCAGT	

			CTCC CTCCGACGTCA		
			AC		
GAM1317	MGC3329	3'	ACTGCAACCCCCGCCTC	44009	AGA
			GAGGC GGTTCAGT		
			CTCCG CCAACGTCA		
			CCC		
GAM1317	MGC4638	3'	ACTGCAACCTCCGTCTC	48938	A
			GAGGC GAGGTTGCAGT		
			CTCTG CTCCAACGTCA		
			C		
GAM1317	MGC5149	3'	TCAGCTCACTGCAACCTCTGCC	72299	—
	TC		GAGGCAGAGGTTGCAGT AGCTGA		
			CTCCGTCTCCAACGTCA TCGACT		
			C		
GAM1317	MGC9912	3'	ACTGCAACCTCCACCTC	54712	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	MLZE	5'	TCAGCTCACTGCAACCTCTGCC	48628	—
	TC		GAGGCAGAGGTTGCAGT AGCTGA		
			CTCCGTCTCCAACGTCA TCGACT		
			C		
GAM1317	MMPL1	3'	ACTGCAGCCTCCACCTC	14713	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCGACGTCA		
			AC		
GAM1317	MOCS3	3'	TCAGCTCACTGCAACCTCCGCC	27160	A —
	TC		GAGGC GAGGTTGCAGT AGCTGA		
			CTCCG CTCCAACGTCA TCGACT		
			C C		
GAM1317	MRPL44	3'	ACTGCAACCTCCACCTC	43312	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	MRPS27	3'	ACTGCAACCTCCGACTC	30633	GCA
			GAG GAGGTTGCAGT		
			CTC CTCCAACGTCA		
			AGC		
GAM1317	MtFMT	3'	TCAGCTCACTGCAACCTCCGCC	57660	A —
	TC		GAGGC GAGGTTGCAGT AGCTGA		

			CTCCG CTCCAACGTCA TCGACT		
			C C		
GAM1317 MUC16	5'	CAGCCACCACATTCCTGCCTC	60526	A GT CA A	
		GAGGCAG G TG GT GCTG			
		I			
		CTCCGTC C AC CA CGAC			
		_ TT AC C			
GAM1317 NDP52	3'	ACTACAGCCTCTGCCTC	19524	C	
		GAGGCAGAGGTTG AGT			
		CTCCGTCTCCGAC TCA			
		A			
GAM1317 NDUFB1	5'	TCAGCTCACTGCAACCTCTGCC	15821	_	
TC		GAGGCAGAGGTTGCAGT AGCTGA			
		CTCCGTCTCCAACGTCA TCGACT			
		C			
GAM1317 NDUFC2	3'	ACTGCAACCTCCACCTC	15823	CA	
		GAGG GAGGTTGCAGT			
		CTCC CTCCAACGTCA			
		AC			
GAM1317 Nup43	3'	ACTGCAACCTCCACCTC	44993	CA	
		GAGG GAGGTTGCAGT			
		CTCC CTCCAACGTCA			
		AC			
GAM1317 OPN4	3'	CAGCTATTTATGAGCCTCTGCC	52717	G _	
		GGCAGAGGTT CA GTAGCTG			
		CCGTCTCCGA GT TATCGAC			
		_ ATT			
GAM1317 OSBPL2	3'	ACCGCAACCTCCGCCTC	57846	A A	
		GAGGC GAGGTTGC GT			
		CTCCG CTCCAACG CA			
		C C			
GAM1317 OSBPL2	3'	ACCGCAACCTCCGCCTC	29195	A A	
		GAGGC GAGGTTGC GT			
		CTCCG CTCCAACG CA			
		C C			
GAM1317 PASK	5'	ACTGCAACCTCTGCCTC	30707		
		GAGGCAGAGGTTGCAGT			
		CTCCGTCTCCAACGTCA			
GAM1317 PELI1	5'	ACTGCAACCTCCTCCTC	40245	CA	
		GAGG GAGGTTGCAGT			

		CTCC CTCCAACGTCA		
		TC		
GAM1317 PELI1	5'	ACTGCAACCTCTGCCTC	40248	
		GAGGCAGAGGTTGCAGT		
		CTCCGTCTCCAACGTCA		
GAM1317 PELI1	5'	ACTGCAAGCTCTGCCTC	40251	G
		GAGGCAGAG TTGCAGT		
		CTCCGTCTC AACGTCA		
		G		
GAM1317 PIP3-E	3'	ACTGCAACCTCTGCCTC	66793	
		GAGGCAGAGGTTGCAGT		
		CTCCGTCTCCAACGTCA		
GAM1317 PPP1R10	5'	TTGTGTCTTCTGCCCT	10741	A T
		AG GGCAGAGG TGCAG		
		TC CCGTCTTC GTGTT		
		C T		
GAM1317 PRO0365	5'	ACTGCAACCTCTGTCTC	26146	
		GAGGCAGAGGTTGCAGT		
		CTCTGTCTCCAACGTCA		
GAM1317 PRO0365	5'	TCAGCTCACTGCAACCTCCACC	26170	CA
	TC	GAGG GAGGTTGCAGT AGCTGA		—
		CTCC CTCCAACGTCA TCGACT		
		AC C		
GAM1317 PRO1992	5'	ACTGCAACCTCTGCCTC	26048	
		GAGGCAGAGGTTGCAGT		
		CTCCGTCTCCAACGTCA		
GAM1317 PRO2955	3'	TCAGCTCACTGCAACCTCTGCC	37647	—
	TC	GAGGCAGAGGTTGCAGT AGCTGA		
		CTCCGTCTCCAACGTCA TCGACT		
		C		
GAM1317 PSPH	3'	ACTGCAAGCTCTGCCTC	15912	G
		GAGGCAGAG TTGCAGT		
		CTCCGTCTC AACGTCA		
		G		
GAM1317 PSTPIP2	3'	TCAGCTCACTGCAACCTCTGCC	44398	—
	TC	GAGGCAGAGGTTGCAGT AGCTGA		

			CTCCGTCTCCAACGTCA TCGACT		
			C		
GAM1317	RAB33B	3'	ACTGCAACCTCCGCCTC 48483	A	
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	RAB39	3'	CTGCAACCTCTGCTTC 76632		
			GAGGCAGAGGTTGCAG		
			CTTCGTCTCCAACGTC		
GAM1317	RAI	5'	ACTGCAACCTCCGCCTC 21868	A	
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	RAP140	3'	ACTGCAAGCTCTGCCTC 30841	G	
			GAGGCAGAG TTGCAGT		
			CTCCGTCTC AACGTCA		
			G		
GAM1317	RASGRP4	3'	AGCTGAACAACCTCTACCT 53647	C	CAG
			AGG AGAGGTTG TAGCT		
			TCC TCTCCAAC GTCGA		
			A AA_		
GAM1317	RASSF2	3'	TCAGCTCACTGCAACATCCGCC 28446	A	G _
	TCT		AGAGGC GA GTTGCAGT AGCTGA		
			TCTCCG CT CAACGTCA TCGACT		
			C A C		
GAM1317	RNF8	3'	TCAGCTCACTGCAACCTCCACC 14241	CA	_
	TC		GAGG GAGGTTGCAGT AGCTGA		
			CTCC CTCCAACGTCA TCGACT		
			AC C		
GAM1317	RNO2	5'	TCAGCTCACTGCAACCTCCACC 52778	CA	_
	TT		GAGG GAGGTTGCAGT AGCTGA		
			TTCC CTCCAACGTCA TCGACT		
			AC C		
GAM1317	SAC2	3'	CAGCCTGGGAAACATCTGCCTC 30055	GG_	G TA
	T		AGAGGCAGA TT CAG GCTG		
			TCTCCGTCT AG GTC CGAC		
			ACAA G _		
GAM1317	SC4MOL	3'	TCAGCTCACTGCAACCTCTGCC 22163		_
	TC		GAGGCAGAGGTTGCAGT AGCTGA		

			CTCCGTCTCCAACGTCA TCGACT	
			C	
GAM1317	SCAMP-4	3'	ACTGCAACCTCTGCCTC 54386	
			GAGGCAGAGGTTGCAGT	
			CTCCGTCTCCAACGTCA	
GAM1317	SCAND2	3'	ACTGCAACATCTGCCTC 41884	G
			GAGGCAGA GTTGCAGT	
			CTCCGTCT CAACGTCA	
			A	
GAM1317	SCYA16	3'	ACTGTAACCTCCACCTC 15951	CA
			GAGG GAGGTTGCAGT	
			CTCC CTCCAATGTCA	
			AC	
GAM1317	SELB	3'	CAGCCACGCCTCAGCCTCT 61914	A TGCA A
			AGAGGC GAGGT GT GCTG	
			TCTCCG CTCCG CA CGAC	
			A C	
GAM1317	SERF1B	3'	ACTGCAACCTCCGCCTC 43405	A
			GAGGC GAGGTTGCAGT	
			CTCCG CTCCAACGTCA	
			C	
GAM1317	SERF1B	3'	TCAGCTCCATGCAACCTCTGCC 43424	GT_
	TC		GAGGCAGAGGTTGCA AGCTGA	
			CTCCGTCTCCAACGT TCGACT	
			ACC	
GAM1317	SFXN2	3'	ACTGCAAACTCTGCCTC 73936	G
			GAGGCAGAG TTGCAGT	
			CTCCGTCTC AACGTCA	
			A	
GAM1317	SIRPB1	3'	ACTGCAACCCCGCCTC 20237	AGA
			GAGGC GGTTCAGT	
			CTCCG CCAACGTCA	
			CCC	
GAM1317	SLC11A1	3'	ATTGCAACCTCCACCTT 59451	CA
			GAGG GAGGTTGCAGT	
			TTCC CTCCAACGTTA	
			AC	
GAM1317	SLC12A8	3'	ACTGCAACCTCTGCTTC 44894	
			GAGGCAGAGGTTGCAGT	

CTTCGTCTCCAACGTCA

GAM1317 SLC2A10 3' ACTGCAACCTCCACTTC 47813 CA  
GAGG GAGGTTGCAGT  
||||| |||||||||  
CTTC CTCCAACGTCA  
AC

GAM1317 SLC2A11 3' CAGCTACTGTCCTGTCCTCTGC 47963 TT\_\_\_\_  
TTC GAGGCAGAGG GCAGTAGCTG  
||||||| |||||||  
CTTCGTCTCC TGTTCATCGAC  
TGTCC

GAM1317 SLC6A14 3' TCAGCTCACTGCAACCTCTGCC 23360 \_  
TT GAGGCAGAGGTTGCAGT AGCTGA  
||||||| |||||  
TTCCGTCTCCAACGTCA TCGACT  
C

GAM1317 SP2 3' CAGCCCCGCCACAACCTCTCCT 11885 C CA A\_\_\_\_  
C GAGG AGAGGTTG GT GCTG  
||||| || |||  
CTCC TCTCCAAC CG CGAC  
\_ AC CCC

GAM1317 SQV7L 5' TCAGCTCACTGCAACCACTGCC 70579 A \_  
TC GAGGCAG GGTTCAGT AGCTGA  
||||| ||||||| |||||  
CTCCGTC CCAACGTCA TCGACT  
A C

GAM1317 SREC 3' ACTGCAAGCTCTGCCTC 13498 G  
GAGGCAGAG TTGCAGT  
||||||| |||||  
CTCCGTCTC AACGTCA  
G

GAM1317 STAF65(gamma) 3' ACTGCAACCTCTGCCTC 29421  
GAGGCAGAGGTTGCAGT  
||||||| |||||  
CTCCGTCTCCAACGTCA

GAM1317 SUN1 3' ACTGCAGCCTCCACCTC 47151 CA  
GAGG GAGGTTGCAGT  
||||| |||||||||  
CTCC CTCCGACGTCA  
AC

GAM1317 SYT13 3' ACTGCAACCTCCGCCTC 93445 A  
GAGGC GAGGTTGCAGT  
||||| |||||||||  
CTCCG CTCCAACGTCA  
C

GAM1317 THEA 3' TCAGCTCACTGCAACCTCGGCC 66296 A \_  
TC GAGGC GAGGTTGCAGT AGCTGA  
||||| ||||||||| |||||

			CTCCG CTCCAACGTCA TCGACT	
			G C	
GAM1317	TNK1	3'	TCAGCTACCACACTGGACTCT 14320	G_ AG TGCA
			AGAG CAG GT GTAGCTGA	
			TCTC GTC CA CATCGACT	
			AG A_ C__	
GAM1317	TOR1B	3'	TCAACTCACTGCAACCTCCGCT 27205	A _ C
			GGC GAGGTTGCAGT AG TGA	
			TCG CTCCAACGTCA TC ACT	
			C C A	
GAM1317	TRIM5	3'	ACTGCAACCTCCACCTCT 52291	CA
			AGAGG GAGGTTGCAGT	
			TCTCC CTCCAACGTCA	
			AC	
GAM1317	TRIM6	3'	ACTGCAACCTCTGCCTC 54127	
			GAGGCAGAGGTTGCAGT	
			CTCCGTCTCCAACGTCA	
GAM1317	TTY7	3'	CAGCCACTCTTTTCCTCCTACC 49179	CA_ TTGC_ A
		TCT	AGAGG GAGG AGT GCTG	
			TCTCC CTCC TCA CGAC	
			ATC TTTTC C	
GAM1317	TU12B1-TY	3'	TCAGCTCACTGCAACCTCTGCC 33407	_
		TC	GAGGCAGAGGTTGCAGT AGCTGA	
			CTCCGTCTCCAACGTCA TCGACT	
			C	
GAM1317	TUBB5	3'	CAGCTCCTACCTCTGACC 20297	_ TGC T
			GG CAGAGGT AG AGCTG	
			CC GTCTCCA TC TCGAC	
			A _ C	
GAM1317	TUBB5	3'	TCAGCTCCTACCTCTGACC 20308	_ TGC T
			GG CAGAGGT AG AGCTGA	
			CC GTCTCCA TC TCGACT	
			A _ C	
GAM1317	TUCAN	3'	TCAGCTCACTGCAACCTCTGCC 30284	_
		TC	GAGGCAGAGGTTGCAGT AGCTGA	
			CTCCGTCTCCAACGTCA TCGACT	
			C	
GAM1317	TUSP	3'	AGTAGCTGACCCACAACCTCTG 39624	G TAG
		ACTC	G CAGAGGTTG CAG CT	



C GTCTCCAAC GTC GA  
 A ACCCIIIA GAT  
 GAM1317 UBAP 3' CAGCACTAACTCCACCTCT 76351 CA GTTGC A  
 AGAGG GAG AGT GCTG  
 ||||| ||| ||| |||||  
 TCTCC CTC TCA CGAC  
 AC AA\_\_\_ \_  
 GAM1317 UBF-fl 3' ACTGCAACCTCTGCCTC 51545  
 GAGGCAGAGGTTGCAGT  
 |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1317 UBF-fl 3' ATTGCAACCTCTGCTTC 51551  
 GAGGCAGAGGTTGCAGT  
 |||||  
 CTTCGTCTCCAACGTTA  
  
 GAM1317 USP22 3' ACTGCAACCTCCACCTC 67997 CA  
 GAGG GAGGTTGCAGT  
 ||| |||||  
 CTCC CTCCAACGTCA  
 AC  
 GAM1317 VCX-8r 3' CAGCTACTCCCCTATCTC 33054 GC A TTGC  
 GAG AG GG AGTAGCTG  
 ||| ||| |||||  
 CTC TC CC TCATCGAC  
 TA C \_\_\_\_  
 GAM1317 VDU1 3' TCAGCTCACTGCAGCCTCCACC 30428 CA \_  
 TC GAGG GAGGTTGCAGT AGCTGA  
 ||| ||||| |||||  
 CTCC CTCCGACGTCA TCGACT  
 AC C  
 GAM1317 VPS33A 3' ACTGCAACCTCCACCTC 43330 CA  
 GAGG GAGGTTGCAGT  
 ||| |||||  
 CTCC CTCCAACGTCA  
 AC  
 GAM1317 WBSCR20A 5' ACCGCAACCTCTGCCTC 49644 A  
 GAGGCAGAGGTTGC GT  
 ||||| ||  
 CTCCGTCTCCAACG CA  
 C  
 GAM1317 ZNF338 3' ACTGCAACGTCCGCCTC 42008 A G  
 GAGGC GA GTTGCAGT  
 ||||| || |||||  
 CTCCG CT CAACGTCA  
 C G  
 GAM1317 ZTL1 3' ACTGCAACCTCTGCCTC 43907  
 GAGGCAGAGGTTGCAGT  
 |||||

CTCCGTCTCCAACGTCA

GAM1317 LOC112724 5' ACTGCAACCTCCACCTC 56490 CA  
GAGG GAGGTTGCAGT  
|||| |||||||||  
CTCC CTCCAACGTCA  
AC

GAM1317 LOC113675 5' ACTGCAACCTCCGCCTC 56566 A  
GAGGC GAGGTTGCAGT  
|||| |||||||||  
CTCCG CTCCAACGTCA  
C

GAM1317 LOC115129 3' TCAGCTCTAAACTCTCTGCCTC 73243 \_ GC T  
GAGGCAGAG GTT AG AGCTGA  
||||||| ||| || |||||  
CTCCGTCTC CAA TC TCGACT  
T A\_ \_

GAM1317 LOC115219 5' ACTGCAACCTCCGCCTC 73291 A  
GAGGC GAGGTTGCAGT  
|||| |||||||||  
CTCCG CTCCAACGTCA  
C

GAM1317 LOC118471 5' CAGCCACTGCAGCTCCCT 73915 CAGA A  
AGG GGTTCAGT GCTG  
||| ||||||| |||  
TCC TCGACGTCA CGAC  
C\_ \_ C

GAM1317 LOC118738 3' CTGCAGCCTCTGCCTCT 75490  
AGAGGCAGAGGTTGCAG  
|||||||||||  
TCTCCGTCTCCGACGTC

GAM1317 LOC119392 3' ACTGCAACCTCTGCCTCT 59130  
AGAGGCAGAGGTTGCAGT  
|||||||||||  
TCTCCGTCTCCAACGTCA

GAM1317 LOC120114 3' TCAGCTCACTGCAATCTCCACC 75539 CA \_  
TC GAGG GAGGTTGCAGT AGCTGA  
|||| ||||||| |||||  
CTCC CTCTAACGTCA TCGACT  
AC C

GAM1317 LOC120939 3' TCAGCTCACTGTAACTCCACC 76262 CA \_  
TC GAGG GAGGTTGCAGT AGCTGA  
|||| ||||||| |||||  
CTCC CTCCAATGTCA TCGACT  
AC C

GAM1317 LOC126364 3' TCAGCTCACTGCAACCTCCGCC 75700 A \_  
TC GAGGC GAGGTTGCAGT AGCTGA  
|||| ||||||| |||||

			CTCCG CTCCAACGTCA TCGACT		
			C C		
GAM1317	LOC126661	3'	TCAGCTCACTGCAACCTCCGCC 74559	A	—
		TC	GAGGC GAGGTTGCAGT AGCTGA		
			CTCCG CTCCAACGTCA TCGACT		
			C C		
GAM1317	LOC126669	3'	AGCCACTGCAAGCCCT 75396	A	AGAGG A
			AG GGC TTGCAGT GCT		
			TC CCG AACGTCA CGA		
			— ——— C		
GAM1317	LOC128077	3'	ACTGCAACCTCCGCCTC 74699	A	
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	LOC128077	3'	ACTGCAACCTCTGCCTC 74702		
			GAGGCAGAGGTTGCAGT		
			CTCCGTCTCCAACGTCA		
GAM1317	LOC128387	3'	ACTGCAACCTCCACTTC 74744	CA	
			GAGG GAGGTTGCAGT		
			CTTC CTCCAACGTCA		
			AC		
GAM1317	LOC128989	3'	ACTGCAACCTCCGCCTC 74801	A	
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	LOC130813	3'	ACCGCAACCTCCGCCTC 75758	A	A
			GAGGC GAGGTTGC GT		
			CTCCG CTCCAACG CA		
			C C		
GAM1317	LOC131308	3'	ACTGCAACCTCTGCTTC 75002		
			GAGGCAGAGGTTGCAGT		
			CTTCGTCTCCAACGTCA		
GAM1317	LOC132625	3'	ACTGCAACCTCCACCTC 75895	CA	
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	LOC133686	3'	CTGCAACCTCCATCTC 75121	CA	
			GAGG GAGGTTGCAG		

	CTCT CTCCAACGTC		
	AC		
GAM1317 LOC135293 3'	ACTGCAACCTCTGCCTC 76171		
	GAGGCAGAGGTTGCAGT		
	CTCCGTCTCCAACGTCA		
GAM1317 LOC135763 3'	ACTGCAACCTCCGCCTC 56782	A	
	GAGGC GAGGTTGCAGT		
	CTCCG CTCCAACGTCA		
	C		
GAM1317 LOC142913 5'	ACTGCAGCCTCCACCTC 76410	CA	
	GAGG GAGGTTGCAGT		
	CTCC CTCCGACGTCA		
	AC		
GAM1317 LOC143187 3'	ACTGCAACCTCCACCTC 59094	CA	
	GAGG GAGGTTGCAGT		
	CTCC CTCCAACGTCA		
	AC		
GAM1317 LOC143241 5'	TCAGTCACTGCAACCTCTGCC 57181		—
TC	GAGGCAGAGGTTGCAGT AGCTGA		
	CTCCGTCTCCAACGTCA TCGACT		
	C		
GAM1317 LOC143425 3'	TTGCAACTCTGCCTCT 87641	G	
	AGAGGCAGAG TTGCAG		
	TCTCCGTCTC AACGTT		
GAM1317 LOC143920 3'	TTGCAACCTCTTCCCCT 76628	A C	
	AG GG AGAGGTTGCAG		
	TC CC TCTCCAACGTT		
	C T		
GAM1317 LOC144248 5'	ACTGCAACCTCCACCTC 76732	CA	
	GAGG GAGGTTGCAGT		
	CTCC CTCCAACGTCA		
	AC		
GAM1317 LOC144317 5'	TCAACTCACTGCAACCTCTTCC 76798	C	— C
TC	GAGG AGAGGTTGCAGT AG TGA		
	CTCC TCTCCAACGTCA TC ACT		
	T C A		
GAM1317 LOC144524 5'	TCAGTCACTGCAACCTCCACC 83137	CA	—
TC	GAGG GAGGTTGCAGT AGCTGA		

		CTCC CTCCAACGTCA TCGACT		
		AC C		
GAM1317	LOC144742 5'	CTGCAACCTTCGCCTC 76944	AG	
		GAGGC AGGTTGCAG		
		CTCCG TCCAACGTC		
		CT		
GAM1317	LOC145622 3'	ACTGCAACTTCTGCCTC 77286		
		GAGGCAGAGGTTGCAGT		
		CTCCGTCTTCAACGTCA		
GAM1317	LOC145719 3'	CAACTCCACCAACCTCTGGCTC 83448	G	CAGT C
	T	AGAG CAGAGGTTG AG TG		
		TCTC GTCTCCAAC TC AC		
		G CACC A		
GAM1317	LOC145720 3'	CAACTCCACCAACCTCTGGCTC 83430	G	CAGT C
	T	AGAG CAGAGGTTG AG TG		
		TCTC GTCTCCAAC TC AC		
		G CACC A		
GAM1317	LOC145725 3'	ACTGCAGCCTCCACCTC 77396	CA	
		GAGG GAGGTTGCAGT		
		CTCC CTCCGACGTCA		
		AC		
GAM1317	LOC145732 3'	ACTGCAGCCTCCACCTC 77418	CA	
		GAGG GAGGTTGCAGT		
		CTCC CTCCGACGTCA		
		AC		
GAM1317	LOC145757 5'	ACTACAACCTCTGCCTC 77448	C	
		GAGGCAGAGGTTG AGT		
		CTCCGTCTCCAAC TCA		
		A		
GAM1317	LOC146050 3'	TCAGTCACTGCAACCTCTGCC 77647		—
	TT	GAGGCAGAGGTTGCAGT AGCTGA		
		TTCCGTCTCCAACGTCA TCGACT		
		C		
GAM1317	LOC146050 3'	TCAGTCACTGCAACCTCTGCT 77648		—
	TC	GAGGCAGAGGTTGCAGT AGCTGA		
		CTTCGTCTCCAACGTCA TCGACT		
		C		
GAM1317	LOC146229 3'	ACTGCAACCTCCACCTC 77726	CA	
		GAGG GAGGTTGCAGT		

	CTCC CTCCAACGTCA		
	AC		
GAM1317 LOC146229 3'	CTGCAACCTCCACCTC	77750	CA
	GAGG GAGGTTGCAG		
	CTCC CTCCAACGTC		
	AC		
GAM1317 LOC146325 3'	CTGCAGCCCCTGCCCCCT	59178	A A
	AG GGCAG GGTTGCAG		
	TC CCGTC CCGACGTC		
	C C		
GAM1317 LOC146346 5'	ACTGCAACTTCTGCCTC	77837	
	GAGGCAGAGGTTGCAGT		
	CTCCGTCTTCAACGTCA		
GAM1317 LOC146455 3'	ACTGCAATCTCTGCCTCT	77901	
	AGAGGCAGAGGTTGCAGT		
	TCTCCGTCTCTAACGTCA		
GAM1317 LOC146784 5'	ACTGCAACCTCCACCTC	78103	CA
	GAGG GAGGTTGCAGT		
	CTCC CTCCAACGTCA		
	AC		
GAM1317 LOC146820 5'	ACTGCAACCTCCGCATC	78147	G A
	GA GC GAGGTTGCAGT		
	CT CG CTCCAACGTCA		
	A C		
GAM1317 LOC146901 3'	ATTGCAACCTCCACCTT	83830	CA
	GAGG GAGGTTGCAGT		
	TTCC CTCCAACGTTA		
	AC		
GAM1317 LOC146909 3'	ACTGCAACCTCCGCCTC	78162	A
	GAGGC GAGGTTGCAGT		
	CTCCG CTCCAACGTCA		
	C		
GAM1317 LOC146952 5'	TCAGTCACTGCAACCTCCACC	83875	CA
TCT	AGAGG GAGGTTGCAGT AGCTGA		
	TCTCC CTCCAACGTCA TCGACT		
	AC C		
GAM1317 LOC147054 3'	CTGCAACTTCCGCCTC	83920	A
	GAGGC GAGGTTGCAG		

		CTCCG CTTCAACGTC			
		C			
GAM1317	LOC147071 5'	ACTGCAACCTCTGCCTC	72990		
		GAGGCAGAGGTTGCAGT			
		CTCCGTCTCCAACGTCA			
GAM1317	LOC147276 3'	TCAGCTCACTGCAACGTCTGCC	78340	G	—
	TC	GAGGCAGA GTTGCAGT AGCTGA			
		CTCCGTCT CAACGTCA TCGACT			
		G C			
GAM1317	LOC147407 3'	ACTGCAACCTCCGCCTC	76319	A	
		GAGGC GAGGTTGCAGT			
		CTCCG CTCCAACGTCA			
		C			
GAM1317	LOC147660 3'	ACAGCAACCTCCGCCTC	78389	A	A
		GAGGC GAGGTTGC GT			
		CTCCG CTCCAACG CA			
		C A			
GAM1317	LOC147817 3'	ACTGCAACCTCCACCTC	78488	CA	
		GAGG GAGGTTGCAGT			
		CTCC CTCCAACGTCA			
		AC			
GAM1317	LOC147841 3'	TCAGCTCAGCAACCTCTGCC	78534	A	—
	TC	GAGGCAGAGGTTGC GT AGCTGA			
		CTCCGTCTCCAACG CA TCGACT			
		A C			
GAM1317	LOC147990 3'	ACTACAACCTCTGCCTC	84086	C	
		GAGGCAGAGGTTG AGT			
		CTCCGTCTCCAAC TCA			
		A			
GAM1317	LOC148046 3'	CAGCGCGGACCCCTGCCTCT	84103	A	— AGTA
		AGAGGCAG GGTT GC GCTG			
		TCTCCGTC CCAG CG CGAC			
		C G —			
GAM1317	LOC148137 3'	ACGGCAACCTCCACCTC	58417	CA	A
		GAGG GAGGTTGC GT			
		CTCC CTCCAACG CA			
		AC G			
GAM1317	LOC148147 3'	ACTGCAATCTCTGCCTC	78670		
		GAGGCAGAGGTTGCAGT			

CTCCGTCTCTAACGTCA

GAM1317 LOC148189 5' ACTGCAACCTCCACCTC 78703 CA  
GAGG GAGGTTGCAGT  
|||| ||||||||  
CTCC CTCCAACGTCA  
AC

GAM1317 LOC148198 3' TCAGTCACTGCAACCTCCATC 70690 CA \_  
TC GAGG GAGGTTGCAGT AGCTGA  
|||| |||||||| |||||  
CTCT CTCCAACGTCA TCGACT  
AC C

GAM1317 LOC148887 5' ACTGCAACATCTGCCTC 84228 G  
GAGGCAGA GTTGCAGT  
|||||| |||||||  
CTCCGTCT CAACGTCA  
A

GAM1317 LOC148918 5' ACTGCAGCCTCCACCTC 79056 CA  
GAGG GAGGTTGCAGT  
|||| ||||||||  
CTCC CTCCGACGTCA  
AC

GAM1317 LOC149171 5' ACTGCAACCTCTGTCTC 79215  
GAGGCAGAGGTTGCAGT  
|||||||||||||  
CTCTGTCTCCAACGTCA

GAM1317 LOC149506 3' ACTGCAACTTCCACCTC 84447 CA  
GAGG GAGGTTGCAGT  
|||| ||||||||  
CTCC CTTCAACGTCA  
AC

GAM1317 LOC149506 3' TCAGTCACTGCAACCTCTGCC 84481 \_  
TC GAGGCAGAGGTTGCAGT AGCTGA  
||||||||||||| |||||  
CTCCGTCTCCAACGTCA TCGACT  
C

GAM1317 LOC149668 3' CAATATAGTGAAACCCCTGCCT 84536 A G G GC\_  
CT AGAGGCAG GGTT CA TA TG  
|||||| ||| || ||  
TCTCCGTC CCAA GT AT AC  
C A G ATA

GAM1317 LOC149684 3' CAGCACTCATCCTCCACCCCT 84611 A CA T C A  
AG GG GAGG TG AGT GCTG  
|| || ||| || ||| |||  
TC CC CTCC AC TCA CGAC  
C AC T \_ \_

GAM1317 LOC149692 3' ACTGTAACCTCTGCCTC 84579  
GAGGCAGAGGTTGCAGT  
|||||||||||||



CTCCGTCTCCAATGTCA

GAM1317 LOC149703 5' TCAGCTTAATGCAACCTCTACC 84660 C GT\_  
TC GAGG AGAGGTTGCA AGCTGA

||||| |||||  
CTCC TCTCCAACGT TCGACT  
A AAT

GAM1317 LOC149711 3' ACTGCAACCTCTGCTTC 84668  
GAGGCAGAGGTTGCAGT  
|||||  
CTTCGTCTCCAACGTCA

GAM1317 LOC150054 5' ACTGCAACCTTCGCCTCT 84825 AG  
AGAGGC AGGTTGCAGT  
|||||  
TCTCCG TCCAACGTCA  
CT

GAM1317 LOC150225 3' ACTGCAACTTCCGCCTC 84977 A  
GAGGC GAGGTTGCAGT  
|||||  
CTCCG CTCAACGTCA  
C

GAM1317 LOC150397 3' ATTGCAACCTCCGCCTC 79839 A  
GAGGC GAGGTTGCAGT  
|||||  
CTCCG CTCCAACGTTA  
C

GAM1317 LOC150696 3' ACTGCAGCCTCCACCTC 58474 CA  
GAGG GAGGTTGCAGT  
|||||  
CTCC CTCCGACGTCA  
AC

GAM1317 LOC150960 3' GCTGCAACCTCCGCCTC 80065 A  
GAGGC GAGGTTGCAGT  
|||||  
CTCCG CTCCAACGTG  
C

GAM1317 LOC151057 3' ACTGCAACCTCTGCCTC 85202  
GAGGCAGAGGTTGCAGT  
|||||  
CTCCGTCTCCAACGTCA

GAM1317 LOC151201 3' TCAGCTCACTGCAACCTCCACC 85292 CA \_  
TC GAGG GAGGTTGCAGT AGCTGA  
|||||  
CTCC CTCCAACGTCA TCGACT  
AC C

GAM1317 LOC151475 5' ACTGCAACCTCCACCTC 85384 CA  
GAGG GAGGTTGCAGT  
|||||

	CTCC CTCCAACGTCA		
	AC		
GAM1317 LOC151475 5'	TCAGTCACTGCAACCTCTGCC 85420	—	
TC	GAGGCAGAGGTTGCAGT AGCTGA		
	CTCCGTCTCCAACGTCA TCGACT		
	C		
GAM1317 LOC151534 3'	TCAGTACTTATCCCCACCCT 56686	CAGA TTGC	
	AGG GG AGTAGCTGA		
	TCC CC TCATCGACT		
	CACC TTAT		
GAM1317 LOC151719 5'	TCAGCCAGACCCACCACTGCCT 80344	A TGCAGTA	
CT	AGAGGCAG GGT GCTGA		
	TCTCCGTC CCA CGACT		
	A CCCAGAC		
GAM1317 LOC151826 3'	TCAGTCACTGCAACCTCCGCC 80367	A —	
TC	GAGGC GAGGTTGCAGT AGCTGA		
	CTCCG CTCCAACGTCA TCGACT		
	C C		
GAM1317 LOC152220 3'	TCAGTCACTGCAACCTCCGCT 85590	A —	
TC	GAGGC GAGGTTGCAGT AGCTGA		
	CTTCG CTCCAACGTCA TCGACT		
	C C		
GAM1317 LOC152245 3'	ACTGCAACCTCCGCCTT 85596	A	
	GAGGC GAGGTTGCAGT		
	TTCCG CTCCAACGTCA		
	C		
GAM1317 LOC152300 3'	TCAGTCACTGCAAGCTCTGCC 80549	G —	
TCT	AGAGGCAGAG TTGCAGT AGCTGA		
	TCTCCGTCTC AACGTCA TCGACT		
	G C		
GAM1317 LOC152445 3'	ACTGCAACCTCTGCCTC 85738		
	GAGGCAGAGGTTGCAGT		
	CTCCGTCTCCAACGTCA		
GAM1317 LOC152582 5'	ACCGCAACCTCTGCCTC 85785	A	
	GAGGCAGAGGTTGC GT		
	CTCCGTCTCCAACG CA		
	C		
GAM1317 LOC152620 3'	TCAGTCACTACAACCTCTGCC 60088	C —	
TC	GAGGCAGAGGTTG AGT AGCTGA		

	CTCCGTCTCCAAC TCA TCGACT		
	A C		
GAM1317 LOC152687 5'	TCAGCCACAGCCTCTGCCTC 80641	CAGTA	
	GAGGCAGAGGTTG GCTGA		
	CTCCGTCTCCGAC CGACT		
	AC__		
GAM1317 LOC152719 5'	TCAGATCACTGCAACCTCTGCC 85857	AG_	
TC	GAGGCAGAGGTTGCAGT CTGA		
	CTCCGTCTCCAACGTCA GACT		
	CTA		
GAM1317 LOC152794 5'	ACTGCAACCTCTACCTC 80670 C		
	GAGG AGAGGTTGCAGT		
	CTCC TCTCCAACGTCA		
	A		
GAM1317 LOC152925 3'	TACTCCAACCTCTGCCTC 80737	C	
	GAGGCAGAGGTTG AGTA		
	CTCCGTCTCCAAC TCAT		
	C		
GAM1317 LOC153077 3'	ACTGCAACCTCCGCCTC 85901	A	
	GAGGC GAGGTTGCAGT		
	CTCCG CTCCAACGTCA		
	C		
GAM1317 LOC153606 5'	ACTGCACCCTCTGCCTC 86071	T	
	GAGGCAGAGG TGCAGT		
	CTCCGTCTCC ACGTCA		
	C		
GAM1317 LOC153688 3'	ACTGCAACCTCCACCTC 86092	CA	
	GAGG GAGGTTGCAGT		
	CTCC CTCCAACGTCA		
	AC		
GAM1317 LOC153883 5'	ACTGCAACCTCCACCCT 80976	A CA	
	AG GG GAGGTTGCAGT		
	TC CC CTCCAACGTCA		
	_ AC		
GAM1317 LOC154075 3'	TCAGTCACTGCAACCTCCGCC 81050	A _	
TC	GAGGC GAGGTTGCAGT AGCTGA		
	CTCCG CTCCAACGTCA TCGACT		
	C C		
GAM1317 LOC154282 5'	ACTGCAACCTCCACCTC 86192	CA	
	GAGG GAGGTTGCAGT		

		CTCC CTCCAACGTCA			
		AC			
GAM1317	LOC154822 3'	ACTGCAACCTCTGTCTC	86256		
		GAGGCAGAGGTTGCAGT			
		CTCTGTCTCCAACGTCA			
GAM1317	LOC154877 3'	ATTGCAACCTCCGCCTT	86281	A	
		GAGGC GAGGTTGCAGT			
		TTCCG CTCCAACGTTA			
		C			
GAM1317	LOC154877 3'	TCAGTCACTGCAACCTCTACC	86311	C	—
	TC	GAGG AGAGGTTGCAGT AGCTGA			
		CTCC TCTCCAACGTCA TCGACT			
		A C			
GAM1317	LOC157247 5'	TCAGTCACTGCAACCTCCACC	81377	CA	—
		GG GAGGTTGCAGT AGCTGA			
		CC CTCCAACGTCA TCGACT			
		AC C			
GAM1317	LOC157349 5'	CAGGGGTACTTCTGCCCT	81410	A	T AGTAG
		AG GGCAGAGGT GC CTG			
		TC CCGTCTTCA TG GAC			
		C _ GG__			
GAM1317	LOC157349 3'	TCAGGCATCAGACCTCTGCCCC	81423	A	GCAGTAG
	T	AG GGCAGAGGTT CTGA			
		TC CCGTCTCCAG GACT			
		C ACTACG_			
GAM1317	LOC157506 3'	ACTGCAATCTCTGCCTC	81436		
		GAGGCAGAGGTTGCAGT			
		CTCCGTCTCTAACGTCA			
GAM1317	LOC157507 5'	ACTGCAACGTCCGCCTC	81450	A G	
		GAGGC GA GTTGCAGT			
		CTCCG CT CAACGTCA			
		C G			
GAM1317	LOC157798 5'	ACTGCAACCTCCGCCTC	86543	A	
		GAGGC GAGGTTGCAGT			
		CTCCG CTCCAACGTCA			
		C			
GAM1317	LOC157858 5'	ACTGCAACCTCTGCCTC	86578		
		GAGGCAGAGGTTGCAGT			

CTCCGTCTCCAACGTCA

GAM1317	LOC158014	5'	ACTGCAATCTCCGCCTC	81643	A	
			GAGGC GAGGTTGCAGT			
			CTCCG CTCTAACGTCA			
			C			
GAM1317	LOC158402	5'	TCAGTCACTGTAACCTCTGCC	86813		—
	TC		GAGGCAGAGGTTGCAGT AGCTGA			
			CTCCGTCTCCAATGTCA TCGACT			
			C			
GAM1317	LOC158476	3'	TCAGTCACTGCAACCTCCGCC	86853	A	—
			GGC GAGGTTGCAGT AGCTGA			
			CCG CTCCAACGTCA TCGACT			
			C C			
GAM1317	LOC158668	3'	TCAGTCACTGCAACCTCTGCC	69376		—
	TC		GAGGCAGAGGTTGCAGT AGCTGA			
			CTCCGTCTCCAACGTCA TCGACT			
			C			
GAM1317	LOC158865	5'	ACTGCAACCTCTGCCTC	86927		
			GAGGCAGAGGTTGCAGT			
			CTCCGTCTCCAACGTCA			
GAM1317	LOC161829	3'	ACTGCAACCTCCGCCTC	82308	A	
			GAGGC GAGGTTGCAGT			
			CTCCG CTCCAACGTCA			
			C			
GAM1317	LOC164714	3'	CAGTCTGCAACCTCCGCT	87223	A	T
			GGC GAGGTTGCAG AGCTG			
			TCG CTCCAACGTC TCGAC			
			C			
GAM1317	LOC169611	3'	TCAGTCACTGCAATCTCCGCC	82779	A	—
	TC		GAGGC GAGGTTGCAGT AGCTGA			
			CTCCG CTCTAACGTCA TCGACT			
			C C			
GAM1317	LOC196047	5'	ACTGCAACCTCCGCCTC	89587	A	
			GAGGC GAGGTTGCAGT			
			CTCCG CTCCAACGTCA			
			C			
GAM1317	LOC196264	3'	ACTGCAACCTCTGCCTC	87598		
			GAGGCAGAGGTTGCAGT			

CTCCGTCTCCAACGTCA

GAM1317 LOC196411 3' ACTGCAACCTCCGCCTC 87662 A  
GAGGC GAGGTTGCAGT  
||||| |||||  
CTCCG CTCCAACGTCA  
C

GAM1317 LOC196418 5' TCAGCCACTGTGGGCCCTGCCT 87698 A \_ TG A  
CT AGAGGCAG GG T CAGT GCTGA  
||||| || | ||| |||||  
TCTCCGTC CC G GTCA CGACT  
\_ G GT C

GAM1317 LOC196529 3' ACTGCAACCTCCACCTC 87767 CA  
GAGG GAGGTTGCAGT  
||| |||||  
CTCC CTCCAACGTCA  
AC

GAM1317 LOC196957 3' ACTGCAGCCTCCACCTC 87813 CA  
GAGG GAGGTTGCAGT  
||| |||||  
CTCC CTCCGACGTCA  
AC

GAM1317 LOC196957 5' TCAGCCACTCCCATCCCTGCCC 87831 A A T C\_ A  
T AG GGCAG GG TG AGT GCTGA  
|| |||| || || ||| |||||  
TC CCGTC CC AC TCA CGACT  
\_ \_ T CC C

GAM1317 LOC196961 3' ACTGCAGCCTCCACCTC 87834 CA  
GAGG GAGGTTGCAGT  
||| |||||  
CTCC CTCCGACGTCA  
AC

GAM1317 LOC196961 5' TCAGCCACTCCCATCCCTGCCC 87852 A A T C\_ A  
T AG GGCAG GG TG AGT GCTGA  
|| |||| || || ||| |||||  
TC CCGTC CC AC TCA CGACT  
\_ \_ T CC C

GAM1317 LOC197114 3' CAACTCCACCAACCTCTGGCTC 89700 G CAGT C  
T AGAG CAGAGGTTG AG TG  
||| ||||| |||  
TCTC GTCTCCAAC TC AC  
G CACC A

GAM1317 LOC197117 3' CAACTCCACCAACCTCTGGCTC 89715 G CAGT C  
T AGAG CAGAGGTTG AG TG  
||| ||||| |||  
TCTC GTCTCCAAC TC AC  
G CACC A

GAM1317 LOC197138 3' ACTGCAGCCTCCACCTC 87907 CA  
GAGG GAGGTTGCAGT  
||| |||||

CTCC CTCCGACGTCA  
 AC  
 GAM1317 LOC197138 5' TCAGCCACTCCCATCCCTGCCC 87925 A A T C\_ A  
 T AG GGCAG GG TG AGT GCTGA  
 || ||||| || || |||||  
 TC CCGTC CC AC TCA CGACT  
 \_ \_ T CC C  
 GAM1317 LOC197358 3' TCAGCTCCCTGCAACCTCCGCC 88050 A T\_  
 TC GAGGC GAGGTTGCAG AGCTGA  
 ||||| |||||  
 CTCCG CTCCAACGTC TCGACT  
 C CC  
 GAM1317 LOC199725 5' TTA CTGCAACCTTCGCCTC 89843 AG  
 GAGGC AGGTTGCAGTAG  
 ||||| |||||  
 CTCCG TCCAACGTCATT  
 CT  
 GAM1317 LOC199786 3' ACTGCAACCTCCGCCTC 88362 A  
 GAGGC GAGGTTGCAGT  
 ||||| |||||  
 CTCCG CTCCAACGTCA  
 C  
 GAM1317 LOC199906 3' TACTGCAACCTCCGCCT 88486 A  
 AGGC GAGGTTGCAGTA  
 ||||| |||||  
 TCCG CTCCAACGTCAT  
 C  
 GAM1317 LOC200014 3' TCAGCTCGCTGCAACCCCCACC 88540 CAGA \_  
 TC GAGG GGTTCAGT AGCTGA  
 ||||| |||||  
 CTCC CCAACGTCG TCGACT  
 ACCC C  
 GAM1317 LOC200093 3' CAGCCACTGCAGCCTC 63088 A  
 GAGGTTGCAGT GCTG  
 ||||| |||||  
 CTCCGACGTCA CGAC  
 C  
 GAM1317 LOC200169 5' ACTGCAACCTCTGCCTC 89938  
 GAGGCAGAGGTTGCAGT  
 ||||| |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1317 LOC200268 3' ACTGCAACCTCTGCCTC 88671  
 GAGGCAGAGGTTGCAGT  
 ||||| |||||  
 CTCCGTCTCCAACGTCA  
  
 GAM1317 LOC200310 3' ACTACAACCTCTGCCTC 65726 C  
 GAGGCAGAGGTTG AGT  
 ||||| |||||

CTCCGTCTCCAAC TCA  
A  
GAM1317 LOC200314 3' ACTGCAACCTCCACCTC 90001 CA  
GAGG GAGGTTGCAGT  
||||| |||||  
CTCC CTCCAACGTCA  
AC  
GAM1317 LOC200339 3' ACTGCAACCTCTGCCTC 90026  
GAGGCAGAGGTTGCAGT  
||||| |||||  
CTCCGTCTCCAACGTCA

GAM1317 LOC200845 5' ACTGCAACCTCCGCCTCT 88894 A  
AGAGGC GAGGTTGCAGT  
||||| |||||  
TCTCCG CTCCAACGTCA  
C  
GAM1317 LOC200860 3' ACTGCAACCTCCACCTC 90155 CA  
GAGG GAGGTTGCAGT  
||||| |||||  
CTCC CTCCAACGTCA  
AC  
GAM1317 LOC201164 3' ACTGCATCCTCTGCCTC 88111 T  
GAGGCAGAGG TGCAGT  
||||| |||||  
CTCCGTCTCC ACGTCA  
T  
GAM1317 LOC201173 5' ACTGCAACCTCTGCCTC 87320  
GAGGCAGAGGTTGCAGT  
||||| |||||  
CTCCGTCTCCAACGTCA

GAM1317 LOC201220 5' ACTGCAACCTCTGCCTC 87340  
GAGGCAGAGGTTGCAGT  
||||| |||||  
CTCCGTCTCCAACGTCA

GAM1317 LOC201245 3' TCAGCTACCACACTGGACTCT 87365 G\_ AG TGCA  
AGAG CAG GT GTAGCTGA  
||||| ||| || |||||  
TCTC GTC CA CATCGACT  
AG A\_ C\_\_  
GAM1317 LOC201294 3' ACTGCAACCTCCGCCTC 88197 A  
GAGGC GAGGTTGCAGT  
||||| |||||  
CTCCG CTCCAACGTCA  
C  
GAM1317 LOC201294 3' TCAGCTCACTGCAACCTCCGCC 88223 A \_  
TC GAGGC GAGGTTGCAGT AGCTGA  
||||| ||||| |||||



		CTCCG CTCCAACGTCA TCGACT		
		C C		
GAM1317	LOC201411 3'	TCAGTCACTGCAACCTCTGCC 62963		—
	TC	GAGGCAGAGGTTGCAGT AGCTGA		
		CTCCGTCTCCAACGTCA TCGACT		
		C		
GAM1317	LOC201627 3'	ACTGCAACCTCCACCTC 89003 CA		
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		AC		
GAM1317	LOC201702 5'	TCAGTCACTGCAACCTCTGAC 89033 G		—
	TC	GAG CAGAGGTTGCAGT AGCTGA		
		CTC GTCTCCAACGTCA TCGACT		
		A C		
GAM1317	LOC202025 3'	ACTGCAACCTCCGCCTC 90277 A		
		GAGGC GAGGTTGCAGT		
		CTCCG CTCCAACGTCA		
		C		
GAM1317	LOC202908 5'	ACTGCAACGTCTGCCTC 89225 G		
		GAGGCAGA GTTGCAGT		
		CTCCGTCT CAACGTCA		
		G		
GAM1317	LOC202934 3'	TCAGTCACTACAACCTCTGCC 90430	C	—
	TC	GAGGCAGAGGTTG AGT AGCTGA		
		CTCCGTCTCCAAC TCA TCGACT		
		A C		
GAM1317	LOC203297 5'	ACTGCAACCTCTGCCTC 75345		
		GAGGCAGAGGTTGCAGT		
		CTCCGTCTCCAACGTCA		
GAM1317	LOC203339 3'	ACTGCAACCACTGCCTC 90541 A		
		GAGGCAG GGTTGCAGT		
		CTCCGTC CCAACGTCA		
		A		
GAM1317	LOC203350 3'	TCAACTGACTGCAACCTCCGCC 90571 A		— C
	TC	GAGGC GAGGTTGCAGT AG TGA		
		CTCCG CTCCAACGTCA TC ACT		
		C G A		
GAM1317	LOC203378 3'	ACGGCAACCTCTGCCTC 90590 A		
		GAGGCAGAGGTTGC GT		

		CTCCGTCTCCAACG CA		
		G		
GAM1317	LOC204804 3'	ACTGCAACCTCGACCTC	89467	CA
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		AG		
GAM1317	LOC219445 5'	ACTGCAGCCTCCGCCTC	91571	A
		GAGGC GAGGTTGCAGT		
		CTCCG CTCCGACGTCA		
		C		
GAM1317	LOC219735 3'	ACTGCAACCTCTGCCTC	93102	
		GAGGCAGAGGTTGCAGT		
		CTCCGTCTCCAACGTCA		
GAM1317	LOC220064 3'	ACTGTAACCTCCGCCTC	93421	A
		GAGGC GAGGTTGCAGT		
		CTCCG CTCCAATGTCA		
		C		
GAM1317	LOC220074 3'	ACTGCAACCTCAGCCTC	59264	A
		GAGGC GAGGTTGCAGT		
		CTCCG CTCCAACGTCA		
		A		
GAM1317	LOC220074 3'	TCAGTCACTGCAACCTCCGCC	59283	A
	T	AGGC GAGGTTGCAGT AGCTGA		—
		TCCG CTCCAACGTCA TCGACT		
		C C		
GAM1317	LOC220662 3'	ACTGCAACCTCCACCTC	91157	CA
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		AC		
GAM1317	LOC220662 3'	ACTGCAACCTCCACTTC	91160	CA
		GAGG GAGGTTGCAGT		
		CTTC CTCCAACGTCA		
		AC		
GAM1317	LOC220846 3'	CAGCCTTTCCACAACCTCTACC	90813	C
	TT	GAGG AGAGGTTG AG GCTG		C__ TA
		TTCC TCTCCAAC TT CGAC		
		A ACC TC		
GAM1317	LOC221035 3'	ACTACAACCTCTGCCTC	93159	C
		GAGGCAGAGGTTG AGT		

CTCCGTCTCCAAC TCA  
A  
GAM1317 LOC221174 5' TCAGCTCACTGCGACCTCCACC 93506 CA \_  
TC GAGG GAGGTTGCAGT AGCTGA  
||||| |||||  
CTCC CTCCAGCGTCA TCGACT  
AC C  
GAM1317 LOC221271 3' TCAGCTCACTGCAACCTCTGCC 91877 \_  
TC GAGGCAGAGGTTGCAGT AGCTGA  
||||| |||||  
CTCCGTCTCCAACGTCA TCGACT  
C  
GAM1317 LOC221296 3' ACTGCAACCTCCACCTC 91954 CA  
GAGG GAGGTTGCAGT  
||||| |||||  
CTCC CTCCAACGTCA  
AC  
GAM1317 LOC221663 5' ACTGCAACCTCCACCTC 93807 CA  
GAGG GAGGTTGCAGT  
||||| |||||  
CTCC CTCCAACGTCA  
AC  
GAM1317 LOC222068 3' TCAGCTCACTGGCAACATCTGC 92713 G \_ \_  
CTC GAGGCAGA GTTGC AGT AGCTGA  
||||| ||||| ||| |||||  
CTCCGTCT CAACG TCA TCGACT  
A G C  
GAM1317 LOC222070 5' ACTGCAACCTCTGCCTC 94146  
GAGGCAGAGGTTGCAGT  
||||| |||||  
CTCCGTCTCCAACGTCA  
  
GAM1317 LOC222224 5' ACTGCAACCTCAGCCTC 94195 A  
GAGGC GAGGTTGCAGT  
||||| |||||  
CTCCG CTCCAACGTCA  
A  
GAM1317 LOC222865 3' TCAGCCACTGCCACAAGCCCCT 92868 C A \_\_\_\_ A  
CCCTCT GAGG AG GGTT GCAGT GCTGA  
||||| ||| ||||| |||||  
CTCC TC CCGA CGTCA CGACT  
C C ACAC C  
GAM1317 LOC223009 5' CAGGCCAGCCTCTGCCTC 94374 CA AG  
GAGGCAGAGGTTG GT CTG  
||||| ||||| ||| |||  
CTCCGTCTCCGAC CG GAC  
C\_ \_  
GAM1317 LOC245771 5' ACTGCAACCCCGTCTC 92880 AGA  
GAGGC GGTTGCAGT  
||||| |||||

	CTCTG CCAACGTCA			
	CCC			
GAM1317 LOC253612 5'	ACTGCAACCTCCGCCTC	96736	A	
	GAGGC GAGGTTGCAGT			
	CTCCG CTCCAACGTCA			
	C			
GAM1317 LOC253664 3'	ATTGCAACCTCTGCCTC	94806		
	GAGGCAGAGGTTGCAGT			
	CTCCGTCTCCAACGTTA			
GAM1317 LOC253666 5'	TCAGCTCACTGCAACCTCCGCC	95069	A	—
TC	GAGGC GAGGTTGCAGT AGCTGA			
	CTCCG CTCCAACGTCA TCGACT			
	C C			
GAM1317 LOC253779 3'	ACTGCAACCTCCGCCTC	97141	A	
	GAGGC GAGGTTGCAGT			
	CTCCG CTCCAACGTCA			
	C			
GAM1317 LOC254082 5'	ATTGCAACCTCCGCTTC	97202	A	
	GAGGC GAGGTTGCAGT			
	CTTCG CTCCAACGTTA			
	C			
GAM1317 LOC254351 3'	ACCGCAACCTCGGCCTC	94991	A	A
	GAGGC GAGGTTGC GT			
	CTCCG CTCCAACG CA			
	G C			
GAM1317 LOC254655 3'	ACTGCAACCTCTGCCTT	95466		
	GAGGCAGAGGTTGCAGT			
	TTCCGTCTCCAACGTCA			
GAM1317 LOC254672 3'	ACTGAAACCTCTGCCTC	94637		G
	GAGGCAGAGGTT CAGT			
	CTCCGTCTCCAA GTCA			
	A			
GAM1317 LOC255040 5'	TCAGCCAAGTCTCCCACCTCT	96383	CA_	GT GCAGTA
	AGAGG GAG T GCTGA			
	TCTCC CTC A CGACT			
	ACC TG AC_____			
GAM1317 LOC255308 3'	CTGCAATCTCTGCCTC	94536		
	GAGGCAGAGGTTGCAG			

CTCCGTCTCTAACGTC

GAM1317 LOC255497 3' ACTGCAACCTCCGCCTC 97183 A  
GAGGC GAGGTTGCAGT  
||||| |||||  
CTCCG CTCCAACGTCA  
C

GAM1317 LOC255919 3' CTGCAACCTCTGCCTC 95032  
GAGGCAGAGGTTGCAG  
||||| |||||  
CTCCGTCTCCAACGTC

GAM1317 LOC255975 5' CAGCCACCTTCGGCCTC 95882 A TTGCA A  
GAGGC GAGG GT GCTG  
||||| ||| || |||  
CTCCG CTTC CA CGAC  
G \_ \_ C

GAM1317 LOC255975 5' CAGGCCAGCCTCTGCCTC 95886 CA AG  
GAGGCAGAGGTTG GT CTG  
||||| ||| |||  
CTCCGTCTCCGAC CG GAC  
C\_ \_

GAM1317 LOC255987 5' CAGGCCAGCCTCTGCCTC 96064 CA AG  
GAGGCAGAGGTTG GT CTG  
||||| ||| |||  
CTCCGTCTCCGAC CG GAC  
C\_ \_

GAM1317 LOC256267 3' TCAGTCACTGCAACCTCCGCC 96809 A \_  
TC GAGGC GAGGTTGCAGT AGCTGA  
||||| ||||| |||||  
CTCCG CTCCAACGTCA TCGACT  
C C

GAM1317 LOC256306 3' TCAGTCACTGCAACCTCCACC 96698 CA \_  
TC GAGG GAGGTTGCAGT AGCTGA  
||| ||||| |||||  
CTCC CTCCAACGTCA TCGACT  
AC C

GAM1317 LOC256360 5' TACTGCAAGCTCCGCCTC 96551 A G  
GAGGC GAG TTGCAGTA  
||||| ||| |||||  
CTCCG CTC AACGTCAT  
C G

GAM1317 LOC256997 3' CAGCCACGCTGTCCTCTGCTCC 95335 AG TT A\_\_  
T AG GCAGAGG GCAGT GCTG  
|| ||||| ||||| |||  
TC CGTCTCC TGTCG CGAC  
CT \_ CAC

GAM1317 LOC257106 3' CAGCTCCCCACCCTCTGCCTC 95384 T CAGT  
GAGGCAGAGG TG AGCTG  
||||| ||| |||||

		CTCCGTCTCC AC	TCGAC		
		C CCC_			
GAM1317	LOC257334	3'	ACTGCAACCTCCGCCT	97274	A
			AGGC GAGGTTGCAGT		
			TCCG CTCCAACGTCA		
			C		
GAM1317	LOC257465	3'	ACTGCAGCCTCCGCCTC	81589	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCGACGTCA		
			C		
GAM1317	LOC51008	5'	ACAGCAACCTCTGCCTC	31957	A
			GAGGCAGAGGTTGC GT		
			CTCCGTCTCCAACG CA		
			A		
GAM1317	LOC51200	3'	ACCACAACCTCTGCCTC	32986	CA
			GAGGCAGAGGTTG GT		
			CTCCGTCTCCAAC CA		
			AC		
GAM1317	LOC51219	5'	ACCGCAACCTCCGCCTC	33108	A A
			GAGGC GAGGTTGC GT		
			CTCCG CTCCAACG CA		
			C C		
GAM1317	LOC51236	3'	CAGCCACCCTCTGCCCT	33199	A TTGCA A
			AG GGCAGAGG GT GCTG		
			TC CCGTCTCC CA CGAC		
			C C		
GAM1317	LOC51696	3'	TCAGCTCACTGCAACCTCTGCC	32558	—
	TC		GAGGCAGAGGTTGCAGT AGCTGA		
			CTCCGTCTCCAACGTCA TCGACT		
			C		
GAM1317	LOC56181	5'	ACTGCAAGCTCTGCCTC	95530	G
			GAGGCAGAG TTGCAGT		
			CTCCGTCTC AACGTCA		
			G		
GAM1317	LOC57107	3'	ACTGCAACCTCCGCCTC	39823	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTCCAACGTCA		
			C		
GAM1317	LOC57146	3'	ACTGCAACCTCCAACCTC	39909	GCA
			GAG GAGGTTGCAGT		

			CTC CTCCAACGTCA		
			AAC		
GAM1317	LOC81034	3'	TCAGCTCACTGCAACCTCCACC	47858	CA
		TC	GAGG GAGGTTGCAGT AGCTGA		—
			CTCC CTCCAACGTCA TCGACT		
			AC C		
GAM1317	LOC89932	3'	ACTGCAACCTCCACCTC	60786	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	LOC89932	3'	TCAGCTCACTGCAACCTCCGTC	60818	A
		TC	GAGGC GAGGTTGCAGT AGCTGA		—
			CTCTG CTCCAACGTCA TCGACT		
			C C		
GAM1317	LOC90141	3'	ACTGCAACTTCCGCCTC	61622	A
			GAGGC GAGGTTGCAGT		
			CTCCG CTTCAACGTCA		
			C		
GAM1317	LOC90288	3'	ACTGCAACCTCCACCTC	62075	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	LOC90333	5'	ACTGCAACCTCCACTTC	62275	CA
			GAGG GAGGTTGCAGT		
			CTTC CTCCAACGTCA		
			AC		
GAM1317	LOC90333	3'	TCAGCTCACTGCAACCTCCTCC	62301	CA
		TC	GAGG GAGGTTGCAGT AGCTGA		—
			CTCC CTCCAACGTCA TCGACT		
			TC C		
GAM1317	LOC90371	5'	ACTGCAACCTCCACCTC	62491	CA
			GAGG GAGGTTGCAGT		
			CTCC CTCCAACGTCA		
			AC		
GAM1317	LOC90408	5'	ACTGCAACCTCTACCTC	62653	C
			GAGG AGAGGTTGCAGT		
			CTCC TCTCCAACGTCA		
			A		
GAM1317	LOC90459	3'	ACTGCAACCTCCGCCTC	62877	A
			GAGGC GAGGTTGCAGT		

		CTCCG CTCCAACGTCA		
		C		
GAM1317	LOC90485	3' ACTGCAACCTCCGCCTC	63004	A
		GAGGC GAGGTTGCAGT		
		CTCCG CTCCAACGTCA		
		C		
GAM1317	LOC91040	3' CAGCCACTGCAGCCTC	64708	A
		GAGGTTGCAGT GCTG		
		CTCCGACGTCA CGAC		
		C		
GAM1317	LOC91115	3' ACTGCAACCTCCACCTC	64916	CA
		GAGG GAGGTTGCAGT		
		CTCC CTCCAACGTCA		
		AC		
GAM1317	LOC91115	3' ACTGCAACCTCCGCCTC	64918	A
		GAGGC GAGGTTGCAGT		
		CTCCG CTCCAACGTCA		
		C		
GAM1317	LOC91115	3' TCAGCTCACTGCAACTTCTGCC	64952	—
	TC	GAGGCAGAGGTTGCAGT AGCTGA		
		CTCCGTCTTCAACGTCA TCGACT		
		C		
GAM1317	LOC91291	5' TCAGCTCACTGCAACCTCGACC	65486	CA —
	TCT	AGAGG GAGGTTGCAGT AGCTGA		
		TCTCC CTCCAACGTCA TCGACT		
		AG C		
GAM1317	LOC91963	5' ACAAACCTGCCTCT	67687	A GCA
		AGAGGCAG GGTT GT		
		TCTCCGTC CCAA CA		
		— AA—		
GAM1317	LOC92267	3' TCAGCTCACTGCAACCTCCACC	68625	CA —
	TC	GAGG GAGGTTGCAGT AGCTGA		
		CTCC CTCCAACGTCA TCGACT		
		AC C		
GAM1317	LOC92303	3' TCAACTCACTGCAACCTCTGCC	68826	A — C
	CT	AG GGCAGAGGTTGCAGT AG TGA		
		TC CCGTCTCCAACGTCA TC ACT		
		— C A		
GAM1317	LOC92466	3' TCAGCTCACTGCAACCTCCGCC	69434	A —
	TC	GAGGC GAGGTTGCAGT AGCTGA		



			CTCCG CTCCAACGTCA TCGACT			
			C C			
GAM1317	LOC92689	3'	ACTGCAACCTCCGCCTC 70211	A		
			GAGGC GAGGTTGCAGT			
			CTCCG CTCCAACGTCA			
			C			
GAM1317	LOC92697	5'	ACCGCAACCTCCGCCTC 70257	A	A	
			GAGGC GAGGTTGC GT			
			CTCCG CTCCAACG CA			
			C C			
GAM1317	LOC92841	3'	ACCGCAACCTCCTCCTC 70702	CA	A	
			GAGG GAGGTTGC GT			
			CTCC CTCCAACG CA			
			TC C			
GAM1317	LOC92841	3'	ACTGCAAGCTCTGCCTC 70705		G	
			GAGGCAGAG TTGCAGT			
			CTCCGTCTC AACGTCA			
			G			
GAM1317	LOC93132	5'	TCAGCTCACTGCAACCTCCGCC 71503	A		—
		TC	GAGGC GAGGTTGCAGT AGCTGA			
			CTCCG CTCCAACGTCA TCGACT			
			C C			
GAM1317	LOC93349	3'	TCAGCTCACTGCAACCTCTGCC 56466			—
		TC	GAGGCAGAGGTTGCAGT AGCTGA			
			CTCCGTCTCCAACGTCA TCGACT			
			C			
GAM1317	LOC93408	5'	ACTGCAACCTCTGCCTC 56472			
			GAGGCAGAGGTTGCAGT			
			CTCCGTCTCCAACGTCA			
GAM1318	ARF3	3'	GCTTTCTGCTTCCTGA 8004	T		
			TCA GAAGCAGAAAGC			
			AGT CTTCGTCTTTTCG			
			C			
GAM1318	EFG2	5'	CTCGCGCCTCCTGCTTCAAGA 50475	A	AAA ACTA	
			TC TGAAGCAG GC CGAG			
			AG ACTTCGTC CG GCTC			
			A CTC C__			
GAM1318	FGFR2	3'	GCCTTCTGCTTCTGA 3763	T	A	
			TCA GAAGCAGAA GC			

				AGT CTTCGTCTT CG			
				— C			
GAM1318	FGFR2	3'	GCCTTCTGCTTCTGA	43359	T	A	
			TCA GAAGCAGAA GC				
			AGT CTTCGTCTT CG				
			— C				
GAM1318	FGFR2	3'	GCCTTCTGCTTCTGA	43371	T	A	
			TCA GAAGCAGAA GC				
			AGT CTTCGTCTT CG				
			— C				
GAM1318	FGFR2	3'	GCCTTCTGCTTCTGA	43482	T	A	
			TCA GAAGCAGAA GC				
			AGT CTTCGTCTT CG				
			— C				
GAM1318	FGFR2	3'	GCCTTCTGCTTCTGA	43492	T	A	
			TCA GAAGCAGAA GC				
			AGT CTTCGTCTT CG				
			— C				
GAM1318	FGFR2	3'	GCCTTCTGCTTCTGA	43502	T	A	
			TCA GAAGCAGAA GC				
			AGT CTTCGTCTT CG				
			— C				
GAM1318	FZD4	3'	CTCATACCTGTCTGCTTCA	24135		A CAC C	
			TGAAGCAGA AG TA GAG				
			ACTTCGTCT TC AT CTC				
			G C__ A				
GAM1318	HR	3'	GCTTCCCTCCTTCATGA	17642		C A_	
			TCATGAAG AG AAGC				
			AGTACTTC TC TTCG				
			C CC				
GAM1318	PPARA	5'	GTGCTTCCTGCTTCAT	17276		A	
			ATGAAGCAG AAGCAC				
			TACTTCGTC TTCGTG				
			C				
GAM1318	TBL1X	3'	CTAGTTGCTTCAGA	18930	A	GAAAGC	C
			TC TGAAGCA ACTA G				
			AG ACTTCGT TGAT C				
			— ——— A				
GAM1318	TCF8	3'	GTGAACTTTCTGCTTCATG	47729		—	
			CATGAAGCAGAAAAG CAC				

		GTACTTCGTCTTTC GTG		
		AA		
GAM1318	UGT1A1	3' CTCATCTCTGCTCTGCTTCAT 4875	AAA	CTAC_
		ATGAAGCAG GCA GAG		
		TACTTCGTC TGT CTC		
		C_ CTCTA		
GAM1318	UGT1A4	3' CTCATCTCTGCTCTGCTTCAT 23060	AAA	CTAC_
		ATGAAGCAG GCA GAG		
		TACTTCGTC TGT CTC		
		C_ CTCTA		
GAM1318	UGT1A9	3' CTCATCTCTGCTCTGCTTCAT 40711	AAA	CTAC_
		ATGAAGCAG GCA GAG		
		TACTTCGTC TGT CTC		
		C_ CTCTA		
GAM1318	C20orf177	3' CTTGTTTACTTTCTGCCTCAGA 62147	A A	CACT
		TC TGA GCAGAAAG ACGAG		
		AG ACT CGTCTTTC TGTTC		
		_ C ATT_		
GAM1318	FLJ12121	3' TGGTGCTTCCACTCCATGA 46460	A CA	A
		TCATG AG GAA GCACTA		
		AGTAC TC CTT CGTGGT		
		C AC _		
GAM1318	FLJ13910	3' TAGTGACTTTTGCCCCATGA 42930	AA	AG
		TCATG GCAGAA CACTA		
		AGTAC CGTTTT GTGAT		
		CC CA		
GAM1318	MGC14376	3' CTCCAGGCTTTCTGCCTC 51847	A	A AC
		GA GCAGAAAGC CT GAG		
		CT CGTCTTTCG GA CTC		
		C _ C_		
GAM1318	MGC20460	5' TCGGCTTCTGCTTCATGG 53849	A	ACTA
		TCATGAAGCAGAA GC CGA		
		GGTACTTCGTCTT CG GCT		
		— — —		
GAM1318	REM	5' GGGACTTTCTGCCCAAGA 25810	A AA	CA
		TC TG GCAGAAAG CT		
		AG AC CGTCTTTC GG		
		A CC AG		
GAM1318	SCYE1	5' CGTGGTCCTCCGCTTCATGA 16469	A AA	C
		TCATGAAGC GA G ACTACG		

				AGTACTTCG CT C TGGTGC			
				C _ C			
GAM1318	SLC12A8	3'	CTCACTGCAACCTCTGCTTC	44898	AA__	CTAC	
			GAAGCAGA GCA GAG				
			CTTCGTCT CGT CTC				
			CCAA CA__				
GAM1318	LOC151647	3'	AGCCCTCTCTGCTTCGTGA	80329	A	CA	
			TCATGAAGCAGA AG CT				
			AGTGCTTCGTCT TC GA				
			C CC				
GAM1318	LOC256950	3'	CGAGAACTCCTGCTTCACGG	95426	A	AA CA A	
			TC TGAAGCAG AG CT CG				
			GG ACTTCGTC TC GA GC				
			C C_ AA _				
GAM1318	LOC90288	3'	CTCGATCTCCTGACTTCATGA	62092	_	AA CACTA	
			TCATGAAG CAG AG CGAG				
			AGTACTTC GTC TC GCTC				
			A C_ TA__				
GAM1318	LOC90470	3'	TGTTTCTGTTTCATGA	62971	G	G	
			TCATGAA CAGAAA CA				
			AGTACTT GTCTTT GT				
			- -				
GAM1319	ARNT2	3'	AAACAACCCGTCATCCCTGC	29450	A	TTTTA	
			GTA GGAT GGGTTGTTT				
			CGT CCTA CCCAACAAA				
			C CGTG_				
GAM1319	LCT	3'	AACCGTAAAAATCCTT	9697	G		
			AAGGATTTTTTA GGTT				
			TTCCTAAAAAT CCAA				
			G				
GAM1319	RPL15	3'	AAACAACCCTAAAAATCCTTAC	11382			
			GTAAGGATTTTTAGGGTTGTTT				
			CATTCCTAAAAATCCCAACAAA				
GAM1319	FBXO30	3'	AACTAAAAAAATCCTGAC	49573	A	AG	
			GT AGGATTTTTT GGTT				
			CA TCCTAAAAA TCAA				
			G AA				
GAM1319	KIAA0494	3'	AACAACCCTTACTTAC	28736	GATTTTTT		
			GTAAG AGGGTTGTT				

		CATTC	TCCCAACAA		
		AT_____			
GAM1319	PRO0641	5'	AAACAACCCCAAAACTTG	26210	GAT A
			TAAG TTTT GGGTTGTTT		
			GTTC AAAA CCAACAAA		
			___ C		
GAM1319	SMT3H2	3'	AACAACATAAAAAATCCTTGC	22670	GG
			GTAAGGATTTTTA GTTGTT		
			CGTTCCTAAAAAT CAACAA		
			A_		
GAM1319	LOC120103	3'	AACCTATGAAAAATCCTTGC	74002	A__
			GTAAGGATTTT GGGTT		
			CGTTCCTAAAAA TCCAA		
			GTA		
GAM1319	LOC129831	3'	AAACAACCCCAATGTCC	74889	TT A
			GGAT TT GGGTTGTTT		
			CCTG AA CCAACAAA		
			T_ C		
GAM1319	LOC133088	5'	AAACAAAATAGAAAAATCCCTG	75075	A AGGG_
		C	GTA GGATTTT TTGTTT		
			CGT CCTAAAAA AACAAA		
			C GATAA		
GAM1319	LOC148089	3'	GGCCCTAAAAATTCCTAC	78637	A
			GTA GGATTTT TAGGGTT		
			CAT CTTAAAAATCCCGG		
			C		
GAM1319	LOC154547	3'	AACAACATAAAAAATCCTTGC	76050	GG
			GTAAGGATTTTTA GTTGTT		
			CGTTCCTAAAAAT CAACAA		
			A_		
GAM1319	LOC158104	3'	ACAGCCAAAAATCCTTA	60313	AG
			TAAGGATTTT GGTGT		
			ATTCCTAAAAA CCGACA		
			—		
GAM1319	LOC205880	5'	AAACAACCATCATCCTGAC	90709	A TTTAG
			GT AGGAT GGTGTTT		
			CA TCCTA CCAACAAA		
			G CTA__		
GAM1319	LOC221561	3'	AACAACATAAAAAATCCTTGC	92130	GG
			GTAAGGATTTTTA GTTGTT		

		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1319	LOC257591	3' AACAAACATAAAAAATCCTTGC	97840	GG
		GTAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1319	LOC51145	3' AGCTAAAATCCTTAC	32393	TAG
		GTAAGGATTTT GGTT		
		CATTCCTAAAA TCGA		
		—		
GAM1320	CTNS	3' ATCTCTTTTCTTTAAGGCTTCA	17037	AA AA TTT
		TGAA CTAA AG GGAGAT		
		ACTT GAATT TC TCTCTA		
		CG _ TTT		
GAM1320	DBT	3' TCTTGAAC TTTTGAGCTTC	8613	AA TG A
		GAA CTAAAAAGTT G GA		
		CTT GAGTTTTTCAA T CT		
		C_ GT_		
GAM1320	DSC2	3' ATCTCCAGTTAATTAAGTG TTC	17064	A AAAGT
	A	TGAA ACTTAA TTGGAGAT		
		ACTT TGAATT GACCTCTA		
		G AATT_		
GAM1320	DSC2	3' ATCTCCAGTTAATTAAGTG TTC	44333	A AAAGT
	A	TGAA ACTTAA TTGGAGAT		
		ACTT TGAATT GACCTCTA		
		G AATT_		
GAM1320	FPRL1	3' TCCTTGCTAAGTTTTCA	7591	AAAA TT
		TGAAA ACTT AGT GGA		
		ACTTTTGAA TCG CCT		
		_ TT		
GAM1320	NDN	3' AACTTTTAAGTTTTCA	10189	A
		TGAAA ACTTAAAA GTT		
		ACTTTTGAATTTT CAA		
		—		
GAM1320	PTGS2	3' CTGAACTTTTGCAAGTTTTCA	6361	A_ TG
		TGAAA ACTT AAAAGTT G		
		ACTTTTGAA TTTTCAA C		
		CG GT		
GAM1320	SORCS1	3' TCGGGACTTTTAAATTCTTCA	53588	AAC G
		TGAA TTAAAAAGTTT GA		

		ACTT AATTTTTCAGG CT	
		CTT G	
GAM1320 TRIM9	3'	CTCTGAGGCTTTTAACATTTTC 53758	CTTA _
A		TGAAAA AAAAGTTT GGAG	
		ACTTTT TTTTCGGA TCTC	
		ACAA G	
GAM1320 BCMP1	3'	ATCTCGAGTCTTATCAAGTTT 48730	AAA T G
CA		TGAAACTT AAG TT GAGAT	
		ACTTTTGAA TTC GA CTCTA	
		CTA T G	
GAM1320 FLJ12960	3'	CTCTGTATTTTTCAGTTTTC 44950	A T
		GAAAACTT AAAAGT TGGAG	
		CTTTTGAA TTTTTA GTCTC	
		C T	
GAM1320 KIAA0471	3'	CTAAACATCTTAAGTTTTC 29393	AAA
		TGAAAACTTAA GTTTGG	
		ACTTTTGAATT CAAATC	
		CTA	
GAM1320 KIAA0826	5'	TCCAAATTGCTAAGTTTTC 82641	AAA
		TGAAAACTTA AGTTTGG	
		ACTTTTGAAT TTAAACCT	
		CG_	
GAM1320 KIAA1656	3'	ATCTCTGGGCCTCAGAGTCCTC 65780	AA AAAAA TG
A		TGA ACTT GTT GAGAT	
		ACT TGAG CGG CTCTA	
		CC ACTC_ GT	
GAM1320 KIAA1938	3'	CTCCAACTTTCAACTTCA 92195	AACTTAA
		TGAA AAAGTTTGGAG	
		ACTT TTTCAAACCTC	
		CAAC__	
GAM1320 PREI3	3'	ACTTTTAAAGTTATTCA 66319	_
		TGAA AACTTAAAAAGT	
		ACTT TTGAATTTTCA	
		A	
GAM1320 SPATA1	5'	CCCGACTCTTAAGTTTTC 42294	AA T
		GAAAACTTAA AGTT GG	
		CTTTTGAATT TCAG CC	
		C_ C	
GAM1320 SPRY1	3'	CTCCTGAACCTTTTAGCTTTCA 65003	A TA _
		TGAAA CT AAAAGTTT GGAG	

		ACTTT GA TTTTCAAG CCTC	
		C _ T	
GAM1320	LOC146901 3'	CAAAGTTCTTAAGTTTTCA 83833	A G
		TGAAAACCTTAA AA TTTG	
		ACTTTTGAATT TT AAAC	
		C G	
GAM1320	LOC151877 3'	AAACTCTTTAAGTTTTTA 85500	A
		TGAAAACCTTAAA AGTTT	
		ATTTTGAATTT TCAAA	
		C	
GAM1320	LOC161742 3'	ATCTTCATCCCTGAAGTTTTCA 82289	AAAAAGTT
		TGAAAACCTT TGGAGAT	
		ACTTTTGAA ACTTCTA	
		GTCCCT_	
GAM1320	LOC196047 3'	CTCCAACTTTGTTTATC 89599	_ TTAA
		GA AAAC AAAGTTTGGAG	
		CT TTTG TTTCAAACCTC	
		A _	
GAM1320	LOC90593 5'	TCCTCTCTTACAAGTTTTCA 63454	AAA TTT
		TGAAAACCTT AAG GGA	
		ACTTTTGAA TTC CCT	
		CA_ TCT	
GAM1320	LOC92703 3'	ATCTCCAAACAAGGAAGTTTCA 56428	A AAAAA
		TGAAA CTT GTTTGGAGAT	
		ACTTT GAA CAAACCTCTA	
		_ GGAA_	
GAM1321	ADH1B 3'	CTTAGACATAAAGTAAAAT 72644	C CAC
		ATTT ACTTT TGTCTGAG	
		TAAA TGAAA ACAGATTC	
		A T_	
GAM1321	AHR 3'	ATCTCAGATGTTAAATAAATG 7875	CAC C T
		CATTT TTT AC GTCTGAGAT	
		GTAAA AAA TG TAGACTCTA	
		TA_ T _	
GAM1321	FDFT1 3'	TAGGAAAGTGAAATG 15518	A
		CATTTCACTTTC CTG	
		GTAAAGTGAAAG GAT	
		-	
GAM1321	JTB 3'	ATCTCAGACAGTGAAAGTGAAA 21959	
	TG	CATTTCACTTTCAGTGTCTGAGAT	



GTAAAGTGAAAGTGACAGACTCTA

GAM1321	KLF4	3'	TCCCAGACAGTGGATATG	14891	CT	A
			CA TTCACTGTCTG GA			
			GT AGGTGACAGAC CT			
			AT C			
GAM1321	PHYH	3'	ACAGTAAAAGTGAAAT	20608		C
			ATTTCACTTT ACTGT			
			TAAAGTGAAA TGACA			
			A			
GAM1321	PKD2	3'	TCCAGGTTGAAAGTGAAA	60096	CTG	A
			TTTCACTTTCA TCTG GA			
			AAAGTGAAAGT GGAC CT			
			T_ _			
GAM1321	WRN	3'	GGGCAGTGAAAATGAAA	5098		C
			TTTCA TTTCACTGTCT			
			AAAGT AAAGTGACGGG			
			A			
GAM1321	ZNF216	3'	ATCTGCACAGCAAAGTGAAA	20017	CA	CTG
			TTTCACTTT CTGT AGAT			
			AAAGTGAAA GACA TCTA			
			C_ CG_			
GAM1321	CG012	5'	CTCACTCTGAAAGTGAA	83218	CT	CT
			TTCAC TTTCA GT GAG			
			AAGTGAAAGT CA CTC			
			CT _			
GAM1321	EIF2C2	3'	ATCTTCTGAGAGTGAAAG	71946	G	T_
			CTTTCACT TC GAGAT			
			GAAAGTGA AG TTCTA			
			G TC			
GAM1321	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT	45802	ACTTTCACT	
	G		CATTTT GTCTGAGAT			
			GTAAAG CAGACTCTA			
			AAACATTT_			
GAM1321	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG	45281	CTT	
			CATTTCA TCACTGTCTGAGAT			
			GTAAAGT AGTGACAGACTCTA			
			C_			
GAM1321	KIAA0984	3'	TTTGTCCAGTGAAAATGAA	65534	C	TC
			TTCA TTTCACTG TGAG			

			AAGT AAAGTGAC GTTT		
			A CT		
GAM1321	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A _	
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1321	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T	
			ATT CACTTTCACTGT		
			TAA GTGAAAGTGACG		
			C		
GAM1321	PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA 53598	CA G	
			TTCAC TTT CT TCTGAGAT		
			AAGTGAAA GG AGACTCTA		
			CC G		
GAM1321	PP35	3'	ATCTCAGACTGAAA 22814	CT	
			TTTCA GTCTGAGAT		
			AAAGT CAGACTCTA		
			—		
GAM1321	PRTD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148	TCAC C_	
			CATTTCACTT TGT TGAG		
			GTAAAGTGAA ACG ACTC		
			TA_ TT		
GAM1321	SEP15	3'	TCCTACAGTAAGAGTGAAA 14934	C CT	
			TTTCACTTT ACTGT GA		
			AAAGTGAGA TGACA CT		
			A TC		
GAM1321	SFXN2	3'	CTCAGGGGAAAAAAGTGAAA 73941	CACTG	
			TTTCACTTT TCTGAG		
			AAAGTGAAA GGA CTC		
			AAAGG		
GAM1321	LOC149703	3'	ATCTCAGACAGCCGTTTGAAA 84647	ACTTTCA	
			TTTC CTGTCTGAGAT		
			AAAG GACAGACTCTA		
			GTTTGCC		
GAM1321	LOC154007	3'	ATCTCAAACCCTTTAGTGAAA 81015	TTCAC T C	
			TTTCACT GT TGAGAT		
			AAAGTGA CA ACTCTA		
			TTTCC_ A		
GAM1321	LOC155004	3'	TCATTTAAGTGAAAAGGAAA 81226	A GTC_	
			TTTC CTTTCACT TGA		

AAAG GAAAGTGA ACT  
 \_ ATTT  
 GAM1321 LOC222134 5' ACAGTGAAGTGAAATG 94136 T  
 CATTTCACCTT CACTGT  
 ||||| ||||  
 GTAAAGTGAA GTGACA

\_  
 GAM1322 ASH1 5' CATTTCGCCAGTCAGCTTACC 37499 C \_  
 GG AAGCTG CTGGCGGAGATG  
 || ||||| |||||  
 CC TTCGAC GACCGCCTTTAC  
 A T

GAM1322 DNASE1L1 3' CAGCAAAATGCCAGCAGCGTGC 22073 A GAGA  
 C GGCA GCTGCTGGCG TGCTG  
 ||| ||||| ||||  
 CCGT CGACGACCGT ACGAC  
 G AAA\_

GAM1322 LIMK1 3' CAGGTGTCCACCAGCAGCTCAG 9784 A\_ C G G  
 C GC AGCTGCTGG GGA AT CTG  
 || ||||| ||| |||  
 CG TCGACGACC CCT TG GAC  
 AC A G \_

GAM1322 LIMK1 3' CAGGTGTCCACCAGCAGCTCAG 33643 A\_ C G G  
 C GC AGCTGCTGG GGA AT CTG  
 || ||||| ||| |||  
 CG TCGACGACC CCT TG GAC  
 AC A G \_

GAM1322 PAX9 5' TCACCATGCAGCTTGCC 20562 \_ C  
 GGCAAGCTGC TGG GG  
 ||||| ||| ||  
 CCGTTCGACG ACC CT  
 T A

GAM1322 RHCG 3' CAGCACCCCCACCTGCTGGCTT 32865 \_ \_ T C AGA  
 GGCC GGC AAGCT GC GG GG TGCTG  
 ||| ||||| ||| |||  
 CCG TTCGG CG CC CC ACGAC  
 G T T A CCC

GAM1322 C20orf150 3' AGCACCCCCAGCACCTGCT 65387 A C C AGA  
 GGCA G TGCTGG GG TGCT  
 ||||| ||||| ||| |||  
 TCGT C ACGACC CC ACGA  
 \_ C \_ C \_

GAM1322 C20orf150 3' CAGCATCTCCCGACACCAACTG 65389 \_ C C GC\_  
 TGCC GGCA AG TG TG GGAGATGCTG  
 ||||| ||| ||| |||||  
 CCGT TC AC AC CCTCTACGAC  
 G A C AGC

GAM1322 C20orf150 3' CTCCACCAGCAACTCC 65397 CA C C  
 GG AG TGCTGG GGAG  
 || || ||||| ||||

CC TC ACGACC CCTC  
 \_ A A  
 GAM1322 CLECSF1 5' GCTCAGCAGGCTTGCC 19243 \_ \_  
 GGCAAGC TGCTG GC  
 ||||| ||||| ||  
 CCGTTCG ACGAC CG  
 G T  
 GAM1322 DKFZP586P0123 5' TTCCGCCAGAAGCTCACC 94840 CA G  
 GG AGCT CTGGCGGAG  
 || ||| |||||  
 CC TCGA GACCGCCTT  
 AC A  
 GAM1322 FKHL18 5' CAGCAGGTCCCAGCAGCCTGGC 79554 G A C AGA  
 G CA GCTGCTGG GG TGCTG  
 || ||||| || |||||  
 C GT CGACGACC CT ACGAC  
 G C \_ GG\_  
 GAM1322 FLJ10157 5' AGCGGCACCAGCAGCCCC 35858 CAA CGGAGA  
 GG GCTGCTGG TGCT  
 || ||||| |||||  
 CC CGACGACC GCGA  
 C\_ ACG\_  
 GAM1322 FLJ10374 3' CATCCCTGGAGCAGCTTCC 36066 C GG A  
 GG AAGCTGCT CGG GATG  
 || ||||| || |||||  
 CC TTCGACGA GTC CTAC  
 \_ G\_ C  
 GAM1322 FLJ13612 3' AGCATCTCCATCCACCA 47310 C C\_  
 TG TGG GGAGATGCT  
 || ||| |||||  
 AC ACC CCTCTACGA  
 C TA  
 GAM1322 FLJ20195 3' TCGCCAGCCGCTTACC 34716 C T  
 GG AAGC GCTGGCGG  
 || ||| |||||  
 CC TTCG CGACCGCT  
 A C  
 GAM1322 GFPT1 5' ATCCCGCCAGCCACTCGCC 9021 A CT A  
 GGC AG GCTGGCGG GAT  
 ||| || ||||| |||  
 CCG TC CGACCGCC CTA  
 C AC \_  
 GAM1322 ILF3 5' CAGTTGAACCCAGCAGCCCGCC 15721 AA CGGAGAT  
 GGC GCTGCTGG GCTG  
 ||| ||||| |||||  
 CCG CGACGACC TGAC  
 CC CAAGT\_  
 GAM1322 KIAA0513 5' CAGCCTCACCAGCAGCTCCCC 28345 CA CG AT  
 GG AGCTGCTGG GAG GCTG  
 || ||||| || |||||

CC TCGACGACC CTC CGAC  
 CC A\_ \_  
 GAM1322 KIAA1280 5' CATCCAGCAGCAGCTGGCC 69713 A G GGA  
 GGC AGCTGCTG C GATG  
 ||| ||||| | |||  
 CCG TCGACGAC G CTAC  
 G \_AC\_  
 GAM1322 KIAA1775 3' AGCATCCTTACAGCTTGC 52374 CT CGGA  
 GCAAGCTG GG GATGCT  
 ||||| || |||||  
 CGTTCGAC TC CTACGA  
 AT \_\_\_\_  
 GAM1322 LANO 5' CCGCCAGCAGCCGGCC 47187 AA  
 GGC GCTGCTGGCGG  
 ||| |||||  
 CCG CGACGACCGCC  
 GC  
 GAM1322 LPAAT-gamma1 3' AGCATCTCCACGCGCGCC 39287 AA T T GC  
 GGC GC GC G GGAGATGCT  
 ||| ||| | |||||  
 CCG CG CG C CCTCTACGA  
 \_ \_ \_A\_  
 GAM1322 P15-2 3' CAGCACCTTTTCTAGCAGCTGC 38006 A CG A  
 C GGCA GCTGCTGG GAG TGCTG  
 ||| ||||| ||| |||||  
 CCGT CGACGATC TTC ACGAC  
 \_ TT C  
 GAM1322 PRIC285 3' CTCCGCCATCAGCCTGCC 61434 A C  
 GGCA GCTG TGGCGGAG  
 ||| ||| |||||  
 CCGT CGAC ACCGCCTC  
 C T  
 GAM1322 SCAMP5 3' CTCCCACCAGAAGCTTGCC 57258 G C\_  
 GGCAAGCT CTGG GGAG  
 ||||| ||| |||  
 CCGTTCGA GACC CCTC  
 A AC  
 GAM1322 UBCE7IP5 3' TCCCACCAGCAGCTTG 30161 C A  
 CAAGCTGCTGG GG GA  
 ||||| || ||  
 GTTCGACGACC CC CT  
 A \_  
 GAM1322 LOC148089 3' CAGCATGGACCCCAGCAGCTCC 78626 CA C AG\_  
 GG AGCTGCTGG GG ATGCTG  
 || ||||| || |||||  
 CC TCGACGACC CC TACGAC  
 \_ \_ AGG  
 GAM1322 LOC148137 3' CAGCATCTGGTGCAGCTGACC 58422 CA TG GG  
 GG AGCTGC GC AGATGCTG  
 || ||||| || |||||

CC TCGACG TG TCTACGAC  
 AG \_ G\_  
 GAM1322 LOC162333 5' CCACCAGCAGCTTCC 87125 C C  
 GG AAGCTGCTGG GG  
 || ||||| ||  
 CC TTCGACGACC CC  
 \_ A  
 GAM1322 LOC164382 3' TTCCACCTACAGCTTGCC 87205 CT C  
 GGCAAGCTG GG GGAG  
 ||||| || |||  
 CCGTTCGAC CC CCTT  
 AT A  
 GAM1322 LOC170370 3' AGCATCTCCACCAGAGTCC 82838 A G C  
 A GCT CTGG GGAGATGCT  
 | || ||| |||||  
 C TGA GACC CCTCTACGA  
 C \_ A  
 GAM1322 LOC222057 3' CAGCATCTCCAGGACGAGCT 92764 \_ \_ GGC  
 AGCT G CT GGAGATGCTG  
 ||| | |||||  
 TCGA C GG CCTCTACGAC  
 G A A\_  
 GAM1322 LOC96597 3' AGCCAGCCAGCAGCATGCC 66905 A GGAGAT  
 GGCA GCTGCTGGC GCT  
 ||| ||||| |||  
 CCGT CGACGACCG CGA  
 A AC\_\_\_\_  
 GAM1323 B3GAT1 3' CAAACTCCTGCCCTCC 37824 TT  
 GGAGGGCAGG GTTTG  
 ||||| ||||  
 CCTCCCGTCC CAAAC  
 T\_  
 GAM1323 B3GAT1 3' CAAACTCCTGCCCTCC 53969 TT  
 GGAGGGCAGG GTTTG  
 ||||| ||||  
 CCTCCCGTCC CAAAC  
 T\_  
 GAM1323 B4GALT1 3' CAAACCACTGCCCTCCT 7665 GTT  
 AGGAGGGCAG GTTTG  
 ||||| ||||  
 TCCTCCCGTC CAAAC  
 AC\_  
 GAM1323 CHD1 3' CAGGGACCTCAACACTGCCCTC 7026 \_ TTTGAG  
 C GGAGGGCAG GTTG CCTG  
 ||||| ||| |||  
 CCTCCCGTC CAAC GGAC  
 A TCCAG\_  
 GAM1323 CYP4A11 3' CAAACTCCTGCCCTGCCCTCC 5752 T\_\_\_\_  
 GGAGGGCAGGT GTTTG  
 ||||| ||||

			CCTCCCGTCCG CAAAC		
			TCCT		
GAM1323	FBXL11	3'	CAAGCCCCAACCTGCCTCCC 24567	AG	___
			GG GGCAGGTT GTTTG		
			CC CCGTCCAA CGAAC		
			CT CCC		
GAM1323	GNB3	3'	GGACAACCTGCCCCTCC 9080	-	
			GGAGGG CAGGTTGTTT		
			CCTCCC GTCCAACAGG		
			C		
GAM1323	GNG5	5'	GCTCTGCCTTCCCTCC 17950	C	TGTTT
			GGAGGG AGGT GAGC		
			CCTCCC TCCG CTCG		
			T T___		
GAM1323	KCNN3	5'	GCTCCCCTCCTGCTCTCC 9560		TTGTTT
			GGAGGGCAGG GAGC		
			CCTCTCGTCC CTCG		
			TCCC__		
GAM1323	KLK13	5'	CAGGCCCGGCCGCCCTGCC 31530		T TT A_
			GGGCAGG TG TG GCCTG		
			CCCGTCC GC GC CGGAC		
			C CC CC		
GAM1323	LHX3	3'	CAAACAGCCTGCCCTCC 27371		
			GGAGGGCAGGTTGTTTG		
			CCTCCCGTCCGACAAAC		
GAM1323	LZTFL1	5'	TAAACAACCTACCCTCCT 39756	C	
			AGGAGGG AGGTTGTTTG		
			TCCTCCC TCCAACAAAT		
			A		
GAM1323	NCF4	3'	CAGGCTCGTGGCCTCCCCTCC 25509	C	TG TT
			GGAGGG AGGT T GAGCCTG		
			CCTCCC TCCG G CTCGGAC		
			C GT__		
GAM1323	NTSR1	3'	CAGACCCATGCCCCCT 10288	A	_ TT
			AGG GGGCA GG GTTTG		
			TCC CCCGT CC CAGAC		
			C A __		
GAM1323	NUMB	3'	CAGGCCATTACCTGCCTCCT 13620	G	T TT A
			AGGAGG CAGGT G TG GCCTG		

			TCCTCC GTCCA C AC CGGAC		
			— — TT —		
GAM1323	RNH	5'	CAGGCTCACAGACCACCCACC 59618	A CA GTT	
			GG GGG GGTT TGAGCCTG		
			CC CCC CCAG ACTCGGAC		
			A CA AC_		
GAM1323	RNH	5'	CAGGCTCACAGACCACCCACC 11363	A CA GTT	
			GG GGG GGTT TGAGCCTG		
			CC CCC CCAG ACTCGGAC		
			A CA AC_		
GAM1323	SORCS2	3'	AGGCCCCCCTGCCCTCC 40412	TTGTTTGA	
			GGAGGGCAGG GCCT		
			CCTCCCGTCC CGGA		
			CCC_____		
GAM1323	TAZ	5'	CAGGCTCAGCTTCGCTGCCCGC 31306	A GTTGT	
	C		GG GGGCAG TTGAGCCTG		
			CC CCCGTC GACTCGGAC		
			G GCTTC		
GAM1323	TNFRSF14	3'	CAGACCACACACCCAGCCCTCC 13782	A T T AGC	
	T		AGGAGGGC GG TGT TG CTG		
			TCCTCCCG CC ACA AC GAC		
			A C C CA_		
GAM1323	TNFRSF6B	5'	AGAGCCCAACTGCCCTCCT 31602	GTTGT A _	
			AGGAGGGCAG TTG GC CT		
			TCCTCCCGTC AAC CG GA		
			_____ C A		
GAM1323	ZNF76	3'	CAGGCCCTGTCTGCCCTCC 12808	TTGTTTGA	
			GGAGGGCAGG GCCTG		
			CCTCCCGTCC CGGAC		
			TGTCC_____		
GAM1323	C1QTNF6	3'	CAGGTGGCCTGCCCTTCT 49140	TG	
			AGGAGGGCAGGT TTTG		
			TCTTCCCGTCCG GGAC		
			GT		
GAM1323	C20orf150	3'	GTTTACAACCTGCCCTCC 65401	TT	
			GGAGGGCAGGTTGT GAGC		
			CCTCCCGTCCAACA TTTG		
			_____		
GAM1323	C20orf162	5'	CAGGCCTTCCACCTGCCCTGCC 54599	_ TGTTTGA	
			GG AGGGCAGGT GCCTG		



			CC TCCCGTCCA	CGGAC	
			G CCTTC__		
GAM1323	FKBP8	3'	CAGGCTCCCTGTCCACTGCCCT	24100	GTTGTTT_
	CC		GGAGGGCAG	GAGCCTG	
			CCTCCCGTC	CTCGGAC	
			ACCTGTCC		
GAM1323	FLJ10700	3'	CAAGCCCCTCCTGCCCTCT	36426	TT__
			GGAGGGCAGG	GTTTG	
			TCTCCCGTCC	CGAAC	
			TCCC		
GAM1323	FLJ13693	3'	CAAACCCAGAGGCTGCCATCCT	45647	G G ____
			AGGA GGCAG TT	GTTTG	
			TCCT CCGTC GA	CAAAC	
			A G GACC		
GAM1323	FLJ13782	3'	CAGGCAACCTACCCCTCT	46163	C_
			GGAGGG AGGTTGTTTG		
			TCTCCC	TCCAACGGAC	
			CA		
GAM1323	FLJ13848	3'	CAGGCCCTCTGCCTGCACTCC	45462	G TGTTTGA
	T		AGGAG GCAGGT	GCCTG	
			TCCTC CGTCCG	CGGAC	
			A TCTCCC_		
GAM1323	FLJ14326	5'	GAGCAGCCCACCCTCCT	49807	CA
			AGGAGGG GGTTGTTT		
			TCCTCCC	CCGACGAG	
			AC		
GAM1323	FLJ23519	5'	CAGGCTCACAGACCACCCACC	69201	A CA GTT
			GG GGG GGTT	TGAGCCTG	
			CC CCC CCAG	ACTCGGAC	
			A CA AC_		
GAM1323	FLJ32865	3'	CAGACACACCTGCCCTCC	58169	_
			GGAGGGCAGGT	TGTTTG	
			CCTCCCGTCCA	ACAGAC	
			C		
GAM1323	GABARAP	3'	GCTCAAACACCACCTCC	23458	GCA T
			GGAGG GGT	GTTTGAGC	
			CCTCC	CCA CAACTCG	
			A__ _		
GAM1323	GMEB2	5'	AGGCCCTCCTGTCCTCCT	24726	TTGTTTGA
			AGGAGGGCAGG	GCCT	

		TCCTCCTGTCC	CGGA	
		TCCC_____		
GAM1323 GP5	3'	GCCACTACACCTGCCCTCTT	15647	T T_ A
		AGGAGGGCAGGT GT TG GC		
		TTCTCCCGTCCA CA AC CG		
		_ TC _		
GAM1323 HA-1	3'	CAGGCCCTGCCCTGCCCTCT	65553	TT TTGA
		GGAGGGCAGG GT GCCTG		
		TCTCCCGTCC CG CGGAC		
		_ TCC_		
GAM1323 HEYL	3'	CAGACCCCTCTCCTGCCCTCT	27392	TT_____
		GGAGGGCAGG GTTTG		
		TCTCCCGTCC CAGAC		
		TCTCCC		
GAM1323 HU-K4	3'	CAGGCTCTCTCCCCTGCTCTCC	24366	TTGTTT
		GGAGGGCAGG GAGCCTG		
		CCTCTCGTCC CTCGGAC		
		CCTCT_		
GAM1323 KIAA0125	5'	CAAGCCCTGCCTGCCTCCC	28895	AG T__
		GG GGCAGGT GTTTG		
		CC CCGTCCG CGAAC		
		CT TCC		
GAM1323 KIAA0125	3'	CAAGCCCTGCCTGCCTCCC	60504	AG T__
		GG GGCAGGT GTTTG		
		CC CCGTCCG CGAAC		
		CT TCC		
GAM1323 KIAA0415	3'	CAGGCTCAAACCTCTTCCCCCTC	92574	CA TT__
C		GGAGGG GG GTTTGAGCCTG		
		CCTCCC CC CAAACTCGGAC		
		_ TTCT		
GAM1323 KIAA0447	3'	AGGGCACCCTGCCCTCCT	71665	T TTGAG
		AGGAGGGCAGG TGT CCT		
		TCCTCCCGTCC ACG GGA		
		C _____		
GAM1323 KIAA0789	5'	CAAGCATTGAACCTTGCCCTCC	63681	_____
		GGAGGGCAGGT TGTTTG		
		CCTCCCGTTCA ACGAAC		
		AGTT		
GAM1323 KIAA0821	3'	CAAGCAAACCTGCCCCCT	29941	A _
		AGG GGGCAGGTT GTTTG		

TCC CCCGTCCAA CGAAC  
 — A  
 GAM1323 KIAA1026 3' CAGGCTCAAACAATTCTCCTGC 71189 —  
 CT GGGCAGG TTGTTTGAGCCTG  
 ||||| |||||  
 TCCGTCC AACAAACTCGGAC  
 TCTT  
 GAM1323 KIAA1036 5' CAGACAACCCACCCCT 29814 A CA  
 AGG GGG GGTTGTTTG  
 ||| ||| |||||  
 TCC CCC CCAACAGAC  
 — AC  
 GAM1323 KIAA1259 3' CAGGCTCGGCACCGGCCCTCC 49830 A T T  
 GGAGGGC GGT GTT GAGCCTG  
 ||||| ||| ||| |||||  
 CCTCCCG CCA CGG CTCGGAC  
 G — —  
 GAM1323 KIAA1904 3' CAGACTCCCCCGCCCCCT 73478 A A\_ TT  
 AGG GGGC GG GTTTG  
 ||| ||| || |||||  
 TCC CCGG CC CAGAC  
 — CC CT  
 GAM1323 MGC10200 3' GCTCAAACAATCCACCCTCCT 58988 CA  
 AGGAGGG GGTTGTTTGAGC  
 ||||| |||||  
 TCCTCCC CTAACAAACTCG  
 AC  
 GAM1323 MGC26766 3' AGACTCCTGCCTGCCCTCT 58818 TGTTT C  
 GGAGGGCAGGT GAG CT  
 ||||| ||| ||  
 TCTCCCGTCCG CTC GA  
 TC\_\_ A  
 GAM1323 NIR3 3' AGGTGGGCAGCCTGCCCCCT 66236 A GA  
 GG GGGCAGGTTGTTT GCCT  
 || ||||| |||  
 CC CCCGTCCGACGGG TGGA  
 C —  
 GAM1323 OPRL1 3' CAGACTAAAGCTGCCCTCCT 6193 G —  
 AGGAGGGCAG TT GTTTG  
 ||||| || |||||  
 TCCTCCCGTC AA CAGAC  
 G AT  
 GAM1323 PLA2G6 3' CAAGCCCAGCCACTGCCCTCC 66487 — —  
 GGAGGGCA GGTT GTTTG  
 ||||| ||| |||||  
 CCTCCCGT CCGA CGAAC  
 CA CC  
 GAM1323 SQV7L 5' CAGGCTCAAGTGATCTGCCCTC 70570 TG  
 CT AGGAGGGCAGGT TTTGAGCCTG  
 ||||| |||||

	TCCTCCCGTCTA GAACTCGGAC		
	GT		
GAM1323 LOC126006 5'	GCTCAGGTCGCCCTGCCCCCT 74428	A	T _
	AGG GGGCAGG TG TTTGAGC		
	TCC CCCGTCC GC GGA CTG		
	_ C T		
GAM1323 LOC126031 5'	GCTCATCCTGCTGCCCTCCT 74433		GTTGTT
	AGGAGGGCAG TGAGC		
	TCCTCCCGTC ACTCG		
	GTCCT_		
GAM1323 LOC129198 3'	CAGGCCCTGTGACCTCCCTCCT 76118	C	TG TTGA
	AGGAGGG AGGT T GCCTG		
	TCCTCCC TCCA G CGGAC		
	_ GT TCC_		
GAM1323 LOC144501 5'	CAGGCTCACTCGCTCACCCCCC 83104	A	CA T TT
T	AGG GGG GGT G TGAGCCTG		
	TCC CCC TCG C ACTCGGAC		
	C AC _ TC		
GAM1323 LOC145082 5'	AGGCTCAAATCATCCTCCT 83234		CAGGTT
	AGGAGGG GTTTGAGCCT		
	TCCTCCT TAAACTCGGA		
	AC_____		
GAM1323 LOC145082 5'	AGGCTCATGCCACCCACCC 83235	CA	T T
	GGG GGT GT TGAGCCT		
	CCC CCA CG ACTCGGA		
	AC C T		
GAM1323 LOC146013 3'	CAGACTGACTGAACCTGCCTCC 83609	AG	_____
C	GG GGCAGGTT GTTTG		
	CC CCGTCAA CAGAC		
	CT GTCAGT		
GAM1323 LOC148181 5'	CAGGCCAGCTCCTCCTGCCTC 78701	AG	TT__ T A
CC	GG GGCAGG GTT G GCCTG		
	CC CCGTCC CGA C CGGAC		
	CT TCCT _ C		
GAM1323 LOC149657 3'	AGGCCAGCCTGCGCCCC 84568	A _	TTTGA
	GG GG GCAGGTTG GCCT		
	CC CC CGTCCGAC CGGA		
	_ G C_____		
GAM1323 LOC149657 3'	AGGCCAGCCTGCGCCCC 84569	A _	TTTGA
	GG GG GCAGGTTG GCCT		

CC CC CGTCCGAC CGGA  
 \_ G C\_\_\_\_  
 GAM1323 LOC149657 3' AGGCCCCAGCCTGCGCCCC 84570 A \_ TTTGA  
 GG GG GCAGGTTG GCCT  
 || || ||||| ||||  
 CC CC CGTCCGAC CGGA  
 \_ G C\_\_\_\_  
 GAM1323 LOC149657 3' AGGCCCCAGCCTGCGCCCC 84571 A \_ TTTGA  
 GG GG GCAGGTTG GCCT  
 || || ||||| ||||  
 CC CC CGTCCGAC CGGA  
 \_ G C\_\_\_\_  
 GAM1323 LOC150622 5' CAAGCCACCTGCCTTCC 79955 T  
 GGAGGGCAGGT GTTTG  
 ||||| ||||  
 CCTTCCGTCCA CGAAC  
 C  
 GAM1323 LOC151808 5' AAGCAAACCTGCCCTCCT 85496 G  
 AGGAGGGCAG TTGTTT  
 ||||| ||||  
 TCCTCCCGTC AACGAA  
 A  
 GAM1323 LOC154990 5' CAGGCCAGCTCCTCCTGCCTC 81221 AG TT\_ T A  
 CC GG GGCAGG GTT G GCCTG  
 || |||| ||| ||||  
 CC CCGTCC CGA C CGGAC  
 CT TCCT \_C  
 GAM1323 LOC157860 5' CAGACTCTCCTGGCCCCCT 86566 A \_ TT\_  
 AGG GGGC AGG GTTTG  
 || |||| || ||||  
 TCC CCCG TCC CAGAC  
 \_ G TCT  
 GAM1323 LOC164582 5' CAGGCTCAAAACCAGGCCCCCT 82539 A A\_ GT  
 AGG GGGC GGTT TTGAGCCTG  
 || |||| ||| |||||  
 TCC CCCG CCAA AACTCGGAC  
 \_ GA \_  
 GAM1323 LOC196463 3' CAGGCCCCACCCACCCACC 87709 A CA\_ T TTTGA  
 GG GGG GG TG GCCTG  
 || || ||| ||||  
 CC CCC CC AC CGGAC  
 A CAC C CC\_\_\_\_  
 GAM1323 LOC196472 5' CAGGCTCAAATGGAGGTCCCTC 87719 \_AGG TG  
 C GGAGGG C T TTTGAGCCTG  
 ||||| | | |||||  
 CCTCCC G G AACTCGGAC  
 T GA\_ GT  
 GAM1323 LOC197003 3' AGGCTCATCTACCCCGCT 87864 A T TT  
 GGC GG TG TGAGCCT  
 ||| || |||||

	TCG CC AT ACTCGGA		
	C C CT		
GAM1323 LOC199923 3'	CAGGCTGTTACCTGCCCCCT 88498	A	TGTTTG
	AGG GGGCAGGT AGCCTG		
	TCC CCCGTCCA TCGGAC		
	_ TTG__		
GAM1323 LOC199926 5'	CAAGCATTGTATCCTGCCCTCC 89878	T	_____
	GGAGGGCAGG TGTTTG		
	CCTCCCGTCC ACGAAC		
	TATGTT		
GAM1323 LOC202316 5'	CAAGCATTGTATCCTGCCCTCC 90338	T	_____
	GGAGGGCAGG TGTTTG		
	CCTCCCGTCC ACGAAC		
	TATGTT		
GAM1323 LOC202908 3'	CAGGCCCAGCTCCTCCTGCCTC 89229	AG	TT__ T A
CC	GG GGCAGG GTT G GCCTG		
	CC CCGTCC CGA C CGGAC		
	CT TCCT _C		
GAM1323 LOC221839 5'	CAAACCCAAGAGCATGCCCTTC 92495	G	_____
T	AGGAGGGCA GTT GTTTG		
	TCTTCCCGT CGA CAAAC		
	A GAACC		
GAM1323 LOC222057 3'	CAGGCCCAGCTCCTCCTGCCTC 92766	AG	TT__ T A
CC	GG GGCAGG GTT G GCCTG		
	CC CCGTCC CGA C CGGAC		
	CT TCCT _C		
GAM1323 LOC255975 3'	CAGGCCCAGCTCCTCCTGCCTC 95887	AG	TT__ T A
CC	GG GGCAGG GTT G GCCTG		
	CC CCGTCC CGA C CGGAC		
	CT TCCT _C		
GAM1323 LOC256878 3'	CAGGCCCAGCTCCTCCTGCCTC 96900	AG	TT__ T A
CC	GG GGCAGG GTT G GCCTG		
	CC CCGTCC CGA C CGGAC		
	CT TCCT _C		
GAM1323 LOC93349 3'	CAAGCTCCCTGCCCTCT 56452	TT	
	GGAGGGCAGG GTTTG		
	TCTCCCGTCC CGAAC		
	CT		
GAM1324 CACNB3 3'	CAGAGCACAACCACAGTGACC 61333	_	A AG
	GG CACTGTGGTT TG TTG		

CC GTGACACCAA AC GAC  
 A C GA  
 GAM1324 C8orf17 5' ACCCACAACCACAGCCCT 39593 CA A A  
 AGG CTGTGGTT TG GT  
 ||| ||||| || ||  
 TCC GACACCAA AC CA  
 C\_ C C  
 GAM1324 SERP1 3' TAGTCCATACCACAGTGCCT 27065 T AG  
 AGGCACTGTGGT ATG TTG  
 ||||| ||| |||  
 TCCGTGACACCA TAC GAT  
 \_ CT  
 GAM1324 LOC142955 5' ACAACTCACCGTGTGC 76439 TGT TAT  
 GCAC GGT GAGTTGT  
 ||| || |||||  
 CGTG CCA CTCAACA  
 TG\_ \_  
 GAM1324 LOC150596 3' CAATGTTGATAACCACAGTTCC 79949 C GA\_  
 T AGG ACTGTGGTTAT GTTG  
 ||| ||||| |||  
 TCC TGACACCAATA TAAC  
 T GTTG  
 GAM1324 LOC51075 3' CATAACCACAAGCCT 31990 AC  
 AGGC TGTGGTTATG  
 ||| |||||  
 TCCG ACACCAATAC  
 A\_  
 GAM1325 ADH1B 3' CTTAGACATAAAGTAAAAT 72644 C CAC  
 ATTT ACTTT TGTCTGAG  
 ||| ||| |||||  
 TAAA TGAAA ACAGATTC  
 A T\_  
 GAM1325 AHR 3' ATCTCAGATGTTAAATAAATG 7875 CAC C T  
 CATTT TTT AC GTCTGAGAT  
 ||| ||| |||||  
 GTAAA AAA TG TAGACTCTA  
 TA\_ T \_  
 GAM1325 FDFT1 3' TAGGAAAGTGAAATG 15518 A  
 CATTTCACTTTC CTG  
 ||||| |||  
 GTAAAGTGAAAG GAT  
 \_  
 GAM1325 JTB 3' ATCTCAGACAGTGAAAGTGAAA 21959  
 TG CATTTCACTTTCAGTGTCTGAGAT  
 |||||  
 GTAAAGTGAAAGTGACAGACTCTA  
 GAM1325 KLF4 3' TCCCAGACAGTGGATATG 14891 CT A  
 CA TTCAGTGTCTG GA  
 || ||||| ||

			GT AGGTGACAGAC CT	
			AT C	
GAM1325	PHYH	3'	ACAGTAAAAGTGAAAT 20608	C
			ATTTCACTTT ACTGT	
			TAAAGTGAAA TGACA	
			A	
GAM1325	PKD2	3'	TCCAGGTTGAAAAGTGAAA 60096	CTG A
			TTTCACTTTCA TCTG GA	
			AAAGTGAAAGT GGAC CT	
			T__ _	
GAM1325	WRN	3'	GGGCAGTGAAAATGAAA 5098	C
			TTTCA TTTCACTGTCT	
			AAAGT AAAGTGACGGG	
			A	
GAM1325	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA CTG
			TTTCACTTT CTGT AGAT	
			AAAGTGAAA GACA TCTA	
			C_ CG_	
GAM1325	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT CT
			TTCACTTTCA GT GAG	
			AAGTGAAAGT CA CTC	
			CT _	
GAM1325	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G T_
			CTTTCACT TC GAGAT	
			GAAAGTGA AG TTCTA	
			G TC	
GAM1325	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT 45802	ACTTTCACT
	G		CATTTT GTCTGAGAT	
			GTAAAG CAGACTCTA	
			AAACATTT_	
GAM1325	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281	CTT
			CATTTCA TCACTGTCTGAGAT	
			GTAAAGT AGTGACAGACTCTA	
			C_	
GAM1325	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C TC
			TTCA TTTCACTG TGAG	
			AAGT AAAGTGAC GTTT	
			A CT	
GAM1325	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A _
			TTTC CTG TCTGAGAT	



		AAAG GAC AGACTCTA		
		— G		
GAM1325 NIR3	3'	GCAGTGAAAGTGCAAT 66242	T	
		ATT CACTTTTCACTGT		
		TAA GTGAAAGTGACG		
		C		
GAM1325 PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA 53598	CA	G
		TTCAC TTT CT TCTGAGAT		
		AAGTGAAA GG AGACTCTA		
		CC G		
GAM1325 PP35	3'	ATCTCAGACTGAAA 22814	CT	
		TTTCA GTCTGAGAT		
		AAAGT CAGACTCTA		
		—		
GAM1325 PRD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148	TCAC	C_
		CATTTCAC TTT TGT TGAG		
		GTAAAGTGAA ACG ACTC		
		TA_ TT		
GAM1325 SEP15	3'	TCCTACAGTAAGAGTGAAA 14934	C	CT
		TTTCACTTT ACTGT GA		
		AAAGTGAGA TGACA CT		
		A TC		
GAM1325 SFXN2	3'	CTCAGGGGAAAAAAGTGAAA 73941	CACTG	
		TTTCACTTT TCTGAG		
		AAAGTGAAA GGA CTC		
		AAAGG		
GAM1325 LOC149703	3'	ATCTCAGACAGCCGTTTGAAA 84647	ACTTTCA	
		TTTC CTGTCTGAGAT		
		AAAG GACAGACTCTA		
		GTTTGCC		
GAM1325 LOC154007	3'	ATCTCAAACCCTTTAGTGAAA 81015	TTCAC T	C
		TTTCACT GT TGAGAT		
		AAAGTGA CA ACTCTA		
		TTTCC_ A		
GAM1325 LOC155004	3'	TCATTTAAGTGAAAGGAAA 81226	A	GTC_
		TTTC CTTTCACT TGA		
		AAAG GAAAGTGA ACT		
		_ ATTT		
GAM1325 LOC222134	5'	ACAGTGAAGTGAAATG 94136	T	
		CATTTCAC TTT CACTGT		

GTAAAGTGAA GTGACA

GAM1326	FGFR1	3'	AGCACTTTAGATCACTTG	43611	A	CTCC
			CAA TGATCTAGA TGCT			
			GTT ACTAGATTT ACGA			
			C C__			
GAM1326	FGFR1	3'	AGCACTTTAGATCACTTG	43618	A	CTCC
			CAA TGATCTAGA TGCT			
			GTT ACTAGATTT ACGA			
			C C__			
GAM1326	FMNL	3'	AGCAGGAGCCTGGCCTGTA	19702	AATGAT	A
			TGCA CTAG CTCCTGCT			
			ATGT GGTC GAGGACGA			
			CC__ C			
GAM1326	GATA6	3'	CAGTGTTAAATCATTTGCA	17915	CTA	TC
			TGCAAATGAT GAC CTG			
			ACGTTTACTA TTG GAC			
			AA_ T_			
GAM1326	GRAF	5'	CAGCAGGAAGAAGGCATTTGCA	30552	A	AGAC
			TGCAAATG TCT TCCTGCTG			
			ACGTTTAC GGA AGGACGAC			
			_ AGA_			
GAM1326	TOMM22	3'	CAGCAGGAGCTCATTTCTCTG	39618	AAT TCT_	A
	CA		TGCA GA AG CTCCTGCTG			
			ACGT CT TC GAGGACGAC			
			CTC TTAC _			
GAM1326	AMOT	3'	CAGCAGGAACCTAAAATATCTG	55718	A	ATC AC
	C		GCA ATG TAG TCCTGCTG			
			CGT TAT ATC AGGACGAC			
			C AAA CA			
GAM1326	C21orf18	3'	AGCATGTCAACCATTTGCA	33843	ATCTA	TCC
			TGCAAATG GAC TGCT			
			ACGTTTAC CTG ACGA			
			CAA_ T_			
GAM1326	CCRK	3'	AGCAGGAGACCCTCTGCA	24011	AAT TCTAGA	
			TGCA GA CTCCTGCT			
			ACGT CT GAGGACGA			
			_ CCCA_			
GAM1326	CORO1A	3'	CAGCAGGGTCAGCCATTCACA	22987	CA	AT A T
			TG AATG CT GAC CCTGCTG			

AC TTAC GA CTG GGACGAC  
 AC C\_ \_ \_  
 GAM1326 DDX37 3' CAGCAGGGCTGGAGATCTCTGC 51024 AAT AGAC  
 A TGCA GATCT TCCTGCTG  
 ||| |||| |||||  
 ACGT CTAGA GGGACGAC  
 CT\_ GGTC  
 GAM1326 DKFZP761D0211 5' AGCAGGAGTCCACATCG 49350 CTA  
 TGAT GACTCCTGCT  
 ||| |||||  
 GCTA CTGAGGACGA  
 CAC  
 GAM1326 FLJ22659 3' CAGCAGGAACCTAGACTC 46259 \_ AC  
 GA TCTAG TCCTGCTG  
 || |||| |||||  
 CT AGATC AGGACGAC  
 C CA  
 GAM1326 HSPBAP1 3' AGCAAAAGGTCAGTTTGCA 44835 \_ AGACTCC  
 TGCAAA TGATCT TGCT  
 |||| |||| |||  
 ACGTTT ACTGGA ACGA  
 G AA\_\_\_\_  
 GAM1326 KIAA1655 5' CAGCAGGAGCCTGGGTC 66598 A  
 GATCTAG CTCCTGCTG  
 ||||| |||||  
 CTGGGTC GAGGACGAC  
 C  
 GAM1326 MADHIP 3' CAGCAGTCATACCCAAATCATT 23636 CTAGACTC\_  
 TGCA TGCAAATGAT CTGCTG  
 ||||| |||||  
 ACGTTTACTA GACGAC  
 AACCCATACT  
 GAM1326 MADHIP 3' CAGCAGTCATACCCAAATCATT 16619 CTAGACTC\_  
 TGCA TGCAAATGAT CTGCTG  
 ||||| |||||  
 ACGTTTACTA GACGAC  
 AACCCATACT  
 GAM1326 MGC15937 3' CAGCAGGAACTCTTCTCACCTG 54707 AA TCT C\_  
 CA TGA AGA TCCTGCTG  
 || ||| ||| |||||  
 GT ACT TCT AGGACGAC  
 CC CT\_ CA  
 GAM1326 NLI-IF 3' AGCAGGAGTCTGTCCTTCA 41044 TC\_  
 TGA TAGACTCCTGCT  
 ||| |||||  
 ACT GTCTGAGGACGA  
 TCCT  
 GAM1326 PPP2R2A 5' AGCAGGGTCACCATTTGCA 10744 ATCTA T  
 TGCAAATG GAC CCTGCT  
 ||||| ||| |||||

ACGTTTAC CTG GGACGA  
 CA\_\_\_\_\_  
 GAM1326 TBX19 3' AGTTAGATCATTTGCA 17647 A  
 TGCAAATGATCT GACT  
 |||||  
 ACGTTTACTAGA TTGA  
 -  
 GAM1326 LOC124222 3' AGCAGGAGCCCTGTTCA 74268 TC A\_  
 TGA TAG CTCCTGCT  
 ||| ||| |||||  
 ACT GTC GAGGACGA  
 T\_ CC  
 GAM1326 LOC197273 5' CAGCAGGAACCTATTGTTTCA 67397 C TG TC AC  
 TG AAA A TAG TCCTGCTG  
 || ||| | ||| |||||  
 AC TTT T ATC AGGACGAC  
 \_ GT\_ CA  
 GAM1326 LOC254228 3' CAGCAGGAGTCTCTGTC 95952 CT  
 GAT AGACTCCTGCTG  
 ||| |||||  
 CTG TCTGAGGACGAC  
 TC  
 GAM1327 LIMK1 3' CCCACAGCTGGAGCAGCTGGA 33644 A AGTCTA  
 TC AGCTGCTC CTGTGGG  
 || ||||| |||||  
 AG TCGACGAG GACACCC  
 G GTC\_\_\_\_  
 GAM1327 NAGA 3' CCCACAGACGTTGCTGAGCAAC 4234 C CTA\_  
 T AG TGCTCAGT CTGTGGG  
 || ||||| |||||  
 TC ACGAGTCG GACACCC  
 A TTGCA  
 GAM1327 KIAA0205 3' CCACAGCAGACAAGGTTGA 29578 G GCTCA A  
 TCAA CT GTCT CTGTGG  
 |||| || ||| |||||  
 AGTT GA CAGA GACACC  
 G A\_\_\_\_ C  
 GAM1327 MYO3B 3' CCCACATGTGTTGTGCAGCCTG 57302 A T TC \_  
 A TCA GCTGC CAG TAC TGTGGG  
 ||| |||| ||| ||| |||||  
 AGT CGACG GTT GTG ACACCC  
 C T \_ T  
 GAM1327 PDK2 3' CCCACAGTAAAGAGGAGACTGA 10503 AG G AGTC  
 TCA CT CTC TACTGTGGG  
 ||| || ||| |||||  
 AGT GA GAG ATGACACCC  
 CA G AA\_  
 GAM1327 PPP1R16B 3' CCCAACCCACTGAGCGCCTGA 61383 A T CTA CTG  
 TCA GC GCTCAGT TGGG  
 ||| || ||||| |||

			AGT CG CGAGTCA	ACCC	
			C _	CCCA__	
GAM1327	PRKRI	5'	CCACCCACCAGCAGCTT	20754	CA CTACT
			AAGCTGCT GT	GTGG	
			TTCGACGA CA	CACC	
			C_ CC__		
GAM1327	LOC153454	3'	CCATTTTtagactGAGAGCTT	80832	G CT_
			AAGCT CTCAGTCTA	GTGG	
			TTCGA GAGTCAGAT	TACC	
			_	TTT	
GAM1328	ATP11A	3'	GCCACGCCGGCAGCTTC	77031	A AT_
			GAAGCTGCC GGC	GC	
			CTTCGACGG CCG	CG	
			_	CAC	
GAM1328	BAP1	3'	AGCGAGGTACTGCAGCTTC	16213	CAG A_
			GAAGCTGC GC	TGCT	
			CTTCGACG TG	GCGA	
			TCA	GA	
GAM1328	BCL7B	3'	GCTGCTGGCAGCTTC	8134	G T
			GAAGCTGCCAG CA	GC	
			CTTCGACGGTC GT	CG	
			-	-	
GAM1328	C18orf1	5'	GCCTCGCCCGGCGGCTTC	60245	A AT_
			GAAGCTGCC GGC	GC	
			CTTCGGCGG CCG	CG	
			C	CTC	
GAM1328	CIS4	5'	GCAGCCTTGCAGCCTC	14877	A C A
			GA GCTGC AGGC	TGC	
			CT CGACG TCCG	ACG	
			C	T _	
GAM1328	DSCR3	3'	TGTGCCCAGCAGTTTC	20198	CA
			GAAGCTGC GGCATG		
			CTTTGACG CCGTGT		
			AC		
GAM1328	EGFL4	5'	GCCGGCCCGGCAGCTTC	61813	A AT
			GAAGCTGCC GGC	GC	
			CTTCGACGG CCG	CG	
			C	GC	
GAM1328	EMS1	3'	GTCACGCGGCAGCTTC	56754	AG A _
			GAAGCTGCC GC	TG C	

			CTTCGACGG CG AC G		
			___ C T		
GAM1328 EMS1	3'	GTCACGCGGCAGCTTC	17854	AG A _	
		GAAGCTGCC GC TG C			
		CTTCGACGG CG AC G			
		___ C T			
GAM1328 ETS2	3'	TGGCGCCTGGCAGTCC	17881	A AT	
		A GCTGCCAGGC GCTA			
		C TGACGGTCCG CGGT			
		C ___			
GAM1328 FUT4	3'	TGTGGCCCCGTGCAGCTTC	8963	CA CAT	
		GAAGCTGC GG GCTATA			
		CTTCGACG CC CGGTGT			
		TG ___			
GAM1328 GNA11	5'	GCACCGGCCTGGGCAGCTTC	76100	_ A__	
		GAAGCTGCC AGGC TGC			
		CTTCGACGG TCCG ACG			
		G GCC			
GAM1328 GRLF1	3'	GTACAGCCCGGCTGGCGGCCTC	78563	A G AT_ A	
		GA GCTGCCAG C GCT TAC			
		CT CGGCGGTC G CGA ATG			
		C _GCC C			
GAM1328 HAS3	3'	GTATGGCCTGACAGCT	18042	C _	
		AGCTG CAGGC ATGC			
		TCGAC GTCCG TATG			
		A G			
GAM1328 HMG20A	3'	GCATCACGCCTAGCAGTTTC	36539	C ___	
		GAAGCTGC AGGC ATGC			
		CTTTGACG TCCG TACG			
		A CAC			
GAM1328 HPS4	5'	TGGGATGCCTGGCTACT	41989	CT G	
		AG GCCAGGCAT CTA			
		TC CGGTCCGTA GGT			
		AT G			
GAM1328 IKBKB	3'	GTACAGCCATGGCAGCT	63210	_ A_	
		AGCTGCCA GGC TGC			
		TCGACGGT CCG ATG			
		A AC			
GAM1328 KCNJ5	3'	GTGGCATCAGCAGCTTC	6097	CAGGC	
		GAAGCTGC ATGCTAT			

			CTTCGACG TACGGTG		
			AC__		
GAM1328	MBD3	3'	GCAGTGGGCTGGCAGCTTC 14095	G_ _	
			GAAGCTGCCAG CA TGC		
			CTTCGACGGTC GT ACG		
			GG G		
GAM1328	MFI2	3'	GCACCTGGCAGCTTT 52814	CA	
			GAAGCTGCCAGG TGC		
			TTTCGACGGTCC ACG		
			—		
GAM1328	MYLK	3'	GCAGATGTCTAGCAGCTTC 97020	C _	
			GAAGCTGC AGGCA TGC		
			CTTCGACG TCTGT ACG		
			A AG		
GAM1328	PCDH12	5'	GCACAGGTTCTTGACAGCTTC 33422	C _ A_	
			GAAGCTGC AGG C TGC		
			CTTCGACG TCT G ACG		
			T T GAC		
GAM1328	PEX1	3'	TATGCTTAGCAGCTTC 4877	C	
			GAAGCTGC AGGCATG		
			CTTCGACG TTCGTAT		
			A		
GAM1328	SGCA	3'	GCTGCTGGCAGCCTC 3428	A G T	
			GA GCTGCCAG CA GC		
			CT CGACGGTC GT CG		
			C _ _		
GAM1328	SLC3A1	3'	TACAGCATGCTGCTT 62247	TGCCA A	
			AAGC GGCATGCT TA		
			TTCG TCGTACGA AT		
			— C		
GAM1328	SPON1	5'	GCCAGCCTGGCAGCCTC 62451	A AT	
			GA GCTGCCAGGC GC		
			CT CGACGGTCCG CG		
			C AC		
GAM1328	TAF1C	3'	AGCGGCCGTTGGCAGCT 19056	_ A	
			AGCTGCCA GGC TGCT		
			TCGACGGT CCG GCGA		
			TG _		
GAM1328	UBE2I	5'	GGCGGCTCTAGCAGCTTC 12492	C _ A	
			GAAGCTGC AG GC TGCT		

			CTTCGACG TC CG GCGG		
			A T _		
GAM1328	UBE4A	3'	AGCTATTCCCAGCAGCTTC 16555	CA C _	
			GAAGCTGC GG AT GCT		
			CTTCGACG CC TA CGA		
			AC T T		
GAM1328	XKRY	5'	AGCAAAATCTGGCAGCT 16253	CA_	
			AGCTGCCAGG TGCT		
			TCGACGGTCT ACGA		
			AAA		
GAM1328	XKRY	5'	AGCAAAATCTGGCAGCT 60014	CA_	
			AGCTGCCAGG TGCT		
			TCGACGGTCT ACGA		
			AAA		
GAM1328	ZFH1B	3'	CGTGCCTGACGCTTC 28924	T C	
			GAAGC G CAGGCATG		
			CTTCG C GTCCGTGC		
			_ A		
GAM1328	AKAP6	3'	GTATAGCATGTAGCAGCTTC 14993	CAG	
			GAAGCTGC GCATGCTATAC		
			CTTCGACG TGTACGATATG		
			A_		
GAM1328	AP1S2	3'	GCACACTTTACAGCAGCTTC 14040	C_ CA	
			GAAGCTGC AGG TGC		
			CTTCGACG TTC ACG		
			ACAT AC		
GAM1328	BRPF3	3'	GTATGGCCGGCAGCTTC 92323	A _	
			GAAGCTGCC GGC ATGC		
			CTTCGACGG CCG TATG		
			_ G		
GAM1328	C16orf44	3'	GTACAACTTAGCAGCTTT 45316	C CA_	
			GAAGCTGC AGG TGC		
			TTTCGACG TTC ATG		
			A AAC		
GAM1328	CGI-96	3'	CATGGCCTGCAGCTTC 31661	C _	
			GAAGCTGC AGGC ATG		
			CTTCGACG TCCG TAC		
			_ G		
GAM1328	DKFZp434F1719	3'	GTCTGCCTGGCTGCCTC 50003	A T T	
			GA GC GCCAGGCA GC		



CT CG CGGTCCGT TG  
 C T C  
 GAM1328 DKFZP564C1940 5' GCATTGCCAGCCTGGCAATTC 25903 C \_\_\_\_\_  
 GAAG TGCCAGGC ATGC  
 ||| ||||| |||  
 CTTT ACGGTCCG TACG  
 A ACCGT  
 GAM1328 DKFZP564O0423 3' GCACCTCTGAACCCGCAGCTTC 91690 \_\_\_\_\_ CA  
 GAAGCTGC CAGG TGC  
 ||||| ||| |||  
 CTTGACG GTCT ACG  
 CCCAA CC  
 GAM1328 DKFZP564P1916 5' GTAGATGTGCAGCTTC 31608 CAG G  
 GAAGCTGC GCAT CTAT  
 ||||| ||| |||  
 CTTGACG TGTA GATG  
 \_\_\_\_\_  
 GAM1328 DKFZP761F241 3' GCAGTGCCTGGCAGTCC 48797 A \_  
 A GCTGCCAGGCA TGC  
 | ||||| |||  
 C TGACGGTCCGT ACG  
 C G  
 GAM1328 DNAL4 3' GCTACCTGGCAGTTTC 19218 CAT  
 GAAGCTGCCAGG GC  
 ||||| ||  
 CTTTGACGGTCC CG  
 AT\_  
 GAM1328 ERAP140 3' GCATACTGGCAGTTTC 75206 GC  
 GAAGCTGCCAG ATGC  
 ||||| |||  
 CTTTGACGGTC TACG  
 A\_  
 GAM1328 FEM1B 5' GCAGCGCCTGGCACTTC 31024 C A\_  
 GAAG TGCCAGGC TGC  
 ||| ||||| |||  
 CTTT ACGGTCCG ACG  
 \_ CG  
 GAM1328 FLJ10824 5' GTGTGCTGGCAGCTTC 72575 G  
 GAAGCTGCCAG CATGC  
 ||||| |||||  
 CTTGACGGTC GTGTG  
 \_  
 GAM1328 FLJ10898 5' GCACTTTGCCAGCAGCTTC 59433 CA \_\_\_\_  
 GAAGCTGC GGCA TGC  
 ||||| ||| |||  
 CTTGACG CCGT ACG  
 A\_ TTC  
 GAM1328 FLJ10979 3' GCATTTGCCTGGCAGCTTT 36934 \_\_\_\_  
 GAAGCTGCCAGGCA TGC  
 ||||| |||

TTTTCGACGGTCCGT ACG  
 TT  
 GAM1328 FLJ11151 3' GCATCTTCTCAGCAGCTTC 67876 C\_\_ C  
 GAAGCTGC AGG ATGC  
 ||||| ||| |||  
 CTTTCGACG TTC TACG  
 ACTC \_  
 GAM1328 FLJ12150 3' GCATGGCCTGGCAGCT 45349 \_  
 AGCTGCCAGGC ATGC  
 ||||| |||  
 TCGACGGTCCG TACG  
 G  
 GAM1328 FLJ12387 3' CACGCCTGCAGCTTC 43064 C A  
 GAAGCTGC AGGC TG  
 ||||| ||| ||  
 CTTTCGACG TCCG AC  
 \_ C  
 GAM1328 FLJ14957 3' AGCATGCCAGCTCCTC 51737 \_ GCCA  
 GA AGCT GGCATGCT  
 || ||| |||||  
 CT TCGA CCGTACGA  
 CC \_  
 GAM1328 FLJ14966 3' GCACGCATGGCAGCTTC 51769 G A  
 GAAGCTGCCA GC TGC  
 ||||| || |||  
 CTTTCGACGGT CG ACG  
 A C  
 GAM1328 FLJ23047 3' TATGTCTGCAACTTC 44627 C C  
 GAAG TGC AGGCATG  
 ||| ||| |||||  
 CTTT ACG TCTGTAT  
 A \_  
 GAM1328 HSN0V1 3' GTATGCCTGGGAGCCTC 34012 A G  
 GA GCT CCAGGCATGC  
 || ||| |||||  
 CT CGA GGTCCGTATG  
 C G  
 GAM1328 ING4 3' ATAGCATGGGGGCAGT 59703 AGG  
 GCTGCC CATGCTAT  
 |||| |||||  
 TGACGG GTACGATA  
 GG\_  
 GAM1328 KIAA0140 3' AGCGGGTGTGTCAGCCTC 27804 A C G A  
 GA GCTG CA GC TGCT  
 || ||| || |||  
 CT CGAC GT TG GCGA  
 C T G G  
 GAM1328 KIAA0376 3' AGCGCCTGGCAGTT 65596 AT  
 AGCTGCCAGGC GCT  
 ||||| |||

TTGACGGTCCG CGA

GAM1328 KIAA0450 5' AGTGGCCAGCAGCTTC 27617 CA A  
GAAGCTGC GGC TGCT  
||||||| ||| ||||  
CTTCGACG CCG GTGA

A\_ \_  
GAM1328 KIAA0682 3' AGCATGCTATCACTTC 29362 C CCA  
GAAG TG GGCATGCT  
|||| || |||||||  
CTTC AC TCGTACGA

\_ TA\_  
GAM1328 KIAA1184 3' GTCTGCCTGGCAAGTTC 42617 GC T  
GAA TGCCAGGCA GC  
||| ||||||| ||  
CTT ACGGTCCGT TG  
GA C

GAM1328 KIAA1404 3' TAGCATGCCAGCAGCTTC 61992 CA  
GAAGCTGC GGCATGCTA  
||||||| |||||||  
CTTCGACG CCGTACGAT  
A\_

GAM1328 KIAA1530 5' GCCTCGCCTGGCGCTTC 67952 T AT\_  
GAAGC GCCAGGC GC  
||||| ||||||| ||  
CTTCG CGGTCCG CG  
\_ CTC

GAM1328 KIAA1600 3' AGCATGCTTGTACTT 71441 C C  
AAG TGC AGGCATGCT  
||| ||| |||||||  
TTC ATG TTCGTACGA

\_ \_  
GAM1328 KIAA1622 5' GCCGCCTGGCAGCCTC 54261 A AT  
GA GCTGCCAGGC GC  
|| ||||||| ||  
CT CGACGGTCCG CG  
C C\_

GAM1328 KIAA1622 5' GCCGCCTGGCAGCCTC 40560 A AT  
GA GCTGCCAGGC GC  
|| ||||||| ||  
CT CGACGGTCCG CG  
C C\_

GAM1328 LANO 5' GTAGCGCCTGGCGC 47191 T AT  
GC GCCAGGC GCTAT  
|| ||||| |||||  
CG CGGTCCG CGATG

\_ \_  
GAM1328 MAGE-E1 3' AGCACCTAGGCGGCTTC 47941 \_ CA  
GAAGCTGCC AGG TGCT  
||||||| ||| ||||

			CTTCGGCGG TCC ACGA		
			A C_		
GAM1328	MAGEA1	3'	GCGTCCAGCAGCTTC 17159	CA	C
			GAAGCTGC GG ATGC		
			CTTCGACG CC TGCG		
			A_ _		
GAM1328	MGC26766	3'	GCCTCTGCCTGGCAGCT 58820	T_	
			AGCTGCCAGGCA GC		
			TCGACGGTCCGT CG		
			CTC		
GAM1328	MGC4832	3'	GCTGCCTGGTAGCTTC 59003	T	
			GAAGCTGCCAGGCA GC		
			CTTCGATGGTCCGT CG		
			-		
GAM1328	NET-7	3'	GCCTGCCATGGCAGCT 24709	_	T
			AGCTGCCA GGCA GC		
			TCGACGGT CCGT CG		
			A C		
GAM1328	OSBPL7	3'	GCAAAATGCCTGCAGCTTC 34808	C	___
			GAAGCTGC AGGCA TGC		
			CTTCGACG TCCGT ACG		
			- AAA		
GAM1328	phorbolin-1	5'	GTATCGCTGACTCAGCAGCTTC 88782	CA	_ T T
			GAAGCTGC GG CA GC ATAC		
			CTTCGACG TC GT CG TATG		
			AC A _ C		
GAM1328	PL6	3'	GTACATCAGCTGGCAGC 22832	GC_	C
			GCTGCCAG ATG TAT		
			CGACGGTC TAC ATG		
			GAC _		
GAM1328	RIL	3'	GTGGGGTGCTGGCAGCCTC 13489	A	G G
			GA GCTGCCAG CAT CTAT		
			CT CGACGGTC GTG GGTG		
			C _ G		
GAM1328	RP4-622L5	3'	GTAGATGCCTGGCACT 38932	C	G
			AG TGCCAGGCAT CTAT		
			TC ACGGTCCGTA GATG		
			- -		
GAM1328	SIAT8C	5'	GCAGCCTGGCAGCCTC 31882	A	A
			GA GCTGCCAGGC TGC		

			CT CGACGGTCCG ACG		
			C _		
GAM1328	SLC38A1	3'	ATAGGCCAGCAGCTTT	47721	CA ATG
			GAAGCTGC GGC CTAT		
			TTTCGACG CCG GATA		
			AC _		
GAM1328	SMARCF1	3'	GTATAGCACTATGGTGCGCTTC	37442	_ GGCA
			GAAGC TGCCA TGCTATAC		
			CTTCG GTGGT ACGATATG		
			C ATC_		
GAM1328	SSB-3	5'	GCAGGGCCTGGCACTTC	55095	C A_
			GAAG TGCCAGGC TGC		
			CTTC ACGGTCCG ACG		
			_ GG		
GAM1328	TXNL2	3'	AGCTGCAGTAGCTTC	21548	CAG T
			GAAGCTGC GCA GCT		
			CTTCGATG CGT CGA		
			A _ _		
GAM1328	ZAK	3'	GCATAGCCTGACAGCT	56129	C _
			AGCTG CAGGC ATGC		
			TCGAC GTCCG TACG		
			A A		
GAM1328	ZF	5'	GCTGCTGGCAGCCTC	41089	A G T
			GA GCTGCCAG CA GC		
			CT CGACGGTC GT CG		
			C _ _		
GAM1328	LOC112724	3'	GCCATGCCCGCAGCTTC	56498	CA _
			GAAGCTGC GGCATG C		
			CTTCGACG CCGTAC G		
			C_ C		
GAM1328	LOC115939	3'	ATGGGCCTGGCAGCCTC	73662	A ATG
			GA GCTGCCAGGC CTAT		
			CT CGACGGTCCG GGTA		
			C _		
GAM1328	LOC124460	3'	ATAGCATGGACTTAGCT	76038	CC G_
			AGCTG AG CATGCTAT		
			TCGAT TC GTACGATA		
			_ AG		
GAM1328	LOC125268	3'	AGGTGCTGGCAGCT	76067	G G
			AGCTGCCAG CAT CT		

TCGACGGTC GTG GA

GAM1328 LOC128936 3' ATGGCACCTTGCAGCTTC 75788 C CA  
GAAGCTGC AGG TGCTAT  
||||||| ||| |||||  
CTTCGACG TCC ACGGTA

T \_  
GAM1328 LOC129011 5' AGCATGCCTTTGGGTGC 74863 T \_  
GC GCC AGGCATGCT  
|| ||| |||||  
CG TGG TCCGTACGA

\_ GTT  
GAM1328 LOC131831 5' GCTCGCCTAGCGGCTTC 75010 C AT  
GAAGCTGC AGGC GC  
||||||| ||| ||  
CTTCGGCG TCCG CG  
A CT

GAM1328 LOC131870 3' GCACCCTGGCAGGTTC 75019 G CA  
GAA CTGCCAGG TGC  
||| ||||| |||  
CTT GACGGTCC ACG  
G C\_

GAM1328 LOC139296 5' TGGAAGGCCTGGCAGCTTC 75830 ATG  
GAAGCTGCCAGGC CTA  
||||||| |||  
CTTCGACGGTCCG GGT  
GAA

GAM1328 LOC146562 3' GCAGCCTGGCGGCCTC 57533 A A  
GA GCTGCCAGGC TGC  
|| ||||| |||  
CT CGGCGGTCCG ACG  
C \_

GAM1328 LOC148166 5' GCCCAGCCTGGCAGCTTC 78692 AT\_  
GAAGCTGCCAGGC GC  
||||||| |||  
CTTCGACGGTCCG CG  
ACC

GAM1328 LOC148710 5' GCATCCCAGTAGCTTC 84196 CA C  
GAAGCTGC GG ATGC  
||||||| || |||  
CTTCGATG CC TACG  
AC \_

GAM1328 LOC149182 3' GTACCTGGCAGCTTC 84376 CA  
GAAGCTGCCAGG TGC  
||||||| |||  
CTTCGACGGTCC ATG

\_  
GAM1328 LOC149386 3' ATAGCATGCTGACCTTC 84402 CTGCCA  
GAAG GGCATGCTAT  
||| |||||

	CTTC	TCGTACGATA		
	CAG	___		
GAM1328	LOC150225	3' GGAATCCCAGCAGTTTC	85002	CA C G
		GAAGCTGC GG AT CT		
		CTTTGACG CC TA GG		
		AC _ A		
GAM1328	LOC151534	3' GCTGGTGCCTTGCAGCTTC	56685	C _
		GAAGCTGC AGGCAT GC		
		CTTCGACG TCCGTG CG		
		T GT		
GAM1328	LOC153768	5' GCGCATGGCAGCTTC	56715	G AT
		GAAGCTGCCA GC GC		
		CTTCGACGGT CG CG		
		A _		
GAM1328	LOC154007	3' TGTGCCTGCAGCCTC	81024	A C
		GA GCTGC AGGCATG		
		CT CGACG TCCGTGT		
		C _		
GAM1328	LOC168512	5' AGCCTCTCTGGCAGCTTT	82712	CAT
		GAAGCTGCCAGG GCT		
		TTTCGACGGTCT CGA		
		CTC		
GAM1328	LOC197423	5' GCACAGTCTGCAGCTTC	77860	C A_
		GAAGCTGC AGGC TGC		
		CTTCGACG TCTG ACG		
		_ AC		
GAM1328	LOC199920	5' GTATAGCATATTTGTTCAATTC	88492	GCTGC C
		GAA CAGG ATGCTATAC		
		CTT GTTT TACGATATG		
		AACTT A		
GAM1328	LOC200205	3' GCCAGCACTGGCAGCTTC	88626	_ AT
		GAAGCTGCCAG GC GC		
		CTTCGACGGTC CG CG		
		A AC		
GAM1328	LOC200268	3' AGTGAGCCGGTAGCTTC	88675	A A
		GAAGCTGCC GGC TGCT		
		CTTCGATGG CCG GTGA		
		_ A		
GAM1328	LOC219700	5' GTAGCCTGGCAGTCC	93067	A A
		A GCTGCCAGGC TGC		

C TGACGGTCCG ATG  
 C \_  
 GAM1328 LOC220776 3' ATAGCATGCAGCGGT 68384 CAG  
 GCTGC GCATGCTAT  
 |||| |||||  
 TGGCG CGTACGATA  
 A\_\_  
 GAM1328 LOC221037 3' GTATAGCATATGTCACAGCT 93157 CCA \_  
 AGCTG GGCA TGCTATAC  
 |||| ||| |||||  
 TCGAC CTGT ACGATATG  
 A\_\_ AT  
 GAM1328 LOC221424 3' GCATGGGGGCTCTGGCAGCT 93627 \_\_\_\_\_  
 AGCTGCCAGG CATGC  
 ||||| ||||  
 TCGACGGTCT GTACG  
 CGGGG  
 GAM1328 LOC222057 3' GCAGCTGGCAGCCTC 92775 A G A  
 GA GCTGCCAG C TGC  
 || ||||| | |||  
 CT CGACGGTC G ACG  
 C \_ \_  
 GAM1328 LOC223009 5' GCATCTTGGCAGCCTC 94376 A C  
 GA GCTGCCAGG ATGC  
 || ||||| ||||  
 CT CGACGGTTC TACG  
 C \_  
 GAM1328 LOC253502 5' GCATGGGCCCAGCGGCTTC 94580 CA \_  
 GAAGCTGC GGC ATGC  
 ||||| ||| ||||  
 CTTTCGGCG CCG TACG  
 AC GG  
 GAM1328 LOC253725 5' GCCTGTGCTGGCAGCCTC 94701 A \_ T  
 GA GCTGCCAG GCA GC  
 || ||||| ||| ||  
 CT CGACGGTC TGT CG  
 C G C  
 GAM1328 LOC255158 3' GTATAGCATGTGTATCTTC 96171 C CAG  
 GAAG TGC GCATGCTATAC  
 |||| ||| |||||  
 CTTC ATG TGTACGATATG  
 T \_  
 GAM1328 LOC255326 3' ATAGCATGTTAGTTTC 96371 CCAG  
 GAAGCTG GCATGCTAT  
 ||||| |||||  
 CTTTGAT TGTACGATA  
 \_  
 GAM1328 LOC255759 5' AGCACCTGGCAGGCT 97479 \_ CA  
 AGC TGCCAGG TGCT  
 ||| ||||| ||||



			TCG ACGGTCC ACGA		
			G _		
GAM1328	LOC255975	5'	GCTGCTGGCAGCCTC	95896	A G T
			GA GCTGCCAG CA GC		
			CT CGACGGTC GT CG		
			C _ _		
GAM1328	LOC256337	5'	GCCTGTGCTGGCAGCCTC	94696	A _ T
			GA GCTGCCAG GCA GC		
			CT CGACGGTC TGT CG		
			C G C		
GAM1328	LOC51337	3'	GCCTCTCCTGGCAGCTTC	33588	CAT_
			GAAGCTGCCAGG GC		
			CTTCGACGGTCC CG		
			TCTC		
GAM1328	LOC91149	3'	ATAGCATGCTTTTGCTC	65070	A TGCC
			GA GC AGGCATGCTAT		
			CT CG TTCGTACGATA		
			_ TT_		
GAM1328	LOC91409	3'	GCATTTCTGACACTTC	65957	C C C_
			GAAG TG CAGG ATGC		
			CTTC AC GTCC TACG		
			_ A TT		
GAM1328	LOC92492	5'	ATGGAGAGCCAGCAGCTTC	69525	CA ATG
			GAAGCTGC GGC CTAT		
			CTTCGACG CCG GGTA		
			A_ AGA		
GAM1329	ACK1	3'	CCATGTTTTCCCACCAG	19342	A
			CTG TGGGAAAGTATGG		
			GAC ACCCTTTTGTACC		
			C		
GAM1329	BCL11B	5'	CCGGCTCCCCCATCAGTG	43187	AA_ A
			CACTGATGGG AGT TGG		
			GTGACTACCC TCG GCC		
			CCC _		
GAM1329	BCL11B	5'	CCGGCTCCCCCATCAGTG	56801	AA_ A
			CACTGATGGG AGT TGG		
			GTGACTACCC TCG GCC		
			CCC _		
GAM1329	BCL7A	3'	CCACCACCCCATCACTG	40639	C AAA A_
			CA TGATGGG GT TGG		

			GT ACTACCC CA ACC		
			C C__ CC		
GAM1329	ESRRA	3'	CCAGGGCTTCCCCATCAG 15481	A	A_
			CTGATGGG AAGT TGG		
			GACTACCC TTCG ACC		
			C GG		
GAM1329	GAD1	3'	TCACACCCTCCCCATTAGT 5874	AA	TA GC
			ACTGATGGG AG TG GA		
			TGATTACCC TC AC CT		
			C_ CC A_		
GAM1329	GBF1	3'	CCAGTGCTTCCCACCAG 14830	A	A _
			CTG TGGGAA GTA TGG		
			GAC ACCCTT CGT ACC		
			C _ G		
GAM1329	HMG20A	3'	CCAGTCTTCTCCCATCATTG 36535	C	_ TA
			CA TGATGGGA AAG TGG		
			GT ACTACCCT TTC ACC		
			T C TG		
GAM1329	IL1R1	3'	CCATGCTTTCCCACCAG 6055	A	
			CTG TGGGAAAGTATGG		
			GAC ACCCTTTCGTACC		
			C		
GAM1329	SIAT1	3'	CTATCTCTCCCATCAG 11661	A	T
			CTGATGGGA AG ATGG		
			GACTACCCT TC TATC		
			C _		
GAM1329	SYCP2	3'	TCACCATACTTTATCTA 26522	_	C
			TGGG AAAGTATGG GA		
			ATCT TTTCATACC CT		
			A A		
GAM1329	TCF2	3'	CCATACTTTCCCACAG 21376	A	
			CTG TGGGAAAGTATGG		
			GAC ACCCTTTCATACC		
			-		
GAM1329	BICD2	3'	CGCCTCAGCTCCCACCGTGTT 70392	T A	AA AT_
			AACAC G TGGGA GT GGCG		
			TTGTG C ACCCT CG CCGC		
			_ C _ ACT		
GAM1329	CDH22	3'	CCAGGTTTCCCCCATCAGAGTT 41154	A	A_ TA
			AAC CTGATGGG AAG TGG		

TTG GACTACCC TTT ACC  
 A CC GG  
 GAM1329 DCAMKL1 3' GCCTTTTCCCATCG 16412 TAT  
 TGATGGGAAAG GGC  
 ||||| ||  
 GCTACCCTTTT CCG  
  
 —  
 GAM1329 DCTN3 3' CCACCCTCCCCCAATCAGTGT 23371 \_ AA\_ TA  
 T AACACTGAT GGG AG TGG  
 ||||| || || ||  
 TTGTGACTA CCC TC ACC  
 A CCC CC  
 GAM1329 DCTN3 3' CCACCCTCCCCCAATCAGTGT 44307 \_ AA\_ TA  
 T AACACTGAT GGG AG TGG  
 ||||| || || ||  
 TTGTGACTA CCC TC ACC  
 A CCC CC  
 GAM1329 DKFZP434J1813 5' CGCCTTTCCACAATG 61786 C A GTAT  
 CA TG TGGGAAA GGCG  
 || ||||| ||  
 GT AC ACCCTTT CCGC  
 A \_ \_  
 GAM1329 DKFZP586B2420 3' TCACCACATCTGCTTCCCACCA 74998 C A A \_ \_ C  
 TG CA TG TGGGAA GTA TGG GA  
 || ||||| || || ||  
 GT AC ACCCTT CGT ACC CT  
 \_ C \_ CTAC A  
 GAM1329 DKFZp761J1523 3' CCACCCACTCCCATCAGTGT 50167 AAGTA  
 ACACTGATGGGA TGG  
 ||||| ||  
 TGTGACTACCCT ACC  
 CACCC  
 GAM1329 FLJ10110 5' CGCCCTACCCCCTCCAGCGT 35821 A AT AAA T  
 AC CTG GGG GTA GGCG  
 || || || || ||  
 TG GAC CCC CAT CCGC  
 C CT C\_ C  
 GAM1329 FLJ11506 3' TCACCACCAGCCCATCAGTGTT 45112 AAAGTA C  
 AACACTGATGGG TGG GA  
 ||||| || ||  
 TTGTGACTACCC ACC CT  
 GACC\_ A  
 GAM1329 FLJ13993 3' CCAAGACCTTTCCCATCCATG 60458 CT TA\_  
 CA GATGGGAAAG TGG  
 || ||||| ||  
 GT CTACCCTTTC ACC  
 AC CAGA  
 GAM1329 FLJ22087 3' CCATACTTTCTAGATGTC 41956 \_  
 GATG GGAAAGTATGG  
 || ||||| ||

		CTGT TCTTTCATACC		
		AGA		
GAM1329	GFPT1	3' TCACCATACTTCATTCAG 9023	TGG A C	
		CTGA GAA GTATGG GA		
		GACT CTT CATACC CT		
		TA_ _ A		
GAM1329	HCA4	3' GTTACACTCCCATCA 77592	AA A	
		TGATGGGA GT TGGC		
		ACTACCCT CA ATTG		
		_ C		
GAM1329	HSA9947	3' CCAGCTCCCCTCAGTG 42020	T AA A	
		CACTGA GGGA GT TGG		
		GTGACT CCCT CG ACC		
		C _ _		
GAM1329	HSRNAFEV	3' TCGCCCGATCCCATCGG 34026	AAGTAT	
		CTGATGGGA GGCGA		
		GGCTACCCT CCGCT		
		AGC_		
GAM1329	KIAA0864	3' CGCCACACTCACTGTCAGT 63248	GAA A	
		ACTGATGG AGT TGGCG		
		TGACTGTC TCA ACCGC		
		AC_ C		
GAM1329	KIAA1055	3' CGCAACCCTTCCATCAGTGT 66061	AA ATG	
		AACTGATGGGA GT GCG		
		TGTGACTACCTT CA CGC		
		CC A_		
GAM1329	KIAA1467	3' TTATTCTTTCCACCTGT 71619	TGA T	
		AC TGGGAAAG ATGG		
		TG ACCCTTTC TATT		
		TCC T		
GAM1329	KIAA1879	5' CCTGCCCTCCCATCAGTGT 73567	AA T	
		AACTGATGGGA GTA GG		
		TGTGACTACCCT CGT CC		
		CC _		
GAM1329	MGC23918	3' CCACCACTCGCCCATCAG 58515	AA A_	
		CTGATGGG AGT TGG		
		GACTACCC TCA ACC		
		GC CC		
GAM1329	MGC3146	3' CCACATCACCATCAGTGTT 48440	GAAA A	
		AACACTGATGG GT TGG		

TTGTGACTACC TA ACC  
 AC\_\_ C  
 GAM1329 PAK7 3' CCACAATGTTTCCCTCAGTG 69646 T GTA\_\_  
 CACTGA GGGAAA TGG  
 ||||| ||||| ||  
 GTGACT CCCTTT ACC  
 \_ GTAAC  
 GAM1329 PCBP3 3' CGCCGAGTCCCCCCTCAGTGTT 40070 T AAAGTA  
 AACACTGA GGG TGGCG  
 ||||| || ||||  
 TTGTGACT CCC GCCGC  
 C CCTGA\_  
 GAM1329 PI4KII 3' CCATCTCCCATCAGTG 37343 AA T  
 CACTGATGGGA G ATGG  
 ||||| || ||||  
 GTGACTACCCT C TACC  
 \_ \_  
 GAM1329 PSMF1 3' CGCTGTCCCCATCAG 22351 AAAGT  
 CTGATGGG ATGGCG  
 ||||| ||||  
 GACTACCC TGTCGC  
 C\_\_  
 GAM1329 TP53TG3 3' CGGAGACTTTCCACCAAGTGT 31103 A ATGG  
 ACACTG TGGGAAAGT CG  
 ||||| ||||| ||  
 TGTGAC ACCCTTTCA GC  
 C GAG\_  
 GAM1329 ZFP100 3' CCAGTTCCCTACCAGTGT 70051 AT\_ AGTA  
 ACACTG GGGAA TGG  
 ||||| |||| ||  
 TGTGAC CCCTT ACC  
 CAT G\_\_  
 GAM1329 LOC128954 5' CCAGCTGCTCCCATCAG 75794 A\_ A  
 CTGATGGGA AGT TGG  
 ||||| || ||||  
 GACTACCCT TCG ACC  
 CG \_  
 GAM1329 LOC133418 3' CCACTGCTTTCCCCACCAG 75090 AT\_ \_  
 CTG GGGAAAGTA TGG  
 || ||||| ||||  
 GAC CCCTTTCGT ACC  
 CAC C  
 GAM1329 LOC134957 3' CGTTTTATCTGCCATCAGTGTT 57663 GAAA TG  
 AACACTGATGG GTA GCG  
 ||||| || ||||  
 TTGTGACTACC TAT TGC  
 GTC\_ TT  
 GAM1329 LOC144114 5' CCAGCTTTCCCTCAATG 82210 C T A  
 CA TGA GGGAAAGT TGG  
 || ||||| ||||

	GT ACT CCCTTTTCG ACC	
	A C _	
GAM1329 LOC145622 3'	ACTTTACCATCAGTGTT 77287	G
	AACACTGATGG AAAGT	
	TTGTGACTACC TTTCA	
	A	
GAM1329 LOC146176 5'	CCATGCCTTCGCATCAATG 77695	C G A
	CA TGATG GAA GTATGG	
	GT ACTAC CTT CGTACC	
	A G C	
GAM1329 LOC149301 5'	TGCACCTTCCCCATCAG 79253	A TATG
	CTGATGGG AAG GCG	
	GACTACCC TTC CGT	
	C CA_	
GAM1329 LOC149566 3'	CCTCCCTCTTCCCATCAG 84488	_ TAT
	CTGATGGGAA AG GG	
	GACTACCCTT TC CC	
	C CCT	
GAM1329 LOC149606 3'	CGCCACCCTCACCATCAGT 79449	GAA TA
	ACTGATGG AG TGGCG	
	TGACTACC TC ACCGC	
	AC_ CC	
GAM1329 LOC150170 5'	TCACTGTTCTCCCATCA 79593	AAGT C
	TGATGGGA ATGG GA	
	ACTACCCT TGTC CT	
	CT_ A	
GAM1329 LOC150175 5'	TCACTGTTCTCCCATCA 79634	AAGT C
	TGATGGGA ATGG GA	
	ACTACCCT TGTC CT	
	CT_ A	
GAM1329 LOC150215 5'	TCACTGTTCTCCCATCA 79642	AAGT C
	TGATGGGA ATGG GA	
	ACTACCCT TGTC CT	
	CT_ A	
GAM1329 LOC150218 5'	TCACTGTTCTCCCATCA 79723	AAGT C
	TGATGGGA ATGG GA	
	ACTACCCT TGTC CT	
	CT_ A	
GAM1329 LOC153577 5'	CCACCAAACCCATAGTGTT 86054	A AAAGTA
	AACACTG TGGG TGG	

		TTGTGAT ACCC ACC		
		_ AAAACC		
GAM1329	LOC153910 3'	TCAAATTTCCCATCAG	80999	GTA
		CTGATGGGAAA TGG		
		GACTACCCTTT ACT		
		AA_		
GAM1329	LOC158435 3'	TGCTACACTCCCATCAG	56718	AA A
		CTGATGGGA GT TGGCG		
		GACTACCCT CA ATCGT		
		_ C		
GAM1329	LOC163479 5'	TCACCATCAGATCCATCAG	82141	AAAGT C
		CTGATGGG ATGG GA		
		GACTACCT TACC CT		
		AGAC_ A		
GAM1329	LOC201633 3'	TACTCTCCATCAGTG	90238	AA
		CACTGATGGG AGTA		
		GTGACTACCT TCAT		
		C_		
GAM1329	LOC253612 3'	CCAGTATTTCCCATCATGT	96744	C GTA
		ACA TGATGGGAAA TGG		
		TGT ACTACCCTTT ACC		
		_ ATG		
GAM1329	LOC253868 3'	CCAGTATTTCCCATAGT	95579	A GTA
		ACTG TGGGAAA TGG		
		TGAT ACCCTTT ACC		
		_ ATG		
GAM1329	LOC255098 3'	CCACTGCTTTCCCCACCAG	95401	AT_ _
		CTG GGGAAAGTA TGG		
		GAC CCCTTTTCGT ACC		
		CAC C		
GAM1329	LOC56834 5'	CCGGCTCTCCCATCAG	39341	A A
		CTGATGGGA AGT TGG		
		GACTACCCT TCG GCC		
		C _		
GAM1329	LOC85414 3'	CCAACTTTCCCCACCAG	52395	AT_ A
		CTG GGGAAAGT TGG		
		GAC CCCTTTCA ACC		
		CAC _		
GAM1329	LOC90462 3'	CCACCTTTCCCATCAGT	62901	TA
		ACTGATGGGAAAG TGG		

			TGACTACCCTTTC ACC		
			C_		
GAM1329	LOC91445	3'	TCACAGGTTTCCCATCAG 60551	GTA GC	
			CTGATGGGAAA TG GA		
			GACTACCCTTT AC CT		
			GG_ A_		
GAM1329	LOC93129	3'	CCAGGGATTTCCTCCATCAGT 71464	_ A__	
			ACTGATGGG AAAGT TGG		
			TGACTACCC TTTTA ACC		
			C GGG		
GAM1330	ASTN	3'	TGGCACACAACGTGTCCA 69339	CAGA CT	
			TGGACAGT GT TGCCA		
			ACCTGTCA CA ACGGT		
			A__ C_		
GAM1330	ATP1A2	5'	CAGGGTCTCCGACTGTCC 5522	A _	
			GGACAGTC GAG TCTTG		
			CCTGTCAG CTC GGGAC		
			C T		
GAM1330	CADPS	3'	GATTTCCTGATGTCCATG 65207	G _	
			CATGGACA TCAG AGTC		
			GTACCTGT AGTC TTAG		
			_ CT		
GAM1330	CHRM1	3'	CAGGTGTCCTGACTGTCC 94786	AG_	
			GGACAGTCAG T CTTG		
			CCTGTCAGTC G GGAC		
			CT T		
GAM1330	CNGB1	3'	GCAGCTCTGACCGTCC 7111	A CT	
			GGAC GTCAGAGT TGC		
			CCTG CAGTCTCG ACG		
			C _		
GAM1330	PMP22	5'	GCGGGTCTCTGACTGCCC 4329	A T	
			GG CAGTCAGAG CTTGC		
			CC GTCAGTCTC GGGCG		
			C T		
GAM1330	BFAR	3'	CTGGCAAGACTCAGGGTCC 60770	AGTCA	
			GGAC GAGTCTTGCCAG		
			CCTG CTCAGAACGGTC		
			GGA__		
GAM1330	C8orf17	5'	TGAGGCTCTGACCATC 39605	CA	
			GA GTCAGAGTCTTG		



		CT CAGTCTCGGAGT			
		AC			
GAM1330	DKFZP586C1324	3' AAGCTTCTGCTGTCCA	69795	T	T
		TGGACAG CAGAG CTT			
		ACCTGTC GTCTT GAA			
		_ C			
GAM1330	FLJ10044	3' GCAAGTCCTGCTGTCCA	35767	T	AGT
		TGGACAG CAG CTTGC			
		ACCTGTC GTC GAACG			
		_ CT_			
GAM1330	FLJ13114	3' CTGAGCAGCCTCTGACTGCCC	44598	A	T T _
		GG CAGTCAGAG CT GC CAG			
		CC GTCAGTCTC GA CG GTC			
		C C _ A			
GAM1330	KIAA0355	3' GCCAGCTGCTGTCCATG	28028	T	AGT T
		CATGGACAG CAG CT GC			
		GTACCTGTC GTC GA CG			
		_ _ C			
GAM1330	KIAA0478	3' GAGACTCCTACTGTCCA	29546	CA	
		TGGACAGT GAGTCTT			
		ACCTGTCA CTCAGAG			
		TC			
GAM1330	KIAA0843	3' CTGGCAGGGCAACCATACCAT	30112	ACAGTCAGA	
		ATGG GTCTTGCCAG			
		TACC CGGGACGGTC			
		ATACCAA_			
GAM1330	KIAA1388	3' TAGGTCTCTGGCTGCCCATG	93581	A	T
		CATGG CAGTCAGAG CTTG			
		GTACC GTCGGTCTC GGAT			
		C T			
GAM1330	KIAA1870	5' GGCAAGACGGTCGTCCA	51831	AG	AGA
		TGGAC TC GTCTTGCC			
		ACCTG GG CAGAACGG			
		CT _			
GAM1330	PNMA5	3' GCATCCTGTGACTGTCC	73598	G	TCT
		GGACAGTCA AG TGC			
		CCTGTCAGT TC ACG			
		G CT_			
GAM1330	SES2	3' CAAACCTCTGACTGCCA	48806	A	TC
		TGG CAGTCAGAG TTG			

ACC GTCAGTCTC AAC  
 — CA  
 GAM1330 TXI1 5' GGCAAGACCTGACCCG 37371 ACA A  
 TGG GTCAG GTCTTGCC  
 ||| |||| |||||  
 GCC CAGTC CAGAACGG

— —  
 GAM1330 LOC148137 3' CTGGCAAGACTGGGACCCA 58426 ACA AG  
 TGG GTC AGTCTTGCCAG  
 ||| || |||||  
 ACC CAG TCAGAACGGTC  
 — GG

GAM1330 LOC151475 5' GCACTTCGCCCTGACTGTCC 85405 A\_ CT\_  
 GGACAGTCAG GT TGC  
 ||||| || |||  
 CCTGTCAGTC CG ACG  
 CC CTTC

GAM1330 LOC158428 3' CAAAACCTCTGACTTACCCAT 70558 AC\_ C  
 ATGG AGTCAGAGT TTG  
 ||| ||||| |||  
 TACC TCAGTCTCA AAC  
 CAT A

GAM1330 LOC204970 3' GCTCTCCACTGTCCATG 89412 C\_  
 CATGGACAGT AGAGT  
 ||||| ||||  
 GTACCTGTCA TCTCG  
 CC

GAM1330 LOC221060 3' GTAGAACCTAACTGTCCAT 93216 C A CT  
 ATGGACAGT AG GT TGC  
 ||||| || |||  
 TACCTGTCA TC CA ATG  
 A \_ AG

GAM1330 LOC221421 3' CTGGCAAGGGACCCAACTGCCC 92277 A CAGAG\_  
 GG CAGT TCTTGCCAG  
 || ||| |||||  
 CC GTCA GGAACGGTC  
 C ACCCAG

GAM1330 LOC253184 5' CTGACAAGACTCCTGCTCA 96246 GA TCA C  
 TG CAG GAGTCTTG CAG  
 || ||| ||||| |||  
 AC GTC CTCAGAAC GTC  
 TC \_ A

GAM1330 LOC57109 3' GGTCTTACTGTCCATG 39853 C AGTCTT  
 CATGGACAGT AG GCC  
 ||||| || |||  
 GTACCTGTCA TC TGG  
 T \_

GAM1330 LOC90631 3' CGAGCCCTGCTGTCCA 63634 T A T  
 TGGACAG CAG G CTTG  
 ||||| ||| | |||

ACCTGTC GTC C GAGC  
 \_ C \_  
 GAM1330 LOC91812 5' CAGGTCCCTGACTGTCC 67238 AGT  
 GGACAGTCAG CTTG  
 ||||| |||  
 CCTGTCAGTC GGAC  
 CCT  
 GAM1330 LOC91813 5' CAGGTCCCTGACTGTCC 67246 AGT  
 GGACAGTCAG CTTG  
 ||||| |||  
 CCTGTCAGTC GGAC  
 CCT  
 GAM1331 APBA2 3' ACTAATGACCACACCTGC 18555 AT ACA G  
 GCAG TGT GT CATTAGT  
 ||| || |||||  
 CGTC ACA CA GTAATCA  
 C\_ C\_ \_  
 GAM1331 B3GALT5 5' CGACTAATACACCTGGAGTGCA 52561 \_ A\_ C |||  
 GAATCTGCT TGTAC GTG ATTAGTC G  
 ||| ||||| |  
 ACGTG CAC TAATCAG C  
 AG AGGTC A |||  
 GAM1331 B3GALT5 5' CGACTAATACACCTGGAGTGCA 52569 \_ A\_ C |||  
 GAATCTGCT TGTAC GTG ATTAGTC G  
 ||| ||||| |  
 ACGTG CAC TAATCAG C  
 AG AGGTC A |||  
 GAM1331 CASP2 5' ACTAATGGAAGAAATCTGCT 52164 GTACAGTG  
 AGCAGATT CATTAGT  
 ||||| |||||  
 TCGTCTAA GTAATCA  
 AGAAG\_  
 GAM1331 CASP2 5' ACTAATGGAAGAAATCTGCT 6894 GTACAGTG  
 AGCAGATT CATTAGT  
 ||||| |||||  
 TCGTCTAA GTAATCA  
 AGAAG\_  
 GAM1331 CTNS 3' ACCACCTCACACAATCTGT 17035 ACA CATT  
 GCAGATTGT GTG GT  
 ||||| || ||  
 TGTCTAACA CAC CA  
 \_ TCCAC  
 GAM1331 PDE4D 3' GACTAATGCACTGTACAATCTG 73582  
 CT AGCAGATTGTACAGTG CATTAGTC  
 |||||  
 TCGTCTAACATGTCACGTAATCAG  
 GAM1331 RASGRP1 3' ACTAAGTAGCACAATCTGT 19201 ACA GCA  
 GCAGATTGT GT TTAGT  
 ||||| || |||

			TGTCTAACA CG AATCA		
			___ ATG		
GAM1331	GAB3	3'	GACCTACCCACTGTACAGTCCA 54628	CA	CATTA
	CT		AG GATTGTACAGTG GTC		
			TC CTGACATGTCAC CAG		
			AC CCATC		
GAM1331	KIAA1416	5'	GACTAATGCACCAGCAG 86460	ACA	
			TTGT GTGCATTAGTC		
			GACG CACGTAATCAG		
			AC_		
GAM1331	LOC146174	3'	CACTGTAAAATCTGCT 77702	G	
			AGCAGATT TACAGTG		
			TCGTCTAA ATGTCAC		
			A		
GAM1331	LOC152762	3'	GACCGCGCGCTGCACAATGC 80651	GA A	ATTA
			GCA TTGT CAGTGC GTC		
			CGT AACA GTCGCG CAG		
			___ C CGC_		
GAM1332	ARHGEF6	3'	CAAACTTGAAGCCAGGC 68198	ACCA	
			GCCTGG CAAGTTTG		
			CGGACC GTTCAAAC		
			GAA_		
GAM1332	BIG1	3'	TCAAACCTTGCAACACTCCAG 21205	CCA___	
			CTGGA CAAGTTTGA		
			GACCT GTTCAAAC		
			CACAAC		
GAM1332	CABC1	5'	TCAAGCTGACCCAGGCGG 39658	ACCACA	
			TCGCCTGG AGTTTGA		
			GGCGGACC TCGAACT		
			CAG___		
GAM1332	CORO2A	3'	TCAAACCTGTGGTCCAGAGA 53403	GC	A
			TC CTGGACCACA GTTTGA		
			AG GACCTGGTGT CAAACT		
			A_ _		
GAM1332	CORO2A	3'	TCAAACCTGTGGTCCAGAGA 12647	GC	A
			TC CTGGACCACA GTTTGA		
			AG GACCTGGTGT CAAACT		
			A_ _		
GAM1332	DISC1	3'	TCAAACCTCCTGACCTCAGGCGA 37892	_ AC	CA
			TCGCCTG G CA AGTTTGA		

		AGCGGAC C GT TCAAAC	
		T CA CC	
GAM1332 EN2	5'	CGGGCGGCCCGAGGCGG 7459	A ACA
		TCGCCTGG CC GTTTG	
		GGCGGACC GG CGGGC	
		C ____	
GAM1332 FOXD2	5'	CAGAGGGGGGCCAGGCGA 15562	A ACAAG
		TCGCCTGG CC TTTG	
		AGCGGACC GG AGAC	
		C GGG__	
GAM1332 GPX3	5'	TCAGGCAGCGGCTCAGGCGA 9125	GA ACA
		TCGCCTG CC GTTTGA	
		AGCGGAC GG CGGACT	
		TC CGA_	
GAM1332 HNF3G	3'	AACTCTGGTCCAGGAGA 72339	G CA
		TC CCTGGACCA AGTT	
		AG GGACCTGGT TCAA	
		A C_	
GAM1332 IL13RA1	3'	TCAAACCTTGAGTCACAAAGA 7778	GCC _ CA
		TC TG GAC CAAGTTTGA	
		AG AC CTG GTTCAAAC	
		AA_ A A_	
GAM1332 KCNS2	3'	CAAACCTTGATTGAAGGGA 68300	G GGACC
		TC CCT ACAAGTTTG	
		AG GGA TGTCAAAC	
		_ AGTTA	
GAM1332 LMO4	5'	CAAACCTTGACAGCAGCGA 22251	_ GACCA
		TCGC CTG CAAGTTTG	
		AGCG GAC GTTCAAAC	
		AC ____	
GAM1332 LZTS1	3'	TCAAACCTTGTTGGCCTCAAGC 40695	CT__ A
		GC GG CCACAAGTTTGA	
		CG CC GGTGTTCAAAC	
		AACT _	
GAM1332 MATK	3'	CAAGGAGGGTCCAGGCGG 57816	ACAAG
		TCGCCTGGACC TTTG	
		GGCGGACCTGG GAAC	
		GAG__	
GAM1332 MATK	3'	CAAGGAGGGTCCAGGCGG 57819	ACAAG
		TCGCCTGGACC TTTG	

			GGCGGACCTGG	GAAC	
			GAG__		
GAM1332	MATK	3'	CAAGGAGGGTCCAGGCGG	9915	ACAAG
			TCGCCTGGACC	TTTG	
			GGCGGACCTGG	GAAC	
			GAG__		
GAM1332	MIR16	3'	TCAAACCTGTGGCCA	33565	A
			TGG CCACAAGTTTGA		
			ACC GGTGTTCAAAC		
			—		
GAM1332	PIK3C2B	3'	AGCTCGGTCCAGGTGA	10559	ACA
			TCGCCTGGACC	AGTT	
			AGTGGACCTGG	TCGA	
			C__		
GAM1332	PLCG2	5'	CAAACCCGGGGCAGGCGG	72463	GA ACAA
			TCGCCTG CC	GTTTG	
			GGCGGAC GG	CAAAC	
			GG CC__		
GAM1332	PLIN	3'	CAAACCTGTGGCCAAAAGA	10640	GCC A
			TC TGG CCACAAGTTTG		
			AG ACC GGTGTTCAAAC		
			AAA _		
GAM1332	POU2AF1	3'	CAGATTTACAGTCCAGGC	20648	CAC
			GCCTGGAC	AAGTTTG	
			CGGACCTG	TTTAGAC	
			ACA		
GAM1332	SLC6A12	3'	CGAATGTGCTCCAGGCGA	11734	C AG
			TCGCCTGGA CACA	TTTG	
			AGCGGACCT GTGT	AAGC	
			C _		
GAM1332	STARD4	3'	TCAAACCTGTAGTACTACAGA	57516	GCC _ C
			TC TGG AC ACAAGTTTGA		
			AG ATC TG TGTTCAAAC		
			AC_ A A		
GAM1332	TP53	3'	TCAAACCTCCTGGGCTCAGGCGA	5043	A_ CA
			TCGCCTGG CCA	AGTTTGA	
			AGCGGACT GGT	TCAAAC	
			CG CC		
GAM1332	TR2	5'	CAAACCTTCCAGGC	72314	CCAC
			GCCTGGA	AAGTTTG	

CGGACCT TTCAAAC

GAM1332 C21orf42 5' TCAAACCTTGTAGCTGTATGA 54207 CC ACC  
TCG TGG ACAAGTTTGA  
||| ||| |||||  
AGT GTC TGTTCAAAC  
AT GA\_

GAM1332 DAZAP1 3' CAAACCTTGTGAACTCGTGA 38536 CT AC  
TCGC GG CACAAGTTTG  
|||| || |||||  
AGTG TC GTGTTCAAAC  
C\_ AA

GAM1332 DBR1 3' AACTCCTGACCTCAGGCGA 32523 \_AC CA  
TCGCCTG G CA AGTT  
||||| | |||  
AGCGGAC C GT TCAA  
T CA CC

GAM1332 DC-TM4F2 3' CAAACCTTGTGACTGC 48171 CT AC  
GC GG CACAAGTTTG  
|| || |||||  
CG TC GTGTTCAAAC  
\_ A\_

GAM1332 DKFZp434N2030 5' TCAAACCTTGTCTCTCGC 65525 CT CAC  
GC GGAC AAGTTTGA  
|| ||| |||||  
CG CCTG TTCAAAC  
CT \_

GAM1332 DKFZP564I1171 3' TCAGAAGCTGAGTCCAGGC 71592 \_ CAAG  
GCCTGGAC CA TTTGA  
||||| || |||  
CGGACCTG GT AGACT  
A CGA\_

GAM1332 DKFZP564O0423 3' TCAAACCTCCTGGCCTCAGGCGA 91699 \_A CA  
TCGCCTG G CCA AGTTTGA  
||||| | ||| |||||  
AGCGGAC C GGT TCAAAC  
T C CC

GAM1332 EPN2 5' CAAACCTTGTGGACAGG 30321 GA  
CCTG CCACAAGTTTG  
||| |||||  
GGAC GGTGTTCAAAC  
A\_

GAM1332 EREG 3' TCAAACCTTATGGGCAGGGA 7510 G GA C  
TC CCTG CCA AAGTTTGA  
|| ||| || |||||  
AG GGAC GGT TTCAAAC  
\_ G\_ A

GAM1332 FLJ10718 3' TCAAACCTCTTAGGCTCAGGCGA 36496 GA ACA\_  
TCGCCTG CC AGTTTGA  
||||| || |||||

		AGCGGAC GG TCAAAC	
		TC ATTC	
GAM1332	FLJ10803	3' TCAAAC	36671 _ TGGACC
		TCG CC ACAAGTTTGA	
		AGT GG TGTTCAAAC	
		A TA__	
GAM1332	FLJ20312	5' TCAAAC	34928 _ AC
		CCT GG CACAAGTTTGA	
		GGA TC GTGTTCAAAC	
		G GT	
GAM1332	FLJ23420	3' CAAGTGGGTCCAGGC	46846 A AG
		GCCTGGACC CA TTTG	
		CGGACCTGG GT GAAC	
		— —	
GAM1332	FREQ	3' TCAGCTGCTGGCCCGGCGA	26585 A CA T
		TCGCCTGG CCA AGTT GA	
		AGCGGGCC GGT TCGA CT	
		C CG _	
GAM1332	H2AV	3' TCAAAC	56858 _AC CA
		TCGCCTG G CA AGTTTGA	
		AGCGGAC C GT TCAAAC	
		T CA CC	
GAM1332	HSA249128	5' GGCGCGGTCCAGGCGG	34153 ACAA
		TCGCCTGGACC GTT	
		GGCGGACCTGG CGG	
		CG__	
GAM1332	KIAA0089	5' AAGCACGGTCCAGGCGG	69960 ACAA
		TCGCCTGGACC GTTT	
		GGCGGACCTGG CGAA	
		CA__	
GAM1332	KIAA0256	3' CAAAC	64417 _ _ CAC
		GC CT GGAC AAGTTTG	
		CG GA CCTG TTCAAAC	
		T GT _	
GAM1332	KIAA1026	3' TCAAC	71207 _AC CA T
		TCGCCTG G CA AGTT GA	
		AGCGGAC C GT TCAA CT	
		T CA CC _	
GAM1332	KIAA1981	3' CAGAGGATGATTCAGGCGA	88341 C CAAG
		TCGCCTGGA CA TTTG	



AGCGGACTT GT AGAC  
 A AGG\_  
 GAM1332 MGC13090 5' TCAAACCTTGTCGCAAGT 51141 C ACC  
 GC TGG ACAAGTTTGA  
 || ||| |||||  
 TG ACC TGTTCAAACT  
 A GCC  
 GAM1332 MGC2452 5' TCAAGGAGATGTGGTCCAGG 50990 AG\_\_  
 CCTGGACCACA TTTGA  
 ||||| |||  
 GGACCTGGTGT GAACT  
 AGAG  
 GAM1332 MYT1L 5' TCAAACCTTGTTGGTGG 66825 TGG  
 CC ACCACAAGTTTGA  
 || |||||  
 GG TGGTGTTCAAACT  
 \_\_\_\_\_  
 GAM1332 NUDT13 3' TCAGTTTGTGACCCAGGGA 63215 G AC AGT  
 TC CCTGG CACA TTGA  
 || ||| ||| |||  
 AG GGACC GTGT GACT  
 \_ CA TT\_  
 GAM1332 PCDH17 3' CAAACCTTGATTAGG 27087 ACC  
 CCTGG ACAAGTTTG  
 ||| |||||  
 GGATT TGTTCAAAC  
 A\_  
 GAM1332 PGRMC1 3' TCAAACCTTGTAATTGTGGT 21895 TG CC  
 GCC GA ACAAGTTTGA  
 ||| || |||||  
 TGG TT TGTTCAAACT  
 TG AA  
 GAM1332 PTDSS2 3' CATGGTGTGGTCCAGGC 47884 AGTT  
 GCCTGGACCACA TG  
 ||||| ||  
 CGGACCTGGTGT AC  
 GGT\_  
 GAM1332 RPS6KB1 3' TCAAACCTTTCCAGGC 12038 ACCAC  
 GCCTGG AAGTTTGA  
 ||||| |||||  
 CGGACC TTCAAAC  
 CTT\_  
 GAM1332 USP22 3' TCAAACCTCCTGACCTCAGGCGA 68023 \_AC CA  
 TCGCCTG G CA AGTTTGA  
 ||||| | || |||||  
 AGCGGAC C GT TCAAAC  
 T CA CC  
 GAM1332 LOC129011 5' CAGACCTGCGGTCCAGGC 74865 A A  
 GCCTGGACC CA GTTTG  
 ||||| || |||

	CGGACCTGG GT CAGAC		
	C C		
GAM1332 LOC130595 5'	CAGGCTCAGTCCAGGC 75748	CACA	
	GCCTGGAC AGTTTG		
	CGGACCTG TCGGAC		
	AC__		
GAM1332 LOC131873 5'	CTGGTGGTCCAGGAGA 75879	G A	
	TC CCTGGACCAC AG		
	AG GGACCTGGTG TC		
	A G		
GAM1332 LOC145978 3'	TCAAACCTTTAACAGGTGA 77600	GACCAC	
	TCGCCTG AAGTTTGA		
	AGTGGAC TTCAAAC		
	AAT__		
GAM1332 LOC146890 5'	TCAGAAGTAGTCAGGCGA 83854	G C AAG	
	TCGCCTG AC AC TTTGA		
	AGCGGAC TG TG AGACT		
	_ A A__		
GAM1332 LOC150622 5'	CTGGTGGTCCAGGGA 79957	G A	
	TC CCTGGACCAC AG		
	AG GGACCTGGTG TC		
	_ G		
GAM1332 LOC152002 3'	CAAACCAGCTCCAGGTGA 80431	CCACAA	
	TCGCCTGGA GTTTG		
	AGTGGACCT CAAAC		
	CGAC__		
GAM1332 LOC153474 3'	TCAGAAGCTGAGTCCAGGC 80847	_ CAAG	
	GCCTGGAC CA TTTGA		
	CGGACCTG GT AGACT		
	A CGA__		
GAM1332 LOC154007 3'	TCAAACCTCCTAGGCTCAGGCGA 81021	GA ACA__	
	TCGCCTG CC AGTTTGA		
	AGCGGAC GG TCAAAC		
	TC ATCC		
GAM1332 LOC154789 5'	TCAAACCTTGAGCAGGC 81141	GACCA	
	GCCTG CAAGTTTGA		
	CGGAC GTTCAAAC		
	GA__		
GAM1332 LOC158301 3'	CAAACCTGTGGTTCCA 81869	_ A	
	TGGA CCACA GTTTG		

ACCT GGTGT CAAAC  
 T C  
 GAM1332 LOC199906 3' TCAAACCTCCTGACCTCAGGCGA 88487 \_ AC CA  
 TCGCCTG G CA AGTTTGA  
 ||||| I || |||||  
 AGCGGAC C GT TCAAACCT  
 T CA CC  
 GAM1332 LOC199991 5' TCAGAGCGTTCCAGGCGA 89916 CC AAG  
 TCGCCTGGA AC TTTGA  
 ||||| || |||||  
 AGCGGACCT TG AGACT  
 \_ CG\_  
 GAM1332 LOC219529 5' TCAAACCTCCTGAGCCCAGGTGA 92974 AC\_ CA  
 TCGCCTGG CA AGTTTGA  
 ||||| || |||||  
 AGTGGACC GT TCAAACCT  
 CGA CC  
 GAM1332 LOC220753 3' CAAACTTGTAGAGGTGGGC 92941 GG \_\_\_\_  
 GCCT ACC ACAAGTTTG  
 ||| ||| |||||  
 CGGG TGG TGTCAAAC  
 \_ AGA  
 GAM1332 LOC221718 3' TCAAACCTATTGGTGAAG 93632 GG C\_  
 CT ACCA AAGTTTGA  
 || ||| |||||  
 GA TGGT TTCAAACCT  
 AG TA  
 GAM1332 LOC253927 3' TCAAACCTTAGACTTCAGGC 95025 CCAC  
 GCCTGGA AAGTTTGA  
 ||||| |||||  
 CGGACTT TTCAAACCT  
 CAGA  
 GAM1332 LOC51028 3' CAAATATGGTCCAGG 32179 CAA  
 CCTGGACCA GTTTG  
 ||||| |||||  
 GGACCTGGT TAAAC  
 A\_  
 GAM1333 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
 GTA GGAT GGGTTGTTT  
 ||| ||| |||||  
 CGT CCTA CCAACAAA  
 C CGTG\_  
 GAM1333 LCT 3' AACCGTAAAAATCCTT 9697 G  
 AAGGATTTTGA GGTT  
 ||||| |||||  
 TTCCTAAAAAT CCAA  
 G  
 GAM1333 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
 GTAAGGATTTTATAGGGTTGTTT  
 ||||| |||||

CATTCCTAAAAATCCCAACAAA

GAM1333 FBXO30 3' AACTAAAAAATCCTGAC 49573 A AG  
GT AGGATTTTT GTT  
|| ||||| |||  
CA TCCTAAAAA TCAA  
G AA

GAM1333 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTT  
GTAAG AGGGTTGTT  
|||| |||||  
CATTC TCCCAACAA  
AT\_\_\_\_

GAM1333 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
TAAG TTTT GGGTTGTT  
||| ||| |||||  
GTTC AAAA CCAACAAA  
\_\_\_\_ C

GAM1333 SMT3H2 3' AACAACATAAAAAATCCTTGC 22670 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1333 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
GTAAGGATTTTT GGGTT  
||||||| |||||  
CGTTCCTAAAAA TCCAA  
GTA

GAM1333 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
GGAT TT GGGTTGTT  
||| || |||||  
CCTG AA CCAACAAA  
T\_ C

GAM1333 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
C GTA GGATTTTT TTGTTT  
|| ||||| |||||  
CGT CCTAAAAA AACAAA  
C GATAA

GAM1333 LOC148089 3' GGCCCTAAAAATTCCTAC 78637 A  
GTA GGATTTTTAGGGTT  
|| |||||  
CAT CTAAAAATCCCGG  
C

GAM1333 LOC154547 3' AACAAACATAAAAAATCCTTGC 76050 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1333 LOC158104 3' ACAGCCAAAAATCCTTA 60313 AG  
TAAGGATTTTT GGTGT  
||||||| |||||

ATTCCTAAAAA CCGACA

GAM1333 LOC205880 5' AAACAACCATCATCCTGAC 90709 A TTTTAG  
GT AGGAT GGTGTGTT  
|| |||| |||||  
CA TCCTA CCAACAAA  
G CTA\_\_

GAM1333 LOC221561 3' AACAAACATAAAAAATCCTTGC 92130 GG  
GTAAGGATTTTGA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA

A\_  
GAM1333 LOC257591 3' AACAAACATAAAAAATCCTTGC 97840 GG  
GTAAGGATTTTGA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA

A\_  
GAM1333 LOC51145 3' AGCTAAAATCCTTAC 32393 TAG  
GTAAGGATTTT GTTG  
||||||| |||  
CATTCCTAAAA TCGA

GAM1334 ACCN2 3' CCTCAGGCTGCCCTCT 39168 T G GCA  
AGAGG GGCAG TT GAGG  
|||| |||| || |||  
TCTCC CCGTC GA CTCC

\_ G \_  
GAM1334 ADAM12 3' CTGCAAACCGCCACCTC 12970 A \_  
GAGGTGGC GGTT GCAG  
|||||| |||| ||||  
CTCCACCG CCAA CGTC

\_ A  
GAM1334 ADCY6 3' CCTTTCCCTGCAACCTC 40617 G TTGC  
GAGGT GCAGG AGAGG  
|||| |||| ||||  
CTCCA CGTCC TTTCC

A C\_  
GAM1334 ADCY6 3' CCTTTCCCTGCAACCTC 30928 G TTGC  
GAGGT GCAGG AGAGG  
|||| |||| ||||  
CTCCA CGTCC TTTCC

A C\_  
GAM1334 ALPPL2 3' ACCTCCACCTGGAGCTGTCACC 68836 G G \_\_\_\_  
GGTGGCAG TT CA GAGGT  
|||||| || || ||||  
CCACTGTC GA GT CTCCA

\_ G CCAC  
GAM1334 AP2B1 3' CCTCTTGCCACCTGCT 7059 T \_  
GGCAGGT GCA GAGG  
|||||| || ||||

TCGTCCA CGT CTCC  
C T

GAM1334 ASGR2 5' CCTCTGCCCCAGCCCC 55155 T A TT  
GG GGC GG GCAGAGG  
|| ||| || |||||  
CC CCG CC CGTCTCC  
\_ A C\_

GAM1334 ATP8B2 3' CTGCAACCTCCACCTC 65224 C  
GAGGTGG AGGTTGCAG  
||||| |||||  
CTCCACC TCCAACGTC

GAM1334 ATRN 3' ACCTCTACTTTGAGACTCACCT 57791 GCA GC\_\_\_\_  
CT AGAGGTG GGTT AGAGGT  
||||| ||| |||||  
TCTCCAC TCAG TCTCCA  
\_\_\_\_ AGTTTCA

GAM1334 AXIN1 3' ACCTCCGTGCAGCCCTCCCACC 60848 CA\_ \_  
TCT AGAGGTGG GGTTGCA GAGGT  
||||| ||||| |||||  
TCTCCACC CCGACGT CTCCA  
CTC GC

GAM1334 B4GALT5 3' CCTCCACCCTGCAACC 16496 G T CA  
GGT GCAGG TG GAGG  
|| ||||| || |||||  
CCA CGTCC AC CTCC  
A C \_

GAM1334 BAK1 5' ACCTCTGCAACCTACAGCACC 91986 GC\_\_\_\_  
GGTG AGGTTGCAGAGGT  
||| |||||  
CCAC TCCAACGTCTCCA  
GACA

GAM1334 BTEB1 5' CCTCCGCAGCCACCGCC 6843 CA A  
GGTGG GGTTGC GAGG  
||||| ||||| |||||  
CCGCC CCGACG CTCC  
A\_ C

GAM1334 BTNL3 5' ACCTCCAAATCATCCATCCACC 21998 A CA T CA\_\_\_\_  
CCT AG GGTGG GG TG GAGGT  
|| ||||| || || |||||  
TC CCACC CC AC CTCCA  
C TA T TAAAC

GAM1334 C1QA 3' CCTCCCCCACCACCTCT 32033 CA TTGCA  
AGAGGTGG GG GAGG  
||||| || |||||  
TCTCCACC CC CTCC  
CA CC\_\_\_\_

GAM1334 CACNA2D2 3' ACCTCCACTCCCACCTC 20076 C GTTGCA  
GAGGTGG AG GAGGT  
||||| || |||||

CTCCACC TC CTCCA  
 C AC\_\_\_\_  
 GAM1334 CAMLG 5' CCGCCACTGCCACCCCT 8235 A GTT AGA  
 AG GGTGGCAG GC GG  
 || ||||| || ||  
 TC CCACCGTC CG CC  
 C AC\_ \_\_\_\_  
 GAM1334 CD81 3' CCTCTGCAGTGCCCCCT 15135 T GG  
 AGG GGCA TTGCAGAGG  
 ||| ||| |||||  
 TCC CCGT GACGTCTCC  
 C \_\_\_\_  
 GAM1334 CISH 3' CCTACTGGCAGCCAGCCTCT 25277 GGCA \_ \_  
 AGAGGT GGTTGC AG AGG  
 ||||| ||||| || |||  
 TCTCCG CCGACG TC TCC  
 A\_\_\_\_ G A  
 GAM1334 CISH 3' CCTACTGGCAGCCAGCCTCT 59014 GGCA \_ \_  
 AGAGGT GGTTGC AG AGG  
 ||||| ||||| || |||  
 TCTCCG CCGACG TC TCC  
 A\_\_\_\_ G A  
 GAM1334 CSK 5' ACCTCTTTGTACCGCACC 15217 G A TGC\_  
 GGTG C GGT AGAGGT  
 |||| | ||| |||||  
 CCAC G CCA TCTCCA  
 \_\_\_\_ TGTT  
 GAM1334 CSNK2A2 5' CTGCAACCTCCACCTC 8562 C  
 GAGGTGG AGGTTGCAG  
 ||||| |||||  
 CTCCACC TCCAACGTC  
 \_\_\_\_  
 GAM1334 DRPLA 3' ACCCCTGTGGCCGCCGCCCT 8666 A A TG A  
 AG GGTGGC GGT CAG GGT  
 || ||||| ||| ||| |||  
 TC CCGCCG CCG GTC CCA  
 C \_ GT C  
 GAM1334 DSCR3 3' CTGCAACCTCCACCTC 20179 C  
 GAGGTGG AGGTTGCAG  
 ||||| |||||  
 CTCCACC TCCAACGTC  
 \_\_\_\_  
 GAM1334 DUOX2 3' ACCCCTGGGCAGGCCCTCT 26019 T AG G A  
 AGAGG GGC GTT CAG GGT  
 ||||| ||| ||| ||| |||  
 TCTCC CCG CGG GTC CCA  
 \_ GA \_ C  
 GAM1334 DUSP2 3' ACCTCCGGCAGGGCTGCTACCT 15345 G \_ A\_  
 C GAGGTGGCAG T TGC GAGGT  
 ||||| ||| ||| |||

			CTCCATCGTC G ACG CTCCA		
			G G GC		
GAM1334	EGFL5	5'	ACCCCTACAACCCTGCAGACT 86609	G_ _ C A	
			GGT GCAGG TTG AG GGT		
			TCA CGTCC AAC TC CCA		
			GA C A C		
GAM1334	EGLN2	5'	ACCCCCAGAGCCACAGCCACCT 54924	A_ GCAGA	
	CT		AGAGGTGGC GGTT GGT		
			TCTCCACCG CCGA CCA		
			ACA GACCC		
GAM1334	EGLN2	5'	ACCCCTTCCCTGCCACC 34093	TTGC A	
			GGTGGCAGG AG GGT		
			CCACCGTCC TC CCA		
			CT_ C		
GAM1334	EHD2	3'	CTGCAACCTCCACCTC 27492	C	
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			—		
GAM1334	ELK1	5'	CCGCCACCACCACCTC 17838	CA T AGA	
			GAGGTGG GGT GC GG		
			CTCCACC CCA CG CC		
			A_ C _		
GAM1334	ERBB3	5'	CCTCCCCTGCCATCCCT 8797	A TTGCA	
			AG GGTGGCAGG GAGG		
			TC CTACCGTCC CTCC		
			C C_		
GAM1334	FBLN5	3'	ACCCTGCAGGACTTGCCACC 20913	_ A	
			GGTGGCAGGT TGCAG GGT		
			CCACCGTTCA ACGTC CCA		
			GG _		
GAM1334	FEZ1	3'	CTGCAACCTCCACCTC 42571	C	
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			—		
GAM1334	FGFR1	3'	ACCTCTCCCTCCACCTC 43624	C TTGC	
			GAGGTGG AGG AGAGGT		
			CTCCACC TCC TCTCCA		
			_ C_		
GAM1334	FGFR1	3'	ACCTCTCCCTCCACCTC 31792	C TTGC	
			GAGGTGG AGG AGAGGT		



			CTCCACC TCC TCTCCA		
			— C—		
GAM1334	FGFR1	3'	ACCTCTCCCTCCACCTC 5199	C	TTGC
			GAGGTGG AGG AGAGGT		
			CTCCACC TCC TCTCCA		
			— C—		
GAM1334	FRAP1	3'	ACCTCACCCCTGCCACCT 17095		TTGCA
			AGGTGGCAGG GAGGT		
			TCCACCGTCC CTCCA		
			CCA—		
GAM1334	HMGA2	5'	CCTCCACCGCCACCTC 12996	A	TGCA
			GAGGTGGC GGT GAGG		
			CTCCACCG CCA CTCC		
			— C—		
GAM1334	HTR6	3'	CCCCTGCTGCCATCTC 6033	GGTT	A
			GAGGTGGCA GCAG GG		
			CTCTACCGT CGTC CC		
			— C		
GAM1334	HYOU1	3'	CCTTCCCCCACCATTCT 59651	CA	TTGCA
			AGAGGTGG GG GAGG		
			TCTTCACC CC TTCC		
			AC CC—		
GAM1334	ICMT	3'	GCACCTGCCACCCCT 24814	A	T
			AG GGTGGCAGGT GC		
			TC CCACCGTCCA CG		
			C —		
GAM1334	IGFBP5	5'	ACCCCAGCCCTCCACCTCT 5188	CA	CAGA
			AGAGGTGG GGTG GGT		
			TCTCCACC CCGAC CCA		
			TC C—		
GAM1334	IGFBP5	5'	CCCCCAACGCCATCTC 5190	AG	CAGA
			GAGGTGGC GTTG GG		
			CTCTACCG CAAC CC		
			— CC—		
GAM1334	IHPK3	5'	ACCCCCCACCACCACCATCT 54022	—	CA TGCAGA
			AGA GGTGG GGT GGT		
			TCTCCACC CCA CCA		
			A A_ CCCC—		
GAM1334	ITGBL1	5'	ACCTCTCCCTCCTGCCGCCTC 16572		TTGC
			GAGGTGGCAGG AGAGGT		

			CTCCGCCGTCC	TCTCCA		
			TCCC			
GAM1334	KCNAB2	3'	ACCCAAGCCTGTACCTCT	13300		GCAGA
			AGAGGTGGCAGGTT	GGT		
			TCTCCACTGTCCGA	CCA		
			AC__			
GAM1334	KCNK2	3'	CCCCTAGGCTCACCTCT	26421	GCA	GC A
			AGAGGTG	GGTT AG GG		
			TCTCCAC	TCGG TC CC		
			__ A_ C			
GAM1334	KLK10	5'	GCATCCTGCCACCCCT	10924	A	T
			AG GGTGGCAGG	TGC		
			TC CCACCGTCC	ACG		
			C	T		
GAM1334	KRT15	5'	ACCTCCTGCCAGCACCTCT	9641	G A	TGCA
			AGAGGTG C GGT	GAGGT		
			TCTCCAC G CCG	CTCCA		
			_ A TC_			
GAM1334	LYZ	3'	CTGCAACCTCCACCTC	4100	C	
			GAGGTGG AGGTTGCAG			
			CTCCACC TCCAACGTC			
			-			
GAM1334	MAK	3'	CTGCAACCTCCACCTC	19758	C	
			GAGGTGG AGGTTGCAG			
			CTCCACC TCCAACGTC			
			-			
GAM1334	MEFV	3'	CTGCAACCTCCACCTC	4136	C	
			GAGGTGG AGGTTGCAG			
			CTCCACC TCCAACGTC			
			-			
GAM1334	MLLT2	3'	ACCCCCGCTCCTGCCGCC	19841	TT	AGA
			GGTGGCAGG GC	GGT		
			CCGCCGTCC CG	CCA		
			T_ CCC			
GAM1334	MPL	3'	CTGCAACCTCCACCTC	18140	C	
			GAGGTGG AGGTTGCAG			
			CTCCACC TCCAACGTC			
			-			
GAM1334	MTMR2	5'	ACCCTGGGAGCCGCCACCTC	32380	A _	G A
			GAGGTGGC GG TT	CAG GGT		

		CTCCACCG CC AG GTC CCA	
		_ G G _	
GAM1334 MYLK2	3'	ACCTCCATGCCCCGCCACCTC 52415	A TT _
		GAGGTGGC GG GCA GAGGT	
		CTCCACCG CC CGT CTCCA	
		C C_ AC	
GAM1334 NF2	3'	ACCCCAGGACCTGCCACTTCT 4248	GCAGA
		AGAGGTGGCAGGTT GGT	
		TCTTCACCGTCCAG CCA	
		GACC_	
GAM1334 OAS3	3'	CCCCAAACTCCACCTCT 20539	C G CAGA
		AGAGGTGG AG TTG GG	
		TCTCCACC TC AAC CC	
		_ A C_	
GAM1334 ORC2L	3'	CCCCAGCTGCCACTCCT 20548	AG G CAGA
		AG GTGGCAG TTG GG	
		TC CACCGTC GAC CC	
		CT _ C_	
GAM1334 OTP	3'	CCTCGCCCGCCGCCTC 49496	A TGCA
		GAGGTGGC GGT GAGG	
		CTCCGCCG CCG CTCC	
		C _	
GAM1334 PDCL	3'	CTGCAACCTCCACCTC 18213	C
		GAGGTGG AGGTTGCAG	
		CTCCACC TCCAACGTC	
		-	
GAM1334 PDE6B	3'	CTGCAACCTCCACCTC 4279	C
		GAGGTGG AGGTTGCAG	
		CTCCACC TCCAACGTC	
		-	
GAM1334 PDGFRB	3'	ACCTCCTGCAGCCCACCACT 65966	CA _
		GGTGG GGTTGCAG AGGT	
		TCACC CCGACGTC TCCA	
		AC C	
GAM1334 PDYN	5'	ACCAGCCACTGCCACCTC 44320	GTT AGA
		GAGGTGGCAG GC GGT	
		CTCCACCGTC CG CCA	
		AC_ A_	
GAM1334 PSD	5'	ACCTCTGCGTGGGCCCCCCT 10925	A T AGGT
		AG GG GGC TGCAGAGGT	

			TC CC CCG GCGTCTCCA		
			C _ GGT_		
GAM1334	RBBP9	3'	CTCTAACCTGCACCTC 70132	G	GC
			GAGGTG CAGGTT AGAG		
			CTCCAC GTCCAA TCTC		
			— —		
GAM1334	RCN1	3'	ACCCGCAGACCTGCCCC 11268	T	_ AGA
			GG GGCAGGT TGC GGT		
			CC CCGTCCA ACG CCA		
			— G C_		
GAM1334	RGS14	3'	ACCCACAGCTGCCACC 21367	G	CAGA
			GGTGGCAG TTG GGT		
			CCACCGTC GAC CCA		
			— ACC_		
GAM1334	RNH	3'	ACCCTGGGGCCCACCAGCCCCT 59614	A	_ CA G A
			AG GG TGG GGTT CAG GGT		
			TC CC ACC CCGG GTC CCA		
			C G AC G _		
GAM1334	RNH	3'	ACCCTGGGGCCCACCAGCCCCT 11359	A	_ CA G A
			AG GG TGG GGTT CAG GGT		
			TC CC ACC CCGG GTC CCA		
			C G AC G _		
GAM1334	RPH3AL	3'	CTGCAACCTCCACCTC 22746	C	
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			—		
GAM1334	SEDL	3'	CTGCAACCTCCACCTC 27333	C	
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			—		
GAM1334	SEDL	3'	CTGCAACCTCCACCTC 27334	C	
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			—		
GAM1334	SELP	3'	ACCCCTTCCTGTCCCACCTCT 11533	_	TTGC A
			AGAGGTGG CAGG AG GGT		
			TCTCCACC GTCC TC CCA		
			CT T_ C		
GAM1334	SELP	3'	TTCTCAACCTACCACCCCT 11538	A	C C
			AG GGTGG AGGTTG AGAG		

			TC CCACC TCCAAC TCTT		
			C A _		
GAM1334	SEPN1	3'	CTGCAACCTCCACCTC	66368	C
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			-		
GAM1334	SLC14A2	5'	CTGCAACCTCCACCTC	23131	C
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			-		
GAM1334	SLC22A1LS	5'	ACCCCCACCCCACTCTCT	23025	_ CA TGCAGA
			AGAG GTGG GGT GGT		
			TCTC CACC CCA CCA		
			T C_ CCC_		
GAM1334	SLC39A4	5'	CCTCTGCGTGACCCCT	34951	A G GGT
			AG GGTG CA TGCAGAGG		
			TC CCAC GT GCGTCTCC		
			C _ _		
GAM1334	SNX15	3'	CTGCAACCTCCACCTC	73741	C
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			-		
GAM1334	SOX12	3'	ACCCACGCGCACCACTCT	22693	CAG T AGA
			AGAGGTGG GT GC GGT		
			TCTCCACC CG CG CCA		
			A_ _ CAC		
GAM1334	STAT3	3'	CTGCATTCTGCCACCCCT	57712	A GT
			AG GGTGGCAG TGCAG		
			TC CCACCGTC ACGTC		
			C TT		
GAM1334	STAT3	3'	CTGCATTCTGCCACCCCT	11997	A GT
			AG GGTGGCAG TGCAG		
			TC CCACCGTC ACGTC		
			C TT		
GAM1334	STAU	5'	CTGCAACCTCCACCTC	16002	C
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			-		
GAM1334	TAT	3'	CTGCAACCTCCACCTC	4468	C
			GAGGTGG AGGTTGCAG		

CTCCACC TCCAACGTC

GAM1334 TBXA2R 3' CTGCAACCTCCACCTC 6488 C  
GAGGTGG AGGTTGCAG  
||||| |||||  
CTCCACC TCCAACGTC

GAM1334 TFAP4 3' ACCCCCCAGCCCCACCTCT 12234 CA CAGA  
AGAGGTGG GGTG GGT  
||||| ||| ||  
TCTCCACC CCGAC CCA  
C\_ CCC\_

GAM1334 TIMM23 3' ACCTCTGACATTTTAACCACCT 60138 CAGGT\_ \_  
CT AGAGGTGG TG CAGAGGT  
||||| || |||||  
TCTCCACC AC GTCTCCA  
AATTTT A

GAM1334 TLR9 3' ACCTCCACACTCACCTCACCTC 33847 GC \_ CA  
T AGAGGTG AGGT TG GAGGT  
||||| ||| || |||||  
TCTCCAC TCCA AC CTCCA  
\_ CTC AC

GAM1334 TNFAIP2 3' ACCTCTGTCCAGAGCCCCTC 20828 T A\_ TT  
GAGG GGC GG GCAGAGGT  
||| ||| || |||||  
CTCC CCG CC TGTCTCCA  
\_ AGA \_

GAM1334 TXNRD2 3' ACCTCACCCCTGCACCTCT 21234 G TTGCA  
AGAGGTG CAGG GAGGT  
||||| ||| |||||  
TCTCCAC GTCC CTCCA  
\_ CCA\_

GAM1334 ZFP36 3' CCTCTCCCCACCTCT 12712 CA TTGC  
AGAGGTGG GG AGAGG  
||||| || |||||  
TCTCCACC CC TCTCC  
C\_ \_

GAM1334 ZNF42 5' ACCCCTGCATTTGTGCGCTC 12782 T A  
GAGGTGGCAGGT GCAG GGT  
||||||| ||| |||  
CTCCGCTGTTTA CGTC CCA  
\_ C

GAM1334 A2BP1 5' CCTTCCGCCGCCTC 38060 A TTGCA  
GAGGTGGC GG GAGG  
||||| || |||||  
CTCCGCCG CC TTCC

GAM1334 ASB16 3' ACCTCCCTCTCCTGCCACCCT 55103 A TTGCA  
AG GGTGGCAGG GAGGT  
|| ||||| |||||

			TC CCACCGTCC	CTCCA		
			— TCTCC			
GAM1334	ATP1B4	3'	CTGCAACCTCCACCTC	23819	C	
			GAGGTGG AGGTTGCAG			
			CTCCACC TCCAACGTC			
			—			
GAM1334	B3GAT3	3'	CCCCAACTACCACCTCT	24188	CA	CAGA
			AGAGGTGG GGTG GG			
			TCTCCACC TCAAC CC			
			A_ C__			
GAM1334	BAG5	3'	CTGCAACCTCCACCTC	16843	C	
			GAGGTGG AGGTTGCAG			
			CTCCACC TCCAACGTC			
			—			
GAM1334	BTN3A1	3'	TGCAACCTCCACCTC	22928	C	
			GAGGTGG AGGTTGCA			
			CTCCACC TCCAACGT			
			—			
GAM1334	C21orf25	3'	CTGCAACCTCCACCTC	63546	C	
			GAGGTGG AGGTTGCAG			
			CTCCACC TCCAACGTC			
			—			
GAM1334	C9orf9	3'	CTGCAACCTCCACCTC	38512	C	
			GAGGTGG AGGTTGCAG			
			CTCCACC TCCAACGTC			
			—			
GAM1334	CENTA1	3'	ACCCAGCCAACCTGCCCTC	22492	T	CAGA
			GAGG GGCAGGTTG GGT			
			CTCC CCGTCCAAC CCA			
			CGAC			
			—			
GAM1334	CLDN1	5'	TGCACCTGCCACCCCT	40852	A	T
			AG GGTGGCAGGT GCA			
			TC CCACCGTCCA CGT			
			C			
			—			
GAM1334	CNOT3	5'	ACCTCTCCTAGCCACCTCT	27213	—	TTGC
			AGAGGTGGC AGG AGAGGT			
			TCTCCACCG TCC TCTCCA			
			A			
			—			
GAM1334	CNOT3	5'	ACCTCTGCCCAGCCCCTCT	27214	T	A TT
			AGAGG GGC GG GCAGAGGT			

TCTCC CCG CC CGTCTCCA  
 \_ A \_  
 GAM1334 CYP2S1 3' ACCTCTGCAACTGCAGCCCTC 47612 TG\_ G  
 GAGG GCAG TTGCAGAGGT  
 |||| ||| |||||  
 CTCC CGTC AACGTCTCCA  
 CGA \_  
 GAM1334 DDR1 3' ACCTCTGCCCTTCCCCTC 25693 T C TT  
 GAGG GG AGG GCAGAGGT  
 |||| || ||| |||||  
 CTCC CC TCC CGTCTCCA  
 \_ T \_  
 GAM1334 DDR1 3' ACCTCTGCCCTTCCCCTC 25702 T C TT  
 GAGG GG AGG GCAGAGGT  
 |||| || ||| |||||  
 CTCC CC TCC CGTCTCCA  
 \_ T \_  
 GAM1334 DDR1 3' ACCTCTGCCCTTCCCCTC 8720 T C TT  
 GAGG GG AGG GCAGAGGT  
 |||| || ||| |||||  
 CTCC CC TCC CGTCTCCA  
 \_ T \_  
 GAM1334 DKFZP434C212 3' CTGCAACCTCCACCTC 68910 C  
 GAGGTGG AGGTTGCAG  
 ||||| |||||  
 CTCCACC TCCAACGTC  
 \_  
 GAM1334 DKFZp434J0226 3' ACCAAGTCACCGGCCACCTC 72328 A T AGA  
 GAGGTGGC GGT GC GGT  
 ||||| ||| || |||  
 CTCCACCG CCA TG CCA  
 G C AA\_  
 GAM1334 DKFZp547H025 3' CTGCAACCTCCACCTC 39356 C  
 GAGGTGG AGGTTGCAG  
 ||||| |||||  
 CTCCACC TCCAACGTC  
 \_  
 GAM1334 DKFZP564O0523 3' CTGCAACCTCCACCTC 49515 C  
 GAGGTGG AGGTTGCAG  
 ||||| |||||  
 CTCCACC TCCAACGTC  
 \_  
 GAM1334 DKFZP566C243 3' CCTCCCCACCTACCCCT 31168 T C T CA  
 AGG GG AGGT G GAGG  
 ||| || ||| | |||  
 TCC CC TCCA C CTCC  
 \_ A \_CC  
 GAM1334 DKFZp586I021 3' ACCTCCGCCAGCCGCCTC 50086 A TGCA  
 GAGGTGGC GGT GAGGT  
 ||||| ||| ||||



		CTCCGCCG CCG	CTCCA		
		A C__			
GAM1334	DKFZp761B1514	3'	ACCCGCCACCTGCCACCTCT	50146	T AGA
			AGAGGTGGCAGGT GC GGT		
			TCTCCACCGTCCA CG CCA		
			C C__		
GAM1334	FER1L4	3'	CTGCAACCTCCACCTC	47345	C
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			—		
GAM1334	FER1L4	3'	CTGCAACCTCCACCTC	47346	C
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			—		
GAM1334	FLJ00060	5'	CCTCCACCTCACCTCT	61094	GC TGCA
			AGAGGTG AGGT GAGG		
			TCTCCAC TCCA CTCC		
			— C__		
GAM1334	FLJ10307	3'	ACCTCCCTCCCTGGCCACCTCT	36003	_ TTGCA
			AGAGGTGGC AGG GAGGT		
			TCTCCACCG TCC CTCCA		
			G CTCC_		
GAM1334	FLJ10700	3'	ACCTCTACCTGTTGCT	36424	TG TGC
			GG GCAGGT AGAGGT		
			TC TGTCCA TCTCCA		
			GT _		
GAM1334	FLJ11078	3'	CCTCCGCGCCCTGCCACT	37030	T A
			GGTGGCAGG TGC GAGG		
			TCACCGTCC GCG CTCC		
			C C		
GAM1334	FLJ11618	3'	CCTCACCAGCCACCTCT	42392	A TGCA
			AGAGGTGGC GGT GAGG		
			TCTCCACCG CCA CTCC		
			A _		
GAM1334	FLJ12363	3'	CTGCAACCTCCACCTC	49678	C
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			—		
GAM1334	FLJ12747	3'	CCTCACTGCAACCTCT	49714	G GTTGCA
			AGAGGT GCAG GAGG		

TCTCCA CGTC CTCC  
 A A\_\_\_\_  
 GAM1334 FLJ12750 3' ACCTTCTGGCCCGCCCCTC 45119 T A TG \_  
 GAGG GGC GGT CAGA GGT  
 |||| ||| ||| |||| |||  
 CTCC CCG CCG GTCT CCA  
 \_ C \_ T  
 GAM1334 FLJ12960 3' TGCAACCTCCACCTC 44954 C  
 GAGGTGG AGGTTGCA  
 ||||| |||||  
 CTCCACC TCCAACGT  
 \_  
 GAM1334 FLJ13840 5' ACCCGCTTCTGCCACCTC 45364 TT AGA  
 GAGGTGGCAGG GC GGT  
 ||||| || |||  
 CTCCACCGTCT CG CCA  
 T\_ C\_  
 GAM1334 FLJ14950 3' CTGCAACCTCCACCTC 51719 C  
 GAGGTGG AGGTTGCAG  
 ||||| |||||  
 CTCCACC TCCAACGTC  
 \_  
 GAM1334 FLJ20174 3' CCTCTGCAACACCTGCT 34687 \_  
 GGCAGGT TGCAGAGG  
 ||||| |||||  
 TCGTCCA ACGTCTCC  
 CA  
 GAM1334 FLJ20255 5' CCTCTGCTGCCAGCCCT 34797 T A T  
 GG GGC GGT GCAGAGG  
 || ||| ||| |||||  
 TC CCG CCG CGTCTCC  
 \_ A T  
 GAM1334 FLJ20294 3' ACCCCAGCCCTCCACCTCT 34869 CA CAGA  
 AGAGGTGG GGTTG GGT  
 ||||| |||| |||  
 TCTCCACC CCGAC CCA  
 TC C\_  
 GAM1334 FLJ20359 3' CCTGTGGGACCCCCACCCCT 35040 A CA G G  
 AG GGTGG GGTT CA AGG  
 || |||| |||| || |||  
 TC CCACC CCAG GT TCC  
 C C\_ G G  
 GAM1334 FLJ22169 3' ACCCCTGCAACCTTCCCT 43996 T C A  
 AGG GG AGGTTGCAG GGT  
 ||| || ||||| |||  
 TCC CT TCCAACGTC CCA  
 \_ \_ C  
 GAM1334 FLJ22246 3' ACCCCTGCAACCTCCCT 47447 TG CA A  
 AGG G GGTTGCAG GGT  
 ||| | ||||| |||

TCC C CCAACGTC CCA  
 CT \_ C  
 GAM1334 FLJ22393 3' ACCCCAGCACCTGCCACC 47057 T AGA  
 GGTGGCAGGT GC GGT  
 ||||| || |||  
 CCACCGTCCA CG CCA  
 \_ ACC  
 GAM1334 FLJ22531 5' CTGCAACCTCCACCTC 45030 C  
 GAGGTGG AGGTTGCAG  
 ||||| |||||  
 CTCCACC TCCAACGTC  
 -  
 GAM1334 FLJ23519 3' ACCCTGGGGCCCACCAGCCCCT 69197 A \_ CA G A  
 AG GG TGG GGTT CAG GGT  
 || || || || || || ||  
 TC CC ACC CCGG GTC CCA  
 C G AC G \_  
 GAM1334 FUK 3' ACCTCCTACTCCCCACCCACCT 58969 CA\_\_ TTGCA  
 CT AGAGGTGG GG GAGGT  
 ||||| || |||||  
 TCTCCACC CC CTCCA  
 CACC TCATC  
 GAM1334 GABBR1 3' CCCCTGCAGCTCCTCT 7606 TGGCA A  
 AGAGG GGTTGCAG GG  
 |||| ||||| ||  
 TCTCC TCGACGTC CC  
 \_ C  
 GAM1334 GABBR1 3' CCCCTGCAGCTCCTCT 41571 TGGCA A  
 AGAGG GGTTGCAG GG  
 |||| ||||| ||  
 TCTCC TCGACGTC CC  
 \_ C  
 GAM1334 GGA2 3' ACCTCTCTCAAGCTGCCACCTC 30456 G C\_  
 GAGGTGGCAG TTG AGAGGT  
 ||||| || |||||  
 CTCCACCGTC AAC TCTCCA  
 G TC  
 GAM1334 GGA2 3' ACCTCTCTCAAGCTGCCACCTC 56869 G C\_  
 GAGGTGGCAG TTG AGAGGT  
 ||||| || |||||  
 CTCCACCGTC AAC TCTCCA  
 G TC  
 GAM1334 GMPPB 5' CTGCAACCTCCACCTC 95734 C  
 GAGGTGG AGGTTGCAG  
 ||||| |||||  
 CTCCACC TCCAACGTC  
 -  
 GAM1334 GNG3 3' ACCCCATTTCTACCACCTTT 24190 C TTGCAGA  
 AGAGGTGG AGG GGT  
 ||||| || |||

			TTTCCACC TCC	CCA		
			A TTTACC_			
GAM1334	GRO3	5'	CCTCCCCGCCAGCTCT	62519	G	A TTGCA
			AGAG TGGC GG	GAGG		
			TCTC ACCG CC	CTCC		
			G C _____			
GAM1334	GTPBG3	3'	CTGCAACCTCCACCTC	50898	C	
			GAGGTGG AGGTTGCAG			
			CTCCACC TCCAACGTC			
			_____			
GAM1334	H-plk	5'	CTGCAACCTCCACCTC	31808	C	
			GAGGTGG AGGTTGCAG			
			CTCCACC TCCAACGTC			
			_____			
GAM1334	HSPC065	3'	CTGCAACCTCCACCTCT	26297	C	
			AGAGGTGG AGGTTGCAG			
			TCTCCACC TCCAACGTC			
			_____			
GAM1334	IL1RAPL1	3'	CCTCATTCCCCACCTCT	26545	CA	TTGCA
			AGAGGTGG GG	GAGG		
			TCTCCACC CC	CTCC		
			___ TTA___			
GAM1334	KIAA0057	3'	CCTCCCCCTGCCACCCT	24420	A	TTGCA
			AG GGTGGCAGG	GAGG		
			TC CCACCGTCC	CTCC		
			___ CC___			
GAM1334	KIAA0063	3'	CTGCAACCTCCACCTC	29625	C	
			GAGGTGG AGGTTGCAG			
			CTCCACC TCCAACGTC			
			_____			
GAM1334	KIAA0161	3'	ACCAACATCTGCCACCTCT	28495		TGCAGA
			AGAGGTGGCAGGT	GGT		
			TCTCCACCGTCTA	CCA		
			CAA___			
GAM1334	KIAA0339	3'	ACCCCTGCCCACCACC	71472	CA TT	A
			GGTGG GG GCAG GGT			
			CCACC CC CGTC CCA			
			A_ __ C			
GAM1334	KIAA0406	3'	ACCCCTTAGCCTACCATCTCT	61328	C	C A
			AGAGGTGG AGGTTG AG GGT			

			TCTCTACC TCCGAT TC CCA		
			A _ C		
GAM1334	KIAA0459	3'	CTGCAACCTCCACCTC 60991	C	
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			—		
GAM1334	KIAA0513	3'	CTGCAACCTCCACCTC 28355	C	
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			—		
GAM1334	KIAA0748	3'	ACCTTGTGACCCCCACCCCT 28932	A CA TG G	
			AG GGTGG GGT CA AGGT		
			TC CCACC CCA GT TCCA		
			C C_ GT _		
GAM1334	KIAA0757	3'	CCTGGCTTCCCCACCTCT 20129	CA TT AG	
			AGAGGTGG GG GC AGG		
			TCTCCACC CC CG TCC		
			_ TT G_		
GAM1334	KIAA0876	3'	ACCCCCGAGAGGCCACCTC 64674	AGG CAGA	
			GAGGTGGC TTG GGT		
			CTCCACCG AGC CCA		
			GAG CC_		
GAM1334	KIAA0953	3'	CCCCTGTGCTCCACCTCT 66782	C GTT A	
			AGAGGTGG AG GCAG GG		
			TCTCCACC TC TGTC CC		
			_ G_ C		
GAM1334	KIAA1030	3'	ACCTCTGCTTCCACTCCCT 93329	TG CA TT	
			AGG G GG GCAGAGGT		
			TCC C CC CGTCTCCA		
			CT A_ TT		
GAM1334	KIAA1274	5'	ACCTCCGGAGCCACCTCT 91363	AGG CA	
			AGAGGTGGC TTG GAGGT		
			TCTCCACCG GGC CTCCA		
			A_ _		
GAM1334	KIAA1297	3'	ACCTCACTGGCCCCACCCCT 72164	A CA CA	
			AG GGTGG GGTTG GAGGT		
			TC CCACC CCGGT CTCCA		
			C _ CA		
GAM1334	KIAA1373	3'	CTGCAACCTCCACCTC 70935	C	
			GAGGTGG AGGTTGCAG		

CTCCACC TCCAACGTC

GAM1334 KIAA1423 3' ACCTCTACAGTCACACTTCT 61720 GCA GT C  
AGAGGTG G TG AGAGGT  
||||| | |||||  
TCTTCAC C AC TCTCCA  
A\_\_TG A

GAM1334 KIAA1530 3' CTGCAACTACCACCTC 67951 CA  
GAGGTGG GGTTCAG  
||||| |||||  
CTCCACC TCAACGTC

GAM1334 KIAA1538 5' ACCCAACCCTGCCACC 71526 \_ CAGA  
GGTGGCAGG TTG GGT  
||||||| ||| |||  
CCACCGTCC AAC CCA  
C \_\_\_\_

GAM1334 KIAA1615 3' CTGCAACCTCCACCTC 68708 C  
GAGGTGG AGGTTGCAG  
||||| |||||  
CTCCACC TCCAACGTC

GAM1334 KIAA1655 3' CTGTAACCTCCACCTC 66607 C  
GAGGTGG AGGTTGCAG  
||||| |||||  
CTCCACC TCCAATGTC

GAM1334 KIAA1656 3' ACCCCTCGGCTGCTACC 65779 G C A  
GGTGGCAG TTG AG GGT  
||||||| ||| |||  
CCATCGTC GGC TC CCA

GAM1334 KIAA1870 3' CCTCCCCTGCCACACTC 51828 \_ TTGCA  
GAG GTGGCAGG GAGG  
||| ||||| |||  
CTC CACCGTCC CTCC  
A C\_\_\_\_

GAM1334 KIAA1884 3' ACCCCTGGCCACACCACCTCT 73334 CA\_ TG A  
AGAGGTGG GGT CAG GGT  
||||||| ||| ||| |||  
TCTCCACC CCG GTC CCA  
ACA \_ C

GAM1334 KIAA1971 3' CTGCAACCTCCACCTC 74216 C  
GAGGTGG AGGTTGCAG  
||||| |||||  
CTCCACC TCCAACGTC

GAM1334 LHPP 3' ACCCCTGCCTCCCCTCCACCCC 42099 A C TT\_\_ A  
T AG GGTGG AGG GCAG GGT  
|| ||||| ||| ||||| |||

			TC CCACC TCC CGTC CCA		
			C _ CCTC C		
GAM1334	LIPG	3'	CCTCTGTCCACACCTC 20096	GCA TT	
			GAGGTG GG GCAGAGG		
			CTCCAC CC TGTCTCC		
			A_ _		
GAM1334	MCLC	3'	CTGCAACCTCCACCTC 30684	C	
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			-		
GAM1334	MGC15854	5'	ACCCTTCCCCTGCCACC 58845	TTGC A	
			GGTGGCAGG AG GGT		
			CCACCGTCC TC CCA		
			CCT_ _		
GAM1334	MGC9912	3'	CTGCAACCTCCACCTC 54717	C	
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			-		
GAM1334	MR	3'	ACCTCTGTTGCCACCACCTTT 48318	CA T	
			AGAGGTGG GGT GCAGAGGT		
			TTTCCACC CCG TGTCTCCA		
			A_ T		
GAM1334	MSE55	3'	ACCTCCCCCGACTGCCACTCT 22939	G G CA_	
			AGAG TGGCAG TTG GAGGT		
			TCTC ACCGTC AGC CTCCA		
			- _ CCC		
GAM1334	NDUFC2	3'	CTGCAACCTCCACCTC 15831	C	
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			-		
GAM1334	NET-5	3'	ACCCCTGCACCCACCCC 21921	T CA T A	
			GG GG GGT GCAG GGT		
			CC CC CCA CGTC CCA		
			_ AC _ C		
GAM1334	NMT1	3'	CTTCAGCCACCAGCCCCT 40782	T A T A	
			AGG GGC GGT GC GAGG		
			TCC CCG CCA CG CTTC		
			_ A C A		
GAM1334	Nup43	3'	CTGCAACCTCCACCTC 45000	C	
			GAGGTGG AGGTTGCAG		

CTCCACC TCCAACGTC

GAM1334 OAZ3 5' ACCTCTGCCACCCACCT 32449 CAG T  
AGGTGG GT GCAGAGGT  
||||| || |||||  
TCCACC CA CGTCTCCA

\_\_\_ C  
GAM1334 phospho1 5' ACCTCTGCTGCCGCCGCC 82366 A T  
GGTGGC GGT GCAGAGGT  
||||| ||| |||||  
CCGCCG CCG CGTCTCCA

\_ T  
GAM1334 PRKRI 5' ACCAGGCAACCTGCCAGCC 20753 \_ AGA  
GG TGGCAGGTTGC GGT  
|| ||||| |||  
CC ACCGTCCAACG CCA  
G GA\_

GAM1334 PRO0365 5' CTGCAACCTCCACCTC 26157 C  
GAGGTGG AGGTTGCAG  
||||| |||||  
CTCCACC TCCAACGTC

\_\_\_  
GAM1334 PTPNS1 3' CCTCCCCACCACTCT 54996 CA TTGCA  
AGAGGTGG GG GAGG  
||||| || |||  
TCTCCACC CC CTCC  
AC \_\_\_\_\_

GAM1334 QKI 3' ACCTCTGCCTCCCCACCCCT 65436 A CA TT  
AG GGTGG GG GCAGAGGT  
|| ||| || |||||  
TC CCACC CC CGTCTCCA  
C C\_ TC

GAM1334 RAGB 5' CCCCTAACCCACCTCT 33605 CAG GC A  
AGAGGTGG GTT AG GG  
||||| ||| |||  
TCTCCACC CAA TC CC

\_\_\_ \_ C  
GAM1334 RNF8 3' CTGCAACCTCCACCTC 14224 C  
GAGGTGG AGGTTGCAG  
||||| |||||  
CTCCACC TCCAACGTC

\_\_\_  
GAM1334 SC65 3' CCCATCCTGCCACTTCT 21287 T CAGA  
AGAGGTGGCAGG TG GG  
||||||| || ||  
TCTTCACCGTCC AC CC

T \_\_\_\_\_  
GAM1334 SCAMP-4 3' ACCCCAGGCTGCCACCCCT 54384 A G CAGA  
AG GGTGGCAG TTG GGT  
|| ||||| ||| |||



			TC CCACCGTC GAC CCA		
			C G C__		
GAM1334	SCAMP5	3'	CCTCCACCTGCCCTCT 57257	T	TGCA
			AGAGG GGCAGGT GAGG		
			TCTCC CCGTCCA CTCC		
			_ C__		
GAM1334	SCYA11	5'	ACCCAGAAACCACCACCTCT 11454	CA	GCAGA
			AGAGGTGG GGTT GGT		
			TCTCCACC CCAA CCA		
			A_ AGAC_		
GAM1334	SCYA16	3'	CTGTAACCTCCACCTC 15958	C	
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAATGTC		
			-		
GAM1334	SCYA3	3'	CCTCCACAGCTACCTCT 59845	AGGT	CA
			AGAGGTGGC TG GAGG		
			TCTCCATCG AC CTCC		
			___ AC		
GAM1334	SH3BGRL2	3'	ACCCCTGTGTGCCTACCACC 48881	C _	A
			GGTGG AGGT TGCAG GGT		
			CCACC TCCG GTGTC CCA		
			A T C		
GAM1334	SIAT4A	3'	ACCTCTGCATTTCCAGCCCC 11665	T A T__	
			GG GGC GG TGCAGAGGT		
			CC CCG CC ACGTCTCCA		
			_ A TTT		
GAM1334	SMOC2	3'	CCCCTGCAGTCACTTC 72371	AGGT	A
			GAGGTGGC TGCAG GG		
			CTTCACTG ACGTC CC		
			___ C		
GAM1334	STK29	3'	ACCTCCACGAGGCCATCCTCT 87573	_	AGG CA
			AGAGG TGGC TTG GAGGT		
			TCTCC ACCG AGC CTCCA		
			T G__ AC		
GAM1334	TNFSF13	5'	ACCCGCCCCGCCACCTC 13741	A TT	AGA
			GAGGTGGC GG GC GGT		
			CTCCACCG CC CG CCA		
			C _ C__		
GAM1334	TOMM40	3'	ACCTCCACCTCCACCTC 20368	C	TGCA
			GAGGTGG AGGT GAGGT		

			CTCCACC TCCA CTCCA		
			— C—		
GAM1334	TRIM5	3'	CTGCAACCTCCACCTCT	52298	C
			AGAGGTGG AGGTTGCAG		
			TCTCCACC TCCAACGTC		
			—		
GAM1334	ULK2	3'	ACCTCCACAACCCTATTT	28000	CA CA
			AGGTGG GGTTG GAGGT		
			TTTATC CCAAC CTCCA		
			— AC		
GAM1334	USP22	3'	CTGCAACCTCCACCTC	68011	C
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			—		
GAM1334	VEGFC	5'	ACCGCTCCCGCCGCCTC	18306	A TT AGA
			GAGGTGGC GG GC GGT		
			CTCCGCCG CC CG CCA		
			— CT C—		
GAM1334	VPS33A	3'	ACCTCACTGCAACCTCCACCTC	43329	C —
			GAGGTGG AGGTTGCA GAGGT		
			CTCCACC TCCAACGT CTCCA		
			— CA		
GAM1334	WBSCR23	3'	ACCTCCACCTCCAGCCTC	46751	— C TGCA
			GAGG TGG AGGT GAGGT		
			CTCC ACC TCCA CTCCA		
			G — C—		
GAM1334	ZNF237	3'	ACCTCTTTTGCTCTACCACCT	26471	C — TGC
			AGGTGG AG GT AGAGGT		
			TCCACC TC CG TCTCCA		
			A T TTT		
GAM1334	LOC112476	3'	ACCTCCACCCTGGCCGCCTC	59109	— T CA
			GAGGTGGC AGG TG GAGGT		
			CTCCGCCG TCC AC CTCCA		
			G C —		
GAM1334	LOC112724	5'	CTGCAACCTCCACCTC	56497	C
			GAGGTGG AGGTTGCAG		
			CTCCACC TCCAACGTC		
			—		
GAM1334	LOC118786	5'	ACCTCTTCCTTTCCTACCAACC	75498	— C TTGC—
			GGT GG AGG AGAGGT		

		CCA CC TCC	TCTCCA		
		A A	TTTCCT		
GAM1334	LOC120939 3'	CTGTAACCTCCACCTC	76253	C	
		GAGGTGG	AGGTTGCAG		
		CTCCACC	TCCAATGTC		
		—			
GAM1334	LOC123096 3'	ACCCCAGCTGCTGCCACTCCT	74197	AG	GTT AGA
		AG GTGGCAG	GC GGT		
		TC CACCGTC	CG CCA		
		CT	GT_ ACC		
GAM1334	LOC124944 3'	ACCTCTGCTGATCCTCCTCT	74372	T	CAGGTT
		AGAGG GG	GCAGAGGT		
		TCTCC CC	CGTCTCCA		
		T	TAGT_		
GAM1334	LOC130733 3'	CTGTTGCCTGCCAGCCCT	74979	A _	T
		AG GG TGGCAGGT	GCAG		
		TC CC ACCGTCCG	TGTC		
		_ G	T		
GAM1334	LOC132625 3'	CTGCAACCTCCACCTC	75905	C	
		GAGGTGG	AGGTTGCAG		
		CTCCACC	TCCAACGTC		
		—			
GAM1334	LOC143187 3'	CTGCAACCTCCACCTC	59097	C	
		GAGGTGG	AGGTTGCAG		
		CTCCACC	TCCAACGTC		
		—			
GAM1334	LOC143915 3'	ACCTCTGCCAGCCACC	82991	AGGTT	
		GGTGGC	GCAGAGGT		
		CCACCG	CGTCTCCA		
		AC_			
GAM1334	LOC144248 5'	CTGCAACCTCCACCTC	76737	C	
		GAGGTGG	AGGTTGCAG		
		CTCCACC	TCCAACGTC		
		—			
GAM1334	LOC144524 5'	CTGCAACCTCCACCTC	83127	C	
		GAGGTGG	AGGTTGCAG		
		CTCCACC	TCCAACGTC		
		—			
GAM1334	LOC144681 3'	CTGAGACCTGCCACCTC	83176	TG	
		GAGGTGGCAGGT	CAG		

		CTCCACCGTCCA GTC		
		GA		
GAM1334	LOC144682 3'	CTGAGACCTGCCACCTC	83178	TG
		GAGGTGGCAGGT CAG		
		CTCCACCGTCCA GTC		
		GA		
GAM1334	LOC145468 3'	ACCTCCACCTCCACCTC	73819	C TGCA
		GAGGTGG AGGT GAGGT		
		CTCCACC TCCA CTCCA		
		- C -		
GAM1334	LOC145813 5'	ACCCCAACAACCTGCCACCCCT	83502	A CAGA
		AG GGTGGCAGGTTG GGT		
		TC CCACCGTCCAAC CCA		
		C AACC		
GAM1334	LOC146184 5'	ACCTCATTAGGCCTGGCCACCT	83618	- GCA_
	CT	AGAGGTGGC AGGTT GAGGT		
		TCTCCACCG TCCGG CTCCA		
		G ATTA		
GAM1334	LOC146229 3'	CTGCAACCTCCACCTC	77748	C
		GAGGTGG AGGTTGCAG		
		CTCCACC TCCAACGTC		
		-		
GAM1334	LOC146229 3'	TGCAACCTCCACCTC	77782	C
		GAGGTGG AGGTTGCA		
		CTCCACC TCCAACGT		
		-		
GAM1334	LOC146784 5'	CTGCAACCTCCACCTC	78112	C
		GAGGTGG AGGTTGCAG		
		CTCCACC TCCAACGTC		
		-		
GAM1334	LOC146952 5'	CTGCAACCTCCACCTCT	83866	C
		AGAGGTGG AGGTTGCAG		
		TCTCCACC TCCAACGTC		
		-		
GAM1334	LOC147817 3'	CTGCAACCTCCACCTC	78499	C
		GAGGTGG AGGTTGCAG		
		CTCCACC TCCAACGTC		
		-		
GAM1334	LOC148189 5'	CTGCAACCTCCACCTC	78708	C
		GAGGTGG AGGTTGCAG		

CTCCACC TCCAACGTC

GAM1334 LOC148426 3' ACCCCTACAATGTCAACCTC 84147 \_ GG C A  
GAGGT GGCA TTG AG GGT  
||||| |||| ||| || |||  
CTCCA CTGT AAC TC CCA  
A \_ A C

GAM1334 LOC149711 5' ACCTCCGCAGCTGCCACCCT 84667 A G A  
AG GGTGGCAG TTGC GAGGT  
|| ||||||| |||| ||||||  
TC CCACCGTC GACG CTCCA

GAM1334 LOC150067 5' ACCCCCCCGGCTGCCATCTC 60339 G CAGA  
GAGGTGGCAG TTG GGT  
||||||||| ||| |||  
CTCTACCGTC GGC CCA  
\_ C

GAM1334 LOC150155 3' ACCTCCGCCTCCACCTC 70850 C TGCA  
GAGGTGG AGGT GAGGT  
||||||| |||| |||||  
CTCCACC TCCG CTCCA  
\_ C \_

GAM1334 LOC150290 3' CCTCTGCTTCCACCTT 79770 CAGGTT  
GAGGTGG GCAGAGG  
||||||| |||||||  
TTCCACC CGTCTCC  
TT \_

GAM1334 LOC150372 3' ACCTCACTGGGCCTGCCTCC 79784 T GCA\_  
GG GGCAGGTT GAGGT  
|| ||||||| |||||  
CC CCGTCCGG CTCCA  
T GTCA

GAM1334 LOC150519 3' ACCTCTGCAACCTGCCACCTC 79912  
GAGGTGGCAGGTTGCAGAGGT  
|||||||||||||||  
CTCCACCGTCCAACGTCTCCA

GAM1334 LOC150519 3' GCAACCAGCCACCTCT 79921 A  
AGAGGTGGC GGTTCG  
||||||||| |||||||  
TCTCCACCG CCAACG  
A

GAM1334 LOC150519 3' TGCAACCTGCCACCTC 79925  
GAGGTGGCAGGTTGCA  
|||||||||||||  
CTCCACCGTCCAACGT

GAM1334 LOC151201 3' CTGCAACCTCCACCTC 85276 C  
GAGGTGG AGGTTGCAG  
||||||| |||||||||

CTCCACC TCCAACGTC

GAM1334 LOC151361 3' ATCTCCCCACCACCACCT 85316 CA T CA  
AGGTGG GGT G GAGGT  
||||| ||| | |||||  
TCCACC CCA C CTCTA  
A \_ \_ CC

GAM1334 LOC151475 5' CTGCAACCTCCACCTC 85402 C  
GAGGTGG AGGTTGCAG  
||||| |||||  
CTCCACC TCCAACGTC

GAM1334 LOC151959 3' CCCC GCCCGCCACCTT 85522 A TT AGA  
GAGGTGGC GG GC GG  
||||| || || ||  
TTCCACCG CC CG CC  
C \_ \_ CC \_

GAM1334 LOC153454 5' ACTTCCAACACCACCTCT 80829 CA GCA  
AGAGGTGG GGTT GAGGT  
||||| ||| |||||  
TCTCCACC CCAA CTTC A  
A \_ AC \_

GAM1334 LOC153688 3' CTGCAACCTCCACCTC 86105 C  
GAGGTGG AGGTTGCAG  
||||| |||||  
CTCCACC TCCAACGTC

GAM1334 LOC154282 5' CTGCAACCTCCACCTC 86199 C  
GAGGTGG AGGTTGCAG  
||||| |||||  
CTCCACC TCCAACGTC

GAM1334 LOC155061 3' ACCAGGACAGCTGCCACCTCT 81263 G CAGA  
AGAGGTGGCAG TTG GGT  
||||||| ||| |||  
TCTCCACCGTC GAC CCA  
\_ AGGA

GAM1334 LOC157349 5' ACCCCTGCACCTGCCAC 81403 T A  
GTGGCAGGT GCAG GGT  
||||||| ||| |||  
CACCGTCCA CGTC CCA

GAM1334 LOC157349 5' ACCCCTGCACCTGCCAC 81404 T A  
GTGGCAGGT GCAG GGT  
||||||| ||| |||  
CACCGTCCA CGTC CCA

GAM1334 LOC157349 5' ACCCCTGCACCTGCCAC 81405 T A  
GTGGCAGGT GCAG GGT  
||||||| ||| |||

CACCGTCCA CGTC CCA  
\_ C  
GAM1334 LOC157349 5' ACCTCTGCACCTCCCAC 81406 C T  
GTGG AGGT GCAGAGGT  
||||| |||||  
CACC TCCA CGTCTCCA  
C \_  
GAM1334 LOC157349 3' ACCTCTGCCCCTGCGCCCCTC 81407 TG\_ TT  
GAGG GCAGG GCAGAGGT  
||||| ||||| |||||  
CTCC CGTCC CGTCTCCA  
CCG C\_  
GAM1334 LOC157918 5' ACCTCCACAACCCATC 86637 CAG CA  
GGTGG GTTG GAGGT  
||||| ||||| |||||  
CTACC CAAC CTCCA  
\_ AC  
GAM1334 LOC157931 3' CCTCCCTCCCACCTCT 86660 C TTGCA  
AGAGGTGG AGG GAGG  
||||||| ||| |||||  
TCTCCACC TCC CTCC  
C \_  
GAM1334 LOC158654 3' ACCCCATAACCACCATCTCT 81962 CA CAGA  
AGAGGTGG GGTG GGT  
||||||| ||||| |||  
TCTCTACC CCAAT CCA  
A\_ ACC\_  
GAM1334 LOC163412 5' ACCCCTGCAACCTCTTGCT 82131 TG C A  
GG G AGGTTGCAG GGT  
|| | ||||| ||||| |||  
TC T TCCAACGTC CCA  
GT C C  
GAM1334 LOC196559 5' ACCGCATAACCTGCCACCTC 89638 CAGA  
GAGGTGGCAGGTTG GGT  
||||||| ||||| |||  
CTCCACCGTCCAAT CCA  
ACG\_  
GAM1334 LOC197131 3' ACCCCTAATGTGCCACCTGCT 87885 \_ G GC A  
AG AGGTGGCA GTT AG GGT  
|| ||||| ||||| ||| |||  
TC TCCACCGT TAA TC CCA  
G G \_ C  
GAM1334 LOC200014 3' TGCAACCCCCACCTC 88545 CA  
GAGGTGG GGTGCA  
||||| |||||  
CTCCACC CCAACGT  
C\_  
GAM1334 LOC200078 3' GCCAACCTGCCCCCTC 88571 T \_  
GAGG GGCAGGTTG C  
||||| ||||| |||

			CTCC CCGTCCAAC G		
			C C		
GAM1334	LOC200301 3'	ACCCCCAAACCTGCCCTC	88735	T	GCAGA
		GAGG GGCAGGTT GGT			
		CTCC CCGTCCAA CCA			
		_ ACCC_			
GAM1334	LOC200314 3'	CTGCAACCTCCACCTC	90009	C	
		GAGGTGG AGGTTGCAG			
		CTCCACC TCCAACGTC			
		-			
GAM1334	LOC200860 3'	CTGCAACCTCCACCTC	90163	C	
		GAGGTGG AGGTTGCAG			
		CTCCACC TCCAACGTC			
		-			
GAM1334	LOC201627 3'	CTGCAACCTCCACCTC	89013	C	
		GAGGTGG AGGTTGCAG			
		CTCCACC TCCAACGTC			
		-			
GAM1334	LOC203504 3'	ACCTCCCCTCCCCACCTCT	90636		CA TTGCA
		AGAGGTGG GG GAGGT			
		TCTCCACC CC CTCCA			
		_ TCCC_			
GAM1334	LOC219406 5'	ACCTCTGCAGTGCATCCCT	93555	TG_ GG	
		AGG GCA TTGCAGAGGT			
		TCC CGT GACGTCTCCA			
		CTA _			
GAM1334	LOC219513 5'	ACCCACCCCTGCTACC	94324	T CAGA	
		GGTGGCAGG TG GGT			
		CCATCGTCC AC CCA			
		C C_			
GAM1334	LOC219988 3'	ACCTCCTTTTGGCTGCCACCT	91618		GTTGCA_
		AGGTGGCAG GAGGT			
		TCCACCGTC CTCCA			
		GGTTTTC			
GAM1334	LOC220662 3'	CTGCAACCTCCACCTC	91168	C	
		GAGGTGG AGGTTGCAG			
		CTCCACC TCCAACGTC			
		-			
GAM1334	LOC221296 3'	CTGCAACCTCCACCTC	91961	C	
		GAGGTGG AGGTTGCAG			



CTCCACC TCCAACGTC

GAM1334 LOC221362 3' ACCTCCATGTGCCTCCCCT 93755 A T G TGCA  
AG GG GGCA GT GAGGT  
|| ||||| || |||||  
TC CC CCGT TA CTCCA  
C T G C\_\_

GAM1334 LOC221431 5' CCTCCCTTGCCACCT 92100 TTGCA  
AGGTGGCAGG GAGG  
||||||| |||||  
TCCACCGTTC CTCC  
C\_\_

GAM1334 LOC221663 5' CTGCAACCTCCACCTC 93813 C  
GAGGTGG AGGTTGCAG  
||||||| |||||||  
CTCCACC TCCAACGTC

GAM1334 LOC221914 3' ACCTCTGCCACCCACATC 93948 GCA T  
GGTG GGT GCAGAGGT  
|||| ||| |||||||  
CTAC CCA CGTCTCCA  
AC\_ C

GAM1334 LOC222166 3' CCTCTGCTCCCTCCTCC 94094 T C TT  
GG GG AGG GCAGAGG  
|| ||| |||||||  
CC CC TCC CGTCTCC  
T \_ CT

GAM1334 LOC254428 3' ACCCCACACTCCCACCTCT 95454 C GT CAGA  
AGAGGTGG AG TG GGT  
||||||| || ||| |||  
TCTCCACC TC AC CCA  
C AC C\_\_

GAM1334 LOC254532 5' ACCTCTGTTTCAGCCAGCTCT 96629 G AGGTT  
AGAG TGGC GCAGAGGT  
|||| ||| |||||||  
TCTC ACCG TGTCTCCA  
G ACT\_\_

GAM1334 LOC255650 3' ACCTCCTGGTGCCACCTC 96709 GGTTG \_  
GAGGTGGCA CAG AGGT  
||||||| ||| |||||  
CTCCACCGT GTC TCCA  
G\_\_ C

GAM1334 LOC256267 3' ACCTCCGGTGATCTGCCCACCT 96793 \_ TG A\_  
CT AGAGGTGG CAGGT C GAGGT  
||||||| ||||| | |||||  
TCTCCACC GTCTA G CTCCA  
C GT GC

GAM1334 LOC256302 3' CCCCTGCTGCCACCTCT 95191 GGTT A  
AGAGGTGGCA GCAG GG  
||||||| ||||| ||

		TCTCCACCGT	CGTC CC		
		_____ C			
GAM1334	LOC256306 3'	CTGCAACCTCCACCTC	96685	C	
		GAGGTGG AGGTTGCAG			
		CTCCACC TCCAACGTC			
		_____			
GAM1334	LOC257438 3'	ACCTCCCTCCCTGGCCACCTCT	93968	_	TTGCA
		AGAGGTGGC AGG GAGGT			
		TCTCCACCG TCC CTCCA			
		G CTCC_			
GAM1334	LOC51236 3'	CCTCACTGCCACCTCT	33202		GTTGCA
		AGAGGTGGCAG GAGG			
		TCTCCACCGTC CTCC			
		A_____			
GAM1334	LOC51725 5'	GCAACCCAGCCACCTC	69865	A_	
		GAGGTGGC GGTTGC			
		CTCCACCG CCAACG			
		AC			
GAM1334	LOC81034 3'	CTGCAACCTCCACCTC	47850	C	
		GAGGTGG AGGTTGCAG			
		CTCCACC TCCAACGTC			
		_____			
GAM1334	LOC81558 3'	ACCTGTGTACCTGCCACATC	47948	G	T G
		GA GTGGCAGGT GCA AGGT			
		CT CACCGTCCA TGT TCCA			
		A _ G			
GAM1334	LOC89932 3'	CTGCAACCTCCACCTC	60798	C	
		GAGGTGG AGGTTGCAG			
		CTCCACC TCCAACGTC			
		_____			
GAM1334	LOC90288 3'	CTGCAACCTCCACCTC	62094	C	
		GAGGTGG AGGTTGCAG			
		CTCCACC TCCAACGTC			
		_____			
GAM1334	LOC90371 5'	CTGCAACCTCCACCTC	62497	C	
		GAGGTGG AGGTTGCAG			
		CTCCACC TCCAACGTC			
		_____			
GAM1334	LOC90630 5'	CCTCACCGACACCTCT	63630	GCA	TGCA
		AGAGGTG GGT GAGG			

		TCTCCAC CCA CTCC		
		AG_ ____		
GAM1334	LOC90786	5' ACCTCCTTTCTACCACTTC	64027	C TTGCA
		GAGGTGG AGG GAGGT		
		CTTCACC TCT CTCCA		
		A TTC_		
GAM1334	LOC91115	3' CTGCAACCTCCACCTC	64935	C
		GAGGTGG AGGTTGCAG		
		CTCCACC TCCAACGTC		
		-		
GAM1334	LOC91208	5' CCTCACCAACACCTCT	65245	GCA TGCA
		AGAGGTG GGT GAGG		
		TCTCCAC CCA CTCC		
		AA_ ____		
GAM1334	LOC91308	3' TGCAACCTCCACCTC	65567	C
		GAGGTGG AGGTTGCA		
		CTCCACC TCCAACGT		
		-		
GAM1334	LOC91445	3' CCTCCTCCTGCCACCCT	60550	A TTGCA
		AG GGTGGCAGG GAGG		
		TC CCACCGTCC CTCC		
		- TC_		
GAM1334	LOC92230	5' CCCCTGCTGCCATCTC	68545	GGTT A
		GAGGTGGCA GCAG GG		
		CTCTACCGT CGTC CC		
		- C		
GAM1334	LOC92267	3' CTGCAACCTCCACCTC	68612	C
		GAGGTGG AGGTTGCAG		
		CTCCACC TCCAACGTC		
		-		
GAM1334	LOC92293	3' CCTCGGGATTCCACCCCT	68763	A CA GCA
		AG GGTGG GGTT GAGG		
		TC CCACC TTAG CTCC		
		C _ GG_		
GAM1334	LOC92335	3' ACCCGAGGACCGCCACCTCT	68970	A GCAGA
		AGAGGTGGC GGTT GGT		
		TCTCCACCG CCAG CCA		
		- GAGC_		
GAM1334	LOC92466	3' ACCTCCGGTGATCTGCCACCT	69418	_ TG A_
	CT	AGAGGTGG CAGGT C GAGGT		

			TCTCCACC GTCTA G CTCCA		
			C GT GC		
GAM1335	CARD15	5'	GCTCACCAGTCCTGTG 42216	T	
			CACAG ACTGGTGAGT		
			GTGTC TGACCACTCG		
			C		
GAM1335	CBFB	3'	CACCATTGGCCATACTGTG 8272	C G AA	
			CACAGTA TGGT AGT TG		
			GTGTCAT ACCG TTA AC		
			_ G CC		
GAM1335	CBFB	3'	CACCATTGGCCATACTGTG 43139	C G AA	
			CACAGTA TGGT AGT TG		
			GTGTCAT ACCG TTA AC		
			_ G CC		
GAM1335	F9	3'	CTATCACAAGGCCAGTAC 3738	GAGTAA	
			GTACTGGT TGATAG		
			CATGACCG ACTATC		
			GAAC__		
GAM1335	LZTS1	3'	CAGTGCTCACCAGCCCTG 40682	TA A	
			CAG CTGGTGAGTA TG		
			GTC GACCACTCGT AC		
			CC G		
GAM1335	PMX1	3'	ACCACCACTTGTCTGTG 42652	T_ _ A	
			CACAG AC TGGTG GT		
			GTGTC TG ACCAC CA		
			TT TTC _		
GAM1335	PMX1	3'	ACCACCACTTGTCTGTG 22584	T_ _ A	
			CACAG AC TGGTG GT		
			GTGTC TG ACCAC CA		
			TT TTC _		
GAM1335	DDM36	3'	CATTTCTCACTAGCACT 40569	A T	
			AGT CTGGTGAG AATG		
			TCA GATCACTC TTAC		
			C T		
GAM1335	FLJ11029	5'	CACCACCACTAGCACCTGTG 60972	TA_ A AA	
			CACAG CTGGTG GT TG		
			GTGTC GATCAC CA AC		
			CAC _ CC		
GAM1335	FLJ12704	5'	CGTGCTCTCACCAGAACTG 46533	A TA_	
			CAGT CTGGTGAG ATG		

		GTCA GACCACTC TGC		
		A TCG		
GAM1335 HES6	3'	CAGCCTTCACCAGCCCTGTG 37835	TA	TAA
		CACAG CTGGTGAG TG		
		GTGTC GACCACTT AC		
		CC CCG		
GAM1335 NYD-SP12	3'	CAATGCCACCTAGTACTGTG 49224	_	A A
		CACAGTACT GGTG GTA TG		
		GTGTCATGA CCAC CGT AC		
		T C A		
GAM1335 OSMR	3'	ACTCCCACTCAGTACTGT 14343	_ _	
		ACAGTACTG GT GAGT		
		TGTCATGAC CA CTCA		
		T CC		
GAM1335 TRIP-Br2	3'	ACCCGCCAGTACTGTG 28575	A	
		CACAGTACTGGTG GT		
		GTGTCATGACCGC CA		
		C		
GAM1335 ZWINT	3'	ATCATTACAGGAAAGACTGTG 22934	A	GGTGA
		CACAGT CT GTAATGAT		
		GTGTCA GA CATTACTA		
		_ AAGGA		
GAM1335 ZWINT	3'	ATCATTACAGGAAAGACTGTG 52220	A	GGTGA
		CACAGT CT GTAATGAT		
		GTGTCA GA CATTACTA		
		_ AAGGA		
GAM1335 LOC123876	5'	CACCACTCATCACTGTG 74244	ACT	AA
		CACAGT GGTGAGT TG		
		GTGTCA CTACTION AC		
		_ CC		
GAM1335 LOC129676	5'	CATTGTCCTCACCAGTAC 75732	_	
		GTACTGGTGAG TAATG		
		CATGACCACTC GTTAC		
		CT		
GAM1335 LOC147004	3'	CATTCACCAGCACTCA 83901	C A	GT
		A AGT CTGGTGA AATG		
		A TCA GACCACT TTAC		
		C C _		
GAM1336 APM1	3'	TACCCTAAACTCTCTGGG 16600	ACTCA	T
		TCCAGAGA AGG GTG		

			GGGTCTCT	TCC CAT		
			CAA_ _			
GAM1336	APPBP2	3'	TTGCATT	TAAGTTCCCTAGGA	21086	_ A CA TG
			TCC AG	GAACT AGGTG A		
			AGG TC	CTTGA TTTAC T		
			A C	A_ GT		
GAM1336	AQP6	5'	CATGCTT	GAGTCCCCTGGG	53915	AGA G
			TCCAG	ACTCAAG TGTG		
			GGGTC	TGAGTTC GTAC		
			CCC	_		
GAM1336	ARAF1	3'	CACTCAGA	ACCTCTCTGGA	63937	AC_ AA
			TCCAGAGA	TC GGTG		
			AGGTCTCT	AG TCAC		
			CCA	AC		
GAM1336	C8orf1	3'	TACTGGCTT	GAATTTTCTGGA	15087	C G_
			TCCAGAGAA	TCAAG T GTG		
			AGGTCTTTT	AGTTC G CAT		
			A	G T		
GAM1336	CA12	3'	CACTTCGGCT	CTCTCTGGA	6875	A CA
			TCCAGAGA	CT AGGTG		
			AGGTCTCT	GG TTCAC		
			C	C_		
GAM1336	CANX	3'	ATTCACACCT	CTGTCCCTC	87480	A_ TCA
			GAG AC	AGGTGTGAAT		
			CTC TG	TCCACACTTA		
			CC	TC_		
GAM1336	CEP1	5'	TAGACCCCGA	ACTCTTTGGA	22817	AC AA G
			TCCAGAGA	TC GGT TG		
			AGGTTTCT	AG CCA AT		
			CA	CC G		
GAM1336	FCAR	3'	TTCCTCGCT	AGAGTTCTCCAGA	55807	CA AA T_
			TC	GAGAACTC GGTG GAA		
			AG	CTCTTGAG TCGC CTT		
			AC	A_ TC		
GAM1336	FCAR	3'	TTCCTCGCT	AGAGTTCTCCAGA	55817	CA AA T_
			TC	GAGAACTC GGTG GAA		
			AG	CTCTTGAG TCGC CTT		
			AC	A_ TC		
GAM1336	HMGCR	3'	ATTCACACAG	GGGCTCTTGGA	5972	_ AA CAAG
			TCCA	GAG CT GTGTGAAT		

		AGGT CTC GA CACACTTA		
		T GG ____		
GAM1336 MME	3'	TACTCTTGTTGAGTTCTATAGA 6143	CAG	__ T
		TC AGAACTCAA GG GTG		
		AG TCTTGAGTT TC CAT		
		ATA GT T		
GAM1336 MME	3'	TACTCTTGTTGAGTTCTATAGA 23490	CAG	__ T
		TC AGAACTCAA GG GTG		
		AG TCTTGAGTT TC CAT		
		ATA GT T		
GAM1336 MME	3'	TACTCTTGTTGAGTTCTATAGA 23500	CAG	__ T
		TC AGAACTCAA GG GTG		
		AG TCTTGAGTT TC CAT		
		ATA GT T		
GAM1336 MME	3'	TACTCTTGTTGAGTTCTATAGA 23512	CAG	__ T
		TC AGAACTCAA GG GTG		
		AG TCTTGAGTT TC CAT		
		ATA GT T		
GAM1336 NEU3	3'	CACCTGAACTCTCTGGA 21846	AC	A
		TCCAGAGA TCA GGTG		
		AGGTCTCT AGT CCAC		
		CA _		
GAM1336 P53AIP1	3'	CACCCACTGAACTTTCTGGA 42080	AC	A_ T
		TCCAGAGA TCA GG GTG		
		AGGTCTTT AGT CC CAC		
		CA CA _		
GAM1336 PAICS	3'	TACCTTTAGTTCTCTG 21260	C	
		CAGAGAACT AAGGTG		
		GTCTCTTGA TTCCAT		
		T		
GAM1336 PIR51	3'	CACTTTTTGTTAAGTTCTTTAG 21364	C	__ T
A		TC AGAGAACT CAAGG GTG		
		AG TTTCTTGA GTTTT CAC		
		A ATT T		
GAM1336 PLSCR1	5'	CATCGCCTGGCCCCGGCTCTCT 40856	A CA	__ _
GGA		TCCAGAGA CT AGGTG TG		
		AGGTCTCT GG TCCGC AC		
		C CCCCCG T		
GAM1336 PTPN1	3'	TATTCACACCTCACGCTCTGGA 11050	AACTCA	
		TCCAGAG AGGTGTGAATA		

			AGGTCTC TCCACACTTAT		
			GCAC__		
GAM1336	RAP1A	3'	GTTTGCACAAAGTTCCTGGA 11248	A	CAAG TG
			TCCAG GAACT GTG AAT		
			AGGTC CTTGA CAC TTG		
			C A__ GT		
GAM1336	SYT4	3'	CACTATATTTGAGTTCTT 62435	GT__	
			GAGAACTCAAG GTG		
			TTCTTGAGTTT CAC		
			ATAT		
GAM1336	TCTA	3'	TAGGCCCTGAGTTTTCTG 42241	A G	
			CAGAGAACTCA GGT TG		
			GTCTTTTGAGT CCG AT		
			C G		
GAM1336	VAT1	3'	CACCCTTCACTGAGTTCTCTGG 21044	_____ T	
	A		TCCAGAGAACTCA AGG GTG		
			AGGTCTCTTGAGT TCC CAC		
			CACT _		
GAM1336	ZFH4	5'	CACCTCAGCTCCCTGGA 45294	A A CA	
			TCCAG GA CT AGGTG		
			AGGTC CT GA TCCAC		
			C C C_		
GAM1336	ZFP103	5'	TATTCCGAGCTCTCTGGA 19026	A AA T	
			TCCAGAGA CTC GG GTG		
			AGGTCTCT GAG CC TAT		
			C _ T		
GAM1336	ZNF202	3'	TTGCAGCCAAGTTCCTGG 12913	A CAA _ TG	
			CCAG GAACT GG TG A		
			GGTC CTTGA CC AC T		
			C A_ G GT		
GAM1336	C1orf25	5'	ATTCACGTCAAGTTCTCTG 72532	CAA GT	
			CAGAGAACT G GTGAAT		
			GTCTCTTGA C CACTTA		
			_ TG		
GAM1336	C20orf177	3'	TACTTTTGAGTTCTC 62154	T	
			GAGAACTCAAGG GTG		
			CTCTTGAGTTTT CAT		
			_		
GAM1336	CG012	3'	GCAGTCTGAGTTCTTCAGA 83221	CA A _	
			TC GAGAACTCA GG TGT		



AG TTCTTGAGT CT ACG  
 AC \_ G  
 GAM1336 CRK7 3' TTCCATCCAGTTCTCTG 33256 CAA T  
 CAGAGAACT GGTG GAA  
 ||||| ||| ||  
 GTCTCTTGA CTAC CTT  
 C\_\_ \_  
 GAM1336 DIO2 3' ATTCACACTGTTGTCCTT 25678 A TCAA  
 GAG AC GGTGTGAAT  
 ||| || |||||  
 TTC TG TCACACTTA  
 C TTG\_  
 GAM1336 DIO2 3' ATTCACACTGTTGTCCTT 5826 A TCAA  
 GAG AC GGTGTGAAT  
 ||| || |||||  
 TTC TG TCACACTTA  
 C TTG\_  
 GAM1336 DKFZP434A043 3' CACACTTAACTCTGTGGA 31187 G ACTCA  
 TCCA AGA AGGTGTG  
 ||| ||| |||||  
 AGGT TCT TTCACAC  
 G CAAA\_  
 GAM1336 DKFZp434F1819 3' TCACACCTCCTTTTTG 50009 ACTCA  
 CAGAGA AGGTGTGA  
 ||||| |||||  
 GTTTTT TCCACACT  
 CC\_\_  
 GAM1336 DPCR1 3' CATCTCTGAGTTCTCAGGA 55120 A \_  
 TCC GAGAACTCA AGGTG  
 ||| ||||| |||||  
 AGG CTCTTGAGT TCTAC  
 A C  
 GAM1336 FLJ10898 3' ATTCACACTGATTTTGTCTGGA 59421 G CTCAA  
 TCCAGA AA GGTGTGAAT  
 ||||| || |||||  
 AGGTCT TT TCACACTTA  
 G TTAG\_  
 GAM1336 FLJ11193 3' TATTTTGAATCTCTG 37154 AC  
 CAGAGA TCAAGGTG  
 ||||| |||||  
 GTCTCT AGTTTTAT  
 A\_  
 GAM1336 FLJ13769 3' CACTCAAGCTCTCTGGA 46603 A CAA  
 TCCAGAGA CT GGTG  
 ||||| || |||  
 AGGTCTCT GA TCAC  
 C AC\_  
 GAM1336 FLJ13782 3' GCCTGAGCTTTCTGGA 46169 A A  
 TCCAGAGA CTCA GGT  
 ||||| ||| |||

AGGTCTTT GAGT CCG  
 C \_  
 GAM1336 FLJ20555 3' CAGACCTCAGCTCTCTGGA 35393 A CA G  
 TCCAGAGA CT AGGT TG  
 ||||| || ||| ||  
 AGGTCTCT GA TCCA AC  
 C C\_ G  
 GAM1336 FLJ23142 3' TTTTGAGTTCCTAGA 44727 C A  
 TC AG GAACTCAAGG  
 || || |||||  
 AG TC CTTGAGTTTT  
 A \_  
 GAM1336 FLJ30092 5' TATTCACACCTCACTTCCTG 58691 A CTCA  
 CAG GAA AGGTGTGAATA  
 ||| ||| |||||  
 GTC CTT TCCACACTTAT  
 \_ CAC\_  
 GAM1336 GRID1 3' TATTCAAGCAAGTTCTCTAGG 68501 \_ CAAG G  
 CC AGAGAACT GT TGAATA  
 || ||||| || |||||  
 GG TCTCTTGA CG ACTTAT  
 A A\_\_ A  
 GAM1336 HPCAL4 3' CATCTTGTGCCCTCTGGA 32732 AACT  
 TCCAGAG CAAGGTG  
 ||||| |||||  
 AGGTCTC GTTCTAC  
 CCGT  
 GAM1336 KIAA0229 3' CATTTTGATTCTCTG 92423 C  
 CAGAGAA TCAAGGTG  
 ||||| |||||  
 GTCTCTT AGTTTTAC  
 \_  
 GAM1336 KIAA0295 3' GCCTTGGGTTCTCCAGA 68105 CA  
 TC GAGAACTCAAGGT  
 || |||||  
 AG CTCTTGGGTTCCG  
 AC  
 GAM1336 KIAA0420 3' TACCCTGCACTCTCTGGA 63366 ACTCA T  
 TCCAGAGA AGG GTG  
 ||||| ||| |||  
 AGGTCTCT TCC CAT  
 CACG\_ \_  
 GAM1336 KIAA0565 3' TATTTTAAAGTCTCTGGA 66897 ACTC  
 TCCAGAGA AAGGTG  
 ||||| |||||  
 AGGTCTCT TTTTAT  
 GAAT  
 GAM1336 KIAA1036 3' CATCTTGGTCCTCCGGA 29816 A A T  
 TCC GAG AC CAAGGTG  
 ||| ||| || |||||

AGG CTC TG GTTCTAC  
 C C \_  
 GAM1336 KIAA1240 3' TATTCATGTTTGAGTTC 66737 G TG  
 GAACTCAA G TGAATA  
 ||||| | |||||  
 CTTGAGTT T ACTTAT  
 \_ GT  
 GAM1336 KIAA1297 5' CACTGCAGCCCGAGTTCTCTGG 72170 AA \_\_\_\_  
 CCAGAGAACTC GGT GTG  
 ||||| ||| |||  
 GGTCTCTTGAG CCG CAC  
 C\_ ACGT  
 GAM1336 KIAA1579 3' CACTTTGATTTCCCTGGA 36605 A C  
 TCCAG GAA TCAAGGTG  
 |||| | |||||  
 AGGTC CTT AGTTTCAC  
 C T  
 GAM1336 MAB21L2 5' TTCGCAGCTCTCTGGA 21233 ACTCAA G  
 TCCAGAGA G TGTGAA  
 ||||| | |||||  
 AGGTCTCT C ACGCTT  
 \_\_\_\_ G  
 GAM1336 MAP2K6 5' CATCTTGATTCCCTG 10868 A C  
 CAG GAA TCAAGGTG  
 ||| || |||||  
 GTC CTT AGTTCTAC  
 C \_  
 GAM1336 MGC21688 3' ATTCACGCAGAGCTCTCTG 58265 A AAG  
 CAGAGA CTC GTGTGAAT  
 |||| | |||||  
 GTCTCT GAG CGCACTTA  
 C A\_\_  
 GAM1336 MMPL1 3' TATTCCTCTGTGTGTTCTCTGG 14722 T A TGT  
 A TCCAGAGAAC CA GG GAATA  
 ||||| || ||| |||||  
 AGGTCTCTTG GT TC CTTAT  
 T G TC\_  
 GAM1336 NDUFB6 3' ATTTACTGAATTTTCTGGA 10197 C AGGT  
 TCCAGAGAA TCA GTGAAT  
 ||||| || |||||  
 AGGTCTTTT AGT CATTTA  
 A \_\_\_\_  
 GAM1336 SSB-4 3' CACTGACTCACAGTTCTCTGGA 55097 CA\_ GT\_  
 TCCAGAGAACT AG GTG  
 ||||| || |||  
 AGGTCTCTTGA TC CAC  
 CAC AGT  
 GAM1336 STAM2 3' TTCAAGCTAGTTCTCTG 19570 CAA G  
 CAGAGAACT GGT TGAA  
 ||||| || |||

			GTCTCTTGA TCG ACTT		
			___ A		
GAM1336	SYT12	3'	TAGCTTGAGTTCCCTAGA 94740	C A	G
			TC AG GAACTCAAG TG		
			AG TC CTTGAGTTC AT		
			A C G		
GAM1336	TED	3'	TATTCACACCTTTCCATCCCTG 31643	A	ACTC
			CAG GA AAGGTGTGAATA		
			GTC CT TTCCACACTTAT		
			C ACCT		
GAM1336	TRAD	3'	CACTCCGTGCAGTTCTCTG 22951	_ A	T
			CAGAGAACT CA GG GTG		
			GTCTCTTGA GT CC CAC		
			C G T		
GAM1336	TRIM22	3'	CATCTACAAGTTCTCTGGA 20286	CA_	
			TCCAGAGAACT AGGTG		
			AGGTCTCTTGA TCTAC		
			ACA		
GAM1336	TUB	3'	ATTCAGAACTTCAAGTTCTCTT 12425	C	CA G_
	GA		TC AGAGAACT AGGT TGAAT		
			AG TCTCTTGA TTCA ACTTA		
			T AC AG		
GAM1336	LOC120939	3'	CATCTCTCGAGTTCTTGGA 76250	G	A GT
			TCCA AGAACTC AG GTG		
			AGGT TCTTGAG TC TAC		
			_ C TC		
GAM1336	LOC122258	3'	CACGCCACGTTCTCTG 59141	TCAA	
			CAGAGAAC GGTGTG		
			GTCTCTTG CCGCAC		
			CAC_		
GAM1336	LOC124842	3'	CACCTTCCTGAGTTCTCAGGA 75658	A	___
			TCC GAGAACTCA AGGTG		
			AGG CTCTTGAGT TCCAC		
			A CCT		
GAM1336	LOC138050	5'	TCCATAATGAACTTCTCTGGA 75299	C_	AG T
			TCCAGAGAA TCA GTG GA		
			AGGTCTCTT AGT TAC CT		
			CA AA _		
GAM1336	LOC146839	5'	ATTCTCTTGAGTTTCTAGA 83806	C	TGT
			TC AGAGAACTCAAGG GAAT		

	AG TCTTTTGAGTTCT CTTA	
	A      _____	
GAM1336 LOC150095 5'	CACACCTTCCCTCTCTG 84855	ACTC
	CAGAGA AAGGTGTG	
	GTCTCT TTCCACAC	
	CCC_	
GAM1336 LOC151094 3'	CACGCTTGGTCCCT 65293	A CA
	AG GAACT AGGTGTG	
	TC CTTGG TTCGCAC	
	C      _	
GAM1336 LOC153603 3'	CATCTTCGAGCTCTCTGGA 80900	A _
	TCCAGAGA CTC AAGGTG	
	AGGTCTCT GAG TTCTAC	
	C C	
GAM1336 LOC153811 3'	ATTCACACAGCTCCCTGGG 80942	A A CAAG
	TCCAG GA CT GTGTGAAT	
	GGGTC CT GA CACACTTA	
	C C _____	
GAM1336 LOC163341 3'	CATCTTGAGCCCCTTGGA 82119	AGAA
	TCCAG CTCAAGGTG	
	AGGTT GAGTTCTAC	
	CCCC	
GAM1336 LOC199800 5'	CACCCAGTGAGGTCTCTGGA 89856	A A_ T
	TCCAGAGA CTCA GG GTG	
	AGGTCTCT GAGT CC CAC	
	G GA _	
GAM1336 LOC254439 3'	TTACACAGCTCTCTGGA 94749	ACTCAA G
	TCCAGAGA G TGTGAA	
	AGGTCTCT C ACACTT	
	_____ G	
GAM1336 LOC255465 3'	GCCTTGAGTCTCTGGA 97289	A
	TCCAGAGA CTCAAGGT	
	AGGTCTCT GAGTTCCG	
	—	
GAM1336 LOC256207 3'	TATTTTCAAGTCTCTGGA 95176	ACTC
	TCCAGAGA AAGGTG	
	AGGTCTCT TTTTAT	
	GAAC	
GAM1336 LOC257354 3'	TACCCTGCACTCTCTGGA 95099	ACTCA T
	TCCAGAGA AGG GTG	

AGGTCTCT TCC CAT  
 CACG\_ \_  
 GAM1336 LOC91308 3' TGTGCCTTAAGTTCTCT 65568 C TG  
 AGAGAACT AAGG TG  
 ||||| ||| ||  
 TCTCTTGA TTCC GT  
 A GT  
 GAM1336 LOC91695 5' TATTCCAATCAAGTTCTCTG 66971 CAAGG T  
 CAGAGAACT TG GAATA  
 ||||| || ||||  
 GTCTCTTGA AC CTTAT  
 ACTA\_ \_  
 GAM1336 LOC93259 5' TACAGCCTTGAGTTCCTTGGA 71826 A \_  
 TCCAG GAACTCAAGG TGTG  
 |||| ||||| ||||  
 AGGTT CTTGAGTTCC ACAT  
 C G  
 GAM1337 HMGB1 3' GTCTATAAAGCATTTAACC 9228 AG A  
 GGT TAGGT CTTTATAGAC  
 || |||| |||||  
 CCA ATTTA GAAATATCTG  
 \_ C  
 GAM1337 PLAGL1 3' GTCTAGCTTAAACCTACTACCT 10615 ACTTTA  
 CA TGAGGTAGTAGGT TAGAC  
 ||||| ||||  
 ACTCCATCATCCA ATCTG  
 AATTCG  
 GAM1337 C20orf54 3' AAGTACCAACTACCTCA 53007 A  
 TGAGGTAGT GGTACTT  
 ||||| |||||  
 ACTCCATCA CCATGAA  
 A  
 GAM1337 DKFZP564D172 3' TCTATAAAGTACTGAATCCGCA 49392 A TAGTA  
 TG GG GGTACTTTATAGA  
 || || |||||  
 AC CC TCATGAAATATCT  
 G TAAG\_  
 GAM1337 KIAA0140 3' TCTATAAGGTGCCACCCC 27816 TA A  
 GG GT GGTACTTTATAGA  
 || || |||||  
 CC CA CCGTGGAATATCT  
 C\_ \_  
 GAM1337 KIAA0435 5' TCTATAAGAGTATACCCCA 28986 A AGTAG \_  
 TG GGT GTACTTT ATAGA  
 || || ||||| ||||  
 AC CCA TATGAGA TATCT  
 C \_ \_ A  
 GAM1337 KIAA1228 3' TCTATAAAGCAGCAGCACTCA 65050 \_ A AGGTA  
 TGAG GT GT CTTTATAGA  
 ||| || |||||

		ACTC CG CG GAAATATCT			
		A A AC__			
GAM1337	PYY2	3' CTATCCTCGCCACTACCTCA 40826	A	ACTTT	
		TGAGGTAGT GGT ATAG			
		ACTCCATCA CCG TATC			
		_ CTCC_			
GAM1337	RAB3IL1	3' TCTCCAGGGTACCCTCCACCCC 25466	A	AGTA	AT
	A	TG GGT GGTACTTT AGA			
		AC CCA CCATGGGA TCT			
		C CCTC CC			
GAM1337	LOC145833	3' GTCTATAAAGCATTTAACC 60303	AG	A	
		GGT TAGGT CTTTATAGAC			
		CCA ATTTA GAAATATCTG			
		_ C			
GAM1337	LOC149271	3' AGGTGGCTACTACCTTA 79236	G		
		TGAGGTAGTAG TACTT			
		ATTCCATCATC GTGGA			
		G			
GAM1338	B3GAT3	3' AAGGACAGATGGACCCA 24186	G		
		TGGGTCCGTCTGT CTT			
		ACCCAGGTAGACA GAA			
		G			
GAM1338	BPESC1	3' AAGCCAAGCACACTTTCCTA 41468	TCCGTC	A	
		TGGG TGTGCTTG CTT			
		ATCC ACACGAAC GAA			
		TTTC_ C			
GAM1338	CTSO	3' AAGTCAGTGGGACAACTCCA 7188	_ CC	G	T
		TGG GT GTCT TGCT GACTT			
		ACC CA CAGG GTGA CTGAA			
		T AA _ _			
GAM1338	KIAA1029	5' AAGCCAAGGCGCGGAGCCA 23469	G	CT G	A
		TGG TCCGT GT CTTG CTT			
		ACC AGGCG CG GAAC GAA			
		G _ _ C			
GAM1338	KIAA1613	3' AAGCAGTCAGGCAGACCCA 64809	C	_	
		TGGGTC GTCTG TGCTT			
		ACCCAG CGGAC ACGAA			
		A TG			
GAM1338	KIAA1867	5' AAGCCACCCGGAGGGACCCA 94820	G	T_	
		TGGGTCC TCTG GCTT			

			ACCCAGG AGGC CGAA		
			G CCAC		
GAM1338	Ubc6p	3'	AGCACAGGCAGACCCA	54149	C
			TGGGTC GTCTGTGCT		
			ACCCAG CGGACACGA		
			A		
GAM1338	LOC255712	5'	AAGTCAGAAGACGGACTCA	97611	GTGCT
			TGGGTCCGTCT TGA		
			ACTCAGGCAGA ACTGAA		
			AG__		
GAM1338	LOC96597	5'	AAGTCAAGTCCCAGAACCCA	66903	CCG T_
			TGGGT TCTG GCTTGACTT		
			ACCCA AGAC TGA		
			__ CC		
GAM1339	A1BG	3'	CAGGCACCCACCACACCCA	55412	A A T
			TG GTGTGGT GTG GTGCCTG		
			AC CACACCA CAC CACGGAC		
			C C C		
GAM1339	AQP6	3'	TACAGGCGCCTGCCACCACGCC	53940	A A T
	CA		TG GTGTGGT GTG GTGCCTGTA		
			AC CGCACCA CGT CGCGGACAT		
			C C C		
GAM1339	AQP6	3'	TACAGGCGCCTGCCACCACGCC	7960	A A T
	CA		TG GTGTGGT GTG GTGCCTGTA		
			AC CGCACCA CGT CGCGGACAT		
			C C C		
GAM1339	ATP8B2	3'	TACAGGCACACACCACACGCT	65233	A
	T		GAGTGTGGT GTGTGTGCCTGTA		
			TTCGCACCA CACACACGGACAT		
			C		
GAM1339	ATP8B2	3'	TACAGGCGTGAGCCACCACACC	65234	A A GTG
	CA		TG GTGTGGT GT TGCCTGTA		
			AC CACACCA CG GCGGACAT		
			C C AGT		
GAM1339	AXL	3'	TACAGGTGTGTGCCACCACACC	41602	A A TG TG
	CG		TG GTGTGGT G TG CCTGTA		
			GC CACACCA C GT GGACAT		
			C C GT GT		
GAM1339	AXL	3'	TACAGGTGTGTGCCACCACACC	8105	A A TG TG
	CG		TG GTGTGGT G TG CCTGTA		



			GC CACACCA C GT GGACAT		
			C C GT GT		
GAM1339	BIN2	3'	TACAGAGACATAACCACACACA 32824	_ AG_	GC
		CTCA	TGAGTGTG GT TGTGT CTGTA		
			ACTCACAC CA ATACA GACAT		
			A CCA GA		
GAM1339	CAMLG	3'	TACAGGCATGCACCACCACGCC 8242	A A	
		CA	TG GTGTGGT GTGTGTGCCTGTA		
			AC CGCACCA CACGTACGGACAT		
			C C		
GAM1339	CCNF	3'	TACAAGCACCCAACCACGCCCA 8324	A AG T C	
			TG GTGTGGT TG GTGC TGTA		
			AC CGCACCA AC CACG ACAT		
			C _ C A		
GAM1339	CDH12	3'	ACAAACACACACACACAC 14487	_ A CC	
			GTGTG GT GTGTGTG TGT		
			CACAC CA CACACAC ACA		
			A _ AA		
GAM1339	CENTD2	5'	ACAGACACACAGAGTCACACAC 57551	_ AG_	C
		ACTCA	TGAGTGTG GT TGTGTG CTGT		
			ACTCACAC CA ACACAC GACA		
			A CTGAG A		
GAM1339	CLECSF12	3'	TACAGTCAGGCACCACCACACC 76698	A A G C	
		CG	TG GTGTGGT GTGT TG CTGTA		
			GC CACACCA CACG AC GACAT		
			C C G T		
GAM1339	COX15	3'	TACAGGCATGGGCCACCACGCC 54319	A A G	
		CA	TG GTGTGGT GT TGTGCCTGTA		
			AC CGCACCA CG GTACGGACAT		
			C C G		
GAM1339	CSF2RB	3'	ACAGACACACACACACAC 4619	GTA C	
			GTGTG GTGTGTG CTGT		
			CACAC CACACAC GACA		
			A_ A		
GAM1339	CSPG3	3'	ACAAACACACACACACAC 15226	_ A CC	
			GTGTG GT GTGTGTG TGT		
			CACAC CA CACACAC ACA		
			A _ AA		
GAM1339	CXCL16	3'	TACAGGTGCTCACCACCACACC 41925	A A T TG	
		CG	TG GTGTGGT GTG G CCTGTA		

			GC CACACCA CAC C GGACAT		
			C C TGT		
GAM1339	CYP1A2	3'	TACAGGCACACACCACCACGC 69120	A	
			GTGTGGT GTGTGTGCCTGTA		
			CGCACCA CACACACGGACAT		
			C		
GAM1339	CYP1A2	3'	TACAGGTGTGAGCCACCACATC 69121	AG	A G TG
	CA		TG TGTGGT GT TG CCTGTA		
			AC ACACCA CG GT GGACAT		
			CT C A GT		
GAM1339	CYP1A2	3'	TACAGGCACACACCACCACGC 5700	A	
			GTGTGGT GTGTGTGCCTGTA		
			CGCACCA CACACACGGACAT		
			C		
GAM1339	CYP1A2	3'	TACAGGTGTGAGCCACCACATC 5701	AG	A G TG
	CA		TG TGTGGT GT TG CCTGTA		
			AC ACACCA CG GT GGACAT		
			CT C A GT		
GAM1339	DNASE1L1	5'	TACAGGCATGAGCCACCACGCC 22080	A	A G
	CA		TG GTGTGGT GT TGTGCCTGTA		
			AC CGCACCA CG GTACGGACAT		
			C C A		
GAM1339	DSCR3	3'	TACAGGTGAGTGCCACCACACT 20190	A TG G	
	CA		TGAGTGTGGT G T TGCCTGTA		
			ACTCACCA C G GTGGACAT		
			C GT A		
GAM1339	DSCR3	3'	TACAGGTGTGAGCCACCACACC 20191	A	A G TG
	CA		TG GTGTGGT GT TG CCTGTA		
			AC CACACCA CG GT GGACAT		
			C C A GT		
GAM1339	ENDOGL1	3'	TACAGGCACACACCATCACCT 17553	T A	
	CA		TGAG GTGGT GTGTGTGCCTGTA		
			ACTC CACTA CACACACGGACAT		
			C C		
GAM1339	F3	3'	TACAGGTGCGCACTACCACACC 67081	A	TG
	A		TG GTGTGGTAGTGTG CCTGTA		
			AC CACACCATCACGC GGACAT		
			GT		
GAM1339	FANCE	3'	TACAGGTGTGAGCCACCACACC 41615	A	A G TG
	A		TG GTGTGGT GT TG CCTGTA		

			AC CACACCA CG GT GGACAT		
			— C A GT		
GAM1339	FGFRL1	3'	CAGACACACACTA 41618 A C		
			TGGT GTGTGTG CTG		
			ATCA CACACAC GAC		
			— A		
GAM1339	GM2A	3'	TACAGGCATGAGCCACTACACC 67783 A A G		
	CA		TG GTGTGGT GT TGTGCCTGTA		
			AC CACATCA CG GTACGGACAT		
			C C A		
GAM1339	INMT	3'	CAGGCACACACCTCCA 22266 TA		
			TGG GTGTGTGCCTG		
			ACC CACACACGGAC		
			TC		
GAM1339	INMT	3'	TACAGGCGTGAGCCACCGCACC 22277 A A GTG		
	CA		TG GTGTGGT GT TGCCTGTA		
			AC CACGCCA CG GCGGACAT		
			C C AGT		
GAM1339	JAK3	3'	TACAGGTGTGCACCACCACACC 4006 A A TG		
	CG		TG GTGTGGT GTGTG CCTGTA		
			GC CACACCA CACGT GGACAT		
			C C GT		
GAM1339	LLGL1	3'	TACAGGCGCCCACCACCACGCC 66881 A A T		
	CA		TG GTGTGGT GTG GTGCCTGTA		
			AC CGCACCA CAC CGCGGACAT		
			C C C		
GAM1339	LTB4R	5'	TACAGGCACATGCCACTACACC 5652 A A		
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CACATCA CGTACACGGACAT		
			C C		
GAM1339	MHC2TA	3'	TACAGGTGTGAACCACCACACC 4186 A A G TG		
	CA		TG GTGTGGT GT TG CCTGTA		
			AC CACACCA CA GT GGACAT		
			C C A GT		
GAM1339	MICB	3'	TACAGACAGGCACCACCACACC 19830 A A G C		
	CA		TG GTGTGGT GTGT TG CTGTA		
			AC CACACCA CACG AC GACAT		
			C C G A		
GAM1339	MPL	3'	TACAGGCGCACACCACCACAC 18152 A		
			GTGTGGT GTGTGTGCCTGTA		

			CACACCA CACACGCGGACAT			
			C			
GAM1339	MTR	3'	TACAGGTGCCCACCACACACC 4217	A	A	T TG
	CG		TG GTGTGGT GTG G CCTGTA			
			GC CACACCA CAC C GGACAT			
			C C C GT			
GAM1339	NCAM1	3'	ACAGACACACACACGCACAC 5220	_	A	C
			GTGTG GT GTGTGTG CTGT			
			CACAC CA CACACAC GACA			
			G _ A			
GAM1339	NDRG3	3'	TACAGGCACCTGCCACCATACC 49302	A	A	T
	CA		TG GTGTGGT GTG GTGCCTGTA			
			AC CATAcca CGT CACGGACAT			
			C C C			
GAM1339	NGFR	3'	ACAGACACACGCACACACAC 10222	_	A	C
			GTGTG GT GTGTGTG CTGT			
			CACAC CA CGCACAC GACA			
			A _ A			
GAM1339	PCDHB9	3'	TACAGGCATGAGCCACCGCACC 38945	A	A	G
	CA		TG GTGTGGT GT TGTGCCTGTA			
			AC CACGCCA CG GTACGGACAT			
			C C A			
GAM1339	PDE6B	3'	TACAGGCATGAGCCACCACGCC 4288	A	A	G
	CA		TG GTGTGGT GT TGTGCCTGTA			
			AC CGCACCA CG GTACGGACAT			
			C C A			
GAM1339	PER2	3'	TACAGGCGTGAGCCACCACGCC 43042	A	A	GTG
	CA		TG GTGTGGT GT TGCCTGTA			
			AC CGCACCA CG GCGGACAT			
			C C AGT			
GAM1339	POU2AF1	3'	ACAGGCGTGAGCCACCGCACCC 20646	A	A	GTG
	A		TG GTGTGGT GT TGCCTGT			
			AC CACGCCA CG GCGGACA			
			C C AGT			
GAM1339	PPEF2	3'	TACAGGCATGAGCCACCGCACC 20674	A	A	G
	CA		TG GTGTGGT GT TGTGCCTGTA			
			AC CACGCCA CG GTACGGACAT			
			C C A			
GAM1339	PPEF2	3'	TACAGGCATGCACCACCACACC 20675	A	A	
	A		TG GTGTGGT GTGTGTGCCTGTA			

			AC CACACCA CACGTACGGACAT		
			— C		
GAM1339	PPID	3'	TACAGGCACGTGCCACCACGCC 87437	A	A TG
	CA		TG GTGTGGT G TGTGCCTGTA		
			AC CGCACCA C GCACGGACAT		
			C C GT		
GAM1339	PRG2	5'	CACCACCGCCCACTCA 10778	TA	T
			TGAGTGTGG GTG GTG		
			ACTCACACC CAC CAC		
			GC —		
GAM1339	PRKR	3'	TACAGGCATGTGCCACCCACCC 10886	A T	A TG
	A		TG GTG GGT G TGTGCCTGTA		
			AC CAC CCA C GTACGGACAT		
			C — C GT		
GAM1339	PRV1	3'	GCTGCTCACCACCACACTCA 73532	A T	—
			TGAGTGTGGT GTG GT GC		
			ACTCACACCA CAC CG CG		
			C T T		
GAM1339	PTGIS	3'	TACAGGCACCCGCCACCACACC 6340	A	A T
	CG		TG GTGTGGT GTG GTGCCTGTA		
			GC CACACCA CGC CACGGACAT		
			C C C		
GAM1339	PTGIS	3'	TACAGGCGCACACCACCACGCC 6341	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CGCACCA CACACGCGGACAT		
			C C		
GAM1339	RHD	3'	TACAAGTGCGCACTACCACACC 32313	A	TG C
	CA		TG GTGTGGTAGTGTG C TGTA		
			AC CACACCATCACGC G ACAT		
			C GT A		
GAM1339	RHD	3'	TACAAGTGCGCACTACCACACC 32622	A	TG C
	CA		TG GTGTGGTAGTGTG C TGTA		
			AC CACACCATCACGC G ACAT		
			C GT A		
GAM1339	RPH3AL	3'	TACAGGTGTGAGCCACCGCACC 22754	A	A G TG
	CA		TG GTGTGGT GT TG CCTGTA		
			AC CACGCCA CG GT GGACAT		
			C C A GT		
GAM1339	SERPINB9	3'	TACAAGCACCCACCACCACACC 14761	A	A T C
	CG		TG GTGTGGT GTG GTGC TGTA		

			GC CACACCA CAC CACG ACAT		
			C C C A		
GAM1339	SHOX	3'	TACAGGCACCCACCACCACACC 22543	A	A T
	CA		TG GTGTGGT GTG GTGCCTGTA		
			AC CACACCA CAC CACGGACAT		
			C C C		
GAM1339	SLC14A2	5'	TACAAGTGTGTGCCACCACAC 23138	A TG	TG C
			GTGTGGT G TG C TGTA		
			CACACCA C GT G ACAT		
			C GT GT A		
GAM1339	SLC16A7	3'	CACAAACACACATACTC 16403	_ A	G
			GAGTGTG GT GT TGTG		
			CTCATAC CA CA ACAC		
			A _ A		
GAM1339	TAF11	3'	TACAGGCACACACTACTGTGCC 18916	A TG	
	CA		TG GTG GTAGTGTGTGCCTGTA		
			AC CGT CATCACACACGGACAT		
			C GT		
GAM1339	TAPBP	3'	TACAGGCACATGCCACCACACC 12133	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CACACCA CGTACACGGACAT		
			C C		
GAM1339	TERF1	3'	TACAGGCACACACCACCAGCCA 33976	A G	A
			TG GT TGGT GTGTGTGCCTGTA		
			AC CG ACCA CACACACGGACAT		
			_ _ C		
GAM1339	TIM3	3'	TACAGGCGTGAGCCACCACATC 51348	AG	A GTG
	CA		TG TGTGGT GT TGCCTGTA		
			AC ACACCA CG GCGGACAT		
			CT C AGT		
GAM1339	TMPRSS3	3'	ACAGGTGCCCCGCCACCACACC 50500	A	A T TG
	A		TG GTGTGGT GTG G CCTGT		
			AC CACACCA CGC C GGACA		
			C C C GT		
GAM1339	TMPRSS3	3'	ACAGGTGCCCCGCCACCACACC 50520	A	A T TG
	A		TG GTGTGGT GTG G CCTGT		
			AC CACACCA CGC C GGACA		
			C C C GT		
GAM1339	TMPRSS3	3'	ACAGGTGCCCCGCCACCACACC 43787	A	A T TG
	A		TG GTGTGGT GTG G CCTGT		

			AC CACACCA CGC C GGACA		
			C C C GT		
GAM1339	TOP2A	3'	TACAGATACTCTACTACACTCA 6533	T	GC
			TGAGTGTGGTAG GTGT CTGTA		
			ACTCACATCATC CATA GACAT		
			T —		
GAM1339	AD7C-NTP	3'	TACAGGCGTGAGCCACCTCACC 27166	A	T A GTG
	CA		TG GTG GGT GT TGCCTGTA		
			AC CAC CCA CG GCGGACAT		
			C T C AGT		
GAM1339	APXL2	5'	TACAGGCGTGTGCCACCACGCC 75195	A	A TG
	CA		TG GTGTGGT GTG TGCCTGTA		
			AC CGCACCA CGT GCGGACAT		
			C C GT		
GAM1339	ASB16	3'	TACAGGTGTGAGCCACCACACC 69942	A	A G TG
	CG		TG GTGTGGT GT TG CCTGTA		
			GC CACACCA CG GT GGACAT		
			C C A GT		
GAM1339	ATP1B4	3'	TACAGGCACACACCACCATGCC 23826	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CGTACCA CACACACGGACAT		
			C C		
GAM1339	BM-002	3'	TACAGGCATGCACCACCACGCC 33525	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CGCACCA CACGTACGGACAT		
			C C		
GAM1339	BTN3A1	3'	TAGGTGCACGCCACCACACCCA 22923	A	A TG
			TG GTGTGGT GTGTG CCTG		
			AC CACACCA CGCAC GGAT		
			C C GT		
GAM1339	C20orf142	3'	TACAGGCATGCGTCACCACACC 74785	A	AG
	A		TG GTGTGGT TGTGTGCCTGTA		
			AC CACACCA GCGTACGGACAT		
			— CT		
GAM1339	C6orf5	3'	TACAGGTGTGAGCCACCACACC 31362	A	A G TG
	CA		TG GTGTGGT GT TG CCTGTA		
			AC CACACCA CG GT GGACAT		
			C C A GT		
GAM1339	C9orf9	3'	ACAGGCGCCCACCACCCCA 38496	T	A T
			TG GGT GTG GTGCCTGT		

			AC CCA CAC CGCGGACA		
			C C C		
GAM1339	CARD6	3'	TACAGGCATGCACCACCACACC 50858	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CACACCA CACGTACGGACAT		
			C C		
GAM1339	CDC14B	3'	TACAGGTGTCAGCCACCGCACCC 52859	A	A GT TG
	CA		TG GTGTGGT GT G CCTGTA		
			AC CACGCCA CG T GGACAT		
			C C AC GT		
GAM1339	CHSY1	3'	TACAGGCACACACCACCACGCC 29904	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CGCACCA CACACACGGACAT		
			C C		
GAM1339	CIP29	3'	TACAGGCACACACCACCACAC 50407	A	
			GTGTGGT GTGTGTGCCTGTA		
			CACACCA CACACACGGACAT		
			C		
GAM1339	COVA1	3'	ACAAACACACACACGCACGC 73257	_ A	CC
			GTGTG GT GTGTGTG TGT		
			CGCAC CA CACACAC ACA		
			G _ AA		
GAM1339	CPSF2	3'	TACAGGCATGCACCACCACGCC 61596	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CGCACCA CACGTACGGACAT		
			C C		
GAM1339	CSR1	3'	ACAGGCACACATGCATGCACAC 32673	GTA__	
			GTGTG GTGTGTGCCTGT		
			CACAC TACACACGGACA		
			GTACG		
GAM1339	DKFZP564G092	5'	ATACAGGCACACACCACCACGC 31533	A	
			GTGTGGT GTGTGTGCCTGTA T		
			CGCACCA CACACACGGACAT A		
			C		
GAM1339	ERO1L	3'	TACAGGTGTCTGCCACCATACC 27432	A	A GT TG
	CA		TG GTGTGGT GT G CCTGTA		
			AC CATACCA CG T GGACAT		
			C C TC GT		
GAM1339	FLJ10535	3'	TACAGGCACACGCCACCACACC 36245	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		



			AC CACACCA CGCACACGGACAT		
			C C		
GAM1339	FLJ10535	3'	TACAGGCATGAGCCACCACACC 36246	A	A G
	CA		TG GTGTGGT GT TGTGCCTGTA		
			AC CACACCA CG GTACGGACAT		
			C C A		
GAM1339	FLJ10687	3'	TACAGGCACGTGCCACCATACT 36410		A TG
	CA		TGAGTGTGGT G TGTGCCTGTA		
			ACTCATACCA C GCACGGACAT		
			C GT		
GAM1339	FLJ10713	3'	TACAGGCACCTGCCACCACACC 36471	A	A T
	CA		TG GTGTGGT GTG GTGCCTGTA		
			AC CACACCA CGT CACGGACAT		
			C C C		
GAM1339	FLJ10718	3'	ACAGGCACGTGCCACCACACCC 36489	A	A TG
	A		TG GTGTGGT G TGTGCCTGT		
			AC CACACCA C GCACGGACA		
			C C GT		
GAM1339	FLJ10829	5'	TACAGGCACGTGCCAACACACC 36713	A	GTA TG
	CA		TG GTGTG G TGTGCCTGTA		
			AC CACAC C GCACGGACAT		
			C AAC GT		
GAM1339	FLJ11800	3'	TACAGGCATGGGCCACCACAGC 46430	AG	A G
	CA		TG TGTGGT GT TGTGCCTGTA		
			AC ACACCA CG GTACGGACAT		
			CG C G		
GAM1339	FLJ12078	3'	ACAAACACACACACACT 46448	GTA	CC
			AGTGTG GTGTGTG TGT		
			TCACAC CACACAC ACA		
			A_ AA		
GAM1339	FLJ12363	3'	TACAGGCACCTGTCACCACACC 49689	A	AG T
	CA		TG GTGTGGT TG GTGCCTGTA		
			AC CACACCA GT CACGGACAT		
			C CT C		
GAM1339	FLJ12363	3'	TACAGGCATGAGCCACCACGCC 49690	A	A G
	CA		TG GTGTGGT GT TGTGCCTGTA		
			AC CGCACCA CG GTACGGACAT		
			C C A		
GAM1339	FLJ12610	3'	AGGCACACACCACCACAC 45509	A	
			GTGTGGT GTGTGTGCCT		

			CACACCA CACACACGGA		
			C		
GAM1339	FLJ12747	3'	TACAGGCATGCGCCACCACACC 49723	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CACACCA CGCGTACGGACAT		
			C C		
GAM1339	FLJ13072	5'	TACAGGTGTGAGCCACCACACC 89823	A	A G TG
	CG		TG GTGTGGT GT TG CCTGTA		
			GC CACACCA CG GT GGACAT		
			C C A GT		
GAM1339	FLJ13114	3'	TACAGGCGTGAGCCACCACACC 44603	A	A GTG
	CA		TG GTGTGGT GT TGCCTGTA		
			AC CACACCA CG GCGGACAT		
			C C AGT		
GAM1339	FLJ13193	3'	ACAGGTGTGTACCACCACGCCC 49757	A	A TG
	A		TG GTGTGGT GTG TGCCTGT		
			AC CGCACCA CAT GTGGACA		
			C C GT		
GAM1339	FLJ14957	3'	TACAGGCATGAGCCACCACGCC 51757	A	A G
	CA		TG GTGTGGT GT TGTGCCTGTA		
			AC CGCACCA CG GTACGGACAT		
			C C A		
GAM1339	FLJ20700	3'	TACAGGTGTGAGCCACCACACC 35585	A	A G TG
	CA		TG GTGTGGT GT TG CCTGTA		
			AC CACACCA CG GT GGACAT		
			C C A GT		
GAM1339	FLJ20958	3'	TACAGGCGTGAGCCACCACACC 42061	A	A GTG
	CA		TG GTGTGGT GT TGCCTGTA		
			AC CACACCA CG GCGGACAT		
			C C AGT		
GAM1339	FLJ21135	3'	ACAGGCGCCCCACCACCAC 45883	A	T_
			GTGGT GTG GTGCCTGT		
			CACCA CAC CGCGGACA		
			C CC		
GAM1339	FLJ21290	3'	CAAGCACACACACAC 46741	GGTA	C
			GTGT GTGTGTGC TG		
			CACA CACACACG AC		
			_____ A		
GAM1339	FLJ21324	5'	TACAGGCATGCGCCACCACGCT 91209		A
	CA		TGAGTGTGGT GTGTGTGCCTGTA		

		ACTCGCACCA CGCGTACGGACAT			
		C			
GAM1339	FLJ22684	3'	TACAGGCACCTGCCACCACATC 46799	AG	A T
	CA		TG TGTGGT GTG GTGCCTGTA		
			AC ACACCA CGT CACGGACAT		
			CT C C		
GAM1339	FLJ22794	3'	TACAGGCAAACGCCACCACACC 91610	A	A G
	CA		TG GTGTGGT GTGT TGCCTGTA		
			AC CACACCA CGCA ACGGACAT		
			C C A		
GAM1339	FLJ23024	3'	TACAGGCATGAGCCACCTCACC 46272	A T	A G
	CA		TG GTG GGT GT TGTGCCTGTA		
			AC CAC CCA CG GTACGGACAT		
			C T C A		
GAM1339	FLJ23556	3'	TACAGGCGTGAGCCACTACACC 45957	A	A GTG
	CA		TG GTGTGGT GT TGCCTGTA		
			AC CACATCA CG GCGGACAT		
			C C AGT		
GAM1339	FLJ31101	3'	TACAGGCACCTGCCACCACGCC 35715	A	A T
	CA		TG GTGTGGT GTG GTGCCTGTA		
			AC CGCACCA CGT CACGGACAT		
			C C C		
GAM1339	FLJ32865	3'	TACAGGCATGCACCACCACGCC 58180	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CGCACCA CACGTACGGACAT		
			C C		
GAM1339	GNG4	3'	TACAGGCGTGAGCCACCACACC 15622	A	A GTG
	CG		TG GTGTGGT GT TGCCTGTA		
			GC CACACCA CG GCGGACAT		
			C C AGT		
GAM1339	GOLPH2	3'	ACAGGCACACAGTCAC 33319		TAG
			GTGG TGTGTGCCTGT		
			CACT ACACACGGACA		
			G_		
GAM1339	GRWD	3'	TACAGGCATGTGCCACCACAC 48971		A TG
			GTGTGGT G TGTGCCTGTA		
			CACACCA C GTACGGACAT		
			C GT		
GAM1339	HSMPP8	3'	TACAGGCATGAGCCACCGCACC 93482	A	A G
	CA		TG GTGTGGT GT TGTGCCTGTA		

AC CACGCCA CG GTACGGACAT  
 C C A  
 GAM1339 IGF2AS 3' ACAGGCACAGCAGCTCACCTCA 33093 T \_ A G  
 TGAG GTG GT GT TGTGCCTGT  
 |||| ||| || || |||||  
 ACTC CAC CG CG ACACGGACA  
 \_ T A \_  
 GAM1339 KIAA0087 3' ACAAACACACACCCACAGAACT 28691 \_ TA CC  
 CA TGAGT GTGG GTGTGTG TGT  
 |||| ||| ||||| |||  
 ACTCA CACC CACACAC ACA  
 AGA \_ AA  
 GAM1339 KIAA0125 5' TACAGACACACAGCAGAGCCAC 28903 A\_\_ C  
 AC GTGTGGT G TGTGTG CTGTA  
 ||||| | ||||| |||||  
 CACACCG C ACACAC GACAT  
 AGA G A  
 GAM1339 KIAA0161 3' TACAGGCACCCACCACCTCACC 28513 A T A T  
 CA TG GTG GGT GTG GTGCCTGTA  
 || ||| ||| |||||  
 AC CAC CCA CAC CACGGACAT  
 C T C C  
 GAM1339 KIAA0337 3' TACAGACACACACGTACGCACA 28837 \_ \_ \_ C  
 CTGCA TG AGTGTG GTA GTGTGTG CTGTA  
 || ||||| ||| ||||| |||||  
 AC TCACAC CAT CACACAC GACAT  
 G G G A  
 GAM1339 KIAA0469 3' TACAGGCGTGTGCCACCACACC 29348 A A TG  
 CA TG GTGTGGT GTG TGCCTGTA  
 || ||||| ||| |||||  
 AC CACACCA CGT GCGGACAT  
 C C GT  
 GAM1339 KIAA0469 3' TACAGGTACCCACCACCACGCC 29349 A A T  
 CA TG GTGTGGT GTG GTGCCTGTA  
 || ||||| ||| |||||  
 AC CGCACCA CAC CATGGACAT  
 C C C  
 GAM1339 KIAA0472 5' TACAGGCTTGTGCCACCACACT 71869 A TG T  
 CA TGAGTGTGGT G TG GCCTGTA  
 ||||| ||| || |||||  
 ACTCACACCA C GT CGGACAT  
 C GT T  
 GAM1339 KIAA0599 3' TACAGGCATGAGCCACCACACC 77188 A A G  
 CA TG GTGTGGT GT TGTGCCTGTA  
 || ||||| || |||||  
 AC CACACCA CG GTACGGACAT  
 C C A  
 GAM1339 KIAA0737 3' TACAGGCATGAGCCACCGCACC 29146 A A G  
 CA TG GTGTGGT GT TGTGCCTGTA  
 || ||||| || |||||

			AC CACGCCA CG GTACGGACAT		
			C C A		
GAM1339	KIAA0841	3'	TACAGGTACGCACCACCACGCC 71395	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CGCACCA CACGCATGGACAT		
			C C		
GAM1339	KIAA1198	3'	TACAGGCACATGCCACCACGCC 63329	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CGCACCA CGTACACGGACAT		
			C C		
GAM1339	KIAA1198	3'	TACAGGCGTGAGCCACCACACC 63330	A	A GTG
	CG		TG GTGTGGT GT TGCCTGTA		
			GC CACACCA CG GCGGACAT		
			C C AGT		
GAM1339	KIAA1373	3'	TACAGGCGTGACCACCACGCC 70950	A	A TG
	CA		TG GTGTGGT GTG TGCCTGTA		
			AC CGCACCA CAC GCGGACAT		
			C C GT		
GAM1339	KIAA1443	3'	TACAGGCACCTGCCACCACACC 63840	A	A T
	CG		TG GTGTGGT GTG GTGCCTGTA		
			GC CACACCA CGT CACGGACAT		
			C C C		
GAM1339	KIAA1493	3'	TACAGGCGCCTGCCACCACACC 64164	A	A T
	CA		TG GTGTGGT GTG GTGCCTGTA		
			AC CACACCA CGT CGCGGACAT		
			C C C		
GAM1339	KIAA1493	3'	TACAGGCGTAAGCCACCACACC 64165	A	A G
	CA		TG GTGTGGT GT TGTGCCTGTA		
			AC CACACCA CG ATGCGGACAT		
			C C A		
GAM1339	KIAA1530	3'	TACAGGCACACACCACAACAC 67960	G	A
			GTGT GT GTGTGTGCCTGTA		
			CACA CA CACACACGGACAT		
			A C		
GAM1339	KIAA1530	3'	TACAGGCGCGCACCACCACGCC 67961	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CGCACCA CACGCGCGGACAT		
			C C		
GAM1339	KIAA1530	3'	TACAGGTGTGAGCCACCGCACT 67962		A G TG
	CA		TGAGTGTGGT GT TG CCTGTA		

			ACTCACGCCA CG GT GGACAT		
			C A GT		
GAM1339	KIAA1559	3'	TACAGGTATGAGCCACCACACC 73075	A	A G
	CA		TG GTGTGGT GT TGTGCCTGTA		
			AC CACACCA CG GTATGGACAT		
			C C A		
GAM1339	KIAA1615	3'	TACAGGCATGAGCCACCGCACCC 68725	A	A G
	CA		TG GTGTGGT GT TGTGCCTGTA		
			AC CACGCCA CG GTACGGACAT		
			C C A		
GAM1339	KIAA1737	3'	TACAGGCCTGAGCCACCACGCT 67361		A GTGT
	CA		TGAGTGTGGT GT GCCTGTA		
			ACTCGCACCA CG CGGACAT		
			C AGTC		
GAM1339	KIAA1784	3'	TACAGGCACACGCTGCCACGCC 65153	A	
	CA		TG GTGTGGTAGTGTGTGCCTGTA		
			AC CGCACCGTCGCACACGGACAT		
			C		
GAM1339	KIAA1821	3'	TACAGGCATGCACCACCACGCC 71795	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CGCACCA CACGTACGGACAT		
			C C		
GAM1339	KIAA1877	3'	TACAGGCACCCGCCACCACGCC 66177	A	A T
	CA		TG GTGTGGT GTG GTGCCTGTA		
			AC CGCACCA CGC CACGGACAT		
			C C C		
GAM1339	KIAA1922	5'	TACAGGCATGTGCCACCACACC 73640	A	A TG
	CG		TG GTGTGGT G TGTGCCTGTA		
			GC CACACCA C GTACGGACAT		
			C C GT		
GAM1339	KIAA1971	3'	TACAGGTGTGAGCCACCACGCC 74226	A	A G TG
	CA		TG GTGTGGT GT TG CCTGTA		
			AC CGCACCA CG GT GGACAT		
			C C A GT		
GAM1339	KLK7	3'	TACAGGTGTGCACCACCACACC 17295	A	A TG
	A		TG GTGTGGT GTGTG CCTGTA		
			AC CACACCA CACGT GGACAT		
			_ C GT		
GAM1339	KLK7	3'	TACAGGTGTGCACCACCACACC 57735	A	A TG
	A		TG GTGTGGT GTGTG CCTGTA		

			AC CACACCA CACGT GGACAT		
			— C GT		
GAM1339	LAMP3	3'	TACAGGCACACACTACCACGC 59493		
			GTGTGGTAGTGTGTGCCTGTA		
			CGCACCATCACACACGGACAT		
GAM1339	MAP-1	3'	TACAGGCATGTGCCACCACGCC 42184	A	A TG
	CA		TG GTGTGGT G TGTGCCTGTA		
			AC CGCACCA C GTACGGACAT		
			C C GT		
GAM1339	MEF-2	3'	TACAGGCGCGAGCCACCACACC 64393	A	A G
	CG		TG GTGTGGT GT TGTGCCTGTA		
			GC CACACCA CG GCGCGGACAT		
			C C A		
GAM1339	MGC2603	3'	TACAGGCATGCGCCACCACGCC 43861	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CGCACCA CGCGTACGGACAT		
			C C		
GAM1339	MGC5149	3'	TACAGGCACGTGCCACCACGCC 72296	A	A TG
	CA		TG GTGTGGT G TGTGCCTGTA		
			AC CGCACCA C GCACGGACAT		
			C C GT		
GAM1339	MMPL1	3'	TACAGGCATGAGCCACCACACC 14721	A	A G
	CA		TG GTGTGGT GT TGTGCCTGTA		
			AC CACACCA CG GTACGGACAT		
			C C A		
GAM1339	MOCS3	3'	TACAGGCGTGAGCCACCACAC 27155	A	GTG
			GTGTGGT GT TGCCTGTA		
			CACACCA CG GCGGACAT		
			C AGT		
GAM1339	MRPL44	3'	TACAGGCACACACCACCATAC 43324	A	
			GTGTGGT GTGTGTGCCTGTA		
			CATACCA CACACACGGACAT		
			C		
GAM1339	MtFMT	3'	TACAGGCACACGCCACCACACG 57656	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CACACCA CGCACACGGACAT		
			G C		
GAM1339	MYO5C	3'	TACAGGCACCTGCCACCACGCC 38109	A	A T
	CA		TG GTGTGGT GTG GTGCCTGTA		

			AC CGCACCA CGT CACGGACAT		
			C C C		
GAM1339	PRO0365	5'	TACAGGCACCTGCCACCACGCC 26168	A	A T
	CA		TG GTGTGGT GTG GTGCCTGTA		
			AC CGCACCA CGT CACGGACAT		
			C C C		
GAM1339	RAB33B	3'	TACAGGCGTGCACTACCACACC 48504	A	TG
	CA		TG GTGTGGTAGTG TGCCTGTA		
			AC CACACCATCAC GCGGACAT		
			C GT		
GAM1339	RES4-25	3'	TACAGACATGTGCCACCACGCC 64653	A	A TG C
	CA		TG GTGTGGT G TGTG CTGTA		
			AC CGCACCA C GTAC GACAT		
			C C GT A		
GAM1339	RNF8	3'	TACAGGCATATGCCATCACACC 14238	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CACACTA CGTATACGGACAT		
			C C		
GAM1339	RNF8	3'	TACAGGCGTGAGCCACCACGCC 14239	A	A GTG
	CA		TG GTGTGGT GT TGCCTGTA		
			AC CGCACCA CG GCGGACAT		
			C C AGT		
GAM1339	SBBI31	3'	ACAGACACACACTGCTA 25875		C
			TGGTAGTGTGTG CTGT		
			ATCGTCACACAC GACA		
			A		
GAM1339	SC4MOL	3'	TACAGGCACCCGCCACCACGCC 22160	A	A T
	CA		TG GTGTGGT GTG GTGCCTGTA		
			AC CGCACCA CGC CACGGACAT		
			C C C		
GAM1339	SCYA22	3'	TACAGGCGTGAGCTATCACACC 90954	A	GTG
	CA		TG GTGTGGTAGT TGCCTGTA		
			AC CACACTATCG GCGGACAT		
			C AGT		
GAM1339	SDC3	3'	ACAGACACCATTGCCCACT 27736	_	T C
			AGTGTGG TAGTG GTG CTGT		
			TCACACC GTTAC CAC GACA		
			C _ A		
GAM1339	SERF1B	3'	TACAGGCGCCTGCCACCACGCC 43420	A	A T
	CA		TG GTGTGGT GTG GTGCCTGTA		



			AC CGCACCA CGT CGCGGACAT		
			C C C		
GAM1339	SFXN2	3'	TACAGGCATGAGCCACCACACC 73953	A	A G
	CA		TG GTGTGGT GT TGTGCCTGTA		
			AC CACACCA CG GTACGGACAT		
			C C A		
GAM1339	SIRPB1	3'	TACAGGCATGTACCACCACACC 20262	A	A TG
	CA		TG GTGTGGT GTG TGCCTGTA		
			AC CACACCA CAT ACGGACAT		
			C C GT		
GAM1339	SLC16A4	3'	TACAGGCACACGCCACCACACC 16283	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CACACCA CGCACACGGACAT		
			C C		
GAM1339	SLC2A10	3'	TACAGGCGCGTGCCACCACACC 47824	A	A TG
	CA		TG GTGTGGT G TGTGCCTGTA		
			AC CACACCA C GCGCGGACAT		
			C C GT		
GAM1339	SSX5	3'	ACACACACACATGCCACAC 40672	—	CC
			GTGTGGTA GTGTGTG TGT		
			CACACCGT CACACAC ACA		
			A —		
GAM1339	SUN1	3'	TACAGGCGCACACCACCACACC 47160	A	A
	CA		TG GTGTGGT GTGTGTGCCTGTA		
			AC CACACCA CACACGCGGACAT		
			C C		
GAM1339	TADA3L	3'	TACAGGCACCCACCACCACGCC 55998	A	A T
	CA		TG GTGTGGT GTG GTGCCTGTA		
			AC CGCACCA CAC CACGGACAT		
			C C C		
GAM1339	TCL6	3'	TACAGGTGTGAGCCACCACTC 40114	—	AGTG TG
			GAGTG TGGT TG CCTGTA		
			CTCAC ACCG GT GGACAT		
			C A__ GT		
GAM1339	TCL6	3'	TACAGGTGTGAGCCACCACTC 40145	—	AGTG TG
			GAGTG TGGT TG CCTGTA		
			CTCAC ACCG GT GGACAT		
			C A__ GT		
GAM1339	TOB2	3'	ACAGGCACCCACCCACACCA 95614	A	TA T
			TG GTGTGG GTG GTGCCTGT		

AC CACACC CAC CACGGACA  
 — — C  
 GAM1339 TRIP-Br2 3' ACAGGCACACACATGCACACAC 28574 A — —  
 CCA TG GTGTG GTA GTGTGTGCCTGT  
 || ||||| ||| |||||  
 AC CACAC CGT CACACACGGACA  
 C A A  
 GAM1339 TU12B1-TY 3' TACAGGCATGCACTACCACACC 33401 A  
 CA TG GTGTGGTAGTGTGTGCCTGTA  
 || |||||  
 AC CACACCATCACGTACGGACAT  
 C  
 GAM1339 TU12B1-TY 3' TACAGGTGCCCACCACCACATC 33402 AG A T TG  
 CA TG TGTGGT GTG G CCTGTA  
 || ||||| ||| |||||  
 AC ACACCA CAC C GGACAT  
 CT C C GT  
 GAM1339 UBF-fl 3' TACACACCACCACGCCCA 51570 A A  
 TG GTGTGGT GTGTGTG  
 || ||||| |||||  
 AC CGCACCA CACACAT  
 C C  
 GAM1339 VMP 3' TACAGGCACCTGCCACCAC 54901 — TGT  
 GTG TGGTAG GTGCCTGTA  
 ||| ||||| |||||  
 CAC ACCGTC CACGGACAT  
 C —  
 GAM1339 VPS33A 3' TACAGGCATGCACCACCACACC 43342 A A  
 CG TG GTGTGGT GTGTGTGCCTGTA  
 || ||||| |||||  
 GC CACACCA CACGTACGGACAT  
 C C  
 GAM1339 ZNF221 3' TACAGGTGCCCCGCCACCACACC 25339 A A T TG  
 CA TG GTGTGGT GTG G CCTGTA  
 || ||||| ||| |||||  
 AC CACACCA CGC C GGACAT  
 C C C GT  
 GAM1339 ZTL1 3' TACAGGCACCCACCACCACACC 43918 A A T  
 CA TG GTGTGGT GTG GTGCCTGTA  
 || ||||| ||| |||||  
 AC CACACCA CAC CACGGACAT  
 C C C  
 GAM1339 LOC112817 3' TACAGGCGCCTGCCACCACGCC 56516 A A T  
 CA TG GTGTGGT GTG GTGCCTGTA  
 || ||||| ||| |||||  
 AC CGCACCA CGT CGCGGACAT  
 C C C  
 GAM1339 LOC124216 3' TACAGGCATGCACCACCACAC 74266 A  
 GTGTGGT GTGTGTGCCTGTA  
 ||||| |||||

		CACACCA CACGTACGGACAT			
		C			
GAM1339	LOC128077 3'	TACAGGTGCCCACCACCACGCC 74717	A	A	T TG
	CA	TG GTGTGGT GTG G CCTGTA			
		AC CGCACCA CAC C GGACAT			
		C C C GT			
GAM1339	LOC128989 3'	ACAAGCACACACATGCAAGCCA 74798	A	GTG	_ C
		TG GT GTA GTGTGTGC TGT			
		AC CG CGT CACACACG ACA			
		_ AA_ A A			
GAM1339	LOC128989 3'	CAGACACACACAC 74807	GGTA	C	
		GTGT GTGTGTG CTG			
		CACA CACACAC GAC			
		_____ A			
GAM1339	LOC132241 3'	TACAGGCATGCGCCACCACACC 75053	A	A	
	CA	TG GTGTGGT GTGTGTGCCTGTA			
		AC CACACCA CGCGTACGGACAT			
		C C			
GAM1339	LOC143187 3'	TACAGGCACACACCACCACGCC 59100	A	A	
	CA	TG GTGTGGT GTGTGTGCCTGTA			
		AC CGCACCA CACACACGGACAT			
		C C			
GAM1339	LOC145453 5'	TACAGGCATGAGCCACCACGCC 77146	A	A	G
	CA	TG GTGTGGT GT TGTGCCTGTA			
		AC CGCACCA CG GTACGGACAT			
		C C A			
GAM1339	LOC146229 3'	TACAGGCGCCACCTCCACACC 77770	A	TA	T
	CA	TG GTGTGG GTG GTGCCTGTA			
		AC CACACC CAC CGCGGACAT			
		C TC C			
GAM1339	LOC146346 5'	TACAGGCATGCACCACCACACC 77845	A	A	
	CA	TG GTGTGGT GTGTGTGCCTGTA			
		AC CACACCA CACGTACGGACAT			
		C C			
GAM1339	LOC146784 5'	TACAGGCATGAGCCACCACGCC 78124	A	A	G
	CA	TG GTGTGGT GT TGTGCCTGTA			
		AC CGCACCA CG GTACGGACAT			
		C C A			
GAM1339	LOC146909 3'	TACAGGCACCCATCACCACACC 78182	A	A	T
	CA	TG GTGTGGT GTG GTGCCTGTA			

		AC CACACCA TAC CACGGACAT		
		C C C		
GAM1339	LOC147671 3'	ACAGGCACCCACCCACACCA	78462	A TA T
		TG GTGTGG GTG GTGCCTGT		
		AC CACACC CAC CACGGACA		
		— — C		
GAM1339	LOC147841 3'	TACAGGCATGCGCCACCACACC	78532	A A
	CA	TG GTGTGGT GTGTGTGCCTGTA		
		AC CACACCA CGCGTACGGACAT		
		C C		
GAM1339	LOC147929 5'	ACAGGCACACGTGTGCACACAC	78572	_ GT_
		GTGTG GTA GTGTGCCTGT		
		CACAC CGT CACACGGACA		
		A GTG		
GAM1339	LOC148189 5'	TACAGGCATGCGCCACCACGCC	78720	A A
	CA	TG GTGTGGT GTGTGTGCCTGTA		
		AC CGCACCA CGCGTACGGACAT		
		C C		
GAM1339	LOC148203 3'	ACAGACACACAGACGTGCACAC	78728	_ G_ C
	AC	GTGTG GTA TGTGTG CTGT		
		CACAC CGT ACACAC GACA		
		A GCAG A		
GAM1339	LOC149577 3'	TACAGGTGTGTGCCACCACACC	84519	A A TG TG
	CG	TG GTGTGGT G TG CCTGTA		
		GC CACACCA C GT GGACAT		
		C C GT GT		
GAM1339	LOC150225 3'	TACAGGCACACGCCACCACACC	85011	A A
	CA	TG GTGTGGT GTGTGTGCCTGTA		
		AC CACACCA CGCACACGGACAT		
		C C		
GAM1339	LOC150960 3'	TACAGGCATGAGCCACCGCACC	80070	A A G
	CA	TG GTGTGGT GT TGTGCCTGTA		
		AC CACGCCA CG GTACGGACAT		
		C C A		
GAM1339	LOC151201 3'	TACAGGCGTGAGCCACCACGCC	85288	A A GTG
	CA	TG GTGTGGT GT TGCCTGTA		
		AC CGCACCA CG GCGGACAT		
		C C AGT		
GAM1339	LOC151568 5'	ACAGGCACAACTCCCCACCC	56688	A T T G
	A	TG GTG GG AGT TGTGCCTGT		

		AC CAC CC TCA ACACGGACA		
		C C C A		
GAM1339	LOC151701 3'	TACAGGCATGCACCACCACACT 85488	A	
	CA	TGAGTGTGGT GTGTGTGCCTGTA		
		ACTCACACCA CACGTACGGACAT		
		C		
GAM1339	LOC151826 3'	TACAGGCACATGCCACCACACC 80363	A	A
	CA	TG GTGTGGT GTGTGTGCCTGTA		
		AC CACACCA CGTACACGGACAT		
		C C		
GAM1339	LOC152137 3'	TACAGGCATGTGTCACCACACC 80483	A	A TG
	CG	TG GTGTGGT G TGTGCCTGTA		
		GC CACACCA T GTACGGACAT		
		C C GT		
GAM1339	LOC152220 3'	ACAGGCACCCGCCACCACACCC 85577	A	A T
	A	TG GTGTGGT GTG GTGCCTGT		
		AC CACACCA CGC CACGGACA		
		C C C		
GAM1339	LOC152343 3'	TACAGGTGTGCACCACCACACC 80569	A	A TG
	CA	TG GTGTGGT GTGTG CCTGTA		
		AC CACACCA CACGT GGACAT		
		C C GT		
GAM1339	LOC152620 3'	TACAGGCACACACAACCACGCC 60085	A	A
	CA	TG GTGTGGT GTGTGTGCCTGTA		
		AC CGCACCA CACACACGGACAT		
		C A		
GAM1339	LOC153077 3'	TACAGGCGCATGCCACCACACC 85914	A	A
	CG	TG GTGTGGT GTGTGTGCCTGTA		
		GC CACACCA CGTACGCGGACAT		
		C C		
GAM1339	LOC153883 5'	TACAGGCACATGCCACCACAC 80984	A	
		GTGTGGT GTGTGTGCCTGTA		
		CACACCA CGTACACGGACAT		
		C		
GAM1339	LOC154739 3'	TACAGGCATGTGCCACCACACT 86238	A TG	
		AGTGTGGT G TGTGCCTGTA		
		TCACACCA C GTACGGACAT		
		C GT		
GAM1339	LOC154790 5'	ACAGGCAGGCAGTACTGCCACA 81146	A	___ G
	CCCA	TG GTGTGGTAGT GT TGCCTGT		

		AC CACACCGTCA CG ACGGACA		
		C TGA G		
GAM1339	LOC154877 3'	TACAGGCGTGAGCCACCACACC 86307	A	A GTG
	CG	TG GTGTGGT GT TGCCTGTA		
		GC CACACCA CG GCGGACAT		
		C C AGT		
GAM1339	LOC157506 3'	TACAGGCATGCGCCACCACGCC 81445	A	A
	CA	TG GTGTGGT GTGTGTGCCTGTA		
		AC CGCACCA CGCGTACGGACAT		
		C C		
GAM1339	LOC157507 5'	TACAGGCATGAGCCACCAAACC 81460	A G	A G
	CA	TG GT TGGT GT TGTGCCTGTA		
		AC CA ACCA CG GTACGGACAT		
		C A C A		
GAM1339	LOC158310 5'	TACAGGCATGCACCACCACAC 86762	A	
		GTGTGGT GTGTGTGCCTGTA		
		CACACCA CACGTACGGACAT		
		C		
GAM1339	LOC158709 3'	TACAGGCGTGAGCCACCGCACC 81984	A	A GTG
	CA	TG GTGTGGT GT TGCCTGTA		
		AC CACGCCA CG GCGGACAT		
		C C AGT		
GAM1339	LOC169611 3'	TACAGCACCCACCACCACACC 82775	A	A T C
	A	TG GTGTGGT GTG GTGC TGTA		
		AC CACACCA CAC CACG ACAT		
		C C C _		
GAM1339	LOC196264 3'	TACAGGCATGCGCCACCACACC 87611	A	A
	CA	TG GTGTGGT GTGTGTGCCTGTA		
		AC CACACCA CGCGTACGGACAT		
		C C		
GAM1339	LOC197358 3'	TACAGGCACGCACCACCACACC 88046	A	A
	CA	TG GTGTGGT GTGTGTGCCTGTA		
		AC CACACCA CACGCACGGACAT		
		C C		
GAM1339	LOC200268 3'	TACAAGTACACACTACCACGCC 88688	A	C
	CA	TG GTGTGGTAGTGTGTGC TGTA		
		AC CGCACCATCACACATG ACAT		
		C A		
GAM1339	LOC200314 3'	CAGGCACACGACACCA 90004	AG	
		TGGT TGTGTGCCTG		

		ACCA GCACACGGAC		
		CA		
GAM1339	LOC200845 5'	TACAGGTGCCACCACACGCC 88905	A	A T TG
	CA	TG GTGTGGT GTG G CCTGTA		
		AC CGCACCA CAC C GGACAT		
		C C C GT		
GAM1339	LOC200860 3'	TACAGGCATGCGCCACCACACC 90172	A	A
	CG	TG GTGTGGT GTGTGTGCCTGTA		
		GC CACACCA CGCGTACGGACAT		
		C C		
GAM1339	LOC201696 3'	TACAGGCATGCGCTAACACACC 63137	A	G
	CA	TG GTGTG TAGTGTGTGCCTGTA		
		AC CACAC ATCGCGTACGGACAT		
		C A		
GAM1339	LOC202459 5'	TACAGGCGTGACCATCACACC 59254	A	A TG
	CA	TG GTGTGGT GTG TGCCTGTA		
		AC CACACTA CAC GCGGACAT		
		C C GT		
GAM1339	LOC203276 3'	TACAGGCATGTGCCACCACACT 90488		A TG
	C	GAGTGTGGT G TGTGCCTGTA		
		CTCACACCA C GTACGGACAT		
		C GT		
GAM1339	LOC203305 3'	TACAGGCATGTGCCACCACACT 90532		A TG
	C	GAGTGTGGT G TGTGCCTGTA		
		CTCACACCA C GTACGGACAT		
		C GT		
GAM1339	LOC203427 3'	TAGGTGCACACCACCACAC 89360	A	TG
		GTGTGGT GTGTG CCTG		
		CACACCA CACAC GGAT		
		C GT		
GAM1339	LOC219673 3'	ACAAGCACATACCACCACAGCC 93017	AG	A C
	A	TG TGTGGT GTGTGTGC TGT		
		AC ACACCA CATAACG ACA		
		CG C A		
GAM1339	LOC219731 5'	TACAGGCTTGCACTACCACACC 93098	A	T
	CA	TG GTGTGGTAGTGTG GCCTGTA		
		AC CACACCATCACGT CGGACAT		
		C T		
GAM1339	LOC219735 3'	TACAGGCGCCTGCCACCACACC 93114	A	A T
	CG	TG GTGTGGT GTG GTGCCTGTA		

		GC CACACCA CGT CGCGGACAT		
		C C C		
GAM1339	LOC220074 3'	TACAGGCGCCTGCTACCACATC 59280	AG	T
	CA	TG TGTGGTAGTG GTGCCTGTA		
		AC ACACCATCGT CGCGGACAT		
		CT C		
GAM1339	LOC220575 3'	TACAGGCATGGGCCACCACACC 76316	A	A G
	CA	TG GTGTGGT GT TGTGCCTGTA		
		AC CACACCA CG GTACGGACAT		
		C C G		
GAM1339	LOC220662 3'	TACAGGCCACACTACCACACC 91178	A	T
	CG	TG GTGTGGTAGTGTG GCCTGTA		
		GC CACACCATCACAC CGGACAT		
		C C		
GAM1339	LOC221035 3'	TACAGGCGTGAGCCACCGCACC 93168	A	A GTG
	CA	TG GTGTGGT GT TGCCTGTA		
		AC CACGCCA CG GCGGACAT		
		C C AGT		
GAM1339	LOC221756 3'	CACGTTTACACTCCACACTCA 92136	T	T C
		TGAGTGTGG AGTGTG GC TG		
		ACTCACACC TCACAT TG AC		
		- T C		
GAM1339	LOC253805 3'	TACAGGCATGCGCCACCATAACC 96435	A	A
	CA	TG GTGTGGT GTGTGTGCCTGTA		
		AC CATAcca CGCGTACGGACAT		
		C C		
GAM1339	LOC254243 3'	TACAGGCATGTGCCACCACACT 97418		A TG
	C	GAGTGTGGT G TGTGCCTGTA		
		CTCACACCA C GTACGGACAT		
		C GT		
GAM1339	LOC254685 3'	TACAGGCACGCACCACGACACC 96488	A	G A
	CA	TG GTGT GT GTGTGTGCCTGTA		
		AC CACA CA CACGCACGGACAT		
		C G C		
GAM1339	LOC255707 3'	TACAGGCGTGAGCCACCAAACC 96962	A G	A GTG
	CA	TG GT TGGT GT TGCCTGTA		
		AC CA ACCA CG GCGGACAT		
		C A C AGT		
GAM1339	LOC257465 3'	TACAGGCGCGTGCCACCACGCC 81600	A	A TG
	CA	TG GTGTGGT G TGTGCCTGTA		



			AC CGCACCA C GCGCGGACAT		
			C C GT		
GAM1339	LOC89932	3'	TACAGGCATGAGCCACCACGCC 60813	A	A G
	CA		TG GTGTGGT GT TGTGCCTGTA		
			AC CGCACCA CG GTACGGACAT		
			C C A		
GAM1339	LOC90038	3'	TACAGGCATGTGCCACCACACT 61160		A TG
	C		GAGTGTGGT G TGTGCCTGTA		
			CTCACACCA C GTACGGACAT		
			C GT		
GAM1339	LOC90459	3'	TACAGGCGCGTGCCACCACACC 62891	A	A TG
	CG		TG GTGTGGT G TGTGCCTGTA		
			GC CACACCA C GCGCGGACAT		
			C C GT		
GAM1339	LOC91250	5'	TACAGGCATCAGCCACCACACC 65326	A	A GT
	CA		TG GTGTGGT GT GTGCCTGTA		
			AC CACACCA CG TACGGACAT		
			C C AC		
GAM1339	LOC91549	5'	TACAGGTGTGAGCCACCACACC 66427	A	A G TG
	CG		TG GTGTGGT GT TG CCTGTA		
			GC CACACCA CG GT GGACAT		
			C C A GT		
GAM1339	LOC92148	5'	TACAGGTGTGAGCCACCGCACC 68336	A	A G TG
	CA		TG GTGTGGT GT TG CCTGTA		
			AC CACGCCA CG GT GGACAT		
			C C A GT		
GAM1339	LOC92170	3'	ACAGGCACACACAGACACA 68367		GTA
			TGTG GTGTGTGCCTGT		
			ACAC CACACACGGACA		
			AGA		
GAM1339	LOC92689	3'	TACAGGTGTGTGCCACCACGCC 70226	A	A TG TG
	CA		TG GTGTGGT G TG CCTGTA		
			AC CGCACCA C GT GGACAT		
			C C GT GT		
GAM1339	LOC92841	3'	TACAGGCATATGCCACCAC 70719	A	
			GTGGT GTGTGTGCCTGTA		
			CACCA CGTATACGGACAT		
			C		
GAM1340	ABCB10	3'	ATGAACTGCTAGGTATTATT 23886	AG	A
			AATAATAC GGTA GTTCAT		

		TTATTATG TCGT CAAGTA		
		GA _		
GAM1340 BPAG1	3'	GCACCTGTATCATTGAA	31429	A _
		TTCAAT ATACAGG GT		
		AAGTTA TATGTCC CG		
		C A		
GAM1340 EML1	3'	ACCATGTATTATTGAA	59728	G
		TTCAATAATACA GGT		
		AAGTTATTATGT CCA		
		A		
GAM1340 HEM1	5'	ATGAACTTCTCAACACCATTGA	18049	AATACA T
		TCAAT GGG AAGTTCAT		
		AGTTA CTC TTCAAGTA		
		CCACAA _		
GAM1340 TTC3	5'	ATCCTTATTATTGAA	12416	C
		TTCAATAATA AGGGT		
		AAGTTATTAT TCCTA		
		-		
GAM1340 FLJ10468	3'	ATGTTTATCCCTGTTTACTGAA	36144	A T TAAGTT
		TTCA TAA ACAGGG CAT		
		AAGT ATT TGTCCC GTA		
		C _ TATT_		
GAM1340 KIAA1280	5'	AACTTACCCAGATTGAG	69707	AATACA
		TTCAAT GGGTAAGTT		
		GAGTTA CCCATTCAA		
		GA__		
GAM1340 NEUROD6	5'	TGAAAACCTGATTATTGAA	42688	A GGTAAG
		TTCAATAAT CAG TTCA		
		AAGTTATTA GTC AAGT		
		_ AA__		
GAM1340 LOC144202	5'	TGAACTGCACATTGTTGAA	76710	ACAGG A
		TTCAATAAT GTA GTTCA		
		AAGTTGTTA CGT CAAGT		
		CA__ _		
GAM1340 LOC221552	3'	AACTTACCTATCATTTGAA	93804	TAATACA
		TTCAA GGGTAAGTT		
		AAGTT TCCATTCAA		
		TACTA__		
GAM1340 LOC257493	3'	AACTTACCTATCATTTGAA	97799	TAATACA
		TTCAA GGGTAAGTT		

			AAGTT	TCCATTCAA		
			TACTA__			
GAM1340	LOC257609	3'	AACTTACCTATCATTTGAA	97939	TAATACA	
			TTCAA	GGGTAAGTT		
			AAGTT	TCCATTCAA		
			TACTA__			
GAM1340	LOC90768	5'	ATGAACTTACTGCGCCATTTGA	63951	TAATACAG	
	A		TTCAA	GGTAAGTTCAT		
			AAGTT	TCATTCAAGTA		
			TACCGCG_			
GAM1341	CTGF	5'	CAGCCCCGAGACGACAG	8575	G	C
			CTGTCGT	TCGGG	CTG	
			GACAGCA	AGCCC	GAC	
			G	C		
GAM1341	LIF	3'	CAGCATGCTCCGACACAGCAG	9730	C	_ CTGAC
			CTGT	GTGTCGG	GC	GCTG
			GACG	CACAGCC	CG	CGAC
			A	T	TA__	
GAM1341	PK428	5'	CAGCACCAGCATTGCATGACAG	13208	CGG	C AC
			CTGTCGTGT	GC	TG	GCTG
			GACAGTACG	CG	AC	CGAC
			TTA	_	CA	
GAM1341	RAGE	3'	CAAGCCCGACCGGGCCAG	26445	_	T C
			CTG	TCG	GTCGGGC	TG
			GAC	GGC	CAGCCCG	AC
			CG	_	A	
GAM1341	UBE3A	5'	CAGGACCCGACACACCAG	55588	TC	_
			CTG	GTGTCGGG	CCTG	
			GAC	CACAGCCC	GGAC	
			CA	A		
GAM1341	FLJ20671	3'	CAGGCCCGCACAAACA	35517	C	T
			TGT	GTG	CGGGCCTG	
			ACA	CAC	GCCCCGAC	
			A	_		
GAM1341	GFR	3'	AGCATCAAGACAAGACA	24465	G	GGGCC C
			TGTC	TGTC	TGA	GCT
			ACAG	ACAG	ACT	CGA
			A	A__	A	
GAM1341	KIAA0376	3'	CAGCATCAGGCCTGAGGTCAG	65597	TCG	G C
			CTG	T	TCGGGCCTGA	GCTG

GAC G AGTCCGGACT CGAC  
 T\_\_G A  
 GAM1341 KIAA0542 5' CGTCAGGCCCGATGGC 66085 GT  
 GTC GTCGGGCCTGACG  
 ||| |||||  
 CGG TAGCCCGGACTGC  
  
 —  
 GAM1341 KIAA1559 3' CAGGCCTGTACACAG 73060 C T  
 CTGT GTG CGGGCCTG  
 |||| |||||  
 GACA CAC GTCCGGAC  
 \_ T  
 GAM1341 LOC255031 5' CAGCGCCAGGGCCACGACAG 97231 GTC G A  
 CTGTCGT GG CCTG CGCTG  
 ||||| || |||||  
 GACAGCA CC GGAC GCGAC  
 \_ G C  
 GAM1342 AP1G1 3' ACTAATGTCCTCTCCT 6671 G GTA  
 AGGAGAGGA GT TAGT  
 ||||| || |||  
 TCCTCTCCT TA ATCA  
 G \_  
 GAM1342 APBA1 3' ACCATACATTATTTCTTCCC 69914 A \_ A  
 GG GAGGAG GTGTAT GT  
 || ||||| ||||| ||  
 CC CTTCTT TACATA CA  
 \_ TAT C  
 GAM1342 APLP1 3' ACGTGGCACCTCCTCACCTTA 17703 A ATA  
 TAAGG GAGGAGGTGT GT  
 ||||| ||||| ||  
 ATTCC CTCCTCCACG CA  
 A GTG  
 GAM1342 ASTN 3' ACTATCTTCCTCTCTCCT 69328 G TGT  
 AGGAGAG AGG ATAGT  
 ||||| || |||||  
 TCCTCTC TCC TATCA  
 \_ TTC  
 GAM1342 ATP6V1G2 3' ACTACATTTAGCCCCTCTCTT 55318 A GTA\_\_  
 AGGAGAGG GGT TAGT  
 ||||| || |||  
 TTCTCTCC CCG ATCA  
 \_ ATTTAC  
 GAM1342 ATP6V1G2 3' ACTACATTTAGCCCCTCTCTT 56278 A GTA\_\_  
 AGGAGAGG GGT TAGT  
 ||||| || |||  
 TTCTCTCC CCG ATCA  
 \_ ATTTAC  
 GAM1342 BMP1 3' ACTGGTGCTCTCTTCTCC 20412 T \_  
 GGAGAGGAGG GTAT AGT  
 ||||| ||||| |||

			CCTCTTCTCT CGTG TCA		
			_ G		
GAM1342	BMP1	3'	ACTGGTGCTCTTCTCC 6827	T	_
			GGAGAGGAGG GTAT AGT		
			CCTCTTCTCT CGTG TCA		
			_ G		
GAM1342	BMP4	3'	ACTACACAGACTGCTTCCTTA 6829	G G G_	A
			TAAGGA AG AG TGT TAGT		
			ATTCCT TC TC ACA ATCA		
			_ G AG C		
GAM1342	BMP4	3'	ACTACACAGACTGCTTCCTTA 55633	G G G_	A
			TAAGGA AG AG TGT TAGT		
			ATTCCT TC TC ACA ATCA		
			_ G AG C		
GAM1342	BMP4	3'	ACTACACAGACTGCTTCCTTA 55637	G G G_	A
			TAAGGA AG AG TGT TAGT		
			ATTCCT TC TC ACA ATCA		
			_ G AG C		
GAM1342	C14orf1	3'	ACTGTGTCTCCTTCCC 23172	AG	TG
			GG AGGAGG TATAGT		
			CC TCCTCT GTGTCA		
			CT _		
GAM1342	COL6A1	3'	ACTAGCCTCCCTCTCCT 8476	_	GTA
			AGGAGAGG AGGT TAGT		
			TCCTCTCC TCCG ATCA		
			C _		
GAM1342	CRYGS	3'	ACTATAATGCCTCTCCTTA 34075	AGGTG	
			TAAGGAGAGG TATAGT		
			ATTCCTCTCC ATATCA		
			GTA_		
GAM1342	DYSF	3'	ACTGGCCTGCCTCCTCCGCC 13020	A_	TA_
			GG GAGGAGGTG TAGT		
			CC CTCCTCCGT GTCA		
			GC CCG		
GAM1342	ELF3	3'	ACTATGGCCTCGCCTCC 15419	AG	G
			GGAG GAGGT TATAGT		
			CCTC CTCCG GTATCA		
			CG _		
GAM1342	EN2	5'	ACCCCTCCTCTCCTTG 7455	T	
			TAAGGAGAGGAGG GT		

			GTTCCTCTCCTCC CA			
			C			
GAM1342	GLUL	5'	TGCGGCCTCCTCTCCT	9047		—
			AGGAGAGGAGGT GTA			
			TCCTCTCCTCCG CGT			
			G			
GAM1342	HEXA	3'	ACTCATCCACCTCCCTCC	4972	A	T —
			GGAG GGAGGTG AT AGT			
			CCTC CCTCCAC TA TCA			
			— C C			
GAM1342	HIVEP1	3'	ACCCTCCTTTTCCTTA	9199		T
			TAAGGAGAGGAGG GT			
			ATTCCTTTTCCTCC CA			
			—			
GAM1342	LZTFL1	3'	ATATCCCTCTCCTTA	39751	A	
			TAAGGAGAGG GGTGT			
			ATTCCTCTCC CTATA			
			C			
GAM1342	MAF	5'	ACTAAACTCCCCCTCC	18097	A A T A	
			GGAG GG GG GT TAGT			
			CCTC CC CC CA ATCA			
			— C T A			
GAM1342	OCRL	3'	TGTCACCTCCTTCCT	7831	G	T
			AGGA AGGAGGTG ATA			
			TCCT TCCTCCAC TGT			
			— —			
GAM1342	OCRL	3'	TGTCACCTCCTTCCT	4265	G	T
			AGGA AGGAGGTG ATA			
			TCCT TCCTCCAC TGT			
			— —			
GAM1342	PCTK1	3'	TACATCTTCCCTGCTTA	52263	G A	
			TAAG AG GGAGGTGTA			
			ATTC TC CTTCTACAT			
			G C			
GAM1342	PCTK1	3'	TACATCTTCCCTGCTTA	52268	G A	
			TAAG AG GGAGGTGTA			
			ATTC TC CTTCTACAT			
			G C			
GAM1342	PCTK1	3'	TACATCTTCCCTGCTTA	20579	G A	
			TAAG AG GGAGGTGTA			

		ATTC TC CTTCTACAT		
		G C		
GAM1342 PTGS1	3'	ACACCCTCTCCTTA	54567	AG
		TAAGGAGAGG GTGT		
		ATTCCTCTCC CACA		
		—		
GAM1342 PTGS1	3'	ACACCCTCTCCTTA	6348	AG
		TAAGGAGAGG GTGT		
		ATTCCTCTCC CACA		
		—		
GAM1342 RAD50	3'	ACTCTGTGCCTCCCTCC	19190	A TG T
		GGAG GGAGG TA AGT		
		CCTC CCTCC GT TCA		
		— GT C		
GAM1342 RAD50	3'	ACTCTGTGCCTCCCTCC	56004	A TG T
		GGAG GGAGG TA AGT		
		CCTC CCTCC GT TCA		
		— GT C		
GAM1342 SPHK2	3'	ACTAATGTTCTCTCC	39245	G TG A
		GGAGAGGA G T TAGT		
		CCTCTCCT T A ATCA		
		— GT —		
GAM1342 SPRR1B	5'	ACCATACAGAGTATTCCTCTCT	87404	G_____ A
T		AGGAGAGGAG TGTAT GT		
		TTCTCTCCTT ACATA CA		
		ATGAG C		
GAM1342 SYNGR1	3'	ACTATGTCACCTCTCCTCT	16308	AG _
		GGAG GAGGTG TATAGT		
		TCTC CTCCAC GTATCA		
		CT T		
GAM1342 TIRAP	3'	ACTCTGTTCTCTTCCC	53564	A TG T
		GG GAGGAGG TA AGT		
		CC CTTCTCC GT TCA		
		— TT C		
GAM1342 TRPV2	5'	GCAGCCTCCTCCTCCT	32266	— _
		AGGAG AGGAGG TGT		
		TCCTC TCCTCC ACG		
		C G		
GAM1342 AAMP	3'	ACTTGCTCCCCTCTCCTT	6560	A T T
		AAGGAGAGG GG GTA AGT		

TTCCTCTCC CC CGT TCA  
 \_ T \_  
 GAM1342 ARHGEF9 5' ACTTCCTCCTCTCCTT 30804 T\_  
 AAGGAGAGGAGG GT  
 ||||| ||  
 TTCCTCTCCTCC CA  
 TT  
 GAM1342 C1orf17 3' ACTACACGATTTCTTCCC 68209 A \_ A  
 GG GAGGAGGT GT TAGT  
 || ||||| || ||||  
 CC CTTCTTTA CA ATCA  
 \_ G C  
 GAM1342 CX46.6 3' TGCGACCCCTTCTCCT 39945 A \_  
 AGGAGAGG GGT GTA  
 ||||| ||| |||  
 TCCTCTTC CCA CGT  
 C G  
 GAM1342 DKFZP586I2223 3' ACTGGGGCGCTCCTCCCT 54907 A G A\_  
 AGG GAGGAG TGT TAGT  
 ||| ||||| ||| ||||  
 TCC CTCCTC GCG GTCA  
 \_ \_ GG  
 GAM1342 DKFZP586I2223 3' ACTGGGGCGCTCCTCCCT 54915 A G A\_  
 AGG GAGGAG TGT TAGT  
 ||| ||||| ||| ||||  
 TCC CTCCTC GCG GTCA  
 \_ \_ GG  
 GAM1342 DKFZP586I2223 3' ACTGGGGCGCTCCTCCCT 31265 A G A\_  
 AGG GAGGAG TGT TAGT  
 ||| ||||| ||| ||||  
 TCC CTCCTC GCG GTCA  
 \_ \_ GG  
 GAM1342 EFS2 3' ACTAGATCCTTCTCTCCT 19617 TGTA  
 AGGAGAGGAGG TAGT  
 ||||| ||||| ||||  
 TCCTCTCTTCC ATCA  
 TAG\_  
 GAM1342 FLJ11210 3' ACTATACTAATCTTCTC 59573 GGT  
 GAGAGGA GTATAGT  
 ||||| ||||| |||||  
 CTCTTCT CATATCA  
 AAT  
 GAM1342 FLJ12387 3' ACTACCCGGGCGCTCCCTC 43063 A \_ TA  
 GAG GGAGGT G TAGT  
 ||| ||||| | ||||  
 CTC CCTCCG C ATCA  
 C GG CC  
 GAM1342 FLJ12649 3' ACTGCAACCTCCGCCTCCT 44774 A\_ GTA  
 AGGAG GGAGGT TAGT  
 ||||| ||||| |||||



		TCCTC CCTCCA GTCA		
		CG AC_		
GAM1342	FLJ13263	3' CATCTTTCCTCTCCTT 47090	—	
		AAGGAGAGGA GGTG		
		TTCCTCTCCT CTAC		
		TT		
GAM1342	FLJ13544	5' CACCTCTGACCTCTCCTT 46576	—	
		AAGGAGAGG AGGTG		
		TTCCTCTCC TCCAC		
		AGTC		
GAM1342	FLJ20257	3' ACCATCATCTTCCTCTCC 38990	_ T A	
		GGAGAGGA GGTG AT GT		
		CCTCTCCT CTAC TA CA		
		T _ C		
GAM1342	FLJ21432	3' ACTATACTTCCTCCTT 44629	T_	
		GAGGAGG GTATAGT		
		TTCCTCC CATATCA		
		TT		
GAM1342	FREQ	3' ACTGACATCTCCTCCCCT 26569	A A	
		AGG GAGGAGGTGT TAGT		
		TCC CTCCTCTACA GTCA		
		C _		
GAM1342	JAM1	5' ACTGCAACCTCCTCCTCC 57911	_ GTA	
		GGAG AGGAGGT TAGT		
		CCTC TCCTCCA GTCA		
		C AC_		
GAM1342	KIAA0217	3' ACCATACACTTTATTCC 67032	AG A	
		GGAG GAGGTGTAT GT		
		CCTT TTTCACATA CA		
		A_ C		
GAM1342	KIAA0326	3' ACTTGGCTCCCCTCTCCT 64317	A T AT	
		AGGAGAGG GG GT AGT		
		TCCTCTCC CC CG TCA		
		_ T GT		
GAM1342	KIAA0638	3' CTGACACCTGCTCTCC 72396	G A	
		GGAGAG AGGTGT TAG		
		CCTCTC TCCACA GTC		
		G _		
GAM1342	KIAA0776	3' ACTATACAACCTCCCCTCT 64822	A G	
		GGAG GGAG TGTATAGT		

			TCTC CCTC ACATATCA		
			C A		
GAM1342	KIAA0789	3'	ACCATATATCTCCCCTTG	63678	AGA A
			TAAGG GGAGGTGTAT GT		
			GTTCC CCTCTATATA CA		
			— C		
GAM1342	KIAA1170	3'	ACTATACATGTTGCCCTCT	69838	A AG—
			GGAG GG GTGTATAGT		
			TCTC CC TACATATCA		
			C GTTG		
GAM1342	LAP1B	5'	ACGTCCTCCTCCCCCTT	64582	A_ _
			AAGG GAGGAGG TGT		
			TTCC CTCCTCC GCA		
			CC T		
GAM1342	MGC10646	3'	ACTATTCCTCCCTCCCTT	51105	A A TGT
			AAGG GAGG GG ATAGT		
			TTCC CTCC CC TATCA		
			_ _ CCT		
GAM1342	NPTXR	3'	ACTGAGTCCCCCTCCTT	54172	A A TG A
			AAGGAG GG GG T TAGT		
			TTCCTC CC CC G GTCA		
			_ _ CT A		
GAM1342	NPTXR	3'	ACTGAGTCCCCCTCCTT	26636	A A TG A
			AAGGAG GG GG T TAGT		
			TTCCTC CC CC G GTCA		
			_ _ CT A		
GAM1342	OR51E2	3'	TACACTTCTCCTTA	47796	GGA
			TAAGGAGA GGTGTA		
			ATTCCTCT TCACAT		
			—		
GAM1342	PLP1	3'	ACTGGCCCTCTTCTT	5003	T A
			GAGAGGAGG GT TAGT		
			TTCTTCTCC CG GTCA		
			— —		
GAM1342	PLUNC	3'	TGCCCCCTCTCCTT	33426	A T
			AAGGAGAGG GG GTA		
			TTCCTCTCC CC CGT		
			— —		
GAM1342	PLUNC	3'	TGCCCCCTCTCCTT	55642	A T
			AAGGAGAGG GG GTA		

TTCCTCTCC CC CGT

GAM1342 PRO1580 3' ACTCATTCCCTCTCTCTTA 37528 \_ A TGTAT  
TAAG GAGAGG GG AGT  
||||| |||  
ATTCTCTCC CC TCA  
T \_ TTAC\_  
GAM1342 PTD004 3' ACTGTGTACCCCCCCCC 25316 AGA A  
GG GG GGTGTATAGT  
|| |||||  
CC CC CCATGTGTCA  
CCC C  
GAM1342 RACGAP1 3' TATATATCTCCCCTTC 25201 A  
GGAG GGAGGTGTATA  
|||||  
CTTC CCTCTATATAT  
C  
GAM1342 RALGPS1A 3' ACACCTATCTCCTTA 27593 GG  
TAAGGAGA AGGTGT  
|||||  
ATTCCTCT TCCACA  
A\_  
GAM1342 RSHL1 3' ACTATGTGCTTCCTGTCC 47892 G TG  
GGA AGGAGG TATAGT  
||| |||||  
CCT TCCTTC GTATCA  
G GT  
GAM1342 SARM 3' CTGATCCTCCTTTCCT 30604 TGTA  
AGGAGAGGAGG TAG  
||||| |||  
TCCTTTCCTCC GTC  
TA\_  
GAM1342 SLC26A9 3' ACTATGCGCCCCCCTCC 53615 A A  
GGAG GG GGTGTATAGT  
||| |||||  
CCTC CC CCGCGTATCA  
C C  
GAM1342 SLC26A9 3' ACTATGCGCCCCCCTCC 56176 A A  
GGAG GG GGTGTATAGT  
||| |||||  
CCTC CC CCGCGTATCA  
C C  
GAM1342 THTPA 3' ACTGTGCCTCTCCCCTC 44258 A T  
GAG GGAGG GTATAGT  
||| |||||  
CTC CCTCT CGTGTCA  
C C  
GAM1342 TOB2 3' ACTGCCAGCCTCCTCTCC 95615 GTA  
GGAGAGGAGGT TAGT  
||||| |||

			CCTCTCCTCCG	GTCA		
			ACC			
GAM1342	TREX1	3'	ACCACTCCTTTCCTTA	49667	GT	
			TAAGGAGAGGAG	GT		
			ATTCCTTTCCTC	CA		
			AC			
GAM1342	TREX1	3'	ACCACTCCTTTCCTTA	55217	GT	
			TAAGGAGAGGAG	GT		
			ATTCCTTTCCTC	CA		
			AC			
GAM1342	TREX1	5'	ACCACTCCTTTCCTTA	53274	GT	
			TAAGGAGAGGAG	GT		
			ATTCCTTTCCTC	CA		
			AC			
GAM1342	TREX1	5'	ACCACTCCTTTCCTTA	53285	GT	
			TAAGGAGAGGAG	GT		
			ATTCCTTTCCTC	CA		
			AC			
GAM1342	TREX1	5'	ACCACTCCTTTCCTTA	33056	GT	
			TAAGGAGAGGAG	GT		
			ATTCCTTTCCTC	CA		
			AC			
GAM1342	TTC2	3'	ACAGTTCACCTCCTCCCTT	12409	A	T A
			AAGG GAGGAGGTG	AT GT		
			TTCC CTCCTCCAC	TG CA		
			—	T A		
GAM1342	UNC93B1	3'	ACTTTGCACCTCCTATCC	48178	G	T
			GGA AGGAGGTGTA	AGT		
			CCT TCCTCCACGT	TCA		
			A	T		
GAM1342	LOC124739	3'	GCTCACCTCCTGCCCT	74328	AG	TAT
			AGG AGGAGGTG	AGT		
			TCC TCCTCCAC	TCG		
			CG	—		
GAM1342	LOC128439	3'	CTAAGCCCCTTCCCT	57352	A	A T A
			AGG GAGG GG	GT TAG		
			TCC CTTC CC	CG ATC		
			—	—	—	A
GAM1342	LOC129961	5'	ACTATTGAATCCTCTCTCA	75738	A	GGTGT
			A GGAGAGGA	ATAGT		

	A TCTCTCCT TATCA	
	C AAGT_	
GAM1342 LOC143196 3'	ATTGTTAATCCCCTCCTT 82904	A A GT
	AAGGAG GG GGT ATAGT	
	TTCCTC CC CTA TGTTA	
	_ _ AT	
GAM1342 LOC145676 5'	ACTAATCCTCATCTCCT 77330	G TGTA
	AGGAGA GAGG TAGT	
	TCCTCT CTCC ATCA	
	A TA_	
GAM1342 LOC146517 3'	TGCACTCTCTCCTTA 77948	GA
	TAAGGAGAG GGTGTA	
	ATTCCTCTC TCACGT	
	_	
GAM1342 LOC150218 5'	ACTTTTACCTCCTCTCC 79717	TAT
	GGAGAGGAGGTG AGT	
	CCTCTCCTCCAT TCA	
	TT_	
GAM1342 LOC199870 3'	ACTGGACACTTCTCTCC 88429	G A
	GGAGAG AGGTGT TAGT	
	CCTCTC TTCACA GTCA	
	_ G	
GAM1342 LOC219401 5'	ACTACAGCCTCCTCCTCTC 92811	T_ A_
	GAGAGGAGG GT TAGT	
	CTCTCCTCC CG ATCA	
	TC AC	
GAM1342 LOC219722 3'	ACTTGTGCTTCTCTCCT 93078	G TG T
	AGGAGAG AGG TA AGT	
	TCCTCTC TTC GT TCA	
	_ GT _	
GAM1342 LOC221935 3'	ACGCTGGCCCTCTCCTT 92613	A_
	AAGGAGAGG GGTGT	
	TTCCTCTCC TCGCA	
	CGG	
GAM1342 LOC222183 3'	ACTACACAGCTCCCTCC 94163	A G A
	GGAG GGAG TGT TAGT	
	CCTC CCTC ACA ATCA	
	_ G C	
GAM1342 LOC254082 5'	ACTACATTTCTCCTCCC 97201	A T A
	GG GAGGAGG GT TAGT	

CC CTCCTCT TA ATCA  
 \_ T C  
 GAM1342 LOC255913 3' ACTGTTTGACCTCCTCCCC 96124 A GT\_  
 GG GAGGAGGT ATAGT  
 || ||||| ||||  
 CC CTCCTCCA TGTCA  
 C GTT  
 GAM1342 LOC256306 5' ACTCGTGCCTTCCCTCCT 96675 A T \_  
 AGGAG GGAGG GTAT AGT  
 |||| |||| |||| ||  
 TCCTC CCTTC CGTG TCA  
 \_ \_ C  
 GAM1342 LOC84548 3' ACTATTTTTGCTCTCCTTA 71250 G TGT  
 TAAGGAGAG AGG ATAGT  
 ||||| || ||||  
 ATTCCTCTC TTT TATCA  
 G T\_\_  
 GAM1342 LOC90141 3' ACTGGTGGTCCTCCTCCTCCT 61623 \_ TGTA\_  
 AGGAG AGGAGG TAGT  
 |||| |||| ||||  
 TCCTC TCCTCC GTCA  
 C TGGTG  
 GAM1342 LOC90333 3' ACTGCAACCTCCTCCTCC 62279 \_ GTA  
 GGAG AGGAGGT TAGT  
 |||| |||| ||||  
 CCTC TCCTCCA GTCA  
 C AC\_  
 GAM1342 LOC90736 3' ATATTTCTGCCTTA 63902 AG  
 TAAGG AGGAGGTGT  
 |||| |||||  
 ATTCC TCCTTTATA  
 G\_  
 GAM1342 LOC91782 3' ACACCTCCCCTCCTTG 67153 A  
 TAAGGAG GGAGGTGT  
 ||||| |||||  
 GTTCCTC CCTCCACA  
 C  
 GAM1343 AVPR2 3' TCCCTAATAAAAATTGGAGCTC 3545 A TTC\_\_ C A  
 TTT AAAGAGCTC CA TA TAG GA  
 ||||| || || ||||  
 TTTCTCGAG GT AT ATC CT  
 \_ TAAAA A C  
 GAM1343 CYP27B1 3' CTTTGCATGTAAGCTCTT 5776 C TCTAC  
 AAAGAGCT ACAT TAGAG  
 ||||| || ||||  
 TTTCTCGA TGTA GTTTC  
 A C\_\_\_\_  
 GAM1343 DLG5 5' TCTCTGAATGAATGTGAATCTC 82923 C\_ TAC  
 T AGAG TCACATTC TAGAGA  
 |||| ||||| |||||

		TCTC AGTGTAA	GTCTCT		
		TA	TAA		
GAM1343	EGFL5	3'	CTCTAATGTCTCGAGCTTTT	86617	___ TCTAC
			AAAGAGCTC ACAT TAGAG		
			TTTTTCGAG TGTA ATCTC		
			CTC _____		
GAM1343	EIF4EBP2	3'	CTAGTCCCCCAGGAGCTCTTT	14590	ACATTCT
			AAAGAGCTC ACTAG		
			TTTCTCGAG TGATC		
			GACCCCC		
GAM1343	LU	3'	CTCCAGGGAATGTGACTCTCC	18752	A C A A
			A AGAG TCACATTCT CT GAG		
			C TCTC AGTGTAAAGG GA CTC		
			C _ _ C		
GAM1343	MAT2A	3'	TCTATTATGAATGTGAAGCCTT	19789	A _ _ C
			AAG GCT CACATTC TA TAGA		
			TTC CGA GTGTAAG AT ATCT		
			_ A T T		
GAM1343	MMP1	3'	TAGAATGTAGCCCTTT	10062	A C
			AAAG GCT ACATTCTA		
			TTTC CGA TGTAAGAT		
			C _		
GAM1343	MPL	3'	CTGCTACTAGATTGTGAGCTC	18141	T C _
			GAGCTCACA TCTA TAG AG		
			CTCGAGTGT AGAT ATC TC		
			T C G		
GAM1343	PRPSAP2	5'	TCAGTAAACATTGAGCTCTT	10907	CA_ C A
			AAGAGCTCA TT TACT GA		
			TTCTCGAGT AA ATGA CT		
			TAC A _		
GAM1343	TGFBR2	3'	TCTCACTGTAAACATTAGCTCT	12270	CACATTC TA_
	TT		AAAGAGCT TAC GAGA		
			TTTCTCGA ATG CTCT		
			TTACAA_ TCA		
GAM1343	TP63	3'	CTCACCATGTGAGCTCTT	13567	TCTACTA
			AAGAGCTCACAT GAG		
			TTCTCGAGTGTA CTC		
			CCA_____		
GAM1343	YWHAZ	3'	TCTTTTAGAATGTAAGCTC	12705	C CT
			GAGCT ACATTCTA AGA		

			CTCGA TGTAAGAT TCT		
			A TT		
GAM1343	C20orf35	3'	TCTCTAGATGGATGTGAACTC 37482	C	TA
			GAG TCACATTC CTAGAGA		
			CTC AGTGTAGG GATCTCT		
			A TA		
GAM1343	C4.4A	3'	TTACTAGACTGTGAGCTC 26947	T	C
			GAGCTCACA TCTA TAG		
			CTCGAGTGT AGAT ATT		
			C C		
GAM1343	CCRL2	3'	TCTTTACAAACGTGAGCTC 14249		ATTCTAC
			GAGCTCAC TAGAGA		
			CTCGAGTG ATTTCT		
			CAAAC__		
GAM1343	CDIPT	3'	CTCACTAGAATGTAAACTC 20889	CTC	CTA
			GAG ACATTCTA GAG		
			CTC TGTAAGAT CTC		
			AAA CA_		
GAM1343	DMWD	3'	CTGGGCAGGAATGTGGCTC 60879	T	A__
			GAGC CACATTCT CTAG		
			CTCG GTGTAAGG GGTC		
			_ ACG		
GAM1343	FLJ12287	3'	TCTACCAAGCACATGAGCTCT 42319		CATT AC_
			AGAGCTCA CT TAGA		
			TCTCGAGT GA ATCT		
			ACAC ACC		
GAM1343	FLJ12476	5'	TCTCCAGCAGAAGTGAAGTTCT 42954	_ A	A A
	TT		AAAGAGCT CAC TTCT CT GAGA		
			TTTCTTGA GTG AAGA GA CTCT		
			A _ C C		
GAM1343	FLJ14564	3'	CTGGAGAATGTGAGC 76502		A
			GCTCACATTCT CTAG		
			CGAGTGTAAGA GGTC		
			-		
GAM1343	GENX-3414	3'	TCCAGTGAATGTGAACTTCTT 14150	_ C	T A
			AAGA G TCACATTC ACT GA		
			TTCT C AGTGTAAG TGA CT		
			T A _ C		
GAM1343	KIAA0435	3'	TCTCCGAGCCATGTGAGC 28987	T_	ACTA
			GCTCACAT CT GAGA		



		CGAGTGTA GA CTCT		
		CC GC__		
GAM1343	KIAA1706	5' TCCCTAGCCAGAGAGCTCTT 92792	ACAT	A_ A
		AAGAGCTC TCT CTAG GA		
		TTCTCGAG AGA GATC CT		
		____ CC C		
GAM1343	KIAA1954	5' CTAGTGAATGTGAGACCCTT 77717	AG_	T
		AAG CTCACATTCT ACTAG		
		TTC GAGTGTAAG TGATC		
		CCA _		
GAM1343	KLF3	3' CTAAAGAATGTGAACACTTT 33273	AGC	AC
		AAAG TCACATTCT TAG		
		TTTC AGTGTAAGA ATC		
		ACA A_		
GAM1343	MGC2835	3' TGGAAATGTGGGCCCTCC 43964	A A	_
		A AG GCTCACATT CTA		
		C TC CGGGTGTA GGT		
		C C A		
GAM1343	MGC2865	3' CTAGTCGCTGGACAGCTCTTT 50450	CA_	TTCT
		AAAGAGCT CA ACTAG		
		TTTCTCGA GT TGATC		
		CAG CGC_		
GAM1343	MGC4832	3' CTCTTATGTCAGCTCTTT 59002	C	TCTACT
		AAAGAGCT ACAT AGAG		
		TTTCTCGA TGTA TCTC		
		C T_____		
GAM1343	My015	3' CTCTAGAGCTGAGCTCTT 66653	CATT	A
		AAGAGCTCA CT CTAGAG		
		TTCTCGAGT GA GATCTC		
		C_ _		
GAM1343	NPTXR	3' TCTCCAGATTGGGTGTGAGCTT 54187	TA_	A
		GAGCTCACATTCT CT GAGA		
		TTCGAGTGTGGG GA CTCT		
		TTA C		
GAM1343	NPTXR	3' TCTCCAGATTGGGTGTGAGCTT 26651	TA_	A
		GAGCTCACATTCT CT GAGA		
		TTCGAGTGTGGG GA CTCT		
		TTA C		
GAM1343	RAP2B	3' TCTGGTGGAAATGTGGCTCTTT 95824	T	_
		AAAGAGC CACATT CTA TAGA		

TTTCTCG GTGTAA GGTGGTCT  
 \_ A  
 GAM1343 STK36 3' CTTTGTTGCCAGCTCTTT 72104 CA TTCT  
 AAAGAGCT CA ACTAGAG  
 ||||| || |||||  
 TTTCTCGA GT TGGTTTC  
 CC \_\_\_\_  
 GAM1343 LOC124470 3' CTCCATGCTGTGAGCTGCTT 75636 \_ TTCTACTA  
 AAG AGCTCACA GAG  
 || ||||| ||  
 TTC TCGAGTGT CTC  
 G CGTAC\_\_\_\_  
 GAM1343 LOC144695 3' CTCCTACTGTGAGCTCTCC 83180 A TTCTACTA  
 A AGAGCTCACA GAG  
 | ||||| ||  
 C TCTCGAGTGT CTC  
 C CATC\_\_\_\_  
 GAM1343 LOC148936 3' CTCTGTAATCATGTGAGCCCTT 84289 A TC\_ T  
 T AAAG GCTCACAT TAC AGAG  
 ||| ||||| || |||  
 TTTC CGAGTGTA ATG TCTC  
 C CTA \_  
 GAM1343 LOC148938 3' CTCTGTAATCATGTGAGCCCTT 84269 A TC\_ T  
 T AAAG GCTCACAT TAC AGAG  
 ||| ||||| || |||  
 TTTC CGAGTGTA ATG TCTC  
 C CTA \_  
 GAM1343 LOC154789 5' CTCTAGTCTTTTGTGGGCTC 81133 TTCT  
 GAGCTCACA ACTAGAG  
 ||||| |||||  
 CTCGGGTGT TGATCTC  
 TTTC  
 GAM1343 LOC158709 5' TCTCTAGTTTTGCATGCCCTTT 81987 A TCA TTCT  
 AAAG GC CA ACTAGAGA  
 ||| || || |||||  
 TTTC CG GT TGATCTCT  
 C TAC TT\_\_\_\_  
 GAM1343 LOC254428 3' CTCCGCAAGATGAGCTCTCC 95457 A CAT ACTA  
 A AGAGCTCA TCT GAG  
 | ||||| || ||  
 C TCTCGAGT AGA CTC  
 C \_\_\_\_ ACGC  
 GAM1343 LOC254910 3' CTCTCAGACATAGCTCTTT 96789 CACAT ACT  
 AAAGAGCT TCT AGAG  
 ||||| || |||  
 TTTCTCGA AGA TCTC  
 TAC\_\_ C\_\_  
 GAM1343 LOC51104 5' AGCAGAACGCGAGCTCTT 32057 ACA A  
 AAGAGCTC TTCT CT  
 ||||| ||| ||

		TTCTCGAG AAGA GA	
		CGC C	
GAM1343	LOC51580	3' CTCTAGATTGTGTAAGCTTTTT 31862	C TCTA
		AAAGAGCT ACAT CTAGAG	
		TTTTTCGA TGTG GATCTC	
		A TTA_	
GAM1343	LOC93496	3' TCTTTACTAGAATGTGAGCTC 72441	C
		GAGCTCACATTCTA TAGAGA	
		CTCGAGTGTAAGAT ATTTCT	
		C	
GAM1344	ADAR	3' ACTTTCTCCGGCAGCT 6620	CAGTT
		AGCTGCT GGAGAAAGT	
		TCGACGG CCTCTTTCA	
GAM1344	ADAR	3' ACTTTCTCCGGCAGCT 31745	CAGTT
		AGCTGCT GGAGAAAGT	
		TCGACGG CCTCTTTCA	
GAM1344	ADAR	3' ACTTTCTCCGGCAGCT 31755	CAGTT
		AGCTGCT GGAGAAAGT	
		TCGACGG CCTCTTTCA	
GAM1344	ALDH3B2	5' ACTTCCTTCAAGAAAACAAGCA 5501	CAG_____ A
		GCTT AAGCTGCT TTGGAG AAGT	
		TTCGACGA AACTTC TTCA	
		ACAAAAG C	
GAM1344	BAZ1B	3' TCTCCTCTAGAGCAGTT 50541	_ TT
		AGCTGCTC AG GGAGA	
		TTGACGAG TC CCTCT	
		A T_	
GAM1344	BLMH	3' TACTCTCCTCATCTCTAACAGC 4611	CTC_ T GA A
	T	AGCTG AG TG GA AGTA	
		TCGAC TC AC CT TCAT	
		AATC T TC C	
GAM1344	CD2AP	3' TTACTTTCTTTTAATGACCA 24017	C GTT
		TG TCA GGAGAAAGTAA	
		AC AGT TTTCTTTCATT	
		C AAT	
GAM1344	CLCA2	3' CTCCCATCAAAGCAGCTT 21537	CA_ T
		AAGCTGCT GT GGAG	

			TTCGACGA TA CCTC		
			AAC C		
GAM1344	CRACC	3'	ACTTTCATGAGCAGTT 41002	GTTGGA	
			AGCTGCTCA GAAAGT		
			TTGACGAGT CTTTCA		
			A_____		
GAM1344	FETUB	3'	CTCCTAAACTGAGCAGT 26879	___	
			GCTGCTCAGTT GGAG		
			TGACGAGTCAA CCTC		
			AT		
GAM1344	GYS1	3'	CTCCAGCTCCAGTTT 88400	CTC	
			AAGCTG AGTTGGAG		
			TTTGAC TCGACCTC		
			C__		
GAM1344	MAPRE2	3'	ACTTTCGCTTAACTGAAAAGC 26539	GC	A__
	TT		AAGCT TCAGTTGG GAAAGT		
			TTCGA AGTCAATT CTTTCA		
			AA CGC		
GAM1344	PSD	5'	TCACCCACTGGGCAGC 10935	T A	
			GCTGCTCAGT GG GA		
			CGACGGGTCA CC CT		
			C A		
GAM1344	RNMT	3'	ACCTTCTTTAGCAGC 13708	CAGTT	A
			GCTGCT GGAGAA GT		
			CGACGA TTTCTT CA		
			_____ C		
GAM1344	RPL17	5'	CTCTCTGAGCAGCT 6388	TT	
			AGCTGCTCAG GGAG		
			TCGACGAGTC TCTC		
			_____		
GAM1344	SORBS1	5'	CTTAAACCACTGAGCAGTT 31154	T AGA	
			AGCTGCTCAGT GG AAG		
			TTGACGAGTCA CC TTC		
			_ AAA		
GAM1344	WDR4	5'	ACCTTCTCCAAGTCTGGCAGCT 53359	T _	A
			AGCTGC CAG TTGGAGAA GT		
			TCGACG GTC AACCTCTT CA		
			_ TG C		
GAM1344	ZNF236	3'	TTACTTCTTTTCCAAACTG 23719	_	__
			CAGTT GGAGAA AGTAA		

GTCAA CCTTTT TCATT  
 A CT  
 GAM1344 BTBD3 3' TCACTTCCTGAAGCAGCTT 30313 \_ TT A  
 AAGCTGCT CAG GG GA  
 ||||| || ||  
 TTCGACGA GTC TC CT  
 A CT A  
 GAM1344 C4.4A 3' ACTTTCTCCTAGCCAGC 26941 CTCA \_  
 GCTG GTT GGAGAAAGT  
 ||| || |||||  
 CGAC CGA CCTCTTTCA  
 \_ T  
 GAM1344 CAPN13 5' TCTCTAACCTGAGAGC 58016 G \_  
 GCT CTCAG TTGGAGA  
 || |||| |||||  
 CGA GAGTC AATCTCT  
 \_ C  
 GAM1344 CHST8 5' TCCCAACAAGCAGCTT 42441 CA A  
 AAGCTGCT GTTGG GA  
 ||||| |||| ||  
 TTCGACGA CAACC CT  
 A \_ \_  
 GAM1344 CITED2 3' ACTTTCTCCAGTGCTCAACT 20294 C CT G  
 AG TG CA TTGGAGAAAGT  
 || || || |||||  
 TC AC GT GACCTCTTTCA  
 A TC \_  
 GAM1344 FGF19 3' ACTTCCCCAGGAGCAGC 17585 AG A A  
 GCTGCTC TTGG GAA GT  
 ||||| |||| || ||  
 CGACGAG GACC CTT CA  
 \_ C \_  
 GAM1344 FLJ14525 3' ACTTTCTCAACAAGC 51412 CA G  
 GCT GTTG AGAAAGT  
 || |||| |||||  
 CGA CAAC TCTTTCA  
 A \_ \_  
 GAM1344 FLJ20519 3' TTA CTTTCAGAGCAACCAGCTT 35348 CTCA GA\_\_  
 AAGCTG GTTG GAAAGTAA  
 |||| || |||||  
 TTCGAC CAAC CTTTCATT  
 \_ GAGA  
 GAM1344 FLJ21195 3' ACTTTTCTGAGCGGC 42448 TTGGA  
 GCTGCTCAG GAAAGT  
 ||||| ||||  
 CGGCGAGTC TTTTCA  
 \_  
 GAM1344 FLJ30681 3' TTTCCAATGAGCAGCTT 91794 G  
 AAGCTGCTCA TTGGAGA  
 ||||| |||||

TTCGACGAGT AACCTTT

GAM1344 HH114 5' CTCTGCTGAGCATCTT 50686 C T  
AAG TGCTCAGT GGAG  
||| ||||| |||  
TTC ACGAGTCG TCTC  
T \_

GAM1344 KIAA0871 3' ACTTTCTTTAAAAAAGC 30297 CAG  
GCT TTGGAGAAAGT  
||| ||||| |||  
CGA AATTTCTTTCA  
AAA

GAM1344 KIAA0876 3' TACTGCAATGCCCTACTGAGCA 64682 T\_ AGAA\_  
TGCTCAGT GG AGTA  
||| ||| |||  
ACGAGTCA CC TCAT  
TC GTAACG

GAM1344 KIAA1029 3' TACTTTCTCCATCCCAGTT 23479 CTCAGT  
AGCTG TGGAGAAAGTA  
||| ||||| |||  
TTGAC ACCTCTTTCAT  
CCT\_

GAM1344 KIAA1091 3' TTACTTTCAGACACCTGAGCAG 69691 T GA\_  
CT AGCTGCTCAG TG GAAAGTAA  
||| ||| |||  
TCGACGAGTC AC CTTTCATT  
C AGA

GAM1344 KIAA1157 3' CTCTCTGAGCAGACTT 72243 \_ TT  
AAG CTGCTCAG GGAG  
||| ||||| |||  
TTC GACGAGTC TCTC  
A \_

GAM1344 KIAA1863 3' TACTCCCTGCCAGAGCAGTT 64875 AGT \_ AA  
AGCTGCTC TGG AG AGTA  
||| ||| |||  
TTGACGAG ACC TC TCAT  
\_ G CC

GAM1344 LIN-28 3' ACTTTCTCCAGGATGC 45144 \_ AG  
GC TC TTGGAGAAAGT  
|| || ||||| |||  
CG AG GACCTCTTTCA  
T \_

GAM1344 MAL2 3' TTACTTTCTGGCTGAAGCA 53559 \_ GG  
TGCT CAGTT AGAAAGTAA  
||| ||| ||||| |||  
ACGA GTCGG TCTTTCATT  
A \_

GAM1344 MCF2L 3' ACCCTCCCAGCGGCTT 60839 CAGTT AAA  
AAGCTGCT GGAG GT  
||| ||| ||| |||

			TTCGGCGA CCTC CA		
			C____ C__		
GAM1344	MGC3222	5'	ACTTCCTAGCTGAACAGC 44291	C	A A
			GCTG TCAGTTGG GAA GT		
			CGAC AGTCGATC CTT CA		
			A _ _		
GAM1344	MOST2	5'	TCTCCACTGCAGCAGCTT 39693	_	T
			AAGCTGCT CAGT GGAGA		
			TTCGACGA GTCA CCTCT		
			C _		
GAM1344	PEX12	5'	TTACCTTTAAGACTGAGCA 4299	GGA	A
			TGCTCAGTT GAA GTAA		
			ACGAGTCAG TTT CATT		
			AA_ C		
GAM1344	PREI3	3'	CTTTAGCTGAGAAGCTT 66321	G	
			AAGCT CTCAGTTGGAG		
			TTCGA GAGTCGATTTC		
			A		
GAM1344	RBBP1	3'	ACCTTCCCAGCAGTTT 43428	CAGTT A	A
			AAGCTGCT GG GAA GT		
			TTTGACGA CC CTT CA		
			_____ _ C		
GAM1344	RBBP1	3'	ACCTTCCCAGCAGTTT 11257	CAGTT A	A
			AAGCTGCT GG GAA GT		
			TTTGACGA CC CTT CA		
			_____ _ C		
GAM1344	SH3GLB1	3'	TACTAATAAGCAGCTT 32055	CA	A
			AAGCTGCT GTTGG GA		
			TTCGACGA TAATC CT		
			A_ A		
GAM1344	SLAC2-B	3'	TACTTTTTTCACCAAAGCTT 30515	GCTCAGT	
			AAGCT TGGAGAAAGTAA		
			TTCGA ACTTTTTTCATT		
			AAACC_		
GAM1344	TLN1	3'	CCACCCTGCCAGCAGCTT 20817	_	T_
			AAGCTGCT CAG TGG		
			TTCGACGA GTC ACC		
			CC CC		
GAM1344	LOC147958	3'	ACTTTCTCCCGCAGC 87177	TCAGTT	
			GCTGC GGAGAAAGT		

CGACG CCTCTTTCA  
 C\_\_\_\_  
 GAM1344 LOC148760 3' ACCTTCTCCAACAAGC 84202 CA A  
 GCT GTTGGAGAA GT  
 ||| ||||| ||  
 CGA CAACCTCTT CA  
 A\_ C  
 GAM1344 LOC150271 3' TACTCTCTCATCAGCACTGAGC 84953 C TG\_\_\_\_ A  
 ACCT AG TGCTCAGT GAGA AGTA  
 || ||||| ||| |||  
 TC ACGAGTCA CTCT TCAT  
 C CGACTA C  
 GAM1344 LOC152065 3' ACCTTCTCCTTGGCAGGCT 85552 \_ T TT A  
 AGC TGC CAG GGAGAA GT  
 ||| ||| ||||| ||  
 TCG ACG GTT CCTCTT CA  
 G \_ \_ C  
 GAM1344 LOC158308 5' ACTCTCCCCACGCCAGAGCGGC 86741 A\_ \_ A A  
 TT AAGCTGCTC GT TGG GA AGT  
 ||||| || ||| |||  
 TTCGGCGAG CG ACC CT TCA  
 AC C C C  
 GAM1344 LOC201626 3' ACTCCCTTCAAGAAAAGCTT 88984 GC AG AA  
 AAGCT TC TTGGAG AGT  
 |||| || ||||| |||  
 TTCGA AG AACTTC TCA  
 AA \_ CC  
 GAM1344 LOC222224 3' TACTTTCTCCACATGTCACTT 94203 C CT GT  
 AAG TG CA TGGAGAAAGTA  
 ||| || ||||| |||||  
 TTC AC GT ACCTCTTTCAT  
 \_ T\_ AC  
 GAM1344 LOC51170 5' TACCCTCTAAAAGCAGTTT 32694 CAG AAA  
 AAGCTGCT TTGGAG GTA  
 ||||| ||||| |||  
 TTTGACGA AATCTC CAT  
 A\_ C\_  
 GAM1344 LOC51619 3' ACTCTCTCCAGCTGCAGC 32015 TC A  
 GCTGC AGTTGGAGA AGT  
 |||| ||||| |||  
 CGACG TCGACCTCT TCA  
 \_ C  
 GAM1344 LOC55580 5' TTA TCTCCCTTCTGGAGCAGTT 34116 AGTT AA\_  
 AGCTGCTC GGAG AGTAA  
 ||||| ||| |||||  
 TTGACGAG CTTC TCATT  
 GT\_ CCC  
 GAM1344 LOC56181 3' TCACTCACTCAGCAGCTT 95541 C T A  
 AAGCTGCT AGT GG GA  
 ||||| ||| |||



TTCGACGA TCA TC CT  
 C C A  
 GAM1344 LOC93097 3' TACTTTCTTATGAGCATGCT 71364 \_ GTTG  
 AGC TGCTCA GAGAAAGTA  
 ||| ||||| |||||  
 TCG ACGAGT TTCTTTCAT  
 T A\_\_  
 GAM1345 CDH3 3' AAAGTTCTTCAAAAGTGCAGC 8378 C C G  
 GT GC ATT TTGAAGAACTTT  
 || || ||| |||||  
 CG CG TGA AACTTCTTGAAA  
 A \_ A  
 GAM1345 COL4A5 3' AAGTTCTTCCAAACAATTC 52967 C \_  
 C ATTGTT GAAGAACTT  
 | ||||| |||||  
 C TAACAA CTTCTTGAA  
 T AC  
 GAM1345 COL4A5 3' AAGTTCTTCCAAACAATTC 52971 C \_  
 C ATTGTT GAAGAACTT  
 | ||||| |||||  
 C TAACAA CTTCTTGAA  
 T AC  
 GAM1345 COL4A5 3' AAGTTCTTCCAAACAATTC 4937 C \_  
 C ATTGTT GAAGAACTT  
 | ||||| |||||  
 C TAACAA CTTCTTGAA  
 T AC  
 GAM1345 FGF23 3' AAAGTCGATTCAACAACAGC 40190 CA GA\_  
 GC TTGTTGAA ACTTT  
 || ||||| |||||  
 CG AACAACTT TGAAA  
 AC AGC  
 GAM1345 KCND3 5' AAAGTTCTCCAGCTCGGCGA 17143 ATT A  
 TCGCC GTTG AGAACTTT  
 ||||| ||||| |||||  
 AGCGG CGAC TCTTGAAA  
 CT\_ C  
 GAM1345 NPC2 3' CTTCAACAACAGTGACTT 21222 CA  
 AAGTCGC TTGTTGAAG  
 ||||| |||||  
 TTCAGTG AACAACTTC  
 AC  
 GAM1345 HERC3 3' AAAGTTCTTGAGGGAATAGCAA 27510 C CA\_ G G  
 CT AGT GC TT TT AAGAACTTT  
 ||| || ||| |||||  
 TCA CG AG GA TTCTTGAAA  
 A ATA G G  
 GAM1345 KIAA1025 3' AAGTTCTTCCAAGAGACTT 63972 GCCA TT  
 AAGTC TTG GAAGAACTT  
 ||||| ||| |||||

		TTCAG AAC CTTCTTGAA	
		AG__ _	
GAM1345 KIAA1303	5'	AAAGCTCTTCAGACAGGACTT 65998	GCCA _ A
		AAGTC TTGT TGAAGA CTTT	
		TTCAG GACA ACTTCT GAAA	
		_ _ G C	
GAM1345 PLXNC1	3'	AAGTTCTTCAGACGACTT 19265	CCATTG
		AAGTCG TTGAAGAACTT	
		TTCAGC GACTTCTTGAA	
		A _ _ _	
GAM1345 SZF1	3'	AAAGTTCTTCAGACTCAGGACT 32229	GCCATTG
T		AAGTC TTGAAGAACTTT	
		TTCAG GACTTCTTGAAA	
		GACTCA_	
GAM1345 LOC255426	3'	AGTGCTTCAACATCGGCAACTT 97157	C AT A
		AAGT GCC TGTTGAAG ACT	
		TTCA CGG ACAACTTC TGA	
		A CT G	
GAM1346 ADH5	3'	GCCTCCAACCTCACAG 5418	AA T
		CTGTGAGGTT GA GGC	
		GACACTCCAA CT CCG	
		C_ _	
GAM1346 CPB2	3'	AGCCATCTCAAGCAAGTTT 8523	G AGGTTA
		AAACT TG AGATGGCT	
		TTTGA AC TCTACCGA	
		_ GAAC_	
GAM1346 CPB2	3'	AGCCATCTCAAGCAAGTTT 33102	G AGGTTA
		AAACT TG AGATGGCT	
		TTTGA AC TCTACCGA	
		_ GAAC_	
GAM1346 GNRH2	5'	AGCCATCTCATCCACAG 7679	A TA
		CTGTG GGT AGATGGCT	
		GACAC CTA TCTACCGA	
		_ C_	
GAM1346 JRKL	3'	CCATCTTAAATGATGTTTT 13661	TGTGAGG
		AAAAC TTAAGATGG	
		TTTTG AATTCTACC	
		TAGTA_	
GAM1346 NAV2	3'	AGTTGTCCATCCTCACAGT 60155	TTAA TG
		ACTGTGAGG GA GCT	

		TGACACTCC CT TGA	
		TAC_ GT	
GAM1346	PCDH12	5' TCGTTTAATCCTCACAGTTT 33423	TTA
		AAACTGTGAGG AGATGG	
		TTTGACACTCC TTTGCT	
		TAA	
GAM1346	TRADD	3' GCCAGCCCTTACAGTTT 13699	TTAAGA
		AAACTGTGAGG TGGC	
		TTTGACATTCC ACCG	
		CG__	
GAM1346	XPR1	3' AGCCATTTCTCCCAGCAGTTTT 16424	GA TTA
		AAACTGT GG AGATGGCT	
		TTTTGACG CC TTTACCGA	
		AC TC_	
GAM1346	AMOT	3' AGCCACCTTTTCACAGTT 55714	GTT A
		AACTGTGAG AAG TGGCT	
		TTGACACTT TTC ACCGA	
		__ C	
GAM1346	C17	3' AGCCATGACCCTCACAG 37857	TTAAG
		CTGTGAGG ATGGCT	
		GACACTCC TACCGA	
		CAG__	
GAM1346	CECR7	5' TTGTCCTGACCCACAGTTT 79627	A A TG
		AAACTGTG GGTTA GA G	
		TTTGACAC CCAGT CT T	
		C C GT	
GAM1346	FLJ10142	3' AGCCATCTTTATACAG 35847	AGGTT
		CTGTG AAGATGGCT	
		GACAT TTCTACCGA	
		AT__	
GAM1346	FLJ10650	5' CCACTTCCCTCGCAG 36381	TT A
		CTGTGAGG AAG TGG	
		GACGCTCC TTC ACC	
		C_ _	
GAM1346	KIAA0014	3' AGCACTGAAACCTCACAAGTCC 27836	A _ AAGATG
		A ACT GTGAGGTT GCT	
		C TGA CACTCCAA CGA	
		C A AGTCA_	
GAM1346	KIAA1332	3' ATCTCAACCTTACAGT 71159	A
		ACTGTGAGGTT AGAT	

			TGACATTCCAA TCTA		
			C		
GAM1346 KIAA1775	3'	CCAGACCTCACAGT	52376	AAGA	
		ACTGTGAGGTT TGG			
		TGACACTCCAG ACC			
GAM1346 KIAA1977	5'	AGCTAGGAAGCCCCACAGTTTT	74279	A AAGA	
		AAAAGTGTG GGTT TGGCT			
		TTTTGACAC CCGA ATCGA			
		— AGG—			
GAM1346 LIN-7-C	3'	CCTTTAACCTCACTAG	37165	AT	
		CT GTGAGGTTAAG GG			
		GA CACTCCAATTT CC			
		T —			
GAM1346 NIBAN	5'	TTTAACGTCACAGTTTT	42004	G	
		AAAAGTGTGA GTTAAG			
		TTTTGACACT CAATTT			
		G			
GAM1346 OR8G1	3'	AGCCATCTTCAATCAGC	91519	GA	—
		GT GGTT AAGATGGCT			
		CG CTAA TTCTACCGA			
		A_ C			
GAM1346 RBMS2	3'	AGCCATCGTTTTTTCACAG	11263	TTAA	
		CTGTGAGG GATGGCT			
		GACACTTT CTACCGA			
		TTG_			
GAM1346 SSB-4	3'	AGCCACTGACTCACAGTT	55096	GTTA A	
		AACTGTGAG AG TGGCT			
		TTGACACTC TC ACCGA			
		AG_ _			
GAM1346 WDR7	3'	AGCCATCTCAACCGCAC	30955	A A	
		GTG GGTT AGATGGCT			
		CAC CCAA TCTACCGA			
		G C			
GAM1346 LOC139397	5'	AGCTGGTCCACCTCACAG	75832	TAAGA	
		CTGTGAGGT TGGCT			
		GACACTCCA GTCGA			
		CCTG_			
GAM1346 LOC143162	3'	AGCCATCATATTCACAGT	76493	GTAA	
		ACTGTGAG GATGGCT			

		TGACACTT	CTACCGA		
		ATA__			
GAM1346	LOC145783 3'	AGCCATCTTCCAAATACAAGT	77478	_ A__	TT
		ACT GTG	GG AAGATGGCT		
		TGA CAT	CC TTCTACCGA		
		A AAA	__		
GAM1346	LOC146176 5'	CCCTTGAACCTCACAGTTTT	77696	G	AT
		AAAACGTGAG	TTAAG GG		
		TTTTGACACTC	AGTTC CC		
		A	__		
GAM1346	LOC150159 3'	AGCCATCTTGATCACAG	57538	GG	
		CTGTGA	TTAAGATGGCT		
		GACACT	AGTTCTACCGA		
		__			
GAM1346	LOC150587 3'	CCACTGCTCACAGTTT	85059	GTTA	A
		AAACTGTGAG	AG TGG		
		TTTGACACTC	TC ACC		
		G__	_		
GAM1346	LOC151057 3'	AGCCATGGTCTCACAG	85206	GT	AAG
		CTGTGAG	T ATGGCT		
		GACACTC	G TACCGA		
		TG	__		
GAM1346	LOC154562 3'	AGCCATCTTACTCA	81090	GT	
		TGAG	TAAGATGGCT		
		ACTC	ATTCTACCGA		
		__			
GAM1346	LOC155060 3'	AGCCATCTTGGCCCTCACAG	86326	_	
		CTGTGAGG	TTAAGATGGCT		
		GACACTCC	GGTTCTACCGA		
		C			
GAM1346	LOC157621 3'	AGCCATCCAGTCATTTACAT	86493	C	TAA__
	TTTT	AAAA TGTGAGGT	GATGGCT		
		TTTT	ACACTTTA CTACCGA		
		T	CTGACC		
GAM1346	LOC157622 3'	AGCCATCCAGTCATTTACAT	86502	C	TAA__
	TTTT	AAAA TGTGAGGT	GATGGCT		
		TTTT	ACACTTTA CTACCGA		
		T	CTGACC		
GAM1346	LOC158332 3'	CAGAAGGAACACACAGTTT	81887	A	AAGA_
		AAACTGTG	GGTT TG		

TTTGACAC CCAA AC  
 A GGAAG  
 GAM1346 LOC196510 3' ATGTTAACCTCTCAGTTCC 87746 A T G  
 A AACTG GAGGTTAA AT  
 I |||| ||||| ||  
 C TTGAC CTCCAATT TA  
 C T G  
 GAM1346 LOC196738 3' AGCCATCATATTCACAGT 87501 GTTAA  
 ACTGTGAG GATGGCT  
 ||||| |||||  
 TGACACTT CTACCGA  
 ATA\_\_  
 GAM1346 LOC200220 3' ATGTTAACCTCTCAGTTCC 88636 A T G  
 A AACTG GAGGTTAA AT  
 I |||| ||||| ||  
 C TTGAC CTCCAATT TA  
 C T G  
 GAM1346 LOC221060 3' AGCCAGCGCCTCACAG 93205 TAAGA  
 CTGTGAGGT TGGCT  
 ||||| ||||  
 GACACTCCG ACCGA  
 CG\_\_  
 GAM1346 LOC253142 5' AGCATCCTGACCCACAG 97382 A A G  
 CTGTG GGTTA GATG CT  
 |||| |||| |||| ||  
 GACAC CCAGT CTAC GA  
 C C \_  
 GAM1346 LOC253394 5' AGCCATCTCAGGGCACAATTTT 97505 C AGGTTA  
 AAAA TGTG AGATGGCT  
 |||| |||| |||||  
 TTTT ACAC TCTACCGA  
 A GGGAC\_  
 GAM1346 LOC81034 3' AGCCATCTTTAAATAGTT 47841 GAGGTT  
 AACTGT AAGATGGCT  
 |||| |||||  
 TTGATA TTCTACCGA  
 AAT\_\_  
 GAM1346 LOC90520 3' AGCCAGGGCCCCACAGTTT 63142 A TAAGA  
 AAACTGTG GGT TGGCT  
 ||||| || ||||  
 TTTGACAC CCG ACCGA  
 C GG\_\_  
 GAM1347 MMP20 3' TCCAAATCAACACAATGCAC 16484 CAGGA  
 GTGCATTGTGTTG TTGGG  
 ||||| ||||  
 CACGTAACACAAC AACCT  
 TA\_\_  
 GAM1347 PIM2 3' TCCCAATCCTACAAAGGAGC 59991 A GTG C  
 GC TT TTG AGGATTGGGA  
 || || || |||||

			CG AG AAC TCCTAACCCCT		
			_ GA_ A		
GAM1347	RXRA	3'	CCCAATCCTTAGCAATGC 11405	GTTGC	
			GCATTGT AGGATTGGG		
			CGTAACG TCCTAACCC		
			AT__		
GAM1347	BRAG	3'	TCCCAATTCCAAAACACAATGC 29477	GCA	
	AC		GTGCATTGTGTT GGATTGGGA		
			CACGTAACACAA CTTAACCCCT		
			AAC		
GAM1347	DKFZp547O146	5'	CCCAATCCCCCAACAC 39564	CA	
			GTGTTG GGATTGGG		
			CACAAC CCTAACCC		
			CC		
GAM1347	KIAA1762	3'	TCCCAATCCCCACAGACACACA 63792	CAT GCA__	
	C		GTG TGTGTT GGATTGGGA		
			CAC ACACAG CCTAACCCCT		
			__ ACACC		
GAM1347	LOC145820	3'	CCCAATCCTTAAGCAATCAC 77512	C GTTGC	
			GTG ATTGT AGGATTGGG		
			CAC TAACG TCCTAACCC		
			_ AAT__		
GAM1347	LOC253980	3'	TCCCAACCCCATTTGCTAACAA 95076	GTT __ A	
			TTGT GCA GG TTGGGA		
			AACA CGT CC AACCCCT		
			AT_ TAC C		
GAM1348	CCNT2	3'	GGTGGTTGTGCTACTGTAT 54266	A	
			ATACAGTAG ACAACCATT		
			TATGTCATC TGTTGGTGG		
			G		
GAM1348	D8S2298E	3'	ATGTTTATTCTGCTGTAT 19035	C C	
			ATACAGTAGAA AA CAT		
			TATGTCGTCTT TT GTA		
			A T		
GAM1348	ERBB2IP	3'	TGGTTATTGTACTGTAT 37988	G C	
			ATACAGTA AA AACCA		
			TATGTCAT TT TTGGT		
			G A		
GAM1348	ICMT	3'	TCAATGAAATCTGTACTGTAT 24819	GAACAAC	
			ATACAGTA CATTGA		

			TATGTCAT	GTAAC		
			GTCTAAA			
GAM1348	PLGL	3'	ATGTAATCGTTGTTATACTGTA	10636	G C A	
	T		ATACAGTA AACAA	ATTG CAT		
			TATGTCAT TTGTTG	TAAT GTA		
			A C _			
GAM1348	PTPRC	3'	ATGTCCTCCTTGTCTACT	11100	CCATT	
			AGTAGAACAA	GACAT		
			TCATCTTGTT	CTGTA		
			CCTC_			
GAM1348	PTPRC	3'	ATGTCCTCCTTGTCTACT	55165	CCATT	
			AGTAGAACAA	GACAT		
			TCATCTTGTT	CTGTA		
			CCTC_			
GAM1348	TGFBR1	3'	GTCAGTTGTTCTAC	16051	CAT	
			GTAGAACAA	TGAC		
			CATCTTGTTG	ACTG		
			_____			
GAM1348	TLL1	3'	ATGTCAATATAGATTACTGTAT	24948	AACAACC	
			ATACAGTAG	ATTGACAT		
			TATGTCATT	TAAGTGA		
			AGATA__			
GAM1348	TMOD2	3'	TCAGAAAGTGTCTACTG	27252	ACCA	
			CAGTAGAAC	TTGA		
			GTCATCTTGT	GAAT		
			GAA_			
GAM1348	ZK1	3'	ATGCAAATAGTTGTTCTATTGT	19462	C GA	
	AT		ATACAGTAGAACAA	ATT CAT		
			TATGTTATCTTGTTG	TAA GTA		
			A AC			
GAM1348	BTBD3	3'	ATGTTGAATGTTATTGTACTGT	30306	G C CA TG	
	AT		ATACAGTA AA AAC	T ACAT		
			TATGTCAT TT TTG	A TGTA		
			G A TA GT			
GAM1348	FLJ14054	3'	TGTTTATTGTTCTAATGTA	44663	G CCATT	
			TACA TAGAACAA	GACA		
			ATGT ATCTTGTT	TTGT		
			A AT__			
GAM1348	HSU84971	3'	ATGTAGTGGTTTTCTACT	25252	AAC A	
			AGTAG AACCAT	TG CAT		



	TCATC TTGGTGAT GTA		
	CTT _		
GAM1348 KIAA0716	3' GTGGTATCTACTGTAT 28165	ACA	
	ATACAGTAGA ACCAT		
	TATGTCATCT TGGTG		
	A_		
GAM1348 KIAA1344	3' TGGTGCTCTACTGTAT 72451	ACA	
	ATACAGTAGA ACCA		
	TATGTCATCT TGGT		
	CG_		
GAM1348 NIP30	3' GTGTTGTTTGGTTCTACTG 46325	AACCAT	
	CAGTAGAAC TGACAT		
	GTCATCTTG GTTGTG		
	GTTT_		
GAM1348 PRKCBP1	5' ATGGTCCGTTTTACTATAT 24833	C	A_
	ATA AGTAGAAC ACCAT		
	TAT TCATTTTG TGGTA		
	A CC		
GAM1348 PSMD10	3' TGTTGAGATTGTTCTACTGT 10995	CCA TG	
	ACAGTAGAACAA T ACA		
	TGTCATCTTGTT A TGT		
	AG_ GT		
GAM1348 TUCAN	3' ATGTCTTTTCTATTCTACTGT 30270	CAACCATT	
	ACAGTAGAA GACAT		
	TGTCATCTT CTGTA		
	ATCTTTT_		
GAM1348 LOC115827	3' ATGTCAATGGCTCGTAC 56621	_ ACAA	
	GTA GA CCATTGACAT		
	CAT CT GGTA ACTGTA		
	G C_		
GAM1348 LOC146227	3' TGTCTGTTGTACTGTAT 77714	G ACCATT	
	ATACAGTA AACA GACA		
	TATGTCAT TTGT CTGT		
	G _		
GAM1348 LOC147219	3' TGTCATTTTACTGTAT 83992	CAACCAT	
	ATACAGTAGAA TGACA		
	TATGTCATTTT ACTGT		
	_____		
GAM1348 LOC150054	3' TCTGTGATCATTCTACTGTTC 84838	T CAAC T	
	A ACAGTAGAA CAT GA		

		C TGTCATCTT GTG CT	
		T ACTA T	
GAM1348	LOC152667 3'	GTGTTGTTTGTTCTACTG 80638	AACCAT
		CAGTAGAAC TGACAT	
		GTCATCTTG GTTGTG	
		GTTT__	
GAM1348	LOC196424 3'	TGGTTTATTTCTACTGTA 87704	C__
		TACAGTAGAA AACCA	
		ATGTCATCTT TTGGT	
		TAT	
GAM1348	LOC199907 3'	ATGTCACAAAGCTACTTACTGT 88462	AACAACCAT
	A	TACAGTAG TGACAT	
		ATGTCATT ACTGTA	
		CATCGAAAC	
GAM1348	LOC203369 3'	ATGTCAATAGTTATAACCTAC 89336	AAC__ C
		GTAG AAC ATTGACAT	
		CATC TTG TAACTGTA	
		CAATA A	
GAM1348	LOC90576 3'	ATGCAAATAGTTGTTCTATTGT 63344	C GA
	AT	ATACAGTAGAACAAC ATT CAT	
		TATGTTATCTTGTTG TAA GTA	
		A AC	
GAM1348	LOC93496 3'	ATGTCACTTAAATCGTACTGTA 72430	_ ACAACCAT
	T	ATACAGTA GA TGACAT	
		TATGTCAT CT ACTGTA	
		G AAATTC__	
GAM1349	AMPD3 3'	GGTGCTCAATAAATGCATATTG 4900	CAA C
	AA	TTCAA GT TTTATTGAGCACC	
		AAGTT CG AAATAACTCGTGG	
		ATA T	
GAM1349	CHRND 3'	TGCTCAATGGCTCCCTGAA 5638	ACA_ TTT
		TTCA AGTC ATTGAGCA	
		AAGT TCGG TAACTCGT	
		CCCC ____	
GAM1349	CNTN3 3'	GGTTTTCAAAAAATTGTTGAA 66696	GTC A C
		TTCAACAA TTT TTGAG ACC	
		AAGTTGTT AAA AACTT TGG	
		__ A T	
GAM1349	CRYBA2 3'	CTCAATAAAGGTTCTGAA 54044	ACA GT
		TTCA A CTTTATTGAG	

			AAGT T GAAATAACTC		
			CC_TG		
GAM1349	CRYBA2	3'	CTCAATAAAGGTTCTGAA 54045	ACA GT	
			TTCA A CTTTATTGAG		
			AAGT T GAAATAACTC		
			CC_TG		
GAM1349	CRYBA2	3'	CTCAATAAAGGTTCTGAA 17798	ACA GT	
			TTCA A CTTTATTGAG		
			AAGT T GAAATAACTC		
			CC_TG		
GAM1349	CYP46	3'	TGCTCAATAAATGTGTGTTGA 21897	AG C	
			TCAACA T TTTATTGAGCA		
			AGTTGT G AAATAACTCGT		
			GT T		
GAM1349	DLEU1	3'	CTCAATAAATCTTTGATGAA 19694	A TC	
			TTCA CAAG TTTATTGAG		
			AAGT GTTT AAATAACTC		
			A CT		
GAM1349	EIF1A	3'	AATAAAATACTTGTTGAA 88599	C_	
			TTCAACAAGT TTTATT		
			AAGTTGTTCA AAATAA		
			TA		
GAM1349	GABPB1	3'	TTGATAAAGATTGTTGAA 17908	G TG	
			TTCAACAA TCTTTAT A		
			AAGTTGTT AGAAATA T		
			_ GT		
GAM1349	GCNT1	3'	GTGCTCAGGGACTT 7654	TTA	
			AAGTCT TTGAGCAC		
			TTCAGG GACTCGTG		
			—		
GAM1349	GNRHR	5'	GTGCTCAACAGTGTGTTTGAA 4642	_ AGT TTA	
			TTCAA CA CT TTGAGCAC		
			AAGTT GT GA AACTCGTG		
			T GT_ C__		
GAM1349	GUCY1B3	3'	GCACCCAATAAATATTTGTTGA 5966	C A__	
	A		TTCAACAAGT TTTATTG GC		
			AAGTTGTTTA AAATAAC CG		
			T CCA		
GAM1349	MEF2D	3'	GGCACTCAATAAATGCT 96914	C CA	
			AGT TTTATTGAG CC		

			TCG AAATAACTC GG		
			T AC		
GAM1349	MEF2D	3'	GGTGCTCAATAAATGAATG 96915	AG _	
			CA TC TTTATTGAGCACC		
			GT AG AAATAACTCGTGG		
			A_ T		
GAM1349	NFATC1	3'	GCAGACAAAGACTTTTGAA 20486	C A GA	
			TTCAA AAGTCTTT TT GC		
			AAGTT TTCAGAAA AG CG		
			_ C A_		
GAM1349	PAG	3'	GGTACTTCTAGACTTGTT 37405	TTATT C	
			AACAAGTCT GAG ACC		
			TTG TTCAGA TTC TGG		
			TC__ A		
GAM1349	PBX3	3'	GGTGCTGCACAGACTTGT 20566	TTAT _	
			ACAAGTCT TG AGCACC		
			TG TTCAGA AC TCGTGG		
			C__ G		
GAM1349	PLA2G2D	3'	GGTGCTCAATTCATGCCTGTGA 24798	A A CTTT	
	A		TTCA CA GT ATTGAGCACC		
			AAGT GT CG TAACTCGTGG		
			_ C TACT		
GAM1349	PLA2G4C	3'	GTGCTCAATAAATGCTTGCTGA 73415	A C	
			TCA CAAGT TTTATTGAGCAC		
			AGT GTTCG AAATAACTCGTG		
			C T		
GAM1349	PML	3'	GGCTGCTCAATAAACACTTGTT 52663	C _	
	GAA		TTCAACAAGT TTTATTGAGCA CC		
			AAGTTGTTCA AAATAACTCGT GG		
			C C		
GAM1349	PML	3'	GGCTGCTCAATAAACACTTGTT 52669	C _	
	GAA		TTCAACAAGT TTTATTGAGCA CC		
			AAGTTGTTCA AAATAACTCGT GG		
			C C		
GAM1349	PML	3'	GGCTGCTCAATAAACACTTGTT 52675	C _	
	GAA		TTCAACAAGT TTTATTGAGCA CC		
			AAGTTGTTCA AAATAACTCGT GG		
			C C		
GAM1349	PML	3'	GGCTGCTCAATAAACACTTGTT 52678	C _	
	GAA		TTCAACAAGT TTTATTGAGCA CC		

			AAGTTGTTCA AAATAACTCGT GG		
			C C		
GAM1349	PX19	3'	CTCAATAAACTTGTGAA 25087	C	
			TTCAACAAGT TTTATTGAG		
			AAGTTGTTCA AAATAACTC		
			T		
GAM1349	SNAP25	3'	TGCTCAATGTGCTGTTGA 55527	A	CTT
			TCAACA GT TATTGAGCA		
			AGTTGT CG GTAACCTCGT		
			_ T _		
GAM1349	SNAP25	3'	TGCTCAATGTGCTGTTGA 11834	A	CTT
			TCAACA GT TATTGAGCA		
			AGTTGT CG GTAACCTCGT		
			_ T _		
GAM1349	SOD3	5'	GCACCCAATAAACATTTGTTG 11863	C	A _
			CAACAAGT TTTATTG GC		
			GTTGTTTA AAATAAC CG		
			C CCA		
GAM1349	TLR9	3'	GGCACTCAATAAATGCT 33851	C	CA
			AGT TTTATTGAG CC		
			TCG AAATAACTC GG		
			T AC		
GAM1349	YWHAZ	3'	TGCTCAATAAATATTG 12706	GTC	
			CAA TTTATTGAGCA		
			GTT AAATAACTCGT		
			AT _		
GAM1349	Z39IG	3'	GGTGCTCAATAAATATCT 23435	TC _	
			AG TTTATTGAGCACC		
			TC AAATAACTCGTGG		
			TAT		
GAM1349	ZNF2	3'	GGTGCTCAATAAATATTT 40806	C	
			AAGT TTTATTGAGCACC		
			TTTA AAATAACTCGTGG		
			T		
GAM1349	AKAP6	3'	GGTATTCAATAAAAATTTACTG 14992	AC	C C
	AA		TTCA AAGT TTTATTGAG ACC		
			AAGT TTTA AAATAACTT TGG		
			CA A A		
GAM1349	CROC4	3'	GTCTTCAATAAAGACTCTTGAA 21020	CA	C
			TTCAA AGTCTTTATTGAG AC		

AAGTT TCAGAAATAACTT TG  
 C\_ C  
 GAM1349 DIS3 3' GGGCACTCAATAAATGTTGA 30232 AGTC CA  
 TCAACA TTTATTGAG CC  
 ||||| ||||| ||  
 AGTTGT AAATAACTC GG  
 AC  
 GAM1349 DKFZp434A1520 3' TGCTCAATAGATGTTTGTGAA 61118 TC  
 TTCAACAAG TTTATTGAGCA  
 ||||| |||||  
 AAGTTGTTT AGATAACTCGT  
 GT  
 GAM1349 E2F6 3' GTGCTCAATAAATGTCTGAA 8717 \_ AGTC  
 TTCA ACA TTTATTGAGCAC  
 ||| || |||||  
 AAGT TGT AAATAACTCGTG  
 C  
 GAM1349 FLJ13352 3' GGTGCTCAATAACTGTTTGTG 44757 TCT  
 CAACAAG TTATTGAGCACC  
 ||||| |||||  
 GTTGTTT AATAACTCGTGG  
 GTC  
 GAM1349 FLJ20255 3' TGCTCAATAAAGCTATTCAGTG 34800 ACA\_ T  
 AA TTCA AG CTTTATTGAGCA  
 ||| || |||||  
 AAGT TC GAAATAACTCGT  
 GACTTA \_  
 GAM1349 FLJ20276 5' TGCAAAAATAAAGACCTTTGAA 34832 CAA GA\_  
 TTCAA GTCTTTATT GCA  
 ||||| ||||| |||  
 AAGTT CAGAAATAA CGT  
 TC\_ AAA  
 GAM1349 FLJ21820 3' GATAAAGAATTGTTGAA 41623 G  
 TTCAACAA TCTTTATT  
 ||||| |||||  
 AAGTTGTT AGAAATAG  
 A  
 GAM1349 GIT2 3' TAATAAAACTTGTTGA 57582 C  
 TCAACAAGT TTTATTG  
 ||||| |||||  
 AGTTGTTCA AAATAAT  
 A  
 GAM1349 GOA 3' TGCTCAATAAACACTTGTTGAA 78078 C  
 TTCAACAAGT TTTATTGAGCA  
 ||||| |||||  
 AAGTTGTTCA AAATAACTCGT  
 C  
 GAM1349 KIAA0830 3' TGCTCAATAAAGTAATTACTGA 69704 AC GT\_  
 TCA AA CTTTATTGAGCA  
 ||| || |||||

			AGT TT GAAATAACTCGT			
			CA AAT			
GAM1349	KIAA0924	3'	CTCAGACTTGTGGAA	29715	A	TTATT
			TTC ACAAGTCT	GAG		
			AAG TGTTCAGA	CTC		
			G	_____		
GAM1349	KIAA1161	5'	CTTCCTAGAGACTTGTT	81750		TT
			AACAAGTCTTTA	GAG		
			TTGTTCAGAGAT	TTC		
			CC			
GAM1349	KIAA1184	3'	GGCGCTCAATAAATGTTGAA	42616	AGTC	A
			TTCAACA TTTATTGAGC	CC		
			AAGTTGT AAATAACTCG	GG		
			_____	C		
GAM1349	KIAA1219	3'	GGCGCCCAGTAAATACTTGTTG	61370	C	A A
	AA		TTCAACAAGT TTTATTG	GC CC		
			AAGTTGTTCA AAATGAC	CG GG		
			T C C			
GAM1349	KIAA1497	3'	GTGCTCAATAAAATGATT	67516	___	
			AGTC TTTATTGAGCAC			
			TTAG AAATAACTCGTG			
			TA			
GAM1349	KIAA1877	3'	GTACAGTTAAGACTTGTTG	66174	T A	
			CAACAAGTCTT ATTG	GC		
			GTTGTTTCAGAA TGAC	TG		
			T A			
GAM1349	KLK15	3'	GGCGCTCAAGGTCACCTGTT	56746	A CTTTA	A
			AACA GT TTGAGC	CC		
			TTGT CA AACTCG	GG		
			C CTGG_ C			
GAM1349	KLK15	3'	GGCGCTCAAGGTCACCTGTT	56748	A CTTTA	A
			AACA GT TTGAGC	CC		
			TTGT CA AACTCG	GG		
			C CTGG_ C			
GAM1349	KLK15	3'	GGCGCTCAAGGTCACCTGTT	43435	A CTTTA	A
			AACA GT TTGAGC	CC		
			TTGT CA AACTCG	GG		
			C CTGG_ C			
GAM1349	KLK15	3'	GGCGCTCAAGGTCACCTGTT	33999	A CTTTA	A
			AACA GT TTGAGC	CC		

TTGT CA AACTCG GG  
 C CTGG\_ C  
 GAM1349 LEC3 3' GGCACCTCATTGTGGCCTTGTTG 30861 T T T CA  
 AA TTCAACAAG CT TA TGAG CC  
 ||||| || || || ||  
 AAGTTGTTT GG GT ACTC GG  
 C T T AC  
 GAM1349 MGC32043 3' CTCAATAAATGTTTGTT 58048 TC  
 AACAAAG TTTATTGAG  
 ||||| |||||  
 TTGTTT AAATAACTC  
 GT  
 GAM1349 MGC5576 3' GGCACCTCAATAAAGATTTGCAG 43922 AA CA  
 AA TTC CAAGTCTTTATTGAG CC  
 || ||||| ||||| ||  
 AAG GTTTAGAAATAACTC GG  
 AC AC  
 GAM1349 OSBPL11 3' GGTGCTCAACACTTGTT 42891 CTTTA  
 AACAAAGT TTGAGCACC  
 ||||| |||||  
 TTGTTCA AACTCGTGG  
 C\_\_\_\_  
 GAM1349 PDGFC 3' TGCAAAGACTTTTTGAA 32501 C ATTGA  
 TTCAA AAGTCTTT GCA  
 ||||| ||||| ||  
 AAGTT TTCAGAAA CGT  
 T \_\_\_\_\_  
 GAM1349 RHOBTB3 3' TGTAAGTCAAAGACTTGTT 29745 \_ GA  
 AACAAAGTCTTT ATT GCA  
 ||||| ||||| || ||  
 TTGTTTCAGAAA TGA TGT  
 C A\_  
 GAM1349 SC65 3' GGTGCTCAATAAATGTTTGTTG 21293 TC  
 CAACAAG TTTATTGAGCACC  
 ||||| ||||| |||||  
 GTTGTTT AAATAACTCGTGG  
 GT  
 GAM1349 SH3BGRL2 3' TAAAGAACTTGTTGAA 48888 \_  
 TTCAACAAGT CTTTA  
 ||||| |||||  
 AAGTTGTTCA GAAAT  
 A  
 GAM1349 TRIM26 3' GGTGCTCAATAAAGACTTGTTG 12892  
 AA TTCAACAAGTCTTTATTGAGCACC  
 ||||| ||||| ||||| |||||  
 AAGTTGTTTCAGAAATAACTCGTGG  
 GAM1349 VEST1 5' TAATAAAGACTTCTGAA 53687 AC  
 TTCA AAGTCTTTATTG  
 ||||| ||||| |||||



			AAGT TTCAGAAATAAT		
			C_		
GAM1349	ZFP95	3'	TGCCCAATAAATATTTGTTGA 59025	C	A
			TCAACAAGT TTTATTG GCA		
			AGTTGTTTA AAATAAC CGT		
			T C		
GAM1349	ZFP95	3'	TGCCCAATAAATATTTGTTGA 27381	C	A
			TCAACAAGT TTTATTG GCA		
			AGTTGTTTA AAATAAC CGT		
			T C		
GAM1349	LOC145482	3'	GGCACTGAGTAAAGATTTGTTG 77231		G CA
	AA		TTCAACAAGTCTTTATT AG CC		
			AAGTTGTTTAGAAATGA TC GG		
			G AC		
GAM1349	LOC145482	3'	GGCACTTTGTAAAGATTTGTT 77232		T CA
			AACAAGTCTTTAT GAG CC		
			TTGTTTAGAAATG TTC GG		
			T AC		
GAM1349	LOC148645	5'	GGTGCTCAGAAAACGTGCT 84184	C_	A
			AGT TTT TTGAGCACC		
			TCG AAA GACTCGTGG		
			TGC A		
GAM1349	LOC149535	3'	GTGCTCAATAAATGTGT 79419	AGTC	
			ACA TTTATTGAGCAC		
			TGT AAATAACTCGTG		
			GT_		
GAM1349	LOC150630	3'	GTGCTCAATAAATACTGAGTGA 85111	ACA	C
	A		TTCA AGT TTTATTGAGCAC		
			AAGT TCA AAATAACTCGTG		
			GAG T		
GAM1349	LOC152225	5'	GGTGCTCAATAAAAGCTTGTT 85594	TC	
			AACAAG TTTATTGAGCACC		
			TTGTTC AAATAACTCGTGG		
			GA		
GAM1349	LOC154141	5'	GTGCTGAGAAGACTTGT 86172	AT	G
			ACAAGTCTTT T AGCAC		
			TGTTCAGAAG A TCGTG		
			_ G		
GAM1349	LOC154562	3'	GGCACTCAATAAATACTTGTT 81092	C	CA
			AACAAGT TTTATTGAG CC		

		TTGTTCA AAATAACTC GG		
		T AC		
GAM1349	LOC157660 3'	GGCACTCAACAAATATTTGTTG 86509	C A	CA
	AA	TTCAACAAGT TTT TTGAG CC		
		AAGTTGTTTA AAA AACTC GG		
		T C AC		
GAM1349	LOC158310 3'	GGTGCTCAATAAATATCTGCCG 86760	AA AG C	
	A	TC CA T TTTATTGAGCACC		
		AG GT A AAATAACTCGTGG		
		CC CT T		
GAM1349	LOC197125 3'	GGCACTCAGTAAATACTTGTTG 87904	C	CA
	AA	TTCAACAAGT TTTATTGAG CC		
		AAGTTGTTCA AAATGACTC GG		
		T AC		
GAM1349	LOC203411 3'	TGCTCAGTCAGACCTGTT 90632	A TT	
		AACA GTCT ATTGAGCA		
		TTGT CAGA TGA CTGT		
		C C_		
GAM1349	LOC256338 3'	CTCAATAAATAATTGTTGAA 94610	GTC	
		TTCAACAA TTTATTGAG		
		AAGTTGTT AAATAACTC		
		AAT		
GAM1349	LOC257494 3'	GGTGCTCAATAAAGACTTGTTG 97796		
	AA	TTCAACAAGTCTTTATTGAGCACC		
		AAGTTGTT CAGAAATAACTCGTGG		
GAM1349	LOC56267 3'	TGCTAAGAGTTGTTGAA 39016	G TATTG	
		TTCAACAA TCTT AGCA		
		AAGTTGTT AGAA TCGT		
		G _		
GAM1349	LOC90874 5'	GGCTCGGACTTGTTGAA 64259	A TTATT A	
		TTCA CAAGTCT GAGC C		
		AAGT GTTCAGG CTCG G		
		G _ C		
GAM1349	LOC91907 3'	GTGCTCAATAAAATGATT 67494	_	
		AGTC TTTATTGAGCAC		
		TTAG AAATAACTCGTG		
		TA		
GAM1350	ARNT2 3'	GCCAATGCCCAGAGTG 29461	A _	
		CACTCTG GC TTGGC		

			GTGAGAC CG AACCG		
			C T		
GAM1350 COL4A2	5'	CCGGGGCCCCAGAGTGGACGA	8466	A	A TGG
		TCG CCACTCTG GCT CTGG			
		AGC GGTGAGAC CGG GGCC			
		A C ____			
GAM1350 EVPL	5'	GCCAGCCAAGCCCAGCCTG	8805	CT	A
		CA CTG GCTTGGCTGGC			
		GT GAC CGAACCGACCG			
		CC C			
GAM1350 GATA2	3'	GCCAAAGCCAGAGTGG	8998	A	_
		CCACTCTG GCTT GGC			
		GGTGAGAC CGAA CCG			
		_ A			
GAM1350 GPC4	3'	CCAAATTCTGCAGAGTGGTC	7551	_	C__
		GACCACTCTG AG TTGG			
		CTGGTGAGAC TC AACC			
		G TTA			
GAM1350 IL22RA2	3'	CCTAAGGCTCAGTGTGGTC	53691	T	GGCT
		GACCAC CTGAGCTT GG			
		CTGGTG GACTCGGA CC			
		T AT__			
GAM1350 KCNA4	5'	CCAGCCAAGCTCTGGAG	9509	_	
		CTCT GAGCTTGGCTGG			
		GAGG CTCGAACCGACC			
		T			
GAM1350 LZTS1	3'	CCAGCCCCCGCCCCAGAGTGG	40684	A_	TT_
		CCACTCTG GC GGCTGG			
		GGTGAGAC CG CCGACC			
		CC CCC			
GAM1350 MTR	3'	GCCATTTGCCCCAGTGTGGTC	4212	T	A_ T__
		GACCAC CTG GC TGGC			
		CTGGTG GAC CG ACCG			
		T CC TTT			
GAM1350 OCLN	5'	GCCAGGTCCAGAGCGCCGA	10316	ACCA	AG
		TCG CTCTG CTTGGC			
		AGC GAGAC GGACCG			
		CGC_ CT			
GAM1350 PIK3R2	3'	GCCAGCCTGGCCAAAATGG	17258	CTC	A T
		CCA TG GCT GGCTGGC			

GGT AC CGG CCGACCG  
AAA \_ T  
GAM1350 POU2AF1 3' GCCTGGGGCTCAGAGTAGT 20652 C \_  
AC ACTCTGAGCTT GGC  
|| ||||| |||  
TG TGAGACTCGGG CCG  
A GT  
GAM1350 PTGS1 3' CAGCCTCAGAGTGGTCGA 54568 GCTT  
TCGACCACTCTGA GGCTG  
||||||| |||  
AGCTGGTGAGACT CCGAC  
  
GAM1350 PTGS1 3' CAGCCTCAGAGTGGTCGA 6349 GCTT  
TCGACCACTCTGA GGCTG  
||||||| |||  
AGCTGGTGAGACT CCGAC  
  
GAM1350 RAMP1 3' CAGGAGTCCAGAGTAGCCGA 19581 ACC AG GG  
TCG ACTCTG CTT CTG  
|| |||| ||| |||  
AGC TGAGAC GAG GAC  
CGA CT \_  
GAM1350 TAZ 5' GCCAGTGTCTCGAGCGGTCGA 3676 A T CTTG  
TCGACC CTC GAG GCTGGC  
||||| ||| ||| |||||  
AGCTGG GAG CTC TGACCG  
C \_ TG\_  
GAM1350 TMC2 3' CCCCACGCTCACAGTGGTCGA 54961 C T CT  
TCGACCACT TGAGC TGG GG  
||||||| |||| ||| ||  
AGCTGGTGA ACTCG ACC CC  
C C \_  
GAM1350 USH3A 3' GCCAGCAGACATCAGAACACAC 53784 ACCAC\_ GCTTG  
CGA TCG TCTGA GCTGGC  
|| |||| |||||  
AGC AGACT CGACCG  
CACACA ACAGA  
GAM1350 bA430M15.1 3' GCTAAGCCCAAAGTGGCTGA 76978 A C A  
TCG CCACT TG GCTTGGC  
|| |||| || |||||  
AGT GGTGA AC CGAATCG  
C A C  
GAM1350 BCMP1 3' CAAGCTCAAAGTGACAGA 48733 GAC C  
TC CACT TGAGCTTG  
|| |||| |||||  
AG GTGA ACTCGAAC  
ACA A  
GAM1350 DKFZp586H0623 3' GCCAGCCAGGTGTAATACAGTC 34072 CACTCTGA  
GAC GCTTGGCTGGC  
|| |||||

CTG TGGACCGACCG  
 ACATAATG  
 GAM1350 FLJ10932 3' AAGCTCAGGGCGGTCTGA 36890 A  
 TCGACC CTCTGAGCTT  
 ||||| |||||  
 AGCTGG GGGACTCGAA  
 C  
 GAM1350 FLJ14775 3' GCCAGCCAAAGTTTGA 51602 T  
 TC GAGCTTGGCTGGC  
 || |||||  
 AG TTTGAACCGACCG  
 —  
 GAM1350 FLJ20004 3' GCTTGAGCCCAGATAGTC 95297 CAC A \_  
 GAC TCTG GCTTG GC  
 ||| ||| ||||| ||  
 CTG AGAC CGAGT CG  
 AT\_ C T  
 GAM1350 KIAA0632 3' CCAGCCTCAGCCAGAG 31424 A T\_  
 CTCTG GCT GGCTGG  
 ||||| ||| |||||  
 GAGAC CGA CCGACC  
 \_ CT  
 GAM1350 MEF-2 5' GCCCCTCAGCTCAGGCGGCCGA 64386 A A T T CT  
 TCG CC C CTGAGCT GG GGC  
 ||| ||| ||||| || |||  
 AGC GG G GACTCGA TC CCG  
 C C \_ C C\_  
 GAM1350 MGC12921 3' GCCAGGAGTCAGAGCGG 63776 A G\_  
 CC CTCTGA CTTGGC  
 || ||||| |||||  
 GG GAGACT GGACCG  
 C GA  
 GAM1350 MGC2306 3' GCCAAAGCCAGAGTGG 50961 A \_  
 CCACTCTG GCTT GGC  
 ||||| ||| |||  
 GGTGAGAC CGAA CCG  
 \_ A  
 GAM1350 PPP1R12C 3' GCCAGGACCAGAGTGGCCG 34279 A AG  
 CG CCACTCTG CTTGGC  
 || ||||| |||||  
 GC GGTGAGAC GGACCG  
 C CA  
 GAM1350 RHOBTB3 3' CCAGCCTGGCCAAAACAGTG 29743 C\_\_ A T  
 CACT TG GCT GGCTGG  
 ||| || ||| |||||  
 GTGA AC CGG CCGACC  
 CAAA \_ T  
 GAM1350 RNF24 3' GCCAGCCAAACTGGGA 23319 G C  
 TCT AG TTGGCTGGC  
 ||| || |||||

AGG TC AACCGACCG  
 G A  
 GAM1350 SCYA21 3' GCCAGGTCCAGAGAGACCGA 11463 ACCA AG  
 TCG CTCTG CTTGGC  
 ||| |||| |||||  
 AGC GAGAC GGACCG  
 CAGA CT  
 GAM1350 SLC37A1 3' GCCAAGCCAGAGAACCGA 38564 ACCA A  
 TCG CTCTG GCTTGGC  
 ||| |||| |||||  
 AGC GAGAC CGAACCG  
 CAA\_ \_  
 GAM1350 X123 5' CCAGCCAAGTGCACAGA 69921 A\_\_  
 TCTG GCTTGGCTGG  
 |||| |||||  
 AGAC TGAACCGACC  
 ACG  
 GAM1350 LOC113444 3' GCCAGGCAGACCCAGCAGCAGC 56557 ACCA \_ AGC G  
 CGA TCG CTCTG TTG CTGGC  
 ||| || ||| ||| |||||  
 AGC GA GAC GAC GACCG  
 CGAC C CCA G  
 GAM1350 LOC116143 3' CCAGCCTGGCCAACATGGTC 73771 CTC A T  
 GACCA TG GCT GGCTGG  
 |||| || ||| |||||  
 CTGGT AC CGG CCGACC  
 ACA \_ T  
 GAM1350 LOC118987 3' GCCTGTTGGCCAGAGTAATC 73956 CC A T T  
 GA ACTCTG GCT GGC GGC  
 || ||||| ||| ||| |||  
 CT TGAGAC CGG TTG CCG  
 AA \_ \_ T  
 GAM1350 LOC149157 3' GCCAGTCAGAATGGCGA 79201 A C GC  
 TCG CCA TCTGA TTGGC  
 ||| ||| |||| |||||  
 AGC GGT AGACT GACCG  
 \_ A \_  
 GAM1350 LOC151124 5' GCCAGCAGGGGCTCAGA 85230 TG  
 TCTGAGCT GCTGGC  
 ||||| |||||  
 AGACTCGG CGACCG  
 GA  
 GAM1350 LOC151632 3' CCAGCCTGGCCAAAATGGTGA 85466 G CTC A T  
 TC ACCA TG GCT GGCTGG  
 || |||| || ||| |||||  
 AG TGGT AC CGG CCGACC  
 \_ AAA \_ T  
 GAM1350 LOC155036 5' CCAACCAAGCCCAGTCAGCGG 86339 A \_ A C  
 CC CT CTG GCTTGG TGG  
 || || ||| ||||| |||

GG GA GAC CGAACC ACC  
C CT C A  
GAM1350 LOC155435 3' CCAGCCAAACCCTCGTGG 81349 TCT C\_\_  
CCAC GAG TTGGCTGG  
|||| ||| |||||  
GGTG CTC AACCGACC  
\_\_ CCA  
GAM1350 LOC202934 3' GCCAACCCCTGTTTAGAGCAGTC 90413 CA TT C  
GAC CTCTGAGC GG TGGC  
||| ||||| || |||  
CTG GAGATTTG CC ACCG  
AC TC A  
GAM1350 LOC222066 3' CCAACCTGGCCAAAGTGGTGA 92743 G C A T C  
TC ACCACT TG GCT GG TGG  
|| ||||| || ||| |||  
AG TGGTGA AC CGG CC ACC  
\_ A \_ T A  
GAM1350 LOC57228 5' CCGAAACCCGGAGCGGCCGA 39998 A A AGC\_  
TCG CC CTCTG TTGG  
||| || ||||| |||  
AGC GG GAGGC AGCC  
C C CCAA  
GAM1350 LOC91813 5' GCCAGAAGCCCAGAGACAGCCG 67252 ACCA\_ A GG  
A TCG CTCTG GCTT CTGGC  
||| |||| ||| |||||  
AGC GAGAC CGAA GACCG  
CGACA C \_  
GAM1351 DDEF1 3' GAGCTTTAGCAGCCTC 59564 A AGATAC A  
GA GCT CTAAAGCT C  
|| ||| ||||| |  
CT CGA GATTTCGA G  
C C \_ \_ C  
GAM1351 DDX3 3' GAGCCTTAGGTATTTG 43759 A A  
TAGATACCTAA GCT C  
||||||| ||| |  
GTTTATGGATT CGA G  
C C  
GAM1351 GRAF 3' GGTAACCTCCCTCCCTAGCTTC 30573 ATACCTAA C  
GAAGCTAG AG TACC  
||||| || |||  
CTTCGATC TC ATGG  
CCTCCC\_ A  
GAM1351 MAT1A 3' AGCTTTAGAATCCCAGC 90825 A\_ AC  
GCT GAT CTAAAGCT  
||| ||| |||||  
CGA CTA GATTTCGA  
CC A\_  
GAM1351 MYLK 3' AGCTTCAGACATTTGGTT 97018 AC A  
AGCTAGAT CT AAGCT  
|||||| || |||||

		TTGGTTTA GA TTCGA	
		CA C	
GAM1351 RGL	3'	GTAGCTAAACTTAGCTTCA 30736	ATACCTAA
		TGAAGCTAG AGCTAC	
		ACTTCGATT TCGATG	
		CAAAA__	
GAM1351 ZFP93	3'	GTAGCCTTAATAACGTTAGTTT 14887	ATACC_ A
CA		TGAAGCTAG TAA GCTAC	
		ACTTTGATT ATT CGATG	
		GCAATA C	
GAM1351 C3orf4	3'	AGCATTGACACATAGCTTCA 39118	GATACC A
		TGAAGCTA TAA GCT	
		ACTTCGAT GTT CGA	
		ACACA_ A	
GAM1351 D2S448	3'	GGCAGGAGTCCTAGCTTCA 73527	_ A AAA
		TGAAGCTAG AT CCT GCT	
		ACTTCGATC TG GGA CGG	
		C A ____	
GAM1351 FLJ12604	3'	AGCTTTAGTATTGACTTCA 64436	CTA C
		TGAAG GATAC TAAAGCT	
		ACTTC TTATG ATTTCGA	
		AG_ _	
GAM1351 FLJ14280	5'	GGTAGCTCCTGGCCAGCTCA 45999	A AGATA TAA
		TGA GCT CC AGCTACC	
		ACT CGA GG TCGATGG	
		_ CC__ TCC	
GAM1351 H2AFJ	3'	GTTGTCAAGTTTCTAGCTTCA 36842	T CTAA_
		TGAAGCTAGA AC AGC	
		ACTTCGATCT TG TTG	
		T AACTG	
GAM1351 KIAA0441	3'	TAGCTTTGTTAATCTAGCCTC 28960	A ACC
		GA GCTAGAT TAAAGCTA	
		CT CGATCTA GTTTCGAT	
		C ATT	
GAM1351 KIAA1128	3'	TAGCTTTATGTGCAGCTTGCA 68483	_ AGA C
		TG AAGCT TAC TAAAGCTA	
		AC TTCGA GTG ATTTCGAT	
		G C__ T	
GAM1351 KIAA1750	3'	TAGCCCCAGGAGTGGGCTTTA 68254	AG A AAA
		TGAAGCT AT CCT GCTA	



		ATTTCGG TG GGA CGAT		
		G_ A CCC		
GAM1351	KPNA5	3' GGTAGCTTCAGGTA	9629	A A
		AG TACCT AAGCTACC		
		TC ATGGA TTCGATGG		
		A C		
GAM1351	MAGEH1	5' GGTAGCTTCAGCGGCAGCAGCT	25924	AGATAC_ A
	TC	GAAGCT CT AAGCTACC		
		CTTCGA GA TTCGATGG		
		CGACGGC C		
GAM1351	MGC12921	3' AGCCCTATTTAGCTTC	63774	CCTAAA
		GAAGCTAGATA GCT		
		CTTCGATTTAT CGA		
		CC_____		
GAM1351	MGC30052	3' AGCTTTAGAATAGCTTC	58532	GATAC
		GAAGCTA CTAAAGCT		
		CTTCGAT GATTTCGA		
		AA_____		
GAM1351	RNF34	3' AGCAAGGGCTGCATCTAGCTTC	47094	A___ AAA
		GAAGCTAGAT CCT GCT		
		CTTCGATCTA GGG CGA		
		CGTC AA_		
GAM1351	TNFRSF19L	3' GTAGCTTTTATCCCAGC	51779	A_ CCT
		GCT GATA AAAGCTAC		
		CGA CTAT TTTCGATG		
		CC _____		
GAM1351	LOC121536	3' AGCAAATCACATTTAGCTTCA	74082	ACCTAAA
		TGAAGCTAGAT GCT		
		ACTTCGATTTA CGA		
		CACTAAA		
GAM1351	LOC255452	3' TAGGTACCTACCTTCA	97544	C A
		TGAAG TAG TACCTA		
		ACTTC ATC ATGGAT		
		C C		
GAM1351	LOC257396	3' GGCAGCTTTAGGCTTAACTT	97139	C ATA A
		AAG TAG CCTAAAGCT CC		
		TTC ATT GGATTTCGA GG		
		A C_ C		
GAM1351	LOC92710	3' GTACAAGGCATCTAGCTT	70359	A AAAGC
		AAGCTAGAT CCT TAC		

			TTCGATCTA GGA ATG		
			C AC__		
GAM1352 CCR2	3'	CAATCTCTGATTCTGTCA	5386	CG	GG
		TGACAGAA AGAG TG			
		ACTGTCTT TCTC AC			
		AG TA			
GAM1352 CYP51	5'	AGCTTCTCTCGTTCCGTC	5779	A	T
		GAC GAACGAGAGGG GCT			
		CTG CTTGCTCTCTT CGA			
		C _			
GAM1352 GABRP	3'	TCAGAGAGTCGCTGTCATTCTG	26402	C G _	TG
TCA		TGACAGAA GA AG GG CTCTGA			
		ACTGTCTT CT TC CT GAGACT			
		A G G GA			
GAM1352 GMPS	5'	GGCACCCCTCCCGCCCCGTC	13918	AGAA	A
		GAC CG GAGGGTGCT			
		CTG GC CTCCCACGG			
		CCCC C			
GAM1352 LIMD1	3'	GGGGACCCTCTCTTCCCATCA	26463	CA_ C	G
		TGA GAA GAGAGGGT CTC			
		ACT CTT CTCTCCCA GGG			
		ACC _ G			
GAM1352 OCRL	3'	CACTCCCCTCGTTCTGTCA	7825	A _	
		TGACAGAACGAG GG GTG			
		ACTGTCTTGCTC CC CAC			
		C T			
GAM1352 OCRL	3'	CACTCCCCTCGTTCTGTCA	4259	A _	
		TGACAGAACGAG GG GTG			
		ACTGTCTTGCTC CC CAC			
		C T			
GAM1352 PYGO2	3'	GCTCCCTCTCGCTCTCTCA	63987	C A	T
		TGA AGA CGAGAGGG GC			
		ACT TCT GCTCTCCC CG			
		C C T			
GAM1352 TCFL4	3'	TCAAAATCACCCTTTCTGTCA	63465	ACGA	CTC_
		TGACAGA GAGGGTG TGA			
		ACTGTCT TTCCAC ACT			
		____ TAAA			
GAM1352 BIRC1	3'	CAGTCTCTCCCATCTGT	15787	C_	G
		ACAGAA GAGAGG TG			

TGTCTT CTCTCT AC  
 ACC G  
 GAM1352 CHERP 3' AGCGCCTTCCACTCCATCA 21096 CA ACGA  
 TGA GA GAGGGTGTCT  
 ||| || |||||  
 ACT CT CTTCCGCGA  
 AC CAC\_  
 GAM1352 DKFZP564K2062 3' TCAGAAGTCTCAGTTCTGTCA 31238 GA GTGC  
 TGACAGAAC GAGG TCTGA  
 ||||| ||| ||||  
 ACTGTCTTG CTCT AGACT  
 A\_ GA\_  
 GAM1352 FLJ10482 3' TCAGAGTGATCTGTCCTGCCA 36165 A AAC G GG  
 TG CAG GA AG TGCTCTGA  
 || ||| || |||||  
 AC GTC CT TC GTGAGACT  
 C \_ G TA  
 GAM1352 FLJ13848 3' CAGAAGGACTTCTCGTTCCTCA 45461 CA GTGC  
 TGA GAACGAGAGG TCTG  
 || ||||| |||  
 ACT CTTGCTCTTC AGAC  
 C\_ AGGA  
 GAM1352 FLJ21802 3' CAGAGCACCAACTTCATC 44980 AC AG  
 GA GAG GGTGCTCTG  
 || ||| |||||  
 CT TTC CCACGAGAC  
 AC AA  
 GAM1352 KIAA1458 3' CAGGACCTCCATTCTGTCA 69002 CGA GTGC  
 TGACAGAA GAGG TCTG  
 ||||| ||| ||||  
 ACTGTCTT CTCC GGAC  
 AC\_ A\_  
 GAM1352 MGC10500 3' GTCCCCCTCGTTTCTGT 48935 A TG  
 ACAGAACGAG GGG C  
 ||||| ||| |  
 TGTCTTGCTC CCC G  
 \_ CT  
 GAM1352 NDP52 3' CATCCTCTCACCTGTCA 19526 AAC  
 TGACAG GAGAGGGTG  
 |||| |||||  
 ACTGTC CTCTCCTAC  
 CA\_  
 GAM1352 SEC24C 3' TCAAGTATCCTGCCACTCTGTC 17000 ACGAG C  
 A TGACAGA AGGGTGCT TGA  
 |||| ||||| |||  
 ACTGTCT TCCTATGA ACT  
 CACCG \_  
 GAM1352 SNRPD3 5' CAGAGCCGA ACTCTCTTCCTGC 14800 A AAC \_  
 CA TG CAG GAGAGGGT GCTCTG  
 || ||| ||||| |||||

AC GTC TTCTCTCA CGAGAC  
 C C\_\_ AGC  
 GAM1352 LOC152328 3' CAAGTGCCCTCCCCTATCA 80523 C AACGA TG C  
 TGA AG GAGGG CT TG  
 ||| || |||| ||||  
 ACT TC CTCCC GA AC  
 A CC\_\_ GT \_  
 GAM1352 LOC158835 3' CATCCCTCTCATTCCATC 82009 CA C \_  
 GA GAA GAGAGGG TG  
 || ||| ||||| ||  
 CT CTT CTCTCCC AC  
 AC A T  
 GAM1352 LOC197003 3' CAGACCTTCTCACACTGCCA 87871 A AAC TGC  
 TG CAG GAGAGGG TCTG  
 || ||| ||||| ||||  
 AC GTC CTCTTCC AGAC  
 C ACA \_  
 GAM1352 LOC257443 3' CAGGACCTCCATTCTGTCA 95846 CGA GTGC  
 TGACAGAA GAGG TCTG  
 ||||| ||| ||||  
 ACTGTCTT CTCC GGAC  
 AC\_ A\_  
 GAM1352 LOC257451 3' GCTCCCTCTCGCTCTCTCA 95557 C A T  
 TGA AGA CGAGAGGG GC  
 ||| ||| ||||| ||  
 ACT TCT GCTCTCCC CG  
 C C T  
 GAM1352 LOC92609 5' CAAAGTCTCTCGTTC 72844 GGT C  
 GAACGAGAG GCT TG  
 ||||| ||| ||  
 CTTGCTCTC TGA AC  
 \_ A  
 GAM1353 FLNA 3' GCCCGCCTGTCACTGCAG 7580 A\_  
 CTGCAGTGACAGGC GC  
 ||||| ||||| ||  
 GACGTCACTGTCCG CG  
 CC  
 GAM1353 Nrap 3' ACTTAGCATGCCCTTCACTGCA 43346 CA \_ CTT  
 GT ACTGCAGTGA GGCA GC AGT  
 ||||| |||| ||| ||  
 TGACGTCACT CCGT CG TCA  
 TC A AT\_  
 GAM1353 Nrap 3' ACTTAGCATGCCCTTCACTGCA 57633 CA \_ CTT  
 GT ACTGCAGTGA GGCA GC AGT  
 ||||| |||| ||| ||  
 TGACGTCACT CCGT CG TCA  
 TC A AT\_  
 GAM1353 ZFX 5' GCCCGCCTGTCACTGCCGT 12718 T A\_  
 AC GCAGTGACAGGC GC  
 || ||||| ||||| ||

			TG CGTCACTGTCCG CG			
			C CC			
GAM1353	C19orf7	3'	GCTATGCCTGCACTGCAG 61129	A	___	
			CTGCAGTG CAGGCA GC			
			GACGTCAC GTCCGT CG			
			_ AT			
GAM1353	FLJ10604	3'	ACTAAGGCCACTGTGCCACTGT 36334	___	GCA	
			GCAGTG ACAG GCCTTAGT			
			TGTCAC TGTC CGGAATCA			
			CG AC_			
GAM1353	FLJ12363	3'	AGGCACCTGTCACCACA 49670	CA	CA	
			TG GTGACAGG GCCT			
			AC CACTGTCC CGGA			
			AC A_			
GAM1353	FLJ14525	3'	ACCAAGGCTGCCCAGTG 51411	G ACA	A	
			CA TG GGCAGCCTT GT			
			GT AC CCGTCGGAA CA			
			G ___ C			
GAM1353	GTF2E1	3'	TTGCTGTCACTACAGT 18621	C	G	
			ACTG AGTGACAG CAG			
			TGAC TCACTGTC GTT			
			A _			
GAM1353	HYPC	5'	GGTGCCTGTCACCGCAG 64610	A	G	
			CTGC GTGACAGGCA CC			
			GACG CACTGTCCGT GG			
			C _			
GAM1353	KIAA0937	3'	CTGCCTGTCACCCAGT 91586	CA		
			ACTG GTGACAGGCAG			
			TGAC CACTGTCCGTC			
			C_			
GAM1353	KIAA1010	3'	GTTGCCTGCCACCCAG 72073	CA	A	
			CTG GTG CAGGCAGC			
			GAC CAC GTCCGTTG			
			C_ C			
GAM1353	KIAA1301	3'	ACTAAAGGCACGTACTGCAGT 66340	ACAGGCA	___	
			ACTGCAGTG GCCTT AGT			
			TGACGTCAT CGGAA TCA			
			GCA___ A			
GAM1353	KIAA1393	3'	ACTAAGGCTACCAAATAC 72095	ACA	C	
			GTG GG AGCCTTAGT			

			CAT CC TCGGAATCA			
			AAA A			
GAM1353	LMOD1	3'	TTGCCTGTCACCCCAGT	24048	CA	
			ACTG GTGACAGGCAG			
			TGAC CACTGTCCGTT			
			CC			
GAM1353	PTDSS2	3'	GCTCCCTGTCACCCAG	47889	CA	C
			CTG GTGACAGG AGC			
			GAC CACTGTCC TCG			
			C_ C			
GAM1353	LOC125704	5'	GCTGCCTGCACTACA	74410	C	A
			TG AGTG CAGGCAGC			
			AC TCAC GTCCGTCG			
			A _			
GAM1353	LOC131368	3'	ACTAAACTATGTGTGACTGCAG	75855		
		T	ACTGCAGT ACA AG TTAGT		G	GGC CC
			TGACGTCA TGT TC AATCA			
			G GTA A_			
GAM1353	LOC145719	5'	GCCGTACCTGTCACGCAGT	83452	A	CA__
			ACTGC GTGACAGG GC			
			TGACG CACTGTCC CG			
			_ ATGC			
GAM1353	LOC145720	5'	GCCGTACCTGTCACGCAGT	83434	A	CA__
			ACTGC GTGACAGG GC			
			TGACG CACTGTCC CG			
			_ ATGC			
GAM1353	LOC158402	3'	CTAAAGTTTGTACACGCA	86803	A	AGCC
			TGC GTGACAGGC TTAG			
			ACG CACTGTTTG AATC			
			C A__			
GAM1353	LOC161176	5'	GCTGCCCATCACGCAG	82260	A	CA
			CTGC GTGA GGCAGC			
			GACG CACT CCGTCG			
			_ AC			
GAM1353	LOC197114	5'	GCCGTACCTGTCATGCAGT	89706	G	CA__
			ACTGCA TGACAGG GC			
			TGACGT ACTGTCC CG			
			_ ATGC			
GAM1353	LOC197117	5'	GCCGTACCTGTCATGCAGT	89720	G	CA__
			ACTGCA TGACAGG GC			

TGACGT ACTGTCC CG  
 \_ ATGC  
 GAM1353 LOC199796 5' ACCAAGGTGAAGCCACTGC 74448 GACA A\_\_ A  
 GCAGT GGC GCCTT GT  
 ||||| ||| ||||| ||  
 CGTCA CCG TGGAA CA  
 \_\_\_\_ AAG C  
 GAM1353 LOC203080 5' ACTAAGGCCGCTGAGCCACAGT 89264 CA GACA A  
 ACTG GT GGC GCCTTAGT  
 ||||| || ||| ||||| ||  
 TGAC CG TCG CGGAATCA  
 AC AG\_\_ C  
 GAM1354 ACCN1 3' TATTAAGCTGGTCTTGTGGA 6584 \_\_ TA CC  
 AA TTTTCAC GGCCA GCTT AATA  
 ||||| ||||| ||||| |||||  
 AAAGGTG CTGGT CGAA TTAT  
 TT \_\_ AA  
 GAM1354 IRF2 5' TTGGTAGCGTGAAAA 9358 GGCCATA T  
 TTTTCAC GCT CCAA  
 ||||| ||| |||||  
 AAAAGTG CGA GGTT  
 \_\_\_\_ T  
 GAM1354 PABPN1 5' ATTGGAAGCTGTCCAGGAAAA 16174 AC CC  
 TTTTC GG ATAGCTTCCAAT  
 ||||| || ||||| ||||| |||||  
 AAAAG CC TGTCGAAGGTTA  
 GA \_\_  
 GAM1354 TPO 5' GAGTTACAGCCGTGAAAA 5046 CA  
 TTTTCACGGC TAGCTT  
 ||||| |||||  
 AAAAGTGCCG ATTGAG  
 AC  
 GAM1354 ARHU 3' TATTAGAAGCTATATTAGCTG 41079 C\_\_ C  
 CGGC ATAGCTTC AATA  
 ||||| ||||| ||||| |||||  
 GTCG TATCGAAG TTAT  
 ATTA A  
 GAM1354 FLJ12998 3' ATTGGTTTTGCCGTGAAAA 42835 CATAGCTT  
 TTTTCACGGC CCAAT  
 ||||| ||||| ||||| |||||  
 AAAAGTGCCG GGTTA  
 TTTT\_\_  
 GAM1354 GNB4 3' AGCCTATAGCTGTGAAAA 41267 C \_  
 TTTTCACGGC ATAG CT  
 ||||| ||||| ||||| |||||  
 AAAAGTGTCG TATC GA  
 A C  
 GAM1354 LOC150418 3' GAGTCGGCCGTGAAGA 65509 ATA  
 TTTTCACGGCC GCTT  
 ||||| ||||| ||||| |||||

			AGAAGTGCCGG	TGAG		
			C__			
GAM1354	LOC199957	3'	GAGTCGGCCGTGAAGA	88505	ATA	
			TTTTCACGGCC	GCTT		
			AGAAGTGCCGG	TGAG		
			C__			
GAM1354	LOC91431	5'	ATTGGAAATGCAAGGCCGTGGA	56922	ATA	__
	AA		TTTTCACGGCC	GC TTCCAAT		
			AAAGGTGCCGG	CG AAGGTTA		
			AA_	TA		
GAM1355	COL5A1	3'	AGCAACCTCGTACCT	3631	C	G
			AGG	ATGAGGTTG CT		
			TCC	TGCTCCAAC GA		
			A	_		
GAM1355	GPRC5C	3'	GAGGAGCCAACCCAGCCT	37850	A A	ATA
			AGGC	TG GGTTGGCT TC		
			TCCG	AC CCAACCGA AG		
			_ C	GG_		
GAM1355	GPRC5C	3'	GAGGAGCCAACCCAGCCT	41846	A A	ATA
			AGGC	TG GGTTGGCT TC		
			TCCG	AC CCAACCGA AG		
			_ C	GG_		
GAM1355	ICAM1	5'	AGTTGCAACCTCAGCCT	71574	A	__
			AGGC	TGAGGTTG GCT		
			TCCG	ACTCCAAC TGA		
			_	GT		
GAM1355	ITIH1	3'	AGCACCTCATGCCT	9411	TG	
			AGGC	ATGAGGT GCT		
			TCCG	TACTCCA CGA		
			__			
GAM1355	NR1I2	5'	GATATAGCCCCATGCT	13969	A	TTG
			GGCATG	GG GCTATATC		
			TCGTAC	CC CGATATAG		
			__			
GAM1355	PRODH	3'	AGCCAACCCCATCCT	32921	C A	
			AGG	ATG GGTTGGCT		
			TCC	TAC CCAACCGA		
			_ C			
GAM1355	SHC1	3'	TGTGCCAACCTGATGCC	11654	G	T
			GGCAT	AGGTTGGC ATA		



			CCGTA TCCAACCG TGT			
			G _			
GAM1355	STAT6	3'	TGGACACTTGCTCATGCC	12026	GTT	CTATA
			GGCATGAG GG TCCA			
			CCGTACTC TC AGGT			
			GT_ AC__			
GAM1355	TYRO3	5'	TGGCAACCTCACACCT	20847	CA	G
			AGG TGAGGTTG CTA			
			TCC ACTCCAAC GGT			
			AC _			
GAM1355	DDR1	3'	TGGACACACTCTCATGTC	8727	GT	GCTATA
			GGCATGAG TG TCCA			
			CTGTACTC AC AGGT			
			TC AC__			
GAM1355	DDR1	3'	TGGACACACTCTCATGTC	25700	GT	GCTATA
			GGCATGAG TG TCCA			
			CTGTACTC AC AGGT			
			TC AC__			
GAM1355	DDR1	3'	TGGACACACTCTCATGTC	25709	GT	GCTATA
			GGCATGAG TG TCCA			
			CTGTACTC AC AGGT			
			TC AC__			
GAM1355	FLJ11370	3'	ATAGATAACCTCACCCC	46369	CA	G
			GG TGAGGTTG CTAT			
			CC ACTCCAAT GATA			
			CC A			
GAM1355	FLJ14888	3'	TGGACATGGTGGCTCATGCCT	51686	GTTG	A
			AGGCATGAG GCTAT TCCA			
			TCCGTACTC TGGTA AGGT			
			GG_ C			
GAM1355	FLJ20195	3'	TGGCCACCTCATGCC	34718	T	
			GGCATGAGGT GGCTA			
			CCGTACTCCA CCGGT			
			_			
GAM1355	KIAA0561	3'	GATACAGCCGACTCCAGCC	65884	A AG	A
			GGC TG GTTGGCT TATC			
			CCG AC CAGCCGA ATAG			
			_ CT C			
GAM1355	KIAA0620	3'	TGGAGGCCAACCCACGGCC	62123	A_ A	ATA
			GGC TG GGTGGCT TCCA			

CCG AC CCAACCGG AGGT  
 GC C \_\_\_\_  
 GAM1355 KIAA1266 3' GTGTGGCCAACCCCATGACC 66126 \_ A  
 GG CATG GGTTGGCTATAT  
 || ||| |||||  
 CC GTAC CCAACCGGTGTG  
 A C  
 GAM1355 MFN2 5' ATAGCCAACCTCAACCT 29597 CA  
 AGG TGAGGTTGGCTAT  
 ||| |||||  
 TCC ACTCCAACCGATA  
 A\_  
 GAM1355 MGC2452 5' ATATAGGCTGATTATGCC 50978 AG TG \_  
 GGCATG GT GC TATAT  
 ||||| || || |||||  
 CCGTAT TA CG ATATA  
 \_ GT G  
 GAM1355 MYO3B 3' TTGGACATATGGTCCATGCCT 57310 AGGTT \_  
 AGGCATG GGCTATA TCCAA  
 ||||| ||||| |||||  
 TCCGTAC CTGGTAT AGGTT  
 \_ AC  
 GAM1355 SDC3 3' TGGCAGGCCAACCTCAGCC 27769 A ATAT  
 GGC TGAGGTTGGCT CCA  
 ||| ||||| |||  
 CCG ACTCCAACCGG GGT  
 \_ AC\_  
 GAM1355 TRIM11 3' GGATGGGAGCCAGCCCCATGCC 72833 A A\_  
 T AGGCATG GGTTGGCT TATCC  
 ||||| ||||| |||||  
 TCCGTAC CCGACCGA GTAGG  
 C GG  
 GAM1355 LOC150005 5' TTGGATTAGTTCAACCTCAGAC 84824 CA \_ T  
 C GG TGAGGTTGG CTA ATCCAA  
 || ||||| ||| |||||  
 CC ACTCCAACCT GAT TAGGTT  
 AG T \_  
 GAM1355 LOC152313 3' GACATAGCCAAATGTC 85662 GAGG A  
 GGCAT TTGGCTAT TC  
 ||||| ||||| ||  
 CTGTA AACCGATA AG  
 \_ C  
 GAM1355 LOC152313 5' GACATAGCCAAATGTC 85663 GAGG A  
 GGCAT TTGGCTAT TC  
 ||||| ||||| ||  
 CTGTA AACCGATA AG  
 \_ C  
 GAM1355 LOC158230 3' TGGGAGGCCCAACCTCCTGCC 81803 T \_ ATA  
 GGCA GAGGTTGG CT TCCA  
 ||||| ||||| || |||||

			CCGT CTCCAACC GG GGGT	
			C C A_	
GAM1355	LOC158857 5'	TGGCCACCATGCCT	86912	GA T
		AGGCAT GGT GGCTA		
		TCCGTA CCA CCGGT		
		— —		
GAM1355	LOC159049 5'	TGGCCACCATGCCT	86975	GA T
		AGGCAT GGT GGCTA		
		TCCGTA CCA CCGGT		
		— —		
GAM1355	LOC196337 3'	AGCCAGCCCACAGCCT	87645	A_ A
		AGGC TG GGTTGGCT		
		TCCG AC CCGACCGA		
		AC _		
GAM1355	LOC199796 5'	GGCCAACCCCATCCT	74456	C A
		AGG ATG GGTTGGCT		
		TCC TAC CCAACCGG		
		_ C		
GAM1355	LOC222031 3'	TGGCCAACCTCCGCCT	94031	AT
		AGGC GAGGTTGGCTA		
		TCCG CTCCAACCGGT		
		C_		
GAM1355	LOC223009 5'	GGCCAAGCTCATGCCT	94380	G
		AGGCATGAG TTGGCT		
		TCCGTACTC AACCGG		
		G		
GAM1355	LOC255798 3'	GGACATGGTGGCTCATGCCT	97005	GTTG A
		AGGCATGAG GCTAT TCC		
		TCCGTACTC TGGTA AGG		
		GG_ C		
GAM1355	LOC257464 5'	GGACACATCTCATGCT	89671	T GCTATA
		GGCATGAGGT G TCC		
		TCGTACTCTA C AGG		
		_ AC_		
GAM1356	ACCN1 3'	TATTAAAAGCTGGTCTTGGA	6584	_ TA CC
	AA	TTTTCAC GGCCA GCTT AATA		
		AAAGGTG CTGGT CGAA TTAT		
		TT _ AA		
GAM1356	IRF2 5'	TTGGTAGCGTGAAAA	9358	GGCCATA T
		TTTTCAC GCT CCAA		

		AAAAGTG	CGA GGTT		
		_____	T		
GAM1356	PABPN1	5'	ATTGGAAGCTGTCCAGGAAAA	16174	AC CC
			TTTTC GG ATAGCTTCCAAT		
			AAAAG CC TGTCGAAGGTTA		
			GA _		
GAM1356	TPO	5'	GAGTTACAGCCGTGAAAA	5046	CA
			TTTTCACGGC TAGCTT		
			AAAAGTGCCG ATTGAG		
			AC		
GAM1356	ARHU	3'	TATTAGAAGCTATATTAGCTG	41079	C__ C
			CGGC ATAGCTTC AATA		
			GTCG TATCGAAG TTAT		
			ATTA A		
GAM1356	FLJ12998	3'	ATTGGTTTTGCCGTGAAAA	42835	CATAGCTT
			TTTTCACGGC CCAAT		
			AAAAGTGCCG GGTTA		
			TTTT__		
GAM1356	GNB4	3'	AGCCTATAGCTGTGAAAA	41267	C _
			TTTTCACGGC ATAG CT		
			AAAAGTGTCG TATC GA		
			A C		
GAM1356	LOC150418	3'	GAGTCGGCCGTGAAGA	65509	ATA
			TTTTCACGGCC GCTT		
			AGAAGTGCCGG TGAG		
			C__		
GAM1356	LOC199957	3'	GAGTCGGCCGTGAAGA	88505	ATA
			TTTTCACGGCC GCTT		
			AGAAGTGCCGG TGAG		
			C__		
GAM1356	LOC91431	5'	ATTGGAAATGCAAGGCCGTGGA	56922	ATA __
	AA		TTTTCACGGCC GC TTCCAAT		
			AAAGGTGCCGG CG AAGGTTA		
			AA_ TA		
GAM1357	BTG2	3'	AGGTTAGCAACTGTGAA	22208	T G
			TTCACA GTTGCTAA TT		
			AAGTGT CAACGATT GA		
			_ G		
GAM1357	CALCR	3'	ACTGCAACTTGTGAA	8216	T TA
			TTCACA GTTGC AGT		

			AAGTGT CAACG TCA		
			T _		
GAM1357 DDX15	3'	TACAACTTGTGCTTATGT	7231	TT _	
		ACATG GC TAAGTTGTA			
		TGTAT CG GTTCAACAT			
		T_ T			
GAM1357 EPHA3	3'	ACAACTTAGTGTAATAT	17863	_	
		ATGTT GCTAAGTTGT			
		TATAA TGATTCAACA			
		TG			
GAM1357 KMO	3'	ACAACTTAACTAGCATGT	13438	C_	
		ACATGTTG TAAGTTGT			
		TGTACGAT ATTCAACA			
		CA			
GAM1357 MBD1	3'	ACATGGCAACGTGTGAA	31785	A	
		TTCACATGTTGCTA GT			
		AAGTGTGCAACGGT CA			
		A			
GAM1357 MBD1	3'	ACATGGCAACGTGTGAA	31770	A	
		TTCACATGTTGCTA GT			
		AAGTGTGCAACGGT CA			
		A			
GAM1357 MBD1	3'	ACATGGCAACGTGTGAA	9944	A	
		TTCACATGTTGCTA GT			
		AAGTGTGCAACGGT CA			
		A			
GAM1357 MBD1	3'	ACATGGCAACGTGTGAA	31778	A	
		TTCACATGTTGCTA GT			
		AAGTGTGCAACGGT CA			
		A			
GAM1357 PIGC	3'	TACATGCTGTAACATATGAA	10557	C TA _	
		TTCA ATGTTGC AGT TGTA			
		AAGT TACAATG TCG ACAT			
		A _ T			
GAM1357 PPP2R5E	3'	TACAATTTTCAAATGTGAA	20728	G CT	
		TTCACAT TTG AAGTTGTA			
		AAGTGTA AAC TTTAACAT			
		_ T_			
GAM1357 TSG	3'	TACAACTTTGGTCATATGAGA	40238	A T _	
		TC CATGT GCTAA GTTGTA			

		AG GTATA TGGTT CAACAT	
		A C T	
GAM1357 CAPS2	3'	ACTTGGCAGCAACATGAG 70602	CA_
		TTCA TGTTGCTAAGT	
		GAGT ACGACGGTTCA	
		ACA	
GAM1357 CDA02	5'	TACAACTTTATGATGTGAA 67851	GTTGCT
		TTCACAT AAGTTGTA	
		AAGTGTA TTCAACAT	
		GTAT__	
GAM1357 FLJ10035	3'	TAGCAACAGCATGTGAA 35749	__
		TTCACATGT TGCTA	
		AAGTGTACG ACGAT	
		ACA	
GAM1357 FLJ23420	5'	TACAACCTGGTCTATGTGGA 46849	TT A
		TTCACATG GCTA GTTGTA	
		AGGTGTAT TGGT CAACAT	
		C_ C	
GAM1357 GSPT2	3'	ATAACTAACATGTGAA 36119	GCTA
		TTCACATGTT AGTTGT	
		AAGTGTACAA TCAATA	
		__	
GAM1357 HNK-1ST	3'	TACAACCTTAGTTTGGATGT 16772	GTT_
		ACAT GCTAAGTTGTA	
		TGTA TGATTCAACAT	
		GGTT	
GAM1357 HYPH	3'	ACATAGCACATGTGAA 94896	T A
		TTCACATGT GCTA GT	
		AAGTGTACA CGAT CA	
		_ A	
GAM1357 IMPACT	3'	ACAATTTCAACATGT 37387	CT
		ACATGTTG AAGTTGT	
		TGTACAAC TTTAACA	
		__	
GAM1357 KIAA0089	3'	ACTACAATATGTGAA 69961	CTA
		TTCACATGTTG AGT	
		AAGTGTATAAC TCA	
		A__	
GAM1357 KIAA0229	3'	ACAACCTTAGAACAGACTGAA 92422	CA_ G
		TTCA TGTT CTAAGTTGT	

			AAGT ACAA GATTCAACA	
			CAG _	
GAM1357	KIAA0256	3'	ACAACTTGTGACATGT 64415	TG T
			ACATGT C AAGTTGT	
			TGTACA G TTCAACA	
			GT _	
GAM1357	KIAA1203	3'	TACAACTTTAGGCCACA 71644	T _
			TGT GCT AAGTTGTA	
			ACA CGG TTCAACAT	
			C AT	
GAM1357	KIAA1260	3'	CAACTTAGCACACGTGAA 60024	A T
			TTCAC TGT GCTAAGTTG	
			AAGTG ACA CGATTCAAC	
			C _	
GAM1357	KIAA1577	3'	TACAACTTATGTATACAT 64481	_ _
			ATGT TGC TAAGTTGTA	
			TACA ATG ATTCAACAT	
			T T	
GAM1357	KIAA1737	3'	ATTTAGCAAATGTGAA 67349	G
			TTCACAT TTGCTAAGT	
			AAGTGTA AACGATTTA	
			-	
GAM1357	NKX2B	5'	TACAACTTTGCGACAT 10236	T
			ATGTTGC AAGTTGTA	
			TACAGCG TTCAACAT	
			T	
GAM1357	OLFM3	3'	TACAACTTGCAATAATGAA 82146	CA T
			TTCA TGTTGC AAGTTGTA	
			AAGT ATAACG TTCAACAT	
			A_ _	
GAM1357	POT1	3'	TACAACTTACAATAATTGAA 31280	CAT_ C
			TTCA GTTG TAAGTTGTA	
			AAGT CAAC ATTCAACAT	
			TAAT _	
GAM1357	SYNPO2	3'	TAACGAAGTAACATGT 71897	AA
			ACATGTTGCT GTTG	
			TGTACAATGA CAAT	
			AG	
GAM1357	TNRC9	3'	ACCTACAATATGTGAA 71287	C A
			TTCACATGTTG TA GT	

	AAGTGTATAAC AT CA		
	— C		
GAM1357 LOC145598 3'	TACAACTTAAGCATTTGAA 77284	C	GC
	TTCA ATGTT TAAGTTGTA		
	AAGT TACGA ATTCAACAT		
	T —		
GAM1357 LOC145854 3'	CAGCTGACCAACATGTGAA 77550		CTA
	TTCACATGTTG AGTTG		
	AAGTGTACAAC TCGAC		
	CAG		
GAM1357 LOC149703 5'	TACAGATAAAACATGTGAA 84658		GCTAAG
	TTCACATGTT TTGTA		
	AAGTGTACAA GACAT		
	AATA—		
GAM1357 LOC158263 3'	ACAACCTCAGGCATGTGA 81840		GCTAA
	TCACATGTT GTTGT		
	AGTGTACGG CAACA		
	ACTC—		
GAM1357 LOC158382 3'	GACTTAACAACATGTGA 86785	C	
	TCACATGTTG TAAGTT		
	AGTGTACAAC ATTCAG		
	A		
GAM1357 LOC158956 3'	CAGCTGACCAACATGTGAA 66641		CTA
	TTCACATGTTG AGTTG		
	AAGTGTACAAC TCGAC		
	CAG		
GAM1357 LOC253003 3'	TACAACTTAAGTGATGT 96894	TG	—
	ATGT CT AAGTTGTA		
	TGTA GA TTCAACAT		
	GT A		
GAM1357 LOC56267 3'	TACAACTTTAACATG 39014		CT
	CATGTTG AAGTTGTA		
	GTACAAT TTCAACAT		
	—		
GAM1357 LOC92360 3'	ACAACTCATCACATGTGA 69068		TGCTA
	TCACATGT AGTTGT		
	AGTGTACA TCAACA		
	CTAC—		
GAM1357 LOC92539 5'	TACAACTTACCTGACATG 69641		GC—
	CATGTT TAAGTTGTA		



			GTACAG ATTCAACAT		
			TCC		
GAM1358	ADAM20	5'	CATAATGACAGCTTCA	13765	C CT
			TGAAGCTG TCAT TG		
			ACTTCGAC AGTA AC		
			_ AT		
GAM1358	AICDA	3'	ATGAAGATGAGCAGATCCA	40323	AAG G
			TG CTGCTCATCTT AT		
			AC GACGAGTAGAA TA		
			CTA G		
GAM1358	ALDH3B2	5'	TCAAGAAAACAAGCAGCTTC	5508	CA__
			GAAGCTGCT TCTTGA		
			CTTCGACGA AGAACT		
			ACAAA		
GAM1358	CLCN6	3'	GGATAAAGCAGCTTCA	41389	C_
			TGAAGCTGCT ATCT		
			ACTTCGACGA TAGG		
			AA		
GAM1358	CLCN6	3'	GGATAAAGCAGCTTCA	41404	C_
			TGAAGCTGCT ATCT		
			ACTTCGACGA TAGG		
			AA		
GAM1358	CLCN6	3'	GGATAAAGCAGCTTCA	7082	C_
			TGAAGCTGCT ATCT		
			ACTTCGACGA TAGG		
			AA		
GAM1358	DCTN1	3'	TTGATTAAAGCAACTTC	14556	C CATC
			GAAG TGCT TTGATCAA		
			CTTC ACGA AATTAGTT		
			A _		
GAM1358	DCTN1	3'	TTGATTAAAGCAACTTC	43477	C CATC
			GAAG TGCT TTGATCAA		
			CTTC ACGA AATTAGTT		
			A _		
GAM1358	DFFB	3'	TGGCAAATGGGCAGCTCCA	87402	A C A
			TG AGCTGCTCAT TTG TCA		
			AC TCGACGGGTA AAC GGT		
			C _ _		
GAM1358	DHFR	3'	TCAACTGAGCAGTTTCA	5815	TC
			TGAAGCTGCTCA TTGA		

			ACTTTGACGAGT AACT		
			C_		
GAM1358	ESR1	3'	TAAAATGGCAGCTTCA 3707	T	C
			TGAAGCTGC CAT TTG		
			ACTTCGACG GTA AAT		
			_ A		
GAM1358	F2RL3	3'	TTTTGATCAAGACGGAGTTTCA 14199	G	CA
			TGAAGCT CT TCTTGATCAAAA		
			ACTTTGA GG AGAACTAGTTTT		
			_ C_		
GAM1358	FGF2	3'	TTTTAATCAAGATAGTGTGCTT 8878	_	C C
	TA		TGAAGC TGCT ATCTTGAT AAAA		
			ATTTTCG GTGA TAGAACTA TTTT		
			T _ A		
GAM1358	GPR30	5'	GAGAGTGAGCAGCTCCA 7691	A	_
			TG AGCTGCTCA TCTT		
			AC TCGACGAGT AGAG		
			C G		
GAM1358	HHLA1	5'	AGGTGAAATAAACAGCTTTA 19127	C	_____
			TGAAGCTG TCATCT		
			ATTTTCGAC AGTGGA		
			AAATAA		
GAM1358	OXR1	3'	TTTTGATTATAATGACAACTTC 35839	C	C CT
	A		TGAAG TG TCAT TGATCAAAA		
			ACTTC AC AGTA ATTAGTTTT		
			A _ AT		
GAM1358	PBP	3'	TTTTGATCAAATTTGAACTTCA 10386	CTGC	TC_
			TGAAG TCA TTGATCAAAA		
			ACTTC AGT AACTAGTTTT		
			A_ TTA		
GAM1358	PDE4B	3'	TGATCAAGACACATGGCTT 10484	GCTCA	
			AAGCT TCTTGATCA		
			TTCGG AGAACTAGT		
			TACAC		
GAM1358	PDGFRB	3'	TTGTAAAAGACAAGAAGCTTCA 65983	G	CA GAT
			TGAAGCT CT TCTT CAA		
			ACTTCGA GA AGAA GTT		
			A AC AAT		
GAM1358	PROX1	3'	TGACAGATGAGCAGCTCA 10896	A	T A
			TGA GCTGCTCATCT G TCA		

ACT CGACGAGTAGA C AGT

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      -  -
GAM1358 TXNIP  3' TTGATCAAGATGCCCA  21355  CT
      TG CATCTTGATCAA
      || |||||
      AC GTAGAACTAGTT
      CC
GAM1358 CORTBP2 3' TTTAATCAAGATGTTTCAG  53079  CT  C
      CTG CATCTTGAT AAA
      ||| ||||| |||
      GAC GTAGAACTA TTT
      TT  A
GAM1358 EFA6R  3' CAATATGAGGCAGCTTCA  30979  _  C
      TGAAGCTGC TCAT TTG
      ||||| ||| |||
      ACTTCGACG AGTA AAC
      G  T
GAM1358 FLJ10242 3' TCCTGACAGCAGCTTCA  35935  CA TT
      TGAAGCTGCT TC GA
      ||||| || ||
      ACTTCGACGA AG CT
      C_ TC
GAM1358 FLJ13456 3' ATCAATTTGCAGCTTCA  65934  TCATC
      TGAAGCTGC TTGAT
      ||||| ||||
      ACTTCGACG AACTA
      TTT__
GAM1358 FLJ20666 3' TTTTGATCAAACCTGATCTTCA 37091  CTGC TC
      TGAAG TCA TTGATCAAAA
      |||| ||| |||||
      ACTTC AGT AACTAGTTTT
      T__ CA
GAM1358 FLJ20666 3' TTTTGATCAAACCTGATCTTCA 35514  CTGC TC
      TGAAG TCA TTGATCAAAA
      |||| ||| |||||
      ACTTC AGT AACTAGTTTT
      T__ CA
GAM1358 FLJ20898 5' CGAGGCGAGCAGCTTCA  44805  AT
      TGAAGCTGCTC CTTG
      ||||| |||
      ACTTCGACGAG GAGC
      CG
GAM1358 FLJ22557 3' CAAAAGGAGCAGCTTCA  45255  ATC
      TGAAGCTGCTC TTG
      ||||| |||
      ACTTCGACGAG AAC
      GAA
GAM1358 H105E3  3' TTGAAGCAGGCAGCTTCA  31929  CAT TGA
      TGAAGCTGCT CT TCAA
      ||||| || |||
```

			ACTTCGACGG	GA	AGTT		
			AC_	___			
GAM1358	HEI10	5'	TTTTGATCAAGATAAGCTGCCT	41001	A T C		
	TA		TGA GC GCT ATCTTGATCAAAA				
			ATT CG CGA TAGAACTAGTTTT				
			C T A				
GAM1358	HLA2	3'	AGGTGAAATAAACAGCTTTA	22984	C_____		
			TGAAGCTG TCATCT				
			ATTCGAC AGTGGA				
			AAATAA				
GAM1358	KIAA1328	3'	TTTGAAACATAAGCAGTTTTCA	61660	C C GA		
			TGAAGCTGCT AT TT TCAAA				
			ACTTTGACGA TA AA AGTTT				
			A C _				
GAM1358	KIAA1789	5'	TCAAGATGATCAGCCTCA	67103	A C		
			TGA GCTG TCATCTTGA				
			ACT CGAC AGTAGAACT				
			C T				
GAM1358	MGC12538	3'	CAAATTGAGCAGCTTCA	51241	TC		
			TGAAGCTGCTCA TTG				
			ACTTCGACGAGT AAC				
			TA				
GAM1358	P17.3	5'	CAGGAAATGAGCAGACCCA	38794	AAG _		
			TG CTGCTCA TCTTG				
			AC GACGAGT AGGAC				
			CCA AA				
GAM1358	PALM	3'	GTCACGGCAGCTTCA	10416	CATCT		
			TGAAGCTGCT TGAT				
			ACTTCGACGG ACTG				
			C_____				
GAM1358	SH3GLB1	3'	TCACTAATAAGCAGCTTC	32056	C CT_		
			GAAGCTGCT AT TGA				
			CTTCGACGA TA ACT				
			A ATC				
GAM1358	SIMRP7	3'	GGGCCTGGTGAGCAGCTTCA	92369	TTGA		
			TGAAGCTGCTCATC TC				
			ACTTCGACGAGTGG GG				
			TCCG				
GAM1358	LOC113763	3'	TCCAGTGACAGCAGCCTCA	56582	A _ T T		
			TGA GCTGC TCA CT GA				

	ACT CGACG AGT GA CT		
	C AC _ C		
GAM1358 LOC126133 3'	TCTGAGGTTGAGCAGCTCA 74445	A	_ _
	TGA GCTGCTCA TCTT GA		
	ACT CGACGAGT GGAG CT		
	_ T T		
GAM1358 LOC132112 3'	GATCAGAACAGCTTTA 75035	C	ATCT
	TGAAGCTG TC TGATC		
	ATTCGAC AG ACTAG		
	A ____		
GAM1358 LOC145758 5'	AAGACGGGCAGCTTCA 83480	A	
	TGAAGCTGCTC TCTT		
	ACTTCGACGGG AGAA		
	C		
GAM1358 LOC145814 3'	GGGATGAACTAGCTTCA 77508	C_	
	TGAAGCTG TCATCTT		
	ACTTCGAT AGTAGGG		
	CA		
GAM1358 LOC150445 3'	TTTTGATCAAATTTGAACTTCA 79871	CTGC TC_	
	TGAAG TCA TTGATCAAAA		
	ACTTC AGT AACTAGTTTT		
	A__ TTA		
GAM1358 LOC151278 3'	TTAAGACAAGTAGCCCCA 80203	AA CA	
	TG GCTGCT TCTTGA		
	AC CGATGA AGAATT		
	CC AC		
GAM1358 LOC153163 5'	AGGTGAAATAAACAGCTTTA 80770	C_____	
	TGAAGCTG TCATCT		
	ATTCGAC AGTGGA		
	AAATAA		
GAM1358 LOC155072 3'	CAAGCTCTGAGCAGCTCCG 86371	A T__	
	TG AGCTGCTCA CTTG		
	GC TCGACGAGT GAAC		
	C CTC		
GAM1358 LOC158117 3'	TTGAGCCTGAGCGGCTTCA 81713	T_ TG	
	TGAAGCTGCTCA CT A		
	ACTTCGGCGAGT GA T		
	CC GT		
GAM1358 LOC164382 3'	TTTGATCAAAGGCAACT 87206	C CATC	
	AG TGCT TTGATCAAA		

		TC ACGG AACTAGTTT		
		A A__		
GAM1358	LOC200982 3'	TTTGATATTGGGACAGCTTCA	90229	_ TCTTG
		TGAAGCTG CTCA ATCAA		
		ACTTCGAC GGGT TAGTTT		
		A TA__		
GAM1358	LOC202868 3'	CAAGCTCTGAGCAGCTCCG	90369	A T__
		TG AGCTGCTCA CTTG		
		GC TCGACGAGT GAAC		
		C CTC		
GAM1358	LOC203069 5'	TTTTGATCTCTTGAGCAGCTTC	89261	TCTT
		GAAGCTGCTCA GATCAAAA		
		CTTCGACGAGT CTAGTTTT		
		TCT_		
GAM1358	LOC203275 3'	TTGAGCCTGAGCGGCTTCA	89329	T_ TG
		TGAAGCTGCTCA CT A		
		ACTTCGGCGAGT GA T		
		CC GT		
GAM1358	LOC221766 3'	CGAGATGAGCAGATCCA	93776	AAG
		TG CTGCTCATCTTG		
		AC GACGAGTAGAGC		
		CTA		
GAM1358	LOC253983 3'	TGGTCATGAGCAGCATCA	96626	A TCT
		TGA GCTGCTCA TGATCA		
		ACT CGACGAGT ACTGGT		
		A _		
GAM1358	LOC254531 5'	TTAGTGAGGAGCAGCTTCA	94990	A _
		TGAAGCTGCTC TC TTGA		
		ACTTCGACGAG AG GATT		
		G T		
GAM1358	LOC256222 5'	TCTAGATGAGCTACTCCA	97224	A CT T
		TG AG GCTCATCT GA		
		AC TC CGAGTAGA CT		
		C AT T		
GAM1358	LOC257447 5'	TAAGGTGGAGCAGCTCCA	83442	A _
		TG AGCTGCTC ATCTTG		
		AC TCGACGAG TGGAAT		
		C G		
GAM1359	ACP2 3'	AGAAAGTTCTAGACTG	7851	GC TC
		CAGT CT AGAACTTTCT		

GTCA GA TCTTGAAAGA

GAM1359 APTX 5' AAGAGAAAGAGATCAGGCA 34655 TCAGAA  
TGCCT CTTTCTCTT  
||||| |||||  
ACGGA GAAAGAGAA  
CTAGA\_

GAM1359 BCL7A 3' AGGCTGTCTCCTTAAGGCACTG 40637 C A\_\_ TT  
CAGTGCCTT AG AC TCT  
||||||| || || |||  
GTCACGGAA TC TG GGA  
T CTC TC

GAM1359 CLC 3' AAGAGAAAATACTGAAAGCACA 25105 A C AAC  
GG CC GTGC TTCAG TTTCTCTT  
|| ||| ||||| |||||  
GG CACG AAGTC AAAGAGAA  
A A ATA

GAM1359 CNK 3' AAGCCCTGAAGGCCTG 14517 T AA  
CAG GCCTTCAG CTT  
||| ||||| |||  
GTC CGGAAGTC GAA  
\_ CC

GAM1359 COL4A3 3' AAGTGCAGGTTCTGAGGGCACC 48549 A TCT  
GG CC GTGCCTTCAGAACTT CTT  
|| ||||| ||||| |||  
GG CACGGGAGTCTTGGA GAA  
C CGT

GAM1359 CSPG4 3' AAGAGAGACCTGGAGACAC 8570 C AAC  
GTG CTTCAG TTTCTCTT  
||| ||||| |||||  
CAC GAGGTC AGAGAGAA  
A C\_\_

GAM1359 CYP1B1 3' AAGAGAAAAGAGAGAAACACTG 3651 CC AGAAC  
CAGTG TTC TTTCTCTT  
||||| ||| |||||  
GTCAC AAG AAAGAGAA  
A\_ AGAGA

GAM1359 DLG3 3' AAGAGAAAAGAGGAGGACTG 40880 G AGAAC  
CAGT CCTTC TTTCTCTT  
||||| ||||| |||||  
GTCA GGAGG AAAGAGAA  
\_ AGA\_\_

GAM1359 DLG5 5' AGGCAGACTCTGAAGGC 82909 A\_ T  
GCCTTCAGA CT TCT  
||||||| || |||  
CGGAAGTCT GA GGA  
CA C

GAM1359 FLT1 3' AAGAGAAACCGGGAGAAGGCAT 8910 AGAAC\_  
GTGCCTTC TTTCTCTT  
||||||| |||||

			TACGGAAG	AAAGAGAA		
			AGGGCC			
GAM1359	GRB10	3'	AGAGAAAATGGCACCTGG	17971	_	TTCAGAAC
			CCAG TGCC	TTTCTCT		
			GGTC ACGG	AAAGAGA		
			C TA_____			
GAM1359	LFG	3'	AAGAGAAAAGGAGCCAAGAACT	76711	GC	CAGAA _
	GG		CCAGT CTT	CTTT CTCTT		
			GGTCA GAA	GAAA GAGAA		
			A_ CCGAG A			
GAM1359	MAN2A2	3'	AAGAGAAAGTTCATTCAC	20391	CCTTCA	
			GTG	GAAC TTTCTCTT		
			CAC	CTTGAAAGAGAA		
			TTA_____			
GAM1359	NLGN3	3'	AAGAAAAGTTCTTAAAACACT	38596	CC C	C
			AGTG TT	AGAACTTT TCTT		
			TCAC AA	TCTTGAAA AGAA		
			AA T	_		
GAM1359	NPAS1	5'	AAGGTCTCCCGAGGGCACT	59879	A_ _	
			AGTGCCTTC	GA ACTTT		
			TCACGGGAG	CT TGGAA		
			CC C			
GAM1359	PLAG1	3'	AGTGTGTTCCAAAGGCATT	10605	CA	TTT
			AGTGCCTT	GAAC CT		
			TTACGGAA	CTTG GA		
			AC	TGT		
GAM1359	PLXNA1	3'	AGAAAATGAAGGCAGTGG	72309	G	GAAC
			CCA TGCCTTCA	TTTCT		
			GGT ACGGAAGT	AAAGA		
			G	A_____		
GAM1359	PPP4R1	3'	AAGAGAAAGTACAGTAAACACT	17620	CCTTCAGA	
			AGTG	ACTTTCTCTT		
			TCAC	TGAAAGAGAA		
			AAATGACA			
GAM1359	ACYP2	3'	AAGAGAAAAATTGTAACACACT	56612	CC _	AAC
	G		CAGTG TT	CAG TTTCTCTT		
			GTCAC AA	GTT AAAGAGAA		
			AC T	AA_		
GAM1359	B3GNT6	3'	AGAAATCAGATGAAGGCAT	22503	GAAC_	
			GTGCCTTCA	TTTCT		



TACGGAAGT AAAGA  
 AGACT  
 GAM1359 BAG5 3' AAGAGAAGGGATAAAGGAC 16835 G CAGAA  
 GT CCTT CTTTCTCTT  
 || ||| |||||  
 CA GGAA GGAAGAGAA  
 \_ ATAG\_  
 GAM1359 BIVM 3' AAGAGAAAAGACTCAAGAACT 34665 GC C AAC  
 G CAGT CTT AG TTTCTCTT  
 ||| ||| || |||||  
 GTCA GAA TC AAAGAGAA  
 AA C AGA  
 GAM1359 C15orf5 3' AGAGAAAAGAAAGCAC 48195 C AGAAC  
 GTGC TTC TTTCTCT  
 ||| ||| |||||  
 CACG AAG AAAGAGA  
 A A\_\_\_\_  
 GAM1359 C20orf80 5' AAGAGAAGAAGATGAAGAAAC 65282 GC GAAC  
 GT CTTCA TTTCTCTT  
 || ||| |||||  
 CA GAAGT GAAGAGAA  
 AA AGAA  
 GAM1359 CLSTN1 3' AGTTCTGAGGACACTGG 30103 C  
 CCAGTG CTTCAGAACT  
 ||||| |||||  
 GGTCAC GGAGTCTTGA  
 A  
 GAM1359 DKFZP434P0111 3' AAGAGAAAGTTTCTGCAC 67368 CTTCA  
 GTGC GAACTTTCTCTT  
 ||| |||||  
 CACG TTTGAAAGAGAA  
 TC\_\_\_\_  
 GAM1359 DORFIN 5' AGAATTCTCTGAAGGAAC 31257 G ACT  
 GT CCTTCAGA TTCT  
 || ||||| |||  
 CA GGAAGTCT AAGA  
 A CTT  
 GAM1359 FLJ10300 5' AAGAGAAAGATGAAGACTCTG 35997 TGC GAA  
 CAG CTTCA CTTTCTCTT  
 ||| ||| |||||  
 GTC GAAGT GAAAGAGAA  
 TCA A\_\_\_\_  
 GAM1359 FLJ20373 3' AAGAGAAGAAGGAAAGGCACAG 35070 A \_AGAAC  
 G CC GTGCCTT C TTTCTCTT  
 || ||||| | |||||  
 GG CACGGAA G GAAGAGAA  
 A A GAA\_\_\_\_  
 GAM1359 FLJ23511 5' AGAGAAAACAAGGCAT 49956 CAGAAC  
 GTGCCTT TTTCTCT  
 ||||| |||||

TACGGAA AAAGAGA  
 CAA\_\_\_\_  
 GAM1359 FLJ30681 3' AGAGAAGAAAGACCACTGG 91782 CCT AGAAC  
 CCAGTG TC TTTCTCT  
 ||||| || |||||  
 GGTCAC AG GAAGAGA  
 C\_\_ AAA\_\_  
 GAM1359 HDAC11 3' GAGCTATAGGCACTGG 45717 TC AACTTT  
 CCAGTGCCT AG CTC  
 ||||| || |||  
 GGTCACGGA TC GAG  
 TA \_\_\_\_\_  
 GAM1359 IKKE 5' AGTGAGCCCTGAAAGCTCTGG 25745 T C AA T  
 CCAG GC TTCAG CTT CT  
 ||| || |||| ||| ||  
 GGTC CG AAGTC GAG GA  
 T A CC T  
 GAM1359 KIAA0680 3' AGAGAAAATTGAAGCAT 28232 C AAC  
 GTGC TTCAG TTTCTCT  
 ||| |||| |||||  
 TACG AAGTT AAAGAGA  
 \_ A\_\_  
 GAM1359 KIAA1228 3' AGGGGGTGATTCTGAGGCACTG 65035 T \_\_ TT  
 CAGTGCCT CAGA ACT CT  
 ||||| ||| ||| ||  
 GTCACGGA GTCT TGG GA  
 \_ TAG GG  
 GAM1359 KIAA1300 5' AGGAACCCTGAAGGCA 62860 AAC  
 TGCCTTCAG TTTCT  
 ||||| ||||  
 ACGGAAGTC AAGGA  
 CC\_  
 GAM1359 KIAA1805 3' AAGAGAAAGTAGAAGCAGCA 79966 \_\_ AGA  
 TGC CTTC ACTTTCTCTT  
 ||| ||| |||||  
 ACG GAAG TGAAAGAGAA  
 AC A\_\_  
 GAM1359 LENG1 5' AAGAGAAAGCTCTGGGCATCCT 84074 \_\_ TT A  
 G CAG TGCC CAGA CTTTCTCTT  
 ||| ||| ||| |||||  
 GTC ACGG GTCT GAAAGAGAA  
 CT \_\_ C  
 GAM1359 LHX6 3' AAGAGAAAACCTCTGGGGTCA 26854 C AC  
 TG CTTCAGA TTTCTCTT  
 || ||||| |||||  
 AC GGGGTCT AAAGAGAA  
 T CA  
 GAM1359 N4BP3 3' AGCTCCAGAAGGCACTGG 66250 A\_ A  
 CCAGTGCCTTC GA CT  
 ||||| ||| ||

GGTCACGGAAG CT GA  
AC C

GAM1359 NASP 3' AGAGGGTGAAGAACTG 67966 GC AGA  
CAGT CTTC ACTTTCT  
|||| ||| |||||  
GTCA GAAG TGGGAGA  
AA \_\_\_\_

GAM1359 SMARCF1 3' AAAATTCTGAAGGAC 20034 G C  
GT CCTTCAGAA TTT  
|| ||||| |||  
CA GGAAGTCTT AAA  
\_ A

GAM1359 SMARCF1 3' AAAATTCTGAAGGAC 57480 G C  
GT CCTTCAGAA TTT  
|| ||||| |||  
CA GGAAGTCTT AAA  
\_ A

GAM1359 SMARCF1 3' AAAATTCTGAAGGAC 37430 G C  
GT CCTTCAGAA TTT  
|| ||||| |||  
CA GGAAGTCTT AAA  
\_ A

GAM1359 TED 3' AAGAGAAAGTCCAGGGACTGG 31630 G TCA A  
CCAGT CCT GA CTTTCTCTT  
|||| ||| || |||||  
GGTCA GGA CT GAAAGAGAA  
G C\_\_ \_

GAM1359 TGIF2 3' AGAAGGGTGCTGAAGGC 41447 AA\_  
GCCTTCAG CTTTCT  
||||| |||||  
CGGAAGTC GGAAGA  
GTG

GAM1359 WBSCR20A 3' AAGAGAAAGAAGAGACAGCA 35958 CT AGAA  
TGC TC CTTTCTCTT  
||| || |||||  
ACG AG GAAAGAGAA  
AC AGAA

GAM1359 LOC115273 3' AGAAAGTTCTGATGGCCAGG 73356 AGT T  
CC GCC TCAGAACTTTCT  
|| ||| |||||  
GG CGG AGTCTTGAAAGA  
AC\_ T

GAM1359 LOC145761 5' AAGAGAAAGTGGGAAGGCATGG 83472 G AGA  
CCA TGCCTTC ACTTTCTCTT  
||| ||||| |||||  
GGT ACGGAAG TGAAAGAGAA  
\_ G\_\_

GAM1359 LOC146179 5' AGAAAGTTTTGGGCCT 77700 T TT  
AG GCC CAGAACTTTCT  
|| ||| |||||

TC CGG GTTTTGAAAGA

— —  
GAM1359 LOC147072 3' AAGAGAAAGTGAGAAGAACTG 60407 GC AGA  
CAGT CTTC ACTTTCTCTT  
|||| ||| |||||  
GTCA GAAG TGAAAGAGAA  
AA AG\_

GAM1359 LOC148758 5' AGAAAGTTCTGAGAAAC 78962 GCC  
GT TTCAGAACTTTCT  
|| |||||  
CA GAGTCTTGAAAGA  
AA\_

GAM1359 LOC148932 3' AGGAATCTGAAGGCACTGG 79103 AC  
CCAGTGCCTTCAGA TTTCT  
||||||| |||  
GGTCACGGAAGTCT AAGGA

—  
GAM1359 LOC149386 5' AAGTTTTGAAAGCACT 84400 C  
AGTGC TTCAGAACTT  
|||| |||||  
TCACG AAGTTTTGAA  
A

GAM1359 LOC150139 3' AGAAAATAGAAAAAGGCGCTGG 79583 CAGAAC\_  
CCAGTGCCTT TTTCT  
||||| |||  
GGTCGCGGAA AAAGA  
AAAGATA

GAM1359 LOC152756 3' AAGATGCAGTTCTGAAAACCTG 85871 TGCC TTC  
CAG TTCAGAACT TCTT  
||| ||||| |||  
GTC AAGTCTTGA AGAA  
CAA\_ CGT

GAM1359 LOC162333 5' AAGAGAAAGCGATGACACTG 87114 CCT GAA  
CAGTG TCA CTTTCTCTT  
|||| ||| |||||  
GTCAC AGT GAAAGAGAA  
\_ AGC

—  
GAM1359 LOC199221 3' AAGAGAAGCTCGAAAGCATGG 80347 G C A A T  
CCA TGC TTC GA CTT CTCTT  
||| ||| ||| ||| |||  
GGT ACG AAG CT GAA GAGAA  
\_ A \_ C \_

GAM1359 LOC203339 3' AGAGAAAATTGGGCCTG 90542 T TCAGAAC  
CAG GCCT TTTCTCT  
||| ||| |||||  
GTC CGGG AAAGAGA  
\_ TTA\_

GAM1359 LOC255017 3' AGAAAGAGGAACTGG 94624 G TCAGAA  
CCAGT CCT CTTTCT  
|||| ||| |||||

GGTCA GGA GAAAGA  
A \_\_\_\_\_  
GAM1359 LOC256021 3' AAGAGAAACAAAGACAACACTG 96512 CCT AGAAC  
G CCAGTG TC TTTCTCTT  
||||| || |||||  
GGTCAC AG AAAGAGAA  
AAC AAAC\_  
GAM1359 LOC90139 3' AGAATCCCGAAGGCAT 55396 A\_ ACT  
GTGCCTTC GA TTCT  
||||||| || |||  
TACGGAAG CT AAGA  
CC \_\_\_\_  
GAM1360 BGN 5' CGGACAGATAGACGTGCGG 8143 GATC \_  
CCGCA CGTC ATCTGTCCG  
|||| ||| |||||  
GGCGT GCAG TAGACAGGC  
\_\_\_\_ A  
GAM1360 EGLN3 5' GGACCTCGATTCTGCGGG 41970 TC TCATCT  
CCCGCAGA CG GTCC  
||||||| || |||  
GGGCGTCT GC CAGG  
TA TC\_\_\_\_  
GAM1360 EGLN3 5' GGACCTCGATTCTGCGGG 52912 TC TCATCT  
CCCGCAGA CG GTCC  
||||||| || |||  
GGGCGTCT GC CAGG  
TA TC\_\_\_\_  
GAM1360 EYA1 3' CAGGGACAGATCCAGCAGG 4953 \_ A\_ C A  
CC GC GATC GTC TCTG  
|| || ||| ||| |||  
GG CG CTAG CAG GGAC  
A AC A \_  
GAM1360 LPIN2 3' CAGAGAGGGATCTGC 27704 G A  
GCAGATCC TC TCTG  
||||||| || |||  
CGTCTAGG AG AGAC  
G \_  
GAM1360 MYO7A 3' AGGGACTGGATCTGCAGGT 4227 C \_ A  
ACC GCAGATCC GTC TCT  
||| ||||| ||| |||  
TGG CGTCTAGG CAG GGA  
A T \_  
GAM1360 PEX14 3' CGGACAGACGCCTTGCCCAGGG 63641 \_\_\_\_ ATC ATC  
T ACCC GCAG CGTC TGTCCG  
|||| ||| ||| |||||  
TGGG CGTT GCAG ACAGGC  
ACC CC\_ \_\_\_\_  
GAM1360 RANBP9 5' CAGAACAACCTGCGGGT 18521 ATCC CA  
ACCCGCAG GT TCTG  
||||||| || |||

TGGGCGTC CA AGAC  
 CAA\_ \_  
 GAM1360 TNFRSF9 3' GACAGATGAGGACAGAGC 7789 AGA\_ G  
 GC TCC TCATCTGTC  
 || ||| |||||  
 CG AGG AGTAGACAG  
 AGAC \_  
 GAM1360 VEGF 3' CGGACAGAAAGACAAATCACAG 12587 GCA CC A\_  
 G CC GAT GTC TCTGTCCG  
 || ||| ||| |||||  
 GG CTA CAG AGACAGGC  
 ACA AA AA  
 GAM1360 C11orf25 3' GACAGATGAGGCAGGAGT 48641 \_ GCAGAT G  
 AC CC CC TCATCTGTC  
 || || ||| |||||  
 TG GG GG AGTAGACAG  
 A AC\_ \_  
 GAM1360 COPB 5' CAGTAGACGGATCCGCGG 33193 A AT  
 CCGC GATCCGTC CTG  
 ||| ||||| |||  
 GGCG CTAGGCAG GAC  
 C AT  
 GAM1360 FLJ10597 3' CGGACAGACAGACATGC 36314 GA C ATC  
 GCA TC GTC TGTCCG  
 ||| ||| |||||  
 CGT AG CAG ACAGGC  
 AC A \_  
 GAM1360 FLJ14166 3' ACTTGTGATGGACCCGCAGGT 44680 C AGA CT  
 ACC GC TCCGTCAT GT  
 ||| || ||||| ||  
 TGG CG AGGTAGTG CA  
 A CCC TT  
 GAM1360 FLJ14525 3' CAGGGAACAGACTGCGGGT 51414 A C CA  
 ACCCGCAG TC GT TCTG  
 ||||| || || |||  
 TGGGCGTC AG CA GGAC  
 \_ A AG  
 GAM1360 FLJ14721 3' CGGACATACGGACATGCGG 51582 GA CATC  
 CCGCA TCCGT TGTCCG  
 |||| |||| |||||  
 GGCGT AGGCA ACAGGC  
 AC T\_  
 GAM1360 KIAA1026 3' GACAGATGGGCTCTGC 71196 T GT  
 GCAGA CC CATCTGTC  
 |||| || |||||  
 CGTCT GG GTAGACAG  
 C \_  
 GAM1360 KPNA6 3' GACAGAACCATCTGAGG 24608 G CC CA  
 CC CAGAT GT TCTGTC  
 || |||| || |||||

GG GTCTA CA AGACAG  
A C\_ \_  
GAM1360 RAB22A 5' CGGACAGGCCGGACCTACGG 59930 C A TCA  
CCG AG TCCG TCTGTCCG  
||| || ||| |||||  
GGC TC AGGC GGACAGGC  
A C C\_  
GAM1360 LOC126432 5' GACAGACAGCCCTGCGGG 74517 ATCC CA  
CCCGCAG GT TCTGTC  
||||| || |||||  
GGGCGTC CG AGACAG  
C\_ AC  
GAM1360 LOC146723 3' GGACAGACCACCTGAGG 78086 G ATCC CA  
CC CAG GT TCTGTCC  
|| ||| || |||||  
GG GTC CA AGACAGG  
A \_ CC  
GAM1360 LOC147072 5' CGGACGCTGGCGGATGTGCG 60408 G TC  
CGCA ATCCGTCA TGTCCG  
||| ||||| |||||  
GCGT TAGGCGGT GCAGGC  
G C\_  
GAM1360 LOC149320 3' CAGTGACAAAGCTGCAGGT 70693 C ATCC T  
ACC GCAG GTCA CTG  
||| ||| ||| |||  
TGG CGTC CAGT GAC  
A GAAA \_  
GAM1360 LOC150372 5' CAGGGACAGATCTGGAGG 79791 CG C A  
CC CAGATC GTC TCTG  
|| ||||| ||| |||  
GG GTCTAG CAG GGAC  
AG A \_  
GAM1360 LOC150577 5' GGGAAGATGCTGCGGGT 85079 ATCCGT GT  
ACCCGCAG CATCT CC  
||||| ||| ||  
TGGGCGTC GTAGA GG  
\_ AG  
GAM1360 LOC153769 3' GCAAATGAACCTACGGGT 80927 C ATCCG C  
ACCCG AG TCAT TGT  
||||| || ||| |||  
TGGGC TC AGTA ACG  
A CA\_ A  
GAM1360 LOC170394 5' CGGACAGGGAGCTCCGC 82850 A TCC CA  
GC GA GT TCTGTCCG  
|| || || |||||  
CG CT CG GGACAGGC  
C \_ AG  
GAM1360 LOC202915 3' GACAGCGGACGGATCCCAGG 90390 GCA AT  
CC GATCCGTC CTGTC  
|| ||||| |||||

GG CTAGGCAG GACAG  
ACC GC  
GAM1360 LOC254173 3' CAGATATGGATCTGC 96841 C  
GCAGATCCGT ATCTG  
||||||| ||||  
CGTCTAGGTA TAGAC  
—  
GAM1361 TNFAIP1 3' CATCAGCTGAGGACAGCAAAC 40917 AG G  
CC GGA TTGCTG CTTGAGCTGATG  
||| ||||| |||||  
CCT AACGAC GGAGTCGACTAC  
CA A  
GAM1361 C1orf2 3' CAGCTGGTTGGGACCAGCAGCC 21681 AA —  
CCC GG GTTGCTGG CT TCAGCTG  
|| ||||| || |||||  
CC CGACGACC GG GGTCGAC  
CC A GTT  
GAM1361 C1orf2 3' CAGCTGGTTGGGACCAGCAGCC 94622 AA —  
CCC GG GTTGCTGG CT TCAGCTG  
|| ||||| || |||||  
CC CGACGACC GG GGTCGAC  
CC A GTT  
GAM1361 C20orf59 3' CATCCCTAGCCAGCAGCTCC 41992 A TC CT  
GGA GTTGCTGGCT AG GATG  
||| ||||| || ||||  
CCT CGACGACCGA TC CTAC  
— — C—  
GAM1361 FLJ20079 3' CATTCTGGTAAACCAGCAGCCT 34490 A CT\_\_ CT  
CC GGA GTTGCTGG TCAG GATG  
||| ||||| ||| ||||  
CCT CGACGACC GGTC TTAC  
C AAAT —  
GAM1361 SSAT2 3' CATCAGCTGAAGCACTCTTC 56041 TTGCTG  
GAAG GCTTCAGCTGATG  
||| |||||  
CTTC CGAAGTCGACTAC  
TCA—  
GAM1361 SYNJ2 3' ATCAGCTTAAGCAATTCC 61763 GTTGCTG C  
GGAA GCTT AGCTGAT  
||| ||| |||||  
CCTT CGAA TCGACTA  
AA— T  
GAM1361 LOC162333 5' CTGAAGCCAGCAATTCC 87131 G  
GGAA TTGCTGGCTTCAG  
||| |||||  
CCTT AACGACCGAAGTC  
—  
GAM1361 LOC222060 5' CACCTCCCACCAGCAACCCCC 94104 AA CTC C  
GG GTTGCTGG AG TG  
|| ||||| |||



CC CAACGACC TC AC  
 CC ACCC C  
 GAM1361 LOC255650 3' CATCAGCCCCAGGCAACTTCC 96711 \_ CTTCA  
 GGAAGTTGC TGG GCTGATG  
 ||||| || |||||  
 CCTTCAACG ACC CGACTAC  
 G C\_\_\_\_  
 GAM1362 BIN3 3' CACCCTCCAGCAGGCAGCCCAG 37955 C AT CA  
 CA TGCTGGGCT CCTGC GA GTG  
 ||||| ||| || |||  
 ACGACCCGA GGACG CT CAC  
 C AC CC  
 GAM1362 CRSP8 3' CACGCAGGAAGCCCACA 80963 C C A  
 TG TGGGCT CCTGC TG  
 || |||| |||| ||  
 AC ACCCGA GGACG AC  
 \_ A C  
 GAM1362 ENG 5' CACTGCCATCCATTGGAGCCCA 3687 C\_ C A  
 GCA TGCTGGGCTCC TG ATG CAGTG  
 ||||| || || |||||  
 ACGACCCGAGG AC TAC GTCAC  
 TT C C  
 GAM1362 HD 3' CACTGTAGTGACAGAGCCCAG 9181 CC \_ \_  
 CA TGCTGGGCTC TG CA TGACAGTG  
 ||||| || || |||||  
 ACGACCCGAG AC GT ATTGTCAC  
 \_ A G  
 GAM1362 IGLL1 5' CACTCTCTAGGGAGCCCACA 39174 C CAT C  
 TG TGGGCTCCCTG GA AGTG  
 || ||||| || |||||  
 AC ACCCGAGGGAT CT TCAC  
 \_ \_ C  
 GAM1362 THBD 3' CACTGCCACACAGGGTCTGCA 4494 T CT CA A  
 TGC GGG CCCTG TG CAGTG  
 ||| || |||| |||||  
 ACG TCT GGGAC AC GTCAC  
 \_ \_ AC C  
 GAM1362 ARHGEF16 3' CACCGTGTCCCAGGGAGCCCAG 27069 CAT \_  
 C GCTGGGCTCCCTG GACA GTG  
 ||||| ||| |||  
 CGACCCGAGGGAC CTGT CAC  
 C\_ GC  
 GAM1362 CABIN1 3' ACCACATGGGAGCCCAG 24479 TGC ACA  
 CTGGGCTCCC ATG GT  
 ||||| || ||  
 GACCCGAGGG TAC CA  
 \_ AC\_  
 GAM1362 FLJ10232 3' ACTGTCAGGAACCCAG 35920 C CTGCA  
 CTGGG TCC TGACAGT  
 |||| || |||||

GACCC AGG ACTGTCA  
 A \_\_\_\_\_  
 GAM1362 FLJ20154 5' GCCTTCAGGCCAGCA 72927 CCCTGCA CA  
 TGCTGGGCT TGA GT  
 ||||| ||| ||  
 ACGACCCGG ACT CG  
 \_\_\_\_\_ TC  
 GAM1362 FLJ21865 3' CACCGCCATGCAGGGCTCGC 42805 T TC ACA  
 GC GGGC CCTGCATG GTG  
 || ||| ||||| |||  
 CG CTCG GGACGTAC CAC  
 \_\_\_\_\_ CGC  
 GAM1362 IRF7 3' CACCGCGGTGCAAGAGCCCAGC 14443 CC GACA  
 GCTGGGCTC TGCAT GTG  
 ||||| |||| |||  
 CGACCCGAG ACGTG CAC  
 A\_ GCGC  
 GAM1362 KIAA0864 3' CACTGTCACTATTAAGGCCAG 63247 CCC\_ A  
 CA TGCTGGGCT TGC TGACAGTG  
 ||||| ||| |||||  
 ACGACCCGG ATG ACTGTCAC  
 AATT \_  
 GAM1362 MFN2 3' ACAAGGCAGGGGCCAGCA 29595 T ATGACA  
 TGCTGGGC CCCTGC GT  
 ||||| |||| ||  
 ACGACCCG GGGACG CA  
 \_ GAA\_\_\_\_  
 GAM1362 MGC3101 3' GTCACACAGAGCCCAGCA 43883 CC CA  
 TGCTGGGCTC TG TGAC  
 ||||| || |||  
 ACGACCCGAG AC ACTG  
 \_ AC  
 GAM1362 SCYB11 3' CACTGCCCAAAGGAGTCCAACA 87442 C CTGCATGA  
 TG TGGGCTCC CAGTG  
 || ||||| ||||  
 AC ACCTGAGG GTCAC  
 A AAACCC\_  
 GAM1362 TIX1 3' CATGTAAGGAGCCCAGCA 61739 C  
 TGCTGGGCTCC TGCATG  
 ||||| ||||  
 ACGACCCGAGG ATGTAC  
 A  
 GAM1362 UBP1 3' CTGCCATAGCCAAGCA 27224 G CCCTGC A  
 TGCT GGCT ATG CAG  
 ||| ||| ||| |||  
 ACGA CCGA TAC GTC  
 A \_\_\_\_\_ C  
 GAM1362 LOC123242 3' ACCATTAAGCAGCCCAGCA 75589 CCCT A CA  
 TGCTGGGCT GC TGA GT  
 ||||| || ||| ||

ACGACCCGA CG ATT CA  
 \_\_\_\_ A AC  
 GAM1362 LOC144058 5' CTGGATGCAGGGCACCCAACA 76666 C CT GA  
 TG TGGG CCCTGCAT CAG  
 || ||| ||||| ||  
 AC ACCC GGGACGTA GTC  
 A AC G\_  
 GAM1362 LOC147160 5' CACAGGGGAGCCCAGCA 83958 GCA  
 TGCTGGGCTCCCT TG  
 ||||| ||  
 ACGACCCGAGGGG AC  
 AC\_  
 GAM1362 LOC148870 5' CACTGCTCCCAGGAGCCCACA 79041 C C CAT \_  
 TG TGGGCTCC TG GA CAGTG  
 || ||||| || || ||||  
 AC ACCCGAGG AC CT GTCAC  
 \_ \_ C\_ C  
 GAM1362 LOC149421 5' CACTGCCAACGTAGAGGGCCCA 79355 C A\_ A  
 GCA TGCTGGGCTC CTGC TG CAGTG  
 ||||| ||| || ||||  
 ACGACCCGGG GATG AC GTCAC  
 A CA C  
 GAM1362 LOC151360 3' CACTGTACACCGTAGCCCACA 85311 C CCCTGCA  
 TG TGGGCT TGACAGTG  
 || |||| |||||  
 AC ACCCGA ACTGTCAC  
 \_ TGCCAC\_  
 GAM1362 LOC151361 3' CACTGTACACCGTAGCCCACA 85320 C CCCTGCA  
 TG TGGGCT TGACAGTG  
 || |||| |||||  
 AC ACCCGA ACTGTCAC  
 \_ TGCCAC\_  
 GAM1362 LOC152286 3' CACTAGACAGCCAGGAGCCCAG 85626 CT A AC\_  
 CA TGCTGGGCTCC GC TG AGTG  
 ||||| || || ||||  
 ACGACCCGAGG CG AC TCAC  
 AC \_ AGA  
 GAM1362 LOC152674 3' CACTGTACCTGGAAGCCCAG 85834 C TGCA  
 CTGGGCT CC TGACAGTG  
 ||||| || |||||  
 GACCCGA GG ACTGTCAC  
 A TCC\_  
 GAM1362 LOC253001 3' ACCATTAAGCAGCCCAGCA 96249 CCCT A CA  
 TGCTGGGCT GC TGA GT  
 ||||| || || ||  
 ACGACCCGA CG ATT CA  
 \_\_\_\_ A AC  
 GAM1362 LOC255030 3' ACTGAGAAGAAGCCCAGC 97267 CC GCATGA  
 GCTGGGCT CT CAGT  
 ||||| || |||

			CGACCCGA GA GTCA	
			A_ AGA__	
GAM1362	LOC51131	3'	ACTGTCACACTCCCAGCA 32277	CTCCC CA
			TGCTGGG TG TGACAGT	
			ACGACCC AC ACTGTCA	
			TC__ _	
GAM1363	CNGA1	3'	CAACTGATAATGTGCAA 59507	GC A
			TTTGACATTA TAG TTG	
			AAACGTGTAAT GTC AAC	
			A_ _	
GAM1363	ESRRG	3'	TGGCAGTCTTATGTGCAA 66396	TAGCT
			TTTGACAT AGATTGCCA	
			AAACGTGTA TCTGACGGT	
			T__	
GAM1363	KCNJ3	3'	GCAATAATGTGCAA 9525	GCTAGA
			TTTGACATTA TTGC	
			AAACGTGTAAT AACG	
			_____	
GAM1363	SDC2	3'	GCAAATTAATGTGTAAA 67132	CTAGA
			TTTGACATTAG TTGC	
			AAATGTGTAATT AACG	
			A__	
GAM1363	USP9X	3'	ATGGCCTGATGCTAATGTGTAA 16206	TAGATT
	A		TTTGACATTAGC GCCAT	
			AAATGTGTAATCG CGGTA	
			TAGTC_	
GAM1363	AMOTL1	3'	GGCAAGTAATGTGCAA 73650	G AGAT
			TTTGACATTA CT TGCC	
			AAACGTGTAAT GA ACGG	
			_____	
GAM1363	BCAR3	3'	AGTAATAATGTGCAA 13098	__
			TTTGACATTA GCT	
			AAACGTGTAAT TGA	
			AA	
GAM1363	DKFZP434B044	3'	TGACAATTAAATGTGCAGA 48930	AGCTA C
			TTTGACATT GATTG CA	
			AGACGTGTAA TTAAC GT	
			A__ A	
GAM1363	MGC3184	3'	ATGACATTTTCTAATGTGCAGA 48235	CT T C
			TTTGACATTAG AGA TG CAT	

			AGACGTGTAATC TTT AC GTA		
			___ T A		
GAM1363	PTD012	3'	ATGGCAATCTAGCTAATGTGCA 25891		
	AA		TTTGCACATTAGCTAGATTGCCAT		
			AAACGTGTAATCGATCTAACGGTA		
GAM1364	ADAM17	3'	ATGCCTGTAATCCCAGCACTTG 41553	_ A	A
			CA GT GCTGGGATTACAG CAT		
			GT CA CGACCCTAATGTC GTA		
			T _ C		
GAM1364	ADAM17	3'	ATGCCTGTAATCCCAGCACTTG 12081	_ A	A
			CA GT GCTGGGATTACAG CAT		
			GT CA CGACCCTAATGTC GTA		
			T _ C		
GAM1364	ADAT1	3'	CTGTAATCCTAGCTACT 23898		
			AGTAGCTGGGATTACAG		
			TCATCGATCCTAATGTC		
GAM1364	AICDA	3'	CTGTAATCCCAGCACT 40326	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
GAM1364	AK1	3'	ATGCCTGTAATCCCAGCACT 4879	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			_ C		
GAM1364	ALDH3A2	3'	ATGCCTGTAATCCCAGCACT 69270	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			_ C		
GAM1364	ALDH3B1	3'	ATGCCTGTAATCCCAGCTACT 91520		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1364	ALDH3B1	3'	CTGTAATCCCAGCACT 91524	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
GAM1364	ALDH8A1	3'	ATGCCTATAATCCCAGCACT 42607	A	C A
			AGT GCTGGGATTA AG CAT		

			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1364	ANKH	3'	ATGCCTGTAATCCCAACACT 53987	AGC	A
			AGT TGGGATTACAG CAT		
			TCA ACCCTAATGTC GTA		
			CA_ C		
GAM1364	ANKH	3'	CTGTAATCCCAGCTACT 53989		
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
GAM1364	ARHGEF6	3'	CTGTGGTCCCAGCTACTCA 68202	C	
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTGGTGTC		
			C		
GAM1364	ATM	3'	CTGTAATCCCAGCACT 56295	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
GAM1364	ATM	3'	CTATAATCCCAGCACT 56303	A	C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1364	ATM	3'	CTGTAATCCCAGCACT 3511	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
GAM1364	ATP1A2	3'	ATGCCTGTAATCCCAGCACT 5521	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	ATP1A2	3'	CTGTAATCTCAGCTACTCA 5524	C	
			A AGTAGCTGGGATTACAG		
			A TCATCGACTCTAATGTC		
			C		
GAM1364	BAAT	3'	ATGTCTCCCCAGCTGC 8112	ATTAC	
			GTAGCTGGG AGACAT		
			CGTCGACCC TCTGTA		
			CC__		
GAM1364	BHMT2	3'	CTGCAATCCCAGCACT 34309	A	A
			AGT GCTGGGATT CAG		

			TCA CGACCCTAA GTC	
			— C	
GAM1364 BRCA1	3'	CTGTAATCCCAGCTACT	23544	
		AGTAGCTGGGATTACAG		
		TCATCGACCCTAATGTC		
GAM1364 BRCA1	3'	CTGTAATCCCAGCACT	23551	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
GAM1364 BRCA1	3'	CTGTAATCCCAGCTACT	23552	
		AGTAGCTGGGATTACAG		
		TCATCGACCCTAATGTC		
GAM1364 BRCA1	3'	CTGTAATCCCAGCACT	23559	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
GAM1364 BRCA1	3'	CTGTAATCCCAGCTACT	23560	
		AGTAGCTGGGATTACAG		
		TCATCGACCCTAATGTC		
GAM1364 BRCA1	3'	CTGTAATCCCAGCACT	23568	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
GAM1364 BRCA1	3'	CTGTAATCCCAGCTACT	23569	
		AGTAGCTGGGATTACAG		
		TCATCGACCCTAATGTC		
GAM1364 BRCA1	3'	CTGTAATCCCAGCACT	23576	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
GAM1364 BRCA1	3'	CTGTAATCCCAGCTACT	23577	
		AGTAGCTGGGATTACAG		
		TCATCGACCCTAATGTC		
GAM1364 BRCA1	3'	CTGTAATCCCAGCACT	23584	A
		AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1364 BRCA1 3' CTGTAATCCCAGCTACT 23585  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1364 BRCA1 3' CTGTAATCCCAGCACT 23592 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 BRCA1 3' CTGTAATCCCAGCTACT 23593  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1364 BRCA1 3' CTGTAATCCCAGCACT 23518 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 BRCA1 3' CTGTAATCCCAGCTACT 23519  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1364 BRCA1 3' CTGTAATCCCAGCACT 23527 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 BRCA1 3' CTGTAATCCCAGCTACT 23528  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1364 BRCA1 3' CTGTAATCCCAGCACT 23535 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 BRCA1 3' CTGTAATCCCAGCTACT 23536  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1364 BRCA1 3' CTGTAATCCCAGCACT 23543 A  
AGT GCTGGGATTACAG  
||| |||||



TCA CGACCCTAATGTC

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GAM1364 BRCA2  3' ATGCCTGTAATCCCAACACTTT 3548 TAGC_  A
      G          CAG  TGGGATTACAG CAT
      ||| ||||| |||
      GTT  ACCCTAATGTC GTA
      TCACA      C
GAM1364 C1orf1 3' CTGTAATCCCAACACT 6859 AGC
      AGT  TGGGATTACAG
      ||| ||||| |||
      TCA  ACCCTAATGTC
      CA_
GAM1364 C5R1   3' CTGTAATCCCAGAACT 8204 AG
      AGT  CTGGGATTACAG
      ||| ||||| |||
      TCA  GACCCTAATGTC
      A_
GAM1364 CARKL  3' ATGCCTGTAATCCCAGCTACT 25183 A
      AGTAGCTGGGATTACAG CAT
      ||||| ||||| |||
      TCATCGACCCTAATGTC GTA
      C
GAM1364 CASP10 3' ATGCCTGTAATCCCAGTACTCT 52098 TA_  A
      G          CAG  GCTGGGATTACAG CAT
      ||| ||||| |||
      GTC  TGACCCTAATGTC GTA
      TCA      C
GAM1364 CASP10 3' ATGCCTGTAATCCCAGTACTCT 52116 TA_  A
      G          CAG  GCTGGGATTACAG CAT
      ||| ||||| |||
      GTC  TGACCCTAATGTC GTA
      TCA      C
GAM1364 CASP6  3' ATGCCTGCAATCCCAGCTACTT 52200 _  A A
      G          CA GTAGCTGGGATT CAG CAT
      || ||||| ||| |||
      GT CATCGACCCTAA GTC GTA
      T      C C
GAM1364 CASP6  3' CTGTAATCCCAGCACT 52203 A
      AGT  GCTGGGATTACAG
      ||| ||||| |||
      TCA CGACCCTAATGTC
      -
GAM1364 CASP6  3' ATGCCTGCAATCCCAGCTACTT 6907 _  A A
      G          CA GTAGCTGGGATT CAG CAT
      || ||||| ||| |||
      GT CATCGACCCTAA GTC GTA
      T      C C
GAM1364 CASP6  3' CTGTAATCCCAGCACT 6910 A
      AGT  GCTGGGATTACAG
      ||| ||||| |||
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TCA CGACCCTAATGTC

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      -
GAM1364 CASP8  3' ATGTCTATAATCCCAGCACT  6913  A    C
      AGT GCTGGGATTA AGACAT
      ||| ||||| |||||
      TCA CGACCCTAAT TCTGTA
      -      A
GAM1364 CASP8  3' ATGTCTATAATCCCAGCACT  52919  A    C
      AGT GCTGGGATTA AGACAT
      ||| ||||| |||||
      TCA CGACCCTAAT TCTGTA
      -      A
GAM1364 CASP8  3' ATGTCTATAATCCCAGCACT  52930  A    C
      AGT GCTGGGATTA AGACAT
      ||| ||||| |||||
      TCA CGACCCTAAT TCTGTA
      -      A
GAM1364 CASP8  3' ATGTCTATAATCCCAGCACT  52942  A    C
      AGT GCTGGGATTA AGACAT
      ||| ||||| |||||
      TCA CGACCCTAAT TCTGTA
      -      A
GAM1364 CD68   3' ATGCCTGTAATCCCAGCACT  59797  A    A
      AGT GCTGGGATTACAG CAT
      ||| ||||| ||||| |||
      TCA CGACCCTAATGTC GTA
      -      C
GAM1364 CHRNA5 3' CTGTAATCCCAGCACT    59755  A
      AGT GCTGGGATTACAG
      ||| ||||| |||||
      TCA CGACCCTAATGTC
      -
GAM1364 CHST5  3' ATGCCTGTAATCCCAGCATTTT 24022  TA_  A
      G      CAG GCTGGGATTACAG CAT
      ||| ||||| ||||| |||
      GTT CGACCCTAATGTC GTA
      TTA      C
GAM1364 CHST5  3' CTGTAATCCCAGCTACTTA  24025  C
      A AGTAGCTGGGATTACAG
      | ||||| |||||
      A TCATCGACCCTAATGTC
      T
GAM1364 CNGB1  3' ATGCCTATAATCCCAGTGCT  7110   G    C A
      AGTA CTGGGATTA AG CAT
      |||| ||||| || |||
      TCGT GACCCTAAT TC GTA
      -      A C
GAM1364 COG7   3' CTGTAATCCCAGCACT    67622  A
      AGT GCTGGGATTACAG
      ||| ||||| |||||
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TCA CGACCCTAATGTC

GAM1364 COL16A1 3' CTGTAATCCTAGCTATT 8500  
AGTAGCTGGGATTACAG  
|||||  
TTATCGATCCTAATGTC

GAM1364 COPA 3' CTGTAATCCCAGCACT 15187 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 CORO2A 3' ATGCCTGTAATCCCAGCACTCT 53400 TA\_ A  
G CAG GCTGGGATTACAG CAT  
||| |||||  
GTC CGACCCTAATGTC GTA  
TCA C

GAM1364 CORO2A 3' ATGCCTGTAATCCCAGCACTCT 12644 TA\_ A  
G CAG GCTGGGATTACAG CAT  
||| |||||  
GTC CGACCCTAATGTC GTA  
TCA C

GAM1364 CPT2 3' ATGCCTGTAATCCCAGCATTTT 3641 TA\_ A  
G CAG GCTGGGATTACAG CAT  
||| |||||  
GTT CGACCCTAATGTC GTA  
TTA C

GAM1364 CRACC 3' CTGTAATCCCAGCACT 41005 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 CTMP 3' CTGTAATCCCAGCACTTTA 53876 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||  
AT TCA CGACCCTAATGTC  
T \_

GAM1364 CTMP 3' CTGTAGTCCCAGCTACTCA 53877 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTGATGTC  
C

GAM1364 CTNNB1 3' TCTGTAATGGTACTG 8581 G GGG  
CAGTA CT ATTACAGA  
||||| || |||||  
GTCAT GG TAATGTCT

GAM1364 CTSS 3' ATGCCTGTAATCCCAGCTACTT 14540 \_ A  
G CA GTAGCTGGGATTACAG CAT  
|| ||||| |||

			GT CATCGACCCTAATGTC GTA		
			T C		
GAM1364	CTSS	3'	CTGTAATCCCAGTACTTG 14542 C G		
			A AGTA CTGGGATTACAG		
			I IIII IIIIIIIIIII		
			G TCAT GACCCTAATGTC		
			T _		
GAM1364	CYP4F3	3'	CTGTAATCCCAGCACTTTA 6115 C A		
			TA AGT GCTGGGATTACAG		
			II IIII IIIIIIIIIII		
			AT TCA CGACCCTAATGTC		
			T _		
GAM1364	DAPP1	3'	ATGCCTGTAATCCCAGGACT 26917 AG A		
			AGT CTGGGATTACAG CAT		
			III IIIIIIIIIII III		
			TCA GACCCTAATGTC GTA		
			G_ C		
GAM1364	DAPP1	3'	TGTAATCCCAGCTACTCA 26920 C		
			A AGTAGCTGGGATTACA		
			I IIIIIIIIIIIIIII		
			A TCATCGACCCTAATGT		
			C		
GAM1364	DBT	3'	CTGTAATCCCAGCACT 8610 A		
			AGT GCTGGGATTACAG		
			III IIIIIIIIIIIII		
			TCA CGACCCTAATGTC		
			_		
GAM1364	DCLRE1C	3'	ATGCCTGTAATCCCAGCTAC 42524 A		
			GTAGCTGGGATTACAG CAT		
			IIIIIIIIIIIIII III		
			CATCGACCCTAATGTC GTA		
			C		
GAM1364	DDOST	3'	ATGCCTGTAATCCCAGCACT 17816 A A		
			AGT GCTGGGATTACAG CAT		
			III IIIIIIIIIIIII III		
			TCA CGACCCTAATGTC GTA		
			_ C		
GAM1364	DFFA	3'	CTGTAATCCCAGCACTG 15302 A		
			CAGT GCTGGGATTACAG		
			IIII IIIIIIIIIIIII		
			GTCA CGACCCTAATGTC		
			_		
GAM1364	DHFR	3'	ATGCCTGTAGTCCCAGCTACTC 5799 C A		
	A		A AGTAGCTGGGATTACAG CAT		
			I IIIIIIIIIIIIIII III		
			A TCATCGACCCTGATGTC GTA		
			C C		
GAM1364	DHFR	3'	CTGTAATCCCAGCGCT 5803 A		
			AGT GCTGGGATTACAG		
			III IIIIIIIIIIIII		

TCG CGACCCTAATGTC

GAM1364 DMC1 3' CTGTAATCCCAGCACT 22972 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 DNASE2 3' ATGCCTGTAGTCCCAGCCACTG 7263 A A  
CAGT GCTGGGATTACAG CAT  
||| |||||  
GTCA CGACCCTGATGTC GTA

GAM1364 DSC1 3' CTGTAATCCCAGCTACTCA 17059 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
C

GAM1364 DSC1 3' CTGTAATCCCAGCTACTCA 44328 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
C

GAM1364 DVL3 3' GTCTGTAATCCCAGCACT 15373 A  
AGT GCTGGGATTACAGAC  
||| |||||  
TCA CGACCCTAATGTCTG

GAM1364 DYRK1A 3' ATGTCTGTAACCAATAATGTA 55198 G GCTG A  
TACA TA GG TTACAGACAT  
||| || |||||  
ATGT AT CC AATGTCTGTA  
A AA\_\_

GAM1364 DYRK1A 3' ATGTCTGTAACCAATAATGTA 55240 G GCTG A  
TACA TA GG TTACAGACAT  
||| || |||||  
ATGT AT CC AATGTCTGTA  
A AA\_\_

GAM1364 DYRK1A 3' ATGTCTGTAACCAATAATGTA 7349 G GCTG A  
TACA TA GG TTACAGACAT  
||| || |||||  
ATGT AT CC AATGTCTGTA  
A AA\_\_

GAM1364 EFG2 5' CTGTAATCCCAGCACT 50476 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 EGFL5 3' CTGTAATCCCAGCACT 86618 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1364 EHHADH 3' CTGTAATCCCAGCACT 8750 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 F2R 3' CTGTAATCCCAGCACT 8837 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 F2RL3 3' CTGCAATCCCAGCACT 14178 A A  
AGT GCTGGGATT CAG  
||| ||||| |||  
TCA CGACCCTAA GTC  
C

GAM1364 F2RL3 3' CTGTAATCCCAGCACTTTA 14179 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||  
AT TCA CGACCCTAATGTC  
T

GAM1364 F2RL3 3' TGTAATCCCAGCTACTCA 14197 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1364 FANCD2 3' CTGTAATCCCAGCACT 52355 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 FCMD 3' CTATAGTCCCAGCTAC 22091 C  
GTAGCTGGGATTA AG  
||| ||||| ||  
CATCGACCCTGAT TC  
A

GAM1364 FGFR1 3' CTGTAATCCCAGCACTTTA 43614 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||  
AT TCA CGACCCTAATGTC  
T

GAM1364 FGFR1 3' CTGTAATCCCAGCACTTTA 43621 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||  
AT TCA CGACCCTAATGTC  
T

GAM1364 FGFR2 3' ATGCCTGTAATCCCAGCACT 43376 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||

			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	FGFR2	3'	ATGCCTGTAATCCCAGCACT 43382	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	FKRP	3'	CTGTAATCCCAGCACT 44185	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	FLRT2	5'	GTCTGTAATCCCAGCGCTCTGT 25064	TA_	
			ACAG GCTGGGATTACAGAC		
			TGTC CGACCCTAATGTCTG		
			TCG		
GAM1364	FUT6	3'	CTGTAATCCCAGCACT 3811	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	GALNT7	3'	CTGTAATCCCAGCTACTTG 54018	_	
			CA GTAGCTGGGATTACAG		
			GT CATCGACCCTAATGTC		
			T		
GAM1364	GNE	3'	CTGTAATCCCAGCACT 18478	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	GP2	3'	ATGCCTGTAATCCCAGC 7680	A	
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1364	GP6	3'	ATGTCTGTAATCCTAGCACTGT 33030	A	
	G		TACAGT GCTGGGATTACAGACAT		
			GTGTCA CGATCCTAATGTCTGTA		
			—		
GAM1364	GPRK7	3'	TCTATAATCCCAGTTAC 57629	C	
			GTAGCTGGGATTA AGA		
			CATTGACCCTAAT TCT		
			A		
GAM1364	GRAF	3'	CTATAATCCCAGCACT 30556	A	C
			AGT GCTGGGATTA AG		

			TCA CGACCCTAAT TC		
			— A		
GAM1364 GRM6	3'	CTGTAATCCCAGCACT	5934	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1364 HFE	3'	CTGTAATCCCAGGGTGCTG	4651	G _	
		CAGTA C TGGGATTACAG			
		GTCGT G ACCCTAATGTC			
		G G			
GAM1364 HIP1	3'	ATGCCTGTAATCCCAGAACT	18055	AG	A
		AGT CTGGGATTACAG CAT			
		TCA GACCCTAATGTC GTA			
		A _ C			
GAM1364 HIP1	3'	CTGTAATCCCAGCACT	18059	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1364 HIP1	3'	GTAATCCCAGCTACTCA	18065	C	
		A AGTAGCTGGGATTAC			
		A TCATCGACCCTAATG			
		C			
GAM1364 HLA-E	3'	ATGCCTGTAATCCCAGCACT	91021	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		C			
GAM1364 HUNK	3'	CTGTAATCCCAGCACT	27449	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1364 IAPP	3'	GTGCCTGTAATCCCAGCTACTC	4696	C	A
A		A AGTAGCTGGGATTACAG CAT			
		A TCATCGACCCTAATGTC GTG			
		C C			
GAM1364 ICA1	3'	TGCAGTCCCAGCTACTCA	42257	C	A
		A AGTAGCTGGGATT CA			
		A TCATCGACCCTGA GT			
		C C			
GAM1364 ICMT	3'	CTGTAATCCCAAAGTGCTG	24812	GC _	
		CAGTA TGGGATTACAG			



			GTCGT ACCCTAATGTC		
			GAA		
GAM1364	IFIT4	3'	ATGCCTGTAATCCCAGCACT 70920	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	IFNAR1	3'	CTGTAATCCCAGCACT 5284	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	IL10	3'	CTGTAATCCCAGCACT 5127	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	IL12RB2	3'	ATGCCTGTAATCCCAGCACT 7768	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	IL17R	3'	CTGTAATCCCAGCAC 26776	A	
			GT GCTGGGATTACAG		
			CA CGACCCTAATGTC		
			—		
GAM1364	IL1R1	3'	CTATAATCCCAGCACT 6057	A	C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1364	IL1R1	3'	CTGTAATCCCAGCTAC 6058		
			GTAGCTGGGATTACAG		
			CATCGACCCTAATGTC		
			—		
GAM1364	IL4R	5'	ATGCCTATAATCCCAGCACT 4699	A	C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1364	IPP	3'	ATGCCTATAATCCCAGCACT 19724	A	C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1364	IRAK1	3'	CTGTAATCCCAGCACT 7808	A	
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1364 ITGAL 3' CTGTAATCCCAGCACT 9391 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 ITGAL 3' CTGTAGTCCCAGCTACTCA 9392 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTGATGTC  
C

GAM1364 JRK 3' CTGTAATCCCAGCACTG 86526 A  
CAGT GCTGGGATTACAG  
||| |||||  
GTCA CGACCCTAATGTC

GAM1364 KAI1 3' CTGTAATCCCAGCACT 9499 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 KCNA7 3' ATGCCTGTGATCCCAGCTACTC 49049 C A  
A AGTAGCTGGGATTACAG CAT  
| ||||| |||  
A TCATCGACCCTAGTGTC GTA  
C C

GAM1364 KNSL1 3' ATGCCTGTAATCCCAGCACT 15747 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

GAM1364 LAMP2 3' CTGTAATCCCAGCACT 25712 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LDLR 3' CTGTAATCCCAGCACT 4985 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LDLR 3' CTGTAATCCCAGCACT 4986 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LEP 3' CTGTAATCCCAGCACT 4048 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1364 LRRC2 3' CTATAATCCCAGCACT 44467 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC

GAM1364 LRRC2 3' CTATAATCCCAGCACT 44468 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC

GAM1364 LRRC2 3' CTGTAATCCCAGCACT 44469 A  
AGT GCTGGGATTACAG  
||| ||||| ||  
TCA CGACCCTAATGTC

GAM1364 LRRC2 3' GTAATCCCAGCTACTCA 44477 C  
A AGTAGCTGGGATTAC  
| ||||| |||||  
A TCATCGACCCTAATG  
C

GAM1364 LUZP1 3' ATGCCTGTAATCGCAGCTACTC 53296 C G A  
A  
A AGTAGCTG GATTACAG CAT  
| ||||| ||||| ||  
A TCATCGAC CTAATGTC GTA  
C G C

GAM1364 LUZP1 3' CTGTAATCCCAGCACT 53299 A  
AGT GCTGGGATTACAG  
||| ||||| ||  
TCA CGACCCTAATGTC

GAM1364 MAFF 3' TCTGTAATCCCAGCACT 24654 A  
AGT GCTGGGATTACAGA  
||| ||||| |||||  
TCA CGACCCTAATGTCT

GAM1364 MCM4 3' CTGTAATCCCAGCACT 61903 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

GAM1364 MIR16 3' ATGCCTGTATTCCCAGCTACTC 33563 C T A  
A  
A AGTAGCTGGGA TACAG CAT  
| ||||| ||||| ||  
A TCATCGACCCT ATGTC GTA  
C T C

GAM1364 MOG 3' CTGTAATCCCAGCACT 10102 A  
AGT GCTGGGATTACAG  
||| ||||| |||||

TCA CGACCCTAATGTC

GAM1364 MSH3 3' ATGCCTGTAATCCCAGCACT 10118 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1364 MTMR8 3' CTGTAATCCCAGCACT 31292 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 MTNR1A 3' CTGTAATCCCAGCTACT 19889  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1364 NFKBIL2 3' CTGTAATCCCAACACT 25525 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1364 NPHP1 3' CTGTAATCCCAACACT 62479 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1364 NPHS1 3' CTATAATCCCAGCACT 16190 A C  
AGT GCTGGGATTA AG  
||| |||||  
TCA CGACCCTAAT TC

GAM1364 NT5C2 3' ATGCCTGTAATCCCATCATCTA 24237 C\_\_\_ A  
CT AGTAG TGGGATTACAG CAT  
|||| |||||  
TCATC ACCCTAATGTC GTA  
TACT C

GAM1364 NT5C2 3' CTGTAATCCCAGCACT 24238 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 OASL 3' CTGTAATCCCAGAACT 13578 AG  
AGT CTGGGATTACAG  
||| |||||  
TCA GACCCTAATGTC  
A\_

GAM1364 OPTN 3' ATGCCTGTAATCCCAGCACT 41767 A A  
AGT GCTGGGATTACAG CAT  
||| |||||

		TCA CGACCCTAATGTC GTA			
		C			
		—			
GAM1364	P2RX7	3'	GTCTGTAATCCCAGCGCT	10374	A
			AGT GCTGGGATTACAGAC		
			TCA CGACCCTAATGTCTG		
		—			
GAM1364	PA2G4	3'	CTGTAATCCCAGCACT	71299	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
		—			
GAM1364	PCDH11X	3'	CTGTAATCCCAGCACT	52007	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
		—			
GAM1364	PCDH11X	3'	CTGTAATCCCAGCACT	52008	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
		—			
GAM1364	PCDH11Y	3'	CTGTAATCCCAGCACT	52060	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
		—			
GAM1364	PCDH11Y	3'	CTGTAATCCCAGCACT	52066	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
		—			
GAM1364	PDE4C	3'	ATGCCTATAATCCCAGCACT	6230	A
			AGT GCTGGGATTACAG CAT		C A
			TCA CGACCCTAAT TC GTA		
			A C		
GAM1364	PDE4C	3'	TGCCTGTAATCCCGGTACT	6238	G
			AGTA CTGGGATTACAG CA		A
			TCAT GGCCCTAATGTC GT		
			C		
GAM1364	PIK3R2	3'	ATGCCTGTAATCCCAGCACT	17256	A
			AGT GCTGGGATTACAG CAT		A
			TCA CGACCCTAATGTC GTA		
			C		
GAM1364	PKD2	3'	CTGTAATCCCAGCACT	60092	A
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1364 PLA2G2D 3' ATGCCTGTAATCCCAACACT 24786 AGC A  
—  
AGT TGGGATTACAG CAT  
||| ||||| |||  
TCA ACCCTAATGTC GTA  
CA\_ C

GAM1364 POLK 3' CTGTAATCCCAGCTACT 32566  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1364 PSD 5' CTGCAATCCCAGCACT 10927 A A  
AGT GCTGGGATT CAG  
||| ||||| |||  
TCA CGACCCTAA GTC  
— C

GAM1364 PSMB2 3' ATGCCTGTAATCCCAGCACT 10947 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
— C

GAM1364 PSMB9 3' CTATAATCCCAGCACT 10960 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC  
— A

GAM1364 PSMD5 3' CTATAATCTCAGCTACTCA 17303 C C  
A AGTAGCTGGGATTA AG  
| ||||| ||  
A TCATCGACTCTAAT TC  
C A

GAM1364 PTAFR 3' CTGTAATCCCAGCACT 6294 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 PTAFR 3' CTGTAGTCCCAGCTACTCA 6295 C  
—  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTGATGTC  
C

GAM1364 RAB3B 3' CTGTAATCCCAGCACT 11185 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 RAB7L1 3' CTGTAATCCCAGCACT 14107 A  
—  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1364 RAB7L1 3' TGCCTGTAATCCCAGC 14110 A  
GCTGGGATTACAG CA  
||||||| ||  
CGACCCTAATGTC GT

C

GAM1364 RAD51L1 5' CTGTAATCCCAGCGCT 56060 A  
AGT GCTGGGATTACAG  
||| |||||  
TCG CGACCCTAATGTC

GAM1364 RBBP5 3' ATGCCTGTAATCCCAGCTAC 17332 A  
GTAGCTGGGATTACAG CAT  
||||||| |||  
CATCGACCCTAATGTC GTA

C

GAM1364 RBBP5 3' CTGTAATCCCAGCACT 17334 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 RBBP9 3' ATGCCTGTAATCCCAGCACTGT 70128 A A  
G TACAGT GCTGGGATTACAG CAT  
||||| ||||| |||  
GTGTCA CGACCCTAATGTC GTA

C

GAM1364 RBL1 3' ATGCCTATAATCCCAGCTACTT 11260 \_ C A  
G CA GTAGCTGGGATTA AG CAT  
|| ||||| || |||  
GT CATCGACCCTAAT TC GTA

T A C

GAM1364 RBM3 3' CTGTAATCCCAGTGACT 70487 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA TGACCCTAATGTC

G

GAM1364 RECQL5 3' ATGTCTGTATTGGCTACTGT 14924 TG GAT  
ACAGTAGC G TACAGACAT  
||||| | |||||  
TGTCATCG T ATGTCTGTA

GT \_

GAM1364 RFC2 3' CTGTAATCCCAACACT 11304 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC

CA\_

GAM1364 RPN1 5' ATGCCTGTAATCCCAGCTACT 11389 A  
AGTAGCTGGGATTACAG CAT  
||||||| |||

			TCATCGACCCTAATGTC GTA			
			C			
GAM1364	SCD	3'	ATGTCTGTTTATTA	17346	C	GATT
			CAGTAG TGG ACAGACAT			
			GTCATC ATT TGTCTGTA			
			A ATT_			
GAM1364	SCN2B	3'	CTGTAATCCCAGCACT	15938	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	SIM2	3'	CTGTAATCCCAGCACT	23783	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	SLC14A1	3'	CTGTAATCCCAGCACT	31839	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	SLC14A2	3'	CTGTAATCCCAGCACT	23132	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	SLC26A4	3'	ATGCCTGTAATCCCAGCACT	4783	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			C			
GAM1364	SLC28A2	3'	CTGTAATCCCAGCGCT	14869	A	
			AGT GCTGGGATTACAG			
			TCG CGACCCTAATGTC			
			—			
GAM1364	SLC2A3	3'	CTGTAATCCCAGCACT	22660	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	SLC2A6	3'	CTGTAATCCCAGCACT	34157	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	SLC31A1	3'	ATGCCTGTAATCCCAGCACT	8511	A	A
			AGT GCTGGGATTACAG CAT			



				TCA CGACCCTAATGTC GTA		
				— C		
GAM1364	SLC31A1	3'	TGTAATCCCAGCTACTCA	8515	C	
			A AGTAGCTGGGATTACA			
			A TCATCGACCCTAATGT			
			C			
GAM1364	SMG1	3'	CTGTAATCCCAGCACT	30651	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	SRGAP1	5'	ATGCCTGTAGTCTCAGCTACTC	72259	C	A
	A		A AGTAGCTGGGATTACAG CAT			
			A TCATCGACTCTGATGTC GTA			
			C C			
GAM1364	STAT3	3'	CTGTAATCCCAGCACT	57713	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	STAT3	3'	CTGTAATCCCAGCACT	11998	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	SULT1A2	3'	ATGTCTGCAATCCCAGCGATTT	72215	TA_	A
	G		CAG GCTGGGATT CAGACAT			
			GTT CGACCCTAA GTCTGTA			
			TAG C			
GAM1364	SULT1A3	3'	ATGTCTGCAATCCCAGCGATTT	12052	TA_	A
	G		CAG GCTGGGATT CAGACAT			
			GTT CGACCCTAA GTCTGTA			
			TAG C			
GAM1364	SULT2A1	3'	ATGCCTGTAATCCCAGCACT	71751	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	SULT2A1	3'	ATGTCTGTAATCCCAGCACT	71752	A	
			AGT GCTGGGATTACAGACAT			
			TCA CGACCCTAATGTCTGTA			
			—			
GAM1364	SUV39H2	3'	CTGTAGTCCCAGCTACTCA	45136	C	
			A AGTAGCTGGGATTACAG			

			A TCATCGACCCTGATGTC		
			C		
GAM1364	SWAP70	3'	CTGTAATCCCAGCACT	71348	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	TBX6	3'	CTGTAATCCCAACTACTTG	54964	— C
			CA GTAG TGGGATTACAG		
			GT CATC ACCCTAATGTC		
			T A		
GAM1364	TCF7	3'	CTGTAATCCCAGCACT	12161	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	TCTA	3'	CTGTAATCCCAACACT	42238	AGC
			AGT TGGGATTACAG		
			TCA ACCCTAATGTC		
			CA_		
GAM1364	TEM7	3'	CTGTAATCCCAGCACT	39884	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	TKTL1	5'	ATGTCTGTCTTTCAGCCAC	24296	A GG TT
			GT GCTG A ACAGACAT		
			CA CGAC T TGTCTGTA		
			C TT C_		
GAM1364	TM7SF3	3'	CTGTAATCCCAATACTG	59666	GC
			CAGTA TGGGATTACAG		
			GTCAT ACCCTAATGTC		
			A_		
GAM1364	TNFRSF10A	3'	ATGCCTGTAATCCCAGCACT	13886	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	TNFRSF10D	3'	ATGCCTGTAATCCCAGCACT	13860	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	TNFSF15	3'	CTGTAATCCCAACACT	17592	AGC
			AGT TGGGATTACAG		

			TCA ACCCTAATGTC		
			CA_		
GAM1364	TRIM14	3'	CTGTAATCCCAGCGCT	52635	A
			AGT GCTGGGATTACAG		
			TCG CGACCCTAATGTC		
			—		
GAM1364	TRIM14	3'	ATGCCTGTAATCCCAGCTACT	28851	A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1364	TRIM9	5'	ATGCCTGTAATCCCAGCTA	30752	A
			TAGCTGGGATTACAG CAT		
			ATCGACCCTAATGTC GTA		
			C		
GAM1364	TRPM8	3'	TGTAATCCCAGCTACTCA	43987	C
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1364	TSN	3'	CTGTAATCCCAGCACACTG	16106	A_
			CAGT GCTGGGATTACAG		
			GTCA CGACCCTAATGTC		
			CA		
GAM1364	TSN	3'	TGCCTGTAATTCAGT	16111	G A
			GCTGG ATTACAG CA		
			TGACT TAATGTC GT		
			— C		
GAM1364	TSNAX	3'	CTGTAATCCCAGCACT	19998	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	TTF2	3'	TGCCTGTAATCCCGACACT	13176	AGC A
			AGT TGGGATTACAG CA		
			TCA GCCCTAATGTC GT		
			CA_ C		
GAM1364	UBE2G2	3'	CTGCAATCCCAGCACT	64855	A A
			AGT GCTGGGATT CAG		
			TCA CGACCCTAA GTC		
			— C		
GAM1364	UBE2G2	3'	CTGTAGTCTCAGCTACTCA	64856	C
			A AGTAGCTGGGATTACAG		

			A TCATCGACTCTGATGTC		
			C		
GAM1364 UC28	3'	ATGCCTGTAATCCCAGCTACT	41288	A	
		AGTAGCTGGGATTACAG	CAT		
		TCATCGACCCTAATGTC	GTA		
			C		
GAM1364 UC28	3'	CTGTAATCCCAGCACT	41290	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
GAM1364 UPK1B	3'	ATGCCTGTAATCCCAGCACT	22715	A	A
		AGT GCTGGGATTACAG	CAT		
		TCA CGACCCTAATGTC	GTA		
			C		
GAM1364 USP14	3'	CTGTAATCCCAGCACT	17658	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
GAM1364 VDR	3'	TGTAATCCCAGCTACTCA	4574	C	
		A AGTAGCTGGGATTACA			
		A TCATCGACCCTAATGT			
			C		
GAM1364 VHL	3'	ATGCCTGTAATCCCAGC	5058	A	
		GCTGGGATTACAG	CAT		
		CGACCCTAATGTC	GTA		
			C		
GAM1364 VHL	3'	ATGCCTGTAATCCCAGCACT	5059	A	A
		AGT GCTGGGATTACAG	CAT		
		TCA CGACCCTAATGTC	GTA		
			C		
GAM1364 VHL	3'	ATGCCTGTAATCCTAGCTACTC	5060	C	A
A		A AGTAGCTGGGATTACAG	CAT		
		A TCATCGATCCTAATGTC	GTA		
			C		
GAM1364 VHL	3'	CTGTAATCCCAGCACT	5069	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
GAM1364 VHL	3'	TCTGTAATCCTAGCTACT	5090		
		AGTAGCTGGGATTACAGA			

TCATCGATCCTAATGTCT

GAM1364 VPS41 3' ATGCCTGTAATCCCAGCTACT 26921 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1364 WIG1 3' CTGTAATCCCAGCACT 94466 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 WSX1 3' CTGTAATCCCAGCACT 16732 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 ZNF136 3' CTGTAATCCCAGCACT 59888 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 ZNF137 3' CTGTAATCCCAGCACT 12862 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 ZNF14 3' ATGCCTCTAATCCCAGCTACTC 40713 C C A  
A A  
A AGTAGCTGGGATTA AG CAT  
| ||||| || |||  
A TCATCGACCCTAAT TC GTA  
C C C

GAM1364 ZNF36 3' CTGTAATCCCAGCACT 93962 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 ZNF74 3' ATGTCCCTGTGGTCCCAGCTAC 12790 C  
TCA A  
A AGTAGCTGGGATTACA GACAT  
| ||||| |||||  
A TCATCGACCCTGGTGT CTGTA  
C CC

GAM1364 ZNF74 3' CTGTAATCTTAACACTGTG 12795 AGC  
TACAGT TGGGATTACAG  
||||| |||||  
GTGTCA ATTCTAATGTC  
CA\_

GAM1364 AF020591 3' ATGCCTGTAATCCCAGCACTCT 27135 TA\_ A  
G CAG GCTGGGATTACAG CAT  
||| ||||| |||

			GTC CGACCCTAATGTC GTA		
			TCA C		
GAM1364	AF020591	3'	CTGTAATCCCAGCACT 27139	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	AF020591	3'	CTGTAGTCCCAGCTACTCA 27140	C	
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTGATGTC		
			C		
GAM1364	AKAP11	3'	CTGTAATCCCAGAACTCTG 57831	TAG_	
			CAG CTGGGATTACAG		
			GTC GACCCTAATGTC		
			TCAA		
GAM1364	AKR1D1	3'	ATGCCTATAATCCCAGCACT 19972	A	C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1364	AKR1D1	3'	TGTAATCCCAGCTACTCA 19978	C	
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1364	APOF	3'	CTGTAATCCCAGCACTGTG 7909	A	
			TACAGT GCTGGGATTACAG		
			GTGTCA CGACCCTAATGTC		
			—		
GAM1364	APXL2	3'	CTGTAATCCCAGCACT 75189	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	ARNTL2	3'	ATGCCTGTAATCCCAGCACT 39454	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	ARNTL2	3'	CTGTAATCCCAACTGCT 39462	C	
			AGTAG TGGGATTACAG		
			TCGTC ACCCTAATGTC		
			A		
GAM1364	ARNTL2	3'	CTGTAATCCCAGTACT 39463	G	
			AGTA CTGGGATTACAG		

TCAT GACCCTAATGTC

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      —
GAM1364 BANP  3' ATGCCTGTAATCCCAGC  66214  A
      GCTGGGATTACAG CAT
      |||||
      CGACCCTAATGTC GTA
      C
GAM1364 BFAR  3' CTGTAATCCCAGCTACTTG  60771  —
      CA GTAGCTGGGATTACAG
      || |||||
      GT CATCGACCCTAATGTC
      T
GAM1364 BIA2  3' CTGTAATCCCAGCACT  71281  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC
      —
GAM1364 BIRC1 3' CTGTAATCCCAGCACT  15788  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC
      —
GAM1364 BLOV1 3' ATGCCTGTAATCCCAGCTACT 76277  A
      AGTAGCTGGGATTACAG CAT
      |||||
      TCATCGACCCTAATGTC GTA
      C
GAM1364 BLOV1 3' CTGTAATCCCAGCACT  76280  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC
      —
GAM1364 BLOV1 3' CTGTAATCCCAGCTACTTG  76281  —
      CA GTAGCTGGGATTACAG
      || |||||
      GT CATCGACCCTAATGTC
      T
GAM1364 BNIP-S 3' GTCTGTAATCCCAGCACT  56274  A
      AGT GCTGGGATTACAGAC
      ||| |||||
      TCA CGACCCTAATGTCTG
      —
GAM1364 C13orf1 3' CTGTAATCCCAGCACT  39969  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC
      —
GAM1364 C1orf24 3' CTATAATCCCAGCACT  53714  A  C
      AGT GCTGGGATTA AG
      ||| ||||| ||
```

TCA CGACCCTAAT TC  
 — A  
 GAM1364 C1QTNF2 3' ATGCCTATAATCCCAGGACT 49124 AG C A  
 AGT CTGGGATTA AG CAT  
 ||| ||||| || |||  
 TCA GACCCTAAT TC GTA  
 G\_ A C  
 GAM1364 C20orf108 3' CTGTAATCCCAGCACT 55045 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1364 C20orf12 3' ATGCCTGTAATCCCAGTTACT 36321 A  
 AGTAGCTGGGATTACAG CAT  
 ||||| ||||| |||  
 TCATTGACCCTAATGTC GTA  
 C  
 GAM1364 C20orf12 3' CTGTAATCCCAGCACT 36322 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1364 C20orf130 3' GTGGCTGTCCCAGCCAC 61758 A TTA A  
 GT GCTGGGA CAG CAT  
 || ||||| ||| |||  
 CA CGACCCT GTC GTG  
 C \_ G  
 GAM1364 C20orf142 3' CTGTAATCCCAGCTACT 74775  
 AGTAGCTGGGATTACAG  
 ||||| |||||  
 TCATCGACCCTAATGTC  
 —  
 GAM1364 C20orf175 3' CTGTAATCCCAACACT 55064 AGC  
 AGT TGGGATTACAG  
 ||| |||||  
 TCA ACCCTAATGTC  
 CA\_  
 GAM1364 C20orf177 3' ATGCCTGTAATCCCAGCTACT 62143 A  
 AGTAGCTGGGATTACAG CAT  
 ||||| ||||| |||  
 TCATCGACCCTAATGTC GTA  
 C  
 GAM1364 C20orf177 3' CTGTAATCCCAGCACT 62146 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1364 C20orf183 3' CTGTAATCCCAGCACT 47803 A  
 AGT GCTGGGATTACAG  
 ||| |||||



TCA CGACCCTAATGTC

—  
GAM1364 C20orf29 3' CTGTAATCCCAGCACT 37126 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 C21orf108 3' CTATAATCCCAGCACT 88720 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC

— A  
GAM1364 C22orf19 3' GTCTGTAATCCCAGCACT 13429 A  
AGT GCTGGGATTACAGAC  
||| |||||  
TCA CGACCCTAATGTCTG

—  
GAM1364 C22orf20 3' ATGCCTGTAATCCCAGCTATT 47425 A  
AGTAGCTGGGATTACAG CAT  
||||| ||||| |||  
TTATCGACCCTAATGTC GTA  
C

GAM1364 C2F 3' CTGTAATCCCAGCACT 20928 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 C6orf10 5' CTGTAATCCCATCATTTGCT 22289 C\_\_\_  
AGTAG TGGGATTACAG  
|||| |||||  
TCGTT ACCCTAATGTC  
TACT

GAM1364 C6orf5 3' CTGTAATCCCAGCACT 31346 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 C6orf5 3' CTGTAATCCCAGCACT 31347 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 C8orf2 3' CTGTAATCCCAGCACT 23163 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 C9orf5 3' TCTGTAATCCCAGCACT 49284 A  
AGT GCTGGGATTACAGA  
||| |||||

TCA CGACCCTAATGTCT

GAM1364 CALN1 3' CTATAATCCCAGCACT 48866 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC

GAM1364 CAMKK2 5' CTGTAATCCCAGCACT 21582 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

GAM1364 CBCIP2 3' CTGTAATCCCAGCACT 51590 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

GAM1364 cerk 3' CTGTAATCCCAGCACT 42846 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

GAM1364 CFLAR 3' CTGTAATCCCAGCACT 13929 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

GAM1364 CG012 5' ATGCCTATATTCTAGCTACTCA 83214 C TAC A  
A AGTAGCTGGGAT AG CAT  
| ||||| || |||  
A TCATCGATCTTA TC GTA  
C TA\_ C

GAM1364 CG012 5' ATGCCTGTAATCCCAACACT 83215 AGC A  
AGT TGGGATTACAG CAT  
||| ||||| |||||  
TCA ACCCTAATGTC GTA  
CA\_ C

GAM1364 CG012 5' CTGTAATCCCAGCTATTTCGGCT 83219  
G CAGT AGCTGGGATTACAG  
||| ||||| |||||  
GTCG TCGACCCTAATGTC  
GCTTA

GAM1364 CGI-203 3' TGTAATCCCAGCTACTCA 39904 C  
A AGTAGCTGGGATTACA  
| ||||| |||||  
A TCATCGACCCTAATGT  
C

GAM1364 CHRFA7A 3' ATGCTTGTAATCCCAGCTACTC 95017 C GA  
A A AGTAGCTGGGATTACA CAT  
| ||||| ||||| |||

			A TCATCGACCCTAATGT GTA		
			C TC		
GAM1364	CLDN15	3'	ATGCCTGTAATCCCAGCACT 56558	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	CNNM4	3'	TCTGTTGTCAACTGCTGTA 39484	CTGG	T
			TACAGTAG GAT ACAGA		
			ATGTCGTC CTG TGTCT		
			AA__ T		
GAM1364	COE2	3'	ATGCCTGTAATCCCAGCTACTT 64247	—	A
	G		CA GTAGCTGGGATTACAG CAT		
			GT CATCGACCCTAATGTC GTA		
			T C		
GAM1364	COE2	3'	CTGTAATCCCAGCACT 64251	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	CPR2	3'	CTGTAATCCCAGCACT 48095	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	CPR2	3'	CTGTAATCCCAGCTACTCA 48096	C	
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTAATGTC		
			C		
GAM1364	CSAD	3'	CTGTAATCCCAGCACT 32028	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	D21S2056E	3'	ATGCCTGTAATCCCAGCTACT 13467		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1364	D21S2056E	3'	CTGTAATCCCAGCACT 13470	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	DCOHN	3'	CTGTAATCCCTGCACT 49600	A	T
			AGT GC GGGATTACAG		

				TCA CG CCCTAATGTC		
				— T		
GAM1364	DDX34	3'	CTGTAATCCCAGCACT	27982	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	DEGS	3'	ATGCCTGTAATCCCAGCTACAT	58613	—	A
	G		CA GTAGCTGGGATTACAG CAT			
			GT CATCGACCCTAATGTC GTA			
			A C			
GAM1364	DEGS	3'	ATGCCTATAATCCCAGCACT	13409	A	C A
			AGT GCTGGGATTA AG CAT			
			TCA CGACCCTAAT TC GTA			
			— A C			
GAM1364	DEGS	3'	ATGCCTGTAATCCCAGCTACAT	13410	—	A
	G		CA GTAGCTGGGATTACAG CAT			
			GT CATCGACCCTAATGTC GTA			
			A C			
GAM1364	DIS3	3'	ATGCCTGTAATCCCAGCTACTT	30227	—	A
	G		CA GTAGCTGGGATTACAG CAT			
			GT CATCGACCCTAATGTC GTA			
			T C			
GAM1364	DKFZP434B168	3'	CTGTAATCCCAGCACT	31253	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	DKFZP434C171	3'	CTGTAATCCCAGCACT	31553	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	DKFZP434C1715	3'	CTGTAATCCCAGCAC	86148	A	
			GT GCTGGGATTACAG			
			CA CGACCCTAATGTC			
			—			
GAM1364	DKFZp434E0519	3'	CTATAATCCCAGCACT	49986	A	C
			AGT GCTGGGATTA AG			
			TCA CGACCCTAAT TC			
			— A			
GAM1364	DKFZp434E2220	5'	TGTAATCCCAGCTACTCA	34304	C	
			A AGTAGCTGGGATTACA			

A TCATCGACCCTAATGT  
 C  
 GAM1364 DKFZP434F091 3' TGTAATCCCAACTACTCA 31284 C C  
 A AGTAG TGGGATTACA  
 I ||||| |||||  
 A TCATC ACCCTAATGT  
 C A  
 GAM1364 DKFZp434G171 3' ATGCCTGTAATCCCAGCACT 79431 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||  
 TCA CGACCCTAATGTC GTA  
 — C  
 GAM1364 DKFZp434G171 3' TGTAATCCCAGCTACTCA 79440 C  
 A AGTAGCTGGGATTACA  
 I ||||| |||||  
 A TCATCGACCCTAATGT  
 C  
 GAM1364 DKFZP434I1735 3' CTGTAATCCCAGCTACT 87801  
 AGTAGCTGGGATTACAG  
 ||||| |||||  
 TCATCGACCCTAATGTC  
  
 GAM1364 DKFZP434L187 5' CTGTAATCCCAGCTACT 68804  
 AGTAGCTGGGATTACAG  
 ||||| |||||  
 TCATCGACCCTAATGTC  
  
 GAM1364 DKFZP434N1511 3' ATGCCTGTAATCCCAGCACT 91415 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||  
 TCA CGACCCTAATGTC GTA  
 — C  
 GAM1364 DKFZP434N161 3' GTCTGTAATCCCAGCACT 78522 A  
 AGT GCTGGGATTACAGAC  
 ||| ||||| |||||  
 TCA CGACCCTAATGTCTG  
 —  
 GAM1364 DKFZp547C176 3' CTGTAATCCCAGCACT 67222 A  
 AGT GCTGGGATTACAG  
 ||| ||||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1364 DKFZp547I094 3' CTGTAATCCCAGCACT 49639 A  
 AGT GCTGGGATTACAG  
 ||| ||||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1364 DKFZp547I094 3' CTGTAGTCACAGCTACT 49640 G  
 AGTAGCTG GATTACAG  
 ||||| |||||

			TCATCGAC CTGATGTC			
			A			
GAM1364	DKFZP564B1023	3'	ATGCCTGTAATCCCAGCTACT	48536		A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1364	DKFZP564B1023	3'	CTGTAATCCCAGCACT	48538	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	DKFZP564I052	3'	CTGTAATCCCAGCACT	66707	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	DKFZP564M182	3'	CTGTAATCCCAGCACT	78033	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	DKFZP564M182	3'	CTGTAATCCCAGCTACT	78034		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
			—			
GAM1364	DKFZp566H0824	3'	CTGTAATCCCAGCACTTTA	34050	C A	
			TA AGT GCTGGGATTACAG			
			AT TCA CGACCCTAATGTC			
			T —			
GAM1364	DKFZP586C1324	3'	ATGCCTGTAATCCCAGCACT	69796	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	DKFZP586M1120	3'	CTGTAATCCCAGCACT	48457	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	DKFZP667O116	3'	TGCCTATAATCCCGGCACT	94287	A	C A
			AGT GCTGGGATTA AG CA			
			TCA CGGCCCTAAT TC GT			
			— A C			
GAM1364	DKFZP761E2110	3'	ATGCCTGTAATCCCAGCAC	48224	A	A
			GT GCTGGGATTACAG CAT			

			CA CGACCCTAATGTC GTA		
			— C		
GAM1364	DKFZP761G1913	3'	ATGCCTGTAATCCCAGCACT	48909	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	DKFZP761G1913	3'	CTGTAATCCCAGCTACTTG	48913	—
			CA GTAGCTGGGATTACAG		
			GT CATCGACCCTAATGTC		
			T		
GAM1364	DKFZp761J139	5'	CTGTAATCCCAGCACT	50108	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	DRF1	3'	CTATAATCCCAGCACT	47030	A C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1364	DRF1	3'	CTGTAATCCCAGCACT	47032	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	DRF1	3'	TGTAATCCCAGCTACTCA	47038	C
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1364	FADS1	3'	ATGCCTGTAATCCCAACACT	25473	AGC A
			AGT TGGGATTACAG CAT		
			TCA ACCCTAATGTC GTA		
			CA_ C		
GAM1364	FADS1	3'	CTGTAATCCCAGCTAC	25476	
			GTAGCTGGGATTACAG		
			CATCGACCCTAATGTC		
			—		
GAM1364	FBXO27	3'	ATGCCTGTAATCCCAGCACT	74504	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	FBXO27	3'	CTGTAATCCCTGCACT	74508	A T
			AGT GC GGGATTACAG		

TCA CG CCCTAATGTC  
 — T  
 GAM1364 FBXO6 3' CTGTAATCCCAGCACT 37383 A  
 AGT GCTGGGATTACAG  
 ||| |||||||||  
 TCA CGACCCTAATGTC

—  
 GAM1364 FBXO9 3' ATGCCTATAATCCCAGCACT 53100 A C A  
 AGT GCTGGGATTA AG CAT  
 ||| ||||||| || |||  
 TCA CGACCCTAAT TC GTA

— A C  
 GAM1364 FBXO9 3' CTATAATCCCAATACT 53102 GC C  
 AGTA TGGGATTA AG  
 ||| ||||||| ||  
 TCAT ACCCTAAT TC  
 A\_ A

— A C  
 GAM1364 FKBP14 3' ATGCCTGTAATCCCAGCACT 35622 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||||||| |||  
 TCA CGACCCTAATGTC GTA

— C  
 GAM1364 FKBP14 3' ATGCCTGTAATCCCAGCACT 35623 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||||||| |||  
 TCA CGACCCTAATGTC GTA

— C  
 GAM1364 FKSG17 3' CTGTAATCCCAGTTACTCA 49329 C  
 A AGTAGCTGGGATTACAG  
 | |||||||||  
 A TCATTGACCCTAATGTC  
 C

—  
 GAM1364 FLJ00060 3' ATGTCTGTAATCCCAGCACTCT 61091 TA\_  
 G CAG GCTGGGATTACAGACAT  
 ||| |||||||||  
 GTC CGACCCTAATGTCTGTA  
 TCA

—  
 GAM1364 FLJ10008 3' GTCTGTAATCCCAGCACT 35729 A  
 AGT GCTGGGATTACAGAC  
 ||| |||||||||  
 TCA CGACCCTAATGTCTG

—  
 GAM1364 FLJ10043 3' CTGTAATCCCAGCACT 35758 A  
 AGT GCTGGGATTACAG  
 ||| |||||||||  
 TCA CGACCCTAATGTC

—  
 GAM1364 FLJ10043 3' CTGTAATCCCAGCTACT 35759  
 AGTAGCTGGGATTACAG  
 |||||||||



TCATCGACCCTAATGTC

GAM1364 FLJ10058 3' ATGCCTGTAATCCCAGCACT 35782 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
\_ C

GAM1364 FLJ10244 3' ATGCCTGTAATCCCAGCTGCT 35940 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCGTCGACCCTAATGTC GTA  
C

GAM1364 FLJ10460 3' CTGTAATCCCAACACT 36127 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1364 FLJ10460 3' CTGTAATCCCAGCACT 36128 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC  
\_

GAM1364 FLJ10460 3' CTGTAATCCCAGCTACTTG 36129 \_  
CA GTAGCTGGGATTACAG  
|| |||||  
GT CATCGACCCTAATGTC  
T

GAM1364 FLJ10547 3' CTGTAATCCCAGCACT 36267 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC  
\_

GAM1364 FLJ10607 3' CTGTAATCCCAGCACT 77113 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC  
\_

GAM1364 FLJ10607 3' CTGTAATCCCAGCTACTCA 77114 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
C

GAM1364 FLJ10613 3' GTCTGTAATCCCAGCACT 38825 A  
AGT GCTGGGATTACAGAC  
||| |||||  
TCA CGACCCTAATGTCTG  
\_

GAM1364 FLJ10650 3' CTGTAATCCCAGCACT 36382 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1364 FLJ10704 3' ATGCCTGTAATCCCAGCTACT 36449 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA

C

GAM1364 FLJ10781 3' CTGTAATCCCAGCACT 36631 A  
AGT GCTGGGATTACAG  
|||  
TCA CGACCCTAATGTC

GAM1364 FLJ10781 3' TGTAATCCCAGCTACTCA 36638 C  
A AGTAGCTGGGATTACA  
|  
A TCATCGACCCTAATGT  
C

GAM1364 FLJ10803 3' CTGTAATCCCAGCACT 36664 A  
AGT GCTGGGATTACAG  
|||  
TCA CGACCCTAATGTC

GAM1364 FLJ10826 3' ATGCCTGTAATCCCAGCTACT 36700 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA

C

GAM1364 FLJ10830 3' ATGCCTGTAGTCCCAGCCACTC 36717 C A A  
A  
A AGT GCTGGGATTACAG CAT  
| |||  
A TCA CGACCCTGATGTC GTA  
C C C

GAM1364 FLJ10830 3' ATGCCTGTAGTTCCAGCTACTC 36718 C A  
A  
A AGTAGCTGGGATTACAG CAT  
| |||  
A TCATCGACCTTGATGTC GTA  
C C

GAM1364 FLJ10989 3' CTGTAATCCCAGCACT 36949 A  
AGT GCTGGGATTACAG  
|||  
TCA CGACCCTAATGTC

GAM1364 FLJ10997 3' TGCCTGACCACCTACTGTA 36957 C GATTA A  
TACAGTAG TGG CAG CA  
||||| |||  
ATGTCATC ACC GTC GT

C A C

GAM1364 FLJ11029 3' CTGTAATCCCAGCACT 60975 A  
AGT GCTGGGATTACAG  
|||

TCA CGACCCTAATGTC

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      -
GAM1364 FLJ11036 3' CTGCGGTTCCAGCTACTCA 36998 C TA
      A AGTAGCTGGGAT CAG
      | ||||| |||
      A TCATCGACCTTG GTC
      C GC
GAM1364 FLJ11042 3' ATGCCTGTAATCCCAGCACT 37004 A A
      AGT GCTGGGATTACAG CAT
      ||| ||||| |||
      TCA CGACCCTAATGTC GTA
      C
GAM1364 FLJ11126 3' ATGCCTATAATCCCAGCAC 37083 A C A
      GT GCTGGGATTA AG CAT
      || ||||| || |||
      CA CGACCCTAAT TC GTA
      A C
GAM1364 FLJ11136 3' CTGTAATCCCAGCACT 37093 A
      AGT GCTGGGATTACAG
      ||| ||||| |||
      TCA CGACCCTAATGTC
      -
GAM1364 FLJ11151 3' CTGTAATCCCAGCACT 67874 A
      AGT GCTGGGATTACAG
      ||| ||||| |||
      TCA CGACCCTAATGTC
      -
GAM1364 FLJ11151 3' CTGTAATCCCAGCTACT 67875
      AGTAGCTGGGATTACAG
      ||||| ||||| |||
      TCATCGACCCTAATGTC
      -
GAM1364 FLJ11267 3' ATGCCTGTAATCCCAGCACT 39003 A A
      AGT GCTGGGATTACAG CAT
      ||| ||||| |||
      TCA CGACCCTAATGTC GTA
      C
GAM1364 FLJ11370 3' ATGCCTGTAATCCCAGCTACT 46370 A
      AGTAGCTGGGATTACAG CAT
      ||||| ||||| |||
      TCATCGACCCTAATGTC GTA
      C
GAM1364 FLJ11637 3' CTGTAATCCCAGCACT 46380 A
      AGT GCTGGGATTACAG
      ||| ||||| |||
      TCA CGACCCTAATGTC
      -
GAM1364 FLJ11700 3' CTGTAATCCCAGCACT 46038 A
      AGT GCTGGGATTACAG
      ||| ||||| |||
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TCA CGACCCTAATGTC

GAM1364 FLJ11700 3' CTGTAATCCCAGCTACTCA 46039 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
C

GAM1364 FLJ11710 5' ATGCCTGTAGTCCCAGCTACTC 45825 C A  
A  
A AGTAGCTGGGATTACAG CAT  
| ||||| |||  
A TCATCGACCCTGATGTC GTA  
C C

GAM1364 FLJ11722 3' ATGCCTGTAATCCCAGGACT 46389 AG A  
AGT CTGGGATTACAG CAT  
||| ||||| |||  
TCA GACCCTAATGTC GTA  
G\_ C

GAM1364 FLJ11722 3' CTGTAATCCCAGCTACT 46391  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1364 FLJ11722 3' TGTAATCCCAGCTACTCA 46401 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1364 FLJ11726 3' CTGTAATCCCAGCACT 46411 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 FLJ11996 3' ATGCCTGTAATCCCAGCTACT 46434 A  
AGTAGCTGGGATTACAG CAT  
||||| |||  
TCATCGACCCTAATGTC GTA  
C

GAM1364 FLJ12056 3' ATGCCTATAATCCCAACACT 46251 AGC C A  
AGT TGGGATTA AG CAT  
||| ||||| |||  
TCA ACCCTAAT TC GTA  
CA\_ A C

GAM1364 FLJ12056 3' ATGCCTGTAATCCCAGCTATT 46252 A  
AGTAGCTGGGATTACAG CAT  
||||| |||  
TTATCGACCCTAATGTC GTA  
C

GAM1364 FLJ12122 3' CTGTAATCCCAGCACT 46462 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

—  
GAM1364 FLJ12178 3' GTCTGTAATCCCAGCACT 47103 A  
AGT GCTGGGATTACAGAC  
||| |||||  
TCA CGACCCTAATGTCTG

—  
GAM1364 FLJ12294 3' CTATAATCCCAGCTACT 47012 C  
AGTAGCTGGGATTA AG  
||| ||||| ||  
TCATCGACCCTAAT TC

A  
GAM1364 FLJ12294 3' CTGTAATCCCAGCACT 47013 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ12331 3' CTATAATCCCAGCACTTTA 46478 C A C  
TA AGT GCTGGGATTA AG  
|| ||| ||||| ||  
AT TCA CGACCCTAAT TC  
T \_ A

GAM1364 FLJ12363 3' CTGTAATCCCAGCACT 49679 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ12547 3' CTGTAATCCCAGCACTGTG 46491 A  
TACAGT GCTGGGATTACAG  
||||| |||||  
GTGTCA CGACCCTAATGTC

—  
GAM1364 FLJ12606 3' CTGTAATCCCAGCACT 45640 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ12618 3' ATGCCTGTAATCTCAGCTACTC 45994 C A  
A  
A AGTAGCTGGGATTACAG CAT  
| ||||| ||||| |||  
A TCATCGACTCTAATGTC GTA  
C C

GAM1364 FLJ12660 3' CTGTAATCCCAGCACT 47141 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ12660 3' CTGTAATCCCAGCTACT 47142  
AGTAGCTGGGATTACAG  
|||||

TCATCGACCCTAATGTC

GAM1364 FLJ12666 3' CTGTAATCCCAGCACT 44767 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ12800 3' CTGTAATCCCAGCACT 43232 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ12949 3' ATGCCTGTAGTCCCAGCTACTC 43442 C A  
A A AGTAGCTGGGATTACAG CAT  
| ||||| |||  
A TCATCGACCCTGATGTC GTA  
C C

GAM1364 FLJ12949 3' CTGTAATCCCAGCACT 43445 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ12985 3' CTGTAATCCCAGCACT 46240 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ13117 3' ATGCCTGTAATCCCAGCACT 43539 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

—  
GAM1364 FLJ13162 3' ATGCCTGTAATCCCAGCTACT 46550 A  
AGTAGCTGGGATTACAG CAT  
||| ||||| |||  
TCATCGACCCTAATGTC GTA  
C

GAM1364 FLJ13162 3' CTGTAATCCCAGCACT 46556 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ13193 3' ATGCCTATAATCCCGGCTACT 49758 C A  
AGTAGCTGGGATTA AG CAT  
||| ||||| || |||  
TCATCGGCCCTAAT TC GTA  
A C

GAM1364 FLJ13193 3' CTGTAATCCCAACACTTTA 49765 C AGC  
TA AGT TGGGATTACAG  
|| ||| |||||

			AT TCA ACCCTAATGTC		
			T CA_		
GAM1364	FLJ13193	3'	CTGTAATCCCAGCACT	49766	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	FLJ13305	3'	ATGCCTGTAATCCCAGC	90125	A
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1364	FLJ13448	3'	CTGTAATCCCAGTTACT	47135	
			AGTAGCTGGGATTACAG		
			TCATTGACCCTAATGTC		
			—		
GAM1364	FLJ13456	3'	CTGTAATCCCAGCACT	65936	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	FLJ13456	3'	CTGTAATCCCAGCTACTCA	65937	C
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTAATGTC		
			C		
GAM1364	FLJ13614	3'	CTGTAATCCCAGCACT	57451	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	FLJ13659	3'	ATGCCTGTAATCCCAGCTACT	47243	A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1364	FLJ13659	3'	CTGTAATCCCAGCACT	47246	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	FLJ13769	3'	ATGCCTATAATCCCAGCACT	46600	A C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1364	FLJ13769	3'	CTGTAATCCCAGCACT	46608	A
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1364 FLJ13848 3' CTGTAATCCCAGCACT 45465 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 FLJ13910 3' CTGCATTTTAGCTCTG 42927 T TA  
CAG AGCTGGGAT CAG  
||| ||||| |||  
GTC TCGATTTTA GTC

GAM1364 FLJ13952 3' ATGCCTGTAACCCCAGCTACT 45613 A A  
AGTAGCTGGG TTACAG CAT  
||| ||||| |||  
TCATCGACCC AATGTC GTA  
C C

GAM1364 FLJ13952 3' ATGCCTGTAATCCCAGCACT 45614 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

GAM1364 FLJ13984 3' CTGTGGTCCCAGCTACTCA 45448 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTGGTGTC  
C

GAM1364 FLJ14100 3' CTGTAATCCCAGCACT 46679 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 FLJ14107 3' ATGCCTGTAATCCCAGCACT 46689 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

GAM1364 FLJ14117 3' ATGCCTGTAGTCCCAGCTACTC 42901 C A  
A AGTAGCTGGGATTACAG CAT  
| ||||| |||  
A TCATCGACCCTGATGTC GTA  
C C

GAM1364 FLJ14117 3' CTGTAATACCAGCTACTCA 42907 C G  
A AGTAGCTGG ATTACAG  
| ||||| |||||  
A TCATCGACC TAATGTC  
C A

GAM1364 FLJ14117 3' CTGTAATCCCAGCACT 42908 A  
AGT GCTGGGATTACAG  
||| |||||



TCA CGACCCTAATGTC

—  
GAM1364 FLJ14225 3' CTGTAATCCCAGCACT 45902 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ14251 3' CTGTAATCCCAGCACT 45970 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ14326 3' ATGCCTATAATCCCAGCTACT 49799 C A  
AGTAGCTGGGATTA AG CAT  
||||||| |||  
TCATCGACCCTAAT TC GTA  
A C

GAM1364 FLJ14326 3' ATGCCTGTAATCCCAGC 49800 A  
GCTGGGATTACAG CAT  
||||||| |||  
CGACCCTAATGTC GTA  
C

GAM1364 FLJ14327 3' ATGCCTGTAATCCCAGCACT 46129 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
C

—  
GAM1364 FLJ14345 3' CTGTAATCCCAGCACT 45334 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ14345 3' CTGTAATCCCAGCTACT 45335  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1364 FLJ14346 3' CTGTAATCCCAGCACT 46709 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ14346 3' CTGTAATCCCAGCACT 46710 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ14397 3' ATGCCTGTAACCCCAGCTACT 51323 A A  
AGTAGCTGGG TTACAG CAT  
||||||| |||||

				TCATCGACCC AATGTC GTA		
				C C		
GAM1364	FLJ14397	3'	CTATAATCCCAGCACT	51325	A	C
			AGT GCTGGGATTA AG			
			TCA CGACCCTAAT TC			
			— A			
GAM1364	FLJ14621	3'	CTGTAATCCCAGCACT	51470	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	FLJ14642	3'	ATGCCTGTAATCCCAGCACT	51493	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	FLJ14642	3'	CTGTAATCCCAGCACT	51499	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	FLJ14888	3'	ATGCCTGTAATCCCAGCACT	51679	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	FLJ20004	3'	ATGCCTGTAATCCCAGCACT	34312	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	FLJ20004	3'	CTGTAATCCCAGCACT	95292	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	FLJ20004	3'	TGCCTGTAATCCCAGCTACT	95301		A
			AGTAGCTGGGATTACAG CA			
			TCATCGACCCTAATGTC GT			
			C			
GAM1364	FLJ20006	3'	CTGTAATCCCAGCACT	34320	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	FLJ20006	3'	CTGTAATCCCAGCTACT	34321		
			AGTAGCTGGGATTACAG			

TCATCGACCCTAATGTC

GAM1364 FLJ20034 3' CTGTAATCCCAGCACT 34371 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ20055 3' CTGAAGTCCCAGCTACTCA 34440 C A  
A AGTAGCTGGGATT CAG  
| ||||| |||  
A TCATCGACCCTGA GTC  
C A

GAM1364 FLJ20055 3' CTGTAATCCCAGCACTTTA 34441 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||  
AT TCA CGACCCTAATGTC  
T —

GAM1364 FLJ20059 3' ATGCCTGTAATCCCAGCACT 34446 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
— C

GAM1364 FLJ20071 3' ATGCCTATAATCCCAGCTACTT 34479 — C A  
G CA GTAGCTGGGATTA AG CAT  
|| ||||| || |||  
GT CATCGACCCTAAT TC GTA  
T A C

GAM1364 FLJ20081 3' CTGTAATCCCAGCACT 34507 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 FLJ20139 3' CTGTAATCCCAACACT 34624 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1364 FLJ20174 3' CTGTAATCCCAAAGTGCTG 34688 GC\_  
CAGTA TGGGATTACAG  
|||| |||||  
GTCGT ACCCTAATGTC  
GAA

GAM1364 FLJ20200 3' TGCCTGTAATCCCTGCACT 34729 A T A  
AGT GC GGGATTACAG CA  
||| || ||||| ||  
TCA CG CCCTAATGTC GT  
— T C

GAM1364 FLJ20211 3' CTGTAATCCCAGCACT 34751 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1364 FLJ20280 3' CTGTAATCCCAGCACT 34849 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 FLJ20280 3' CTGTAATCCCTGCTACT 34850 T  
AGTAGC GGGATTACAG  
||||| |||||  
TCATCG CCCTAATGTC  
T

GAM1364 FLJ20340 3' ATGCCTGTAATCCCAGCATTTT 34972 TA\_ A  
G CAG GCTGGGATTACAG CAT  
||| ||||| |||  
GTT CGACCCTAATGTC GTA  
TTA C

GAM1364 FLJ20340 3' TGTAATCCCAGCTACTCA 34979 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1364 FLJ20359 3' ATGCCTGTAATCCCAGCACT 35035 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

GAM1364 FLJ20452 3' ATGCCTGTAATCCCAGCACT 35196 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

GAM1364 FLJ20464 3' ATGCCTATAATCCGAGCTACT 35228 G C A  
AGTAGCT GGATTA AG CAT  
||||| ||||| |||  
TCATCGA CCTAAT TC GTA  
G A C

GAM1364 FLJ20464 3' ATGCCTGTAATCCCAGCACT 35229 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

GAM1364 FLJ20464 3' ATGCCTGTAATCTCAGCTACT 35230 A  
AGTAGCTGGGATTACAG CAT  
||||| ||||| |||  
TCATCGACTCTAATGTC GTA  
C

GAM1364 FLJ20627 3' ATGCCTGTAATCCCAGCACT 35471 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||

			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	FLJ20627	3'	GTCATCTCAGCTACTCA 35475	C	T	
			A AGTAGCTGGGAT AC			
			I			
			A TCATCGACTCTA TG			
			C C			
GAM1364	FLJ20695	3'	ATGCCTGTAATCCCAGCACT 35556	A		A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	FLJ20700	3'	ATGCCTGTAATCCCAGCACT 35570	A		A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	FLJ20783	3'	CTGTAATCCCAGCACT 35661	A		
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	FLJ20825	3'	ATGCCTGTAATCCCAACTCTTG 35693	T C		A
			CAG AG TGGGATTACAG CAT			
			GTT TC ACCCTAATGTC GTA			
			C A C			
GAM1364	FLJ20825	3'	ATGCCTGTAATCCCAGCTACT 35694			A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1364	FLJ20825	3'	CTGTAATCCCAGCACT 35696	A		
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	FLJ20972	3'	ATGCCTATAATCCCAGGTA 46722	G		C A
			AGTA CTGGGATTA AG CAT			
			TCAT GACCCTAAT TC GTA			
			G A C			
GAM1364	FLJ21106	3'	CTGTAATCCCAGCACT 46995	A		
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	FLJ21144	3'	ATGCCTGTAATCCCAGCACT 42875	A		A
			AGT GCTGGGATTACAG CAT			

TCA CGACCCTAATGTC GTA  
 — C  
 GAM1364 FLJ21162 3' ATGCCTATAATCCCAGCACT 45892 A C A  
 AGT GCTGGGATTA AG CAT  
 ||| ||||| || |||  
 TCA CGACCCTAAT TC GTA  
 — A C  
 GAM1364 FLJ21162 3' CTATAAACCCAGCTACTCA 45894 C A C  
 A AGTAGCTGGG TTA AG  
 | ||||| ||| ||  
 A TCATCGACCC AAT TC  
 C A A  
 GAM1364 FLJ21240 3' ATGCCTGTAATATCAGCTACTC 45837 C GG A  
 A A AGTAGCTG ATTACAG CAT  
 | ||||| ||||| |||  
 A TCATCGAC TAATGTC GTA  
 C TA C  
 GAM1364 FLJ21272 3' ATGCCTGTAATCCCAGC 46735 A  
 GCTGGGATTACAG CAT  
 ||||| |||  
 CGACCCTAATGTC GTA  
 C  
 GAM1364 FLJ21551 3' CTGTAATCCCAGCTAC 45628  
 GTAGCTGGGATTACAG  
 |||||  
 CATCGACCCTAATGTC  
  
 GAM1364 FLJ21657 3' CTGTAATCCCAACACT 42509 AGC  
 AGT TGGGATTACAG  
 ||| |||||  
 TCA ACCCTAATGTC  
 CA\_  
 GAM1364 FLJ21687 3' CTGTAATCCCAGCACT 45857 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
  
 —  
 GAM1364 FLJ21870 3' ATGCCTGTAATCCCAGCACT 43458 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||  
 TCA CGACCCTAATGTC GTA  
 — C  
 GAM1364 FLJ22054 3' CTGTAATCCAAGCTGC 94395 G  
 GTAGCT GGATTACAG  
 ||||| |||||  
 CGTCGA CCTAATGTC  
 A  
 GAM1364 FLJ22054 3' CTGTAATCCCAGCACT 94396 A  
 AGT GCTGGGATTACAG  
 ||| |||||

TCA CGACCCTAATGTC

GAM1364 FLJ22167 3' ATGCCTGTAATCCCAGCATTTT 44565 TA\_ A  
G CAG GCTGGGATTACAG CAT

||| |||||  
GTT CGACCCTAATGTC GTA  
TTA C

GAM1364 FLJ22167 3' CTGTAATCCCAGCTACTTA 44572 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
T

GAM1364 FLJ22313 3' GTCTGTAATCCCAGCACT 42344 A  
AGT GCTGGGATTACAGAC  
||| |||||  
TCA CGACCCTAATGTCTG

GAM1364 FLJ22692 3' CTGTAATCCCAGCACT 46802 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 FLJ23022 3' TGCCTGTAATCCCTGCACT 46814 A T A  
AGT GC GGGATTACAG CA  
||| || ||||| ||  
TCA CG CCCTAATGTC GT  
\_ T C

GAM1364 FLJ23042 3' ATGCCTGTAATCCCAGCTACT 47170 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1364 FLJ23042 3' CTGTAATCCCAGCACT 47172 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 FLJ23120 3' CTGTAATCCCAGCTACTCA 85148 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
C

GAM1364 FLJ23235 3' ATGCCTGTAATCCCAGCACT 46305 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
C

GAM1364 FLJ23323 3' CTGTAATCCCAAAGTGCTG 45051 GC\_  
CAGTA TGGGATTACAG  
|||||

				GTCGT ACCCTAATGTC		
				GAA		
GAM1364	FLJ23447	3'	ATGCCTGTAATCCCAGCACT	45710	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	FLJ23476	3'	ATGCCTGTAATCCCAACATTCT	44958	TAGC_	A
	G		CAG TGGGATTACAG CAT			
			GTC ACCCTAATGTC GTA			
			TTACA C			
GAM1364	FLJ23499	3'	ATGCCTGTAATCCCAGCACT	42816	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	FLJ23499	3'	ATGCCTGTAATCCCAGCACT	42817	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	FLJ23499	3'	CTGTAATCCCAGCTACT	42821		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
			— C			
GAM1364	FLJ23537	3'	ATGCCTGCAATCCCAGCTACTT	46021	_	A A
	G		CA GTAGCTGGGATT CAG CAT			
			GT CATCGACCCTAA GTC GTA			
			T C C			
GAM1364	FLJ25012	3'	ATGCCTGTAATCCAGTACT	58088	G G	A
			AGTA CTGG ATTACAG CAT			
			TCAT GACC TAATGTC GTA			
			— — C			
GAM1364	FLJ25012	3'	CTATGGTCCCAGCTACTCA	58089	C	C
			A AGTAGCTGGGATTA AG			
			A TCATCGACCCTGGT TC			
			C A			
GAM1364	FLJ25012	3'	CTGTAATCCCAGCACT	58090	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	FLJ25179	3'	ATGCCTGTAATCCCAGCACT	58354	A	A
			AGT GCTGGGATTACAG CAT			



			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	FLJ30046	3'	CTGCAATGTTTGCTACTGTA 58100	TG G A	
			TACAGTAGC G ATT CAG		
			I		
			ATGTCATCG T TAA GTC		
			TT G C		
GAM1364	FLJ30092	3'	CTGTAATCCCAGCACT 58689 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	FLJ30681	3'	CTGTAATCCCAGCTACT 91786		
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
			—		
GAM1364	FLJ31455	3'	CTGTAATCCCAGCACT 58623 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	FLJ31737	3'	CTGTAATCCCAGCACT 58694 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	FUSIP1	3'	ATGCCTGTAATCTCAGCTACTC 53955 C	A	
	A		A AGTAGCTGGGATTACAG CAT		
			I		
			A TCATCGACTCTAATGTC GTA		
			C C		
GAM1364	FUSIP1	3'	CTGTAATCCCAGCACT 53957 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	GALNT6	3'	ATGCCTGTAGTCGCAGCTACTC 23290 C	G A	
	A		A AGTAGCTG GATTACAG CAT		
			I		
			A TCATCGAC CTGATGTC GTA		
			C G C		
GAM1364	GCN2	3'	ATGCCTGTAGTCCCAGCTACT 62768	A	
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTGATGTC GTA		
			C		
GAM1364	GLTP	3'	CTGTAATCCCAGCACT 33159 A		
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1364 GLTP 3' CTGTAGTTCAGCTACTCA 33160 C  
A AGTAGCTGGGATTACAG  
I |||||  
A TCATCGACCTTGATGTC  
C

GAM1364 GP5 3' CTGTAATCCCAGCACT 15645 A  
AGT GCTGGGATTACAG  
III |||||  
TCA CGACCCTAATGTC

GAM1364 HES2 3' CTGTAATCCCAGCACT 38854 A  
AGT GCTGGGATTACAG  
III |||||  
TCA CGACCCTAATGTC

GAM1364 HSD17B7 3' TGTAGTCCCAGCTACTCA 33037 C  
A AGTAGCTGGGATTACA  
I |||||  
A TCATCGACCCTGATGT  
C

GAM1364 HSH2 3' ATGCCTGTAATCCCAGCTACTT 51671 \_ A  
G CA GTAGCTGGGATTACAG CAT  
II ||||| III  
GT CATCGACCCTAATGTC GTA  
T C

GAM1364 HSMPP8 3' CTATAATCCCAGCGCT 93474 A C  
AGT GCTGGGATTA AG  
III ||||| II  
TCG CGACCCTAAT TC  
A

GAM1364 HSPC043 3' ATGCCTGTAATCCCAGCACT 67719 A A  
AGT GCTGGGATTACAG CAT  
III ||||| III  
TCA CGACCCTAATGTC GTA  
C

GAM1364 HSPC043 3' CTGTAATCCCAGCTACT 67720  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1364 ICAM4 3' CTGTAATCCCAGCACT 7749 A  
AGT GCTGGGATTACAG  
III |||||  
TCA CGACCCTAATGTC

GAM1364 ICAM4 3' CTGTAATCCCAGCACT 42353 A  
AGT GCTGGGATTACAG  
III |||||

TCA CGACCCTAATGTC

GAM1364 IL10RB 3' ATGCCTATAATCCCAGCTACT 5275 C A  
AGTAGCTGGGATTA AG CAT  
||||| |||  
TCATCGACCCTAAT TC GTA  
A C

GAM1364 IMAGE:4907098 3' CTGTAATCCCAGCACT 91658 A  
AGT GCTGGGATTACAG  
||| |||||||  
TCA CGACCCTAATGTC

GAM1364 INE1 3' CTGTAATCCCAGCTCTTTGT 13374 T\_  
ACAG AGCTGGGATTACAG  
||| |||||||  
TGTT TCGACCCTAATGTC  
TC

GAM1364 ING1-like 3' CTGTAATCCCAGCACT 54155 A  
AGT GCTGGGATTACAG  
||| |||||||  
TCA CGACCCTAATGTC

GAM1364 JAM1 3' ATGCCTGTAATCCCAGCTGCT 57887 A  
AGTAGCTGGGATTACAG CAT  
||||| |||  
TCGTCGACCCTAATGTC GTA  
C

GAM1364 JAM1 3' CTATAATCCCAGAGGCTG 57894 AG C  
CAGT CTGGGATTA AG  
||| ||||| ||  
GTCG GACCCTAAT TC  
GA A

GAM1364 JAM1 3' ATGCCTGTAATCCCAGCTGCT 57915 A  
AGTAGCTGGGATTACAG CAT  
||||| |||  
TCGTCGACCCTAATGTC GTA  
C

GAM1364 JAM1 3' CTATAATCCCAGAGGCTG 57923 AG C  
CAGT CTGGGATTA AG  
||| ||||| ||  
GTCG GACCCTAAT TC  
GA A

GAM1364 JAM1 3' ATGCCTGTAATCCCAGCTGCT 57942 A  
AGTAGCTGGGATTACAG CAT  
||||| |||  
TCGTCGACCCTAATGTC GTA  
C

GAM1364 JAM1 3' CTATAATCCCAGAGGCTG 57949 AG C  
CAGT CTGGGATTA AG  
||| ||||| ||

			GTCG GACCCTAAT TC		
			GA A		
GAM1364	JAM1	3'	ATGCCTGTAATCCCAGCTGCT 33749	A	
			AGTAGCTGGGATTACAG CAT		
			TCGTCGACCCTAATGTC GTA		
			C		
GAM1364	JAM1	3'	CTATAATCCCAGAGGCTG 33756	AG	C
			CAGT CTGGGATTA AG		
			GTCG GACCCTAAT TC		
			GA A		
GAM1364	KALI	3'	CTGTAATCCCAGTACT 53592	G	
			AGTA CTGGGATTACAG		
			TCAT GACCCTAATGTC		
			—		
GAM1364	KATII	3'	CTATAATCCCAGCACT 32646	A	C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1364	KBRAS2	3'	ATGCCTGTAATCCCAGCTAC 34192	A	
			GTAGCTGGGATTACAG CAT		
			CATCGACCCTAATGTC GTA		
			C		
GAM1364	KIAA0042	3'	CTGTAATCCCAGCACT 29610	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	KIAA0090	3'	ATGCCTGTAATCCCAGC 88438	A	
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1364	KIAA0159	3'	CTGTAATCCCAGCACT 29507	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	KIAA0159	3'	TGTAATCCCAGCTACTCA 29511	C	
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1364	KIAA0184	3'	CTGTAATCCCAGCACT 65194	A	
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

—  
GAM1364 KIAA0226 3' CTGTAATCCCAGCACT 63514 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 KIAA0226 3' CTGTAATCCCAGCTACTTG 63515 —  
CA GTAGCTGGGATTACAG  
|| |||||  
GT CATCGACCCTAATGTC  
T

GAM1364 KIAA0252 3' CTGTAATCCCAGCACT 62791 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 KIAA0266 3' CTGTAATCCCAGCACT 41331 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 KIAA0266 3' CTGTAATCCCAGCACT 41332 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 KIAA0268 3' CTGTGTTTTAGCTAATGTA 70002 G T  
TACA TAGCTGGGAT ACAG  
|||| ||||| |||  
ATGT ATCGATTTTG TGTC  
A

—  
GAM1364 KIAA0355 3' CTGTAATCCCAGCACT 28025 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 KIAA0391 3' ATGCCTGTGGTCCCAGCTACTC 27904 C A  
A  
A AGTAGCTGGGATTACAG CAT  
| ||||| |||  
A TCATCGACCCTGGTGTC GTA  
C C

GAM1364 KIAA0420 3' ATGCCTATAATCCCAACACT 63352 AGC C A  
AGT TGGGATTA AG CAT  
||| ||||| |||  
TCA ACCCTAAT TC GTA  
CA\_ A C

GAM1364 KIAA0441 3' ATGCCTGTAATCCCAGCACT 28952 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||

TCA CGACCCTAATGTC GTA  
 — C  
 GAM1364 KIAA0445 5' CTGTAATCCCAGCACT 27953 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC

—  
 GAM1364 KIAA0471 3' TCTGTAATCCCAGCACT 29400 A  
 AGT GCTGGGATTACAGA  
 ||| |||||  
 TCA CGACCCTAATGTCT

—  
 GAM1364 KIAA0472 3' ATGCCTGTAATCCAAGATACTC 71859 C G G A  
 A AGTA CT GGATTACAG CAT  
 | ||| || ||||| |||  
 A TCAT GA CCTAATGTC GTA  
 C A A C

GAM1364 KIAA0514 3' ATGCCTGTAATCCCAGCACT 28077 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||  
 TCA CGACCCTAATGTC GTA

— C  
 GAM1364 KIAA0547 3' TGTAATCCCAGCTACTCA 28918 C  
 A AGTAGCTGGGATTACA  
 | |||||  
 A TCATCGACCCTAATGT  
 C

GAM1364 KIAA0563 3' CTGTAATCCCAGCACT 29187 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC

—  
 GAM1364 KIAA0565 3' TCTGTAATTGCTATTG 66900 TGG  
 CAGTAGC GATTACAGA  
 ||||| |||||  
 GTTATCG TTAATGTCT

—  
 GAM1364 KIAA0618 3' ATGCCTGTAATCCCAGC 29161 A  
 GCTGGGATTACAG CAT  
 ||||| |||  
 CGACCCTAATGTC GTA  
 C

GAM1364 KIAA0635 3' CTGTAATCCCAGCACT 27696 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC

—  
 GAM1364 KIAA0694 3' ATGCCTATAATCCCAATACTTT 72579 C GC C A  
 A TA AGTA TGGGATTA AG CAT  
 || ||| ||||| || |||

			AT TCAT ACCCTAAT TC GTA		
			T A_ A C		
GAM1364	KIAA0694	3'	CTGTAATCCCAGCACT 72580	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	KIAA0752	3'	ATGCCTGCAATCCCAGCTACT 67048	A	A
			AGTAGCTGGGATT CAG CAT		
			TCATCGACCCTAA GTC GTA		
			C C		
GAM1364	KIAA0794	3'	ATGCCTGTAATCCCAACACT 80409	AGC	A
			AGT TGGGATTACAG CAT		
			TCA ACCCTAATGTC GTA		
			CA_ C		
GAM1364	KIAA0794	3'	CTGTAATCCCAGCTACTCA 80411	C	
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTAATGTC		
			C		
GAM1364	KIAA0795	3'	CTATAATCCCAGCACT 46590	A	C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1364	KIAA0825	3'	CTGTAATCCCAGCACT 61025	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	KIAA0825	3'	GTGCCTGCAATCCCAGCTACTC 61027	C	A A
	A		A AGTAGCTGGGATT CAG CAT		
			A TCATCGACCCTAA GTC GTG		
			C C C		
GAM1364	KIAA0831	3'	CTGTAATCCCAGCTACT 29972		
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
GAM1364	KIAA0831	3'	CTGTAATCCCGGCACT 29973	A	
			AGT GCTGGGATTACAG		
			TCA CGGCCCTAATGTC		
			—		
GAM1364	KIAA0852	5'	CTGTAATCCCAGCACT 30077	A	
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1364 KIAA0853 3' ATGTCTGTAGTCACAGCTACTC 30537 C G  
A A AGTAGCTG GATTACAGACAT

I ||||| |||||  
A TCATCGAC CTGATGTCTGTA  
C A

GAM1364 KIAA0872 3' ATGCCTGTAATCCCAGCACT 30061 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

— C  
GAM1364 KIAA0872 3' CTGTAATCCCAGCACT 30062 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

—  
GAM1364 KIAA0889 3' ATGCCTGTAATCCCAGCACT 31129 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

— C  
GAM1364 KIAA0907 3' CTGTAATCCCAGCACT 30173 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

—  
GAM1364 KIAA0907 3' CTGTAATCCCAGCACT 30174 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

—  
GAM1364 KIAA0912 3' CTGTAATCCCAGCACT 64409 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

—  
GAM1364 KIAA0918 3' TCTGTAAGATGGGGCTACTGT 73136 GGGA\_  
ACAGTAGCT TTACAGA  
||||| |||||  
TGTCATCGG AATGTCT  
GGTAG

GAM1364 KIAA0930 3' CTGTAATCCCAGCACT 70542 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

—  
GAM1364 KIAA1032 3' ATGCCTGTAGTCCCAGCTACTC 66151 C A  
A A AGTAGCTGGGATTACAG CAT  
I ||||| ||||| |||



			A	TCATCGACCCTGATGTC	GTA		
			C		C		
GAM1364	KIAA1056	3'	CTGTAATCCCAGCACT	29695	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			-				
GAM1364	KIAA1056	3'	CTGTAATCCCAGCTGCT	29696			
			AGTAGCTGGGATTACAG				
			TCGTGACCCCTAATGTC				
GAM1364	KIAA1086	3'	CTATAATCCCAGCACT	70744	A		C
			AGT GCTGGGATTA AG				
			TCA CGACCCTAAT TC				
			- A				
GAM1364	KIAA1086	3'	CTGTAATCCCAGCACT	70745	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			-				
GAM1364	KIAA1130	3'	ATGCCTGTAATCCCAGCACT	62412	A		A
			AGT GCTGGGATTACAG CAT				
			TCA CGACCCTAATGTC GTA				
			- C				
GAM1364	KIAA1130	3'	ATGCCTGTAATCCCAGTGCT	62413	G		A
			AGTA CTGGGATTACAG CAT				
			TCGT GACCCTAATGTC GTA				
			- C				
GAM1364	KIAA1130	3'	TGTAATCCCAGCTACTCA	62428	C		
			A AGTAGCTGGGATTACA				
			A TCATCGACCCTAATGT				
			C				
GAM1364	KIAA1164	3'	ATGCCTGTAATCCCAGTACT	69503	G		A
			AGTA CTGGGATTACAG CAT				
			TCAT GACCCTAATGTC GTA				
			- C				
GAM1364	KIAA1191	3'	CTGTAATCCCAGCACT	39954	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			-				
GAM1364	KIAA1204	3'	TCTGTAATCCCCAACACT	69220	AGC		
			AGT TGGGATTACAGA				

			TCA ACCCTAATGTCT		
			CA_		
GAM1364	KIAA1228	3'	CTGTAATCCCAGCACT	65041	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	KIAA1244	3'	CTGTAATCCCAGCACT	71989	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	KIAA1244	3'	CTGTAATCCCAGCTACTTA	71990	C
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTAATGTC		
			T		
GAM1364	KIAA1253	3'	ATGCCTGTGGTCCCAGCTACTG	91896	A
			CAGTAGCTGGGATTACAG CAT		
			GTCATCGACCCTGGTGTC GTA		
			C		
GAM1364	KIAA1271	3'	CTGTAATCCCAGCACT	69542	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	KIAA1271	3'	GTCTGTAATCCCAGCTATT	69551	
			AGTAGCTGGGATTACAGAC		
			TTATCGACCCTAATGTCTG		
			—		
GAM1364	KIAA1276	3'	CTGTAATCCCATCACT	66430	AGC
			AGT TGGGATTACAG		
			TCA ACCCTAATGTC		
			CT_		
GAM1364	KIAA1277	3'	ATGCCTATAATCCCAGCACT	64450	A C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1364	KIAA1328	3'	CTGTAATCCCAGGCTTTG	61646	T _
			CAG AGC TGGGATTACAG		
			GTT TCG ACCCTAATGTC		
			_ G		
GAM1364	KIAA1348	3'	ATGCCTGTAATCCCAGCTACT	68571	A
			AGTAGCTGGGATTACAG CAT		

			TCATCGACCCTAATGTC GTA			
			C			
GAM1364	KIAA1348	3'	CTGTAATCCCAGCACTGTG 68575	A		
			TACAGT GCTGGGATTACAG			
			GTGTCA CGACCCTAATGTC			
			—			
GAM1364	KIAA1364	3'	ATGCCTGTAATCCCAGCACT 63586	A		A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	KIAA1364	3'	CTGTAATCCCAGCTACTTG 63593	—		
			CA GTAGCTGGGATTACAG			
			GT CATCGACCCTAATGTC			
			T			
GAM1364	KIAA1377	3'	ATGCCTGTAATCCCAGCACT 67174	A		A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	KIAA1404	3'	CTGTAATCCCAGCACT 61987	A		
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	KIAA1423	3'	TAGTCCCAGCTACTCA 61728	C		
			A AGTAGCTGGGATTA			
			A TCATCGACCCTGAT			
			C			
GAM1364	KIAA1456	3'	ATGCCTGTAATCCCAGCACT 66988	A		A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	KIAA1456	3'	ATGCCTGTAATCCCAGCCACTT 66989	— A		A
	G		CA GT GCTGGGATTACAG CAT			
			GT CA CGACCCTAATGTC GTA			
			T C C			
GAM1364	KIAA1473	3'	ATGCCTGTAATCCCAGCTACT 70663			A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1364	KIAA1473	3'	CTGTAATCCCAGCACT 70667	A		
			AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

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GAM1364 KIAA1486 3' CTGTAATCCCAGCACTCTG 67379 TA_
      CAG GCTGGGATTACAG
      ||| |||||
      GTC CGACCCTAATGTC
      TCA
GAM1364 KIAA1554 3' CTGTAATCCCAGCTACCTG 95152 _
      CAG TAGCTGGGATTACAG
      ||| |||||
      GTC ATCGACCCTAATGTC
      C
GAM1364 KIAA1559 3' ATGCCTGTAATCCCAGCACT 73057 A A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      - C
GAM1364 KIAA1559 3' ATGCCTGTAATCCCAGCTACTT 73058 _ A
      G CA GTAGCTGGGATTACAG CAT
      || |||||
      GT CATCGACCCTAATGTC GTA
      T C
GAM1364 KIAA1559 3' CTGTAATCCCAGCACT 73064 A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC
      -
GAM1364 KIAA1586 5' CTGTAATCCCAGCACT 92329 A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC
      -
GAM1364 KIAA1614 3' ATGCCTATAATCCCAGCTACTT 70117 _ C A
      G CA GTAGCTGGGATTA AG CAT
      || |||||
      GT CATCGACCCTAAT TC GTA
      T A C
GAM1364 KIAA1614 3' ATGCCTGTAATCCCAGAACT 70118 AG A
      AGT CTGGGATTACAG CAT
      ||| |||||
      TCA GACCCTAATGTC GTA
      A_ C
GAM1364 KIAA1630 3' ATGCCTGTAATCCCAGCACT 38030 A A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      - C
GAM1364 KIAA1656 5' CTGTAATCCCAGCACT 65794 A
      AGT GCTGGGATTACAG
      ||| |||||
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TCA CGACCCTAATGTC

GAM1364 KIAA1674 3' CTGTAATCCCAGCACT 68777 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

GAM1364 KIAA1715 3' ATGCCTGTAATCCTAGCTACTC 68117 C A  
A AGTAGCTGGGATTACAG CAT  
| |||||  
A TCATCGATCCTAATGTC GTA  
C C

GAM1364 KIAA1735 3' CTGTAGTCCCAGCTACTCA 87627 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTGATGTC  
C

GAM1364 KIAA1751 3' ATGCCTGTAATCCCAGAACT 71688 AG A  
AGT CTGGGATTACAG CAT  
||| |||||  
TCA GACCCTAATGTC GTA  
A\_ C

GAM1364 KIAA1811 5' CTGTAATCCCAGCACT 64796 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 KIAA1829 3' TGTAATCCCAGCTACTCA 61958 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1364 KIAA1872 3' ATGCCTGTAATCCCAGCACTCT 62923 TA\_ A  
G CAG GCTGGGATTACAG CAT  
||| |||||  
GTC CGACCCTAATGTC GTA  
TCA C

GAM1364 KIAA1872 3' ATGCCTGTAATCCCAGCTACT 62924 A  
AGTAGCTGGGATTACAG CAT  
||| |||||  
TCATCGACCCTAATGTC GTA  
C

GAM1364 KIAA1872 3' CTATAATCCCAGCACT 62929 A C  
AGT GCTGGGATTA AG  
||| |||||  
TCA CGACCCTAAT TC

GAM1364 KIAA1872 3' CTGTAATCCCAGACTTTG 62931 T \_  
CAG AG CTGGGATTACAG  
||| || |||||

GTT TC GACCCTAATGTC  
 \_ A  
 GAM1364 KIAA1941 3' CTGTAATCCCAGCACT 74838 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
  
 \_  
 GAM1364 KIAA1948 5' ATGCCTATAATCCCAGCTACT 82399 C A  
 AGTAGCTGGGATTA AG CAT  
 ||||| || |||  
 TCATCGACCCTAAT TC GTA  
 A C  
 GAM1364 KIAA1951 3' CTGTAATCCCAGCACT 73761 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
  
 \_  
 GAM1364 KIAA1954 3' CTGTAATCCCAGCACT 77719 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
  
 \_  
 GAM1364 KIAA1958 3' CTATAATCCCAGCACT 81902 A C  
 AGT GCTGGGATTA AG  
 ||| ||||| ||  
 TCA CGACCCTAAT TC  
 A  
 GAM1364 KIAA1979 3' CTGTAATCCCAGCACT 88278 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
  
 \_  
 GAM1364 KIAA1979 3' CTGTAATCCCAGCTACTCA 88279 C  
 A AGTAGCTGGGATTACAG  
 | |||||  
 A TCATCGACCCTAATGTC  
 C  
 GAM1364 KLHL6 3' CTGTAATCCCAGCCCTATG 55303 GTA\_  
 CA GCTGGGATTACAG  
 || |||||  
 GT CGACCCTAATGTC  
 ATCC  
 GAM1364 KLHL8 3' CTGTAATCCAGCTACTCA 62854 C  
 A AGTAGCTGGGATTACAG  
 | |||||  
 A TCATCGACCTTAATGTC  
 C  
 GAM1364 KR18 3' CTGTAATCCCAGTACT 52745 G  
 AGTA CTGGGATTACAG  
 ||| |||||

TCAT GACCCTAATGTC

GAM1364 KREMEN 3' ATGCCTGTAATCCCAGCACT 49404 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1364 KREMEN 3' CTGTAATCCCAGCTACT 49406  
AGTAGCTGGGATTACAG  
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TCATCGACCCTAATGTC

GAM1364 LHPP 5' CTGTAATCCCAGCACT 42101 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LIAS 3' CTGTAATCCCAGCACTTTA 70635 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||  
AT TCA CGACCCTAATGTC  
T

GAM1364 LIM 3' CTGTAATCCCAGCACT 21302 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LIM 3' CTGTAATCCCAGCTACTCA 21303 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
C

GAM1364 LRG 3' CTGTAATCCCAGCACT 53750 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LRRFIP1 3' TGCCTGTAATCTCAGTAC 16420 G A  
GTA CTGGGATTACAG CA  
||| ||||| ||  
CAT GACTCTAATGTC GT

GAM1364 LRRFIP1 3' TGTAATCCCAGCCACT 16421 A  
AGT GCTGGGATTACA  
||| |||||  
TCA CGACCCTAATGT  
C

GAM1364 LSR68 3' TGCCTATAATCCCAGCTACTCA 37937 C C A  
A AGTAGCTGGGATTA AG CA  
| ||||| || ||

			A TCATCGACCCTAAT TC GT		
			C            A C		
GAM1364	LYSAL1	3'	CTGTAATCCCAGCACT    16918	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	MACF1	3'	CTGTAATCCCAGCACT    52316	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	MAWBP	3'	ATGCCTGTAATCCCAGCACT 42106	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			—            C		
GAM1364	MCAM	3'	CTGTAATCCCAGCACT    21454	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	MESDC2	3'	CTGTAATCCCAGTACT    72492	G	
			AGTA CTGGGATTACAG		
			TCAT GACCCTAATGTC		
			—		
GAM1364	MESDC2	3'	TGTAATCCCAGCTACTCA    72503	C	
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1364	METL	3'	ATGCCTGTAATCCCAGCCACT 37253	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			C            C		
GAM1364	MGC10765	3'	ATGCCTGTAATCCCAGCACT 44299	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			—            C		
GAM1364	MGC10765	3'	CTGTAATCCCAGCTAC    44301		
			GTAGCTGGGATTACAG		
			CATCGACCCTAATGTC		
			—		
GAM1364	MGC10771	3'	ATGCCTGTAATCCCAGCACT 44451	A	A
			AGT GCTGGGATTACAG CAT		



			TCA CGACCCTAATGTC GTA			
			- C			
GAM1364	MGC10814	5'	ATGCCTGTAATCCCAGCACT	51036	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			- C			
GAM1364	MGC10814	3'	CTGTAATCCCAGCACT	51038	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			-			
GAM1364	MGC10999	3'	ATGCCTGTAATCCCAGCACTGT	50225	A	A
	G		TACAGT GCTGGGATTACAG CAT			
			GTGTCA CGACCCTAATGTC GTA			
			- C			
GAM1364	MGC11287	5'	GTCTATAATCCCAGCACTGTG	48834	A	C
			TACAGT GCTGGGATTA AGAC			
			GTGTCA CGACCCTAAT TCTG			
			- A			
GAM1364	MGC11386	3'	CTATAATCCCAGCACT	51950	A	C
			AGT GCTGGGATTA AG			
			TCA CGACCCTAAT TC			
			- A			
GAM1364	MGC13017	3'	TCTGTAATCCCAGCTACT	54694		
			AGTAGCTGGGATTACAGA			
			TCATCGACCCTAATGTCT			
			-			
GAM1364	MGC13053	3'	CTGTAATCCCAGTACT	51131	G	
			AGTA CTGGGATTACAG			
			TCAT GACCCTAATGTC			
			-			
GAM1364	MGC13523	3'	TGCCTGTAATTTCACTA	53031	C GG	A
			TAG TG ATTACAG CA			
			ATC AC TAATGTC GT			
			- TT C			
GAM1364	MGC14126	3'	CTGTAATCCCAGCACT	51854	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			-			
GAM1364	MGC14817	3'	CTGTAATCCCAGCACT	50336	A	
			AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

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      —
GAM1364 MGC15397 3' CTGTAATCCCAGCACT    54679    A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      —
GAM1364 MGC15631 3' ATGCCTGTAATCCCAGTGCT  51259    G    A
      AGTA CTGGGATTACAG CAT
      ||| ||||| |||
      TCGT GACCCTAATGTC GTA

      —      C
GAM1364 MGC15631 3' CTGTCATCCCAGCTAC    51263    T
      GTAGCTGGGAT ACAG
      ||||| |||
      CATCGACCCTA TGTC

      C
GAM1364 MGC16142 3' ATGCCTATAATCCCAGCACT  51291    A    C A
      AGT GCTGGGATTA AG CAT
      ||| ||||| || |||
      TCA CGACCCTAAT TC GTA

      —      A C
GAM1364 MGC16142 3' ATGCCTATAATCCCAGCTACT 51292    C A
      AGTAGCTGGGATTA AG CAT
      ||||| || |||
      TCATCGACCCTAAT TC GTA

      A C
GAM1364 MGC16332 3' ATGCCTGTAATCCCAACACT  56774    AGC    A
      AGT  TGGGATTACAG CAT
      ||| ||||| |||
      TCA  ACCCTAATGTC GTA
      CA_      C
GAM1364 MGC16385 3' CTGTAATCCCAGCACT    58887    A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      —
GAM1364 MGC16703 3' ATGCCTGTAATCCCAGCACT  73098    A    A
      AGT GCTGGGATTACAG CAT
      ||| ||||| |||
      TCA CGACCCTAATGTC GTA

      —      C
GAM1364 MGC20235 3' CTGTAATCCCAGTACT    58894    G
      AGTA CTGGGATTACAG
      ||| |||||
      TCAT GACCCTAATGTC

      —
GAM1364 MGC20235 3' CTGTAGTCCCAGCTACTCA  58895    C
      A AGTAGCTGGGATTACAG
      | |||||
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			A TCATCGACCCTGATGTC		
			C		
GAM1364	MGC22805	3'	ATGCCTGTAATCCCAGCTACTT 58080	—	A
	G		CA GTAGCTGGGATTACAG CAT		
			GT CATCGACCCTAATGTC GTA		
			T C		
GAM1364	MGC2396	3'	ATGCCTGTAATCCCAGCTACT 53460		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1364	MGC2562	3'	CTATAATCCCAGCACT 50437	A C	
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1364	MGC2562	3'	CTGTAATCCCAGCACT 50438	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	MGC26641	3'	CTGTAATCCCAACTACTCA 58657	C C	
			A AGTAG TGGGATTACAG		
			A TCATC ACCCTAATGTC		
			C A		
GAM1364	MGC2731	3'	ATGCCTGTAATCCCAGCTACT 43948		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1364	MGC29762	3'	CTGTAATCCCAGCACT 58472	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	MGC29891	3'	CTGTAATCCCAACT 58204	AGC	
			AGT TGGGATTACAG		
			TCA ACCCTAATGTC		
			CA_		
GAM1364	MGC29891	3'	CTGTAATCCCAGCACT 58205	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	MGC29937	3'	ATGCCTGTAATCCCAGCACT 58110	A A	
			AGT GCTGGGATTACAG CAT		

				TCA CGACCCTAATGTC GTA		
				— C		
GAM1364	MGC29937	3'	ATGCCTGTAATCCCAGTTACTC 58111	C		A
	A		A AGTAGCTGGGATTACAG CAT			
			I               III			
			A TCATTGACCCTAATGTC GTA			
			C C			
GAM1364	MGC3207	3'	CTGTAATCCCAGCACT 62558	A		
			AGT GCTGGGATTACAG			
			III			
			TCA CGACCCTAATGTC			
			—			
GAM1364	MGC39350	3'	CTGTAATCCCAGCACT 58654	A		—
			AGT GCTGGG ATTACAG			
			III			
			TCA CGACCC TAATGTC			
			— C			
GAM1364	MGC4248	3'	CTGTAATCCCAGCACT 50327	A		
			AGT GCTGGGATTACAG			
			III			
			TCA CGACCCTAATGTC			
			—			
GAM1364	MGC4663	3'	CTATAATCCCAGCACTTTA 44505	C A		C
			TA AGT GCTGGGATTA AG			
			II             II			
			AT TCA CGACCCTAAT TC			
			T — A			
GAM1364	MGC5254	3'	CTGTAATCCCAGCACT 50410	A		
			AGT GCTGGGATTACAG			
			III			
			TCA CGACCCTAATGTC			
			—			
GAM1364	MGC5384	3'	ATGCCTGTAATCCCAGCACT 48269	A		A
			AGT GCTGGGATTACAG CAT			
			III             III			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	MKRN4	3'	CTGTAATCCCAGCACT 47746	A		
			AGT GCTGGGATTACAG			
			III			
			TCA CGACCCTAATGTC			
			—			
GAM1364	MOST2	5'	ATGCCTGTAGTCCCAGCTACTC 39674	C		A
	A		A AGTAGCTGGGATTACAG CAT			
			I               III			
			A TCATCGACCCTGATGTC GTA			
			C C			
GAM1364	MOST2	5'	CTGTAATCCCAGCACT 39684	A		
			AGT GCTGGGATTACAG			
			III			

TCA CGACCCTAATGTC

—  
GAM1364 MRP63 3' CTGTAATCCCAACACTTTA 43807 C AGC  
TA AGT TGGGATTACAG  
|| ||| |||||  
AT TCA ACCCTAATGTC  
T CA\_

GAM1364 MRPL56 3' CTGTAATCCCAACACT 51688 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1364 MRPS10 3' CTGTAATCCCAGCACT 36292 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 MRPS10 3' GTGCCTGTAATCCCAGCTACTC 36298 C A  
A AGTAGCTGGGATTACAG CAT  
| ||||| |||  
A TCATCGACCCTAATGTC GTG  
C C

GAM1364 MT-ACT48 3' ATGCCTGTAATCCCAGCACT 24686 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

—  
GAM1364 N4BP2 3' CTGTAATCCCAGCACT 36403 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 NDUFC2 3' ATGCCTGTAATCCCAGCACT 15825 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

—  
GAM1364 NDUFC2 3' CTGCAATCCCAGCTACTCA 15832 C A  
A AGTAGCTGGGATT CAG  
| ||||| |||  
A TCATCGACCCTAA GTC  
C C

GAM1364 NMNAT 3' CTGTAATCCCAGCACT 42956 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 NMT2 3' CTGTAATCCCAGCACT 16664 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

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      -
GAM1364 NPTXR  3' CTGTAATCCCAGCACT   54178  A
      AGT GCTGGGATTACAG
      ||| |||
      TCA CGACCCTAATGTC

      -
GAM1364 NPTXR  3' CTGTAATCCCAGCACT   26642  A
      AGT GCTGGGATTACAG
      ||| |||
      TCA CGACCCTAATGTC

      -
GAM1364 OCLM   5' ATGCCTATAATCCCAGCACT  42347  A      C A
      AGT GCTGGGATTA AG CAT
      ||| ||| ||| |||
      TCA CGACCCTAAT TC GTA
      -       A C
GAM1364 ORC6L  3' ATGCCTGTAATCCCAGCTCCT 26722  T      A
      AG AGCTGGGATTACAG CAT
      || ||| ||| ||| |||
      TC TCGACCCTAATGTC GTA
      C       C
GAM1364 ORC6L  3' CTGTAATCCCAGCACT   26724  A
      AGT GCTGGGATTACAG
      ||| |||
      TCA CGACCCTAATGTC

      -
GAM1364 PAFAH2 3' ATGCCTGTAATCCCAGCACT  4760   A      A
      AGT GCTGGGATTACAG CAT
      ||| ||| ||| |||
      TCA CGACCCTAATGTC GTA
      -       C
GAM1364 PAFAH2 3' CTATAATCCCAGCTACTCA  4762   C      C
      A AGTAGCTGGGATTA AG
      | ||| ||| ||| |||
      A TCATCGACCCTAAT TC
      C       A
GAM1364 PB1    3' CTGTAATCCCAGCACT   37021  A
      AGT GCTGGGATTACAG
      ||| |||
      TCA CGACCCTAATGTC

      -
GAM1364 PDCD7  3' CTGTAATCCCAACACT   72138  AGC
      AGT TGGGATTACAG
      ||| |||
      TCA ACCCTAATGTC
      CA_
GAM1364 phorbolin-1 3' CTGTAATCCCAGCACT   88778  A
      AGT GCTGGGATTACAG
      ||| |||
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TCA CGACCCTAATGTC

—  
GAM1364 PILR(ALPHA) 3' CTGTAATCCCAGCTACT 25546  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1364 PIWIL2 3' CTGTAGTCCCAGCTACTCA 36055 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTGATGTC  
C

GAM1364 PNPASE 3' ATGCCTGTAATCCTAGCTACTC 70870 C A  
A A AGTAGCTGGGATTACAG CAT  
| ||||| |||  
A TCATCGATCCTAATGTC GTA  
C C

GAM1364 POFUT1 3' ATGCCTGTAATCCCAGCACT 70465 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
— C

GAM1364 POLYDOM 3' ATGCCTGTAATTCCAGCTACTC 44424 C A  
A A AGTAGCTGGGATTACAG CAT  
| ||||| |||  
A TCATCGACCTTAATGTC GTA  
C C

GAM1364 POLYDOM 3' CTGTAATCCCAGCACT 44425 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 PPP1R3B 3' ATGCCTGTAATCCCAGCACT 44815 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
— C

GAM1364 PPP1R3B 3' TGCCTGTAATCCCTGCACT 44826 A T A  
AGT GC GGGATTACAG CA  
||| || ||||| ||  
TCA CG CCCTAATGTC GT  
— T C

GAM1364 PRDM14 3' ATGCCTGTGGTTCCAGCCACTC 44444 C A A  
A A AGT GCTGGGATTACAG CAT  
| ||| ||||| |||  
A TCA CGACCTTGGTGTC GTA  
C C C

GAM1364 PRDM14 3' CTGTAATCCCAGCACT 44447 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1364 PRO0038 3' ATGCCTATAATCCCAACACCCT 26090 TAGC\_ C A  
G CAG TGGGATTA AG CAT

||| ||||| || |||  
GTC ACCCTAAT TC GTA  
CCACA A C

GAM1364 PRO0255 3' CTGTAATCTCAGCACT 26141 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACTCTAATGTC

GAM1364 PRO0478 3' ATGCCTGTAATCCCAGCACT 26183 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

— C  
GAM1364 PRO0478 5' CTGTAATCCCAGCACT 26187 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 PRO0478 3' CTGTAATCCCAGCCTG 26188 TA  
CAG GCTGGGATTACAG  
||| |||||  
GTC CGACCCTAATGTC

—  
GAM1364 PRO0478 5' CTGTAATCCCAGGTACT 26189 G  
AGTA CTGGGATTACAG  
||| |||||  
TCAT GACCCTAATGTC  
G

GAM1364 PRO0478 3' TGTAATCCCAGCTACTCA 26198 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1364 PRO0611 3' ATGCCTGTAATCCCAGCACT 26007 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

— C  
GAM1364 PRO0618 3' CTGTAATCCCAGCACTTTA 26200 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||  
AT TCA CGACCCTAATGTC

T —  
GAM1364 PRO1048 5' TCTGTAATCCCAGCACT 37525 A  
AGT GCTGGGATTACAGA  
||| |||||



TCA CGACCCTAATGTCT

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      -
GAM1364 PRO1496 3' ATGCCTGTAATCCCAGCACT 37757 A A
      AGT GCTGGGATTACAG CAT
      ||| |||
      TCA CGACCCTAATGTC GTA
      - C
GAM1364 PRO1580 5' ATGCCTTGTCCCAGCTTCT 37530 T TAC A
      AG AGCTGGGAT AG CAT
      || ||| |||
      TC TCGACCCTG TC GTA
      T T C
GAM1364 PRO1777 3' ATGCCTGTAATCCCAGCATTCT 37762 TA_ A
      G CAG GCTGGGATTACAG CAT
      ||| |||
      GTC CGACCCTAATGTC GTA
      TTA C
GAM1364 PRO1853 3' ATGCCTGTAATCCCAGCACT 37771 A A
      AGT GCTGGGATTACAG CAT
      ||| |||
      TCA CGACCCTAATGTC GTA
      - C
GAM1364 PRO2015 3' CTGTAATCCCAGCACT 37557 A
      AGT GCTGGGATTACAG
      ||| |||
      TCA CGACCCTAATGTC
      -
GAM1364 PRO2198 5' CTGTAATCCCGGCACT 37791 A
      AGT GCTGGGATTACAG
      ||| |||
      TCA CGGCCCTAATGTC
      -
GAM1364 PRO2730 3' CTGTAATCCCAGCACT 47415 A
      AGT GCTGGGATTACAG
      ||| |||
      TCA CGACCCTAATGTC
      -
GAM1364 PRO2859 3' ATGCCTGTAATCCCAGCACT 37614 A A
      AGT GCTGGGATTACAG CAT
      ||| |||
      TCA CGACCCTAATGTC GTA
      - C
GAM1364 PRO2949 3' ATGCCTGTAATCCCAGCACT 37619 A A
      AGT GCTGGGATTACAG CAT
      ||| |||
      TCA CGACCCTAATGTC GTA
      - C
GAM1364 PSR 3' CTGTAATCCCAGCACT 65180 A
      AGT GCTGGGATTACAG
      ||| |||
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TCA CGACCCTAATGTC

GAM1364	PTD012	3'	ATGCCTATAATCCCAGCACT	25890	A	C A
			AGT GCTGGGATTA AG CAT			
			TCA CGACCCTAAT TC GTA			
			— A C			
GAM1364	PTK6	3'	ATGCCTGTAATCCCAGCACT	19934	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	PTRF	3'	ATGCCTGTAATCCCAGCTACT	63497		A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1364	RAB4B	5'	ATGCCTGTAATCCCAGCACT	32372	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	RAB4B	5'	ATGCCTGTAATCCCAGCTACT	32373		A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1364	RHOBTB3	3'	CTGTAATCCCAGCTACT	29744		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
			C			
GAM1364	RNO2	5'	CTGTAATCCCAGCACT	52769	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	RoXaN	3'	ATGCCTGTAATCCCAGC	46632		A
			GCTGGGATTACAG CAT			
			CGACCCTAATGTC GTA			
			C			
GAM1364	RoXaN	3'	CTATAATCCCAGCACTCTG	46641	TA_	C
			CAG GCTGGGATTA AG			
			GTC CGACCCTAAT TC			
			TCA A			
GAM1364	RoXaN	3'	TCTGTAATCCCAGCTACTCA	46659	C	
			A AGTAGCTGGGATTACAGA			

			A TCATCGACCCTAATGTCT		
			C		
GAM1364	Rpo1-2	3'	ATGCCTGTAGTTCCAGCTACTC 38697	C	A
	A		A AGTAGCTGGGATTACAG CAT		
			I               III		
			A TCATCGACCTTGATGTC GTA		
			C C		
GAM1364	RRP4	3'	CTATAATCCCAGCACT 26563	A C	
			AGT GCTGGGATTA AG		
			III           II		
			TCA CGACCCTAAT TC		
			— A		
GAM1364	SAMHD1	3'	ATGCCTGTAATCCCAGCACT 61308	A A	
			AGT GCTGGGATTACAG CAT		
			III             III		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	SC65	3'	CTGTAATCCCAGCACTG 21288	A	
			CAGT GCTGGGATTACAG		
			GTCA CGACCCTAATGTC		
			—		
GAM1364	SCIN	3'	CTGTAATCCCAGCACT 52424	A	
			AGT GCTGGGATTACAG		
			III		
			TCA CGACCCTAATGTC		
			—		
GAM1364	SCYA5	3'	CTGTAATCCCAGCTACT 11450		
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
			—		
GAM1364	SEMA3E	3'	CTGTAATCCCAGCACT 24881	A	
			AGT GCTGGGATTACAG		
			III		
			TCA CGACCCTAATGTC		
			—		
GAM1364	SEMA5A	3'	ATGCCTATAATCCCAGCACT 14252	A C A	
			AGT GCTGGGATTA AG CAT		
			III           II III		
			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1364	SGKL	3'	ATGCCTATAATCCCAGCTACTT 25140	— C A	
	G		CA GTAGCTGGGATTA AG CAT		
			II           II III		
			GT CATCGACCCTAAT TC GTA		
			T A C		
GAM1364	SGKL	3'	ATGCCTTTAGTCCCAGCTACTC 25141	C C A	
	A		A AGTAGCTGGGATTA AG CAT		
			I           II III		

			A TCATCGACCCTGAT TC GTA		
			C T C		
GAM1364	SGKL	3'	CTGTAATCCCAGCACT 25142	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	SLC7A11	3'	TCTGTAATCATATCTAC 26757	C G	
			GTAG TG GATTACAGA		
			CATC AT CTAATGTCT		
			T A		
GAM1364	SLC7A11	3'	TCTGTAATCCCAGCACT 26758	A	
			AGT GCTGGGATTACAGA		
			TCA CGACCCTAATGTCT		
			—		
GAM1364	SMAP-5	3'	CTGTAATCCCAGCACT 47931	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	SNAPC1	3'	ATGCCTGTAATCCCAGC 11838	A	
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1364	SPTLC2	3'	ATGCCTGTAATCCCAGCTAC 16797	A	
			GTAGCTGGGATTACAG CAT		
			CATCGACCCTAATGTC GTA		
			C		
GAM1364	SS18L1	3'	CTGTAATCCCAGCACT 65344	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	SS18L1	3'	CTGTAATCCCAGCTACT 65345		
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
			—		
GAM1364	TA-LRRP	3'	ATGCCTATAATCCCAGCACT 31068	A	C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1364	TACTILE	3'	CTGTAATCCCAGCACT 19469	A	
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1364 THEA 3' CTGTAATCCCAGCACT 66282 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 TIP47 3' CTGTAATCCCAGCACT 19479 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 TMG4 3' ATGCCTGTAATCCCAGCACT 43988 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1364 TRIAD3 3' ATGCCTATAATCCCAGGTACTC 94500 C G C A  
A  
A AGTA CTGGGATTA AG CAT  
| ||| ||||| || |||  
A TCAT GACCCTAAT TC GTA  
C G A C

GAM1364 TRIM38 3' CTGTAATCCCAGAACTATGT 20986 GTAG\_  
ACA CTGGGATTACAG  
||| |||||  
TGT GACCCTAATGTC  
ATCAA

GAM1364 UBF-fl 3' CTGTAATCCCAGCACT 51564 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 VPS4B 3' ATGCCTGTAATCCCAGCACT 16821 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1364 VPS4B 3' TGTAATCCCAGCTACTCA 16826 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1364 WBSCR21 3' CTGTAATCCCAGCTACT 48476  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1364 WBSCR23 3' CTGTAATCCCAGCACT 46759 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1364 WBSCR23 3' CTGTAATCCCAGCTACT 46760  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1364 WBSCR23 3' GTCTGTAGTCCCAGCTACTCA 46770 C  
A AGTAGCTGGGATTACAGAC  
| |||||  
A TCATCGACCCTGATGTCTG  
C

GAM1364 YEA 3' ATGCCTGTAATCCCAGCTACTT 51528 \_ A  
G CA GTAGCTGGGATTACAG CAT  
|| ||||| ||  
GT CATCGACCCTAATGTC GTA  
T C

GAM1364 YME1L1 3' CTGTAATCCCAGCACT 26528 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 YME1L1 3' CTGTAATCCCAGCACT 57778 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 YME1L1 3' TCTGTAATCCCAGCACT 57781 A  
AGT GCTGGGATTACAGA  
||| |||||  
TCA CGACCCTAATGTCT

GAM1364 YME1L1 3' TCTGTAATCCCAGCACT 26531 A  
AGT GCTGGGATTACAGA  
||| |||||  
TCA CGACCCTAATGTCT

GAM1364 ZAK 3' CTGTAATCCCAGCACT 56125 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 ZFP106 3' CTGTAATCCCAGCACT 42466 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 ZFP106 3' CTGTAATCCCAGCTCT 42467 T  
AG AGCTGGGATTACAG  
|| |||||

TC TCGACCCTAATGTC

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      —
GAM1364 ZIM3   3' ATGCCTGTAATCCCAGTACT 53536  G      A
      AGTA CTGGGATTACAG CAT
      ||| ||||| |||
      TCAT GACCCTAATGTC GTA
      —      C
GAM1364 ZNF197 3' ATGCCTGTAATCCCAGCACT 22763  A      A
      AGT GCTGGGATTACAG CAT
      ||| ||||| |||
      TCA CGACCCTAATGTC GTA
      —      C
GAM1364 ZNF197 3' GTAATCCCAGCTACTCA 22766  C
      A AGTAGCTGGGATTAC
      | ||||| |||
      A TCATCGACCCTAATG
      C
GAM1364 ZNF271 3' CTGTAATCCCAACACT 95250  AGC
      AGT TGGGATTACAG
      ||| ||||| |||
      TCA ACCCTAATGTC
      CA_
GAM1364 ZNF297B 5' ATGCCTATAATCCCAACACTTT 25774  C AGC      C A
      A      TA AGT TGGGATTA AG CAT
      || ||| ||||| || |||
      AT TCA ACCCTAAT TC GTA
      T CA_      A C
GAM1364 ZNF297B 5' CTGTAATCCCAGCACT 25781  A
      AGT GCTGGGATTACAG
      ||| ||||| |||
      TCA CGACCCTAATGTC
      —
GAM1364 ZNF297B 3' CTGTAATCCCAGCACT 25782  A
      AGT GCTGGGATTACAG
      ||| ||||| |||
      TCA CGACCCTAATGTC
      —
GAM1364 ZNF297B 3' CTGTAATCCCAGCTACT 25783
      AGTAGCTGGGATTACAG
      ||||| ||||| |||
      TCATCGACCCTAATGTC
      —
GAM1364 ZNF33A 3' ATGCCTGTAATCCCAGCACT 91344  A      A
      AGT GCTGGGATTACAG CAT
      ||| ||||| |||
      TCA CGACCCTAATGTC GTA
      —      C
GAM1364 ZNF347 3' ATGCCTGTAATCCCAACACT 50845  AGC      A
      AGT TGGGATTACAG CAT
      ||| ||||| |||
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		TCA ACCCTAATGTC GTA		
		CA_ C		
GAM1364	LOC112687 3'	CTATAATCCCAGCACT 72859	A	C
		AGT GCTGGGATTA AG		
		TCA CGACCCTAAT TC		
		— A		
GAM1364	LOC113201 3'	ATGCCTATAGTCCCAGCTACT 56549		C A
		AGTAGCTGGGATTA AG CAT		
		TCATCGACCCTGAT TC GTA		
		A C		
GAM1364	LOC115129 5'	CTATAATCCCAGCACT 73229	A	C
		AGT GCTGGGATTA AG		
		TCA CGACCCTAAT TC		
		— A		
GAM1364	LOC115129 5'	CTGTAATCCCAGCTACT 73231		
		AGTAGCTGGGATTACAG		
		TCATCGACCCTAATGTC		
GAM1364	LOC115129 5'	CTGTAATCCCAGGTACT 73232	G	
		AGTA CTGGGATTACAG		
		TCAT GACCCTAATGTC		
		G		
GAM1364	LOC115273 3'	ATGCCTGTAATCCCAGTTACT 73357		A
		AGTAGCTGGGATTACAG CAT		
		TCATTGACCCTAATGTC GTA		
		C		
GAM1364	LOC115761 3'	ATGCCTGTAATCCCAGCACTGT 91737	A	A
	G	TACAGT GCTGGGATTACAG CAT		
		GTGTCA CGACCCTAATGTC GTA		
		— C		
GAM1364	LOC116228 3'	CTGTAATCCCAGCACT 73798	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC116349 3'	CTGTAATCCCAGCACT 73830	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC119504 5'	ATGCCTGTAATCCCAGCTACT 73989		A
		AGTAGCTGGGATTACAG CAT		



			TCATCGACCCTAATGTC GTA		
			C		
GAM1364	LOC119504	5'	CTGTAATCCCAGCACT 73990	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC122704	3'	CTGTAATCCCAGCACT 74139	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC122704	3'	TGTAATCCCAGCTACTCA 74145	C	
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1364	LOC122970	3'	CTGTAATCCCAGTACT 74178	G	
			AGTA CTGGGATTACAG		
			TCAT GACCCTAATGTC		
			—		
GAM1364	LOC126282	3'	CTGTAATCCCAGCACT 74472	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC126282	3'	CTGTAATCCCAGCACT 74473	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC127262	3'	ATGCCTGTAATCCCAGC 76107		A
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1364	LOC127428	3'	ATGCCTATAATCCCAGCGCT 74662	A	C A
			AGT GCTGGGATTA AG CAT		
			TCG CGACCCTAAT TC GTA		
			— A C		
GAM1364	LOC130162	3'	ATGTCTGTAATCCCAGCACT 74909	A	
			AGT GCTGGGATTACAGACAT		
			TCA CGACCCTAATGTCTGTA		
			—		
GAM1364	LOC130535	3'	ATGCCTGTAATCCCAGC 76147		A
			GCTGGGATTACAG CAT		

CGACCCTAATGTC GTA  
C  
GAM1364 LOC130535 3' CTGTAGTCCCAGCTACTCA 76151 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTGATGTC  
C  
GAM1364 LOC130589 3' CTGTAATCCCAGCACT 57132 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC  
—  
GAM1364 LOC130951 3' CTGTAATCCCAACACTTTG 57143 TAGC\_  
CAG TGGGATTACAG  
||| |||||  
GTT ACCCTAATGTC  
TCACA  
GAM1364 LOC131744 3' ATGCCTGTAATCCCAGCACTGT 75868 A A  
A TACAGT GCTGGGATTACAG CAT  
||||| |||||  
ATGTCA CGACCCTAATGTC GTA  
— C  
GAM1364 LOC131965 3' ATGCCTGTAATCCCAGCACT 75027 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
— C  
GAM1364 LOC131965 3' TGTAATCCCAGCTACTCA 75034 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C  
GAM1364 LOC132625 3' ATGCCTGTAATCCCAACACTTT 75898 TAGC\_ A  
GT ACAG TGGGATTACAG CAT  
||| |||||  
TGTT ACCCTAATGTC GTA  
TCACA C  
GAM1364 LOC132625 3' CTGTGTTCCCAGCTACTCA 75906 C T  
A AGTAGCTGGGA TACAG  
| |||||  
A TCATCGACCCT GTGTC  
C T  
GAM1364 LOC133926 3' ATGCCTGTAATCCCAGCGCT 75131 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCG CGACCCTAATGTC GTA  
— C  
GAM1364 LOC134147 3' CTGTAATCCCAGCACT 57161 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1364 LOC134147 3' GTGCCTGTAATCCCAGCTACTC 57166 C A  
A A AGTAGCTGGGATTACAG CAT

I |||||  
A TCATCGACCCTAATGTC GTG  
C C

GAM1364 LOC137362 3' ATGCCTGTAATCCCAACACTTT 75263 TAGC\_ A  
G CAG TGGGATTACAG CAT

||| |||||  
GTT ACCCTAATGTC GTA  
TCACA C

GAM1364 LOC138241 3' CTGTAATCCCAACACT 75308 AGC  
AGT TGGGATTACAG

||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1364 LOC138428 3' ATGCCTGTAATCCCTGCTACT 75331 T A  
AGTAGC GGGATTACAG CAT

||||| |||||  
TCATCG CCCTAATGTC GTA  
T C

GAM1364 LOC138428 3' CTATAATCCCAGCACT 75335 A C  
AGT GCTGGGATTA AG

||| |||||  
TCA CGACCCTAAT TC  
A

GAM1364 LOC143310 3' CTGTAATCCCAGCACT 76532 A  
AGT GCTGGGATTACAG

||| |||||  
TCA CGACCCTAATGTC

GAM1364 LOC143888 3' CTGTAATCCCAGCACT 76659 A  
AGT GCTGGGATTACAG

||| |||||  
TCA CGACCCTAATGTC

GAM1364 LOC143943 3' ATGCCTGTAATCCCAGCACT 82994 A A  
AGT GCTGGGATTACAG CAT

||| |||||  
TCA CGACCCTAATGTC GTA

GAM1364 LOC144289 3' CTGTAATCCCAGCTACT 83024  
AGTAGCTGGGATTACAG

|||||  
TCATCGACCCTAATGTC

GAM1364 LOC144289 3' TCTGTAATCCCAGCACT 83029 A  
AGT GCTGGGATTACAGA

||| |||||

TCA CGACCCTAATGTCT

GAM1364 LOC144465 3' ATGCCTGTAATCCCCAAACT 76852 AGC A  
AGT TGGGATTACAG CAT  
||| |||||  
TCA ACCCTAATGTC GTA  
AA\_ C

GAM1364 LOC144465 3' ATGCCTGTAATCCCAGCTACT 76853 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1364 LOC144465 3' TGTAATCCCAGCTACTCA 76857 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1364 LOC144481 3' ATGCCTGTAATCCCAATACT 83093 GC A  
AGTA TGGGATTACAG CAT  
||| |||||  
TCAT ACCCTAATGTC GTA  
A\_ C

GAM1364 LOC144481 3' ATGCCTGTAATCCCAGCTACT 83094 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1364 LOC144486 3' CTGTAATCCCAGCACGCTG 83083 A\_  
CAGT GCTGGGATTACAG  
||| |||||  
GTCG CGACCCTAATGTC  
CA

GAM1364 LOC144524 3' ATGCCTGTAGTCCCAGCTACTT 83121 C A  
A AGTAGCTGGGATTACAG CAT  
| |||||  
A TCATCGACCCTGATGTC GTA  
T C

GAM1364 LOC144817 3' CTGTAATCCCAGCACT 76967 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LOC145216 3' CTGTAATCCCAGCACT 83265 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LOC145216 3' CTGTAATCCCAGCTACTCA 83266 C  
A AGTAGCTGGGATTACAG  
| |||||

			A TCATCGACCCTAATGTC		
			C		
GAM1364	LOC145231	3'	ATGCCTATAATCCCAGCACT	83278	A C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1364	LOC145231	3'	ATGCCTGTAATCCCAGCACT	83279	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	LOC145231	3'	ATGCCTGTAATCCCAGCTACTT	83280	— A
	G		CA GTAGCTGGGATTACAG CAT		
			GT CATCGACCCTAATGTC GTA		
			T C		
GAM1364	LOC145299	3'	CTGTAATCCCAGCACT	83314	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC145333	3'	CTGTAATCCCAGCACT	83326	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC145387	3'	CTGTAATCCCAGCACT	83354	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC145438	3'	ATGCCTGTAGCCCCAGCTACTC	83334	C AT A
	A		A AGTAGCTGGG TACAG CAT		
			A TCATCGACCC ATGTC GTA		
			C CG C		
GAM1364	LOC145438	3'	CTGTAATCCCAGCACT	83336	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC145453	3'	CTGTAATCTGAGCAC	77140	A G
			GT GCT GGATTACAG		
			CA CGA TCTAATGTC		
			— G		
GAM1364	LOC145482	3'	CTGTAATCCCAGCTACT	77229	
			AGTAGCTGGGATTACAG		

TCATCGACCCTAATGTC

GAM1364 LOC145483 3' CTGTAATCCCAACACT 77242 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1364 LOC145663 3' CTGTAATCCCAGCAATTG 83413 A  
CAGT GCTGGGATTACAG  
||| |||||  
GTTA CGACCCTAATGTC  
A

GAM1364 LOC145757 3' ATGCCTGTAATCCCAGCACT 77454 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
\_ C

GAM1364 LOC145757 3' GTAGTCCCAGCTACTCA 77470 C  
A AGTAGCTGGGATTAC  
| |||||  
A TCATCGACCCTGATG  
C

GAM1364 LOC145820 3' CTGTAATCCCAGCACT 77513 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LOC145824 3' ATGCCTGTAATCCCAGCACT 77523 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
\_ C

GAM1364 LOC145955 3' ATGCCTGTAATCCCAACACT 83588 AGC A  
AGT TGGGATTACAG CAT  
||| |||||  
TCA ACCCTAATGTC GTA  
CA\_ C

GAM1364 LOC146059 3' ATGCCTGTAATCCCAGCACT 77619 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
\_ C

GAM1364 LOC146059 3' TGTAATCCCAGCTACTCA 77623 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1364 LOC146229 3' CTGTAATCCCAGCACTCTG 77751 TA\_  
CAG GCTGGGATTACAG  
||| |||||

		GTC CGACCCTAATGTC		
		TCA		
GAM1364	LOC146272 5'	CTGTAATCCCAGCACT	77787	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC146332 3'	CTGTAATCCCAACACT	77824	AGC
		AGT TGGGATTACAG		
		TCA ACCCTAATGTC		
		CA_		
GAM1364	LOC146540 3'	ATGCCTGTAGTCCCAGCTACTC	77970	C
	A	A AGTAGCTGGGATTACAG CAT		A
		A TCATCGACCCTGATGTC GTA		
		C C		
GAM1364	LOC146540 3'	CTGTAATCCCAGCACT	77974	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC146667 3'	ATGCCTGTAATCCCAGCACT	83702	A
		AGT GCTGGGATTACAG CAT		A
		TCA CGACCCTAATGTC GTA		
		C		
GAM1364	LOC146669 3'	CTGTAATCCAGCACTGTG	78058	A
		TACAGT GCTGG ATTACAG		G
		GTGTCA CGACC TAATGTC		
		— —		
GAM1364	LOC146713 3'	CTGTAATCCCAGCACT	83725	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC146723 3'	CTGTAATCCCAGCTACT	78083	
		AGTAGCTGGGATTACAG		
		TCATCGACCCTAATGTC		
		—		
GAM1364	LOC146728 3'	ATGCCTGTGGTCCCAGCTACTC	83746	C
	A	A AGTAGCTGGGATTACAG CAT		A
		A TCATCGACCCTGGTGTC GTA		
		C C		
GAM1364	LOC146756 3'	CTGTAATCCCAGCACT	83776	A
		AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1364 LOC146756 3' CTGTAATCCCAGCACT 83777 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LOC146780 3' ATGCCTGTAATCCCTGCACTTA 83786 C A T A  
A AGT GC GGGATTACAG CAT  
| ||| || ||||| |||  
A TCA CG CCCTAATGTC GTA  
T \_ T C

GAM1364 LOC146901 3' ATGCCTATAATCCCAGCTACT 83829 C A  
AGTAGCTGGGATTA AG CAT  
||||||| || |||  
TCATCGACCCTAAT TC GTA  
A C

GAM1364 LOC146901 3' CTGTAATCCCCGCACT 83839 A T  
AGT GC GGGATTACAG  
||| || |||||  
TCA CG CCCTAATGTC  
\_ C

GAM1364 LOC146923 3' CTGTAATCCCAGCACT 78192 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LOC146975 5' CTATAATCCCAGCACT 78223 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC  
A

GAM1364 LOC147057 3' ATGCCTGTAATCCCAGCACT 83909 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

GAM1364 LOC147071 3' CTGTAATCCCAGCACT 72998 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

GAM1364 LOC147599 3' ATGCCTGTAATCCCAGCACCCCT 84040 TA\_ A  
G CAG GCTGGGATTACAG CAT  
||| ||||| |||  
GTC CGACCCTAATGTC GTA  
CCA C

GAM1364 LOC147660 3' CTGTAATCCCAGCAC 78392 A  
GT GCTGGGATTACAG  
|| |||||



CA CGACCCTAATGTC

GAM1364 LOC147664 3' ATGCCTGTAATCCCAGCTACTT 78403 \_ A  
G CA GTAGCTGGGATTACAG CAT

|| |||||  
GT CATCGACCCTAATGTC GTA  
T C

GAM1364 LOC147664 3' CTGTAATCCCAACACT 78408 AGC  
AGT TGGGATTACAG  
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TCA ACCCTAATGTC  
CA\_

GAM1364 LOC147669 3' CTGTAATCCCAGCACT 84061 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

GAM1364 LOC147700 3' ATGCCTGTAATCCCAGCTACT 59193 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1364 LOC147700 3' CTGTAATCCCAACACT 59197 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1364 LOC147727 5' CTATAATCCCAGCTACTCA 78467 C C  
A AGTAGCTGGGATTA AG  
| |||||  
A TCATCGACCCTAAT TC  
C A

GAM1364 LOC147837 3' ATGCCTGTAATCCCAGCTACT 78512 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1364 LOC147837 3' CTGTAATCCCAGCACT 78515 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LOC147990 3' CTGTAATCCCAGCACT 84092 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

GAM1364 LOC147990 3' CTGTAATCTCAGCTACTCA 84093 C  
A AGTAGCTGGGATTACAG  
| |||||

			A	TCATCGACTCTAATGTC C			
GAM1364	LOC148147	3'	CTGTAATCCCAGCACT	78680	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			-				
GAM1364	LOC148198	3'	ATGCCTGTAATCCCAGCTACT	70676		A	
			AGTAGCTGGGATTACAG CAT				
			TCATCGACCCTAATGTC GTA				
			C				
GAM1364	LOC148198	3'	CTGTAATCCCAGCACT	70681	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			-				
GAM1364	LOC148254	3'	TGCCTGTAATCCCTGCACT	78760	A T		A
			AGT GC GGGATTACAG CA				
			TCA CG CCCTAATGTC GT				
			_ T C				
GAM1364	LOC148343	3'	TGCCTGTAATCCCCGCACT	78796	A T		A
			AGT GC GGGATTACAG CA				
			TCA CG CCCTAATGTC GT				
			_ C C				
GAM1364	LOC148397	3'	ATGCCTGTAATCCTAGCTATT	78812			A
			AGTAGCTGGGATTACAG CAT				
			TTATCGATCCTAATGTC GTA				
			C				
GAM1364	LOC148397	3'	CTGTAATCCCGGCACTGTG	78817	A		
			TACAGT GCTGGGATTACAG				
			GTGTCA CGGCCCTAATGTC				
			-				
GAM1364	LOC148534	3'	ATGCCTGTAATCCCAGCACT	78894	A		A
			AGT GCTGGGATTACAG CAT				
			TCA CGACCCTAATGTC GTA				
			C				
GAM1364	LOC148734	3'	CTGTAATCCCAGCACT	78954	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			-				
GAM1364	LOC148749	3'	CTGTAATCCCAGCACT	78960	A		
			AGT GCTGGGATTACAG				

TCA CGACCCTAATGTC

GAM1364 LOC148758 5' ATGCCTATAATCCCAGCTACTT 78965 \_ C A  
G CA GTAGCTGGGATTA AG CAT  
|| ||||| || |||  
GT CATCGACCCTAAT TC GTA  
T A C

GAM1364 LOC148758 5' ATGCCTGTAATCCCAGAACT 78966 AG A  
AGT CTGGGATTACAG CAT  
||| ||||| |||  
TCA GACCCTAATGTC GTA  
A\_ C

GAM1364 LOC148809 3' ATGCCTATAATCCCAGCTTCT 79000 T C A  
AG AGCTGGGATTA AG CAT  
|| ||||| || |||  
TC TCGACCCTAAT TC GTA  
T A C

GAM1364 LOC148809 5' CTGTAATCCCAGCACT 79003 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

GAM1364 LOC148918 5' CTGTAATCCCAGCACT 79071 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

GAM1364 LOC148936 3' CTGTAATCCCAGCACT 84290 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

GAM1364 LOC148938 3' CTGTAATCCCAGCACT 84270 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

GAM1364 LOC149073 3' CTATAATCCCAGCACT 84324 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC

GAM1364 LOC149073 3' GTGCCTGTAATCCCAGCTACTC 84331 C A  
A A AGTAGCTGGGATTACAG CAT  
| ||||| ||| |||  
A TCATCGACCCTAATGTC GTG  
C C

GAM1364 LOC149113 3' CTGTAATCCCAGAACTTTA 79164 C AG  
TA AGT CTGGGATTACAG  
|| ||| ||||| |||

		AT TCA GACCCTAATGTC		
		T A_		
GAM1364	LOC149113 3'	CTGTAATCCCAGCACT	79165	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC149194 5'	CTGTAATCCCAGCTACTCA	79225	C
		A AGTAGCTGGGATTACAG		
		A TCATCGACCCTAATGTC		
		C		
GAM1364	LOC149194 5'	GTCTGTAATCCCAGCACT	79229	A
		AGT GCTGGGATTACAGAC		
		TCA CGACCCTAATGTCTG		
		—		
GAM1364	LOC149271 3'	CTGTAATCCCAGCACT	79240	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC149319 3'	GTCTGTAATCCCAGCACT	79301	A
		AGT GCTGGGATTACAGAC		
		TCA CGACCCTAATGTCTG		
		—		
GAM1364	LOC149579 5'	CTGTAATCCCAGCACT	71133	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC149606 3'	GTCTGTAGTCCCAGCTACTCA	79455	C
		A AGTAGCTGGGATTACAGAC		
		A TCATCGACCCTGATGTCTG		
		C		
GAM1364	LOC149628 3'	CTATAATCCCAGCTACT	79462	C
		AGTAGCTGGGATTA AG		
		TCATCGACCCTAAT TC		
		A		
GAM1364	LOC149628 3'	CTGTAATCCCAGCACT	79463	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC149668 3'	ATGCCTGTAATCCCAGCACT	84534	A
		AGT GCTGGGATTACAG CAT		A

		TCA CGACCCTAATGTC GTA			
		— C			
GAM1364	LOC149705 3'	CTGTAATCCCAACACTTTG	84623	TAGC_	
		CAG TGGGATTACAG			
		GTT ACCCTAATGTC			
		TCACA			
GAM1364	LOC149837 3'	TGGAAATCCCAGCTAT	84747	A_	
		GTAGCTGGGATT CA			
		TATCGACCCTAA GT			
		AG			
GAM1364	LOC150139 3'	ATGCCTGTAATCCCAGCTG	79584	A	
		TAGCTGGGATTACAG CAT			
		GTCGACCCTAATGTC GTA			
		C			
GAM1364	LOC150185 3'	ATGCCTGTAATCCCAACACT	84905	AGC	A
		AGT TGGGATTACAG CAT			
		TCA ACCCTAATGTC GTA			
		CA_ C			
GAM1364	LOC150319 3'	ATGCCTGTAATCCCAGCACT	79647	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		— C			
GAM1364	LOC150319 3'	ATGCCTGTAATCCCAGTTACTC	79648	C	A
	A	A AGTAGCTGGGATTACAG CAT			
		A TCATTGACCCTAATGTC GTA			
		C C			
GAM1364	LOC150343 3'	CTGTAATCCCAGCACT	79672	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1364	LOC150358 3'	ATGCCTGTAATCCCAGCACT	84921	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		— C			
GAM1364	LOC150358 3'	CTGTAATCCCAGGTACTCA	84922	C G	
		A AGTA CTGGGATTACAG			
		A TCAT GACCCTAATGTC			
		C G			
GAM1364	LOC150358 3'	ATGCCTATAATCCCAGCACT	84920	A	C A
		AGT GCTGGGATTA AG CAT			

			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1364	LOC150372	3'	ATGCCTGTAATCCCAGC 79786	A	
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1364	LOC150481	3'	CTGTAATCCCAGCACT 79884	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC150622	3'	CTGTAATCCCAACACT 79958	AGC	
			AGT TGGGATTACAG		
			TCA ACCCTAATGTC		
			CA_		
GAM1364	LOC150630	3'	ATGCCTATAATCCCAGCTACT 85099	C A	
			AGTAGCTGGGATTA AG CAT		
			TCATCGACCCTAAT TC GTA		
			A C		
GAM1364	LOC150630	3'	ATGCCTGTAATCCCAGCACT 85100	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	LOC150889	3'	ATGCCTGTAATCCCAGCACT 80024	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	LOC150935	3'	ATGCCTGTAATCCCAGCGCT 80031	A	A
			AGT GCTGGGATTACAG CAT		
			TCG CGACCCTAATGTC GTA		
			— C		
GAM1364	LOC150998	3'	CTGTGGTCCCAGCTAC 85183		
			GTAGCTGGGATTACAG		
			CATCGACCCTGGTGTC		
GAM1364	LOC151196	3'	CTGTAACCCCAGCTACTCA 85265	C	A
			A AGTAGCTGGG TTACAG		
			A TCATCGACCC AATGTC		
			C C		
GAM1364	LOC151196	3'	CTGTAATCCCAGCACT 85266	A	
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1364 LOC151248 3' CTGTAATCCCAGCACT 80186 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LOC151248 3' TGTAATCCCAGCTACTCA 80193 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1364 LOC151429 3' ATGCCTGTAATCCCAGC 85344 A  
GCTGGGATTACAG CAT  
||||||| |||  
CGACCCTAATGTC GTA  
C

GAM1364 LOC151429 3' CTGTAATCCCAGCACT 85352 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LOC151446 3' ATGCCTGTAATCCCAGCTACTG 85375 A  
CAGTAGCTGGGATTACAG CAT  
||||||| |||  
GTCATCGACCCTAATGTC GTA  
C

GAM1364 LOC151556 3' CTGTAATCCCAGTACT 80274 G  
AGTA CTGGGATTACAG  
||| |||||  
TCAT GACCCTAATGTC

GAM1364 LOC151556 3' TGTAATCCCAGCTACTCA 80283 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1364 LOC151602 3' CTGTAATCCCAACACT 80294 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1364 LOC151602 3' CTGTAATCCCAGCTACTCA 80295 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
C

GAM1364 LOC151614 3' CTGTAATCCCAGCACT 80304 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

GAM1364 LOC151623 3' ATGCCTGTGGTCTCAGCTACTC 85456 C A  
A A AGTAGCTGGGATTACAG CAT

I |||||  
A TCATCGACTCTGGTGTC GTA  
C C

GAM1364 LOC151904 3' CTGTAATCCCAGCACT 80390 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC

GAM1364 LOC152263 3' CTGTAATCCCAGCACT 85674 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LOC152263 3' TCCATAATCCTAGCTGCT 85676 CA  
AGTAGCTGGGATTA GA  
||||| ||  
TCGTCGATCCTAAT CT  
AC

GAM1364 LOC152316 3' ATGCCTGTAATCCCAGCACTTT 85609 C A A  
A TA AGT GCTGGGATTACAG CAT  
|| ||| |||||  
AT TCA CGACCCTAATGTC GTA  
T \_ C

GAM1364 LOC152426 3' CTGTAATCCCAGCACT 85714 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LOC152445 3' ATGCCTGTAATCCCAACTACT 85746 C A  
AGTAG TGGGATTACAG CAT  
|||| |||||  
TCATC ACCCTAATGTC GTA  
A C

GAM1364 LOC152453 3' ATGCCTGTAATCCCAGCACT 80592 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1364 LOC152453 3' ATGCCTGTAATCCCAGCTACT 80593 A  
AGTAGCTGGGATTACAG CAT  
||||| |||  
TCATCGACCCTAATGTC GTA  
C

GAM1364 LOC152453 3' CTGTAATCCCAACT 80595 AGC  
AGT TGGGATTACAG  
||| |||||



			TCA ACCCTAATGTC			
			CA_			
GAM1364	LOC152453	3'	CTGTAATCCCAGCACT	80596	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	LOC152453	3'	CTGTAATCCCAGTTACTCA	80597	C	
			A AGTAGCTGGGATTACAG			
			A TCATTGACCCTAATGTC			
			C			
GAM1364	LOC152627	5'	TGTAATCCCAGCTACTCA	80632	C	
			A AGTAGCTGGGATTACA			
			A TCATCGACCCTAATGT			
			C			
GAM1364	LOC152804	3'	ATGCCTGTAATCCCAGCTACT	85878		A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1364	LOC152860	3'	ATGTCTGTAATCCCAGCTACTG	80696		
			CAGTAGCTGGGATTACAGACAT			
			GTCATCGACCCTAATGTCTGTA			
GAM1364	LOC152860	3'	CTATAATCCCAGCACT	80701	A	C
			AGT GCTGGGATTA AG			
			TCA CGACCCTAAT TC			
			— A			
GAM1364	LOC152926	3'	ATGCCTGTAATCCCAGCACT	80744	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1364	LOC153077	3'	CTATAATCCCAGCTACTCA	85909	C	C
			A AGTAGCTGGGATTA AG			
			A TCATCGACCCTAAT TC			
			C A			
GAM1364	LOC153260	3'	CTGTAATCCCAGCACT	80804	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	LOC153561	3'	ATGCCTGTAATCCCAGCACT	80888	A	A
			AGT GCTGGGATTACAG CAT			

TCA CGACCCTAATGTC GTA  
 — C  
 GAM1364 LOC153579 3' CTGTAATCCCAGTACT 80895 G  
 AGTA CTGGGATTACAG  
 |||| |||||  
 TCAT GACCCTAATGTC  
  
 —  
 GAM1364 LOC153642 3' CTATAGTCTCAGCTACTCA 80907 C C  
 A AGTAGCTGGGATTA AG  
 | ||||| ||  
 A TCATCGACTCTGAT TC  
 C A  
 GAM1364 LOC153642 3' CTGTAATCCCAGGACT 80908 AG  
 AGT CTGGGATTACAG  
 ||| |||||  
 TCA GACCCTAATGTC  
 G\_  
 GAM1364 LOC153682 3' ATGCCTGTAATCCCAGCACT 86084 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||  
 TCA CGACCCTAATGTC GTA  
 — C  
 GAM1364 LOC153688 3' ATGCCTATAATCCCAGCACT 86095 A C A  
 AGT GCTGGGATTA AG CAT  
 ||| ||||| || |||  
 TCA CGACCCTAAT TC GTA  
 — A C  
 GAM1364 LOC154092 3' TCTGTAATCCCAGCACT 86161 A  
 AGT GCTGGGATTACAGA  
 ||| |||||  
 TCA CGACCCTAATGTCT  
  
 —  
 GAM1364 LOC154215 3' ATGTCTGTAATATACACACAC 81053 AGC GG\_  
 GT TG ATTACAGACAT  
 || || |||||  
 CA AC TAATGTCTGTA  
 CAC ATA  
 GAM1364 LOC154403 3' CTGTAATCCCAGAACTTTA 81071 C AG  
 TA AGT CTGGGATTACAG  
 || ||| |||||  
 AT TCA GACCCTAATGTC  
 T A\_  
 GAM1364 LOC154739 5' ATGTCTATAATTCCAGCTACTC 86225 C C  
 A A AGTAGCTGGGATTA AGACAT  
 | ||||| |||||  
 A TCATCGACCTTAAT TCTGTA  
 C A  
 GAM1364 LOC154791 3' ATGCCTGTAATCCCAGCTACT 81154 A  
 AGTAGCTGGGATTACAG CAT  
 ||||| ||||| |||

			TCATCGACCCTAATGTC	GTA		
			C			
GAM1364	LOC154791	3'	CTGTAATCCCAGCACT	81156	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	LOC154992	3'	CTGTAATCCCAGAACTTTA	81215	C	AG
			TA AGT CTGGGATTACAG			
			AT TCA GACCCTAATGTC			
			T A_			
GAM1364	LOC155006	3'	ATGCCTGTAATCCCAGCACT	81229	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC	GTA		
			—			
			C			
GAM1364	LOC155006	3'	ATGCCTGTAATCCCAGCACT	81230	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC	GTA		
			—			
			C			
GAM1364	LOC155006	3'	CTGTAATCCCAGCTACTTG	81237	—	
			CA GTAGCTGGGATTACAG			
			GT CATCGACCCTAATGTC			
			T			
GAM1364	LOC155072	3'	CTGTAATCCCAGCACT	86375	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	LOC155072	3'	CTGTAATCCCAGCACT	86376	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	LOC155438	3'	CTGTAATCCCAGTACCT	86393	TA	
			AG GCTGGGATTACAG			
			TC TGACCCTAATGTC			
			CA			
GAM1364	LOC157278	3'	CTGTAATCCCAGCACT	86423	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1364	LOC157292	5'	CTGTAATCTCAGTTACTCA	86413	C	
			A AGTAGCTGGGATTACAG			

			A TCATTGACTCTAATGTC		
			C		
GAM1364	LOC157464	5'	CTGTAATCCCAGCACT	86448	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC157657	3'	ATGCCTGTAATCCCACTACT	81516	C A
			AGTAG TGGGATTACAG CAT		
			TCATC ACCCTAATGTC GTA		
			A C		
GAM1364	LOC157657	3'	CTGTAATCCCAGCACT	81518	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC157660	3'	CTGTAATCCCAGCACT	86507	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC158160	3'	TGTAGTCCCACTACTCA	73082	C C
			A AGTAG TGGGATTACA		
			A TCATC ACCCTGATGT		
			C A		
GAM1364	LOC158187	3'	CTGTAGTCCCAGCTAC	86691	
			GTAGCTGGGATTACAG		
			CATCGACCCTGATGTC		
			—		
GAM1364	LOC158191	3'	CTGTAATCCCAGCACT	81775	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC158292	5'	ATGCCTGTAATCCCAGCACT	86728	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	LOC158292	5'	TGTAATCCCAGCTACTCA	86732	C
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1364	LOC158310	3'	CTGTAATCCCAGCACT	86753	A
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1364 LOC158819 5' ATGCCTGTAATCCCAGCTTCT 86901 T A  
AG AGCTGGGATTACAG CAT  
|| |||||  
TC TCGACCCTAATGTC GTA  
T C

GAM1364 LOC158819 3' CTGTAATCCCAGCACT 86903 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LOC158819 5' CTGTAATCCCAGCACT 86904 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1364 LOC158863 3' CTGTAATCCCAACACT 86923 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1364 LOC158987 3' CTGTAATCCCAACACT 86961 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1364 LOC159036 3' ATGCCTGTAATCCCAGCACT 86969 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
C

GAM1364 LOC159053 3' CTGTAATCCCAGGACT 86978 AG  
AGT CTGGGATTACAG  
||| |||||  
TCA GACCCTAATGTC  
G\_

GAM1364 LOC161823 3' ATGCCTGTAATCCCAGCACT 82300 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
C

GAM1364 LOC170395 3' CTGCAGTCCCAGCTACTCA 76368 C A  
A AGTAGCTGGGATT CAG  
| |||||  
A TCATCGACCCTGA GTC  
C C

GAM1364 LOC170395 3' CTGTAATCCCAGCACT 76369 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

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GAM1364 LOC196047 5' CTGTAATCCCAGTACT    89600    G
                    AGTA CTGGGATTACAG
                    ||| |||||
                    TCAT GACCCTAATGTC

      -
GAM1364 LOC196528 3' CTATAATCCCAGCACT    87764    A    C
                    AGT GCTGGGATTAG
                    ||| ||||| ||
                    TCA CGACCCTAAT TC

      -      A
GAM1364 LOC197196 3' CTGTAATCCCAGCACT    89733    A
                    AGT GCTGGGATTACAG
                    ||| |||||
                    TCA CGACCCTAATGTC

      -
GAM1364 LOC197201 3' ATGCCTGTAATCTCAGCTACTC 87933    C    A
      A      A AGTAGCTGGGATTACAG CAT
                    | ||||| |||
                    A TCATCGACTCTAATGTC GTA
                    C      C
GAM1364 LOC197201 3' CTGTAATCCCAGCACT    87936    A
                    AGT GCTGGGATTACAG
                    ||| |||||
                    TCA CGACCCTAATGTC

      -
GAM1364 LOC197319 3' CTGTAATCCCAGCACT    87969    A
                    AGT GCTGGGATTACAG
                    ||| |||||
                    TCA CGACCCTAATGTC

      -
GAM1364 LOC197319 3' CTGTAATCCCAGCTCCT    87970    T
                    AG AGCTGGGATTACAG
                    || |||||
                    TC TCGACCCTAATGTC
                    C
GAM1364 LOC199733 3' CTGAAATCCCAGCTACTG    89849    A
                    CAGTAGCTGGGATT CAG
                    ||||| |||
                    GTCATCGACCCTAA GTC
                    A
GAM1364 LOC199786 3' CTGTAATCCCAGCACT    88380    A
                    AGT GCTGGGATTACAG
                    ||| |||||
                    TCA CGACCCTAATGTC

      -
GAM1364 LOC200014 3' CTGTAATCCCACCACT    88526    AGC
                    AGT TGCGATTACAG
                    ||| |||||
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		TCA ACCCTAATGTC		
		CC_		
GAM1364	LOC200251 5'	CTGTAATCCCAGCTACTCA	88665	C
		A AGTAGCTGGGATTACAG		
		A TCATCGACCCTAATGTC		
		C		
GAM1364	LOC200317 3'	CTGTAATCCCAGCTACTTG	88794	_
		CA GTAGCTGGGATTACAG		
		GT CATCGACCCTAATGTC		
		T		
GAM1364	LOC200470 3'	CTGTAATCCCAACACT	90062	AGC
		AGT TGGGATTACAG		
		TCA ACCCTAATGTC		
		CA_		
GAM1364	LOC200728 3'	CTGTAATCCCAGCACT	90115	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		-		
GAM1364	LOC200803 3'	ATGCCTGTAATCCTAGCTACTC	88879	C
	A	A AGTAGCTGGGATTACAG CAT		A
		A TCATCGATCCTAATGTC GTA		
		C C		
GAM1364	LOC200803 3'	TGCCTGTAATCCCACCACT	88881	AGC
		AGT TGGGATTACAG CA		A
		TCA ACCCTAATGTC GT		
		CC_ C		
GAM1364	LOC200918 3'	TGTAATCCCAGCTACTTA	88943	C
		A AGTAGCTGGGATTACA		
		A TCATCGACCCTAATGT		
		T		
GAM1364	LOC200940 3'	ATGCCTGTAATCCCAGCTACTT	88950	_
	G	CA GTAGCTGGGATTACAG CAT		A
		GT CATCGACCCTAATGTC GTA		
		T C		
GAM1364	LOC201173 3'	CTGTAATCCCAGCACT	87328	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		-		
GAM1364	LOC201182 5'	ATGCCTGTAATCCCAGCTAC	89763	A
		GTAGCTGGGATTACAG CAT		

		CATCGACCCTAATGTC GTA		
		C		
GAM1364	LOC201220 3'	CTGTAATCCCAGCACT	87349	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC201252 3'	ATGCCTGTAATCCCACTACT	88165	C A
		AGTAG TGGGATTACAG CAT		
		TCATC ACCCTAATGTC GTA		
		A C		
GAM1364	LOC201252 3'	CTGTAATCCCAGAACT	88168	AG
		AGT CTGGGATTACAG		
		TCA GACCCTAATGTC		
		A_		
GAM1364	LOC201564 3'	ATGCCTGTAATCCCAGCTACTT	80435	— A
	G	CA GTAGCTGGGATTACAG CAT		
		GT CATCGACCCTAATGTC GTA		
		T C		
GAM1364	LOC201685 3'	ATGTCTATGGTCCCAGCTACTC	90239	C C
	A	A AGTAGCTGGGATTA AGACAT		
		A TCATCGACCCTGGT TCTGTA		
		C A		
GAM1364	LOC201685 3'	CTGTAATCCCAGCACT	90241	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC201689 3'	CTGTAATCCCAGCACT	67144	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC201868 3'	CTGTAATCCCAGCACT	89077	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC201868 3'	TGTAATCCCAGCTACTCA	89084	C
		A AGTAGCTGGGATTACA		
		A TCATCGACCCTAATGT		
		C		
GAM1364	LOC201895 3'	CTGTAATCCCAGCACT	89087	A
		AGT GCTGGGATTACAG		



TCA CGACCCTAATGTC

GAM1364 LOC201895 3' GTGCCTGTAATCCCAGCTACTC 89091 C A  
A A AGTAGCTGGGATTACAG CAT

I ||||||||||||| III  
A TCATCGACCCTAATGTC GTG  
C C

GAM1364 LOC201911 3' CTGTAATCCCAGCACT 90261 A  
AGT GCTGGGATTACAG  
III |||||||||||||  
TCA CGACCCTAATGTC

GAM1364 LOC202868 3' CTGTAATCCCAGCACT 90373 A  
AGT GCTGGGATTACAG  
III |||||||||||||  
TCA CGACCCTAATGTC

GAM1364 LOC202868 3' CTGTAATCCCAGCACT 90374 A  
AGT GCTGGGATTACAG  
III |||||||||||||  
TCA CGACCCTAATGTC

GAM1364 LOC203025 3' ATGCCTGTAATCCCAACACTTT 89249 TAGC\_ A  
G CAG TGGGATTACAG CAT  
III ||||||||||||| III  
GTT ACCCTAATGTC GTA  
TCACA C

GAM1364 LOC203246 3' CTGTAATCCCAGCACT 89304 A  
AGT GCTGGGATTACAG  
III |||||||||||||  
TCA CGACCCTAATGTC

GAM1364 LOC203276 3' GTCTATAATTCCAGCTACTCA 90487 C C  
A AGTAGCTGGGATTA AGAC  
I ||||||||||||| III  
A TCATCGACCTTAAT TCTG  
C A

GAM1364 LOC203305 3' GTCTATAATTCCAGCTACTCA 90531 C C  
A AGTAGCTGGGATTA AGAC  
I ||||||||||||| III  
A TCATCGACCTTAAT TCTG  
C A

GAM1364 LOC203350 3' ATGCCTGTAATCCCAGCACT 90560 A A  
AGT GCTGGGATTACAG CAT  
III ||||||||||||| III  
TCA CGACCCTAATGTC GTA

GAM1364 LOC203350 3' ATGCCTGTAGTTGCAGCTACTC 90561 C G A  
A A AGTAGCTG GATTACAG CAT  
I ||||||| ||||||| III

			A TCATCGAC TTGATGTC GTA		
			C G C		
GAM1364	LOC203378	3'	CTGTAATCCCGGCACT	90602	A
			AGT GCTGGGATTACAG		
			TCA CGGCCCTAATGTC		
			—		
GAM1364	LOC203378	3'	CTGTAGTTCCAGCTACTG	90603	
			CAGTAGCTGGGATTACAG		
			GTCATCGACCTTGATGTC		
GAM1364	LOC219406	3'	CTGCAATCCCAGCTACT	93559	A
			AGTAGCTGGGATT CAG		
			TCATCGACCCTAA GTC		
			C		
GAM1364	LOC219406	3'	CTGTAATCCCAGCACT	93560	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
GAM1364	LOC219540	3'	CTGTAATCCCAGCTACTTG	93598	—
			CA GTAGCTGGGATTACAG		
			GT CATCGACCCTAATGTC		
			T		
GAM1364	LOC219627	3'	ATGCCTGTAATCCCAACACT	92175	AGC A
			AGT TGGGATTACAG CAT		
			TCA ACCCTAATGTC GTA		
			CA_ C		
GAM1364	LOC219627	3'	CTGTAATCCCAGCACT	92177	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
GAM1364	LOC219627	3'	GTGCCTGTAATCCCAGCTACTC	92185	C A
	A		A AGTAGCTGGGATTACAG CAT		
			A TCATCGACCCTAATGTC GTG		
			C C		
GAM1364	LOC219649	3'	ATGCCTATAATCCCAGC	92950	C A
			GCTGGGATTA AG CAT		
			CGACCCTAAT TC GTA		
			A C		
GAM1364	LOC219649	3'	CTGTAATCCCAGCTACT	92956	
			AGTAGCTGGGATTACAG		

TCATCGACCCTAATGTC

GAM1364 LOC219649 3' GTCTGTAATCCCAGCACT 92961 A  
AGT GCTGGGATTACAGAC  
||| |||||  
TCA CGACCCTAATGTCTG

—  
GAM1364 LOC219672 5' ATGCCTGTAATCCCAGCACT 91328 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

— C  
GAM1364 LOC219673 3' CTGTAATCCCAGCACT 93031 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 LOC219722 5' CTGTAATCCCAGCACT 93081 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 LOC220370 3' ATGCCTGTAATCCCAACACTCT 92824 T C\_\_ A  
G CAG AG TGGGATTACAG CAT  
||| || |||||  
GTC TC ACCCTAATGTC GTA  
— ACA C

GAM1364 LOC220506 3' CTATAATCCCAGCACTTTA 74077 C A C  
TA AGT GCTGGGATTA AG  
|| ||| |||||  
AT TCA CGACCCTAAT TC  
T — A

GAM1364 LOC220662 3' CTGTAATCCCAGCACT 91169 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 LOC220662 3' CTGTAATCCCAGCACT 91170 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1364 LOC220662 3' CTGTAATCCCAGCTACTTG 91171 \_  
CA GTAGCTGGGATTACAG  
|| |||||  
GT CATCGACCCTAATGTC  
T

GAM1364 LOC220662 3' CTGTCATCCCAGCTACTCA 91172 C T  
A AGTAGCTGGGAT ACAG  
| |||||

		A TCATCGACCCTA TGTC		
		C C		
GAM1364	LOC220906 3'	ATGCCTGTAATCCCAACACT	91396	AGC A
		AGT TGGGATTACAG CAT		
		TCA ACCCTAATGTC GTA		
		CA_ C		
GAM1364	LOC221042 3'	CTGTAATCCCAGCGCT	93185	A
		AGT GCTGGGATTACAG		
		TCG CGACCCTAATGTC		
		—		
GAM1364	LOC221178 3'	ATGCCTGTAATCCCAGCACT	93527	A A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		— C		
GAM1364	LOC221178 3'	ATGCCTGTAATCCCAGCTACTG	93528	A
		CAGTAGCTGGGATTACAG CAT		
		GTCATCGACCCTAATGTC GTA		
		C		
GAM1364	LOC221271 3'	CTGTAATCCCAGCACT	91856	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC221271 3'	CTGTAATCCCAGCTACT	91857	
		AGTAGCTGGGATTACAG		
		TCATCGACCCTAATGTC		
		—		
GAM1364	LOC221474 3'	CTGTAATCCCAGCACT	92381	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC221474 3'	TGTAATCCCAGCTACTCA	92389	C
		A AGTAGCTGGGATTACA		
		A TCATCGACCCTAATGT		
		C		
GAM1364	LOC221477 3'	CTGTAATCCCAGCTAC	92152	
		GTAGCTGGGATTACAG		
		CATCGACCCTAATGTC		
		—		
GAM1364	LOC221489 3'	CTGTAATCCCAGCACT	93641	A
		AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

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      -
GAM1364 LOC221490 3' CTGTAATCCCAGCACT   93658   A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1364 LOC221543 3' CTGTAATCCCAGCACT   93740   A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1364 LOC221543 5' CTGTAATCCCAGCACTCTG  93741   TA_
      CAG GCTGGGATTACAG
      ||| |||||
      GTC CGACCCTAATGTC
      TCA

GAM1364 LOC221931 3' ATGCCTGTAATCCCAGCACT  93993   A       A
      AGT GCTGGGATTACAG CAT
      ||| ||||| |||
      TCA CGACCCTAATGTC GTA
      C
      -
GAM1364 LOC221954 5' CTGTAATCCCAGCACT   94000   A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1364 LOC221962 3' CTGTAATCCCAGCACT   92681   A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1364 LOC222066 3' CTGTAATCCCAGCTATT   92744
      AGTAGCTGGGATTACAG
      |||||
      TTATCGACCCTAATGTC

      -
GAM1364 LOC222160 5' ATGCCTGTAATCCCAGCACT  94118   A       A
      AGT GCTGGGATTACAG CAT
      ||| ||||| |||
      TCA CGACCCTAATGTC GTA
      C
      -
GAM1364 LOC222160 3' CTGTAATCCCAGCTACT   94125
      AGTAGCTGGGATTACAG
      |||||
      TCATCGACCCTAATGTC

      -
GAM1364 LOC222182 3' CTGTAATCCCTTAGCTACTCA  94189   C   _
      A AGTAGCT GGGATTACAG
      | ||||| |||||
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		A TCATCGA CCCTAATGTC		
		C TT		
GAM1364	LOC222865 3'	CTGTAATCCCAGCACT 92860	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC253612 3'	CTGTAATCCCAACACT 96748	AGC	
		AGT TGGGATTACAG		
		TCA ACCCTAATGTC		
		CA_		
GAM1364	LOC253612 3'	GTCTGTAATCCCAGCTACT 96755		
		AGTAGCTGGGATTACAGAC		
		TCATCGACCCTAATGTCTG		
GAM1364	LOC253639 3'	ATGCCTGTAATCCCAGCTACT 95818		A
		AGTAGCTGGGATTACAG CAT		
		TCATCGACCCTAATGTC GTA		
		C		
GAM1364	LOC253927 3'	ATGCCTGTAATCCCAGCACT 95023	A	A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		— C		
GAM1364	LOC254045 3'	ATGCCTGTAATCCCAATACT 96502	GC	A
		AGTA TGGGATTACAG CAT		
		TCAT ACCCTAATGTC GTA		
		A_ C		
GAM1364	LOC254045 3'	ATGCCTGTAATCCCAGCTACT 96503		A
		AGTAGCTGGGATTACAG CAT		
		TCATCGACCCTAATGTC GTA		
		C		
GAM1364	LOC254243 3'	GTCTATAATTCCAGCTACTCA 97416	C	C
		A AGTAGCTGGGATTA AGAC		
		A TCATCGACCTTAAT TCTG		
		C A		
GAM1364	LOC254249 5'	TGCTTGTCCTCCAGCTACTG 95449	TAC	A
		CAGTAGCTGGGAT AG CA		
		GTCATCGACCCTG TC GT		
		T_ _		
GAM1364	LOC254531 5'	ATGCCTGTAATCCCAGCTACTT 94980	_	A
	G	CA GTAGCTGGGATTACAG CAT		

			GT CATCGACCCTAATGTC GTA		
			T C		
GAM1364	LOC254531 5'	CTGTAATCCCAGCACT	94985	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1364	LOC255042 3'	ATGCCTGTAATCCTAGCTACTC	95312	C	A
	A	A AGTAGCTGGGATTACAG CAT			
		A TCATCGATCCTAATGTC GTA			
		C C			
GAM1364	LOC255042 3'	CTGTAATCCCAGCACT	95315	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1364	LOC255042 3'	CTGTAATCCCAGCACT	95316	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1364	LOC255177 3'	CTGTAATCCCAGCACT	96605	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1364	LOC255196 3'	ATGCCTATAATCCCAGCACT	97164	A	C A
		AGT GCTGGGATTA AG CAT			
		TCA CGACCCTAAT TC GTA			
		A C			
GAM1364	LOC255196 5'	CTGTAATCCCAGCACT	97169	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1364	LOC255231 3'	CTGTAATCCCAGCACT	95373	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1364	LOC255252 3'	ATGCCTATAATCCCAGCACT	95006	A	C A
		AGT GCTGGGATTA AG CAT			
		TCA CGACCCTAAT TC GTA			
		A C			
GAM1364	LOC255326 3'	CTGTAATCCCAGACTGTG	96376	AG	
		TACAGT CTGGGATTACAG			

GTGTCA GACCCTAATGTC

—  
GAM1364 LOC255328 3' ATGTCTGTAATCCCAGCACT 96557 A  
AGT GCTGGGATTACAGACAT  
||| |||||||||  
TCA CGACCCTAATGTCTGTA

—  
GAM1364 LOC255461 3' CTGTAATCCCAGCACT 97319 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

—  
GAM1364 LOC255516 3' CTGTAATCCCAGCACT 97332 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

—  
GAM1364 LOC255624 3' CTGTAATCCCAGCACT 94523 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

—  
GAM1364 LOC255671 3' CTGTAATCCCAGCTGCT 97255  
AGTAGCTGGGATTACAG  
|||||||  
TCGTCGACCCTAATGTC

GAM1364 LOC255671 3' TCTGTAATCCCAGCACT 97264 A  
AGT GCTGGGATTACAGA  
||| |||||||||  
TCA CGACCCTAATGTCT

—  
GAM1364 LOC255937 3' ATGCCTGTAATCCCAGCTACT 95987 A  
AGTAGCTGGGATTACAG CAT  
||||||| |||  
TCATCGACCCTAATGTC GTA  
C

GAM1364 LOC255937 3' CTGTAATCCCAGCTCT 95988 T  
AG AGCTGGGATTACAG  
|| |||||||||  
TC TCGACCCTAATGTC

—  
GAM1364 LOC255971 3' CTATAATCCCAGCACT 96533 A C  
AGT GCTGGGATTA AG  
||| ||||||| ||  
TCA CGACCCTAAT TC

— A  
GAM1364 LOC256073 3' CTGTAATCCCAATGCT 96664 GC  
AGTA TGGGATTACAG  
|||| |||||||



		TCGT ACCCTAATGTC		
		A_		
GAM1364	LOC256207 3'	TCTGTAATTGCTATTG	95179	TGG
		CAGTAGC GATTACAGA		
		GTTATCG TTAATGTCT		
		—		
GAM1364	LOC256267 3'	ATGCCTGTAATCCCAGCACT	96797	A A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		— C		
GAM1364	LOC256277 3'	CTGTAATCCCAGCACT	94698	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC256520 3'	TGTAATCCCAGCTACTCA	95981	C
		A AGTAGCTGGGATTACA		
		A TCATCGACCCTAATGT		
		C		
GAM1364	LOC256980 3'	TCTGTAATCCCAGCACTCTG	95223	TA_
		CAG GCTGGGATTACAGA		
		GTC CGACCCTAATGTCT		
		TCA		
GAM1364	LOC257354 3'	ATGCCTATAATCCCAACACT	95085	AGC C A
		AGT TGGGATTA AG CAT		
		TCA ACCCTAAT TC GTA		
		CA_ A C		
GAM1364	LOC257480 3'	CTGTAATCCCAGCACT	77869	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1364	LOC257539 3'	ATGCCTGTAATCCCAGCACT	97699	A A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		— C		
GAM1364	LOC257578 3'	ATGCCTGTAATCCCAGCACT	97819	A A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		— C		
GAM1364	LOC257596 3'	CTGTAATCCCAGCACT	97933	A
		AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1364 LOC257596 5' CTGTAATCCCAGCACTCTG 97934 TA\_

—

CAG GCTGGGATTACAG

||| |||||

GTC CGACCCTAATGTC

TCA

GAM1364 LOC51145 3' TGTAATCCCAGCTACTCA 32400 C

A AGTAGCTGGGATTACA

| |||||

A TCATCGACCCTAATGT

C

GAM1364 LOC51333 3' CTGTAATCCCAGCACT 33567 A

AGT GCTGGGATTACAG

||| |||||

TCA CGACCCTAATGTC

GAM1364 LOC51333 3' CTGTAATCCCAGCTACTG 33568

—

CAGTAGCTGGGATTACAG

|||||

GTCATCGACCCTAATGTC

GAM1364 LOC51652 3' ATGCCTATAATCCCAGTGCT 32191 G C A

AGTA CTGGGATTA AG CAT

|||| ||||| || |||

TCGT GACCCTAAT TC GTA

— A C

GAM1364 LOC51716 3' TGCCTGTAATCCCTGC 32795 T A

GC GGGATTACAG CA

|| ||||| ||

CG CCCTAATGTC GT

T C

GAM1364 LOC51759 3' ATGCCTGTAATCCCAGCTGCT 72812 A

AGTAGCTGGGATTACAG CAT

|||||

TCGTGACCCTAATGTC GTA

C

GAM1364 LOC55974 3' ATGCCTGTAATCCCAGATACT 38130 G A

AGTA CTGGGATTACAG CAT

|||| ||||| |||

TCAT GACCCTAATGTC GTA

A C

GAM1364 LOC55974 3' CTGTAATCCCAGCACT 38131 A

AGT GCTGGGATTACAG

||| |||||

TCA CGACCCTAATGTC

GAM1364 LOC57118 3' CTGTAATCCCAACACT 39867 AGC

—

AGT TGGGATTACAG

||| |||||

			TCA ACCCTAATGTC		
			CA_		
GAM1364	LOC63929	3'	ATGCCTGTAATCCTGGCTACT 42041	TG	A
			AGTAGC GGATTACAG CAT		
			TCATCG CCTAATGTC GTA		
			GT C		
GAM1364	LOC64167	3'	CTGTAATCCCAGCACT 42279	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC89890	3'	CTGTAATCCCAGCTAC 60578		
			GTAGCTGGGATTACAG		
			CATCGACCCTAATGTC		
			—		
GAM1364	LOC90038	3'	GTCTATAATTCCAGCTACTCA 61159	C	C
			A AGTAGCTGGGATTA AGAC		
			A TCATCGACCTTAAT TCTG		
			C A		
GAM1364	LOC90092	3'	CTGTAATCCCAGCACT 61405	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC90092	3'	CTGTAATCCCAGCACT 61406	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC90141	3'	ATGCCTACAATCCCAGCACT 61625	A	AC A
			AGT GCTGGGATT AG CAT		
			TCA CGACCCTAA TC GTA		
			CA C		
			—		
GAM1364	LOC90155	5'	ATGCCTGTAATCCCAGCACT 61691	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			C		
			—		
GAM1364	LOC90321	3'	ATGCCTATAATCTCAGCAC 62260	A	C A
			GT GCTGGGATTA AG CAT		
			CA CGACTCTAAT TC GTA		
			A C		
			—		
GAM1364	LOC90321	3'	ATGCCTGCAATCCCAGCTACT 62261		A A
			AGTAGCTGGGATT CAG CAT		

			TCATCGACCCTAA GTC GTA		
			C C		
GAM1364	LOC90408	5'	ATGCCTGTAATCCCAGCACT	62656	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	LOC90509	3'	CTGTAATCCCAGCACT	63104	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC90538	3'	TCTGTAATCCCAGCACT	63196	A
			AGT GCTGGGATTACAGA		
			TCA CGACCCTAATGTCT		
			—		
GAM1364	LOC90580	3'	ATGTCTGTAATCCCAGC	63371	
			GCTGGGATTACAGACAT		
			CGACCCTAATGTCTGTA		
			—		
GAM1364	LOC90591	3'	ATGCCTGTAATCCCAGCTACAT	63414	— A
	G		CA GTAGCTGGGATTACAG CAT		
			GT CATCGACCCTAATGTC GTA		
			A C		
GAM1364	LOC90591	3'	CTGTAATCCCAGCACT	63423	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC90591	3'	CTGTAATCCCAGCACT	63424	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC90624	3'	CTGTAATCCCGCACT	63603	A T
			AGT GC GGGATTACAG		
			TCA CG CCCTAATGTC		
			— —		
GAM1364	LOC90639	3'	CTGCAATCCCAGCACTTTA	63656	C A A
			TA AGT GCTGGGATT CAG		
			AT TCA CGACCCTAA GTC		
			T — C		
GAM1364	LOC90777	3'	CTATAATCTCAGCAC	63967	A C
			GT GCTGGGATTA AG		

			CA CGACTCTAAT TC		
			— A		
GAM1364	LOC90918	5'	ATGCCTGTAATCCCAGCTACT	64350	A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1364	LOC90979	3'	CTGTAATCCCAGCACT	64526	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC90982	5'	ATGTCTCTTTCCAGCTCT	64537	T TTAC
			AG AGCTGGGA AGACAT		
			TC TCGACCTT TCTGTA		
			— TC—		
GAM1364	LOC91035	3'	CTATAATCCCAGCACT	64669	A C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1364	LOC91056	3'	ATGCCTGTAATCCCAGCACT	94756	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			C		
GAM1364	LOC91250	5'	CTGTAATCCCAGTTACT	65323	
			AGTAGCTGGGATTACAG		
			TCATTGACCCTAATGTC		
			—		
GAM1364	LOC91250	5'	TCTGTAATCCCCGCACT	65330	A T
			AGT GC GGGATTACAGA		
			TCA CG CCCTAATGTCT		
			C		
GAM1364	LOC91286	3'	ATGCCTGTAATCCTAGCCACT	65451	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGATCCTAATGTC GTA		
			C C		
GAM1364	LOC91380	3'	CTGTAATCCCAACTAC	65860	C
			GTAG TGGGATTACAG		
			CATC ACCCTAATGTC		
			A		
GAM1364	LOC91380	3'	TGCCTGTAATCCCGGCACT	65864	A A
			AGT GCTGGGATTACAG CA		

			TCA CGGCCCTAATGTC GT		
			— C		
GAM1364	LOC91380	3'	TGTAATCCCAGCTACTCA 65865	C	
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1364	LOC91574	3'	TCTGTAATCCCAGCACT 66521	A	
			AGT GCTGGGATTACAGA		
			TCA CGACCCTAATGTCT		
			—		
GAM1364	LOC91664	3'	CTGTAATCCCAGCACT 66872	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC91750	3'	CTGTAATCCCAGCACT 67061	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC91796	5'	ATGCCTGTAATCCCAGCACT 67210	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	LOC91812	3'	GTGCCTGTAATCCCAGCTACTC 67242	C	A
	A		A AGTAGCTGGGATTACAG CAT		
			A TCATCGACCCTAATGTC GTG		
			C C		
GAM1364	LOC91813	3'	GTGCCTGTAATCCCAGCTACTC 67259	C	A
	A		A AGTAGCTGGGATTACAG CAT		
			A TCATCGACCCTAATGTC GTG		
			C C		
GAM1364	LOC91963	5'	CTGTAATCCCAGCTACTTG 67694	—	
			CA GTAGCTGGGATTACAG		
			GT CATCGACCCTAATGTC		
			T		
GAM1364	LOC92078	3'	CTATAATCCCAGCACT 67980	A	C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1364	LOC92078	3'	TGTAATCCCAACTACTCA 67990	C	C
			A AGTAG TGGGATTACA		

			A TCATC ACCCTAATGT		
			C A		
GAM1364	LOC92228	3'	CTGTAATCCCAGCACT	68541	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC92267	3'	CTGTAATCCCAGCACT	68613	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC92270	5'	CTGTAATCCCAGCACT	68630	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC92270	5'	TGTAATCCCAGCTACTCA	68637	C
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1364	LOC92283	3'	ATGCCTGTAATCCCAGCACT	68744	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	LOC92299	3'	CTGTAATCCCAGCACT	68809	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1364	LOC92405	3'	ATGTCTGTAATCCCAGCTACT	69192	
			AGTAGCTGGGATTACAGACAT		
			TCATCGACCCTAATGTCTGTA		
			—		
GAM1364	LOC92421	3'	ATGCCTATAATCCCAGCACT	69212	A C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1364	LOC92465	5'	ATGCCTGTAATCCCAGCACT	69402	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1364	LOC92465	3'	ATGTCTGTAGTCCCAGCCACTC	69403	C A
	A		A AGT GCTGGGATTACAGACAT		

A TCA CGACCCTGATGTCTGTA  
 C C  
 GAM1364 LOC92465 3' CTGTAATCCCAGCACT 69406 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1364 LOC92465 5' TGTAATCCCAGCTACTCA 69415 C  
 A AGTAGCTGGGATTACA  
 | |||||  
 A TCATCGACCCTAATGT  
 C  
 GAM1364 LOC92466 3' ATGCCTGTAATCCCAGCACT 69422 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||  
 TCA CGACCCTAATGTC GTA  
 — C  
 GAM1364 LOC92482 3' CTGTAATCCCAGCACT 69488 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1364 LOC92573 5' CTGTAATCCCAGCACT 69805 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1364 LOC92573 5' TCTGTAATCCCAGCTTCT 69811 T  
 AG AGCTGGGATTACAGA  
 || |||||  
 TC TCGACCCTAATGTCT  
 T  
 GAM1364 LOC92661 5' ATGCCTATAATCCCAGC 70078 C A  
 GCTGGGATTA AG CAT  
 ||||| || |||  
 CGACCCTAAT TC GTA  
 A C  
 GAM1364 LOC92771 3' TGTAATCCCAGCTACTCA 53078 C  
 A AGTAGCTGGGATTACA  
 | |||||  
 A TCATCGACCCTAATGT  
 C  
 GAM1364 LOC93132 5' CTGTAATCCCAGCACT 71488 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1364 LOC93613 3' ATGCCTGTAATCCCAGCACT 72694 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||



TCA CGACCCTAATGTC GTA  
 — C  
 GAM1364 LOC93613 3' CTGTAATCCCAGCTATT 72698  
 AGTAGCTGGGATTACAG  
 |||||  
 TTATCGACCCTAATGTC

GAM1364 LOC96597 5' CTGTAATCCCAGCTACTCA 66913 C  
 A AGTAGCTGGGATTACAG  
 | |||||  
 A TCATCGACCCTAATGTC  
 C

GAM1365 CALB1 3' AAATGCTAATGTAATCATTTAT 17020 C ACAA  
 C GA AAATGATTG AGCATTT  
 || ||||| |||||  
 CT TTTACTAAT TCGTAAA  
 A GTAA

GAM1365 CYP1B1 3' AAATGCTTCATTTGTATGTCA 3649 A TG T CAA  
 TGACA A A TGA AGCATTT  
 |||| | ||| |||||  
 ACTGT T T ACT TCGTAAA  
 A GT T —

GAM1365 GBE1 3' TTTGAATCATTTGTCA 3852 GA  
 TGACAAATGATT CAAA  
 ||||| |||||  
 ACTGTTTACTAA GTTT

GAM1365 NSF 3' AAATGCTGTTCTCAATCATTGT 63068 A CAA\_  
 CA TGACAA TGATTGA AGCATTT  
 ||||| ||||| |||||  
 ACTGTT ACTAACT TCGTAAA  
 — CTTG

GAM1365 TSN 3' ATGCTTTGCTTTGTC 16105 TGATTGA  
 GACAAA CAAAGCAT  
 ||||| |||||  
 CTGTTT GTTTCGTA  
 C —

GAM1365 AMOT 3' TTGCCAATCATTTGCA 55731 A A  
 TG CAAATGATTG CAA  
 || ||||| |||||  
 AC GTTTACTAAC GTT  
 — C

GAM1365 FLJ12592 5' GCTGTCAACCATTGGTCA 49696 A A AA  
 TGAC AATG TTGACA GC  
 ||| ||| ||||| ||  
 ACTG TTAC AACTGT CG  
 G C —

GAM1365 FLJ14437 3' AAATGCTTTGAGATCATTGGTC 50823 A GA  
 A TGAC AATGATT CAAAGCATTT  
 ||| ||||| |||||

ACTG TTAGTAG GTTTCGTAAA  
 G A\_  
 GAM1365 FLJ23018 3' TGTCAGCCATTGTCA 45655 AT  
 TGACAAATG TGACA  
 ||||| ||||  
 ACTGTTTAC ACTGT  
 CG  
 GAM1365 ITM3 3' AAATGCTTTGTATATTTTCTCA 48160 C TGATTG  
 TGA AAA ACAAAGCATT  
 ||| ||| |||||  
 ACT TTT TGTTTCGTAAA  
 C TATA\_  
 GAM1365 KIAA1240 5' AAATGCTTTATCAATTTTGT 66726 T C  
 CAAA GATTGA AAAGCATT  
 ||| ||||| |||||  
 GTTT TTAAC TTTTCGTAAA  
 \_ A  
 GAM1365 KIAA1866 3' TTGCCACTCATTTGTCA 60938 T A  
 TGACAAATGA TG CAA  
 ||||| || |||  
 ACTGTTTACT AC GTT  
 C C  
 GAM1365 KRT6 3' AAATGCTTTGTCTGTCA 82217 T  
 TGAT GACAAAGCATT  
 ||| |||||  
 ACTG CTGTTTCGTAAA  
 T  
 GAM1365 MOCS3 3' AAATGCTTTCTAAATCATTTTC 27145 C GAC  
 A TGA AAATGATT AAAGCATT  
 ||| ||||| |||||  
 ACT TTTACTAA TTTTCGTAAA  
 \_ ATC  
 GAM1365 SLC5A7 3' AAATGCTTTGTTTTTC 41501 TT  
 GA GACAAAGCATT  
 || |||||  
 CT TTGTTTCGTAAA  
 T\_  
 GAM1365 YME1L1 3' AAATGCTTTGTCAATCATTTGT 57774  
 CA TGACAAATGATTGACAAAGCATT  
 |||||  
 ACTGTTTACTAACTGTTTCGTAAA  
 GAM1365 YME1L1 3' AAATGCTTTGTCAATCATTTGT 57785  
 CA TGACAAATGATTGACAAAGCATT  
 |||||  
 ACTGTTTACTAACTGTTTCGTAAA  
 GAM1365 YME1L1 3' AAATGCTTTGTCAATCATTTGT 26524  
 CA TGACAAATGATTGACAAAGCATT  
 |||||

ACTGTTTACTAACTGTTTCGTAAA

GAM1365 ZFP95 3' AAATGCTTTAGTTAGCATCTTC 59024 CAA A \_  
A TGA ATG TTGAC AAAGCATT  
||| ||| ||||| |||||  
ACT TAC GATTG TTTTCGTAAA  
TC\_ \_ A

GAM1365 ZFP95 3' AAATGCTTTAGTTAGCATCTTC 27380 CAA A \_  
A TGA ATG TTGAC AAAGCATT  
||| ||| ||||| |||||  
ACT TAC GATTG TTTTCGTAAA  
TC\_ \_ A

GAM1365 LOC115294 3' AAATGCTTTGTAGACTATTT 73011 A G  
AAATG TT ACAAAGCATT  
||||| ||| |||||  
TTTAT AG TGTTTCGTAAA  
C A

GAM1365 LOC144509 5' GCTACCATCATTTGTCA 76862 TGACAA  
TGACAAATGAT AGC  
||||||| |||  
ACTGTTTACTA TCG  
CCA\_\_

GAM1365 LOC151790 3' TGCTTTTATCTATCATCTGTCA 80346 A T C\_  
TGACA ATGAT GA AAAGCA  
||||| ||||| ||| |||||  
ACTGT TACTA CT TTTTCGT  
C T AT

GAM1366 ADH7 5' GGCACAAGCTGCTGTTATA 5420 CAC ACA  
TATAACAGC CTTG GTC  
||||||| ||||| |||  
ATATTGTCG GAAC CGG  
TC\_ A\_\_

GAM1366 BACH2 3' ACTAGTTTGGTAACTGTTA 41481 CC TT \_  
TAACAG ACC GAC AGT  
||||| ||| ||| |||  
ATTGTC TGG TTG TCA  
AA T\_ A

GAM1366 G6PT1 3' AAGGTGACTTGTTATA 7596 \_C  
TATAACA G CACCTT  
||||||| | |||||  
ATATTGT C GTGGAA  
T A

GAM1366 H3F3B 3' GACTTGTTGGGTAGCTATTA 18021 C C T \_  
TAA AGC ACCT GACA GTC  
||| ||| ||||| ||||| |||  
ATT TCG TGGG TTGT CAG  
A A \_ T

GAM1366 MNT 3' ACTGTATTCTAGTGGCTGTTCA 39701 T CTTG\_  
A AACAGCCAC ACAGT  
| ||||| |||||

		A TTGTCGGTG	TGTCA	
		C	ATCTTA	
GAM1366 PHEMX	3'	GACCATTTCAGGCTGTTG	19120	ACCT CA_
		TAACAGCC TGA	GTC	
		GTTGTCGG	ACT CAG	
		_____	TAC	
GAM1366 PHEMX	3'	GACCATTTCAGGCTGTTG	57360	ACCT CA_
		TAACAGCC TGA	GTC	
		GTTGTCGG	ACT CAG	
		_____	TAC	
GAM1366 PHEMX	3'	GACCATTTCAGGCTGTTG	57365	ACCT CA_
		TAACAGCC TGA	GTC	
		GTTGTCGG	ACT CAG	
		_____	TAC	
GAM1366 PHEMX	3'	GACCATTTCAGGCTGTTG	57369	ACCT CA_
		TAACAGCC TGA	GTC	
		GTTGTCGG	ACT CAG	
		_____	TAC	
GAM1366 RFXAP	3'	GACTTAATCATGGCTGTT	5014	CCT C__
		AACAGCCA TGA	AGTC	
		TTGTCGGT	ACT TCAG	
		_____	AAT	
GAM1366 SMN1	3'	ACTGGTGGACATGGCTGTTCA	43153	T ____ TTGA
		A AACAGCCA CC	CAGT	
		A TTGTCGGT	GG GTCA	
		C	ACA TG__	
GAM1366 SMN1	3'	ACTGGTGGACATGGCTGTTCA	4429	T ____ TTGA
		A AACAGCCA CC	CAGT	
		A TTGTCGGT	GG GTCA	
		C	ACA TG__	
GAM1366 SMT3H1	3'	GACTGTCACTTGCTGTTA	59959	CACCT
		TAACAGC	TGACAGTC	
		ATTGTCG	ACTGTCAG	
		TTC__		
GAM1366 SNAI1	3'	GACTGTGAGTAATGGCTGT	19969	CC_ G
		ACAGCCA TT	ACAGTC	
		TGTCGGT	GA TGTCAG	
		AAT	G	
GAM1366 SS18 A	3'	ACTGTGTTTCAAATGGACTGTT	18881	_ CC ____
		TAACAG CCA	TTGA CAGT	

ATTGTC GGT AACT GTCA  
 A A\_ TTGT  
 GAM1366 UPK1B 3' CAAGGTGCCTGTTATA 22716 C  
 TATAACAG CACCTTG  
 ||||| |||||  
 ATATTGTC GTGGAAC  
 C  
 GAM1366 DKFZP434A0225 3' ACTGTTGGAATGGCTGTT 93904 CC TG  
 AACAGCCA T ACAGT  
 ||||| | ||||  
 TTGTCGGT G TGTCA  
 AA GT  
 GAM1366 FLJ10462 3' ACTGTCAAATGTCACCTGTTAT 36138 CC\_ C\_  
 G TATAACAG AC TTGACAGT  
 ||||| || |||||  
 GTATTGTC TG AACTGTCA  
 CAC TA  
 GAM1366 FLJ11175 3' GACCAATGTTATGGCTGTT 37134 CCT \_\_\_\_  
 AACAGCCA TGACA GTC  
 ||||| |||| ||  
 TTGTCGGT ATTGT CAG  
 \_\_\_\_ AAC  
 GAM1366 FLJ13491 5' GACTTCCAGCAGCTGTTA 44885 CAC T C  
 TAACAGC CT GA AGTC  
 ||||| || || ||||  
 ATTGTCG GA CT TCAG  
 AC\_ C \_  
 GAM1366 FLJ20079 3' GTTAAGATGGCTGATATA 34498 A C  
 TATA CAGCCA CTTGAC  
 ||| ||||| |||||  
 ATAT GTCGGT GAATTG  
 A A  
 GAM1366 FLJ23518 3' CGACTGTCAAGTGAATGAGCTG 45306 \_ C\_\_\_\_ |||  
 TTG AACAGC CA CTTGACAGTC G  
 ||||| || ||||| ||  
 TTGTCG GT GAACTGTCAG C  
 A AAGT |||  
 GAM1366 FLJ32334 3' ACTGCCCTCAGGGTGGCTGTTA 57980 \_\_\_\_  
 TAACAGCCACCTTGA CAGT  
 ||||| ||||| ||||  
 ATTGTCGGTGGGACT GTCA  
 CCC  
 GAM1366 KIAA0418 5' GACCACAGTGTGGCTGT 27556 C ACA  
 ACAGCCAC TTG GTC  
 ||||| || ||  
 TGTCGGTG GAC CAG  
 T AC\_  
 GAM1366 KIAA0438 3' TTAAGATAGCTGTTGTA 29075 CAC  
 TATAACAGC CTTGA  
 ||||| |||||

	ATGTTGTCG GAATT	
	ATA	
GAM1366 KIAA0459	3' GACTGTTGTCAGCAGCTGTTA 60996	CACCT_
	TAACAGC TGACAGTC	
	ATTGTCG GTTGTGTCAG	
	ACGACT	
GAM1366 KIAA1280	5' GACTGTCCGTGGTGGCTGT 69716	TT_
	ACAGCCACC GACAGTC	
	TGTCGGTGG CTGTGTCAG	
	TGC	
GAM1366 KIAA1376	3' GACTGTCAAGATTGT 63622	CCAC
	ACAG CTTGACAGTC	
	TGTT GAACTGTGTCAG	
	A_	
GAM1366 KIAA1962	3' ACAGTTAAAAGCTGTTATA 81915	CACC A
	TATAACAGC TTGAC GT	
	ATATTGTCG AATTG CA	
	AA_ A	
GAM1366 MGC19606	3' TCAGGATGGGGCTGTCATA 53042	A AC_
	TATACAGCC CTTGA	
	ATA TGTCGG GGA CT	
	C GGTA	
GAM1366 MGC3178	3' ACTGTCAAGAGTCTTGT 47981	CC _
	ACAG AC CTTGACAGT	
	TGTT TG GAACTGTCA	
	C_ A	
GAM1366 MPPE1	5' AAGCATGGCTGTTATA 43559	C_
	TATAACAGCCA CTT	
	ATATTGTCGGT GAA	
	AC	
GAM1366 NMP200	3' GACGTGGTGGTGGCTGTT 27174	TTGA _
	AACAGCCACC CA GTC	
	TTGTCGGTGG GT CAG	
	TG_ G	
GAM1366 NUDT13	3' ACTGCCAAAATGTGCCTGTTGT 63212	C C_ A
A	TATAACAG CAC TTG CAGT	
	ATGTTGTC GTG AAC GTCA	
	C TAA C	
GAM1366 NYD-SP25	5' ACTGTCAAGGTGTCCATTGTA 53183	CAGC
	TATAA CACCTTGACAGT	

ATGTT GTGGA ACTGTCA  
 ACCT  
 GAM1366 PC4 3' ACTGTCAAATGTTAT 22011 GCCACC  
 ATAACA TTGACAGT  
 ||||| |||||  
 TATTGT AACTGTCA  
 AA\_\_\_\_  
 GAM1366 PDE1C 3' GACTGTCAATGCCGTTA 17220 A CACC  
 TAAC GC TTGACAGTC  
 ||| || |||||  
 ATTG CG AACTGTCAG  
 C T\_\_\_\_  
 GAM1366 PEPP3 3' GACTGCCTGGGAGATGGCTGTT 30040 \_\_\_\_ TGA  
 A TAACAGCCA CCT CAGTC  
 ||||| || |||||  
 ATTGTCGGT GGG GTCAG  
 AGA TCC  
 GAM1366 PRO1992 5' TAAGGTGGCTAGTATA 26060 AC  
 TATA AGCCACCTTG  
 ||| |||||  
 ATAT TCGGTGGAAT  
 GA  
 GAM1366 PTGES2 3' GACCCTCAGTGGCTGT 46881 CT CA  
 ACAGCCAC TGA GTC  
 ||||| ||| |||  
 TGTCGGTG ACT CAG  
 \_\_\_\_ CC  
 GAM1366 SRP9 3' GACTGTCACTAACTGTTATG 79192 CCACCT  
 TATAACAG TGACAGTC  
 ||||| |||||  
 GTATTGTC ACTGTCAG  
 AAC\_\_\_\_  
 GAM1366 SYNE-1 5' GACCATCAAGGTGCTG 30968 C CA  
 CAGC ACCTTGA GTC  
 ||| ||||| |||  
 GTCG TGGA ACT CAG  
 \_\_\_\_ AC  
 GAM1366 ZNF185 3' ACTCAGAGAGGTGGCTATTG 23105 C GAC\_  
 TAA AGCCACCTT AGT  
 ||| ||||| |||  
 GTT TCGGTGGAG TCA  
 A AGAC  
 GAM1366 LOC130507 3' GACTTCCATGGCTTGTTATA 74951 \_\_\_\_ CCT AC  
 TATAACA GCCA TG AGTC  
 ||||| ||| || |||  
 ATATTGT CGGT AC TCAG  
 T \_\_\_\_ CT  
 GAM1366 LOC134359 5' ACTGTCAGGTTGCCGT 75182 A C T  
 AC GC ACCT GACAGT  
 || || ||| |||||

	TG CG TGG A CTGTCA		
	C T _		
GAM1366 LOC143914 5'	GACTGTCAAAGTGGTTGT 76612	C	
	ACAGCCAC TTGACAGTC		
	TGTTGGTG AACTGTCAG		
	A		
GAM1366 LOC144465 5'	ACTATCAAGTGAACCACTGTTA 76851	C_	C C
TG	TATAACAG CAC TTGA AGT		
	GTATTGTC GTG AACT TCA		
	ACCAA _ A		
GAM1366 LOC148078 3'	GACCCGTAAGTGGCTGT 84112	C	ACA
	ACAGCCAC TTG GTC		
	TGTCGGTG AAT CAG		
	_ GCC		
GAM1366 LOC150378 5'	GACTGATGTGAGGTGGCT 79745	A_	
	AGCCACCTTG CAGTC		
	TCGGTGGAGT GTCAG		
	GTA		
GAM1366 LOC153727 5'	GACTGTCAAACTTGTT 86152	CCACC	
	AACAG TTGACAGTC		
	TTGTT AACTGTCAG		
	CAA_		
GAM1366 LOC163231 5'	TCAGCAGGTGGCTGTTA 82443	_	
	TAACAGCCACCT TGA		
	ATTGTCGGTGGA ACT		
	CG		
GAM1366 LOC201931 3'	ACTTCTGTGGCTGTTTA 89108	T	CTT C
	A AACAGCCAC GA AGT		
	A TTGTCGGTG CT TCA		
	T T_ _		
GAM1366 LOC253698 3'	ACTGTCAAGAGCCGTGTTA 94887	_	CAC
	TAACA GC CTTGACAGT		
	ATTGT CG GAACTGTCA		
	GC A_		
GAM1366 LOC256158 5'	GACAGGCGAGGTGGCCGTCATG 97665	A A	ACA
	TAT AC GCCACCTTG GTC		
	GTA TG CGGTGGAGC CAG		
	C C GGA		
GAM1366 LOC90906 3'	CAAGGTGGCTGTTATA 64293		
	TATAACAGCCACCTTG		



ATATTGTCGGTGGAAC

GAM1366 LOC91012 3' TAAGGTGGTTGCTATA 64643 A  
TATA CAGCCACCTTG  
|||||  
ATAT GTTGGTGGAAT  
C

GAM1367 CLCN5 5' TGAAATACCTAAGCTGCTCCAA 3595  
TTGGAGCAG GTTTCA  
||||| |||||  
AACCTCGTC TAAAGT  
GAATCCA

GAM1367 FLRT2 5' ATTGAAAAATGAGGTCTGC 25056 GT CTC  
GCAG TTCATT CAAT  
||||| |||||  
CGTC GAGTAA GTTA  
TG AAA

GAM1367 IL17 3' TGGGGAAAATGAAACCCTCC 9333 CA  
GGAG GGTTTCAT TCTCCA  
||||| |||||  
CCTC CCAAAGTA AGGGGT  
AA

GAM1367 NLGN1 5' TGAAGATGCTGCTCCAA 30026 G  
TTGGAGCAG TTTCA  
||||| |||||  
AACCTCGTC GAAGT  
GTA

GAM1367 POLG 3' GTGATAAACCTGCTCCAA 10682  
TTGGAGCAGGTT TCAT  
||||| |||||  
AACCTCGTCCAA AGTG  
AT

GAM1367 TPK1 3' GGAGAACCTGTCCAA 42384 G TTCAT  
TTGGA CAGGT TCTCC  
||||| |||||  
AACCT GTCCA AGAGG

GAM1367 C1orf8 5' GAGAATGAAACCCTC 16832 CA  
GAG GGTTTCATTCTC  
||| |||||  
CTC CCAAAGTAAGAG

GAM1367 CLIC6 3' TGGAGAACATGTTCCAA 82536 G TTCAT  
TTGGAGCA GT TCTCCA  
||||| || |||||  
AACCTTGT CA AGAGGT  
A

GAM1367 CLIPR-59 3' TGGAGAATTTCAATGCCCCGA 31374 A GGTTTC  
TTGG GCA ATTCTCCA  
||||| |||||

AGCC CGT TAAGAGGT  
 C AACTT\_  
 GAM1367 DKFZP547L112 3' TGGAGAACTCTTGCTCCA 66532 TTTCA  
 TGGAGCAGG TTCTCCA  
 ||||| |||||  
 ACCTCGTTC AAGAGGT  
 TC\_\_\_\_  
 GAM1367 EPS8R3 5' GGACCACCTGCTCCAA 55701 TTCATTG  
 TTGGAGCAGGT TCC  
 ||||| |||  
 AACCTCGTCCA AGG  
 CC\_\_\_\_  
 GAM1367 EPS8R3 5' GGACCACCTGCTCCAA 57404 TTCATTG  
 TTGGAGCAGGT TCC  
 ||||| |||  
 AACCTCGTCCA AGG  
 CC\_\_\_\_  
 GAM1367 FLJ20552 3' AGAACAAAACCTGCTCCAA 35389 G CA  
 TTGGAGCAG TTT TTCT  
 ||||| ||| |||  
 AACCTCGTC AAA AAGA  
 \_ AC  
 GAM1367 FLJ22865 5' TGGAGAAAACCTGCTCTAA 47071 GTTTCA  
 TTGGAGCAG TTCTCCA  
 ||||| |||||  
 AATCTCGTC AAGAGGT  
 AA\_\_\_\_  
 GAM1367 KIAA0372 5' ATTGAAATTTGTTACCTACTCC 27663 C TT TTCTC  
 AA TTGGAG AGGT CA CAAT  
 ||||| ||| |||  
 AACCTC TCCA GT GTTA  
 A TT TAAA  
 GAM1367 PRO0132 5' ATGAAACCACTCCAA 26101 CA  
 TTGGAG GGTTTCAT  
 ||||| |||||  
 AACCTC CCAAAGTA  
 A\_  
 GAM1367 TEX27 3' AGAGTGGAACCCGCTGCAA 41658 G A  
 TTG AGC GGTTTCATTCT  
 ||| ||| |||||  
 AAC TCG CCAAGGTGAGA  
 G C  
 GAM1367 LOC149373 3' ATTGGGGTGATGATACCCACCC 79312 AGCA T \_  
 CAA TTGG GGT TCATT CTCCAAT  
 ||| ||| ||||| |||||  
 AACC CCA AGTAG GGGGTTA  
 CCAC T T  
 GAM1367 LOC152687 3' TTGGAGAATATTGCTCC 80643 GTTTC  
 GGAGCAG ATTCTCCAA  
 ||||| |||||

CCTCGTT TAAGAGGTT  
 A\_\_\_\_  
 GAM1367 LOC51202 3' ATTGGAGAATGAAACCTGCTCC 33017  
 AA TTGGAGCAGGTTTCATTCTCCAAT  
 |||||  
 AACCTCGTCCAAAGTAAGAGGTTA

GAM1368 ACADL 3' CTCTTTCTTCAAACAA 7841 T T  
 TTGTTTGA GA GGAG  
 ||||| || ||||  
 AACAAACT CT TCTC  
 T T

GAM1368 CSPG3 3' CTCTCCATCACCAAAT 15229 A  
 GTTTG TGATGGAGAG  
 |||| |||||  
 TAAAC ACTACCTCTC  
 C

GAM1368 MPO 3' CTCCTTAAACAAGAGTT 4201 A TGAT  
 AACTC TTGTTTGA GGAG  
 |||| ||||| ||||  
 TTGAG AACAAATT CCTC

GAM1368 PCDHB7 3' CTCTTGAAGTCAAGCAAT 38443 GAT\_  
 ATTGTTTGAT GGAG  
 ||||| ||||  
 TAACGAACTG TCTC  
 AAGT

GAM1368 PSG7 3' TCCCCATCATGATGAG 10941 GTTTG A  
 CTCATT ATGATGG GA  
 |||| ||||| ||  
 GAGTAG TACTACC CT  
 C

GAM1368 XYLB 3' CTCCCACCCAAACAATGGG 17559 ATGAT  
 CTCATTGTTTG GGAG  
 ||||| ||||  
 GGGTAACAAAC CCTC  
 CCAC\_

GAM1368 YWHAZ 3' CTCCCCACCCTGAAAAAATGA 12702 G GATGA\_ A  
 GTT AACTCATT TTT TGG GAG  
 ||||| || ||||  
 TTGAGTAA AAA ACC CTC  
 A AGTCCC C

GAM1368 FLJ12154 3' CTCCACTGTGAACAGTAAG 41670 C G GA  
 CT ATTGTTT AT TGGAG  
 || ||||| || ||||  
 GA TGACAAG TG ACCTC  
 A \_ TC

GAM1368 FLJ20580 3' CCCCCATCACTCAATGAG 35424 TT AT  
 CTCATTG TGATG GG  
 ||||| |||| ||

		GAGTAAC ACTAC CC		
		TC CC		
GAM1368	FLJ20986	5' CATCACAAACAATAAGTT 44544	C	A
		AACT ATTGTTTG TGATG		
		TTGA TAACAAAC ACTAC		
		A _		
GAM1368	KIAA0794	3' TCTCCCTAAAGAATGAGTT 80415	G	ATGAT
		AACTCATT TTTG GGAGA		
		TTGAGTAA AAAT CCTCT		
		G C__		
GAM1368	KIAA1157	3' CTCCCCATCATCTTTGTGCAA 72242	TT__	A
		TTGT GATGATGG GAG		
		AACG CTACTION CTC		
		TGTTT C		
GAM1368	KIAA1189	3' CTATTATCACCAAACAATATGT 72042	TC	A _
	T	AAC ATTGTTTG TGATGG AG		
		TTG TAACAAAC ACTATT TC		
		TA C A		
GAM1368	PRO1048	3' CTCCATCATCAAAACGCAGT 37516	__	
		ATTGT TTGATGATGGAG		
		TGACG AACTACTACCTC		
		CAA		
GAM1368	RGS17	3' CCACACAAAACAATGA 24840	GA	A
		TCATTGTTT TG TGG		
		AGTAACAAA AC ACC		
		AC _		
GAM1368	LOC143038	3' CCATTAGCTAAACAAT 76452	A_	
		ATTGTTTG TGATGG		
		TAACAAAT ATTACC		
		CG		
GAM1368	LOC158263	3' CTCTCCATCACCCAGTGA 81846	TTTGA	
		TCATTG TGATGGAGAG		
		AGTGAC ACTACCTCTC		
		CC__		
GAM1368	LOC162333	5' CTCTCCATCAAGAATGA 87130	TG	GA
		T TTT TGATGGAGAG		
		A AAG ACTACCTCTC		
		GT A_		
GAM1368	LOC201799	3' CCTATCAAATAATGA 89057	AT	
		TCATTGTTTGATG GG		

AGTAATAAACTAT CC

GAM1368 LOC50999 3' CTCCTTACCTAACAATGA 32100 TGA T  
TCATTGTT TGA GGAG  
||||||| ||| |||  
AGTAACAA ATT CCTC  
TCC \_

GAM1368 LOC89919 3' CTATTCACCAACAATGAGTT 60720 T A \_  
AACTCATTGTT G TGA TGG  
||||||| | ||| |||  
TTGAGTAACAA C ACT ATC  
\_C T

GAM1369 FCMD 3' ACAACTATTCACCCTACCT 22086 C GTTAGT  
AG TAGGG ATAGTTGT  
|| ||||| |||||  
TC ATCCC TATCAACA  
C ACT\_\_

GAM1369 MPDZ 3' CAACCCAACCCCTAGCT 13817 AGTATA  
AGCTAGGGGTT GTTG  
||||||| |||  
TCGATCCCCAA CAAC  
CC\_\_

GAM1369 C12orf4 3' ACTGGTGATCAACCCCTAACTT 39809 C AGTA\_\_  
A TAAG TAGGGGTT TAGT  
||| ||||| |||  
ATTC ATCCCCAA GTCA  
A CTAGTG

GAM1369 DKFZP434F0318 3' CAACCATTCCCTAACTCC 48005 T\_\_ A  
GGGGTTAG AT GTTG  
||||||| || |||  
CCTCAATC TA CAAC  
CCT C

GAM1369 U5-100K 3' ACAATCCAACCTCCCTAGC 59678 GTT ATA  
GCTAGGG AGT GTTGT  
||||||| ||| |||||  
CGATCCC TCA TAACA  
\_\_ ACC

GAM1370 AF1Q 3' GTGTCCCTTCTTCACACCTACT 22366 CT CAT \_  
AG GG TGTGAAGGA ACAC  
|| || ||||| |||  
TC CC ACACCTTCTT TGTG  
AT \_\_ CCC

GAM1370 ANKH 3' TTCTAATGCCAGGTT 53994 G T  
AA CTGGCATTG GAA  
|| ||||| |||  
TT GACCGTAAT CTT  
G \_

GAM1370 ANXA8 3' GTGTGAGCACAATGCCA 73081 AAGGA  
TGGCATTGTG ACAC  
||||||| |||

			ACCGTAACAC	TGTG		
			GAG__			
GAM1370	ANXA8	3'	GTGTGAGCACAATGCCA	7894	AAGGA	
			TGGCATTGTG	ACAC		
			ACCGTAACAC	TGTG		
			GAG__			
GAM1370	CD59	3'	TCCTGAGCAGTGCCAGCTT	5215	GA	
			AAGCTGGCATTGT	AGGA		
			TTCGACCGTGACG	TCCT		
			AG			
GAM1370	DUSP2	3'	GGTGCCCCTCTGCCTGCCTGC	15348	T TT GA AA	
			GC GGCA GT AGG CACC			
			CG CCGT CG TCC GTGG			
			T C_ TC CC			
GAM1370	EFNB2	3'	GGTGCCCCAGGATGCCACGC	14575	_ G AA AA	
			GC TGGCATT TG GG CACC			
			CG ACCGTAG AC CC GTGG			
			C G _ C_			
GAM1370	FANCC	3'	GTACTCCTGGTGCCCGC	70526	T GTGA AC	
			GC GGCATT AGGA AC			
			CG CCGTGG TCCT TG			
			C _ _ CA			
GAM1370	FGF8	3'	TCCCCACAATGCCAG	52550	AA	
			CTGGCATTGTG GGA			
			GACCGTAACAC CCT			
			C_			
GAM1370	FGF8	3'	TCCCCACAATGCCAG	52551	AA	
			CTGGCATTGTG GGA			
			GACCGTAACAC CCT			
			C_			
GAM1370	FGF8	3'	TCCCCACAATGCCAG	52552	AA	
			CTGGCATTGTG GGA			
			GACCGTAACAC CCT			
			C_			
GAM1370	FGF8	3'	TCCCCACAATGCCAG	20386	AA	
			CTGGCATTGTG GGA			
			GACCGTAACAC CCT			
			C_			
GAM1370	GLS	3'	TGTTCCCTTAGCTGCACCAG	29791	CATT G	
			CTGG GT AAGGAACA			

			GACC CG TTCCTTGT			
			ACGT A			
GAM1370	GYG2	3'	TGTTTCAGGGAAACAATGTCAGC 14051		GAAG__	
	TT		AAGCTGGCATTGT GAACA			
			TTCGACTGTAACA CTTGT			
			AAGGGA			
GAM1370	LZTFL1	3'	CCATCACAATGCAGCTT 39753	G	A	
			AAGCTG CATTGTGA GG			
			TTCGAC GTAACACT CC			
			— A			
GAM1370	MAN2A2	3'	GGTATTCCTTCAGCCA 20399	ATTG	C	
			TGGC TGAAGGAA ACC			
			ACCG ACTTCCTT TGG			
			— A			
GAM1370	MAPRE2	3'	GTGTTCTCCATCAGC 26542	GCATT	A	
			GCTG GTG AGGAACAC			
			CGAC TAC TCCTTGTG			
			— C			
GAM1370	MX1	3'	TGTCCCTTCACAAACCCA 10146	CA	A	
			TGG TTGTGAAGG ACA			
			ACC AACACTTCC TGT			
			CA C			
GAM1370	MYO1D	3'	GGTGCCAGGGAGCACTGCCAGC 71770	T	GAA__ AA	
	TT		AAGCTGGCA TGT GG CACC			
			TTCGACCGT ACG CC GTGG			
			C AGGGA —			
GAM1370	PFKFB4	3'	GGTGCCCCTTCAGGCCTGCT 15873	T	ATTG	AA
			AGC GGC TGAAGG CACC			
			TCG CCG ACTTCC GTGG			
			T G__ CC			
GAM1370	PXMP3	3'	TGCTCCTTCATTTTACTACTT 4349	C	CATT	A
			AAG TGG GTGAAGGA CA			
			TTC ATC TACTTCCT GT			
			— ATTT C			
GAM1370	RGS5	3'	GTATTCCTTCACTATTTTCGCTT 13238	T	C	T C
			AAGC GG AT GTGAAGGAA AC			
			TTCG CT TA CACTTCCTT TG			
			— T T A			
GAM1370	SET	3'	GTGCTCTAATGCCAAGTT 11557	—	GTGAA	A
			AGCT GGCATT GGA CAC			

TTGA CCGTAA TCT GTG  
 A \_\_\_\_\_ C  
 GAM1370 SFRP5 3' TCCTTGCCCTGCCAGCT 11581 TT G  
 AGCTGGCA GT AAGGA  
 ||||| || ||||  
 TCGACCGT CG TTCCT  
 CC \_  
 GAM1370 SLC24A1 5' GGTGTTCCCTGCTGTCCAGCTT 16377 C T GAA  
 AAGCTGG AT GT GGAACACC  
 ||||| || || |||||  
 TTCGACC TG CG CCTTGTGG  
 \_ T TC\_  
 GAM1370 TBL1X 3' TGTTCCCTCCGCCACT 18941 C ATT T  
 AG TGGC G GAAGGAACA  
 || ||| | |||||  
 TC ACCG C CTTCTTGT  
 - - - -  
 GAM1370 UBE1 3' GTGTTCCCTCATCATCC 12464 C T A  
 GG AT GTGA GGAACAC  
 || || || || |||||  
 CC TA TACT CCTTGTG  
 \_ C C  
 GAM1370 VBP1 3' GTGTCTTTGCAATGCCA 12572 TG GA  
 TGGCATTG AAG ACAC  
 ||||| || |||  
 ACCGTAAC TTC TGTG  
 GT \_  
 GAM1370 C11orf21 3' GGTGCCCCCAATGCCAGGCT 26245 \_ TGAA AA  
 AGC TGGCATTG GG CACC  
 || ||||| || |||  
 TCG ACCGTAAC CC GTGG  
 G C\_\_ CC  
 GAM1370 CDH22 3' GGTGTTCAATAAATGCTAGC 41158 GTGAAG  
 GCTGGCATT GAACACC  
 ||||| |||||  
 CGATCGTAA CTTGTGG  
 ATAA\_  
 GAM1370 CDIPT 3' GTGTCCCCACCGCCCACTT 20890 CT ATT AA A  
 AAG GGC GTG GGA CAC  
 || || || || |||  
 TTC CCG CAC CCT GTG  
 AC C\_\_ C\_ \_  
 GAM1370 COL12A1 3' GGTGTTCCCTCACCCACCAGCT 15183 CATT A  
 AGCTGG GTGA GGAACACC  
 |||| ||| |||||  
 TCGACC CACT CCTTGTGG  
 ACC\_ \_  
 GAM1370 COL12A1 3' GGTGTTCCCTCACCCACCAGCT 54665 CATT A  
 AGCTGG GTGA GGAACACC  
 |||| ||| |||||



TCGACC CACT CCTTGTGG  
ACC\_ \_  
GAM1370 CRMP5 3' TGCCCTCGCCAGCTT 39296 ATTGT A AA  
AAGCTGGC GA GG CA  
||||| || ||  
TTCGACCG CT CC GT  
\_ \_ CC  
GAM1370 FLJ10849 3' TGTTCCTCGCATTACCTGCTT 36759 T CAT\_ AA  
AAGC GG TGTG GGAACA  
|||| ||| |||||  
TTCG CC ACGC CCTTGT  
T ACTT \_  
GAM1370 FLJ10932 3' GGTGCTCCTTCACAATGGCCCG 36896 T \_ A  
T GC GGC ATTGTGAAGGA CACC  
|| ||| ||||| |||  
TG CCG TAACACTTCCT GTGG  
C G C  
GAM1370 FLJ11703 3' GTGCCCCTTCACGGTACC 46384 C AA  
GG ATTGTGAAGG CAC  
|| ||||| |||  
CC TGGCACTTCC GTG  
A CC  
GAM1370 FLJ12649 3' GTGTTCTTTTGGCTGCCAGT 44783 TTGT  
GCTGGCA GAAGGAACAC  
||||| |||||  
TGACCGT TTTCCTTGTG  
CGGT  
GAM1370 FLJ13224 3' TCCCAACAATGCCACCT 45622 C GAA  
AG TGGCATTGT GGA  
|| ||||| |||  
TC ACCGTAACA CCT  
C AC\_  
GAM1370 FLJ23537 3' TGTCCAGATGCCAGC 46028 GTGAA A  
GCTGGCATT GGA CA  
||||| ||| ||  
CGACCGTAG CCT GT  
A\_ \_  
GAM1370 FLJ32865 3' TGTCCCCCAGGTCCTGCCAGCT 58188 TTG\_ AA A  
AGCTGGCA TG GGA CA  
||||| || ||| ||  
TCGACCGT AC CCT GT  
CCTGG CC \_  
GAM1370 KCNE4 3' GGCATTCTTCACAGTGGGTT 54755 GG CA  
AGCT CATTGTGAAGGAA CC  
||| ||||| ||| ||  
TTGG GTGACACTTCCTT GG  
\_ AC  
GAM1370 KIAA0185 3' GGTGTTCTTCAGCCTCAGC 62973 \_ ATTG  
GCT GGC TGAAGGAACACC  
||| ||| ||||| |||

CGA CCG ACTTCCTTGTGG  
CT \_\_\_\_

GAM1370 KIAA0459 3' CTTCCAATGCCAGTTT 60993 T  
AAGCTGGCATTG GAAG  
||||||| |||  
TTTGACCGTAAC CTTC

GAM1370 KIAA0513 3' CCCTCGCTCTGATGCCAACT 28349 C \_\_\_\_ A  
AG TGGCATT GTGA GG  
|| ||||| ||| ||  
TC ACCGTAG CGCT CC  
A TCT C

GAM1370 KIAA0984 3' TTTTACAAAACCAGCT 65535 CA  
AGCTGG TTGTGAAG  
||||| |||||  
TCGACC AACATTTT  
AA

GAM1370 MGC11335 3' TGTTCTGTTGCCAGGTT 48021 G TTGTGA  
AA CTGGCA AGGAACA  
|| ||||| |||||  
TT GACCGT TCCTTGT  
G TG\_\_\_\_

GAM1370 MGC17998 3' TTCAGTACATTGCCAGCT 58745 T AAG  
AGCTGGCA TGTG GAA  
||||||| ||| |||  
TCGACCGT ACAT CTT  
T GA\_

GAM1370 MYO18B 5' GGTGCTCCTTCGCTCCTGCTT 50888 T CATT A  
AAGC GG GTGAAGGA CACC  
||| || ||||| |||  
TTCG CC CGCTTCCT GTGG  
T T\_\_\_\_ C

GAM1370 NIN283 3' TTCCTTCAGGCTGCTACT 50079 C TTG  
AG TGGCA TGAAGGAA  
|| ||||| |||||  
TC ATCGT ACTTCCTT  
\_ CGG

GAM1370 NK4 3' GGTTCTGCGCAGCT 14872 AT A\_ A  
GGC TGTG AGGAAC C  
||| ||| ||||| |  
TCG ACGC TCCTTG G  
\_ CG C

GAM1370 POLR3F 5' TTCCTTCACAGAGTTGCCA 59941 \_\_\_\_  
TGGCA TTGTGAAGGAA  
||||| |||||  
ACCGT GACACTTCCTT  
TGA

GAM1370 PPP1R16A 5' CCCCCGAGGGTGCCAGTCC 51863 A G\_ AA  
A GCTGGCATT TG GG  
| ||||| || ||

C TGACCGTGG GC CC  
 C GA CC  
 GAM1370 PRO0650 5' TTCACGTGCAATGCCAAGTT 26217 \_ AAG  
 AGCT GGCATTGTG GAA  
 |||| ||||| ||  
 TTGA CCGTAACGT CTT  
 A GCA  
 GAM1370 PRO0800 3' TTCCTCCTTTGCCAGCT 37744 TTGT A  
 AGCTGGCA GA GGAA  
 ||||| || |||  
 TCGACCGT CT CCTT  
 TTC\_ \_  
 GAM1370 PRO2000 5' TTCCTTCATTTGCTCCAGTT 26065 CATT\_  
 AGCTGG GTGAAGGAA  
 ||||| |||||  
 TTGACC TACTTCCTT  
 TCGTT  
 GAM1370 SDF1 3' TGCTCCCTCACATGTC 90863 T A A  
 GGCAT GTGA GGA CA  
 |||| ||| ||| ||  
 CTGTA CACT CCT GT  
 \_ C C  
 GAM1370 SSTK 3' GGCGTCCCTTCCCAACCAGC 49345 CA T A A  
 GCTGG TTG GAAGG AC CC  
 |||| ||| ||||| || ||  
 CGACC AAC CTTCC TG GG  
 \_ C C C  
 GAM1370 STRIN 3' TTTCAACAATACCACTT 32772 C C  
 AAG TGG ATTGTGAAG  
 ||| ||| |||||  
 TTC ACC TAACACTTT  
 \_ A  
 GAM1370 TXI1 5' CTTTCGCACTGCCAAGC 37369 \_ T  
 GCT GGCA TGTGAAGG  
 ||| ||| |||||  
 CGA CCGT ACGCTTTC  
 A C  
 GAM1370 ZNF281 3' CCTTTCAATGCAACTT 25025 CTG T  
 AAG GCATTG GAAGG  
 ||| ||||| |||||  
 TTC CGTAAC TTTCC  
 AA\_ \_  
 GAM1370 LOC119188 5' TGTCCCACAATGCCA 73963 AA A  
 TGGCATTGTG GGA CA  
 ||||| ||| ||  
 ACCGTAACAC CCT GT  
 \_ \_  
 GAM1370 LOC138399 5' GTGCTGACATGCCAGC 75330 T GA GA  
 GCTGGCAT GT AG AC  
 ||||| || || ||

	CGACCGTA CA TC TG	
	_ G_ G_	
GAM1370 LOC142972 3'	GTGTGAGCACAATGCCA 65130	AAGGA
	TGGCATTGTG ACAC	
	ACCGTAACAC TGTG	
	GAG__	
GAM1370 LOC143158 5'	GTGTTCTCCCACTGCCA 76491	T T A
	TGGCA TG GA GGAACAC	
	ACCGT AC CT CCTTGTG	
	C C _	
GAM1370 LOC145988 5'	GTGCCCTCTGCCAGCT 77612	TTGT A AA
	AGCTGGCA GA GG CAC	
	TCGACCGT CT CC GTG	
	_____ CC	
GAM1370 LOC146229 3'	TTCAGTGAATGCCAGCT 77784	G__
	AGCTGGCATT TGAA	
	TCGACCGTAA ACTT	
	GTG	
GAM1370 LOC146506 3'	GTGCTCCCATGCCAGCTT 77935	T TGAA A
	AAGCTGGCAT G GGA CAC	
	TTCGACCGTA C CCT GTG	
	_____ C	
GAM1370 LOC148397 3'	TCCTTCACAATGACAGC 78823	G
	GCTG CATTGTGAAGGA	
	CGAC GTAACACTTCCT	
	A	
GAM1370 LOC149670 5'	TTCTCTCCAATGCCAGC 79494	T AG
	GCTGGCATTG GA GAA	
	CGACCGTAAC CT CTT	
	_ CT	
GAM1370 LOC149803 3'	CATAAAATGCCAGCTT 79539	__
	AAGCTGGCAT TGTG	
	TTCGACCGTA ATAC	
	AA	
GAM1370 LOC150113 5'	TGTCCTTCAGACGCCAGCTT 87217	A G A
	AAGCTGGC TT TGAAGGA CA	
	TTCGACCG AG ACTTCCT GT	
	C _ _	
GAM1370 LOC159184 5'	CCTTCATGCAGCAGCTT 60047	__ TTG
	AAGCTG GCA TGAAGG	

TTCGAC CGT ACTTCC  
 GA \_\_\_\_  
 GAM1370 LOC160942 5' GTGTCCCCAGGATGCAGCCAGC 87073 \_\_\_\_ G AA A  
 TT AAGCTGGC ATT TG GGA CAC  
 ||||| ||| ||| |||  
 TTCGACCG TAG AC CCT GTG  
 ACG G C\_ \_  
 GAM1370 LOC162083 5' TCCTGTCCAGCGCCAGCTT 82338 A T \_  
 AAGCTGGC TTG GA AGGA  
 ||||| ||| ||| |||  
 TTCGACCG GAC CT TCCT  
 C \_ G  
 GAM1370 LOC196759 3' GTGCTGACATGCCAGC 87518 T GA GA  
 GCTGGCAT GT AG AC  
 ||||| || || ||  
 CGACCGTA CA TC TG  
 \_ G\_ G\_  
 GAM1370 LOC201164 3' GTGTTAGGCAAGCCAGCTT 88123 A GAAGG  
 AAGCTGGC TTGT AACAC  
 ||||| ||| ||| |||  
 TTCGACCG AACG TTGTG  
 \_ GA\_\_\_\_  
 GAM1370 LOC219988 5' GTGTTCCCTCCTGTTCTCAGC 91626 CATTGT A  
 GCTGG GA GGAACAC  
 |||| || |||||  
 CGACT CT CCTTGTG  
 CTTGTC \_  
 GAM1370 LOC220565 3' GTGTAACAGTGCCAGC 90753 GAAGGA  
 GCTGGCATTGT ACAC  
 ||||| ||| |||  
 CGACCGTGACA TGTG  
 A\_\_\_\_  
 GAM1370 LOC221964 3' TTTATCCAATGCCAACT 93985 C T AG  
 AG TGGCATTG GA GA  
 || ||||| || ||  
 TC ACCGTAAC CT TT  
 A \_ AT  
 GAM1370 LOC253150 3' TGTTCCCTGGATGTTGCCAGCT 95520 TT GA \_  
 T AAGCTGGCA GT AGG AACA  
 ||||| || ||| |||  
 TTCGACCGT TA TCC TTGT  
 TG GG C  
 GAM1370 LOC51133 5' GGTATTCCTTCATCCACAGC 32283 GCATT C  
 GCTG GTGAAGGAA ACC  
 ||| ||||| |||  
 CGAC TACTTCCTT TGG  
 ACC\_\_ A  
 GAM1370 LOC55893 5' GGC GTTCCCATGATGCCAGGCT 37863 \_ TG AA A  
 AGC TGGCAT TG GGAAC CC  
 || ||||| || ||||| ||

			TCG ACCGTA AC CCTTG GG		
			G GT _ C		
GAM1370	LOC93259	5'	TCCTTTGTGCCTAGCT 71827	_	TGT
			AGCT GGCAT GAAGGA		
			TCGA CCGTG TTTCCT		
			T _		
GAM1371	A1BG	3'	TCCCAAAGTGCTGGGAT 55436		A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			-		
GAM1371	ABCC1	3'	CTGCCCCTGGTGCCCTGAGA 39124	C _	TTG
			TC CA GCACT AGGGGCAG		
			AG GT CGTGG TCCCGTC		
			A CC _		
GAM1371	ABCC1	3'	CTGCCCCTGGTGCCCTGAGA 39132	C _	TTG
			TC CA GCACT AGGGGCAG		
			AG GT CGTGG TCCCGTC		
			A CC _		
GAM1371	ABCC1	3'	CTGCCCCTGGTGCCCTGAGA 17179	C _	TTG
			TC CA GCACT AGGGGCAG		
			AG GT CGTGG TCCCGTC		
			A CC _		
GAM1371	ACADSB	3'	TCCCAAAGTGCTGGGAT 7849		A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			-		
GAM1371	ADAM19	3'	CTGCCCCAGCTCTGAGA 52706	C CA	TTGA
			TC CAG CT GGGGCAG		
			AG GTC GA CCGTC		
			A TC _		
GAM1371	ADAMTS4	3'	TCCCAAAGTGCTGGGAT 17518		A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			-		
GAM1371	ADAMTS4	3'	TCCCAAAGTGCTGGGAT 17519		A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			-		
GAM1371	ADCY6	5'	CCTCACAAAGTGCTGGGAT 30924		A
			ATCCCAGCACTTTG GGGG		

		TAGGGTCGTGAAAC CTCC			
		A			
GAM1371	ADCY6	5'	CCTTCCAAAGTGCTGGGAT	30927	AG
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC TCC			
		CT			
GAM1371	ADRA1A	3'	TCCCAAAGTGCTGGGAT	52791	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
		—			
GAM1371	AIM1	3'	TCCCAAATGCTGGGAT	91829	C A
		ATCCCAGCA TTTG GGG			
		TAGGGTCGT AAAC CCT			
		A —			
GAM1371	ALDH1B1	3'	TCCCAAAGTGCTGGGAT	5499	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
		—			
GAM1371	APAF1	3'	TCCCAAAGTGCTGAGAT	6740	C A
		ATC CAGCACTTTG GGG			
		TAG GTCGTGAAAC CCT			
		A —			
GAM1371	APAF1	3'	TCCCAAAGTGCTGAGAT	25049	C A
		ATC CAGCACTTTG GGG			
		TAG GTCGTGAAAC CCT			
		A —			
GAM1371	APM1	3'	TCCCAAAGTGCTGGGAT	16602	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
		—			
GAM1371	APM1	3'	TCCCAAAGTGCTGGGAT	16603	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
		—			
GAM1371	APOL1	3'	TCCCAAAGTGCTGGGAT	13353	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
		—			
GAM1371	APPL	3'	TCCCAAAGTGCTGGGAT	23931	A
		ATCCCAGCACTTTG GGG			

GAM1371	AQP6	3'	TCCCAAAGTGCTGGGAT	7962		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	AQP6	3'	TCCCAAAGTGCTGGGAT	53942		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	ARSF	5'	TCCCAAAGTGCTGGGAT	64603		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	ATP7A	3'	TCCCAAAGTGCTGGGAT	3530		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	ATP8B2	3'	TCCCAAAGTGCTGAGAT	65238	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A			
GAM1371	AXL	3'	TCCCAAAGTGCTGAGAT	8108	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A			
GAM1371	AXL	3'	TCCCAAAGTGCTGAGAT	41605	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A			
GAM1371	B4GALT5	3'	TCCCAAAGTGCTGGGAT	16513		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	BAZ2B	5'	TCCCAAAGTGCTGGGAT	25623		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	BCL10	3'	TCCCAAAGTGCTGGGAT	14063		A
			ATCCCAGCACTTTG GGG			



Accession	Gene	Strand	Sequence	Position	Orientation	Quality
GAM1371	CAMLG	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	8245	+	A
GAM1371	CASP8	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	6921	+	A
GAM1371	CASP8	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	52927	+	A
GAM1371	CASP8	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	52938	+	A
GAM1371	CASP8	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	52953	+	A
GAM1371	CBFA2T2	3'	TCCCAAAGTGCCAGGAT ATCC GCACTTTG GGG               TAGG CGTGAAAC CCT AC	17477	+	CA A
GAM1371	CCNF	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	8327	+	A
GAM1371	CDH1	3'	GCCCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGGGC               TAGGGTCGTGAAAC CCCC C	15146	+	A
GAM1371	CHRNA4	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	5635	+	A
GAM1371	CIAS1	5'	TCTCAAAGTGCTGGGAT ATCCCAGCACTTTGAGG 	16905	+	

TAGGGTCGTGAAACTCT

GAM1371	CLECSF11	5'	TCCCAAAGTGCTGAGAT	55278	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A			
			—			
GAM1371	CLECSF12	3'	TCCCAAAGTGCTGGGAT	76702		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			—			
GAM1371	COX15	3'	TCCCAAAGTGCTGAGAT	54321	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A			
			—			
GAM1371	CXCL16	3'	TCCCAAAGTGCTGGGAT	41926		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			—			
GAM1371	CYP1A2	3'	TCCCAAAGTGCTGGGAT	69130		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			—			
GAM1371	CYP1A2	3'	TCCCAAAGTGCTGGGAT	5710		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			—			
GAM1371	CYP2B6	3'	TCCCAAAGTGCTGGGAT	5741		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			—			
GAM1371	CYP4F3	3'	TCCCAAAGTGCTGGGAT	6126		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			—			
GAM1371	CYP51	3'	TCCCAAAGTGCTGGGAT	5788		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			—			
GAM1371	DFFB	3'	TCCCAAAGTGCTGGGAT	87396		A
			ATCCCAGCACTTTG GGG			

Accession	Gene	Strand	Sequence	Position	Context	Quality
GAM1371	DFFB	3'	TCCCAAAGTGCTGGGATG TATCCAGCACTTTG GGG             GTAGGGTCGTGAAAC CCT	87397		A
GAM1371	DHFR	3'	TCCCAAAGTGCTGGGAT ATCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	5817		A
GAM1371	DISC1	3'	TCCCAAAGTGCTGAGAT ATC CAGCACTTTG GGG               TAG GTCGTGAAAC CCT A	37894	C	A
GAM1371	DNASE1L1	5'	TCCCAAAGTGCTGGGAT ATCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	22082		A
GAM1371	DSC3	3'	TCCCAAAGTGCTGGGAT ATCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	44346		A
GAM1371	DSC3	3'	TCCCAAAGTGCTGGGAT ATCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	8681		A
GAM1371	DSCR3	3'	TCCCAAAGTGCTGAGAT ATC CAGCACTTTG GGG               TAG GTCGTGAAAC CCT A	20194	C	A
GAM1371	DSCR3	3'	TCCCAAAGTGCTGGGAT ATCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	20195		A
GAM1371	EIF2S3	3'	CCTCACAAAGTGCTGGGAT ATCCAGCACTTTG GGGG             TAGGGTCGTGAAAC CTCC A	7415		A
GAM1371	EPB72	3'	TCTGCCTCCAAAGTGCTGG CCAGCACTTTG GGGGCAGA 	14612		A

GGTCGTGAAAC CTCCGTCT

GAM1371	EVC	3'	CCCCAAAGTGCTGAGAT	27292	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCC			
			A			
GAM1371	FANCF	3'	TCCCAAAGTGCTGGGAT	42681		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			A			
GAM1371	FCAR	3'	TCCCAAAGTGCTGAGAT	55753	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A			
GAM1371	FCAR	3'	TCCCAAAGTGCTGAGAT	55764	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A			
GAM1371	FCAR	3'	TCCCAAAGTGCTGAGAT	55775	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A			
GAM1371	FCAR	3'	TCCCAAAGTGCTGAGAT	55786	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A			
GAM1371	FCAR	3'	TCCCAAAGTGCTGGGAT	55803		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			A			
GAM1371	FCAR	3'	TCCCAAAGTGCTGAGAT	8858	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A			
GAM1371	FCGR2A	3'	TCCCAAAGTGCTGGGATG	79265		A
			TATCCCAGCACTTTG GGG			
			GTAGGGTCGTGAAAC CCT			
			A			
GAM1371	FEZ1	3'	TCCCAAAGTGCTGGGAT	42581		A
			ATCCCAGCACTTTG GGG			

TAGGGTCGTGAAAC CCT

GAM1371 FGF5 3' CCCCAAAGTGCTGGGAT 52481 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCC

GAM1371 FGF5 3' CCCCAAAGTGCTGGGAT 15535 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCC

GAM1371 FGFR3 3' CTGCCCTCAGAGACTG 3770 CA  
CAG CTTTGAGGGGCAG  
||| |||||  
GTC GAGACTCCCCGTC  
A

GAM1371 FUT1 3' TCCCAAAGTGCTGGGAT 3797 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 FY      5' CTGCCCCTCAATTCCCAGGA 8971      CAGCACT  
                         TCC    TTGAGGGGCAG  
                         |||    |||||  
                         AGG    AACTCCCCGTC  
                         ACCCTT\_

GAM1371 FZD4 3' TCCCAAAGTGCTGGGAT 24152 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 GHR 3' TCCCAAAGTGCTGGGAT 3889 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 GLTSCR1 5' TCCCAAAGTGCTGAGAT 31677 C A  
ATC CAGCACTTTG GGG  
||| ||||| |||  
TAG GTCGTGAAAC CCT  
A

GAM1371 GNA11 3' CTGCCCCCAAAAAAGCAGAGG 76098 CCA AC\_ A  
TA TATC GC TTTG GGGGCAG  
|||| || ||| |||||  
ATGG CG AAAC CCCCCTC  
AGA AAA C

GAM1371 GRAF 3' CCCCAAAGTGCTGGGAT 30553 A  
ATCCCAGCACTTTG GGG  
|||||

TAGGGTCGTGAAAC CCC

GAM1371 GRM7	5'	TCCAAAAGTGCTGGGAT	5947	GA
		ATCCCAGCACTTT GGG		
		TAGGGTCGTGAAA CCT		
		A_		
GAM1371 HCS	3'	CCCCAAAGTGCTGGGAT	38463	A
		ATCCCAGCACTTTG GGG		
		TAGGGTCGTGAAAC CCC		
		-		
GAM1371 HCS	3'	TCCCAAAGTGCTGGGAT	38479	A
		ATCCCAGCACTTTG GGG		
		TAGGGTCGTGAAAC CCT		
		-		
GAM1371 HLCS	5'	TCCCAAAGTGCTGGGAT	4677	A
		ATCCCAGCACTTTG GGG		
		TAGGGTCGTGAAAC CCT		
		-		
GAM1371 HPCA	3'	CTGCCTTTTAGCACTTGGATA	9254	C CACT
		TATCC AG TTGAGGGGCAG		
		ATAGG TC GATTTTCCGTC		
		T AC__		
GAM1371 HSD17B1	5'	TCCCAAAGTGCTGGGAT	4691	A
		ATCCCAGCACTTTG GGG		
		TAGGGTCGTGAAAC CCT		
		-		
GAM1371 HTR1D	3'	TCCCAAAGTGCTGGGAT	6003	A
		ATCCCAGCACTTTG GGG		
		TAGGGTCGTGAAAC CCT		
		-		
GAM1371 HUNK	3'	TCCCAAAGTGCTGAGAT	27462	C A
		ATC CAGCACTTTG GGG		
		TAG GTCGTGAAAC CCT		
		A _		
GAM1371 ICMT	3'	TCCCAAAGTGCTGGGAT	24820	A
		ATCCCAGCACTTTG GGG		
		TAGGGTCGTGAAAC CCT		
		-		
GAM1371 IL11	3'	TCCCAAAGTGCTGGGAT	5338	A
		ATCCCAGCACTTTG GGG		

Accession	Gene	Strand	Sequence	Start	End	Score	Match
GAM1371	IMPA2	5'	CCTTGCAAAGTGCTGGGAT ATCCCAGCACTTTG             TAGGGTCGTGAAAC GT	95237			AG
GAM1371	INMT	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG             TAGGGTCGTGAAAC CCT	22278			A
GAM1371	LNK	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG             TAGGGTCGTGAAAC CCT	18472			A
GAM1371	LTB4R	5'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG             TAGGGTCGTGAAAC CCT	5654			A
GAM1371	LYZ	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG             TAGGGTCGTGAAAC CCT	4109			A
GAM1371	LZTS1	3'	TCCCAAAGTGCTGAGAT ATC CAGCACTTTG               TAG GTCGTGAAAC A	40697		C	A
GAM1371	MATN3	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG             TAGGGTCGTGAAAC CCT	9939			A
GAM1371	MDM2	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG             TAGGGTCGTGAAAC CCT	9973			A
GAM1371	MDM2	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG             TAGGGTCGTGAAAC CCT	22511			A
GAM1371	MDM2	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG             TAGGGTCGTGAAAC CCT	22515			A

GAM1371	MDM2	3'	TCCCAAAGTGCTGGGAT	22519	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	MDM2	3'	TCCCAAAGTGCTGGGAT	22523	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	MEFV	3'	TCCCAAAGTGCTGGGAT	4155	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	MHC2TA	3'	TCCCAAAGTGCTGGGAT	4191	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	MHC2TA	3'	TCCCAAAGTGCTGGGAT	4192	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	MICB	3'	TCCCAAAGTGCTGGGAT	19835	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	MPL T	3'	TCTGCCTCCCAAAGTGCTGGGA	18158	A
			ATCCCAGCACTTTG GGGGCAGA		
			TAGGGTCGTGAAAC CTCCGTCT		
			C		
GAM1371	MTR	3'	TCCCAAATGCTGGGAT	4220	C A
			ATCCCAGCA TTTG GGG		
			TAGGGTCGT AAAC CCT		
			A		
GAM1371	NCOA6	5'	TCCACAAAGTGCTGGGAT	25978	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			A		
GAM1371	NDRG3	3'	TCCCAAAGTGCTGGGAT	49307	A
			ATCCCAGCACTTTG GGG		



GAM1371	NONO	3'	TCCCCAAAATGCTGGGAT	82022	C	A
			ATCCCAGCA TTTG GGG			
			TAGGGTCGT AAAC CCT			
			A _			
GAM1371	NQO1	3'	TCCCCAAAGTGCTGGGAT	6169		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	PCDHA9	3'	TCCCCAAAATGCTGGGAT	25770	C	A
			ATCCCAGCA TTTG GGG			
			TAGGGTCGT AAAC CCT			
			A _			
GAM1371	PCDHA9	3'	TCCCCAAAGTGCTGGGAT	25771		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	PCDHB11	3'	TCCCCAAAGTGCTGGGAT	38424		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	PER2	3'	TCCCCAAAGTGCTGGGAT	43045		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	PIGR	3'	TCTCAAAGTACTGGGAT	72608	C	
			ATCCCAG ACTTTGAGG			
			TAGGGTC TGAAACTCT			
			A			
GAM1371	PIGR	3'	TCTGCCTCCCAAAGTGCTGGGA	72609		A
	T		ATCCCAGCACTTTG GGGGCAGA			
			TAGGGTCGTGAAAC CTCCGTCT			
			C			
GAM1371	PIK3C2B	3'	TCCCCAAAGTGCTGGGAT	10577		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	PIK3CD	3'	TCCCCAAAGTGCTGGGAT	17250		A
			ATCCCAGCACTTTG GGG			

GAM1371	PLA2G10	5'	CCTTCCAAAGTGCTGGGAT	13085		AG
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC TCC			
			CT			
GAM1371	PMCHL1	3'	TCCCAAAGTGCTGGGAT	49075		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	PPEF2	3'	TCCCAAAGTGCTGGGAT	20677		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	PPID	3'	TCCCAAAGTGCTGGGAT	87438		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	PPP2R5B	5'	TCTGCCCCCAGGACTGGG	20712	CAC	A
			CCCAG TTTG GGGGCAGA			
			GGGTC GGAC CCCCCTCT			
			A__ C			
GAM1371	PRKR	3'	TCCCAAAGTGCTGGGAT	10887		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	PSG6	3'	TCCCAAAGTGCTAGGAT	10939	C	A
			ATCC AGCACTTTG GGG			
			TAGG TCGTGAAAC CCT			
			A			
GAM1371	PTGES	3'	TCCCAAAGTGCTGGGATG	16864		A
			TATCCAGCACTTTG GGG			
			GTAGGGTCGTGAAAC CCT			
GAM1371	PTGIS	3'	TCCCAAAGTGCTAGGAT	6344	C	A
			ATCC AGCACTTTG GGG			
			TAGG TCGTGAAAC CCT			
			A			
GAM1371	PTGIS	3'	TCCCAAAGTGCTGGGAT	6345		A
			ATCCCAGCACTTTG GGG			

TAGGGTCGTGAAAC CCT

GAM1371	PTPN1	3'	CCCCCCCACCTTTGGGAT	11049	CACTT	A
			ATCCCAG TG GGGGC			
			TAGGGTT AC CCCCC			
			TCC__ C			
GAM1371	PTPN18	3'	TCCCAAAGTGCTGAGAT	26871	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A _			
GAM1371	RAB36	3'	TCCCAAAGTGCTGGGAT	16975		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	RAB36	3'	TCCCAAAGTGCTGGGAT	16976		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	RABL2A	3'	TCCCAAAGTGCTGGGAT	25505		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	RABL2B	3'	TCCCAAAGTGCTGGGAT	23006		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	RAD1	5'	TCCCAAAGCGCTGGGAT	55914	A	A
			ATCCCAGC CTTTG GGG			
			TAGGGTCG GAAAC CCT			
			C _			
GAM1371	RAI3	3'	TCCCAAAGTGCTGGGATG	14287		A
			TATCCCAGCACTTTG GGG			
			GTAGGGTCGTGAAAC CCT			
			_			
GAM1371	RGS9	5'	TCCCAAAGTGCTGGGAT	13838		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	RHD	3'	TCCCAAAGTGCTGGGAT	32318		A
			ATCCCAGCACTTTG GGG			

Accession	Gene	Strand	Sequence	Position	Start	End	RefSeq	GenBank
GAM1371	RHD	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	32627			A	
GAM1371	RPH3AL	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	22757			A	
GAM1371	RPP30	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	21172			A	
GAM1371	SCML2	3'	CCTTGCAAAATGCTGGGAT ATCCCAGCA TTTG GGG               TAGGGTCGT AAAC TCC A GT	20313			C	AG
GAM1371	SEDL	3'	CCACCTCAGGAAGTGCTGGGAT ATCCCAGCACTT TGAGG GG                 TAGGGTCGTGAA ACTCC CC GG A	27329				
GAM1371	SEDL	3'	TCCCAAAGTGCTAGGAT ATCC AGCACTTTG GGG               TAGG TCGTGAAAC CCT A	27363	C		A	
GAM1371	SEDL	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	27364			A	
GAM1371	SEPN1	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	66381			A	
GAM1371	SERPINB9	3'	TCCCAAAGTGCTAGGAT ATCC AGCACTTTG GGG               TAGG TCGTGAAAC CCT A	14766	C		A	
GAM1371	SERPINB9	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG 	14767			A	

GAM1371	SH3BP2	3'	TCCCAAAGTGCTGGGAT	11613		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	SHOX	3'	TCCCAAAGTGCTGGGATG	22546		A
			TATCCCAGCACTTTG GGG			
			GTAGGGTCGTGAAAC CCT			
GAM1371	SIL	5'	TCCCAAAATGCTGGGAT	11698	C	A
			ATCCCAGCA TTTG GGG			
			TAGGGTCGT AAAC CCT			
			A _			
GAM1371	SLA2	3'	TCCCAAAGTGCTGGGAT	49908		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	SLC14A2	5'	TCTCAAAGTGCTGGGAT	23141		
			ATCCCAGCACTTTGAGG			
			TAGGGTCGTGAAACTCT			
GAM1371	SLC24A1	3'	TCCCAAAGTGCTGGGAT	16379		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	SLC39A1	3'	TCTATTTTTTAAAGTGC	27054		GC
			GCACTTTGAGGG AGA			
			CGTGAAATTTTT TCT			
			A _			
GAM1371	SNX15	3'	TCCCAAAGTGCTGAGAT	73750	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A _			
GAM1371	SPN	3'	TCCCAAAGTGCTGAGAT	11929	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A _			
GAM1371	SULT2B1	5'	TCCCAAAGTGCTGGGAT	16032		A
			ATCCCAGCACTTTG GGG			

Accession	Protein	Position	Sequence	Start	End	Score	Identity
GAM1371	TAPBP	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	12136			A
GAM1371	TAPBP	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	12137			A
GAM1371	TBXA2R	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	6506			A
GAM1371	TERF1	3'	TCCCAAAGTGCTGAGAT ATC CAGCACTTTG GGG               TAG GTCGTGAAAC CCT A	33980	C		A
GAM1371	TERF2	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	18949			A
GAM1371	TES	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	72010			A
GAM1371	TIMM23	3'	TCCCAAAGTGCCGAGAT ATC GCACTTTG GGG               TAG CGTGAAAC CCT AGC	60142	CCA		A
GAM1371	TIMM44	3'	TCTGCCCCCCAGCTCTGCCAGGA TCC GCA TTG GGGGCAGA                   AGG CGT GAC CCCC GTCT AC CTC	71422	CA	CT_	A
GAM1371	TIRAP	3'	CCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCC	53569			A
GAM1371	TNFRSF10B	3'	TCCGAAAGTGCTGGGAT ATCCCAGCACTTT GGG 	13881			GA

			TAGGGTTCGTGAAA CCT			
			G_			
GAM1371	TNFRSF9	3'	TCCCAAAGTGCTGGGAT 7794	A		
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	TPMT	3'	CCACCCAAAGTGCTAGGAT 4535	C	A	_
			ATCC AGCACTTTG GG GG			
			TAGG TCGTGAAAC CC CC			
			A _ A			
GAM1371	TPMT	3'	TCCCAAAGTGCTGGGAT 4546	A		
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	TRAF5	3'	TCCCAAAGTGCTGAGAT 16088	C	A	
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A -			
GAM1371	TRPM6	3'	TCCCAAAGTGCTGGGAT 34547	A		
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	TRPV1	3'	TCCCAAAGTGCTGGGAT 38097	A		
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	TRPV1	3'	TCCCAAAGTGCTGGGAT 38098	A		
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	TRPV1	3'	TCCCAAAGTGCTGGGAT 54815	A		
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	TRPV1	3'	TCCCAAAGTGCTGGGAT 54816	A		
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	TRPV1	3'	TCCCAAAGTGCTGGGAT 54847	A		
			ATCCCAGCACTTTG GGG			

GAM1371	TRPV1	3'	TCCCAAAGTGCTGGGAT	54848		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	TRPV1	3'	TCCCAAAGTGCTGGGAT	54880		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	TRPV1	3'	TCCCAAAGTGCTGGGAT	54881		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	TSG	3'	CTGCCCAAAGTGCTG	40233	GAG	
			CAGCACTTT GGGCAG			
			GTCGTGAAA CCGTC			
GAM1371	TUFT1	3'	TCCCAAAGTGCTAGGAT	39266	C	A
			ATCC AGCACTTTG GGG			
			TAGG TCGTGAAAC CCT			
			A			
GAM1371	UGDH	3'	TCCCAAAGTGCTGGGAT	12546		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	UMPS	3'	TCTCAAAGTGCTGGGAT	4559		
			ATCCCAGCACTTTGAGG			
			TAGGGTCGTGAAACTCT			
GAM1371	VENTX2	3'	TCCCAAAGTGCTGGGAT	27119		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	VIPR2	3'	TCCCAAAGTGCTGGGAT	12616		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	WHSC1	5'	TCCCAAAGTGCTGGGAT	23670		A
			ATCCCAGCACTTTG GGG			



Accession	Gene	Strand	Sequence	Position	RefSeq	GenBank
GAM1371	WHSC1	5'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	29918		A
GAM1371	WHSC1	5'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	55836		A
GAM1371	WHSC1	5'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	55853		A
GAM1371	XRCC2	3'	TCCCAAAGTGCTAGGAT ATCC AGCACTTTG GGG               TAGG TCGTGAAAC CCT A	18330	C	A
GAM1371	YES1	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	18357		A
GAM1371	ZNF133	5'	TCCCAAATGCTGGGAT ATCCCAGCA TTTG GGG               TAGGGTCGT AAAC CCT A	12842	C	A
GAM1371	ZNF135	3'	TCCACATGTGCTGGGA TCCCAGCAC TG GGG              AGGGTCGTG AC CCT T_ A	12855	TT	A
GAM1371	ZNF74	5'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	12804		A
GAM1371	AAK1	3'	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	29855		A
GAM1371	AD7C-NTP	3'	CCTTCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG 	27163		AG

				TAGGGTCGTGAAAC	TCC			
				CT				
GAM1371	AF9Q34	3'	TCTGCCCCCTGCAGCTGG	50741	ACTT			
			CCAGC	TG AGGGGCAGA				
			GGTCG	AC TCCCCGTCT				
			_____	G				
GAM1371	APOL2	3'	TCCCAAAGTGCTGGGAT	48054		A		
			ATCCCAGCACTTTG	GGG				
			TAGGGTCGTGAAAC	CCT				
			_____					
GAM1371	ARHF	3'	TCCCAAAGTGCTGGGAT	38749		A		
			ATCCCAGCACTTTG	GGG				
			TAGGGTCGTGAAAC	CCT				
			_____					
GAM1371	ARHGAP11A	3'	TCCCAAAGTGCTGGGAT	28802		A		
			ATCCCAGCACTTTG	GGG				
			TAGGGTCGTGAAAC	CCT				
			_____					
GAM1371	ARPP-19	3'	TCCCAAAGTGCTGGGAT	21804		A		
			ATCCCAGCACTTTG	GGG				
			TAGGGTCGTGAAAC	CCT				
			_____					
GAM1371	ASB16	3'	TCCCAAAGTGCTGGGAT	69945		A		
			ATCCCAGCACTTTG	GGG				
			TAGGGTCGTGAAAC	CCT				
			_____					
GAM1371	ASE-1	3'	TCCCAAAGTGCTAGGATA	23955	C		A	
			TATCC	AGCACTTTG	GGG			
			ATAGG	TCGTGAAAC	CCT			
			A	_____				
GAM1371	BAG5	3'	TCGGCCCCC	AAAGTGCTGGGA	16854		A	A
	T		ATCCCAGCACTTTG	GGGGC	GA			
			TAGGGTCGTGAAAC	CCCCG	CT			
			C	G				
GAM1371	BAGE	3'	CCTTCCAAAGTGCCGAGAT	6808	CCA		AG	
			ATC	GCACTTTG	GGG			
			TAG	CGTGAAAC	TCC			
			AGC	CT				
GAM1371	BNIP-S	3'	TCCCAAAGTGCCGAGAT	56268	CCA		A	
			ATC	GCACTTTG	GGG			

		TAG CGTGAAAC CCT			
		AGC _			
GAM1371	BTN3A1	3'	TCCCAAAGTGCTGGGAT	22926	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			-		
GAM1371	C1orf24	3'	TCCCAAAGTGCTGGGAT	53727	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			-		
GAM1371	C1orf34	3'	TCTGCCTCCTAAAGTGCTGGGA	60681	A
	T		ATCCCAGCACTTTG GGGGCAGA		
			TAGGGTCGTGAAAT CTCCGTCT		
			C		
GAM1371	C1QTNF6	3'	TCTCAAAATGCTGGGAT	49153	C
			ATCCCAGCA TTTGAGG		
			TAGGGTCGT AAACCTCT		
			A		
GAM1371	C20orf142	3'	TCCCAAAGTGCTGGGAT	74787	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			-		
GAM1371	C22orf19	3'	TCCCAAAGTGCTAGGAT	13435	C A
			ATCC AGCACTTTG GGG		
			TAGG TCGTGAAAC CCT		
			A		
GAM1371	C2F	3'	TCCCAAAGTGCTGGGAT	20933	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			-		
GAM1371	C3F	3'	TCCGCCTCCCAAAGTGCTGGGA	19299	A A
	T		ATCCCAGCACTTTG GGGGC GA		
			TAGGGTCGTGAAAC CTCCG CT		
			C C		
GAM1371	C6orf33	3'	CTCAAGTACTGGGATA	55879	C T
			TATCCCAG ACTT GAG		
			ATAGGGTC TGAA CTC		
			A		
GAM1371	C6orf5	3'	TCCCAAAGTGCTAGGAT	31363	C A
			ATCC AGCACTTTG GGG		

		TAGG TCGTGAAAC CCT			
		A _			
GAM1371	C6orf5	3'	TCCCAAAGTGCTGGGAT	31364	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
GAM1371	C9orf9	3'	TCCCAAAGTGCTGGGAT	38527	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
GAM1371	C9orf9	3'	TCCCAAAGTGCTGGGAT	38528	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
GAM1371	CABIN1	3'	TCCACCCCTCGACGCCGGGATG	24482	A ACT CA
		TATCCC GC TTGAGGGG GA			
		GTAGGG CG AGCTCCCC CT			
		C C_ AC			
GAM1371	CDC14B	3'	TCCCAAAGTGCTGGGAT	52861	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
GAM1371	CENPH	3'	CCTACCGAAGTGCTAGGAT	43272	C AG
		ATCC AGCACTTTG GGG			
		TAGG TCGTGAAGC TCC			
		A CA			
GAM1371	CLSTN1	3'	CCCGAAGTCAAAGTGCTGG	30104	_____
		CCAGCACTTTGA GGG			
		GGTCGTGAAACT CCC			
		GAAG			
GAM1371	COLEC12	3'	TCCCAAAGTGCTGGGA	47874	A
		TCCCAGCACTTTG GGG			
		AGGGTCGTGAAAC CCT			
GAM1371	COLEC12	3'	TCTTGCAAAGTGCTGGGAT	47875	AG
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC TCT			
		GT			
GAM1371	COQ7	3'	TCCCAAAGTGCTGGGAT	32335	A
		ATCCCAGCACTTTG GGG			

TAGGGTCGTGAAAC CCT

GAM1371 CPSF2 3' TCCCAAAGTGCTGGGAT 61600 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 CPSF2 3' TCCCAAAGTGCTGGGAT 61601 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 CST7 5' CTGCCCCCTGGGCTGGGA 13326 A TTG  
TCCCAGC CT AGGGGCAG  
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AGGGTTCG GG TCCCCGTC

GAM1371 DCOHM 3' TCCCAAAGTGCTGGGAT 49612 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 DKFZp434A2417 3' TCCCAAAGTGCTGGGAT 66109 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 DKFZP434D193 3' CCCACTGCAAGCCTGGGATA 88877 CAC \_ \_  
TATCCAG TTTG AG GGG  
||||||| ||| |||||  
ATAGGGTC GAAC TC CCC  
C G A

GAM1371 DKFZP434F0318 3' TCCCAAAGTGCTGGGAT 48015 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 DKFZP434J037 3' TCCCAAAGTGCTGGGAT 48219 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 DKFZp547H025 3' TCCCAAAGTGCTGGGAT 39367 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 DKFZP564K0322 3' TCCCAAATGCTGGGAT 49363 C A  
ATCCCAGCA TTTG GGG  
||||| |||||

		TAGGGTCGT AAAC CCT			
		A _			
GAM1371	DKFZP566I1024	3'	TCCCAAAGTGCTGGGAT	70108	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	DKFZp761J139	5'	TCCCAAAGTGCTGGGAT	50120	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	DKFZp761N1114	3'	TCCCAAAGTGCTGGGAT	79027	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	DRIM	3'	TCCCAAAGTGCTGGGAT	27182	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	DSCR6	3'	TCCCAAAGTGCTGGGAT	38553	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	EVI5	3'	TCCCAAAGTGCTGGGAT	19013	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	EVI5	3'	TCCCAAAGTGCTGGGAT	19014	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	FBP17	3'	TCCCAAAGTGCTGAGAT	72808	C A
			ATC CAGCACTTTG GGG		
			TAG GTCGTGAAAC CCT		
			A _		
GAM1371	FER1L4	3'	TCTGCCTCCCAAAGTGCTGGGA	47363	A
T			ATCCCAGCACTTTG GGGGCAGA		
			TAGGGTCGTGAAAC CTCCGTCT		
			C		
GAM1371	FLB6421	3'	TCCCAAAGTGCTGGGAT	39233	A
			ATCCCAGCACTTTG GGG		

GAM1371	FLJ00060	5'	TCCCAAAGTGCTGGGAT	61103		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	FLJ10101	3'	TCCCAAAGTGCTGGGATG	45274		A
			TATCCCAGCACTTTG GGG			
			GTAGGGTCGTGAAAC CCT			
GAM1371	FLJ10298	3'	TCCCAAAGTGCTGGGAT	35993		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	FLJ10346	5'	TCCCAAAGTGCTGGGAT	36048		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	FLJ10535	3'	TCCCAAAGTGCTGGGAT	36251		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	FLJ10535	3'	TCCCAAAGTGCTGGGAT	36252		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	FLJ10560	3'	TCCCAAAGTGCTGGGAT	36284		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	FLJ10687	3'	TCCCAAAGTGCTGAGAT	36414	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A			
GAM1371	FLJ10713	3'	TCCCAAATGCTGGGA	36474	C	A
			TCCCAGCA TTTG GGG			
			AGGGTCGT AAAC CCT			
			A			
GAM1371	FLJ10901	3'	CCTTTCAAAGTGCTGGGAT	36818		
			ATCCCAGCACTTTGAGGGG			

TAGGGTCGTGAAACTTTCC

GAM1371	FLJ10922	3'	CCACCCAAAGTGCTGG	36872	A	_
			CCAGCACTTTG GG GG			
			GGTCGTGAAAC CC CC			
			_ A			
GAM1371	FLJ10956	3'	TCCCAAAGTGCTGGGAT	36920	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	FLJ12610	3'	TCCCAAAGTGCTGGGAT	45517	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	FLJ12687	3'	TCTCAAAGTGCTGGGAT	46205		
			ATCCCAGCACTTTGAGG			
			TAGGGTCGTGAAACTCT			
			_			
GAM1371	FLJ12747	3'	TCCCAAAGTGCTGGGAT	49726	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	FLJ12788	3'	CCTTCAAAGGGCTGGGA	42544	A	
			TCCCAGC CTTTGAGGG			
			AGGGTCG GAAACTTCC			
			G			
GAM1371	FLJ12975	3'	TCCCAAAGTGCTGAGAT	69591	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A			
			_			
GAM1371	FLJ12975	3'	TCCCAAAGTGCTGGGAT	69592	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	FLJ13072	5'	TCCCAAAGTGCTGGGAT	89829	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	FLJ13102	3'	TCCCAAAGTGCTGGGAT	46017	A	
			ATCCCAGCACTTTG GGG			



			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	FLJ13114	3'	TCCCAAAGTGCTGGGAT	44604	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	FLJ13193	3'	TCTGCCTCCCAAAGTGCTGGGA	49774	A
	T		ATCCCAGCACTTTG GGGGCAGA		
			TAGGGTCGTGAAAC CTCCGTCT		
			C		
GAM1371	FLJ13197	3'	TCCCAAAGTGCTGGGAT	44864	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	FLJ13305	5'	TGACCCAAAGTGCTGGGAT	90133	A GG
			ATCCCAGCACTTTG GG CA		
			TAGGGTCGTGAAAC CC GT		
			— A —		
GAM1371	FLJ13952	3'	TCCCAAAGTGCTGGGAT	45619	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	FLJ14351	3'	TCCCAAAGTGCTAGGAT	45332	C A
			ATCC AGCACTTTG GGG		
			TAGG TCGTGAAAC CCT		
			A —		
GAM1371	FLJ14442	3'	TCCCAAAGTGCTGAGAT	51376	C A
			ATC CAGCACTTTG GGG		
			TAG GTCGTGAAAC CCT		
			A —		
GAM1371	FLJ14950	3'	TCCCAAAGTGCTGGGAT	51729	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	FLJ14957	3'	TCCCAAAGTGCTGAGAT	51761	C A
			ATC CAGCACTTTG GGG		
			TAG GTCGTGAAAC CCT		
			A —		
GAM1371	FLJ20045	3'	TCCCAAAGTGCTGGGAT	34431	A
			ATCCCAGCACTTTG GGG		

			TAGGGTCGTGAAAC CCT	
		—		
GAM1371	FLJ20079	3'	TCCCAAAGTGCTGGGAT 34502	A
			ATCCCAGCACTTTG GGG	
			TAGGGTCGTGAAAC CCT	
		—		
GAM1371	FLJ20097	3'	TCCCAAAGTGCTGGGAT 34564	A
			ATCCCAGCACTTTG GGG	
			TAGGGTCGTGAAAC CCT	
		—		
GAM1371	FLJ20136	3'	TCCCAAAGTGCTGGGAT 34618	A
			ATCCCAGCACTTTG GGG	
			TAGGGTCGTGAAAC CCT	
		—		
GAM1371	FLJ20320	3'	TCTCAAAGTGCTGGGAT 34945	
			ATCCCAGCACTTTGAGG	
			TAGGGTCGTGAAACTCT	
		—		
GAM1371	FLJ20342	3'	TCCCAAAGTGCTGGGAT 34997	A
			ATCCCAGCACTTTG GGG	
			TAGGGTCGTGAAAC CCT	
		—		
GAM1371	FLJ20344	3'	TCCCAAAGTGCTGGGAT 35018	A
			ATCCCAGCACTTTG GGG	
			TAGGGTCGTGAAAC CCT	
		—		
GAM1371	FLJ20452	3'	TCCCAAAGTGCTGGGAT 35206	A
			ATCCCAGCACTTTG GGG	
			TAGGGTCGTGAAAC CCT	
		—		
GAM1371	FLJ20507	3'	TCCCAAAGTGCTGGGAT 35301	A
			ATCCCAGCACTTTG GGG	
			TAGGGTCGTGAAAC CCT	
		—		
GAM1371	FLJ20507	3'	TCCCAAAGTGCTGGGAT 60236	A
			ATCCCAGCACTTTG GGG	
			TAGGGTCGTGAAAC CCT	
		—		
GAM1371	FLJ20671	3'	TCCCAAAGTGCTGGGAT 35531	A
			ATCCCAGCACTTTG GGG	

TAGGGTCGTGAAAC CCT

GAM1371 FLJ20700 3' TCCCAAAGTGCTGGGAT 35587 A  
ATCCCAGCACTTTG GGG  
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TAGGGTCGTGAAAC CCT

GAM1371 FLJ21302 3' TCCCAAAGTGCTGGGAT 43222 A  
ATCCCAGCACTTTG GGG  
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TAGGGTCGTGAAAC CCT

GAM1371 FLJ21438 3' GCCCCTCAGTCTGG 61522 C TT  
CCAG ACT GAGGGGC  
||| ||| |||||  
GGTC TGA CTCCCCG

GAM1371 FLJ22002 3' TCCCAAAGTGCTAGGAT 45779 C A  
ATCC AGCACTTTG GGG  
||| ||||| |||  
TAGG TCGTGAAAC CCT  
A

GAM1371 FLJ22184 3' TCCGCCCTTTGGCCTAGGA 46985 CA\_ ACTTT A  
TCC GC GAGGGGC GA  
||| || ||||| ||  
AGG CG TTCCCCG CT  
ATC GT\_ C

GAM1371 FLJ22316 5' TCCCAAAGTGCTGGGAT 46923 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 FLJ22405 3' CCCCATCTTTGCTGGGAT 42519 CTTT \_  
ATCCCAGCA GA GGGG  
||||||| || |||  
TAGGGTCGT CT CCCC  
TT\_ A

GAM1371 FLJ22529 3' TCCCAAAGTGCTGGGA 45577 A  
TCCCAGCACTTTG GGG  
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AGGGTCGTGAAAC CCT

GAM1371 FLJ22684 3' CCCCAAAGTGCTGGGAT 46788 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCC

GAM1371 FLJ22794 3' CCTTCCAAAGTGCTGGGAT 91605 AG  
ATCCCAGCACTTTG GGG  
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		TAGGGTCGTGAAAC TCC			
		CT			
GAM1371	FLJ22969	3'	TCCCAAAGTGCTGGGAT	68663	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
-					
GAM1371	FLJ23024	3'	TCCCAAAGTGCTGGGAT	46277	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
-					
GAM1371	FLJ23209	3'	TCCCAAAGTGCTAGGAT	46055	C A
			ATCC AGCACTTTG GGG		
			TAGG TCGTGAAAC CCT		
			A -		
GAM1371	FLJ23323	3'	TCCCAAAGTGCTGGGAT	45057	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
-					
GAM1371	FLJ23356	3'	CCTCCAAAGTGCTGGGAT	49936	A
			ATCCCAGCACTTTG GGGG		
			TAGGGTCGTGAAAC CTCC		
-					
GAM1371	FLJ23392	3'	TCCCAAAGTGCTGGGAT	45548	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
-					
GAM1371	FLJ23537	3'	CCCACAGGCCAGAGTGCTGAGA	46024	C AG_____
			TC CAGCACTTTG GGG		
			AG GTCGTGAGAC CCC		
			A CGGACA		
GAM1371	FLJ23556	3'	TCCCAAAGTGCTGGGAT	45958	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
-					
GAM1371	FLJ31101	3'	TCCCAAAGTGCTGGGAT	35720	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
-					
GAM1371	FLJ31153	3'	TCCCAAAGCGCTGGGAT	58130	A A
			ATCCCAGC CTTTG GGG		

		TAGGGTCG GAAAC CCT			
		C _			
GAM1371	FLJ32334	3'	TCCCAAAGTGCTGGGAT	57985	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
GAM1371	FLJ32865	3'	TCCCAAAGTGCTGGGAT	58185	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
GAM1371	FLJ32894	3'	TCCCAAAGTGCTGGGAT	58342	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
GAM1371	GMEB2	3'	CTGCCCCTTAGCTACTGAGG	24731	_ CACT
		CC CAG TTGAGGGGCAG			
		GG GTC GATTCCCCGTC			
		A ATC_			
GAM1371	GMPPB	5'	TCCCAAAGTGCTGGGAT	95754	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
GAM1371	GNG4	3'	TCCCAAAGCGCTGGGAT	15625	A A
		ATCCCAGC CTTTG GGG			
		TAGGGTCG GAAAC CCT			
GAM1371	GP5	3'	TCCCAAAGTGCTGGGAT	15657	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
GAM1371	GREB1	3'	TCCAAAAGTGCTGGGAT	27887	GA
		ATCCCAGCACTTT GGG			
		TAGGGTCGTGAAA CCT			
GAM1371	GREB1	3'	TCCCAAAGTGCTGGGAT	27888	A
		ATCCCAGCACTTTG GGG			
		TAGGGTCGTGAAAC CCT			
GAM1371	GRIM19	3'	CTGCCCCTCCCCACTGGGA	31994	CACTTT
		TCCCAG GAGGGGCAG			

			AGGGTC CTCCCCGTC		
			ACCC__		
GAM1371	GTPBG3	3'	TCCCAAAGTGCTGGGAT 50911	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	H2AV	3'	CCTTCCAAAGTGCTGGGAT 56847	AG	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC TCC		
			CT		
GAM1371	HABP2	3'	TCTGCCCCCCGCTGCTG 14699	CTT A	
			CAGCA TG GGGGCAGA		
			GTCGT GC CCCCCTCT		
			C__ C		
GAM1371	HARS2	3'	TCCCAAAGTGCTGGGAT 55038	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	HEMK	3'	CTGCCCTCACCAGGATG 32430	CAGCACTT	
			TATCC TGAGGGGCAG		
			GTAGG ACTCCCCGTC		
			ACC_____		
GAM1371	HRH4	3'	TCCCAAAGTGCTGGGAT 41258	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	HSNOV1	3'	TCCCAAAGTGCTGGGAT 34014	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	HSNOV1	3'	TCCGAAAGTGCTAGGAT 34015	C GA	
			ATCC AGCACTTT GGG		
			TAGG TCGTGAAA CCT		
			A G_		
GAM1371	HSPC065	3'	TCTCAAAGTGCTGGGAT 26328		
			ATCCCAGCACTTTGAGG		
			TAGGGTCGTGAAACTCT		
			—		
GAM1371	JM11	3'	TCCCAAAGTGCTGGGAT 53271	A	
			ATCCCAGCACTTTG GGG		

GAM1371	KIAA0022	3'	TCCCAAAGTGCTGGGAT	29671		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	KIAA0057	3'	CTGCCCCAAAGTGC	24424	GA	
			GCACTTT GGGGCAG			
			CGTGAAA CCCCCTC			
GAM1371	KIAA0063	3'	TCCCAAAGTGCTGGGAT	29643		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	KIAA0087	3'	TCCCAAATGCTGGGAT	28704	C	A
			ATCCCAGCA TTTG GGG			
			TAGGGTCGT AAAC CCT			
GAM1371	KIAA0090	3'	TCCCAAAGTGCCGGGAT	88449	A	A
			ATCCC GCACTTTG GGG			
			TAGGG CGTGAAAC CCT			
GAM1371	KIAA0210	5'	TCCCAAAGTGCTGGGAT	28489		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	KIAA0391	3'	TCCCAAAGTGCTGGGAT	27924		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	KIAA0459	3'	TCCCAAAGTGCTAGGAT	61007	C	A
			ATCC AGCACTTTG GGG			
			TAGG TCGTGAAAC CCT			
GAM1371	KIAA0469	3'	TCCCAAAGTGCTAGGAT	29355	C	A
			ATCC AGCACTTTG GGG			
			TAGG TCGTGAAAC CCT			
GAM1371	KIAA0469	3'	TCCCAAAGTGCTGGGAT	29356		A
			ATCCCAGCACTTTG GGG			

			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	KIAA0472	5'	TCCCAAAGTGCTGGGAT	71871	A
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			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	KIAA0475	3'	CCTTCCAAAGTGCTGGGAT	29489	AG
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC TCC		
			CT		
GAM1371	KIAA0478	3'	TCCCAAAGTGCTAGGAT	29559	C A
			ATCC AGCACTTTG GGG		
			TAGG TCGTGAAAC CCT		
			A —		
GAM1371	KIAA0495	3'	TCCCAAAGTGCTGGGAT	62599	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	KIAA0513	3'	TCCCAAAGTGCTGGGAT	28376	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	KIAA0513	3'	TCTGCCTCTAAGCGCTG	28380	A TG
			CAGC CTT AGGGGCAGA		
			GTCG GAA TCTCCGTCT		
			C —		
GAM1371	KIAA0527	3'	TCCCAAAGTGCTAGGAT	95810	C A
			ATCC AGCACTTTG GGG		
			TAGG TCGTGAAAC CCT		
			A —		
GAM1371	KIAA0555	3'	TCCCAAAGTGCTAGGAT	28888	C A
			ATCC AGCACTTTG GGG		
			TAGG TCGTGAAAC CCT		
			A —		
GAM1371	KIAA0557	3'	TCCCAAAGTGCTGGGAT	78009	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	KIAA0561	3'	TCCCAAAGTGCTGGGAT	65898	A
			ATCCCAGCACTTTG GGG		



TAGGGTCGTGAAAC CCT

		—			
GAM1371	KIAA0562	3'	TCCGCCTCCCAAAGTGCTGG	28159	A A
			CCAGCACTTTG GGGGC GA		
			GGTCGTGAAAC CTCCG CT		
			C C		
GAM1371	KIAA0594	3'	TCCCAAAGTGCTGGGAT	64904	A
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			TAGGGTCGTGAAAC CCT		
		—			
GAM1371	KIAA0599	3'	TCCCAAAGTGCTGGGAT	77192	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
		—			
GAM1371	KIAA0607	3'	CCCCTCAAGTGTAAGGA	72568	CA T
			TCC GCACTT GAGGGG		
			AGG TGTGAA CTCCCC		
			AA —		
GAM1371	KIAA0660	3'	TCTGCCTGTTAATGCTGGGA	24517	CT G
			TCCCAGCA TTGA GGGCAGA		
			AGGGTCGT AATT TCCGTCT		
			— G		
GAM1371	KIAA0682	3'	TCCCAAAGTGCTGAGAT	29371	C A
			ATC CAGCACTTTG GGG		
			TAG GTCGTGAAAC CCT		
			A —		
GAM1371	KIAA0737	3'	TCCCAAAGTGCTGGGAT	29148	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
		—			
GAM1371	KIAA0781	3'	TCTGTGGCAAGTGCTGG	67458	T AGGG
			CCAGCACTT G GCAGA		
			GGTCGTGAA C TGTCT		
			— GG —		
GAM1371	KIAA0798	3'	TCCCAAAGTGCTGGGAT	27730	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
		—			
GAM1371	KIAA0841	3'	TCCCAAAGTGCTGGGAT	71402	A
			ATCCCAGCACTTTG GGG		

			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	KIAA0861	3'	TCCCAAAGTGCTGGGAT 88934	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	KIAA0924	3'	TCCGAAAGTGCTGGGAT 29723	GA	
			ATCCCAGCACTTT GGG		
			TAGGGTCGTGAAA CCT		
			G_		
GAM1371	KIAA1026	3'	TCCCAAAGTGCTGGGAT 71209	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	KIAA1054	3'	TCCCAAATGCTGGGAT 68452	C A	
			ATCCCAGCA TTTG GGG		
			TAGGGTCGT AAAC CCT		
			A _		
GAM1371	KIAA1143	3'	TCCCAAAGTGCTGGGAT 68689	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	KIAA1155	3'	TCCCAAAGTGCTGGGAT 62243	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	KIAA1185	3'	TCCCAAAGTGCTGGGAT 62609	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	KIAA1185	3'	TCTGCCCCCTCAAAGTGCTGGGA 62610		
	T		ATCCCAGCACTTTGAGGGGCAGA		
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			—		
GAM1371	KIAA1193	3'	TCCCAAAGTGCTGGGAT 67650	A	
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			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	KIAA1198	3'	CCCCAAAGTGCTGGGAT 63297	A	
			ATCCCAGCACTTTG GGG		

TAGGGTCGTGAAAC CCC		
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	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
GAM1371 KIAA1198	3' TCCCAAAGTGCTGGGAT 63336	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
GAM1371 KIAA1198	3' TCCCAAAGTGCTGGGAT 63337	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
GAM1371 KIAA1198	3' TCTCAAAGTGCTGGGAT 63341	
	ATCCCAGCACTTTGAGG	
	TAGGGTCGTGAAACTCT	
GAM1371 KIAA1200	3' TCCCAAAGTGCTGGGAT 62382	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
GAM1371 KIAA1254	3' TCTACCTCCCAAAGTGCTGGGA 70025	A C
T	ATCCCAGCACTTTG GGGG AGA	
	TAGGGTCGTGAAAC CTCC TCT	
	C A	
GAM1371 KIAA1257	3' TCCCAAAGTGCTGGGAT 62761	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
GAM1371 KIAA1287	3' TCCCAAAGTGCTGGGAT 78329	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
GAM1371 KIAA1320	5' TCCCAAAGTGCTGGGAT 69311	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
GAM1371 KIAA1328	5' TCCCAAAGTGCTGGGAT 61655	A
	ATCCCAGCACTTTG GGG	

TAGGGTCGTGAAAC CCT					
GAM1371	KIAA1349	5'	TCCCAAAGTGCTGAGAT	70759	C A
			ATC CAGCACTTTG GGG		
			TAG GTCGTGAAAC CCT		
			A		
GAM1371	KIAA1373	3'	TCCCAAAGTGCTGAGAT	70953	C A
			ATC CAGCACTTTG GGG		
			TAG GTCGTGAAAC CCT		
			A		
GAM1371	KIAA1373	3'	TCTCAAAGTGCTGGGAT	70954	
			ATCCCAGCACTTTGAGG		
			TAGGGTCGTGAAACTCT		
GAM1371	KIAA1443	3'	TCCCAAAGTGCTGGGAT	63842	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	KIAA1465	3'	TCTCAAAGTGCTGGGAT	60836	
			ATCCCAGCACTTTGAGG		
			TAGGGTCGTGAAACTCT		
GAM1371	KIAA1467	3'	TCTGCCTCCCAAAGTGCTGGGA	71617	A
	T		ATCCCAGCACTTTG GGGGCAGA		
			TAGGGTCGTGAAAC CTCCGTCT		
			C		
GAM1371	KIAA1493	3'	TCTGCCTCCCAAAGTGCTGGGA	64167	A
	T		ATCCCAGCACTTTG GGGGCAGA		
			TAGGGTCGTGAAAC CTCCGTCT		
			C		
GAM1371	KIAA1508	3'	CCTACCAAAGTGCTGGGAT	61881	AG
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC TCC		
			CA		
GAM1371	KIAA1571	3'	TCCCAAAGTGCTGGGAT	60963	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	KIAA1615	3'	TCCCAAAGTGCTGGGAT	68734	A
			ATCCCAGCACTTTG GGG		

GAM1371	KIAA1615	3'	TCCCAAAGTGCTGGGAT	68735		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	KIAA1655	3'	TCCCAAAGTGCTGGGAT	66631		A
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			TAGGGTCGTGAAAC CCT			
GAM1371	KIAA1668	3'	TCCCAAAGTGCTGGGAT	66482		A
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			TAGGGTCGTGAAAC CCT			
GAM1371	KIAA1671	3'	TCCCAAAGTGCTGGGAT	65695		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	KIAA1727	3'	TCCCAAAGTGCTGGGAT	64067		A
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			TAGGGTCGTGAAAC CCT			
GAM1371	KIAA1755	3'	TCCCAAAGTGCTGGGAT	61356		A
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			TAGGGTCGTGAAAC CCT			
GAM1371	KIAA1784	3'	TCCCAAAGTGCTGGGAT	65156		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	KIAA1817	3'	CTGCCCTCACTGATGGG	68227	G CTT	
			CCCA CA TGAGGGGCAG			
			GGGT GT ACTCCCCGTC			
			A C__			
GAM1371	KIAA1829	3'	TCCCAAAGTGCTGAGAT	61956	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A			
GAM1371	KIAA1829	3'	TCCCAAAGTGCTGGGAT	61957		A
			ATCCCAGCACTTTG GGG			

GAM1371	KIAA1853	5'	CCCCCTCAAGCTGTGA	69395	C	ACT	
			TC CAGC TTGAGGGGC				
			AG GTCG AACTCCCCG				
			T ____				
GAM1371	KIAA1924	3'	TCCCAAAGTGCTGGGAT	73689		A	
			ATCCCAGCACTTTG GGG				
			TAGGGTCGTGAAAC CCT				
			____				
GAM1371	KIAA1971	3'	TCCCAAAGTGCTGGGAT	74228		A	
			ATCCCAGCACTTTG GGG				
			TAGGGTCGTGAAAC CCT				
			____				
GAM1371	KIAA1975	5'	TCCACCTCCCAAAGTGCTAGGA	73979	C	A	CA
		T	ATCC AGCACTTTG GGGG GA				
			TAGG TCGTGAAAC CTCC CT				
			A C AC				
GAM1371	KLK7	3'	TCCCAAAGTGCTGGGAT	17298		A	
			ATCCCAGCACTTTG GGG				
			TAGGGTCGTGAAAC CCT				
			____				
GAM1371	KLK7	3'	TCCCAAAGTGCTGGGAT	57738		A	
			ATCCCAGCACTTTG GGG				
			TAGGGTCGTGAAAC CCT				
			____				
GAM1371	LAMP3	3'	TCCCAAAGTGCTGGGAT	59497		A	
			ATCCCAGCACTTTG GGG				
			TAGGGTCGTGAAAC CCT				
			____				
GAM1371	LANO	3'	TCCGTAAAGTGCTGGGATA	36625		A	
			TATCCCAGCACTTTG GGG				
			ATAGGGTCGTGAAAT CCT				
			G				
GAM1371	LEC3	3'	CTGCTTTTAAAGGC	30859	AC		
			GC TTTGAGGGGCAG				
			CG AAATTTTCGTC				
			GA				
GAM1371	LGALS12	3'	CCACCAGGAGCCTGGGATA	52388	CA	GA	_
			TATCCCAG CTTT GG GG				

			ATAGGGTC GAGG CC CC		
			C_ A_ A		
GAM1371	LIECG3	3'	TCCGCCTCCCAAAGTGCTGGGA 87413	A	A
		T	ATCCCAGCACTTTG GGGGC GA		
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			C C		
GAM1371	LY75	3'	TCCCAAAGTGCTGGGAT 9843	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	MAD4	3'	CTGCCCCTTCCAGCTGGG 21275	ACTTT	
			CCCAGC GAGGGGCAG		
			GGGTCG TTCCCCGTC		
			ACC_		
GAM1371	MAIL	3'	TCCCAAATGCTGGGAT 48653	C	A
			ATCCCAGCA TTTG GGG		
			TAGGGTCGT AAAC CCT		
			A _		
GAM1371	MAP-1	3'	TCTGAAAGTGCTGGGAT 42185	G	
			ATCCCAGCACTTT AGG		
			TAGGGTCGTGAAA TCT		
			G		
GAM1371	MCLC	3'	TCCCAAAGTGCTGGGAT 30693	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	MGC10200	3'	TCCCAAAGTGCTGGGAT 58995	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	MGC10911	5'	TCCCAAAGTGCCGGGATG 50211	A	A
			TATCCC GCACTTTG GGG		
			GTAGGG CGTGAAAC CCT		
			C _		
GAM1371	MGC12518	3'	TCCCAAAGTGCTGGGAT 64086	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	MGC13138	3'	TCCGCAAGTGCTGGGAT 53026	T	A
			ATCCCAGCACTT G GGG		

				TAGGGTCTGTGAA C CCT			
				_ G			
GAM1371	MGC21675	3'	TCCCAAAGTGCTGAGAT	53488	C	A	
		ATC CAGCACTTTG GGG					
		TAG GTCGTGAAAC CCT					
		A _					
GAM1371	MGC21738	3'	TCCCAAAGTGCTGGGAT	58920		A	
		ATCCCAGCACTTTG GGG					
		TAGGGTCTGTGAAAC CCT					
		_					
GAM1371	MGC2474	3'	TCCCAAAGTGCTGGGAT	43731		A	
		ATCCCAGCACTTTG GGG					
		TAGGGTCTGTGAAAC CCT					
		_					
GAM1371	MGC2474	3'	TCTGCCTCCCAAAGTGCTGGGA	43733		A	
	T		ATCCCAGCACTTTG GGGGCAGA				
		TAGGGTCTGTGAAAC CTCCGTCT					
		C					
GAM1371	MGC2477	5'	TCCCAAAGTGCTGGGAT	44069		A	
		ATCCCAGCACTTTG GGG					
		TAGGGTCTGTGAAAC CCT					
		_					
GAM1371	MGC2603	3'	TCCCAAAGTGCTGAGAT	43863	C	A	
		ATC CAGCACTTTG GGG					
		TAG GTCGTGAAAC CCT					
		A _					
GAM1371	MGC3123	3'	CTACCCCTTAGCAGGA	44097	CA	ACTT	C
		TCC GC TGAGGGG AG					
		AGG CG ATTCCCC TC					
		A_ _ _ _ A					
GAM1371	MGC4766	5'	TCCCAAAGTGCTGGGAT	48778		A	
		ATCCCAGCACTTTG GGG					
		TAGGGTCTGTGAAAC CCT					
		_					
GAM1371	MGC5149	3'	TCCCAAAGCGCTGGGAT	72300	A	A	
		ATCCCAGC CTTTG GGG					
		TAGGGTCTG GAAAC CCT					
		C _					
GAM1371	MKRN4	3'	CCTTCCAAAGTGCTGGGAT	47739		AG	
		ATCCCAGCACTTTG GGG					



			TAGGGTCGTGAAAC TCC		
			CT		
GAM1371	MLN64	3'	TCTGCCCCACCTTGCCAGGG 94412	A_	CTTTGA
			CCC GCA GGGGCAGA		
			GGG CGT CCCCCTCT		
			AC TCCA__		
GAM1371	MLZE	5'	TCCCAAAGTGCTGGGAT 48629	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	moblak	3'	TCCAAAAGTGCTGGGAT 55513	GA	
			ATCCCAGCACTTT GGG		
			TAGGGTCGTGAAA CCT		
			A_		
GAM1371	moblak	3'	TCCCAAAGTGCTGGGAT 55514	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	MRPL20	3'	TCCCAAAGTGCTGGGAT 35741	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	MRPL44	3'	TCCCAAAGTGCTGGGAT 43327	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	MRPS27	3'	TCCCAAAGTGCTGGGATG 30645	A	
			TATCCCAGCACTTTG GGG		
			GTAGGGTCGTGAAAC CCT		
			—		
GAM1371	MYO5C	3'	TCCCAAAGTGCTAGGAT 38112	C	A
			ATCC AGCACTTTG GGG		
			TAGG TCGTGAAAC CCT		
			A —		
GAM1371	NAPG	5'	TCCCAAAGTGCTGGGAT 96731	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	NDP52	3'	CCGTCCCAAAGTGCTGGGAT 19527	_	G
			ATCCCAGCACTTTG A GG		

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			C G		
GAM1371	NICN1	3'	CCTTCCAAAGTGCTGGGAT 50290	AG	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC TCC		
			CT		
GAM1371	NINJ2	3'	TCCCAAAGTGCTGGGAT 33288	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	Nup43	3'	TCCCAAATGCTGGGAT 45009	C A	
			ATCCCAGCA TTTG GGG		
			TAGGGTCGT AAAC CCT		
			A —		
GAM1371	NXN	3'	TCCCAAAGTGCTGGGAT 42425	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	OSBPL2	3'	TCCCAAAGTGCTGGGAT 57872	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	OSBPL2	3'	TCCCAAAGTGCTGGGAT 29221	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	PASK	5'	TCCCAAAGTGCTGGGAT 30726	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	PELI1	5'	TCCCAAAGTGCTGGGAT 40287	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	PELI1	5'	TCCGCTTCCCAAAGTGCTGG 40288	A A	
			CCAGCACTTTG GGGGC GA		
			GGTCGTGAAAC CTTCG CT		
			C C		
GAM1371	PP2447	5'	TCCCAAAGTGCTGGGATG 47322	A	
			TATCCCAGCACTTTG GGG		

GTAGGGTCGTGAAAC CCT

GAM1371 PRO0245 5' TCCCAAAGTGCTGAGAT 26136 C A  
ATC CAGCACTTTG GGG  
||| ||||| |||  
TAG GTCGTGAAAC CCT  
A

GAM1371 PRO0365 5' TCCCAAAGTGCTGGGAT 26171 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 PRO1483 3' CCACCAAAGAGTGCTGAGA 37719 C GA \_  
TC CAGCACTTT GG GG  
|| ||||| ||  
AG GTCGTGAGA CC CC  
A AA A

GAM1371 PRO1992 3' TCCCAAAGTGCTGGGAT 26063 A  
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GAM1371 PRO2955 3' TCCCAAAGTGCTGGGAT 37648 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 PSPH 3' TCCCAAAGTGCTGGGAT 15918 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 PSTPIP2 3' TCCCAAAGTGCTGGGAT 44399 A  
ATCCCAGCACTTTG GGG  
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TAGGGTCGTGAAAC CCT

GAM1371 PTPRN2 3' CTGCCCCTCTTCCCGGGAT 55603 AGCACTTT  
ATCCC GAGGGGCAG  
|||| |||||  
TAGGG CTCCCCGTC  
CCCTT\_\_

GAM1371 PTPRN2 3' CTGCCCCTCTTCCCGGGAT 55607 AGCACTTT  
ATCCC GAGGGGCAG  
|||| |||||  
TAGGG CTCCCCGTC  
CCCTT\_\_

GAM1371 RAB21 3' TCCCAAAGTGCTGGGAT 30391 A  
ATCCCAGCACTTTG GGG  
||||||| |||

TAGGGTCGTGAAAC CCT

		—			
GAM1371	RAB25	3'	TCCACCCCTCACAGACTAGGA 72881	C	CA T CA
			TCC AG CT TGAGGGG GA		
			AGG TC GA ACTCCCC CT		
			A A_ C AC		
GAM1371	RAB33B	3'	TCCCAAAGTGCTGGGAT 48508	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
		—			
GAM1371	RAB39	3'	CCTCCAAAGTGCTGG 76630	A	
			CCAGCACTTTG GGGG		
			GGTCGTGAAAC CTCC		
		—			
GAM1371	RAP140	3'	TCCCAAAGTGCTGGGAT 30848	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
		—			
GAM1371	RNF8	3'	TCCCAAAGTGCTGAGAT 14242	C	A
			ATC CAGCACTTTG GGG		
			TAG GTCGTGAAAC CCT		
			A —		
GAM1371	RNO2	5'	TCCCAAAGTGCTGGGAT 52779	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
		—			
GAM1371	Rpo1-2	3'	TCCGAAAGTGCTAGGAT 49880	C	GA
			ATCC AGCACTTT GGG		
			TAGG TCGTGAAA CCT		
			A G_		
GAM1371	Rpo1-2	3'	TCCGAAAGTGCTAGGAT 38711	C	GA
			ATCC AGCACTTT GGG		
			TAGG TCGTGAAA CCT		
			A G_		
GAM1371	SC4MOL	3'	TCCCAAAGTGCTGGGAT 22164	A	
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
		—			
GAM1371	SCAMP-4	3'	TCCCAAAGTGCTGGGATA 54401	A	
			TATCCCAGCACTTTG GGG		

ATAGGGTCGTGAAAC CCT

GAM1371	SCYA16	3'	TCCAAAAGTGCTGGGAT	15969		GA
			ATCCCAGCACTTT GGG			
			TAGGGTCGTGAAA CCT			
			A_			
GAM1371	SCYA22	3'	TCCCAAAGTGCTGAGAT	90959	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A			
GAM1371	SCYA22	3'	TCCCAAAGTGCTGGGAT	90960		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	SCYA22	3'	TCCCAAAGTGCTGGGAT	90961		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	SEC6	3'	CTGCCTTTAGAAACGCGGGA	71595	A AC	G
			TCCC GC TTT AGGGGCAG			
			AGGG CG AAG TTTCCGTC			
			_ CA A			
GAM1371	SERF1B	3'	TCCCAAAGTGCTGGGAT	43425		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	SFRS10	3'	CTGCCCTAGAGCTGGGATA	15975	A TTGA	
			TATCCCAGC CT GGGGCAG			
			ATAGGGTCG GA TCCCGTC			
			A			
GAM1371	SIRPB1	3'	TCCCAAAGTGCTGGGAT	20266		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	SLC11A1	3'	TCCCAAAGTGCTGGGA	59462		A
			TCCCAGCACTTTG GGG			
			AGGGTCGTGAAAC CCT			
			-			
GAM1371	SLC16A4	3'	CCTCCAAAGTGCTGGGAT	16278		A
			ATCCCAGCACTTTG GGGG			

TAGGGTCGTGAAAC CTCC

GAM1371	SPRY2	3'	CTCAAAGTATGAGATA	19557	C GC
			TATC CA ACTTTGAG		
			ATAG GT TGAAACTC		
			A A_		
GAM1371	SREC	3'	CCCCAAAGTGCTGGGATG	13499	A
			TATCCCAGCACTTTG GGG		
			GTAGGGTCGTGAAAC CCC		
GAM1371	STAF65(gamma)	3'	TCCCAAAGTGCTGGGAT	29445	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	SYTL4	5'	TCCCAAAGTGCTGGGAT	54946	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	TADA3L	3'	TCCCAAAGTGCCGGGAT	55999	A A
			ATCCC GCACTTTG GGG		
			TAGGG CGTGAAAC CCT		
			C _		
GAM1371	TCL6	5'	TCCCAAAGTGCTGGGAT	40089	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	TCL6	5'	TCCCAAAGTGCTGGGAT	40115	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	TCL6	5'	TCTCAAAGTGCTGGGAT	40148	
			ATCCCAGCACTTTGAGG		
			TAGGGTCGTGAAACTCT		
GAM1371	TCL6	5'	TCTCAAAGTGCTGGGAT	40163	
			ATCCCAGCACTTTGAGG		
			TAGGGTCGTGAAACTCT		
GAM1371	TCL6	5'	TCCCAAAGTGCTGGGAT	24990	A
			ATCCCAGCACTTTG GGG		

			TAGGGTCGTGAAAC CCT	
GAM1371	TCL6	3'	<div> <div>TCCCAAAGTGCTGGGAT</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	24991 A
GAM1371	TCL6	5'	<div> <div>TCCCAAAGTGCTGGGAT</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	27006 A
GAM1371	TCL6	3'	<div> <div>TCCCAAAGTGCTGGGAT</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	27007 A
GAM1371	THEA	3'	<div> <div>TCCCAAAGTGCTGGGAT</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	66298 A
GAM1371	TIP-1	3'	<div> <div>TCTGCCCTCGGGGACTGG</div> <div>CCAG CTTTGAGGGGCAGA</div> <div>         </div> <div>GGTC GGGGCTCCCCGTCT</div> <div>AG</div> </div>	27508 CA
GAM1371	TRIM16	3'	<div> <div>TCCCAAAGTGCTGGGAT</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	21344 A
GAM1371	TRIM5	3'	<div> <div>TCCCAAAGTGCTGGGAT</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	52304 A
GAM1371	TRIM5	3'	<div> <div>TCCCAAAGTGCTGGGAT</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	52368 A
GAM1371	TRIM6	3'	<div> <div>TCCCAAAGTGCTGGGAT</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	54146 A
GAM1371	TU12B1-TY	3'	<div> <div>CCTTCCAAAGTGCTGGGAT</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> </div>	33375 AG

			TAGGGTCGTGAAAC TCC			
			CT			
GAM1371	TUCAN	3'	CCTTCCAAAGTGCTGGGAT 30274		AG	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC TCC			
			CT			
GAM1371	TUCAN	3'	TCCCAAAGTGCTGGGAT 30285		A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	TUSP	3'	TCCCAAAGTGCTGGGAT 39642		A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	USP22	3'	TCCCAAAGTGCTGGGAT 68026		A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	VDU1	3'	TCCCAAAGTGCTGGGAT 30429		A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	VEZATIN	5'	CCTACCAAAATACCTGGGATA 34225		CAC_	AG
			TATCCAG TTTG GGG			
			ATAGGGTC AAAC TCC			
			CATA CA			
GAM1371	ZNF17	3'	TCCCAAAGTGCTGGGAT 82394		A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	ZNF338	3'	TCCCAAAGTGCTGGGAT 42018		A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			-			
GAM1371	ZNF33A	3'	TCCAAAACAAAGTGCCAGGA 91353		CA	AG__
			TCC GCACTTTG GGG			
			AGG CGTGAAAC CCT			
			AC AAAA			
GAM1371	ZTL1	3'	CCTCACAAAGTGCTAGGAT 43912		C	A
			ATCC AGCACTTTG GGGG			



	<p>           TAGG TCGTGAAAC CTCC                A    A            GAM1371 LOC112687 3' TCCCAAAGTGCTGGGAT 72869 A                      ATCCCAGCACTTTG GGG                                                      TAGGGTCGTGAAAC CCT         </p>	
	<p>           —            GAM1371 LOC112817 3' TCCCAAAGTGCTGGGAT 56517 A                      ATCCCAGCACTTTG GGG                                                      TAGGGTCGTGAAAC CCT         </p>	
	<p>           —            GAM1371 LOC113026 3' GCATTCCAAAGTGCTGGGAT 55902 AG G                      ATCCCAGCACTTTG G GC                                                        TAGGGTCGTGAAAC T CG                      CT A         </p>	
	<p>           GAM1371 LOC113523 5' TCCCAAAGTGCTGGGAT 73050 A                      ATCCCAGCACTTTG GGG                                                      TAGGGTCGTGAAAC CCT         </p>	
	<p>           —            GAM1371 LOC115548 3' TCCCAAAGTGCTGGGAT 73462 A                      ATCCCAGCACTTTG GGG                                                      TAGGGTCGTGAAAC CCT         </p>	
	<p>           —            GAM1371 LOC116411 5' TCCCAAAGTGCCGAGAT 73873 CCA A                      ATC GCACTTTG GGG                                                        TAG CGTGAAAC CCT                      AGC         </p>	
	<p>           —            GAM1371 LOC120114 3' TCCCAAAGTGCTGGGAT 75540 A                      ATCCCAGCACTTTG GGG                                                      TAGGGTCGTGAAAC CCT         </p>	
	<p>           —            GAM1371 LOC120224 5' TCCCAAAGTGCTGGGAT 57105 A                      ATCCCAGCACTTTG GGG                                                      TAGGGTCGTGAAAC CCT         </p>	
	<p>           —            GAM1371 LOC124216 3' TCCCAAAGTGCTGGGAT 74267 A                      ATCCCAGCACTTTG GGG                                                      TAGGGTCGTGAAAC CCT         </p>	
	<p>           —            GAM1371 LOC125194 5' TCCCAAAGTGCTGGGAT 74399 A                      ATCCCAGCACTTTG GGG                                         </p>	

	TAGGGTCGTGAAAC CCT	
	—	
GAM1371 LOC126272 3'	TCCCAAAGTGCTGGGAT 76090	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
	—	
GAM1371 LOC126661 3'	TCCCAAAGTGCTGGGAT 74560	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
	—	
GAM1371 LOC128077 3'	TCCCAAAGTGCTGGGAT 74723	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
	—	
GAM1371 LOC128989 3'	TCCCAAAGTGCTGGGAT 74818	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
	—	
GAM1371 LOC130813 3'	TCCCAAAGTGCTGGGAT 75779	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
	—	
GAM1371 LOC132625 3'	TCCCAAAGTGCTGGGAT 75915	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
	—	
GAM1371 LOC135154 3'	TCCCAAAGTGCTGGGAT 75223	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
	—	
GAM1371 LOC142820 5'	TCCCAAAGTGCTGGGAT 76399	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
	—	
GAM1371 LOC142927 5'	TCCCAAAGTGCTGGGAT 76434	A
	ATCCCAGCACTTTG GGG	
	TAGGGTCGTGAAAC CCT	
	—	
GAM1371 LOC143153 3'	TCCCAAAGTGCTGGGAT 76469	A
	ATCCCAGCACTTTG GGG	

GAM1371	LOC143154	3'	TCCCAAAGTGCTGGGAT	76486	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	LOC144317	5'	TCCCAAAGTGCTGGGAT	76800	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	LOC144524	5'	TCCCAAAGTGCTGGGAT	83138	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	LOC144603	3'	CCCCATCTTTGCTGGGAT	60367	CTTT _
			ATCCCAGCA GA GGGG		
			TAGGGTCGT CT CCCC		
			TT_ A		
GAM1371	LOC145009	3'	TCCCAAAGTGCTGGGAT	60351	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	LOC145082	5'	GCCCCTCAAAGTGCTGGGAT	83241	
			ATCCCAGCACTTTGAGGGGC		
			TAGGGTCGTGAAACTCCCCG		
GAM1371	LOC145268	5'	CCTTCCAAAGTGCTGGGATG	77056	AG
			TATCCCAGCACTTTG GGG		
			GTAGGGTCGTGAAAC TCC		
			CT		
GAM1371	LOC145622	3'	TCCCAAAGTGCTGGGAT	77316	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	LOC145873	5'	TCCCAAAGTGCTAGGAT	77555	C A
			ATCC AGCACTTTG GGG		
			TAGG TCGTGAAAC CCT		
			A _		
GAM1371	LOC146050	3'	TCCCAAAGTGCTGGGAT	77649	A
			ATCCCAGCACTTTG GGG		

	TAGGGTCGTGAAAC CCT	
GAM1371 LOC146050 3'	<div> <div>—</div> <div>TCCCAAAGTGCTGGGAT 77650</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	A
GAM1371 LOC146108 3'	<div> <div>—</div> <div>CCTTCCAAAGTGCTGGGAT 77663</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC TCC</div> <div>CT</div> </div>	AG
GAM1371 LOC146229 3'	<div> <div>—</div> <div>TCCAAAAGTGCTGGGAT 77774</div> <div>ATCCCAGCACTTT GGG</div> <div>     </div> <div>TAGGGTCGTGAAA CCT</div> <div>A_</div> </div>	GA
GAM1371 LOC146229 3'	<div> <div>—</div> <div>TCCCAAAGTGCTGGGAT 77775</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	A
GAM1371 LOC146229 3'	<div> <div>—</div> <div>TCCCAAAGTGCTGGGAT 77776</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	A
GAM1371 LOC146316 5'	<div> <div>—</div> <div>CTGCCCCAGAGCTGGGA 60870</div> <div>TCCCAGC CT GGGGCAG</div> <div>              </div> <div>AGGGTCG GA CCCCCTC</div> <div>A ____</div> </div>	A TTGA
GAM1371 LOC146325 3'	<div> <div>—</div> <div>CTGCCCCCTCACCTGCCTGGGA 59179</div> <div>TCCCAG CA TGAGGGGCAG</div> <div>              </div> <div>AGGGTC GT ACTCCCCGTC</div> <div>C CC_</div> </div>	_ CTT
GAM1371 LOC146337 5'	<div> <div>—</div> <div>CCTTACAAAGTGCTGGGATG 83658</div> <div>TATCCCAGCACTTTG AGGG</div> <div>     </div> <div>GTAGGGTCGTGAAAC TTCC</div> <div>A</div> </div>	—
GAM1371 LOC146429 5'	<div> <div>—</div> <div>TCCCAAAGTGCTGGGAT 83674</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	A
GAM1371 LOC146443 5'	<div> <div>—</div> <div>TCCCAAAGTGCTGGGAT 77886</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> </div>	A

			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	LOC146455	3'	TCCCAAATGCTGGGAT	77910	C A
			ATCCCAGCA TTTG GGG		
			TAGGGTCGT AAAC CCT		
			A —		
GAM1371	LOC146599	5'	TCCCAAAGTGCTAGGAT	78029	C A
			ATCC AGCACTTTG GGG		
			TAGG TCGTGAAAC CCT		
			A —		
GAM1371	LOC146784	5'	TCCCAAAGTGCTGGGAT	78126	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	LOC146909	3'	TCCCAAAGTGCTGAGAT	78185	C A
			ATC CAGCACTTTG GGG		
			TAG GTCGTGAAAC CCT		
			A —		
GAM1371	LOC146909	3'	TCCCAAAGTGCTGGGAT	78186	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	LOC147080	5'	TCCCAAAGTGCTGGGAT	83938	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	LOC147160	5'	TCCCAAAGTGCTGGGAT	83974	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	LOC147166	3'	TCCCAAAGTGCTGGGAT	78291	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
			—		
GAM1371	LOC147429	3'	GCCTCCCAAAGTGCTGGGAT	78359	A
			ATCCCAGCACTTTG GGGGC		
			TAGGGTCGTGAAAC CTCCG		
			C		
GAM1371	LOC147694	3'	TCTCAAAGTGCTGGGAT	78455	
			ATCCCAGCACTTTGAGG		

TAGGGTCGTGAAACTCT

GAM1371 LOC147817 3' CCTCCAAAATGCTGGGAT 78493 C A  
ATCCCAGCA TTTG GGGG  
||||||| ||| |||  
TAGGGTCGT AAAC CTCC  
A \_

GAM1371 LOC147817 3' TCCCAAAGTGCTGGGAT 78506 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 LOC147841 3' TCCCAAAGTGCTAGGAT 78535 C A  
ATCC AGCACTTTG GGG  
||| ||||| |||  
TAGG TCGTGAAAC CCT  
A \_

GAM1371 LOC147990 3' TCCCAAAGTGCTGGGAT 84102 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 LOC148137 3' TCCCAAAGTGCTGGGAT 58441 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 LOC148147 3' CCACCCAAAGTGCTGGGAT 78676 A \_  
ATCCCAGCACTTTG GG GG  
||||||| || ||  
TAGGGTCGTGAAAC CC CC

GAM1371 LOC148189 5' TCCCAAAGTGCTGGGAT 78723 A  
ATCCCAGCACTTTG GGG  
||||||| |||  
TAGGGTCGTGAAAC CCT

GAM1371 LOC148195 3' CCTGGCAAATGCTGGGAT 84126 C AG  
ATCCCAGCA TTTG GGG  
||||||| ||| |||  
TAGGGTCGT AAAC TCC  
A GG

GAM1371 LOC148443 3' TCTCAAATGCTGGGAT 78863 C  
ATCCCAGCA TTTGAGG  
||||||| |||||  
TAGGGTCGT AAAC TCT

GAM1371 LOC148709 5' TCCCAAAGTGCTGGGAT 78951 A  
ATCCCAGCACTTTG GGG  
||||||| |||

	TAGGGTCGTGAAAC CCT	
GAM1371 LOC148887 5'	<div> <div>—</div> <div>TCCCAAAGTGCTGGGAT 84248</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	A
GAM1371 LOC149171 5'	<div> <div>—</div> <div>CCTCCAAAGTGCTGG 79216</div> <div>CCAGCACTTTG GGGG</div> <div>     </div> <div>GGTCGTGAAAC CTCC</div> </div>	A
GAM1371 LOC149194 3'	<div> <div>—</div> <div>TCCAAAAGTGCTGGGAT 79231</div> <div>ATCCCAGCACTTT GGG</div> <div>     </div> <div>TAGGGTCGTGAAA CCT</div> </div>	GA
GAM1371 LOC149276 5'	<div> <div>A_</div> <div>CCCATAAGCTCTGGGATA 84384</div> <div>TATCCCAG CTT GGG</div> <div>         </div> <div>ATAGGGTC GAA CCC</div> <div>TC TA_</div> </div>	CA TGA
GAM1371 LOC149421 3'	<div> <div>TCCCAAAGTGCTGGGAT 79364</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	A
GAM1371 LOC149478 3'	<div> <div>—</div> <div>TCCCAAAGTGCTGGGAT 79382</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	A
GAM1371 LOC149506 3'	<div> <div>—</div> <div>TCTCAAAGTGTTGGGATA 84484</div> <div>TATCCCAGCACTTTGAGG</div> <div>     </div> <div>ATAGGGTTGTGAAACTCT</div> </div>	
GAM1371 LOC149577 3'	<div> <div>TCCCAAATGCTGGGAT 84521</div> <div>ATCCCAGCA TTTG GGG</div> <div>         </div> <div>TAGGGTCGT AAAC CCT</div> </div>	C A
GAM1371 LOC149577 3'	<div> <div>A _</div> <div>TCCCAAAGTGCTGGGAT 84522</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>	A
GAM1371 LOC149684 5'	<div> <div>—</div> <div>TCCCAAAGTGCTGGGAT 84618</div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> </div>	A

	TAGGGTCGTGAAAC CCT	
GAM1371 LOC149703 5'	<p>—</p> <p>TCCCAAAGTGCTGGGAT 84661</p> <p>ATCCCAGCACTTTG GGG</p> <p>           </p> <p>TAGGGTCGTGAAAC CCT</p>	A
GAM1371 LOC149711 3'	<p>—</p> <p>TCCGAAAGTGCTGGGAT 84692</p> <p>ATCCCAGCACTTT GGG</p> <p>           </p> <p>TAGGGTCGTGAAA CCT</p>	GA
GAM1371 LOC149821 5'	<p>G_</p> <p>TCCCAAAGTGCTGGGAT 84768</p> <p>ATCCCAGCACTTTG GGG</p> <p>           </p> <p>TAGGGTCGTGAAAC CCT</p>	A
GAM1371 LOC150054 5'	<p>—</p> <p>TCCCAAAGTGCTGGGAT 84837</p> <p>ATCCCAGCACTTTG GGG</p> <p>           </p> <p>TAGGGTCGTGAAAC CCT</p>	A
GAM1371 LOC150166 5'	<p>—</p> <p>TCCCAAAGTGCTGGGAT 84890</p> <p>ATCCCAGCACTTTG GGG</p> <p>           </p> <p>TAGGGTCGTGAAAC CCT</p>	A
GAM1371 LOC150225 3'	<p>—</p> <p>TCCCAAAGTGCTGGGAT 85013</p> <p>ATCCCAGCACTTTG GGG</p> <p>           </p> <p>TAGGGTCGTGAAAC CCT</p>	A
GAM1371 LOC150282 5'	<p>—</p> <p>GCCCCCAAAGTGCTGGGAT 79727</p> <p>ATCCCAGCACTTTG GGGGC</p> <p>            </p> <p>TAGGGTCGTGAAAC CCCC</p> <p>C</p>	A
GAM1371 LOC150397 3'	<p>TCCCAAAGTGCTGGGAT 79852</p> <p>ATCCCAGCACTTTG GGG</p> <p>           </p> <p>TAGGGTCGTGAAAC CCT</p>	A
GAM1371 LOC150407 3'	<p>—</p> <p>TCCCAAAGTGCTGGGAT 79833</p> <p>ATCCCAGCACTTTG GGG</p> <p>           </p> <p>TAGGGTCGTGAAAC CCT</p>	A
GAM1371 LOC150630 5'	<p>—</p> <p>TCCCAAAGTGCTGGGAT 85114</p> <p>ATCCCAGCACTTTG GGG</p> <p>           </p>	A



GAM1371	LOC151201	3'	TCTGCCTCCCCAAAGTGCTGGG	85295	A	
		AT	ATCCCAGCACTTTG	GGG	GGCAGA	
			TAGGGTCGTGAAAC	CC	CCGTCT	
			C	T		
GAM1371	LOC151475	5'	TCCCAAAGTGCTGGGAT	85421	A	
			ATCCCAGCACTTTG	GGG		
			TAGGGTCGTGAAAC	CCT		
GAM1371	LOC151614	3'	TCCAAAGAAAGTGCTGGGAT	80310	GAG	
			ATCCCAGCACTTT	GGG		
			TAGGGTCGTGAAA	CCT		
			GAAA			
GAM1371	LOC151826	3'	TCCCAAAGTGCTGGGAT	80368	A	
			ATCCCAGCACTTTG	GGG		
			TAGGGTCGTGAAAC	CCT		
GAM1371	LOC151979	5'	TCCCAAAGTGCTGGGAT	80426	A	
			ATCCCAGCACTTTG	GGG		
			TAGGGTCGTGAAAC	CCT		
GAM1371	LOC152343	3'	TCCCAAAGTGCTGGGAT	80571	A	
			ATCCCAGCACTTTG	GGG		
			TAGGGTCGTGAAAC	CCT		
GAM1371	LOC152348	3'	TCCCAAAGTGCTGGGAT	85700	A	
			ATCCCAGCACTTTG	GGG		
			TAGGGTCGTGAAAC	CCT		
GAM1371	LOC152445	3'	TCCCAAAGTGCTGGGAT	85763	A	
			ATCCCAGCACTTTG	GGG		
			TAGGGTCGTGAAAC	CCT		
GAM1371	LOC152620	3'	TCCCAAAGTGCTGAGAT	60089	C	A
			ATC	CAGCACTTTG	GGG	
			TAG	GTCGTGAAAC	CCT	
			A			
GAM1371	LOC152794	5'	TCTCAAAGTGCTGGGAT	80684		
			ATCCCAGCACTTTG	GAGG		

TAGGGTCGTGAAACTCT

GAM1371	LOC152851	3'	TCCCAAAGTGCTGGGAT	80715	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	LOC153077	3'	TCCCAAAGTGCTGGG	85918	A
			CCCAGCACTTTG GGG		
			GGGTCGTGAAAC CCT		
GAM1371	LOC153606	5'	TCCCAAAGTGCTGGGAT	86076	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	LOC153688	3'	TCCCAAAGTGCTAGGAT	86122	C A
			ATCC AGCACTTTG GGG		
			TAGG TCGTGAAAC CCT		
			A		
GAM1371	LOC153811	3'	TCTCAAAGTGCTGGGAT	80958	
			ATCCCAGCACTTTGAGG		
			TAGGGTCGTGAAACTCT		
GAM1371	LOC154141	5'	TCCCAAAGTGCTGGGAT	86174	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	LOC154282	5'	TCCCAAAGTGCTGGGAT	86210	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	LOC154726	5'	TCCCAAAGTGCTGGGAT	81109	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	LOC154877	3'	TCCCAAAGTGCTGGGAT	86312	A
			ATCCCAGCACTTTG GGG		
			TAGGGTCGTGAAAC CCT		
GAM1371	LOC154877	5'	TCCGAAAGTGCTGGGAT	86313	GA
			ATCCCAGCACTTT GGG		

Accession	Gene	Position	Sequence	Length	Quality	Flags
GAM1371	LOC154930	3'	TCTGCCTCCCAAAGTGCTGG	81183	A	
			CCAGCACTTTG GGGGCAGA			
			GGTCGTGAAAC CTCCGTCT			
GAM1371	LOC155372	3'	TCCACCTCCCAAAGTGCTGAGA	81344	C	A CA
			ATC CAGCACTTTG GGGG GA			
			TAG GTCGTGAAAC CTCC CT			
			A C AC			
GAM1371	LOC157247	5'	TCCCAAAGTGCTGGGAT	81378	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC157506	3'	TCCCAAAGTGCTGGGAT	81446	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC157507	5'	TCCCAAAGTGCTGGGAT	81462	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC157681	5'	TCCCAAAGTGCTGGGA	81545	A	
			TCCCAGCACTTTG GGG			
			AGGGTCGTGAAAC CCT			
GAM1371	LOC157858	5'	TCTCAAAGTGCTGGGAT	86606		
			ATCCCAGCACTTTGAGG			
			TAGGGTCGTGAAACTCT			
GAM1371	LOC158310	5'	TCCCAAAGTGCTGGGAT	86764	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC158402	5'	TCCGCCTCCCAAAGTGCTGG	86815	A	A
			CCAGCACTTTG GGGGC GA			
			GGTCGTGAAAC CTCCG CT			
			C C			
GAM1371	LOC158476	3'	TCCCAAAGTGCTGGGAT	86855	A	
			ATCCCAGCACTTTG GGG			

Accession	Gene	Position	Strand	Sequence	Start	End	Quality
GAM1371	LOC158668	3'	+	TCCCAAAGTGCTGAGAT ATC CAGCACTTTG GGG               TAG GTCGTGAAAC CCT A _	69377		C A
GAM1371	LOC158709	3'	+	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	81986		A
GAM1371	LOC158865	5'	-	TCCGAAAATGCTGGGAT ATCCCAGCA TTT GGG               TAGGGTCGT AAA CCT _ AG	86942		C GA
GAM1371	LOC160646	3'	+	TCTGCCTCCCAAAGTGCTGGGA ATCCCAGCACTTTG GGGGCAGA               TAGGGTCGTGAAAC CTCCGTCT C	82232		A
GAM1371	LOC163590	5'	+	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	58865		A
GAM1371	LOC170082	5'	+	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	82565		A
GAM1371	LOC170409	5'	+	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	82868		A
GAM1371	LOC196529	3'	+	TCCCAAAGTGCTGGGATG TATCCCAGCACTTTG GGG             GTAGGGTCGTGAAAC CCT	87783		A
GAM1371	LOC196955	5'	-	TCTGCCCCCCAGCCCTGG CCAG TTG GGGGCAGA               GGTC GAC CCCCCTCT CC_ C	77391		CACT A
GAM1371	LOC197358	3'	+	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG 	88051		A

GAM1371	LOC199699	3'	TCCCAAAGTGCTGGGAT	88314		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC199725	5'	TCCCAAAGTGCTGGGAT	89841		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC199775	5'	TCCCAAAGTGCTGGGAT	88359		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC199786	3'	CCAACCAAAGTGCTGGGAT	88373		AG_
			ATCCCAGCACTTTG GG			
			TAGGGTCGTGAAAC CC			
			CAA			
GAM1371	LOC199786	3'	TCCCAAAGTGCTAGGAT	88394	C	A
			ATCC AGCACTTTG GGG			
			TAGG TCGTGAAAC CCT			
			A			
GAM1371	LOC199786	3'	TCCCAAAGTGCTGGGAT	88395		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC199986	5'	TCCACCCTTCAGTGCTGGGA	89910		TT CA
			TCCCAGCACT GAGGGG GA			
			AGGGTCGTGA CTTCCC CT			
			AC			
GAM1371	LOC200014	3'	TCCCAAAGTGCTGGGAT	88541		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC200169	5'	TCCCAAAGTGCTGGGAT	89959		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC200301	5'	TCCCAAAGTGCTGGGAT	88753		A
			ATCCCAGCACTTTG GGG			

GAM1371	LOC200310	3'	TCCCAAAGTGCTAGGAT	65744	C	A
			ATCC AGCACTTTG GGG			
			TAGG TCGTGAAAC CCT			
			A			
GAM1371	LOC200314	3'	TCCCAAAGTGCTGGGAT	90018		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC200316	5'	TCCCAAAGTGCTGGGAT	88774		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC200316	3'	TCCCAAAGTGCTGGGAT	88775		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC200845	5'	TCCCAAAGTGCTGGGAT	88908		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC200860	3'	TCCCAAAGTGCTGGGAT	90177		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC201164	3'	TCCGCCTCCCAAAGTGCTGGGA	88125		A A
	T		ATCCCAGCACTTTG GGGGC GA			
			TAGGGTCGTGAAAC CTCCG CT			
			C C			
GAM1371	LOC201194	3'	CTGCCCTACTGCAGAGATA	89777	CCA	CTTTG
			TATC GCA AGGGGCAG			
			ATAG CGT TCCCCGTC			
			AGA CA__			
GAM1371	LOC201294	3'	TCCCAAAGTGCTGGGAT	88224		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC201411	3'	TCCCAAAGTGCTGGGAT	62964		A
			ATCCCAGCACTTTG GGG			

	<p> TAGGGTCGTGAAAC CCT  —  GAM1371 LOC201627 3' TCCCAAAGTGCTGGGAT 89025 A  ATCCCAGCACTTTG GGG               TAGGGTCGTGAAAC CCT </p>	
	<p> —  GAM1371 LOC201705 5' TCCCAAAGTGCTGGGAT 90255 A  ATCCCAGCACTTTG GGG               TAGGGTCGTGAAAC CCT </p>	
	<p> —  GAM1371 LOC201799 3' CCCGCCAAGCTGGGATA 89056 ACT A_  TATCCCAGC TTG GGG                 ATAGGGTCG AAC CCC  — CG </p>	
	<p> —  GAM1371 LOC202460 5' TCCCAAAGTGCTGGGAT 89188 A  ATCCCAGCACTTTG GGG               TAGGGTCGTGAAAC CCT </p>	
	<p> —  GAM1371 LOC202934 3' TCTCAAAGTGCTGGGAT 90431  ATCCCAGCACTTTGAGG               TAGGGTCGTGAAACTCT </p>	
	<p> GAM1371 LOC203197 3' TCCCAAAGTGCTGGGAT 89296 A  ATCCCAGCACTTTG GGG               TAGGGTCGTGAAAC CCT </p>	
	<p> —  GAM1371 LOC203339 3' TCCCAAAGTGCTGGGAT 90551 A  ATCCCAGCACTTTG GGG               TAGGGTCGTGAAAC CCT </p>	
	<p> —  GAM1371 LOC203369 3' TCCCAAAGTGCTGGGAT 89345 A  ATCCCAGCACTTTG GGG               TAGGGTCGTGAAAC CCT </p>	
	<p> —  GAM1371 LOC203378 3' TCCCAAAGTGCTGGGAT 90617 A  ATCCCAGCACTTTG GGG               TAGGGTCGTGAAAC CCT </p>	
	<p> —  GAM1371 LOC205251 5' TCCCAAAGTGCTGGGAT 90673 A  ATCCCAGCACTTTG GGG              </p>	

Accession	Gene	Position	Strand	Sequence	Start	End	RefSeq	GenBank
GAM1371	LOC219294	3'	+	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	93011	93011	A	
GAM1371	LOC219295	3'	+	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	92996	92996	A	
GAM1371	LOC219445	5'	+	TCTCAAAGTGCTGGGAT ATCCCAGCACTTTGAGG             TAGGGTCGTGAAACTCT	91580	91580		
GAM1371	LOC219673	5'	+	TCCCAAAGTGCTAGGAT ATCC AGCACTTTG GGG               TAGG TCGTGAAAC CCT A	93045	93045	C	A
GAM1371	LOC219731	5'	+	CCTTCCAAAGTGCTGGGATG TATCCCAGCACTTTG GGG             GTAGGGTCGTGAAAC TCC CT	93093	93093		AG
GAM1371	LOC219894	3'	+	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	93288	93288		A
GAM1371	LOC220064	3'	+	CCTACCAAAGTGCTGG CCAGCACTTTG GGG             GGTCGTGAAAC TCC CA	93423	93423		AG
GAM1371	LOC220074	3'	+	TCCCAAAGTGCTAGGAT ATCC AGCACTTTG GGG               TAGG TCGTGAAAC CCT A	59284	59284	C	A
GAM1371	LOC220074	3'	+	TCCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG             TAGGGTCGTGAAAC CCT	59285	59285		A
GAM1371	LOC221060	3'	+	CCTTCCAAAGTGCTGGGAT ATCCCAGCACTTTG GGG 	93208	93208		AG



			TAGGGTCGTGAAAC	TCC		
			CT			
GAM1371	LOC221663	5'	TCCCAAAGTGCCGGGAT	93825	A	A
			ATCCC GCACTTTG GGG			
			TAGGG CGTGAAAC CCT			
			C _			
GAM1371	LOC221964	3'	TCCCAAAGTGCTGGGAT	93983		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	LOC222070	5'	TCCCAAAGTGCTGGGAT	94162		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	LOC245771	5'	CCTTTCAAAGTGCTGGGAT	92883		
			ATCCCAGCACTTTGAGGGG			
			TAGGGTCGTGAAACTTTCC			
			_			
GAM1371	LOC253842	5'	TCCCAAAGTGCTGGGAT	97391		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	LOC253917	5'	CTGCCCTGGGGAGC	96261	A	G
			GC CTTT AGGGGCAG			
			CG GGGG TCCCCGTC			
			A _			
GAM1371	LOC254100	3'	TCCCAAAGTGCTGGGAT	96419		A
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
			_			
GAM1371	LOC254295	5'	TCTGCCTCCAAAGTGCTGGGAT	96178		A
			ATCCCAGCACTTTG GGGGCAGA			
			TAGGGTCGTGAAAC CTCCGTCT			
			_			
GAM1371	LOC254655	3'	TCTCAAAGTGCTGGGAT	95475		
			ATCCCAGCACTTTGAGG			
			TAGGGTCGTGAAACTCT			
			_			
GAM1371	LOC254672	3'	TCCCAAAGTGCTGGGAT	94648		A
			ATCCCAGCACTTTG GGG			

TAGGGTCGTGAAAC CCT

GAM1371	LOC255149	5'	CCCAAAAGCCTGGGATA	97586	CA	GA
			TATCCCAG CTTT GGG			
			ATAGGGTC GAAA CCC			
			C_ A_			
GAM1371	LOC255308	3'	CCTCACAAAGTGCCGGGAT	94533	A	A
			ATCCC GCACTTTG GGGG			
			TAGGG CGTGAAAC CTCC			
			C A			
GAM1371	LOC255338	5'	TCCCAAAGTGCTGGGAT	95933	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC255465	3'	TCTCAAAGTGCTGGGAT	97303		
			ATCCCAGCACTTTGAGG			
			TAGGGTCGTGAAACTCT			
GAM1371	LOC255707	3'	TCCCAAAGTGCTGGGAT	96964	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC256221	3'	TCCCAAAGTGCTGGGAT	95213	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC256360	5'	TCCCAAAGTGCTGAGAT	96552	C	A
			ATC CAGCACTTTG GGG			
			TAG GTCGTGAAAC CCT			
			A _			
GAM1371	LOC256364	5'	TCCCAAAGTGCTGGGAT	94803	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC257128	5'	TCCCAAATGCTGGGAT	96088	C	A
			ATCCCAGCA TTTG GGG			
			TAGGGTCGT AAAC CCT			
			A _			
GAM1371	LOC257463	3'	TCCCAAAGTGCTGGGAT	71071	A	
			ATCCCAGCACTTTG GGG			

GAM1371	LOC257465	3'	TCCCAAAGTGCTGGGAT	81602	A			
			ATCCCAGCACTTTG GGG					
			TAGGGTCGTGAAAC CCT					
GAM1371	LOC51008	5'	TCCCAAAGTGCTGGGAT	31971	A			
			ATCCCAGCACTTTG GGG					
			TAGGGTCGTGAAAC CCT					
GAM1371	LOC51015	3'	TCTGCTTTCCAAAGTATAGGA	32121	CAGC	AG		
			TCC ACTTTG GGGCAGA					
			AGG TGAAAC TTCGTCT					
			ATA_ CT					
GAM1371	LOC51094	5'	TCTGCCCCCTGGGGCTGAGA	32046	C	A	TGA	
			TC CAGC CTT GGGGCAGA					
			AG GTCG GGG CCCCCTCT					
			A _ TC_					
GAM1371	LOC51193	5'	TCCCAAAGTGCTGGGAT	32911	A			
			ATCCCAGCACTTTG GGG					
			TAGGGTCGTGAAAC CCT					
GAM1371	LOC51219	5'	TCCCAAAGTGCTGGGAT	33128	A			
			ATCCCAGCACTTTG GGG					
			TAGGGTCGTGAAAC CCT					
GAM1371	LOC51696	3'	TCCCAAAGTGCTGGGAT	32559	A			
			ATCCCAGCACTTTG GGG					
			TAGGGTCGTGAAAC CCT					
GAM1371	LOC56181	5'	TCCCAAAGTGCTGGGAT	95542	A			
			ATCCCAGCACTTTG GGG					
			TAGGGTCGTGAAAC CCT					
GAM1371	LOC57107	3'	TCCCAAAGTGCTGGGAT	39844	A			
			ATCCCAGCACTTTG GGG					
			TAGGGTCGTGAAAC CCT					
GAM1371	LOC57146	3'	TCCCAAAGTGCTGGGAT	39929	A			
			ATCCCAGCACTTTG GGG					

GAM1371	LOC81034	3'	<div> <div>—</div> <div>TCCCAAAGTGCTGGGAT</div> <div>47859</div> <div>A</div> </div> <div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>			
GAM1371	LOC89231	3'	<div> <div>—</div> <div>TCCCAAAGTGCTGGGAT</div> <div>92737</div> <div>A</div> </div> <div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>			
GAM1371	LOC89932	3'	<div> <div>—</div> <div>TCCCAAATGCTGGGAT</div> <div>60819</div> <div>C</div> <div>A</div> </div> <div> <div>ATCCCAGCA TTTG GGG</div> <div>     </div> <div>TAGGGTCGT AAAC CCT</div> </div>			
GAM1371	LOC89932	3'	<div> <div>A</div> <div>—</div> <div>TCCCAAAGTGCTGGGAT</div> <div>60820</div> <div>A</div> </div> <div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>			
GAM1371	LOC90110	5'	<div> <div>—</div> <div>TCCCAAAGTGCTGGGAT</div> <div>61514</div> <div>A</div> </div> <div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>			
GAM1371	LOC90155	3'	<div> <div>—</div> <div>CTGCCCTCACCCGCTAGGA</div> <div>61693</div> <div>C</div> <div>ACTT</div> </div> <div> <div>TCC AGC TGAGGGGCAG</div> <div>       </div> <div>AGG TCG ACTCCCCGTC</div> </div>			
GAM1371	LOC90288	3'	<div> <div>A</div> <div>CCCC</div> <div>TCCCAAAGTGCTGGGAT</div> <div>62106</div> <div>A</div> </div> <div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> <div>TAGGGTCGTGAAAC CCT</div> </div>			
GAM1371	LOC90333	3'	<div> <div>—</div> <div>TCCACCTCCCAAAGTGCTGAGA</div> <div>62302</div> <div>C</div> <div>A</div> <div>CA</div> </div> <div> <div>ATC CAGCACTTTG GGGG GA</div> <div>       </div> <div>TAG GTCGTGAAAC CTCC CT</div> </div>			
GAM1371	LOC90485	3'	<div> <div>A</div> <div>C</div> <div>AC</div> <div>TCCCAAAGTGCTGGGA</div> <div>63027</div> <div>A</div> </div> <div> <div>TCCCAGCACTTTG GGG</div> <div>     </div> <div>AGGGTCGTGAAAC CCT</div> </div>			
GAM1371	LOC90485	3'	<div> <div>—</div> <div>TCCCAAAGTGCTGGGAT</div> <div>63028</div> <div>A</div> </div> <div> <div>ATCCCAGCACTTTG GGG</div> <div>     </div> </div>			

		TAGGGTCGTGAAAC CCT		
		—		
GAM1371	LOC90591 3'	TCCCAAAGTGCTGGGAT	63443	A
		ATCCCAGCACTTTG GGG		
		TAGGGTCGTGAAAC CCT		
		—		
GAM1371	LOC90591 3'	TCCCAAAGTGCTGGGATG	63444	A
		TATCCCAGCACTTTG GGG		
		GTAGGGTCGTGAAAC CCT		
		—		
GAM1371	LOC90918 3'	TCCCAAAGTGCCGGGAT	64361	A A
		ATCCC GCACTTTG GGG		
		TAGGG CGTGAAAC CCT		
		C		
		—		
GAM1371	LOC91115 3'	TCCCAAAGTGCTGGGAT	64954	A
		ATCCCAGCACTTTG GGG		
		TAGGGTCGTGAAAC CCT		
		—		
GAM1371	LOC91250 5'	TCCCAAAGTGCTGGGAT	65328	A
		ATCCCAGCACTTTG GGG		
		TAGGGTCGTGAAAC CCT		
		—		
GAM1371	LOC91308 3'	TCCCAAAGTGCTGGGAT	65565	A
		ATCCCAGCACTTTG GGG		
		TAGGGTCGTGAAAC CCT		
		—		
GAM1371	LOC91373 3'	TCCCAAAGTGCTGGGAT	65844	A
		ATCCCAGCACTTTG GGG		
		TAGGGTCGTGAAAC CCT		
		—		
GAM1371	LOC91893 3'	TCCCAAAGTGCTGGGAT	67463	A
		ATCCCAGCACTTTG GGG		
		TAGGGTCGTGAAAC CCT		
		—		
GAM1371	LOC92148 5'	TCTCAAAGTGCTGGGAT	68337	
		ATCCCAGCACTTTGAGG		
		TAGGGTCGTGAAACTCT		
		—		
GAM1371	LOC92303 3'	TCCCAAAGTGCTGGGAT	68827	A
		ATCCCAGCACTTTG GGG		

GAM1371	LOC92482	3'	CCTTCCAAAGTGCTGGGAT	69487	AG	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC TCC			
			CT			
GAM1371	LOC92661	5'	TCCCAAAGTGCTGGGAT	70087	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC92689	3'	TCCCAAAGTGCTGGGAT	70231	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC92697	5'	GCCCCCAAAGTGCCGAGAT	70272	CCA	A
			ATC GCACTTTG GGGGC			
			TAG CGTGAAAC CCCC			
			AGC C			
GAM1371	LOC92841	3'	TCCCAAAGTGCTGGGAT	70724	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC93129	3'	TCCCAAAGTGCTGGGAT	71469	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC93349	3'	TCCCAAAGTGCTGGGA	56467	A	
			TCCCAGCACTTTG GGG			
			AGGGTCGTGAAAC CCT			
GAM1371	LOC93356	3'	TCCCAAATGCTGGGAT	72080	C	A
			ATCCCAGCA TTTG GGG			
			TAGGGTCGT AAAC CCT			
			A			
GAM1371	LOC93408	5'	TCCCAAAGTGCTGGGAT	56483	A	
			ATCCCAGCACTTTG GGG			
			TAGGGTCGTGAAAC CCT			
GAM1371	LOC93496	3'	TCCCAAAGTGCTGGGAT	72438	A	
			ATCCCAGCACTTTG GGG			

TAGGGTCGTGAAAC CCT

GAM1371 LOC93626 3' CTGCCCCCAAAAAAGCAGAGG 72769 CCA AC\_ A  
TA TATC GC TTTG GGGGCAG

|||| || |||| |||||  
ATGG CG AAAC CCCCCTC  
AGA AAA C

GAM1372 BAPX1 3' CCAAGGGGTGCGAAACCCT 6811 \_ A  
AGGGTTTC ACCCC TGG

|||||| |||| |||  
TCCCAAAG TGGGG ACC  
CG A

GAM1372 CA6 3' ACTTAAAGGAAATGGAACCCT 6869 C\_ CA  
AGGGTTTCA CC TGGGT

|||||| || ||||  
TCCCAAGGT GG ATTCA  
AAA AA

GAM1372 MAML1 3' GCACAGGGTGAGACCCT 28591 CA G  
AGGGTTTCACCC TG GT

|||||| || ||  
TCCCAGAGTGGG AC CG  
\_ A

GAM1372 MAN2C1 5' GCTCATGGAGCGGAACCCT 72919 ACC  
AGGGTTTC CCATGGGT

|||||| |||||  
TCCCAAGG GGTACTCG  
CGA

GAM1372 MYO15A 5' ACGCAGGGTGAAACCC 32667 CA G  
GGGTTTCACCC TG GT

|||||| || ||  
CCCAAAGTGGG AC CA  
\_ G

GAM1372 PA2G4 3' ACCAACATGGCGAAACCCT 71298 ACC \_  
AGGGTTTC CCATG GGT

|||||| |||| ||  
TCCCAAAG GGTAC CCA  
C\_ AA

GAM1372 PRX 3' AACTTCCTGAGATGAAACTC 40514 CCC T T  
GGGTTTCA CA GGG AGTT

|||||| || || ||||  
CTCAAAGT GT CCT TCAA  
AGA \_ \_

GAM1372 PRX 3' AACTCCCTGAGGTGAAACTC 40513 C T T  
GGGTTTCACC CA GGG AGTT

|||||| || || ||||  
CTCAAAGTGG GT CCC TCAA  
A \_ \_

GAM1372 SORCS2 3' AACCACCCATGGAGACTGGAAC 40410 CC\_ A  
CT GGGTTTCA CCATGGGT GTT

|||||| |||| |||| |||

		TCCAAGGT GGTACCCA CAA CAGA C	
GAM1372	SULT1C1	3' ACAC TTTGAGGGAAACCCT 6463 AGGGTTTC CC CA GG GT                     TCCCAAAG GG GT TC CA _ A T A	A C T _
GAM1372	USP14	3' GCCACATGGTGAAACCCT 17660 AGGGTTTCACC ATG GGT                  TCCCAAAGTGG TAC CCG _ A	CC _
GAM1372	ZNF136	3' ACCCATATTTGAGAGAAACCCT 59884 AGGGTTTC ATGGGT                  TCCCAAAG TACCCA AGAGTTTA	ACCC_
GAM1372	ZNF26	5' ACTCATACAGGAGTGAAACCC 72978 GGGTTTCAC CC ATGGGT                     CCCAAAGTG GG TACTCA A ACA	_ C_
GAM1372	ZNF266	3' ACTCACATTGGAGAGAAACCCT 88320 AGGGTTTC CCA TGGGT                     TCCCAAAG GGT ACTCA AGA TAC	ACC _
GAM1372	ZNF266	3' ACTCACTGGGGAGAAACCCT 88321 AGGGTTTC CCCC A TGGGT                        TCCCAAAG GGGGT ACTCA A C	A _
GAM1372	ZNF267	3' AATTTATATGGGAGTGAAACCC 12734 AGGGTTTCAC CCCATG AGTT                        TCCCAAAGTG GGGTAT TTAA A AT_	_ GGT
GAM1372	ZNF268	3' ACTCATGCCGAAGAGAAACCCT 62898 AGGGTTTC CATGGGT                        TCCCAAAG GTACTCA AGAAGCC	ACCC_
GAM1372	ATP9A	3' CCCTGAAGTGAAACCCT 62041 AGGGTTTCAC CA GGG                  TCCCAAAGTG GT CCC AA _	CC T
GAM1372	BDG-29	3' ACCCACGGAAATGAAAGCCT 72350 AGG TTTCA CC TGGGT 	G CC_ A



		TCC AAAGT GG ACCCA	
		G AAA C	
GAM1372 BLZF1	5'	AACGTATTCGGAAGCGAAACC 13368	ACCCCA TA__
	CT	AGGGTTTC TGGG GTT	
		TCCCAAAG GCCT CAA	
		CGAAG_ TATG	
GAM1372 C20orf45	3'	AAGTGTTTCATAAATGAAACCCT 32104	CCCC GG G
		AGGGTTTCA ATG TA TT	
		TCCCAAAGT TAC GT AA	
		AAA_ TT G	
GAM1372 CAMKK2	3'	ACTTCAGGGTGAAATCCT 21575	CAT
		AGGGTTTCACCC GGGT	
		TCCTAAAGTGGG TTCA	
		AC_	
GAM1372 CSAD	3'	GCCAATAAGGTGAAACCCT 32029	CCATG
		AGGGTTTCACC GGT	
		TCCCAAAGTGG CCG	
		AATAA	
GAM1372 DKFZp434I1610	3'	CACTGGAGTGAAACCCT 63451	C _
		AGGGTTTCAC CCA TG	
		TCCCAAAGTG GGT AC	
		A C	
GAM1372 DKFZP564B1023	3'	ACCAACATGGAGAAACCCT 48535	ACC _
		AGGGTTTC CCATG GGT	
		TCCCAAAG GGTAC CCA	
		A_ AA	
GAM1372 DKFZP564I052	3'	CTGGCCAACATGGTGAAACCCT 66706	CCA_ G
		AGGGTTTCACC TGG TAG	
		TCCCAAAGTGG ACC GTC	
		TACA G	
GAM1372 FLJ11457	3'	ACTGATGGAGTGAAATCC 45394	C G
		GGGTTTCAC CCAT GGT	
		CCTAAAGTG GGTA TCA	
		A G	
GAM1372 FLJ12606	3'	ACCTGGGCAACATGGTGAAACC 45639	_____ A
	CT	AGGGTTTCACC CC TGGGT	
		TCCCAAAGTGG GG GTCCA	
		TACAAC _	
GAM1372 FLJ13193	3'	CCTGGTCTACATGGTGAAACCC 49764	_____ T
		GGGTTTCACC CCA GG	

		CCCAAAGTGG	GGT CC	
		TACATCT	_	
GAM1372	FLJ13902	3'	CCTGGGCAATAGAGCGAGACCC 45042	AC_____ T
		T	AGGGTTTC	CCCA GG
			TCCCAGAG	GGGT CC
			CGAGATAAC	_
GAM1372	FLJ14100	3'	CTGGCTAACACGGTGAAACCCT 46678	CCA_ G
			AGGGTTTCACC	TGG TAG
			TCCCAAAGTGG	ATC GTC
			CACA	G
GAM1372	FLJ20034	3'	CTAGCCAACATGGTGAAACCC 34368	CCA_ G
			GGGTTTCACC	TGG TAG
			CCCAAAGTGG	ACC ATC
			TACA	G
GAM1372	FLJ20700	3'	ACTGGCCAACAGAATGAAACCC 35569	CCCCA_ G
		T	AGGGTTTCA	TGG TAGT
			TCCCAAAGT	ACC GTCA
			AAGACA	G
GAM1372	FLJ21603	3'	ACCACAGAGTGAGACCCT 45421	CCCA _
			AGGGTTTCAC	TG GGT
			TCCCAGAGTG	AC CCA
			AG__	A
GAM1372	HSZFP36	3'	AACTACTCACACTGGAGAGAAA 63473	ACC ____
		CCCT	AGGGTTTC	CCA TGGGTAGTT
			TCCCAAAG	GGT ACTCATCAA
			AGA	CAC
GAM1372	HSZFP36	3'	ACTCACACCGGAGAGAAACCCT 63477	AC_ CA__
			AGGGTTTC	CC TGGGT
			TCCCAAAG	GG ACTCA
			AGA	CCAC
GAM1372	HSZFP36	3'	ACTCACACTGGAGTGAAACCCT 63478	C ____
			AGGGTTTCAC	CCA TGGGT
			TCCCAAAGTG	GGT ACTCA
			A	CAC
GAM1372	KIAA0266	3'	CATGGTGAAACCCT 41329	CC
			AGGGTTTCACC	ATG
			TCCCAAAGTGG	TAC
			—	
GAM1372	KIAA0565	3'	AACCTCCAACATGGTGAAACCC 66883	CCATG TA
			GGGTTTCACC	GG GTT

		CCCAAAGTGG	CC CAA		
		TACAA TC			
GAM1372	KIAA1271	3'	GCCAACAGGGTGAAACCC	69546	CATG
			GGGTTTCACCC	GGT	
			CCCAAAGTGGG	CCG	
			ACAA		
GAM1372	KIAA1554	3'	CCTGGGTGACAGAGTGAGACCC	95150	_____ T
		T	AGGGTTTCAC	CCCA GG	
			TCCCAGAGTG	GGGT CC	
			AGACAGT	_	
GAM1372	KIAA1559	3'	CCTGGTTAACATGGTGAAACCC	73061	_____ T
		T	AGGGTTTCACC	CCA GG	
			TCCCAAAGTGG	GGT CC	
			TACAATT	_	
GAM1372	LCE	3'	AACTTTCCAAATGAAACCC	44025	CCCCA T
			GGGTTTCA	TGGG AGTT	
			CCCAAAGT	ACCT TCAA	
			AA_____	T	
GAM1372	MAP3K2	3'	TCAGGAGATGAAACCCT	21735	CC_ A
			AGGGTTTCA	CC TGG	
			TCCCAAAGT	GG ACT	
			AGA	_	
GAM1372	MESDC1	3'	TCATAGGTGAAACCC	42596	CC
			GGGTTTCACC	ATGG	
			CCCAAAGTGG	TACT	
			A_		
GAM1372	MGC11386	3'	CTGGCCAACATGGTGAAACCCT	51951	CCA_ G
			AGGGTTTCACC	TGG TAG	
			TCCCAAAGTGG	ACC GTC	
			TACA	G	
GAM1372	MGC12466	5'	ACTCACACTGGAGTGAAACCTT	79030	C ____
			AGGGTTTCAC	CCA TGGGT	
			TTCCAAAGTG	GGT ACTCA	
			A	CAC	
GAM1372	MGC2562	3'	CATGGTGAAACCCT	50435	CC
			AGGGTTTCACC	ATG	
			TCCCAAAGTGG	TAC	
			—		
GAM1372	PRO0456	3'	ACCTGGCGGACAGAGTGAGACC	26173	C____ A_
		CT	AGGGTTTCAC	CC TGGGT	

		TCCCAGAGTG GG GTCCA	
		AGACA CG	
GAM1372 RoXaN	3'	GGCTAACATGGTGAAACCC 46651	CC GG
		GGGTTTCACC ATG TAGTT	
		CCCAAAGTGG TAC ATCGG	
		— A—	
GAM1372 SETBP1	3'	AACCACCAAAAACTGAAACCC 31456	CCCCATG A
		GGGTTTCA GGT GTT	
		CCCAAAGT CCA CAA	
		CAAAAA_ C	
GAM1372 LOC116228	3'	GCCAACAGGGTGAAACCCT 73799	CATG
		AGGGTTTCACCC GGT	
		TCCCAAAGTGGG CCG	
		ACAA	
GAM1372 LOC152627	3'	ACCCAGGTGAAACCC 80624	CCA
		GGGTTTCACC TGGGT	
		CCCAAAGTGG ACCCA	
		—	
GAM1372 LOC152702	3'	ACTCATAGTGGAAGAAACCCT 80645	ACC —
		AGGGTTTC CCA TGGGT	
		TCCCAAAG GGT ACTCA	
		AAA GAT	
GAM1372 LOC152804	3'	CTAGTCAACATGGTGAAACCC 85880	CCA_ G
		GGGTTTCACC TGG TAG	
		CCCAAAGTGG ACT ATC	
		TACA G	
GAM1372 LOC203276	3'	CTGGCCAACATGGTGAAACCCT 90483	CCA_ G
		AGGGTTTCACC TGG TAG	
		TCCCAAAGTGG ACC GTC	
		TACA G	
GAM1372 LOC203305	3'	CTGGCCAACATGGTGAAACCCT 90527	CCA_ G
		AGGGTTTCACC TGG TAG	
		TCCCAAAGTGG ACC GTC	
		TACA G	
GAM1372 LOC221477	3'	GCCAACAGGGTGAAACCC 92154	CATG
		GGGTTTCACCC GGT	
		CCCAAAGTGGG CCG	
		ACAA	
GAM1372 LOC254243	3'	CTGGCCAACATGGTGAAACCCT 97412	CCA_ G
		AGGGTTTCACC TGG TAG	

	TCCCAAAGTGG ACC GTC	
	TACA G	
GAM1372 LOC255671 3'	CCCACATGGTGAAACCCT 97254	CCA
	AGGGTTTCACC TGGG	
	TCCCAAAGTGG ACCC	
	TAC	
GAM1372 LOC256112 3'	ACTCATATAAGACAGAAACCCT 96360	ACCCC__
	AGGGTTTC ATGGGT	
	TCCCAAAG TACTCA	
	ACAGAATA	
GAM1372 LOC256112 3'	AACACACTTGAGGTGAAACCCT 96359	C TGG A
	AGGGTTTCACC CA GT GTT	
	TCCCAAAGTGG GT CA CAA	
	A TCA _	
GAM1372 LOC256207 3'	AACCTCCAACATGGTGAAACCC 95163	CCATG TA
	GGGTTTCACC GG GTT	
	CCCAAAGTGG CC CAA	
	TACAA TC	
GAM1372 LOC55974 3'	GACTAACATGGTGAAACCC 38132	CC GG
	GGGTTTCACC ATG TAGTT	
	CCCAAAGTGG TAC ATCAG	
	_ A_	
GAM1372 LOC90038 3'	CTGGCCAACATGGTGAAACCCT 61155	CCA_ G
	AGGGTTTCACC TGG TAG	
	TCCCAAAGTGG ACC GTC	
	TACA G	
GAM1372 LOC90591 3'	ACTCGCTGAAGAGAAACCCT 63409	ACCC _
	AGGGTTTC CA TGGGT	
	TCCCAAAG GT GCTCA	
	AGAA C	
GAM1372 LOC90639 3'	CATGGGTGAAACCCT 63653	C
	AGGGTTTCACCC ATG	
	TCCCAAAGTGGG TAC	
	-	
GAM1372 LOC91818 5'	ACTTGAGGATGAAACCCT 67268	C _ TG
	AGGGTTTCA CC CA GGT	
	TCCCAAAGT GG GT TCA	
	A A _	
GAM1373 BCL7A 3'	ACTCTGCTGTGAAGC 40636	GAA T
	GCTTCACAG CAG GT	

CGAAGTGTC GTC CA  
 \_\_\_\_ T  
 GAM1373 CDKN2B 3' ACACTCACCATGAAGCGAAACA 54352 C CA AAC  
 TGT TCGCTTCA GG AGTGT  
 ||| ||||| || |||||  
 ACA AGCGAAGT CC TCACA  
 A A\_ AC\_  
 GAM1373 FBXL7 3' CACCATCCTAGCGAGGCA 24542 TCAC ACA  
 TGTCTCGCT AGGA GTG  
 ||||| ||| |||  
 ACGGAGCGA TCCT CAC  
 \_\_\_\_ AC\_  
 GAM1373 HSPC213 3' ATTGTTCTGTAAAGAAAACA 33209 CTCG C  
 TGT CTT ACAGGAACAGT  
 ||| ||| |||||  
 ACA GAA TGTCCTTGTTA  
 AAA\_ A  
 GAM1373 KIAA0356 3' CACTGTTCTAGTGAGC 66189 T \_  
 GCT CAC AGGAACAGTG  
 ||| ||| |||||  
 CGA GTG TCCTTGTCAC  
 \_ A  
 GAM1373 LOC124895 5' CCTGTGAAGGGAGACA 74350 G  
 TGTCTC CTTACAGG  
 ||||| |||||  
 ACAGAG GAAGTGTCC  
 G  
 GAM1373 LOC222029 5' ACACTGTTCCCAGGGCACAGAC 94033 C\_ CACA  
 A TGTCT GCTT GGAACAGTGT  
 |||| ||| |||||  
 ACAGA CGGG CCTTGTCACA  
 CA AC\_  
 GAM1374 ALPP 3' AGGACACTGGTCGAGAGCCAA 68832 GCCC C  
 TTGGT CTCGACCAG GTCCT  
 |||| ||||| |||||  
 AACCG GAGCTGGTC CAGGA  
 A\_ A  
 GAM1374 GLUL 3' GGTCACGGGGCACCAA 9042 TC  
 TTGGTGCCCC GACC  
 ||||| |||  
 AACCACGGGG CTGG  
 CA  
 GAM1374 FLJ11000 3' GGCCGAGGGGCAGCAA 36961 G A  
 TTG TGCCCCTCG CC  
 ||| ||||| |||  
 AAC ACGGGGAGC GG  
 G C  
 GAM1374 FLJ13769 3' GACGCTGGACTCGACACGAA 46611 G CCCC \_  
 TT GTG TCGA CCAGCGTC  
 || ||| ||| |||||

	AA CAC AGCT GGTCGCAG	
	G ____ CA	
GAM1374 MAP1LC3A 3'	CTAGTCAGAGGGCACCAA 50707	_ C C
	TTGGTGCCC CT GAC AG	
	AACCACGGG GA CTG TC	
	A _ A	
GAM1374 RALGPS1A 3'	GGAGCCATGAGGCACCAA 27607	CC ACCA G
	TTGGTGCC TCG GC TCC	
	AACCACGG AGT CG AGG	
	__ AC__ _	
GAM1374 LOC130470 3'	ACACTAGACAGAAGGCACTAA 74943	CC GACC_ C
	TTGGTGCC TC AG GT	
	AATCACGG AG TC CA	
	A_ ACAGA A	
GAM1374 LOC146108 3'	GCTCCGTCAGGGGCACCAA 77668	C C_
	TTGGTGCCCCT GAC AGC	
	AACCACGGGGA CTG TCG	
	_ CC	
GAM1374 LOC147991 5'	GTTGACCAGGAGGCACCAA 78603	_ CGAC
	TTGGTGCC CCT CAGC	
	AACCACGG GGA GTTG	
	A CCA_	
GAM1374 LOC148490 3'	AGGAGCATCGAAGGGCACCGA 78883	C CCA G
	TTGGTGCCC TCGA GC TCCT	
	AGCCACGGG AGCT CG AGGA	
	A A__ _	
GAM1374 LOC154791 5'	GGACGCCGTTGGGCACCA 81159	CT ACCA
	TGGTGCCC CG GCGTCC	
	ACCACGGG GC CGCAGG	
	TT ____	
GAM1374 LOC220021 3'	TGCTGGTCAAGGGGCACGAA 93400	G C
	TT GTGCCCCT GACCAGCG	
	AA CACGGGGA CTGGTCGT	
	G A	
GAM1374 LOC254556 5'	GGAAACGAAAGGCACCAA 94617	CC ACCAGCG
	TTGGTGCC TCG TCC	
	AACCACGG AGC AGG	
	AA AA_____	
GAM1375 BBS4 3'	AGCTAGATCCTATCA 52279	TA
	TGATAG ATCTAGCT	

		ACTATC TAGATCGA		
		C_		
GAM1375	PAG	3' AGCTAGATCACTACA 37398	A A	
		TG TAGT ATCTAGCT		
		AC ATCA TAGATCGA		
		_ C		
GAM1375	TNS	5' CAACCATGAGCTGGTGCCCATC 42627	A_ AT CA	
	A	TGAT GTA CTAGCTCA GTTG		
		ACTA CGT GGTCGAGT CAAC		
		CC _ AC		
GAM1375	UBE2V1	3' CAACTGTGAAAAGACACATCA 41789	A AA AGC	
		TGAT GT TCT TCACAGTTG		
		ACTA CA AGA AGTGTCAAC		
		_ C_ AA_		
GAM1375	UBE2V1	3' CAACTGTGAAAAGACACATCA 42367	A AA AGC	
		TGAT GT TCT TCACAGTTG		
		ACTA CA AGA AGTGTCAAC		
		_ C_ AA_		
GAM1375	UBE2V1	3' CAACTGTGAAAAGACACATCA 12514	A AA AGC	
		TGAT GT TCT TCACAGTTG		
		ACTA CA AGA AGTGTCAAC		
		_ C_ AA_		
GAM1376	USP14	3' AGCCTGGCCACATGGTGAA 17655	_ A	
		TTCAC ATGTGGCCA GTT		
		AAGTG TACACCGGT CGA		
		G C		
GAM1376	C1orf16	3' CATGTCCCCAGCCACATGGGAA 29228	A CAAGTTAT	
		TTC CATGTGGC CATG		
		AAG GTACACCG GTAC		
		G ACCCCT_		
GAM1376	FLJ10702	3' CATGATAAAGTCAGCACACA 36439	_ CAAG_	
		TGTG GC TTATCATG		
		ACAC CG AATAGTAC		
		A ACTGA		
GAM1376	FLJ14281	3' CATGATCTGTTTGGCCACATG 46213	TT_	
		CATGTGGCCAAG ATCATG		
		GTACACCGGTTT TAGTAC		
		GTC		
GAM1376	HYPK	3' AGCCTGGCCAACATGTGAA 33077	_ A	
		TTCACATGT GGCCA GTT		



AAGTGTACA CCGGT CGA  
 A C  
 GAM1376 KIAA0445 5' CATGATAACTCTGTGACATAGA 27951 AC G CA  
 A TTC ATGT GC AGTTATCATG  
 ||| |||| || |||||  
 AAG TACA TG TCAATAGTAC  
 A\_ G TC  
 GAM1376 KIAA1189 3' TGGTAGCTACACATG 72048 GCCA  
 CATGTG AGTTATCA  
 ||||| |||||  
 GTACAC TCGATGGT  
 A\_\_  
 GAM1376 LIPI 5' CATAATAACTTGTGCCA 79565 \_ C  
 TGGC CAAGTTAT ATG  
 ||| ||||| |||  
 ACCG GTTCAATA TAC  
 T A  
 GAM1376 SEMA4F 3' GACCTGGCCACATGTG 14941 A  
 CACATGTGGCCA GTT  
 ||||| |||  
 GTGTACACCGGT CAG  
 C  
 GAM1376 ZNF300 3' CATGACCCCTAAAGCTACATGT 53475 CA\_ TTA  
 ACATGTGGC AG TCATG  
 ||||| || ||||  
 TGTACATCG TC AGTAC  
 AAA CCC  
 GAM1376 LOC149579 5' CATGATAACTCTGTGACATAGA 71131 AC G CA  
 A TTC ATGT GC AGTTATCATG  
 ||| |||| || |||||  
 AAG TACA TG TCAATAGTAC  
 A\_ G TC  
 GAM1376 LOC92223 5' CATGATAGTTCCACATGGAA 68520 A CCA GT  
 TTC CATGTGG A TATCATG  
 ||| ||||| | |||||  
 AAG GTACACC T ATAGTAC  
 \_ C\_ TG  
 GAM1377 NRAP 3' CCAGCTGCAGAGTGAT 20508 \_  
 ATCACTTTGCAG GG  
 ||||| ||  
 TAGTGAGACGTC CC  
 GA  
 GAM1377 SLC16A7 3' TAATCCTACAAAGTGA 16405 CA  
 TCACTTTG GGGATTA  
 ||||| |||||  
 AGTGAAAC TCCTAAT  
 A\_  
 GAM1377 XYLB 3' ATCAGCTGAAAAGTGAT 17558 G G\_  
 ATCACTTT CAG GAT  
 ||||| ||| |||

			TAGTGAAA GTC CTA		
			A GA		
GAM1377	C8orf13	3'	CATTAGTAAAGGAGCAAAGTGA 81569	AGGGA	
			TCAC TTTGC TTACTAATG		
			AGTGAAACG AATGATTAC		
			AGGA_		
GAM1377	FLJ21477	3'	CATCCGTGTCCCTGCAAAGGA 47146	A	T TA
			TC CTTTGCAGGGAT AC ATG		
			AG GAAACGTCCCTG TG TAC		
			_ _ CC		
GAM1377	HZFW1	3'	CATCAGTATTGGTAAAGTGA 47458	AGGGAT	A
			TCAC TTTGC TACT ATG		
			AGTGAAATG ATGA TAC		
			GTT_ _ C		
GAM1377	LOC256021	3'	ATTAAACCCCAAAGTGAT 96514	CA	A AC
			ATCACTTTG GGG TT TAAT		
			TAGTGAAAC CCC AA ATTA		
			_ _ A _		
GAM1377	LOC51291	5'	GGTCCCTGCAGAGCGAT 33364	A	
			ATC CTTTGCAGGGATT		
			TAG GAGACGTCCCTGG		
			C		
GAM1378	CA2	3'	CACAATTGTTGACTAAAATGCT 3560	A	_
	GC		GTAGCATTTTAG TGACA TTGTG		
			CGTCGTAAAATC GTTGT AACAC		
			A T		
GAM1378	KIAA0471	3'	CAGTTTGCATCTAAAAGACTAC 29390	CA	AC_
			GTAG TTTTAGATG ATTG		
			CATC AAAATCTAC TGAC		
			AG GTT		
GAM1378	LOC219894	5'	CACAATGTCATCTTATTTAAAT 93276	T_ _ _	
	GT		GCATTT AGATGACATTGTG		
			TGTAAA TCTACTGTAACAC		
			TTTAT		
GAM1379	CACNG3	5'	GAGAGCTCCAGAAAGGAAATCC 21542	CC	GA T
	CA		TGGGAT TCT CT GAGCTCTC		
			ACCCTA GGA GA CTCGAGAG		
			AA AA C		
GAM1379	CD97	3'	AGACTGATGTCAGAGGCCCCA 54346	AT	TTG C
			TGGG CCTCTGAC AG TCT		

			ACCC GGAGACTG TC AGA		
			C_ TAG _		
GAM1379	CD97	3'	AGACTGATGTCAGAGGCCCCA 8358	AT	TTG C
			TGGG CCTCTGAC AG TCT		
			ACCC GGAGACTG TC AGA		
			C_ TAG _		
GAM1379	FMOD	3'	AGCAGAGTCAGGAGACCCCA 8928	A CT	GA
			TGGG TC CTGACTT GCT		
			ACCC AG GACTGAG CGA		
			C AG A_		
GAM1379	GJA5	3'	GAGCTCAAAGTTCCCA 17941	TCCTCTG	_
			TGGGA ACTT GAGCTC		
			ACCCT TGAA CTCGAG		
			_____ A		
GAM1379	MOX2	3'	AGCCTTAAGGATCCCA 66928	CTGACT	_
			TGGGATCCT TGAG CT		
			ACCCTAGGA ATTC GA		
			_____ C		
GAM1379	PKD1	3'	CATGTCAGAGGACCCCA 4310	A	T
			TGGG TCCTCTGAC TG		
			ACCC AGGAGACTG AC		
			C T		
GAM1379	SLC7A6	3'	GAGCGAAGCCAGAGGATCCC 14307	A	GA
			GGGATCCTCTG CTT GCTC		
			CCCTAGGAGAC GAA CGAG		
			C G_		
GAM1379	KIAA0514	5'	GAGGTAGGAGTCAGGGAACCC 28083	A T	GA T
			GGG TCC CTGACTT GC CTC		
			CCC AGG GACTGAG TG GAG		
			A _ GA _		
GAM1379	KIAA0561	3'	AGTTCAAGCCAGAAAACCCA 65873	ATCC	A
			TGGG TCTG CTTGAGCT		
			ACCC AGAC GAACTTGA		
			AAA_ C		
GAM1379	KIAA1054	3'	GAGAGCTCAAATCATTCCA 68436	TCCTC	C
			TGGGA TGA TTGAGCTCTC		
			ACCTT ACT AACTCGAGAG		
			T_ A		
GAM1379	TBDN100	3'	AGAGCTCAAAGAAAGCCCA 46949	ATCC	GAC
			TGGG TCT TTGAGCTCT		

ACCC AGA AACTCGAGA  
 GAA\_ A\_  
 GAM1379 WIT-1 5' GAGCCGCAGTCGGAGGACCCCA 31827 A \_ A  
 TGGG TCCTCTGACT TG GCTC  
 ||| ||||| || |||  
 ACCC AGGAGGCTGA GC CGAG  
 C C \_  
 GAM1379 LOC137964 5' AGAGTGTCAGAGGATACCA 75277 G \_ TTGA  
 TGG ATCCTCTG AC GCTCT  
 || ||||| || |||  
 ACC TAGGAGAC TG TGAGA  
 A C \_  
 GAM1379 LOC145824 3' GATGCTGAAGTGAGAGGATCCC 77525 G G \_  
 A TGGGATCCTCT ACTT AGC TC  
 ||||| ||| ||| ||  
 ACCCTAGGAGA TGAA TCG AG  
 G G T  
 GAM1379 LOC150280 5' GAGAGCTCTTATGGAGAACGCC 79711 ATC\_ GACTT  
 GG CTCT GAGCTCTC  
 || ||| |||||  
 CC GAGG CTCGAGAG  
 GCAA TATT\_  
 GAM1379 LOC154427 3' AGAACTCAGCCAGGATTCCA 86217 CTGAC C  
 TGGGATCCT TTGAG TCT  
 ||||| ||| |||  
 ACCTTAGGA GACTC AGA  
 CC\_ A  
 GAM1379 LOC158476 5' GAGTCAGAAGACCCA 86845 A C  
 TGGG TC TCTGACTT  
 ||| || |||||  
 ACCC AG AGACTGAG  
 \_ A  
 GAM1379 LOC200032 5' GAGCTCAAAGTTCCCA 84322 TCCTCTG \_  
 TGGGA ACTT GAGCTC  
 ||| ||| |||||  
 ACCCT TGAA CTCGAG  
 \_ A  
 GAM1379 LOC219529 5' AGAATCAAGGACCAAGGATCCC 92965 CTGA\_ GC  
 A TGGGATCCT CTTGA TCT  
 ||||| ||| |||  
 ACCCTAGGA GAACT AGA  
 ACCAG A\_  
 GAM1379 LOC255952 3' AGAGCCCAATGGATTCCA 97632 TCTGAC A  
 TGGGATCC TTG GCTCT  
 ||||| || |||||  
 ACCTTAGG AAC CGAGA  
 T\_ C  
 GAM1379 LOC90620 3' AGAGCTCAAGGTGGGACTCCA 63569 GA CTGA  
 TGG TCCT CTTGAGCTCT  
 || ||| |||||

ACC AGGG GAACTCGAGA  
 TC TG\_\_  
 GAM1380 CSPG3 3' GACAGGAGTAAGGATTTG 15230 TGG C  
 CAG CT ACTCCTGTC  
 ||| || |||||  
 GTT GA TGAGGACAG  
 TAG A  
 GAM1380 DUSP4 5' GACAGGAGCCGCGACCGGCA 7337 ACA G TCA\_  
 A TTGC GT GC CTCCTGTC  
 |||| || || |||||  
 AACG CA CG GAGGACAG  
 GC\_ G CGCC  
 GAM1380 GTF2I 3' TGACAGGAATGAATCTCAC 52226 C\_\_ C  
 GTGG TCA TCCTGTCA  
 |||| || |||||  
 CACT AGT AGGACAGT  
 CTA A  
 GAM1380 GTF2I 3' TGACAGGAATGAATCTCAC 52227 C\_\_ C  
 GTGG TCA TCCTGTCA  
 |||| || |||||  
 CACT AGT AGGACAGT  
 CTA A  
 GAM1380 PCDHA9 3' AGCTGTGAGCCACTGTGC 25755 TC  
 GCACAGTGGCTCAC CT  
 ||||| ||  
 CGTGTACCGAGTG GA  
 TC  
 GAM1380 TDGF1 3' GTGAGCAACTGTGCAA 12202 G  
 TTGCACAGT GCTCAC  
 ||||| |||||  
 AACGTGTCA CGAGTG  
 A  
 GAM1380 TRIM9 5' TGACAGGCTTGAGCCACCGCGC 30770 ACA CT  
 AG TTGC GTGGCTCA CCTGTCA  
 |||| ||||| |||||  
 GACG CACCGAGT GGACAGT  
 CGC TC  
 GAM1380 VNN1 3' ACAGCCATGCACTGTGCAA 16239 G TCACTC  
 TTGCACAGTG C CTGT  
 ||||| | |||||  
 AACGTGTCAC G GACA  
 \_ TACC\_  
 GAM1380 ATP8A1 3' GACATAAGCACTGTGCAA 20338 GCTCA CC  
 TTGCACAGTG CT TGTC  
 ||||| || |||||  
 AACGTGTCAC GA ACAG  
 \_\_\_\_ AT  
 GAM1380 D2S448 3' ACAGGAGTGGAATGTACA 73514 C GTGG T  
 TG ACA C CACTCCTGT  
 || ||| | |||||

AC TGT G GTGAGGACA  
 A AA\_\_  
 GAM1380 DKFZP434O047 5' CAGGCAAGTCACTGTACAA 31506 C CACT  
 TTG ACAGTGGCT CCTG  
 ||| ||||| |||  
 AAC TGTCAGTGA GGAC  
 A AC\_\_  
 GAM1380 FER1L4 3' CAGGTGTGAGCCACCATGC 47335 CA T  
 GCA GTGGCTCAC CCTG  
 ||| ||||| |||  
 CGT CACCGAGTG GGAC  
 AC T  
 GAM1380 FLJ13102 3' CAGGCATGAGCCACCATGC 46005 CA CT  
 GCA GTGGCTCA CCTG  
 ||| ||||| |||  
 CGT CACCGAGT GGAC  
 AC AC  
 GAM1380 FLJ22316 5' CAGGCATGAGCCACTGCACAG 46917 CA CT  
 TTG CAGTGGCTCA CCTG  
 ||| ||||| |||  
 GAC GTCACCGAGT GGAC  
 AC AC  
 GAM1380 FLJ25416 3' TGACAGGAATGCTGCCAGCAA 58815 ACAG T\_ C  
 TTGC TGGC CA TCCTGTCA  
 ||| ||| || |||||  
 AACG ACCG GT AGGACAGT  
 \_\_\_\_ TC A  
 GAM1380 KIAA1161 5' CAGGCATGAGCCACCACGC 81739 ACA CT  
 GC GTGGCTCA CCTG  
 || ||||| |||  
 CG CACCGAGT GGAC  
 CAC AC  
 GAM1380 KIAA1855 3' GGAAGCCACTGTCAA 92343 C CAC  
 TTG ACAGTGGCT TCC  
 ||| ||||| |||  
 AAC TGTCACCGA AGG  
 \_\_\_\_  
 GAM1380 MGC5149 3' CAGGCGTGAGCCACCGC 72288 ACA T  
 GC GTGGCTCAC CCTG  
 || ||||| |||  
 CG CACCGAGTG GGAC  
 C\_\_ C  
 GAM1380 RNF13 3' TGACAGGAGCGGTCTAT 23464 CT A  
 GTGG C CTCCTGTCA  
 ||| | |||||  
 TATC G GAGGACAGT  
 TG C  
 GAM1380 SARCOSIN 3' GACAGGAATCCTGTGCA 20232 T CTCAC  
 TGCACAG GG TCCTGTC  
 ||||| || |||||

ACGTGTC CT AGGACAG  
 \_ A\_  
 GAM1380 SIPL 3' ACAGGAGTATTAGTACAT 36850 \_ C\_  
 GTG GCT ACTCCTGT  
 ||| ||| |||||  
 TAC TGA TGAGGACA  
 A TTA  
 GAM1380 SMOC2 5' TGACAGGAGCGAGGGCGGACGC 72378 ACA\_ GG A  
 AA TTGC GT CTC CTCCTGTCA  
 ||| || ||| |||||  
 AACG CG GAG GAGGACAGT  
 CAGG G\_ C  
 GAM1380 TBCC 3' CAGGCGTGAGCCACCACGC 12139 ACA T  
 GC GTGGCTCAC CCTG  
 || ||||| |||  
 CG CACCGAGTG GGAC  
 CAC C  
 GAM1380 LOC124871 3' TAGGCATGAGCCACTGTGC 74349 CT  
 GCACAGTGGCTCA CCTG  
 ||||| |||  
 CGTGTCACCGAGT GGAT  
 AC  
 GAM1380 LOC147276 3' CAGGCATGAGCCACTGCGC 78332 A CT  
 GC CAGTGGCTCA CCTG  
 || ||||| |||  
 CG GTCACCGAGT GGAC  
 C AC  
 GAM1380 LOC155036 5' GAGTCAAGGCCACTGTACAA 86342 C C\_  
 TTG ACAGTGGCT ACTC  
 ||| ||||| |||  
 AAC TGTACCGG TGAG  
 A AAC  
 GAM1380 LOC200282 5' CAGGTGTGAGCCACCGTGCA 88706 A T  
 TGCAC GTGGCTCAC CCTG  
 ||| ||||| |||  
 ACGTG CACCGAGTG GGAC  
 C T  
 GAM1380 LOC200742 3' GGAGTGAGCCATGTGCAA 88869 G  
 TTGCACA TGGCTCACTCC  
 ||||| |||||  
 AACGTGT ACCGAGTGAGG  
 \_  
 GAM1380 LOC202934 3' CAGATGTGAGCCACTGTGC 90405 TC  
 GCACAGTGGCTCAC CTG  
 ||||| |||  
 CGTGTCACCGAGTG GAC  
 TA  
 GAM1380 LOC221336 3' GTGACCACTGTGCAA 92274 C  
 TTGCACAGTGG TCAC  
 ||||| |||

AACGTGTCACC AGTG

GAM1380 LOC255465 3' CAGATGTGAGCCACTGTGC 97282 TC  
GCACAGTGGCTCAC CTG  
||||||| |||  
CGTGTACCCGAGTG GAC

TA

GAM1380 LOC91380 3' TAGGTGTGAGCCACTGTGC 65862 T  
GCACAGTGGCTCAC CCTG  
||||||| |||  
CGTGTACCCGAGTG GGAT

T

GAM1380 LOC93349 3' TGACAGGAGTGAGCCAC 56470  
GTGGCTCACTCCTGTCA  
|||||||  
CACCGAGTGAGGACAGT

GAM1381 ABCC3 3' ACGTGGACCCAAACAATGTGC 39147 TG A T GAA  
G CATTGT TG GT TTACGT  
| ||||| || |||||  
C GTAACA AC CA GGTGCA  
GT A C \_

GAM1381 ACAA1 5' TGTGGTTCTGCGCGTGTGC 7839 TGT \_  
GCAT ATGTGT GAATTACG  
||| ||||| |||||  
CGTG TGCGCG CTTGGTGT

\_ T

GAM1381 ACTC 3' GTTTACACACGTGCAAT 60186 AATT  
ATTGTATGTGTG AC  
||||||| ||  
TAACGTGCACAC TG

ATT\_

GAM1381 ADAM12 3' ATGTTGATTACAGTGCAGTGCG 12966 G ATT  
C GTGCATTGTAT TGTGA ACGT  
||||||| ||||| |||  
CGCGTGACGTG ACATT TGTA

\_ AGT

GAM1381 ADAMTS13 3' TCGCAACAGTGCGC 57377 ATG  
GTGCATTGT TGTGA  
||||||| |||||  
CGCGTGACA ACGCT

GAM1381 ADAMTS6 3' ATGTAATTTGTGCAGATTTGT 26549 TTGTA TG  
GCA TGTG AATTACGT  
||| ||||| |||||  
TGT ACGT TTAATGTA

TTAG\_ GT

GAM1381 ADH1B 3' CACATATACAAATGTAT 72641 \_  
GTGCATT GTATGTGTG  
||||||| |||||



		TATGTAA CATATACAC			
		A			
GAM1381	AGL	3' ATGTGAGGAAACATGCAAAGCA 5362	A	GTGAA	
	T	GTGC TTGTATGT TTACGT			
		TACG AACGTACA AGTGTA			
		A AAGG_			
GAM1381	AGL	3' ATGTGAGGAAACATGCAAAGCA 5368	A	GTGAA	
	T	GTGC TTGTATGT TTACGT			
		TACG AACGTACA AGTGTA			
		A AAGG_			
GAM1381	AGL	3' ATGTGAGGAAACATGCAAAGCA 5376	A	GTGAA	
	T	GTGC TTGTATGT TTACGT			
		TACG AACGTACA AGTGTA			
		A AAGG_			
GAM1381	AGL	3' ATGTGAGGAAACATGCAAAGCA 5343	A	GTGAA	
	T	GTGC TTGTATGT TTACGT			
		TACG AACGTACA AGTGTA			
		A AAGG_			
GAM1381	AGL	3' ATGTGAGGAAACATGCAAAGCA 5355	A	GTGAA	
	T	GTGC TTGTATGT TTACGT			
		TACG AACGTACA AGTGTA			
		A AAGG_			
GAM1381	AGL	3' ATGTGAGGAAACATGCAAAGCA 3447	A	GTGAA	
	T	GTGC TTGTATGT TTACGT			
		TACG AACGTACA AGTGTA			
		A AAGG_			
GAM1381	AGTR1	3' CACATATATATATATGTAT 16707	—		
		GTGCAT TGTATGTGTG			
		TATGTA ATATATACAC			
		TAT			
GAM1381	AGTR1	3' CACATATATATATATGTAT 49006	—		
		GTGCAT TGTATGTGTG			
		TATGTA ATATATACAC			
		TAT			
GAM1381	AGTR1	3' CACATATATATATATGTAT 49431	—		
		GTGCAT TGTATGTGTG			
		TATGTA ATATATACAC			
		TAT			
GAM1381	AGTR1	3' CACATATATATATATGTAT 5471	—		
		GTGCAT TGTATGTGTG			

			TATGTA ATATATACAC		
			TAT		
GAM1381	AGTR1	3'	CACATATATATATATGTAT 23777	___	
			GTGCAT TGTATGTGTG		
			TATGTA ATATATACAC		
			TAT		
GAM1381	ANK2	3'	TCTATGTACAATGTAT 6710	T	
			GTGCATTGTATGTG GA		
			TATGTAACATGTAT CT		
			—		
GAM1381	ANK2	3'	TCTATGTACAATGTAT 40604	T	
			GTGCATTGTATGTG GA		
			TATGTAACATGTAT CT		
			—		
GAM1381	ANK3	3'	GTGCAATTAGCAATGCAGTGTA 40630	G G	ACGT
	T		GTGCATTGTAT TGT AATT		
			TATGTGACGTA ACG TTAA		
			— A CGTGT		
GAM1381	AQP3	3'	ATGTGTGTGCATGTGTGTGCAT 59589	TGT	AAT
			GTGCAT ATGTGTG TACGT		
			TACGTG TGTACGT GTGTA		
			TG_ GT_		
GAM1381	AQP3	3'	GTGTGTGTGCATGTGTGTGCAT 59591	TG_	TG AAT
			GTGCAT TATG TG TAC		
			TACGTG GTAC GT GTG		
			TGT GT GT_		
GAM1381	ARF3	3'	GTGTTTGCCTGCATGTGTGCGC 8005	TGT	TG AAT_
			GTGCAT ATG TG TAC		
			CGCGTG TAC GC GTG		
			TG_ GT GTTT		
GAM1381	ARHGEF6	3'	ATGTGTGTGCGTGACGTGCGC 68196	_	TG AAT
			GTGCAT TGTATG TG TACGT		
			CGCGTG ACGTGC GT GTGTA		
			C GT _		
GAM1381	ARHGEF6	3'	GTGTGCATATGTGTGTGCGTGC 68205	T	___ AAT GT
	AC		GCAT GTAT GTGTG TAC		
			CGTG CGTG TATAC GTG		
			_ TGTG GT_		
GAM1381	ASPH	5'	TCGACATGCAGTGTGC 50625	TG	G
			G CATTGTATGT TGA		

C GTGACGTACA GCT  
 GT \_  
 GAM1381 ASTN 3' ACGTGTGCACACACAATGCAC 69327 AT AAT  
 GTGCATTGT GTGTG TACGT  
 ||||| ||| |||  
 CACGTAACA CACAC GTGCA  
 \_ GT\_  
 GAM1381 ATP11A 3' ACGTGAGCTCCCACACGTACAC 77015 \_ AA\_  
 ATGCAC AT TGTATGTGTG TTACGT  
 || ||||| |||  
 TA ACATGCACAC AGTGCA  
 C CCTCG  
 GAM1381 ATP11A 3' CACACATGCATGCAC 77020 T  
 GTGCAT GTATGTGTG  
 |||| |||||  
 CACGTA CGTACACAC  
 \_  
 GAM1381 ATP11A 3' TACACATGCACATGTAC 77034 \_  
 GTGCAT TGTATGTGTG  
 |||| |||||  
 CATGTA ACGTACACAT  
 C  
 GAM1381 ATP11A 3' TCACACACGTGTATGCAC 77035 \_ TA  
 GTGCAT TG TGTGTGA  
 |||| || |||||  
 CACGTA GT ACACACT  
 T GC  
 GAM1381 ATP11A 3' TCACATATGTACATGTAC 77036 \_  
 GTGCAT TGTATGTGTGA  
 |||| |||||  
 CATGTA ATGTATACACT  
 C  
 GAM1381 ATP11A 3' TGTGATACACACATGCATGTAC 77038 T A GT  
 GTGCAT GTATGTGTG ATTAC  
 |||| ||||| |||  
 CATGTA CGTACACAC TAGTG  
 \_ A TG  
 GAM1381 ATP6V0D1 3' GTGTGTGCGCGTGTGTGTGC 16268 TG TGT AAT  
 G CAT ATGTGTG TAC  
 | || ||||| |||  
 C GTG TGC GCGT GTG  
 GT TG\_ GT\_  
 GAM1381 ATP7A 3' CACACATATATATGTAC 3519 \_  
 GTGCAT TGTATGTGTG  
 |||| |||||  
 CATGTA ATATACACAC  
 T  
 GAM1381 ATP8A2 3' TCACTACGTGTGATGTAT 93519 TG \_  
 GTGCAT TATGT GTGA  
 |||| |||| |||

TATGTA GTGCA CACT  
 GT T  
 GAM1381 ATRN 3' ATGTAACAAACCTGCATGTTGT 57808 TG \_ GAA  
 GCAC TGCAT TATGT GT TTACGT  
 |||| |||| || ||||  
 ACGTG GTACG CA AATGTA  
 TT TC AAC  
 GAM1381 ATRN 3' ATGTAACAAACCTGCATGTTGT 23832 TG \_ GAA  
 GCAC TGCAT TATGT GT TTACGT  
 |||| |||| || ||||  
 ACGTG GTACG CA AATGTA  
 TT TC AAC  
 GAM1381 B4GALT6 3' ACGTGATGAGTTATTTGGTGCA 59862 T TGTGA  
 C GTGCATTG ATG ATTACGT  
 |||||| || ||||  
 CACGTGGT TAT TAGTGCA  
 T TGAG\_  
 GAM1381 BACH2 3' ATGTAATTTAATTCAATGCAT 41486 TATGTG  
 GTGCATTG TGAATTACGT  
 |||||| ||||||  
 TACGTAAC ATTTAATGTA  
 TTA\_\_\_\_  
 GAM1381 BAZ2A 5' GTGGTTCGCAAGAAGCAT 25609 ATTGTATG  
 GTGC TGTGAATTAC  
 ||| ||||||  
 TACG ACGCTTGGTG  
 AAGA\_\_\_\_  
 GAM1381 BCAT1 3' ATGTAGTTTGTAGTATCAATGT 66199 TG T \_ TG  
 GT G CATTG ATG TG AATTACGT  
 | |||| || || ||||  
 T GTAAC TAT AT TTGATGTA  
 GT \_ G GT  
 GAM1381 BCL11A 3' ACGTTGGTTTGTATGTAGTGT 43156 TG T TG \_  
 GC G CATTGTATG G AATTA CGT  
 | |||||| | |||| ||  
 C GTGATGTAT T TTGGT GCA  
 GT \_ GT T  
 GAM1381 BCL2L2 3' CGCGTGTGCATGTGCAC 14467 \_ TG  
 GTGCAT TGTA TGTG  
 |||| || ||  
 CACGTG ACGT GCGC  
 T GT  
 GAM1381 BCL7A 3' TGGTTTGTACAATGTAC 40646 GTGT  
 GTGCATTGTAT GAATTA  
 |||||| ||||  
 CATGTAACATG TTTGGT  
 \_\_\_\_\_  
 GAM1381 BDKRB2 3' GTGCTACGTACATGTGAGGCAT 5264 A TG AAT  
 GTGC T TATGTGTG TAC  
 ||| | |||||| ||

			TACG A GTACATGC GTG		
			G GT ATC		
GAM1381	BHMT2	3'	TCATGCTGTGGTGCAT 34311	TG T	
			GTGCAT TA GTGTGA		
			TACGTG GT CGTACT		
			GT _		
GAM1381	BRF2	3'	ATGGGTTTGTGTGTATGGTGTG 37009	_ TG TG TG ACGT	
	AT		GTG CAT TA TG AATT		
			TAC GTG AT GT TTGG		
			T GT GT GT GTA		
GAM1381	BSN	3'	ATGTGCGTGCGTGCGTGTGTGT 12916	TG _ TG AAT	
			G CAT TGTATG TG TACGT		
			T GTG GCGTGC GC GTGTA		
			GT T GT _		
GAM1381	BSN	3'	GTGTATGTGCGTGCGTGCG 12927	T TG AAT	
			TGCAT GTATG TG TAC		
			GCGTG CGTGC GT GTG		
			_ GT AT_		
GAM1381	BTAF1	3'	GGATATATTTGTATATATATGT 72456	T TG TACGT	
	AC		GTGCAT GTATGTG AAT		
			CATGTA TATATAT TTA		
			_ GT TATAGGG		
GAM1381	BTAF1	3'	TGTGTGCATACATATGTAT 72459	TTG AAT T	
			GTGCA TATGTGTG TACG		
			TATGT ATACATAC GTGT		
			_ GT_ C		
GAM1381	BTAF1	3'	TTTCAATCATATATATAATATA 72460	C ATTACGT	
	T		GTG ATTGTATGTGTGA		
			TAT TAATATATATACT		
			A AACTTTG		
GAM1381	C11orf8	3'	GGTTTATATATATAAGTAT 7818	A	
			GTGC TTGTATGTGTGAATT		
			TATG AATATATATATTTGG		
			-		
GAM1381	CACNA1C	5'	ATGTGATAACATATATGGGGTG 5557	G A_	
	TAC		GTGCATT TATGTGTG ATTACGT		
			CATGTGG GTATATAC TAGTGTA		
			G AA		
GAM1381	CAV2	3'	TTTACATATATAGTCAC 6943	C	
			GTG ATTGTATGTGTGAA		

CAC TGATATATACATTT

GAM1381 CCNT2 3' TGTAATTCTTTACAATG 54270 TGTGT  
CATTGTA GAATTACG  
||||| |||||  
GTAACAT CTTAATGT  
TT\_\_

GAM1381 CCR2 3' GTGATTCACAGTGTGA 5384 TG G  
T TAT TGTGAATTAC  
| ||| |||||  
A GTG ACACTTAGTG  
GT \_

GAM1381 CDH11 3' ATGTATGTACAATAACAATGTAC 53361 G AAT  
GTGCATTGTAT TGTG TACGT  
||||||| ||| ||||  
CATGTAACATA ACAT ATGTA  
\_ GT\_

GAM1381 CDH11 3' TCTATATGTAGTGCAT 53365 T  
GTGCATTGTATGTG GA  
||||||| ||  
TACGTGATGTATAT CT

GAM1381 CDH13 3' TTCATATATACAGGCAT 6996 A  
GTGC TTGTATGTGTGAA  
||| |||||  
TACG GACATATATACTT

GAM1381 CHS1 3' TACACATGTAGTGATAC 3588 \_  
GTG CATTGTATGTGTG  
||| |||||  
CAT GTGATGTACACAT  
A

GAM1381 CKTSF1B1 3' GCGTAGTTCGTGTGCATGAGTG 25369 G TG\_\_  
T GCATT TATG T GAATTACGT  
||||| ||| | |||||  
TGTGA GTAC G CTTGATGCG  
\_ GT TG

GAM1381 CLK1 5' GCGTGATTCCCGTGATTGCG 94463 TTG TGT  
TGCA TATG GAATTACGT  
||| ||| |||||  
GCGT GTGC CTTAGTGCG  
TA\_ C\_\_

GAM1381 CLN6 3' GCGTGGAATTCGTGTGTGTGTGT 35407 TG TG\_ TG \_  
GTGT CAT TATG TGAATT ACGT  
||| ||| ||||| |||||  
GTG GTGT GCTTAG TGCG  
GT TGT GT G

GAM1381 CLN6 3' TGTGTCTTGTATATGTGTGCGC 35412 TGT TG AT GT  
GTGCAT ATGTG A TAC  
||||| ||||| | |||

		CGCGTG TATAT T GTG	
		TG_ GT CT TG	
GAM1381	CMAR	3' GTCTAGTCACGCATGCAGTGT 17778	ATT_
		GCATTGTATGTGTGA AC	
		TGTGACGTACGCACT TG	
		GATC	
GAM1381	CNGB3	3' GTGATTTTCATGCAGTG 38873	TGT
		CATTGTATG GAATTAC	
		GTGACGTAC TTTAGTG	
		—	
GAM1381	COL11A1	3' TGCATATACAGGTAC 54655	A
		GTGC TTGTATGTGTG	
		CATG GACATATACGT	
		—	
GAM1381	COL11A1	3' TGCATATACAGGTAC 8496	A
		GTGC TTGTATGTGTG	
		CATG GACATATACGT	
		—	
GAM1381	COL1A2	3' ATTGAGTTGTATCGTGTGGTGT 3612	TG _ TG A CGT
	AT	GTGCAT TATG TG A TTA	
		TATGTG GTGC AT T AGT	
		GT T GT G TA	
GAM1381	COL4A6	3' GTGGGTGCGTAGGATGTGT 53319	TG G TG GAA
		G CATT TATG T TTAC	
		T GTAG ATGC G GGTG	
		GT G GT _	
GAM1381	CPNE3	3' ATGTGGTTTGCAGGTTGCTGTG 14025	T _ G TG
	C	GCAT GTA T TG AATTACGT	
		CGTG CGT G AC TTGGTGTA	
		T TG GT	
GAM1381	CREBL2	3' ATGTAATTCATGTAATTGTAT 7143	TTGTA TG
		GTGCA TG TGAATTACGT	
		TATGT AT ACTTAATGTA	
		TA_ GT	
GAM1381	CRIM1	3' TACACATACAATTTAT 33176	C
		GTG ATTGTATGTGTG	
		TAT TAACATACACAT	
		T	
GAM1381	CRY2	3' TGCCTGTTTGTGTGTGCATGCA 72212	T TG TG TACGT
	T	GTGCAT GTA TG AAT	

			TACGTA CGT GT TTG		
			_ GT GT TCCGTG		
GAM1381	CSF2RB	3'	CACACGTACATGCAC 4620	T	
			GTGCAT GTATGTGTG		
			CACGTA CATGCACAC		
			-		
GAM1381	CSNK1G3	3'	ATGTGAACCTTGTTCAGTGTA 15222		TGTGTGAA
		T	GTGCATTGTA TTACGT		
			TATGTGACGT AGTGTA		
			TGTTCCA_		
GAM1381	CSPG3	3'	GTGGTTCTGCATGTGTGATG 15235	TG	_ GT
			CAT TATGTGT GAATTAC		
			GTA GTGTACG CTTGGTG		
			GT T		
GAM1381	CSPG3	3'	GTGTGTCTGCGTGTGCCATGTG 15236	TG T TG	_ AT GT
		C	G CAT GTA TGT GA TAC		
			C GTA CGT GCG CT GTG		
			GT C GT T GT		
GAM1381	CTGF	3'	GTGTATATATATATATATATGT 8576	_	A _ GT
		AC	GTGCAT TGTATGTGTG AT TAC		
			CATGTA ATATATATAT TA GTG		
			T A T		
GAM1381	CTLA4	5'	GTGTGCACATGTGTAATACAT 17811	C	AAT
			GTG ATTGTATGTGTG TAC		
			TAC TAATGTGTACAC GTG		
			A GT_		
GAM1381	CTNND2	3'	TGCATGTGCATGCAT 7186	T	
			GTGCAT GTATGTGTG		
			TACGTA CGTGTACGT		
			-		
GAM1381	CYB5	3'	TGTAATTTACTTATTATAAGCA 8596	A	TGT_ GT
		T	GTGC TTGTA GTGAATTAC		
			TACG AATAT CATTTAATG		
			_ TATT TG		
GAM1381	CYP24	3'	GTGTATGTGCATATGAAGCAC 5769	A TG	TG AAT
			GTGC T TATG TG TAC		
			CACG A ATAC GT GTG		
			A GT GT AT_		
GAM1381	DACH	3'	GTTGGTCATATGTACAGTATAT 54970	C	ATT
			GTG ATTGTATGTGTGA AC		



TAT TGACATGTATACT TG  
 A GGT  
 GAM1381 DDX3 3' TGCATGTGCTGTGCAT 7228 T  
 GTGCAT GTATGTGTG  
 ||||| |||||  
 TACGTG CGTGTACGT  
 T  
 GAM1381 DDX6 3' TATATATATAAAGCAC 15290 A  
 GTGC TTGTATGTGTG  
 ||| |||||  
 CACG AATATATATAT  
 A  
 GAM1381 DMRT1 3' GTAATTTAACAGTGCA 41699 ATGTG  
 TGCATTGT TGAATTAC  
 ||||| |||||  
 ACGTGACA ATTTAATG  
  
 GAM1381 DMXL1 3' ATGTATGTATACGTGTGTGTGT 18576 TG TG\_ AAT  
 GT G CAT TATGTGTG TACGT  
 | ||| ||||| |||||  
 T GTG GTGCATAT ATGTA  
 GT TGT GT\_  
 GAM1381 DNMT1 3' GTCCGTTACATGTGTGGTACA 7269 C TG TACGT  
 T GTG AT TATGTGTGAAT  
 ||| || |||||  
 TAC TG GTGTACACTTG  
 A GT CCTG  
 GAM1381 DPYSL3 3' GTGTTGAGAGCGTGTGTAGTGC 7318 TG GAAT\_ GT  
 GCATTGTA TGT TAC  
 ||||| ||| |||  
 CGTGATGT GCG GTG  
 GT AGAGTT  
 GAM1381 DVL3 3' TATGCATACATGCAC 15375 T  
 GTGCAT GTATGTGTG  
 ||||| |||||  
 CACGTA CATACGTAT  
  
 GAM1381 DXF68S1E 3' ATGCTTTATGTATGCATATGTA 60002 \_ TG TTACGT  
 T GTGCAT TGTATG TGAA  
 ||||| ||||| |||  
 TATGTA ACGTAT ATTT  
 T GT CGTA  
 GAM1381 DXF68S1E 3' ATGTAAACTGTGTATGCATATA 60003 A AA\_\_\_\_  
 AGTAT TTGTATGTGTG TTACGT  
 ||||| |||||  
 AATATACGTAT AATGTA  
 \_ GTGTCA  
 GAM1381 DXF68S1E 3' CATATATACATGTGTGT 60004 TG \_  
 G CAT TGTATGTGTG  
 | ||| |||||

			T GTG ACATATATAC		
			GT T		
GAM1381	E2F1	3'	GTGTGAGCATGTGTGTGTCAT 84801	TG_	GAAT GT
			GTGCAT TATGTGT TAC		
			TACGTG GTGTACG GTG		
			TGT AGT_		
GAM1381	E2F1	3'	GTGTGTCCACATGTGTGTGTCAT 84802	TG_	T AT
			GTGCAT TATGTG GA TAC		
			TACGTG GTACAC CT GTG		
			TGT _ GT		
GAM1381	ED1	3'	GTGTATATAAACTATATATAAT 7374	_ GAAT_	GT
			GTAT TGCATTGTATGT GT TAC		
			ATGTAATATATA CA ATG		
			T AATAT TG		
GAM1381	EDNRA	5'	CGCGCGTACAGTCAT 64106 C		
			GTG ATTGTATGTGTG		
			TAC TGACATGCGCGC		
			—		
GAM1381	EFNA3	3'	TCTATATATAATGTAC 17068	T	
			GTGCATTGTATGTG GA		
			CATGTAATATATAT CT		
			—		
GAM1381	EGFL5	3'	ATGTGTCTCATACATATGCTGT 86612	TT	AT
	AC		GTGCA GTATGTGTGA TACGT		
			CATGT TATACATACT GTGTA		
			CG CT		
GAM1381	EGLN1	5'	GTGGTGTACGTGCAGAGCGC 41897	A	TGA
			GTGC TTGTATGTG ATTAC		
			CGCG GACGTGCAT TGGTG		
			A G_		
GAM1381	EGR3	3'	ACATATACATGTGAGTGTAC 59549	_____	
			GTGCAT TGTATGTGT		
			CATGTG ACATATACA		
			AGTGT		
GAM1381	EGR3	3'	ATGTATGTGTATGTATATGCAT 59550	T	GT AAT
			GTGCAT GTATGT G TACGT		
			TACGTA TATGTA T ATGTA		
			_ TG GT_		
GAM1381	EGR3	3'	ATGTGTATGTATATGCATGCAT 59551	T	TGAAT
			GTGCAT GTATGTG TACGT		

TACGTA CGTATAT GTGTA  
 \_ GTAT\_  
 GAM1381 EGR3 3' GCGTGCTCGCGTGTGTGTGTAT 59557 TGT TG AT  
 GTGCAT A TGTGA TACGT  
 ||||| | |||| ||||  
 TATGTG T GCGCT GTGCG  
 TG\_GT C\_  
 GAM1381 EIF1A 3' TTAGATGTTTATACATGTAATG 88606 TACGT  
 TAC GTGCATTGTATGTGTGAAT  
 |||||  
 CATGTAATGTACATATTTG  
 TAGATTT  
 GAM1381 EIF1A 3' GTTTATACATGTAATGTAC 88604  
 GTGCATTGTATGTGTGAAT  
 |||||  
 CATGTAATGTACATATTTG  
  
 GAM1381 EMP1 3' ATGTAATTTGCATTACTCTG 7442 TT T TG  
 CA GTA GTG AATTACGT  
 || ||| |||||  
 GT CAT TAC TTAATGTA  
 CT \_ GT  
 GAM1381 ENTPD6 5' GTGTGGCGGAGCGCGCGGTGCA 6971 TA G\_ AAT GT  
 T GTGCATTG TGT TG TAC  
 ||||| ||| || |||  
 TACGTGGC GCG GC GTG  
 GC AG GGT  
 GAM1381 EP300 3' GTGGTTCAAGTGTGCAC 7476 TGTATGTG  
 GTGCAT TGAATTAC  
 ||||| |||||  
 CACGTG ACTTGGTG  
 TGA\_\_\_\_  
 GAM1381 EPHA2 5' GCGTGCAGGCGTGCGGGTGTGC 15406 TG \_ G AAT  
 G CATT GTATGT TG TACGT  
 | |||| || |||||  
 C GTGG CGTGCG AC GTGCG  
 GT G G \_\_\_\_  
 GAM1381 EPHA8 3' ATGGGATCTCATGTGAACAGTG 40054 TG A TG \_ TA  
 TGT G CATTGT TG TGA AT CGT  
 | |||| || ||| |||  
 T GTGACA GT ACT TA GTA  
 GT A GT C GG  
 GAM1381 ESR1 3' TCATGTATACAGTCAT 3710 C TG  
 GTG ATTGTATG TGA  
 ||| ||||| |||  
 TAC TGACATAT ACT  
 \_ GT  
 GAM1381 ETV3 3' CTCCATTCATATATATGATGT 17882 TG TACGT  
 GCAT TATGTGTGAAT  
 ||| |||||

			TGTA ATATATACTTA		
			GT CCTCA		
GAM1381	ETV5	3'	TATACATAGATGCAT 15490	G	
			GTGCATT TATGTGTG		
			TACGTAG ATACATAT		
			—		
GAM1381	EXT2	5'	CGCATGCGCAGTGCGC 4633	AT	
			GTGCATTGT GTGTG		
			CGCGTGACG TACGC		
			CG		
GAM1381	EYA2	3'	TCATGTGGACAGTGCAC 17886	A TG	
			GTGCATTGT TG TGA		
			CACGTGACA GT ACT		
			G GT		
GAM1381	F13A1	3'	TGTAGTTTTGTGATGCAT 91061	TG TGTGT	
			GTGCAT TA GAATTACG		
			TACGTA GT TTTGATGT		
			GT ———		
GAM1381	F2R	3'	ATGTGTGTATATGTAGATGTAT 8835	G AAT	
			GTGCATT TATGTGTG TACGT		
			TATGTAG ATGTATAT GTGTA		
			— GT_		
GAM1381	F7	3'	CACACATCAGTGCAC 39026	T	
			GTGCATTG ATGTGTG		
			CACGTGAC TACACAC		
			—		
GAM1381	F7	3'	CACACATGGATGCAC 39027	G	
			GTGCATT TATGTGTG		
			CACGTAG GTACACAC		
			—		
GAM1381	F7	3'	CGCACATGCCAATGCAC 39029	—	
			GTGCATTG TATGTGTG		
			CACGTAAC GTACACGC		
			C		
GAM1381	F7	3'	TACACATGGATGCAC 39030	G	
			GTGCATT TATGTGTG		
			CACGTAG GTACACAT		
			—		
GAM1381	F7	3'	CACACATCAGTGCAC 3716	T	
			GTGCATTG ATGTGTG		

CACGTGAC TACACAC

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GAM1381 F7      3' CACACATGGATGCAC      3717      G
                  -
                  GTGCATT TATGTGTG
                  ||||| |||||
                  CACGTAG GTACACAC

GAM1381 F7      3' CGCACATGCCAATGCAC      3719      -
                  -
                  GTGCATTG TATGTGTG
                  ||||| |||||
                  CACGTAAC GTACACGC
                  C
GAM1381 F7      3' TACACATGGATGCAC      3720      G
                  -
                  GTGCATT TATGTGTG
                  ||||| |||||
                  CACGTAG GTACACAT

GAM1381 FACL2   3' TGTATTATATACAAGCAC      40885      A      TGAAT
                  -
                  GTGC TTGTATGTG      TACG
                  ||| ||||| |||
                  CACG AACATATAT      ATGT
                  -      T_____
GAM1381 FAT2    3' CGTGTGTACACATGTGT      7544      TGT      AAT
                  -
                  GCAT ATGTGTG      TACG
                  ||| ||||| |||
                  TGTG TACACAT      GTGC
                  _____ GT_
GAM1381 FAT2    3' GTGTACACATGTGTAGAGTGTA      7545      G      AAT      GT
      T
                  GTGCATT TAT      GTGTG      TAC
                  ||||| ||| ||||| |||
                  TATGTGA ATG TACAC      GTG
                  G TG      AT_
GAM1381 FCMD    3' TGTGCCACATACAATGC      22098      TGAAT
                  -
                  GCATTGTATGTG      TACG
                  ||||| ||||| |||
                  CGTAACATACAC      GTGT
                  C_____
GAM1381 FCRH1   3' TTTATAAATACAGTGTGT      53628      TG      G
                  -
                  G CATTGTAT TGTGAA
                  | ||||| |||||
                  T GTGACATA ATATTT
                  GT      A
GAM1381 FGF9    3' ACTTTGTGCGCATGCATAATGTA      8889      AT      ATTACGT
      T
                  GTGCATTGT      GTGTGA
                  ||||| |||||
                  TATGTAATA TACGCT
                  CG      GTTTCA
GAM1381 FGFR3   3' GCGTGTGTGTGTGTGTGTGTGCAC      3771      TGT      TG      AAT
                  -
                  GTGCAT ATG TG      TACGT
                  ||||| ||| || |||||
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			CACGTG TGT GT GTGCG		
			TG_ GT GT_		
GAM1381 FGR	5'	ATGTGCATGCGCGTGTGTGCAC 17894	TGT	AAT	
		GTGCAT ATGTGTG TACGT			
		CACGTG TCGCGCT GTGTA			
		TG_ AC_			
GAM1381 FGR	5'	GCGTATGAGCATGTGCATGCGC 17896	T	GAAT	
		GTGCAT GTATGTGT TACGT			
		CGCGTA CGTGTACG ATGCG			
		_ AGT_			
GAM1381 FHOD1	3'	CGTATGCATATGCATGTGCAT 60194	_	AATTACGT	
		GTGCAT TGTATGTGTG			
		TACGTG ACGTATACGT			
		T A TGCA			
GAM1381 FHOD1	3'	GTGTGCATGCATATGCATGTGC 60196	_	GAAT_ GT	
AT		GCAT TGTATGTGT TAC			
		CGTG ACGTATACG GTG			
		T TACGT T			
GAM1381 FHOD1	3'	GTGTGTATGCATGTGAGTGTGT 60197	TG _TG	AAT	
		G CA T TATGTGTG TAC			
		T GT A GTACGTAT GTG			
		GT G GT GT_			
GAM1381 FHOD1	3'	GTGTGTGTGCATGCATATGCAT 60198	_	TG AAT	
		GTGCAT TGTATG TG TAC			
		TACGTA ACGTAC GT GTG			
		T GT GT_			
GAM1381 FLT1	3'	ATGTAATTTATGCAAGGTAT 8914	ATTGTA		
		GTGC TGTGTGAATTACGT			
		TATG ACGTATTTAATGTA			
		GA_			
GAM1381 FOG2	3'	GTGTAGCACATATGGTTTGC 23878	C TG	GAAT	
		GTG AT TATGTGT TAC			
		CGT TG ATACACG GTG			
		T GT AT_			
GAM1381 FOS	3'	ATGTAGCAAAACGCATGGAGTG 17904	TG G	GAA_	
TGT		G CATT TATGTGT TTACGT			
		T GTGA GTACGCA GATGTA			
		GT G AAAC			
GAM1381 FOSB	3'	GTGTGCGTGCGCGTGAGTGTGT 22110	TG G	AAT_	
		G CATT TATGTGTG TAC			

T GTGA GTGCGCGT GTG  
 GT \_ GCGT  
 GAM1381 G6PC 3' GCGTAGCTGGCATACAGGTGC 3827 TG A GTGAA  
 G C TTGTATGT TTACGT  
 | | ||||| |||||  
 C G GACATACG GATGCG  
 GT \_ GTC\_  
 GAM1381 GA 3' CACACATGTAATCCAT 25172 C  
 GTG ATTGTATGTGTG  
 ||| |||||  
 TAC TAATGTACACAC  
 C  
 GAM1381 GAB2 3' TATGTGATTTATGGTGGCATGT 54460 G \_\_\_\_\_  
 GTTGTGTAT TATGTGT GAATTACGT A  
 ||||| ||||| |  
 GTGTACG TTTAGTGTA T  
 T GTGGTA  
 GAM1381 GAB2 3' TATGTGATTTATGGTGGCATGT 24503 G \_\_\_\_\_  
 GTTGTGTAT TATGTGT GAATTACGT A  
 ||||| ||||| |  
 GTGTACG TTTAGTGTA T  
 T GTGGTA  
 GAM1381 GABRA2 3' ATGTACAGTATGTATATAGTGA 5863 \_ TG AAT  
 CAT GTG CATTGTATG TG TACGT  
 ||| ||||| || |||||  
 TAC GTGATATAT AT ATGTA  
 A GT GAC  
 GAM1381 GABRA2 3' GTGATCCAACATGTACAGT 5865 GA\_ GT  
 ATTGTATGTGT ATTAC  
 ||||| |||||  
 TGACATGTACA TAGTG  
 ACC  
 GAM1381 GARP 3' ACGTGGCCGCCACGCAGTGTGC 18593 TG TA T AA  
 G CATTG TG GTG TTACGT  
 | |||| || ||| |||||  
 C GTGAC AC CGC GGTGCA  
 GT GC \_ C\_  
 GAM1381 GAS2 3' TGTAATTCATACATGAGCTGAC 17912 G TTG GT  
 GT CA TATGTGTGAATTAC  
 || || |||||  
 CA GT GTACATACTTAATG  
 \_ CGA TG  
 GAM1381 GJA1 3' TAATGCACATATGGTGT 3905 TG GA  
 GCAT TATGTGT ATTA  
 ||| ||||| |||  
 TGTG ATACACG TAAT  
 GT \_  
 GAM1381 GNRHR 5' ACACATATAAATGCAC 4639 \_  
 GTGCATT GTATGTGT  
 ||||| |||||

			CACGTAA TATACACA		
			A		
GAM1381	GOT1	3'	GTGATGTGCGTAGTGCAT 9096	TG	TG GA
			GTGCAT TATG T ATTAC		
			TACGTG ATGC G TAGTG		
			__ GT __		
GAM1381	GPR48	3'	ATGTAGTTTGTATAAAATGT 37501	GTA	TG
			GCATT TGTG AATTACGT		
			TGTAA ATAT TTGATGTA		
			A__ GT		
GAM1381	GPR85	3'	TTCTGCACATTCAGTGTAT 38581	T	_
			GTGCATTG ATGTGT GAA		
			TATGTGAC TACACG CTT		
			T T		
GAM1381	GPX3	3'	GCGTGATTGTGTGTGTGTGCAT 9122	TGT	TG G
			GTGCAT ATG T AATTACGT		
			TACGTG TGT G TTAGTGCG		
			TG_ GT_		
GAM1381	GRB10	5'	GTGTGGAGTCCAAGCGGTGCAT 17984	A	TG GAAT
			GTGCATTGT TG T TAC		
			TACGTGGCG AC G GTG		
			A CT AGGT		
GAM1381	GRIN2B	3'	GTGGATTGTGCGTGCATGTGTG 5904	TG	_ TG A GT
	T		G CAT TGTATGTG A TTAC		
			T GTG ACGTGCGT T GGTG		
			GT T GT A		
GAM1381	GTF2H1	3'	CACACATATATGTAC 18005	T	
			GTGCAT GTATGTGTG		
			CATGTA TATACACAC		
			—		
GAM1381	GTF2IRD1	3'	ATGTAATTTATGTACAAAATGT 32893	GTA	TG
	AT		GTGCATT TG TGAATTACGT		
			TATGTAA AT ATTTAATGTA		
			AAC GT		
GAM1381	GUCY1A2	5'	CGCACGGCGATGCGC 5960	A	
			GTGCATTGT TGTGTG		
			CGCGTAGCG GCACGC		
			—		
GAM1381	GUCY1A2	3'	GTTTATCACACATACAAGTAT 5961	A	ATT
			GTGC TTGTATGTGTGA AC		



TATG AACATACACACT TG  
 \_ ATT  
 GAM1381 GYPA 3' TTACATATATATAAGTGC 87452 \_\_\_\_  
 GCAT TGTATGTGTGA  
 |||| |||||  
 CGTG ATATATACATT  
 AAT  
 GAM1381 HDAC7A 3' TGAGTGAGGCGTGTGTGTGAGC 33453 A TG TG AA GT  
 G TGC T TATG TG TTAC  
 ||| |||| || ||||  
 GCG A GTGT GC AGTG  
 \_GT GT GG AGTG  
 GAM1381 HDAC7A 3' TGAGTGAGGCGTGTGTGTGAGC 31212 A TG TG AA GT  
 G TGC T TATG TG TTAC  
 ||| |||| || ||||  
 GCG A GTGT GC AGTG  
 \_GT GT GG AGTG  
 GAM1381 HDC 3' GTGTGCTTATGTGTACATGCAT 9197 T TG AT\_  
 GTGCAT GTATG TGA TAC  
 |||| |||| || ||  
 TACGTA CATGT ATT GTG  
 \_ GT CGT  
 GAM1381 HFE 3' ATGTGATTTACGCTCATTGTA 57316 T TAT  
 TGCA TG GTGTGAATTACGT  
 |||| || |||||  
 ATGT AC CGCATTTAGTGTA  
 T T\_  
 GAM1381 HFE 3' ATGTGATTTACGCTCATTGTA 4648 T TAT  
 TGCA TG GTGTGAATTACGT  
 |||| || |||||  
 ATGT AC CGCATTTAGTGTA  
 T T\_  
 GAM1381 HIS1 3' ATGTAACATTATATACATGTGT 21312 \_ TGAA  
 AT GTGCAT TGTATGTG TTACGT  
 |||| ||||| ||||  
 TATGTG ACATATAT AATGTA  
 T TAC\_  
 GAM1381 HLCS 3' ATGTGTGTGCGTGCGTGTGTGC 4660 TG \_ TG AAT  
 G CAT TGTATG TG TACGT  
 | ||||| || ||||  
 C GTG GCGTGC GT GTGTA  
 GT T GT \_\_\_\_  
 GAM1381 HLCS 3' GTGTGCCCGCATATGTGTGTGC 4672 TG TGT AAT\_ GT  
 CAT ATGTGTG TAC  
 || ||||| ||  
 GTG TATACGC GTG  
 GT TG\_ CCGT T  
 GAM1381 HLCS 3' GTGTGCGTGCGTGTGTGCGC 4673 TGT TG AAT  
 GTGCAT ATG TG TAC  
 |||| || || ||

			CGCGTG TGC GC GTG		
			TG_ GT GT_		
GAM1381 HLF	3'	GTGTGGTCAGCGGTATGTGCGT 9221	T	_____	AT_ GT
		GTGC	T GTATGTG TGA TAC		
			G CGTGTAT ACT GTG		
			_ GGCG GGT T		
GAM1381 HMGN1	3'	ACAGATTTGAACATGTAGTGTA 17116		G	ACGT
		C	GTGCATTGTATGT TGAATT		
			CATGTGATGTACA GTTTAG		
			A ACA		
GAM1381 HOXC11	3'	GCGTGAGTGCGTGTGTACATGT 60174	_	TG	AA_
		GCAC	TGCAT TGTATG TG TTACGT		
			ACGTG ACATGT GC AGTGCG		
			T GT GTG		
GAM1381 HSD17B1	5'	CACATATACAATCAT 4681	C		
			GTG ATTGTATGTGTG		
			TAC TAACATATACAC		
			-		
GAM1381 HTR2C	3'	ATGTATGCCATGTATGTTGCAT 6020	TT	TGAAT	
			GTGCA GTATGTG TACGT		
			TACGT TATGTAC ATGTA		
			TG CGT_		
GAM1381 HTR2C	3'	GTGTCCTGCATGTATGCCATGT 6023	T	TG AAT_	GT
		AT	GTGCAT GTATG TG TAC		
			TATGTA CGTAT AC GTG		
			C GT GTCCT		
GAM1381 IARS	3'	TACACATACATGCAC 9293	T		
			GTGCAT GTATGTGTG		
			CACGTA CATAACACAT		
			-		
GAM1381 IARS	3'	TACACATACATGCAC 25513	T		
			GTGCAT GTATGTGTG		
			CACGTA CATAACACAT		
			-		
GAM1381 IGF2R	3'	CACACATACGTGCAC 6050	T		
			GTGCAT GTATGTGTG		
			CACGTG CATAACACAC		
			-		
GAM1381 IGFBP1	3'	GCACATTTATATATATATGTAT 5179	T	TACGT	
			GTGCAT GTATGTGTGAAT		

TATGTA TATATATATTTA  
 \_ CACGT  
 GAM1381 IGFBP4 3' GCGTGTGCACGTGTGCGTGTGC 7759 TG T TG AAT  
 G CAT GTA TGTG TACGT  
 I III III III IIII  
 C GTG CGT GCAC GTGCG  
 GT \_ GT GT\_  
 GAM1381 IGFBP4 3' GTGTGCACGTGTGCGTGTGC 7761 TG T TG AAT GT  
 G CAT GTA TGTG TAC  
 I III III III III  
 C GTG CGT GCAC GTG  
 GT \_ GT GT\_  
 GAM1381 IGFBP4 3' GTGTGCGTGTGCGTGTGCGTGTGT 7762 TG \_ TG AAT\_ GT  
 GT G CAT TGTATG TG TAC  
 I III IIII II III  
 T GTG GCGTGC GT GTG  
 GT T GT GCGT  
 GAM1381 IGJ 3' GTGTAGAGAACATATATGCAT 58317 T GTGAAT  
 GTGCAT GTATGT TAC  
 IIII IIII III  
 TACGTA TATACA GTG  
 \_ AGAGAT  
 GAM1381 IL18R1 3' ATGTGATTTAATGTTTGTAGTG 13906 TGTG\_  
 C GCATTGTA TGAATTACGT  
 IIIIII IIIIIII  
 CGTGATGT ATTTAGTGTA  
 TTGTA  
 GAM1381 IL1A 3' TTGACAGTTCATATGTACCATG 62468 T ACGT  
 TAC GTGCAT GTATGTGTGAATT  
 IIIII IIIIIIIII  
 CATGTA CATGTATACTTGA  
 C CAGTTG  
 GAM1381 IL21R 3' ATGTGTGTGTGTGTCATATGCAT 41424 \_ TG AAT  
 GTGCAT TGTATG TG TACGT  
 IIIII IIIII II IIII  
 TACGTA ACGTGT GT GTGTA  
 T GT \_  
 GAM1381 IL21R 3' GTGTGCATATGTGTGTGTGTGC 41431 TG TG\_ AAT GT  
 G CAT TATGTGTG TAC  
 I III IIIII III  
 C GTG GTGTATAC GTG  
 GT TGT GT\_  
 GAM1381 IL21R 3' GTGTGTGCATATGCATGTGTGT 41432 TG \_ AAT  
 G CAT TGTATGTGTG TAC  
 I III IIIIIII III  
 T GTG ACGTATACGT GTG  
 GT T GT\_  
 GAM1381 IL21R 3' GTGTGTGTGCATATGCATGTGT 41433 TG T AAT\_  
 G CAT GTATGTGTG TAC  
 I III IIIIIII III

T GTA CGTATACGT GTG  
 GT \_ GTGT  
 GAM1381 IMMP2L 5' GCGTGATCGCGAGCATGTGTGC 50729 T TG A\_\_\_\_  
 GTGCGC T GTATG TG ATTACGT  
 ||||| || |||||  
 G CGTGT AC TAGTGCG  
 \_ GT GAGCGC  
 GAM1381 INSR 3' GTGTGCTCACGTGTGTATGCAC 70981 TGT TG AT\_ GT  
 TGCAT A TGTGA TAC  
 ||||| | ||||| ||  
 ACGTA T GCACT GTG  
 TG\_ GT CGT T  
 GAM1381 IREB2 3' ATGTATCACATATGATGCA 66425 TG TGAAT  
 TGCAT TATGTG TACGT  
 ||||| ||||| |||||  
 ACGTA ATACAC ATGTA  
 GT T\_\_\_\_  
 GAM1381 ITGAM 3' ATGTGCAAGTGTATGCACGTGT 5287 TG \_ TG GAAT  
 GC G CAT TGTATG T TACGT  
 | ||| ||||| | |||||  
 C GTG ACGTAT G GTGTA  
 GT C GT AAC\_  
 GAM1381 ITGAM 3' GTGTGCACGTGTGCGTGTGC 5291 TG T TG AAT GT  
 G CAT GTA TGTG TAC  
 | ||| ||| ||||| ||  
 C GTG CGT GCAC GTG  
 GT \_ GT GT\_  
 GAM1381 ITGAM 3' GTGTGCATGTGTGCGAGTGTGT 5292 TG \_ TG AAT  
 G CATT GTATG TG TAC  
 | |||| ||||| || |||  
 T GTGA CGTGT AC GTG  
 GT G GT GT\_  
 GAM1381 ITGAM 3' GTGTGCGTGTGCGTGCATGTGC 5293 \_ TG AAT\_ GT  
 AC GTGCAT TGTATG TG TAC  
 ||||| ||||| || |||  
 CACGTG ACGTGC GT GTG  
 T GT GCGT  
 GAM1381 ITGAM 3' GTGTGTCCATGTGTGTGCAGTG 5294 \_\_\_\_ T AT GT  
 TGT CATTGTAT GTG GA TAC  
 ||||| ||| || |||  
 GTGACGTG TAC CT GTG  
 TGTG \_ GT  
 GAM1381 ITGAM 3' GTGTGTGCACGTGTGCGTGTGC 5295 TG T TG AAT\_  
 G CAT GTA TGTG TAC  
 | ||| ||| ||||| ||  
 C GTG CGT GCAC GTG  
 GT \_ GT GTGT  
 GAM1381 ITGB3 3' TGTAATTTAAAATTGTGATGTG 4000 TG TG TGTG GT  
 T G CAT TA TGAATTAC  
 | ||| || |||||

			T GTA GT ATTTAATG		
			GT GT TAAA TG		
GAM1381	ITM2B	3'	TTCTATATATACAATG 41820	—	
			CATTGTATGTGT GAA		
			GTAACATATATA CTT		
			T		
GAM1381	ITPKB	3'	ATGTGCTAATATGCAAATGATG 9421	TG TG A AAT_	
	TGC		G CAT T TGTGTG TACGT		
			C GTA A ACGTAT GTGTA		
			GT GT A AATC		
GAM1381	JRK	3'	ACGTAGTTTGCATTCCAGCG 86519	AT TAT TG	
			TGC TG GTG AATTACGT		
			GCG AC TAC TTGATGCA		
			— CT_ GT		
GAM1381	JRKL	3'	ATAAATTACATGTACACATGTA 13660	— A CGT	
	T		GTGCAT TGTATGTGTGA TTA		
			TATGTA ACATGTACATT AAT		
			C A A		
GAM1381	KAL1	3'	TACATATACATGTAT 4016	T	
			GTGCAT GTATGTGTG		
			TATGTA CATATACAT		
			—		
GAM1381	KCNJ3	3'	TCAAGCATGCAATAATGTGC 9526	TG — G	
			G CAT TGTATGT TGA		
			C GTA ACGTACG ACT		
			GT ATA A		
GAM1381	KERA	3'	TTCATTTGTGCAGTGTAT 22873	T	
			GTGCATTGTATG GTGAA		
			TATGTGACGTGT TACTT		
			T		
GAM1381	KHK	3'	ATGTAAAGAGCATATAATGTA 21400	GTGAA	
			TGCATTGTATGT TTACGT		
			ATGTAATATACG AATGTA		
			AGA_		
GAM1381	KHK	3'	ATGTAAAGAGCATATAATGTA 4030	GTGAA	
			TGCATTGTATGT TTACGT		
			ATGTAATATACG AATGTA		
			AGA_		
GAM1381	KIF3C	3'	CGTGTGCGTGTGCGTGTCAT 9600	T TG AAT	
			GTGCAT GTA TGTG TACG		

			TACGTG CGT GCGT GTGC		
			_ GT _		
GAM1381	KIF3C	3'	GCGTG CATGTGCGTGTGCGTGT 9605	TG _ TG AAT_	
			GTGC CAT TGTA TGTG TACGT		
			GTG GCGT GCGT GTGCG		
			GT T GT GTAC		
GAM1381	KIF3C	3'	GTGTGCGTG CATGTGCGTGTGC 9609	TG T AAT_ GT	
			G CAT GTATGTGTG TAC		
			C GTG CGTGTACGT GTG		
			GT _ GCGT		
GAM1381	KIF3C	3'	GTGTGCGTGTGCGTG CATGTGC 9610	TG T TG AAT_ GT	
			G CAT GTATG TG TAC		
			C GTA CGTGC GT GTG		
			GT _ GT GCGT		
GAM1381	KLRC1	3'	GTTTGCATTTGCAGTGCAT 9616	T TG	
			GTGCATTGTA GTG AAT		
			TACGTGACGT TAC TTG		
			T GT		
GAM1381	KLRC1	3'	GTTTGCATTTGCAGTGCAT 23649	T TG	
			GTGCATTGTA GTG AAT		
			TACGTGACGT TAC TTG		
			T GT		
GAM1381	KLRC2	3'	ATTTGCGTTTGCAGTGCAT 94527	TG TG	
			GTGCATTGTA TG AAT		
			TACGTGACGT GC TTA		
			TT GT		
GAM1381	KNSL1	3'	GTTTGTATATAATACAATGTGT 15750	TG _ AATT	
			G CATTGTAT GTGTG AC		
			T GTAACATA TATAT TG		
			GT A GTT_		
GAM1381	LAMC2	3'	TGATGCGCATCAATGTAT 18715	T GA	
			GTGCATTG ATGTGT ATTA		
			TATGTAAC TACGCG TAGT		
			_ _		
GAM1381	LAMP2	3'	TATATATATATATGCAC 25718	_	
			GTGCAT TGTATGTGTG		
			CACGTA ATATATATAT		
			T		
GAM1381	LDB2	5'	GTGAGCGTGTGTGCGTGCG 7093	T TG AA	
			TGCAT GTATG TG TTAC		

			GCGTG CGTGT GC AGTG		
			_ GT G_		
GAM1381	LFG	3'	GCGTG CAGCCAGCATGTGCAGT 76722	GAAT__	
	G		CATTGTATGTGT TACGT		
			GTGACGTGTACG GTGCG		
			ACCGAC		
GAM1381	LFNG	3'	GCGTGTGCGTGTGCGTGTGTGT 92641	TG _ TG AAT	
			G CAT TGTA TGTG TACGT		
			T GTG GCGT GCGT GTGCG		
			GT T GT _		
GAM1381	LFNG	3'	GTGCCTGTGCGTGTGCGTGTGC 92645	TG T TG AAT_ GT	
			G CAT GTA TGTG TAC		
			C GTG CGT GCGT GTG		
			GT _ GT GTCC		
GAM1381	LILRB4	3'	CATATATAAAATGCAT 22432	G	
			GTGCATT TATGTGTG		
			TACGTAA ATATATAC		
			A		
GAM1381	LY6E	3'	ACGTGGGTGTGCAGTGAC 9828	TG GTGAA	
			GTGCATTGTA T TTACGT		
			CACGTGACGT G GGTGCA		
			GT _		
GAM1381	LY6E	3'	CGTGGGTGTGCAGTGAC 9829	TG GTGAA	
			GTGCATTGTA T TTACG		
			CACGTGACGT G GGTGC		
			GT _		
GAM1381	MADH3	3'	GCCCAGTGCATATGCAATGTAT 19737	AATTACGT	
			GTGCATTGTATGTGTG		
			TATGTAACGTATACGT		
			GACCCG		
GAM1381	MADH6	3'	TATGTAATTATTTATGTATGGT 18767	TG TG_	
	GCA		GCAT TATGTG AATTACGT A		
			CGTG ATGTAT TTAATGTA T		
			GT TTA		
GAM1381	MADH9	3'	GTGTAAATACATAGAATGTAT 19751	G GAAT	
			GTGCATT TATGTGT TAC		
			TATGTAA ATACATA GTG		
			G AAT_		
GAM1381	MAN1A1	3'	TCATACATTGGTGTAT 91904	T	
			GTGCATTG ATGTGTGA		

TATGTGGT TACATACT

GAM1381 MAP3K12 3' TATATATATATATGCGC 20866 \_  
GTGCAT TGTATGTGTG  
||||| ||||||||  
CGCGTA ATATATATAT  
T

GAM1381 MAP3K7IP2 3' TTCTATATGTATAGTGTA 30665 \_  
TGCATTGTATGTGT GAA  
||||||||||| |||  
ATGTGATATGTATA CTT  
T

GAM1381 MAPK14 3' ATGTGAGCACATGCGTATATGT 57331 TG T AA\_  
GC G CAT GTATGTGTG TTACGT  
| ||| ||||||| |||||  
C GTA TATGCGTAC AGTGTA  
GT \_ ACG

GAM1381 MAPK14 3' GCGTGTTAGTGTGTGTGCATGT 57333 TG \_ TG AAT\_  
GTGT CAT TGTATG TG TACGT  
||| ||||| || |||||  
GTG ACGTGT GT GTGCG  
GT T GT GATT

GAM1381 MAPK14 3' ATGTGAGCACATGCGTATATGT 57342 TG T AA\_  
GC G CAT GTATGTGTG TTACGT  
| ||| ||||||| |||||  
C GTA TATGCGTAC AGTGTA  
GT \_ ACG

GAM1381 MAPK14 3' GCGTGTTAGTGTGTGTGCATGT 57344 TG \_ TG AAT\_  
GTGT CAT TGTATG TG TACGT  
||| ||||| || |||||  
GTG ACGTGT GT GTGCG  
GT T GT GATT

GAM1381 MAPK14 3' ATGTGAGCACATGCGTATATGT 7157 TG T AA\_  
GC G CAT GTATGTGTG TTACGT  
| ||| ||||||| |||||  
C GTA TATGCGTAC AGTGTA  
GT \_ ACG

GAM1381 MAPK14 3' GCGTGTTAGTGTGTGTGCATGT 7159 TG \_ TG AAT\_  
GTGT CAT TGTATG TG TACGT  
||| ||||| || |||||  
GTG ACGTGT GT GTGCG  
GT T GT GATT

GAM1381 MAPRE3 3' TGGTAAAAGTACATGCCATGTG 24668 TG T GAA GT  
T G CAT GTATGTGT TTAC  
| ||| ||||||| |||||  
T GTA CGTACATG AATG  
GT C AA\_ GTG

GAM1381 MARK1 3' CATACATATATGAGGTAC 37844 AT\_\_  
GTGC TGTATGTGTG  
||| |||||||||



			CATG ATATACATAC			
			GAGT			
GAM1381	MATN1	3'	GCGTGTGTGTATGCGTG	9921	T	TG AAT
			GTGCA TGTATG TG TACGT			
			TACGT GCGTAT GT GTGCG			
			— GT —			
GAM1381	MATN1	3'	GTGTGTATGCGTG	9925	TG _	AAT
			G CAT TGTATGTGTG TAC			
			T GTG ACGTGCGTAT GTG			
			GT T GT_			
GAM1381	MATN1	3'	GTGTGTATGCGTG	9926	TG _	AATTACGT
			G CAT TGTATGTGTG			
			T GTG ACGTGCGTAT			
			GT T GTG TGC			
GAM1381	MATN1	3'	GTGTGTGTGTGTGCACGTGCGC	9927	_	TG AAT
			GTGCAT TGTATG TG TAC			
			CGCGTG ACGTGT GT GTG			
			C GT GT_			
GAM1381	MEF2A	3'	TTTACATATATATGTAT	18787	T	
			GTGCAT GTATGTGTGAA			
			TATGTA TATATACATTT			
			—			
GAM1381	MEF2C	3'	TTATATGTGCCGTGTGT	9992	TG T	
			G CAT GTATGTGTGA			
			T GTG CGTGTATATT			
			GT C			
GAM1381	MEOX2	3'	TTTTCATATGTGATGTAT	19806	TG T	
			GTGCAT TATGTG GAA			
			TATGTA GTATAC TTT			
			GT T			
GAM1381	METTL1	3'	ACATGTATATGTGTAC	43507	_	
			GTGCAT TGTATGTGT			
			CATGTG ATATGTACA			
			T			
GAM1381	METTL1	3'	ACATGTATATGTGTAC	43513	_	
			GTGCAT TGTATGTGT			
			CATGTG ATATGTACA			
			T			
GAM1381	METTL1	3'	ACATGTATATGTGTAC	18123	_	
			GTGCAT TGTATGTGT			

CATGTG ATATGTACA  
 T  
 GAM1381 MHC2TA 3' CACATGTGCACATGCAC 4163 \_  
 GTGCAT TGTATGTGTG  
 ||||| |||||  
 CACGTA ACGTGTACAC  
 C  
 GAM1381 MHC2TA 3' TATGTGCACATGCACGTGTGTG 4187 \_\_\_\_\_ AATTACGT  
 CAC CAT TGTATGTGTG  
 || |||||  
 GTG ACGTACACGT  
 TGTGC GTA TG  
 GAM1381 MMP11 3' GTAAATGTGTGTACAGTGTGT 19874 TG TG GAA  
 G CATTGTATG T TTAC  
 | ||||| | |||  
 T GTGACATGT G AATG  
 GT GT TA\_  
 GAM1381 MNT 3' TTGTGAACGCATGTGATGC 39721 TG GAA T  
 GCAT TATGTGT TTACG  
 ||| ||||| |||  
 CGTA GTACGCA AGTGT  
 GT \_ TT  
 GAM1381 MPP2 3' GTGTATGTGTGTGCGTGTGCAC 59829 \_ TG AAT  
 GTGCAT TGTATG TG TAC  
 ||||| ||||| || |||  
 CACGTG GCGTGT GT GTG  
 T GT AT\_  
 GAM1381 MPP2 3' GTGTGTGCACGTGCGTGTGTGT 59830 TG \_ AATTACGT  
 G CAT TGTATGTGTG  
 | ||| |||||  
 T GTG GCGTGCACGT  
 GT T GTG TGC  
 GAM1381 MPP2 3' GTGTGTGCGTGTGCACGTGCG 59831 \_ TG AAT  
 TGCAT TGTA TGTG TAC  
 ||||| ||| ||| |||  
 GCGTG ACGT GCGT GTG  
 C GT GT\_  
 GAM1381 MSL3L1 3' ATGTGTGTGTGTACAGTGCG 54364 TG AAT  
 TGCATTGTATG TG TACGT  
 ||||| ||| ||| |||  
 GCGTGACATGT GT GTGTA  
 GT \_  
 GAM1381 MTMR8 3' TACATATACAATGTGT 31298 TG  
 G CATTGTATGTGTG  
 | |||||  
 T GTAACATATACAT  
 GT  
 GAM1381 MTMR8 3' TGTAATATTTGCGTATGGTGT 31299 TG TGA GT  
 GCAT TATGTG ATTAC  
 ||| ||||| |||

			TGTG ATGCGT TAATG		
			GT TTA TG		
GAM1381	MTRR	3'	TACTTAAATTACACATGTAGAG 43772	A	A C
	CAT		GTGC TTGTATGTGTGA TTA GT		
			TACG GATGTACACATT AAT CA		
			A A T TG		
GAM1381	MTRR	3'	TACTTAAATTACACATGTAGAG 10135	A	A C
	CAT		GTGC TTGTATGTGTGA TTA GT		
			TACG GATGTACACATT AAT CA		
			A A T TG		
GAM1381	MYCL1	5'	CGCATGTGCGTGTGTGC 18163	TG _	
			G CAT TGTATGTGTG		
			C GTG GCGTGTACGC		
			GT T		
GAM1381	MYCL1	5'	GCGGCGCGCATGTGCGTGTGT 18166	TG T	AATTA
			G CAT GTATGTGTG CGT		
			T GTG CGTGTACGC GCG		
			GT _ GCG_		
GAM1381	MYCL2	3'	ATGTATATATGTATATATATAT 18173	T	AAT__
	GTAT		GCAT GTATGTGTG TACGT		
			TGTA TATATATAT ATGTA		
			_ GTATAT		
GAM1381	MYCL2	3'	ATGTATATATGTATATATATAT 18174	T	AAT__
	GTAT		GCAT GTATGTGTG TACGT		
			TGTA TATATATAT ATGTA		
			_ GTATAT		
GAM1381	MYCL2	3'	ATGTATATATGTATATATATAT 18175	T	AAT__
	GTAT		GCAT GTATGTGTG TACGT		
			TGTA TATATATAT ATGTA		
			_ GTATAT		
GAM1381	MYD88	3'	CACACATATATGTAC 10165	T	
			GTGCAT GTATGTGTG		
			CATGTA TATACACAC		
			_		
GAM1381	MYEOV	3'	ATGTCTGCCATGCGTACAGGCA 57047	A	AATT
	T		GTGC TTGTATGTGTG ACGT		
			TACG GACATGCGTAC TGTA		
			_ CGTC		
GAM1381	NCF1	3'	GTGAGCATGTGTGCATGCAT 81330	T	TG AA
			GTGCAT GTATG TG TTAC		

			TACGTA CGTGT AC AGTG		
			— GT G—		
GAM1381	NCSTN	3'	GTAAATATATATAATG 73754	AA	
			CATTGTATGTGTG TTAC		
			GTAATATATATAT AATG		
			A—		
GAM1381	NLGN3	3'	CACACATATATGTAT 38598	T	
			GTGCAT GTATGTGTG		
			TATGTA TATACACAC		
			—		
GAM1381	NPY1R	3'	TCTTATAAATAATGCAC 6181	A T	
			GTGCATTGT TGTG GA		
			CACGTAATA ATAT CT		
			A T		
GAM1381	NRAS	3'	TACCTATACAATGTAT 10277	T	
			GTGCATTGTATG GTG		
			TATGTAACATAT CAT		
			C		
GAM1381	NRF1	3'	CATATATATAAAGTAT 60119	A	
			GTGC TTGTATGTGTG		
			TATG AATATATATAC		
			A		
GAM1381	NRXN1	3'	TCACATATATACATATGTAT 16635	—	
			GTGCAT TGTATGTGTGA		
			TATGTA ATATATACT		
			TAC		
GAM1381	NRXN1	3'	TCACATATATACATATGTAT 57032	—	
			GTGCAT TGTATGTGTGA		
			TATGTA ATATATACT		
			TAC		
GAM1381	NRXN3	3'	CACACAGCGATGCAT 16581	A	
			GTGCATTGT TGTGTG		
			TACGTAGCG ACACAC		
			—		
GAM1381	NRXN3	3'	CACACAGCGATGCAT 57276	A	
			GTGCATTGT TGTGTG		
			TACGTAGCG ACACAC		
			—		
GAM1381	OAS3	3'	GTGTGAGCACATGTGTGCAT 20543	TGT GAAT GT	
			GTGCAT ATGTGT TAC		

			TACGTG TACACG GTG		
			TG_ AGT_		
GAM1381	OXTR	3'	GCGTATGTTTGTGTATAAGGTA 6211	ATTG	TG _
	C		GTGC TATG TGAAT TACGT		
			CATG ATAT GTTTG ATGCG		
			GA_ GT T		
GAM1381	OXTR	3'	GTGGGAATGTAAATGGTGCAC 6215	TG A	TG GAA
			GTGCAT T TG T TTAC		
			CACGTG A AT A GGTG		
			GT A GT AG_		
GAM1381	PACE4	3'	GTGTGCGTGCAAGCAT 56351	A	TG GAATT
			GTGC TTGTATG T AC		
			TACG AACGTGC G TG		
			_ GT _		
GAM1381	PAK4	3'	GTGTGCACGCGTGTGAGTGTGC 19691	TG _TG	AAT
			G CA T TATGTGTG TAC		
			C GT A GTGCGCAC GTG		
			GT G GT GT_		
GAM1381	PAX4	3'	ATGTATGTATGTGTGCATGCG 20553	T	TG AAT
			TGCAT GTATG TG TACGT		
			GCGTACGTGT AT ATGTA		
			_ GT GT_		
GAM1381	PAX4	3'	ATGTATGTGTGCATGCGTGCGC 20554	T	TG AAT
			GTGCAT GTATG TG TACGT		
			CGCGTG CGTAC GT ATGTA		
			_ GT GT_		
GAM1381	PCDHA11	5'	GTGGTAAATGCAGTGCAC 49033		GTGTGA
			GTGCATTGTAT ATTAC		
			CACGTGACGTA TGGTG		
			AA_		
GAM1381	PCDHA11	5'	GTGGTAAATGCAGTGCAC 38202		GTGTGA
			GTGCATTGTAT ATTAC		
			CACGTGACGTA TGGTG		
			AA_		
GAM1381	PCDHGA1	3'	GTAGTGTAGTGCGGTGTGC 38285	TG	GTGTGA
			G CATTGTAT ATTAC		
			C GTGGCGTG TGATG		
			GT ATG_		
GAM1381	PCDHGA10	3'	GTAGTGTAGTGCGGTGTGC 38292	TG	GTGTGA
			G CATTGTAT ATTAC		

			C GTGGCGTG	TGATG			
			GT ATG__				
GAM1381	PCDHGA11	3'	GTAGTGTAGTGC	CGGTGTGC	38299	TG	GTGTGA
			G CATTGTAT	ATTAC			
			C GTGGCGTG	TGATG			
			GT ATG__				
GAM1381	PCDHGA11	3'	GTAGTGTAGTGC	CGGTGTGC	49463	TG	GTGTGA
			G CATTGTAT	ATTAC			
			C GTGGCGTG	TGATG			
			GT ATG__				
GAM1381	PCDHGA12	3'	GTAGTGTAGTGC	CGGTGTGC	13595	TG	GTGTGA
			G CATTGTAT	ATTAC			
			C GTGGCGTG	TGATG			
			GT ATG__				
GAM1381	PCDHGA2	3'	GTAGTGTAGTGC	CGGTGTGC	38309	TG	GTGTGA
			G CATTGTAT	ATTAC			
			C GTGGCGTG	TGATG			
			GT ATG__				
GAM1381	PCDHGA3	3'	GTAGTGTAGTGC	CGGTGTGC	38316	TG	GTGTGA
			G CATTGTAT	ATTAC			
			C GTGGCGTG	TGATG			
			GT ATG__				
GAM1381	PCDHGA4	3'	GTAGTGTAGTGC	CGGTGTGC	38323	TG	GTGTGA
			G CATTGTAT	ATTAC			
			C GTGGCGTG	TGATG			
			GT ATG__				
GAM1381	PCDHGA5	3'	GTAGTGTAGTGC	CGGTGTGC	38330	TG	GTGTGA
			G CATTGTAT	ATTAC			
			C GTGGCGTG	TGATG			
			GT ATG__				
GAM1381	PCDHGA6	3'	GTAGTGTAGTGC	CGGTGTGC	38337	TG	GTGTGA
			G CATTGTAT	ATTAC			
			C GTGGCGTG	TGATG			
			GT ATG__				
GAM1381	PCDHGA7	3'	GTAGTGTAGTGC	CGGTGTGC	38344	TG	GTGTGA
			G CATTGTAT	ATTAC			
			C GTGGCGTG	TGATG			
			GT ATG__				
GAM1381	PCDHGA8	3'	GTAGTGTAGTGC	CGGTGTGC	49455	TG	GTGTGA
			G CATTGTAT	ATTAC			

			C GTGGCGTG	TGATG		
			GT ATG__			
GAM1381	PCDHGA9	3'	GTAGTGTAGTGCGGTGTGC	38351	TG	GTGTGA
			G CATTGTAT ATTAC			
			C GTGGCGTG	TGATG		
			GT ATG__			
GAM1381	PCDHGB1	3'	GTAGTGTAGTGCGGTGTGC	38358	TG	GTGTGA
			G CATTGTAT ATTAC			
			C GTGGCGTG	TGATG		
			GT ATG__			
GAM1381	PCDHGB2	3'	GTAGTGTAGTGCGGTGTGC	38365	TG	GTGTGA
			G CATTGTAT ATTAC			
			C GTGGCGTG	TGATG		
			GT ATG__			
GAM1381	PCDHGB3	3'	GTAGTGTAGTGCGGTGTGC	38372	TG	GTGTGA
			G CATTGTAT ATTAC			
			C GTGGCGTG	TGATG		
			GT ATG__			
GAM1381	PCDHGB4	3'	GTAGTGTAGTGCGGTGTGC	13602	TG	GTGTGA
			G CATTGTAT ATTAC			
			C GTGGCGTG	TGATG		
			GT ATG__			
GAM1381	PCDHGB5	3'	GTAGTGTAGTGCGGTGTGC	38379	TG	GTGTGA
			G CATTGTAT ATTAC			
			C GTGGCGTG	TGATG		
			GT ATG__			
GAM1381	PCDHGB6	3'	GTAGTGTAGTGCGGTGTGC	38386	TG	GTGTGA
			G CATTGTAT ATTAC			
			C GTGGCGTG	TGATG		
			GT ATG__			
GAM1381	PCDHGB7	3'	GTAGTGTAGTGCGGTGTGC	38393	TG	GTGTGA
			G CATTGTAT ATTAC			
			C GTGGCGTG	TGATG		
			GT ATG__			
GAM1381	PCDHGC3	3'	GTAGTGTAGTGCGGTGTGC	50519	TG	GTGTGA
			G CATTGTAT ATTAC			
			C GTGGCGTG	TGATG		
			GT ATG__			
GAM1381	PCDHGC3	3'	GTAGTGTAGTGCGGTGTGC	10456	TG	GTGTGA
			G CATTGTAT ATTAC			

			C GTGGCGTG	TGATG		
			GT	ATG__		
GAM1381	PCDHGC4	3'	GTAGTGTAGTGC	GGTGTGC	38400	TG GTGTGA
			G CATTGTAT	ATTAC		
			C GTGGCGTG	TGATG		
			GT	ATG__		
GAM1381	PCDHGC5	3'	GTAGTGTAGTGC	GGTGTGC	38407	TG GTGTGA
			G CATTGTAT	ATTAC		
			C GTGGCGTG	TGATG		
			GT	ATG__		
GAM1381	PCK1	3'	GTGTGTGTGCATGTATGTGCAC		59945	T AAT_
			GTGCAT GTATGTGTG	TAC		
			CACGTG TATGTACGT	GTG		
			—	GTGT		
GAM1381	PCK1	3'	TGTGTGCATGTATGTGCAC		59947	T AATTACGT
			GTGCAT GTATGTGTG			
			CACGTG TATGTACGT			
			—	GTG TG		
GAM1381	PCLO	3'	CACACATATAAGTAT		94223	A
			GTGC TTGTATGTGTG			
			TATG AATATACACAC			
			—			
GAM1381	PCSK1	3'	TTATACATTTGATGTAT		4780	T
			GTGCATTG ATGTGTGA			
			TATGTAGT TACATATT			
			T			
GAM1381	PCSK2	3'	GTGTGCATGTGTGTATAAGTGC		10468	— __TG AAT GT
	AC		TGCATT GTAT G TG	TAC		
			ACGTGA TATG T AC	GTG		
			A TG GT GT_			
GAM1381	PDE6B	3'	ACATGTACATATGTGTAC		4269	—
			GTGCAT TGTATGTGT			
			CATGTG ACATGTACA			
			TAT			
GAM1381	PDE6B	3'	CACATGTACATATGTGT		4273	TG _
			G CAT TGTATGTGTG			
			T GTA ACATGTACAC			
			GT T			
GAM1381	PDE7A	3'	ATGTTTGTGCATGTGTGACTGT		65520	TG _TG AATT
	GC		G CA T TATGTGTG	ACGT		



			C GT A GTGTACGT TGTA		
			GT C GT GTT_		
GAM1381	PDHA1	3'	ATGCAGTTTGTACATTAGTGCA 4292	T TG A	
	T		GTGCATTG ATGTG AATT CGT		
			TACGTGAT TACAT TTGA GTA		
			_ GT C		
GAM1381	PEA15	3'	CGTGTGTGTGCGTGTGCGC 13652	TGT TG AAT	
			GTGCAT ATG TG TACG		
			CGCGTG TGC GT GTGC		
			___ GT GT_		
GAM1381	PIGH	3'	TTATGGATGTAGTGCAT 15879	G	
			GTGCATTGTAT TGTGA		
			TACGTGATGTA GTATT		
			G		
GAM1381	PITPNB	3'	GTGTATATATGTATGTGTGCAT 24780	_ AAT	
			GTGCAT TGTATGTGTG TAC		
			TACGTG GTATGTATAT GTG		
			T AT_		
GAM1381	PKNOX1	3'	GTGTGTGCGCGTGTGTGC 15883	TG TGT AAT	
			G CAT ATGTGTG TAC		
			C GTG TGC GCGT GTG		
			GT ___ GT_		
GAM1381	PLA2G4A	3'	ATGTAGGGATATATACTGTAT 72550	TT GAA	
			GTGCA GTATGTGT TTACGT		
			TATGT CATATATA GATGTA		
			___ GG_		
GAM1381	PLAG1	3'	TGGCTTATCATGTATATCGTGT 10611	T TG ATTACGT	
	AC		GTGCAT GTATG TGA		
			CATGTG TATAT ACT		
			C GT ATTCGGTG		
GAM1381	PLEK	3'	ATGTAAC TCACCATGTGGTGTG 10629	TG TG T A	
	C		G CAT TATG GTGA TTACGT		
			C GTG GTAC CACT AATGTA		
			GT GT _ C		
GAM1381	PLXNA1	3'	GTACATGTATATATATGCAT 72313	_ TG AAT	
			GTGCAT TGTATG TG TAC		
			TACGTA ATATAT AC ATG		
			T GT _		
GAM1381	PMP2	3'	ATGCCTCCATGCATATATGTGT 10671	TG _ AATTACGT	
	GT		G CAT TGTATGTGTG		

			T GTG ATATACGTAC			
			GT T CTCCGTA			
GAM1381	PMP2	3'	GCGTGTGTGTATACACATGCAT 10672	_	TG	AAT
			GTGCAT TGTATG TG TACGT			
			TACGTA ACATAT GT GTGCG			
			C GT _			
GAM1381	PMP2	3'	GTGATAATACACATGCA 10674	A_		
			TGTATGTGTG ATTAC			
			ACGTACACAT TAGTG			
			AA			
GAM1381	PMP22	3'	GTAGATGTATATATGGTGC 4331	TG	TGAA	
			GCAT TATGTG TTAC			
			CGTG ATATAT GATG			
			GT GTA_			
GAM1381	PMX1	3'	TGCACACTTATATATACTGT 42665	T	ATTACGT	
	AT		GTGCA TGTATGTGTGA			
			TATGT ATATATATATT			
			C CACACGTA			
GAM1381	PMX1	3'	TGCACACTTATATATACTGT 22598	T	ATTACGT	
	AT		GTGCA TGTATGTGTGA			
			TATGT ATATATATATT			
			C CACACGTA			
GAM1381	POLK	3'	TGTAATTCAAAGATTAATGTG 32571	TG	TATGTG	GT
	T		G CATTG TGAATTAC			
			T GTAAT ACTTAATG			
			GT TAGAAA TG			
GAM1381	POV1	3'	GTGTGCACAACATGCAATGTGT 13265	TG	_ AAT	GT
			G CATTGTATGT GTG TAC			
			T GTAACGTACA CAC GTG			
			GT A GT_			
GAM1381	PPARGC1	3'	GCGTGTGTGTCATGTATGTGTGT 25160	TG	T	AAT
			G CAT GTATGTGTG TACGT			
			T GTG TATGTACGT GTGCG			
			GT _ GT_			
GAM1381	PPARGC1	3'	GTGTGCGTGTGTGCATGTAT 25161	T	TG	AAT
			GTGCAT GTATG TG TAC			
			TATGTA CGTGT GC GTG			
			_ GT GT_			
GAM1381	PPAT	3'	ATGTAGATGTACATATACATGT 10695	T	AA_	
	AC		GTGCAT GTATGTGTG TTACGT			

			CATGTA CATATACAT GATGTA			
			— GTA			
GAM1381	PPP1CB	3'	TCTGCATATGATGTAT 10715 TG T			
			GTGCAT TATGTG GA			
			TATGTA ATACGT CT			
			GT —			
GAM1381	PPP1R2	3'	GTCTGTACATGTGCGTGAC 20694 T AATT			
			GTGCAT GTATGTGTG AC			
			CACGTG CGTGTACAT TG			
			— GTC—			
GAM1381	PPP2R5C	3'	TTGTACATACATTGTAT 10763 T TG			
			GTGCA TGTATGTG A			
			TATGT ACATACAT T			
			T GT			
GAM1381	PPP4R1	3'	TTAGACGTATAATGTAT 17622 G			
			GTGCATTGTATGT TGA			
			TATGTAATATGCA ATT			
			G			
GAM1381	PRDM2	3'	ATGTAGCAATATATCAGTGAC 31844 T GAA			
			GTGCATTG ATGTGT TTACGT			
			CACGTGAC TATATA GATGTA			
			— AC—			
GAM1381	PRDM2	3'	GCGTG CATGTGTGCGTGCGTGT 24249 TG _ TG AAT_			
	GTGT		CAT TGTATG TG TACGT			
			GTG GCGTGC GT GTGCG			
			GT T GT GTAC			
GAM1381	PROX1	3'	TTCATATATATGTGTAT 10897 T			
			GTGCAT GTATGTGTGAA			
			TATGTG TATATATACTT			
			—			
GAM1381	PSAP	3'	ATGTAATCCCACTGTAATAGC 69355 _ T T			
	AT		GTGC ATTGTA GTG GAATTACGT			
			TACG TAATGT CAC CTTAATGTA			
			A _ C			
GAM1381	PSME3	3'	GTGTATGTGTATGTGCCATGCA 19375 T GT AAT_ GT			
	C		GTGCAT GTATGT G TAC			
			CACGTA CGTGTA T GTG			
			C TG GTAT			
GAM1381	PSME3	3'	TATGCACATATGTGTATGCAT 19376 TG_ AATTACGT			
			GTGCAT TATGTGTG			

		TACGTA GTATACAC		
		TGT GTA TG		
GAM1381	PTGER2	3' CGTTATACACATATAGTGTAC 6305	AATT	T
		GTGCATTGTATGTGTG ACG		
		CATGTGATATACACAT TGC		
		AT__ C		
GAM1381	PTGER2	3' TACACATATAGTGTAC 6307		
		GTGCATTGTATGTGTG		
		CATGTGATATACACAT		
GAM1381	PTGFRN	3' ATATTATGCAATGCAC 67185	—	
		GTGCATTGTATG TGT		
		CACGTAACGTAT ATA		
		T		
GAM1381	PTPN14	3' ATTCACACATACCATGTAT 18252	T	
		GTGCAT GTATGTGTGAAT		
		TATGTA CATACACTTA		
		C		
GAM1381	PTPN2	3' ATGTGTGTAATGTATAATGTAC 11053	GTGAAT	
		GTGCATTGTATGT TACGT		
		CATGTAATATGTA GTGTA		
		ATGT__		
GAM1381	RAB23	3' ATTGAATTACATTGTGCAATGC 32782	—	A CGT
	AT	GTGCATTGTATG TGTGA TTA		
		TACGTAACGTGT ACATT AGT		
		T A TA		
GAM1381	RAP1B	3' TCATGCATAAGTGTAT 31601	G	
		GTGCATT TATGTGTGA		
		TATGTGA ATACGTA		
		—		
GAM1381	RARA	3' CACACATGCGCGTGCGC 6364	—	
		GTGCAT TGTATGTGTG		
		C GCGTG GCGTACACAC		
		C		
GAM1381	RARG	3' GTGCCTAATGCTGTGTGATGCA 6383	TG	— GAAT GT
	C	GTGCAT TAT GTGT TAC		
		CACGTA GTG CGTA GTG		
		GT T ATCC		
GAM1381	RASSF1	3' GCGTGAATGTATGTAATGTGT 23209	TG	TG GAA
		G CATTGTATG T TTACGT		

			T GTAATGTAT A AGTGCG			
			GT GT ____			
GAM1381	RBBP9	3'	TACACATACAATCCAT 70139 C			
			GTG ATTGTATGTGTG			
			TAC TAACATACACAT			
			C			
GAM1381	RBP3	3'	GTGTATATACACATATATATGT 11266 _ AAT_ GT			
			GTAT TGCAT TGTATGTGTG TAC			
			ATGTG ATATATACAC ATG			
			T ATAT TG			
GAM1381	RECK	3'	TGTAGTTCATGTAAATAATACA 40873 C A TG GT			
			T GTG ATTGT TG TGAATTAC			
			TAC TAATA AT ACTTGATG			
			A A GT TG			
GAM1381	REV3L	5'	GTGATTCCCGGCGGTGGCGC 11298 _ ATG T			
			GTGC ATTGT TG GAATTAC			
			CGCG TGGCG GC CTTAGTG			
			G ____ C			
GAM1381	RHEB2	3'	ATGTAATCATCAAAATGATGCA 18831 TG ATG _ A			
			T GTGCAT T TG TGA TTACGT			
			TACGTA A AC ACT AATGTA			
			GT AA_ T _			
GAM1381	ROCK2	3'	TCACACTACAATGCAC 66018 T			
			GTGCATTGTA GTGTGA			
			CACGTAACAT CACACT			
			-			
GAM1381	ROCK2	3'	TCATACATATATGTGT 66019 TG T			
			G CAT GTATGTGTGA			
			T GTA TATACATACT			
			GT _			
GAM1381	RORB	3'	TTATACATGCACATGCAC 22611 _			
			GTGCAT TGTATGTGTGA			
			CACGTA ACGTACATATT			
			C			
GAM1381	RTN1	3'	GGCTGATTTACATGTATGGTTA 40911 C TG CGT			
			C GTG AT TATGTGTGAATTA			
			CAT TG ATGTACATTTAGT			
			_ GT CGGG			
GAM1381	RXRA	3'	GTGTGGTGTAAACATGTATGTG 11417 T GA__ GT			
			C GCAT GTATGTGT ATTAC			

CGTG TATGTACA TGGTG  
 \_ AATG TG  
 GAM1381 SCG3 3' ATGTAATTTGTGTATTAGTG 25095 T TG  
 CATTG ATG TGAATTACGT  
 ||||| ||| |||||  
 GTGAT TAT GTTTAATGTA  
 \_ GT  
 GAM1381 SCN4A 3' GTGTGAACACGTGTGTGTGTGT 4417 G TG\_\_ GAAT GT  
 GC CAT TATGTGT TAC  
 ||| ||||| |||  
 GTG GTGCACA GTG  
 T TGTGT AGT\_  
 GAM1381 SCO1 3' ATGTGATTTTTAGCTAAGTGGT 15945 TG TG AT\_ GT\_  
 GTGC CAT T GT GAATTACGT  
 ||| | || |||||  
 GTG G CG TTTAGTGTA  
 GT GT AAT ATT  
 GAM1381 SCO1 3' CATATACGTGCAC 15946 T  
 GTGCAT GTATGTGTG  
 ||||| |||||  
 CACGTG CATATATAC  
 \_  
 GAM1381 SDC4 3' ATGTAGTTCATGGCTACTGTAC 11475 TT TG  
 GTGCA GTA TGTGAATTACGT  
 ||||| ||| |||||  
 CATGT CAT GTACTTGATGTA  
 \_ CG  
 GAM1381 SEDL 3' TCACCACAATGGTGTAT 27354 TG A \_  
 GTGCAT T TGTG TGA  
 ||||| | |||||  
 TATGTG A ACAC ACT  
 GT\_ C  
 GAM1381 SERPINB3 3' CACATATAAATGTAC 22625 G  
 GTGCATT TATGTGTG  
 ||||| |||||  
 CATGTAA ATATACAC  
 \_  
 GAM1381 SERPINB4 3' CACATATAAATGTAC 65279 G  
 GTGCATT TATGTGTG  
 ||||| |||||  
 CATGTAA ATATACAC  
 \_  
 GAM1381 SFTPA2 3' GTGACTGACATGTACGATTCAC 22651 C GAA  
 GTG ATTGTATGTGT TTAC  
 ||| ||||| |||  
 CAC TAGCATGTACA AGTG  
 T GTC  
 GAM1381 SH3BP5 3' CGTTTTTCATGGTAATGCAT 16741 TATG TT  
 GTGCATTG TGTGAA ACG  
 ||||| ||||| |||

TACGTAAT GTACTT TGC  
 G\_\_ T\_  
 GAM1381 SHOX2 5' GTGTGTTTCGTGTGGATGCAC 11656 GTA TG \_  
 GTGCATT TG TGAAT TAC  
 ||||| || ||||| ||  
 CACGTAG GT GCTTG GTG  
 \_\_ GT T  
 GAM1381 SLA 3' GCATGTATGTATGCAC 22171 \_  
 GTGCAT TGTATGTGT  
 ||||| |||||  
 CACGTA GTATGTACG  
 T  
 GAM1381 SLC1A5 3' GTGTGTGCACGTGTGTGTGTGT 18847 TG TG\_ AAT  
 G CAT TATGTGTG TAC  
 | ||| ||||| ||  
 T GTG GTGCACGT GTG  
 GT TGT GT\_  
 GAM1381 SLC1A5 3' GTGTGTGCACGTGTGTGTGTGT 78538 TG TG\_ AAT  
 G CAT TATGTGTG TAC  
 | ||| ||||| ||  
 T GTG GTGCACGT GTG  
 GT TGT GT\_  
 GAM1381 SLC38A2 3' ATTTATCGTACGTCACAGTGTA 38588 \_ ATTACGT  
 T  
 GTGCATTGT ATGTGTGA  
 ||||| |||||  
 TATGTGACA TGCATGCT  
 C ATTTA  
 GAM1381 SLC38A2 3' TATTAACTTTGTGTATATAGTG 38592 TG TTACGT  
 TA  
 TGCATTGTATG TGAA  
 ||||| |||||  
 ATGTGATATAT GTTT  
 GT CAATTATG  
 GAM1381 SLC4A4 3' GTGTATATATGTGCAATGT 13642 AAT  
 GCATTGTATGTGTG TAC  
 ||||| ||||| ||  
 TGTAACGTGTATAT GTG  
 AT\_  
 GAM1381 SLC4A7 3' TACATATGTAATGTGT 13228 TG  
 G CATTGTATGTGTG  
 | ||||| |||||  
 T GTAATGTATACAT  
 GT  
 GAM1381 SLC4A7 3' TACATATGTAATGTGT 13229 TG  
 G CATTGTATGTGTG  
 | ||||| |||||  
 T GTAATGTATACAT  
 GT  
 GAM1381 SLC6A6 3' ATGTAATTGTGGGTATGTGTGC 11728 T TG \_\_\_\_  
 GTGCG T GTATG TG AATTACGT  
 | |||| | |||||

G CGTGT AT TTAATGTA  
 \_ GT GGGTG  
 GAM1381 SLC7A6 3' TAATGCATATGTGAAGCAT 14314 A TG GA  
 GTGC T TATGTGT ATTA  
 ||||| ||||| ||||  
 TACG A GTATACG TAAT  
 A GT \_  
 GAM1381 SLC9A6 3' TAAAATTTGCACATGTGATTGT 21009 \_ TG TG ACGT  
 GCA T TATGTG AATT  
 ||| ||||| ||||  
 TGT A GTACAC TTAA  
 T GT GT AATG  
 GAM1381 SMP1 3' ACGTGGTTCTGGTGGGATGCAC 26694 G GTGT  
 GTGCATT TAT GAATTACGT  
 ||||| ||| |||||  
 CACGTAG GTG CTTGGTGCA  
 G GT\_  
 GAM1381 SNAP25 3' ATGTGATTTATGCATTTATGCA 55525 TGT  
 T GTGCAT ATGTGTGAATTACGT  
 ||||| |||||  
 TACGTA TACGTATTTAGTGTA  
 TT\_  
 GAM1381 SNAP25 3' ATGTGATTTATGCATTTATGCA 11832 TGT  
 T GTGCAT ATGTGTGAATTACGT  
 ||||| |||||  
 TACGTA TACGTATTTAGTGTA  
 TT\_  
 GAM1381 SNRP70 5' GTGACCTCGCGCGTGCCTGTG 78548 TG T A\_ GT  
 C G CA TGTATGTGTGA TTAC  
 | || ||||| ||||  
 C GT GCGTGCGCGCT AGTG  
 GT C CC  
 GAM1381 SOCS5 3' ATGTAAGCATGTATACACTGTG 25795 TG T TG AA  
 C G CA TGTATG TG TTACGT  
 | || ||||| || |||||  
 C GT ACATAT AC AATGTA  
 GT C GT G\_  
 GAM1381 SON 3' ATGTGCTGCTAAATATAGTGCA 49828 GT\_ AAT  
 C GTGCATTGTAT GTG TACGT  
 ||||| ||| |||||  
 CACGTGATATA CGT GTGTA  
 AAT C\_  
 GAM1381 SORBS1 3' CGTATGCATATGCACGTGCA 31153 \_ AATTACGT  
 TGCAT TGTATGTGTG  
 ||||| |||||  
 ACGTG ACGTATACGT  
 C A TGCA  
 GAM1381 SOX13 3' TGTATGTGTGCGCGTGCA 19088 AAT\_  
 TGTATGTGTG TACG  
 ||||| ||||



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          ACGTGCGCGT  ATGT
            GTGT
GAM1381 SOX13  3' TGTGTGCGCGTGACGTGTGT 19089  TG _      AATTACGT
            G CAT TGTATGTGTG
            | ||| |||||
            T GTG ACGTGCGCGT
            GT C      GTG TG
GAM1381 SPG7   3' GTCTAGTCACGCATGCAGTGT 11904      ATT_
            GCATTGTATGTGTGA  AC
            ||||| ||
            TGTGACGTACGCACT  TG
            GATC
GAM1381 SPOCK  3' TATGCATGCATGTAC      62820      T
            GTGCAT GTATGTGTG
            ||||| |||||
            CATGTA CGTACGTAT
            -
GAM1381 SPON1  3' GTGAGACACATAACAATGC  62455      GAA
            GCATTGTATGTGT  TTAC
            ||||| |||
            CGTAACATACACA  AGTG
            G_
GAM1381 STAT5B 3' GTGTGTGTGCGTTGGTGCAC  24915      T TG AAT
            GTGCATTG ATG TG  TAC
            ||||| || || ||
            CACGTGGT TGC GT  GTG
            _ GT GT_
GAM1381 STK10  3' GTGTGGCACGTGCGGGGTGT  19989  TG A      GAAT
            G C TTGTATGTGT  TAC
            | | ||||| |||
            T G GGC GTGCACG  GTG
            GT G      GT_
GAM1381 STS    3' CACACATACAGTATAT      4448      C
            GTG ATTGTATGTGTG
            ||| |||||
            TAT TGACATACACAC
            A
GAM1381 SULT1C1 3' GTGAATGTATACAATGTA  6468      TG GAA
            TGCATTGTATG T  TTAC
            ||||| | |||
            ATGTAACATAT A  AGTG
            GT _
GAM1381 SWAP70 3' GCGGTTACATATGTGGTTGTGC 71351  TG _TG      ATTA
            G CA T TATGTGTGA  CGT
            | || ||||| |||
            C GT G GTATACATT  GCG
            GT T GT      G_
GAM1381 SYNGR1 3' TTCTATATATAAGATGTAT  16326      G      _
            GTGCATT TATGTGT GAA
            ||||| ||||| |||

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TATGTAG ATATATA CTT  
 A T  
 GAM1381 TACC1 3' CACACATACATGTAT 20791 T  
 GTGCAT GTATGTGTG  
 ||||| |||||  
 TATGTA CATAACACAC  
 —  
 GAM1381 TBX3 3' GCGTGGTTTATATGTCCGG 33354 T  
 TTG ATGTGTGAATTACGT  
 ||| |||||  
 GGC TGTATATTTGGTGCG  
 C  
 GAM1381 TCERG1 3' GTTTTTACATATATGTGCAT 21997 T TT  
 GTGCAT GTATGTGTGAA AC  
 ||||| ||||| ||  
 TACGTG TATATACATTT TG  
 — T—  
 GAM1381 TCF20 3' ACGTGATTCTTTATGTTGTGT 66952 TG TGT  
 GCAT TATG GAATTACGT  
 |||| ||| |||||  
 TGTG GTAT CTTAGTGCA  
 TT TT—  
 GAM1381 TDG 3' GTGCTTTATGTACATGAGATGT 12193 G — T GT  
 AC GTGCATT TATGT GTGAA TAC  
 ||||| |||| ||||| ||  
 CATGTAG GTACA TATTT GTG  
 A TG C  
 GAM1381 TEK 3' ATGTGATATATAAGTGTACATA 4859 — — A  
 TGTGC CAT TGTATG TGTG ATTACGT  
 ||| ||||| ||||| |||||  
 GTA ACATGT ATAT TAGTGTA  
 T GA A  
 GAM1381 TEM6 3' CGTGTGTGCATGCGTGCG 42743 AAT—  
 TGTATGTGTG TACG  
 ||||| ||||| |||||  
 GCGTGCGTAC GTGC  
 GTGT  
 GAM1381 TEM6 3' GTGTGTGCGTGTGTGCATGCG 42748 T TG AAT—  
 TGCAT GTATG TG TAC  
 ||||| ||||| || |||  
 GCGTACGTGT GC GTG  
 — GT GTGT  
 GAM1381 TFAP2C 3' ATTCATATATATACAGGGTAT 12231 AT—  
 GTGC TGTATGTGTGAAT  
 ||||| ||||| |||||  
 TATG ATATATATACTTA  
 GGAC  
 GAM1381 TFAP2C 3' GTGAGTGTGCAGTACAGTGTGT 12232 TG G AA—  
 G CATTGTAT TGTG TTAC  
 | ||||| ||||| |||||

			T GTGACATG ACGT AGTG		
			GT _ GTG		
GAM1381	TFEB	5'	GTGAACATATATGCATGTAC 92129	T	AA
			GTGCAT GTATGTGTG TTAC		
			CATGTA CGTATATAC AGTG		
			_ A_		
GAM1381	TIMM17A	3'	TCTGCATAAACGATGTAT 20938	A	_
			GTGCATTGT TGTGT GA		
			TATGTAGCA ATACG CT		
			A T		
GAM1381	TKTL1	3'	TGCATATGCAAGTAC 24299	A	
			GTGC TTGTATGTGTG		
			CATG AACGTATACGT		
			-		
GAM1381	TLL1	3'	ATGTTGAACATAATAGTGTAT 24949	A	GAATT
			GTGCATTGT TGTGT ACGT		
			TATGTGATA ATACA TGTA		
			_ AGT__		
GAM1381	TMEM1	3'	GTGAAGCCAGATATGCAATGTG 12338	TG	G AA_ GT
	T		G CATTGTATGT TG TTAC		
			T GTAACGTATA AC AGTG		
			GT G CGA		
GAM1381	TNFRSF11B	5'	ACGTGATGAGCGTACGGGTGC 10350	TG A	GTGA
			G C TTGTATGT ATTACGT		
			C G GGCATGCG TAGTGCA		
			GT_ AG_		
GAM1381	TNFSF13B	5'	TGCCATGTAGTGCAC 21653	T	
			GTGCATTGTATG GTG		
			CACGTGATGTAC CGT		
			-		
GAM1381	TPMT	3'	ACGAGTTACGTGTGTGTGTGCA 4528	TG_ TG	ATTA
	C		GTGCAT TA TGTGA CGT		
			CACGTG GT GCATT GCA		
			TGT GT GA_		
GAM1381	TRAF5	3'	CATATATATAAAGTAT 16076	A	
			GTGC TTGTATGTGTG		
			TATG AATATATATAC		
			A		
GAM1381	TRHDE	3'	GTGTATAATTATGTGCAATGT 25388	TGAAT_ GT	
			GCATTGTATGTG TAC		

			TGTAACGTGTAT	GTG		
			TAATAT			
GAM1381	TRHDE	3'	GTGTATGCATATGTATATGTAC	25389	T	AAT_
			GTGCAT GTATGTGTG	TAC		
			CATGTA TATGTATAC	GTG		
			_	GTAT		
GAM1381	TRIM9	3'	ATGTAGTTTACACTGAATTGC	30753	TTG T	
			GCA TA GTGTGAATTACGT			
			CGT GT CACATTTGATGTA			
			TAA _			
GAM1381	TRPC1	3'	GTGTTTTGCAGACAATGCAT	12393	ATG TG T	
			GTGCATTGT TG AA TAC			
			TACGTAACA AC TT GTG			
			G_ GT T			
GAM1381	TRPC5	3'	TTACATAAATAGTGTGT	25003	TG A	
			G CATTGT TGTGTGA			
			T GTGATA ATACATT			
			GT A			
GAM1381	TRPM2	5'	CGCATGTGCATGTAC	12398	T	
			GTGCAT GTATGTGTG			
			CATGTA CGTGTACGC			
			-			
GAM1381	TRPM2	3'	CGTGGTGGTGCCAATGTGC	12401	TG TAT TG GA	
			G CATTG G T ATTACG			
			C GTAAC C G TGGTGC			
			GT _ GT G_			
GAM1381	TRPM6	3'	CACACTGTGTAGTGTAT	34532	-	
			GTGCATTGTAT GTGTG			
			TATGTGATGTG CACAC			
			T			
GAM1381	TRPM8	3'	GTAGTTCACAATAATGTAT	43986	ATG	
			GTGCATTGT TGTGAATTAC			
			TATGTAATA ACACTTGATG			
			-			
GAM1381	TRPS1	3'	ACGTGAGAACTAGACAATGTA	26073	ATGT GAA	
	C		GTGCATTGT GT TTACGT			
			CATGTAACA CA AGTGCA			
			GAT_ AAG			
GAM1381	TRPS1	3'	TGTACATACACATGCAC	26083	- GT	
			GTGCAT TGTATGT G			

CACGTA ACATACA T  
C TG  
GAM1381 TTN 3' ATGTAGTTCTTTTCATGCAAGT 55918 A TGT\_  
AT GTGC TTGTATG GAATTACGT  
||||| |||||  
TATG AACGTAC CTTGATGTA  
\_ TTTT  
GAM1381 TTN 3' ATGTAGTTCTTTTCATGCAAGT 55936 A TGT\_  
AT GTGC TTGTATG GAATTACGT  
||||| |||||  
TATG AACGTAC CTTGATGTA  
\_ TTTT  
GAM1381 TTN 3' ATGTAGTTCTTTTCATGCAAGT 55948 A TGT\_  
AT GTGC TTGTATG GAATTACGT  
||||| |||||  
TATG AACGTAC CTTGATGTA  
\_ TTTT  
GAM1381 TUBA3 3' GTTAATTTGTATGTAGCAGTGT 20026 \_ TG CGT  
AT GTGCATTGT ATGTG AATTA  
||||| |||||  
TATGTGACG TGTAT TTAAT  
A GT TG  
GAM1381 UBE2E3 3' ATGTGGTTCATGCTGTTGTG 20993 TG T  
CAT TA GTGTGAATTACGT  
||| |||||  
GTG GT CGTACTTGGTGTA  
TT \_  
GAM1381 UBE4A 3' ATGTAAGATTTCATTTCAGTGTGC 16560 TG T TGTGAA  
G CATTG ATG TTACGT  
| ||||| |||||  
C GTGAC TAC AATGTA  
GT T TTAG\_  
GAM1381 USP1 3' GTGTATTCACAATGGTGTAT 12559 TG ATG \_  
GTGCAT T TGTGAAT TAC  
||||| | ||||| |||  
TATGTG A ACACTTA GTG  
GT\_ T  
GAM1381 USP11 3' GTGTGTGTATATATAAAGCAC 16205 A GT AAT  
GTGC TTGTATGT G TAC  
||||| ||||| | |||  
CACG AATATATA T GTG  
A TG GT\_  
GAM1381 USP6 3' GTAATTGTATATGGGGTGTAC 91149 G TG A  
GTGCATT TATGTG A TTAC  
||||| ||||| | |||  
CATGTGG GTATAT T AATG  
G GT\_  
GAM1381 UTY 3' ATGTATTTTATATGTGTGTGTA 23069 TGT T  
T GTGCAT ATGTGTGAA TACGT  
||||| ||||| |||||

			TATGTG TGTATATTT ATGTA		
			TG_ T		
GAM1381	UTY	3'	GTGTACACACATGTATAATATA 23071	C	AAT_ GT
	T		GTG ATTGTATGTGTG TAC		
			TAT TAATATGTACAC GTG		
			A ACAT		
GAM1381	VIL2	3'	GTGTTTTATGCATGTAATGGAC 12600	G	T
			GT CATTGTATGTGTGAA TAC		
			CA GTAATGTACGTATTT GTG		
			G T		
GAM1381	VLDLR	3'	GTGAACTTGTGCTATAGTGTA 69522		T TG A_ GT
	T		GTGCATTGTA GTG A TTAC		
			TATGTGATAT CGT T AGTG		
			_ GT CAA		
GAM1381	VSX1	3'	GTGGTTCAATGTACTGTAT 27469	TT	G
			GTGCA GTATGT TGAATTAC		
			TATGT CATGTA ACTTGGTG		
			— —		
GAM1381	WBSCR1	3'	ATTCACACGTGTGTGTGT 49257	TG	TGT
			G CAT ATGTGTGAAT		
			T GTG TGCACACTTA		
			GT TG_		
GAM1381	WBSCR1	3'	ATTCACACGTGTGTGTGT 42225	TG	TGT
			G CAT ATGTGTGAAT		
			T GTG TGCACACTTA		
			GT TG_		
GAM1381	WHSC1	3'	GTAGTTTACGCGGAGCAC 29916		ATTGTA
			GTGC TGTGTGAATTAC		
			CACG GCGCATTTGATG		
			AG_		
GAM1381	WHSC1	3'	GTAGTTTACGCGGAGCAC 55834		ATTGTA
			GTGC TGTGTGAATTAC		
			CACG GCGCATTTGATG		
			AG_		
GAM1381	WHSC1	3'	GTAGTTTACGCGGAGCAC 55851		ATTGTA
			GTGC TGTGTGAATTAC		
			CACG GCGCATTTGATG		
			AG_		
GAM1381	WHSC1	3'	GTAGTTTACGCGGAGCAC 55860		ATTGTA
			GTGC TGTGTGAATTAC		

CACG GCGCATTTGATG  
AG\_\_\_\_  
GAM1381 WIG1 3' GTGGATTTCACACATATAATTG 94470 \_ \_ GT  
C GCA TTGTATGTGTGAA TTAC  
||| ||||| |||  
CGT AATATACACACTT GGTG  
T TA  
GAM1381 WNT15 3' CATGTGTGCCAATGCAC 12678 \_ TG  
GTGCATTG TATG TG  
||||| ||| ||  
CACGTAAC GTGT AC  
C GT  
GAM1381 WNT5A 3' GCGTGATTTGTATATTTCACTG 12669 T T\_ TG  
CA TG ATGTG AATTACGT  
|| || |||| |||||  
GT AC TATAT TTAGTGCG  
C TT GT  
GAM1381 WWOX 3' CGCAGCGCGTGCGGTGCA 55609 GAATTA  
TGCATTGTATGTGT CG  
||||||| ||  
ACGTGGCGTGCGCG GC  
AC\_\_\_\_  
GAM1381 XDH 3' ATGTAATTTGTAAACACAATG 4594 ATG TG  
CATTGT TG AATTACGT  
||||| || |||||  
GTAACA AT TTAATGTA  
CAA GT  
GAM1381 XDH 3' ATGTAATTTGTAAACACAATG 59415 ATG TG  
CATTGT TG AATTACGT  
||||| || |||||  
GTAACA AT TTAATGTA  
CAA GT  
GAM1381 XRCC1 3' CACACACACGATGCAT 20850 A  
GTGCATTGT TGTGTG  
||||||| |||||  
TACGTAGCA ACACAC  
C  
GAM1381 ZFH1B 3' ATGTGCTCGCACTACAATGCAT 28922 T AT  
GTGCATTGTA GTGTGA TACGT  
||||||| ||||| |||||  
TACGTAACAT CACGCT GTGTA  
\_ C\_  
GAM1381 ZFH1B 3' TTCATACTGTAGTGTAC 28926 T  
GTGCATTGTA GTGTGAA  
||||||| |||||  
CATGTGATGT CATACTT  
\_  
GAM1381 ZFP37 3' CATATATACATGTAT 12715 T  
GTGCAT GTATGTGTG  
||||| |||||

TATGTA CATATATAC

GAM1381 ZNF136 3' TCACACATGAATGTGT 59892 TG G  
G CATT TATGTGTGA  
| ||| |||||  
T GTAA GTACACACT  
GT \_

GAM1381 ZNF146 3' CGTATGCATATATGTATGTAC 23085 \_ AATTACGT  
GTGCAT TGTATGTGTG  
||||| |||||  
CATGTA GTATATACGT  
T A TGCA

GAM1381 ZNF175 3' ATGTATATAAGCATATATATAA 23090 C AAT\_\_\_\_  
TATAT ATTGTATGTGTG TACGT  
||||||| ||||  
TAATATATATAC ATGTA  
A GAATAT

GAM1381 ZNF175 3' ATGTGTATGTATGCGTATGTAT 23091 \_ TG AAT  
GTGCAT TGTATG TG TACGT  
||||| ||||| || |||||  
TATGTA GCGTAT AT GTGTA  
T GT \_\_\_\_

GAM1381 ZNF175 3' GTGCGCCTTATGTATATAAGCA 23096 A TG ATTACGT  
T GTGC TTGTATG TGA  
||||| ||||| |||  
TACG AATATAT ATT  
\_ GT CCGCGTGT

GAM1381 ZNF175 3' GTGTATGTATGCGTATGTATGT 23097 \_ AAT\_ GT  
AT GTGCAT TGTATGTGTG TAC  
||||| ||||| ||||| |||  
TATGTA GTATGCGTAT GTG  
T GTAT

GAM1381 ZNF175 3' TGTATGTATATATATATGCAT 23099 TTG AAT  
GTGCA TATGTGTG TACG  
||||| ||||| |||||  
TACGT ATATATAT ATGT  
\_ GT\_

GAM1381 ZNF264 3' GTGGTTTCTACTGAATGCAT 12763 GTAT T  
GTGCATT GTG GAATTAC  
||||| ||| |||||  
TACGTAA CAT TTTGGTG  
GT\_ C

GAM1381 ZNF289 3' TTCGTATGTGTGGTGTGT 65336 TG TG  
G CAT TATGTGTGAA  
| ||| |||||  
T GTG GTGTATGCTT  
GT GT

GAM1381 ZNF289 3' TTTGTTACTTCGTATGTGTGGT 65337 TG TG TT\_ T  
GTGT CAT TATGTGTGAA ACG  
||| ||||| |||



			GTG GTGTATGCTT TGT		
			GT GT CAT TTA		
GAM1381	ZNF36	3'	ACGATAAGTTGTATATATGATC 93958	C TG	TG A _
	AC		GTG AT TATGTG A TTA CGT		
			CAC TA ATATAT T AAT GCA		
			_ GT GT G A		
GAM1381	ZNF8	3'	GGTAAGTCCACATAGTGTAC 64070	TG	T A GT
			GTGCAT TATGTG GA TTAC		
			CATGTG ATACAC CT AATG		
			_ _ G GT		
GAM1381	ZNF80	3'	ATGTTTTGATGAATACAATGTA 23074	G G	TT
	T		GTGCATTGTAT TGT AA ACGT		
			TATGTAACATA GTA TT TGTA		
			A G T_		
GAM1381	ABHD3	3'	TGTAGTTCTTTGGGTGCAT 56376	GTATGTGT	
			GTGCATT GAATTACG		
			TACGTGG CTTGATGT		
			GTTT_		
GAM1381	ACTR1A	3'	GTGTGTGCACATGCGAGTGC 62967	TG A	AAT
			G C TTGTATGTGTG TAC		
			C G AGCGTACACGT GTG		
			GT_ GT_		
GAM1381	AD024	3'	TACATGTGCACAATGTGC 40342	TG _	
			G CAT TGTATGTGTG		
			C GTA ACGTGTACAT		
			GT AC		
GAM1381	AKAP11	3'	GTGTGCTCGTTGCATATACAGT 57833	TG AT_	GT
	GT		CATTGTATGTG A TAC		
			GTGACATATAC T GTG		
			GT GCTCGT		
GAM1381	AKAP11	3'	CACATGTGTAGTGTGT 32702	TG	
			G CATTGTATGTGTG		
			T GTGATGTGTACAC		
			GT		
GAM1381	AKAP11	3'	TCTTCTATACACATGTGTAGTG 32715	TG	AATTACGT
	TGT		G CATTGTATGTGTG		
			T GTGATGTGTACAC		
			GT ATATCTTCTT		
GAM1381	AKAP8	3'	GTAGTGCACCATATGGTGTGT 19604	TG TG	T A
			G CAT TATG GTG ATTAC		

T GTG ATAC CAC TGATG  
 GT GT \_ G  
 GAM1381 AKAP9 3' TGGAATTTGTATATATAAGCAT 19242 A TG ACGT  
 GTGC TTGTATGTG AATT  
 |||| ||||| ||||  
 TACG AATATATAT TTAA  
 \_ GT GGTC  
 GAM1381 AKL3L 3' ATGTTAACCATATATGCTGTAT 32803 TT AATT  
 GTGCA GTATGTGTG ACGT  
 |||| ||||| ||||  
 TATGT CGTATATAC TGTA  
 \_ CAAT  
 GAM1381 AKR1D1 3' ACGAAGTGCATGTGGCAGTGTG 19970 TG \_ GA A  
 C G CATTGT ATGTGT ATT CGT  
 | |||| ||||| ||||  
 C GTGACG TGTACG TGA GCA  
 GT G \_ A  
 GAM1381 ALDH5A1 3' TACATATATAGGTAC 6551 A  
 GTGC TTGTATGTGTG  
 |||| ||||| ||||  
 CATG GATATATACAT  
 \_  
 GAM1381 AP3S2 3' TCACATGTGCAGTCAT 19523 C  
 GTG ATTGTATGTGTGA  
 |||| ||||| ||||  
 TAC TGACGTGTACACT  
 \_  
 GAM1381 API5 3' GTGTATATATATATATATGCAT 21691 \_ AAT  
 GTGCAT TGTATGTGTG TAC  
 |||| ||||| ||||  
 TACGTA ATATATATAT GTG  
 T AT\_  
 GAM1381 ARHGEF15 3' GTGTGTGTACATGTGCATGTGT 30261 TG T AAT\_  
 G CAT GTATGTGTG TAC  
 | |||| ||||| ||||  
 T GTA CGTGTACAT GTG  
 GT \_ GTGT  
 GAM1381 ARHU 3' GTTTTATGCGTGTGACAGTGTA 41076 \_ TTACGT  
 T TGCATTGT ATGTGTGAA  
 ||||| ||||| |||||  
 ATGTGACA TCGTATTT  
 GTG TG T  
 GAM1381 ARHU 3' TACATTATAATGTAC 41077 T  
 GTGCATTGTA GTGTG  
 ||||| ||||| |||||  
 CATGTAATAT TACAT  
 \_  
 GAM1381 AXOT 3' ATGAATATATACATACACATGT 43078 \_ A A  
 AT GTGCAT TGTATGTGTG ATT CGT  
 ||||| ||||| ||||| |||||

			TATGTA ACATACATAT TAA GTA		
			C A _		
GAM1381	B3GNT5	3'	ATGTAGAAAAATGTGTACAATG 49424	TG GAA_	
	T		GCATTGTATG T TTACGT		
			TGTAACATGT A GATGTA		
			GT AAAA		
GAM1381	BA108L7.2	3'	ATGATACACATGTGTATGTGTA 48256	TG_ A CGT	
	C		GTGCAT TATGTGTG ATTA		
			CATGTG GTGTACAC TAGT		
			TAT A A		
GAM1381	BCCIP	3'	ATGTTTTTCATACATCTGATGTA 54303	GT TT	
	T		GTGCATT ATGTGTGAA ACGT		
			TATGTAG TACATACTT TGTA		
			TC T_		
GAM1381	BCMP1	3'	ATGTAATTTATTTCAGACTGTAT 48732	TT A T	
			GTGCA GT TG GTGAATTACGT		
			TATGT CA AC TATTTAATGTA		
			_ G T		
GAM1381	BCoR	3'	CACCATGTACAGTGTGT 34863	TG _	
			G CATTGTATGTG TG		
			T GTGACATGTAC AC		
			GT C		
GAM1381	BHLHB2	3'	GTGTATGTGCGTGTGCGTGAC 13381	T TG AAT_	
			GTGCAT GTA TGTG TAC		
			CACGTG CGT GCGT GTG		
			_ GT GTAT		
GAM1381	BIRC8	5'	CACACGTGTGTGTGCGC 52903	TG_	
			GTGCAT TATGTGTG		
			CGCGTG GTGCACAC		
			TGT		
GAM1381	BLOV1	3'	CATACATATACATGTGT 76279	TG _	
			G CAT TGTATGTGTG		
			T GTA ATATACATAC		
			GT C		
GAM1381	BLOV1	3'	TACATATACATGTGTAT 76284	_	
			GTGCAT TGTATGTGTG		
			TATGTG ACATATACAT		
			T		
GAM1381	BMF	3'	TATGTTCTTCACATGCATATGT 53163	G _ T_ TACGT	
	GT		CAT TGTATGTG GAAT		

			GTA ACGTACAC CTTG	
			T T TT TA TG	
GAM1381 BPESC1	3'	GGTATGTAGCATGTAGTGCAC 41475		GTGAAT GT
		GTGCATTGTATGT TAC		
		CACGTGATGTACG ATG		
		ATGT__ GT		
GAM1381 BRAG	3'	ATATTTATTTGCAGTACAGTGC 29468		G TG TACGT
GC		GTGCATTGTAT TG AAT		
		CGCGTGACATG AC TTA		
		_ GT TTTATAT		
GAM1381 BRAG	3'	ATGTGAATAACATGTGGTGTA 29469	TG	GTGAA
		TGCAT TATGT TTACGT		
		ATGTG GTACA AGTGTA		
		GT ATA__		
GAM1381 BRP44I	3'	GTATTTCCATGCAGTGTAT 32245	TGT	T
		GTGCATTGTATG GAA TAC		
		TATGTGACGTAC CTT ATG		
		__ T		
GAM1381 BTBD2	3'	TGCACATTGCAATGCAT 35107	_	
		GTGCATTGTA TGTGTG		
		TACGTAACGT ACACGT		
		T		
GAM1381 BTBD3	3'	GTGTGATAGTCTTCAGGTGCAG 30312	G T_ _	GT
TGCG		CATTGTAT TG GA ATTAC		
		GTGACGTG AC CT TAGTG		
		G TT GA TG		
GAM1381 BTBD3	3'	TGCGCACCCATGCGCATGCA 30315	_	T AATTACGT
		TGCAT TGTATG GTG		
		ACGTA GCGTAC CAC		
		C C GCG TG		
GAM1381 BTF3	5'	CGTCCCCGCGTGTGTGCGC 95945	TGT TG	AATT
		GTGCAT A TGTG ACG		
		CGCGTG T GCGC TGC		
		__ GT CCC_		
GAM1381 C11orf11	3'	GTGTTGGCGCGTATGCATGTGC 93260	TG _	G T GT
		G CAT TGTATGTGT AAT AC		
		C GTA GTATGCGCG TTG TG		
		GT C G _		
GAM1381 C11orf14	3'	ATGTCTGCACGTGTGCATGCAT 40226	T TG	AATT
		GTGCAT GTA TGTG ACGT		

TACGTA CGT GCAC TGTA  
 \_ GT GTC\_  
 GAM1381 C11orf25 3' CACATGTATAATATGC 48638 GC  
 GT ATTGTATGTGTG  
 || |||||  
 CG TAATATGTACAC  
 TA  
 GAM1381 C11orf25 3' TTCACTGTACAATGTGT 48647 TG T  
 G CATTGTATG GTGAA  
 | ||||| ||||  
 T GTAACATGT CACTT  
 GT \_  
 GAM1381 C20orf13 3' ATGTAAAGAGAACATACAGTAA 34754 \_\_\_\_ GTGAA  
 TGCAC CAT TGTATGT TTACGT  
 ||| ||||| |||||  
 GTA ACATACA AATGTA  
 ATG AGAGA  
 GAM1381 C20orf13 3' GAGTGTGTGCGCGTATGTGCGC 34755 T AAT GT  
 GTGCAT GTATGTGTG TAC  
 ||||| ||||| |||  
 CGCGTG TATGCGCGT GTG  
 \_ GT\_ AGT  
 GAM1381 C20orf80 3' GACTGCATTACACATGCGATG 65287 TACGT  
 T GCATTGTATGTGTGAAT  
 |||||  
 TGTAGCGTACACACTTA  
 CGTCAGT  
 GAM1381 C21orf108 3' TCTGCCGTATAATGTAC 88726 T \_  
 GTGCATTGTATG GT GA  
 ||||| || ||  
 CATGTAATATGC CG CT  
 \_ T  
 GAM1381 C21orf18 3' ATTCAGTATAATGCAGTGTAT 33844 \_ \_  
 GTGCATTGTAT GTG TGAAT  
 ||||| ||| |||||  
 TATGTGACGTA TAT ACTTA  
 A G  
 GAM1381 C21orf51 3' GTGTGAAATGCTATATAGTGCA 54199 \_ GAAT GT  
 TGCATTGTAT GTGT TAC  
 ||||| ||| |||  
 ACGTGATATA CGTA GTG  
 T AAGT  
 GAM1381 C3IP1 3' GTGTACTATATGTACGTTGTGC 41283 TG T AAT  
 G CA TGTATGTGTG TAC  
 | || ||||| |||  
 C GT GCATGTATAT GTG  
 GT T CAT  
 GAM1381 C3orf4 3' ATGTGGTTTACTTTAAGCGATG 39119 A T\_  
 C GCATTGT TG GTGAATTACGT  
 ||||| || |||||

CGTAGCG AT CATTGGTGTA  
A TT  
GAM1381 C5orf3 3' TGTGGTTTATTAATGCCATGTA 37965 T GT GT  
C GTGCAT GTAT GTGAATTAC  
||||| ||| |||||  
CATGTA CGTA TATTTGGTG  
C AT TG  
GAM1381 C5orf5 3' TCCATCATGCAGTGTAC 33470 \_ T  
GTGCATTGTATG TG GA  
||||||| || ||  
CATGTGACGTAC AC CT  
T \_  
GAM1381 C5orf6 3' GCGTGAGAGTGTGTGCGTGCAT 33484 T TG GAA  
GTGCAT GTATG T TTACGT  
||||| ||| | |||||  
TACGTG CGTGT G AGTGCG  
\_ GT AG\_  
GAM1381 C8orf13 3' CACATGTGTACAGTGC 81567 \_  
GCATTGTAT GTGTG  
||||||| |||||  
CGTGACATG TACAC  
TG  
GAM1381 C8orf13 3' GTAGGTCAACTACAGTGCG 81576 T G A  
TGCATTGTA GT TGA TTAC  
||||||| || ||| |||||  
GCGTGACAT CA ACT GATG  
\_ \_ G  
GAM1381 C9orf7 3' ATGTATATGTGTGTGGGTGCAC 34164 \_TG TG AAT  
GTGCA T TATG TG TACGT  
||||| | ||| || |||||  
CACGT G GTGT AT ATGTA  
G GT GT \_  
GAM1381 CACNA1I 3' TATATATATATATGCAT 40837 \_  
GTGCAT TGTATGTGTG  
||||| |||||  
TACGTA ATATATATAT  
T  
GAM1381 CAMTA1 3' GTGGTAAACGGGTAATGCAT 67918 TA GTGA  
GTGCATTG TGT ATTAC  
||||||| ||| |||||  
TACGTAAT GCA TGGTG  
GG AA\_  
GAM1381 CARD9 3' CATGCATGCATTGTAT 53380 T  
GTGCA TGTATGTGTG  
||||| |||||  
TATGT ACGTACGTAC  
T  
GAM1381 CARD9 3' CATGCATGCATTGTAT 42284 T  
GTGCA TGTATGTGTG  
||||| |||||

TATGT ACGTACGTAC  
 T  
 GAM1381 caspr5 3' CACACATATGTGTAT 55381 T  
 GTGCAT GTATGTGTG  
 ||||| |||||  
 TATGTG TATACACAC  
  
 —  
 GAM1381 CCNG2 3' GTGATTTTTATATATGTAATGT 15128 — GT  
 GCATTGTATGTGTGA ATTAC  
 ||||| |||||  
 TGTAATGTATATATT TAGTG  
 TT  
 GAM1381 CDC14A 3' ATTTACATGTACAGTGTTA 13392 T  
 G GCATTGTATGTGTGAAT  
 | ||||| |||||  
 A TGTGACATGTACATTTA  
 T  
 GAM1381 CENTG3 3' ATGTTTGTGTACATATTTGATG 49206 TG T AATT\_  
 TGT G CATTG ATGTGTG ACGT  
 | |||| |||||  
 T GTAGT TATACAT TGTA  
 GT T GTGTT  
 GAM1381 CG012 5' ATGTGTCAGCTGCATGCAGTG 83216 \_ GAAT  
 CATTGTATGT GT TACGT  
 ||||| || |||||  
 GTGACGTACG CG GTGTA  
 T ACT\_  
 GAM1381 CGI-142 3' ATGTAATTCATATATTAAAGCA 32174 A T  
 TGC TTG ATGTGTGAATTACGT  
 ||| ||| ||||| |||||  
 ACG AAT TATATACTTAATGTA  
 A \_  
 GAM1381 CHIC1 3' CACACATGCGTGTGTGC 82034 TG \_  
 G CAT TGTATGTGTG  
 | ||| |||||  
 C GTG GCGTACACAC  
 GT T  
 GAM1381 CHST3 3' GCGTATAGACATACATACATGT 14977 T AAT\_  
 AC GTGCAT GTATGTGTG TACGT  
 ||||| ||||| |||||  
 CATGTA CATAACATAC ATGCG  
 \_ AGAT  
 GAM1381 CKAP4 3' TGAATTGCGTGTGCAGGGCGC 22391 A TG TG A  
 GTGC TTGTA TG A TTA  
 |||| |||| || ||||  
 CGCG GACGT GC T AGT  
 G GT GT A  
 GAM1381 CLDN15 3' CACACACACAGTGCAC 56560 A  
 GTGCATTGT TGTGTG  
 ||||| |||||

			CACGTGACA ACACAC		
			C		
GAM1381	CLSTN3	3'	CCGGGTGTACATATATAATGTA 28207		AATTA T
	T		GTGCATTGTATGTGTG CG		
			TATGTAATATATACAT GC		
			GTGG_ CC		
GAM1381	CLSTN3	3'	TACATATATAATGTAT 28211		
			GTGCATTGTATGTGTG		
			TATGTAATATATACAT		
GAM1381	CMAS	3'	GTGATATATATATATTGTGC 37953	T	A
			GCAT GTATGTGTG ATTAC		
			CGTG TATATATAT TAGTG		
			T A		
GAM1381	CPR2	3'	GTGTATATATATGTACATGTGT 48103	_	A _ GT
	AT		GTGCAT TGTATGTGTG AT TAC		
			TATGTG ACATGTATAT TA GTG		
			T A T		
GAM1381	CPR2	3'	TCGCATGTATGAGTAT 48105	A TG	
			GTGC T TATGTGTGA		
			TATG A ATGTACGCT		
			_ GT		
GAM1381	CSMD1	5'	GTGTCGCGTGCGTGTGGAGTAT 52642	A TG	TG AAT
			GTGC T TATG TG TAC		
			TATG G GTGC GC GTG		
			A GT GT GCT		
GAM1381	CSMD1	5'	GTGTCGCGTGCGTGTGGAGTAT 73128	A TG	TG AAT
			GTGC T TATG TG TAC		
			TATG G GTGC GC GTG		
			A GT GT GCT		
GAM1381	CSR1	3'	CACACATACACATGCAC 32675	_	
			GTGCAT TGTATGTGTG		
			CACGTA ACATACACAC		
			C		
GAM1381	CSR1	3'	CACACATACACATGCAT 32676	_	
			GTGCAT TGTATGTGTG		
			TACGTA ACATACACAC		
			C		
GAM1381	CSR1	3'	CACACATACACGTGCAC 32677	_	
			GTGCAT TGTATGTGTG		



Accession	Gene	Strand	Sequence	Position	Orientation	Notes
GAM1381	CSR1	3'	CACACATACATATGCAC GTGCAT TGTATGTGTG               CACGTA ACATACACAC	32678	—	
GAM1381	CSR1	3'	CACACATATATGCAC GTGCAT GTATGTGTG               CACGTA TATACACAC	32679	T	
GAM1381	CSR1	3'	CACACATGCATGCAC GTGCAT GTATGTGTG               CACGTA CGTACACAC	32680	T	
GAM1381	CSR1	3'	CACACATGCATGCAC GTGCAT GTATGTGTG               CACGTA CGTACACAC	32681	T	
GAM1381	CSR1	3'	CATACATGCATGCAC GTGCAT GTATGTGTG               CACGTA CGTACATAC	32682	T	
GAM1381	CSR1	3'	CATATATACACATGCAC GTGCAT TGTATGTGTG               CACGTA ACATATATAC	32683	—	
GAM1381	CSR1	3'	CCCCTCCTCACACATACATGTG GTGCAT TGTATGTGTGA               CACGTG ACATACACACT T CCTCCCCG	32684	—	ATTACGT
GAM1381	CSR1	3'	TACACATGCATGCAC GTGCAT GTATGTGTG               CACGTA CGTACACAT	32689	T	
GAM1381	CSR1	3'	TACATGTGCACATGCAC GTGCAT TGTATGTGTG               CACGTA ACGTGTACAT	32690	—	
GAM1381	CYP3A7	3'	ATTCTGTACGTGCATTGTGC G CA TGTATGT GAAT 	5716	TG T	GT_

C GT ACGTGCA CTTA  
 GT T TGT  
 GAM1381 CYYR1 3' GCCTACCTTTATATGTATAAAG 53673 A TTACGT  
 CAT GTGC TTGTATGTGTGAA  
 |||| |||||  
 TACG AATATGTATATTT  
 A CCATCCGT  
 GAM1381 DCAMKL1 3' ATGTATCATTATGGCAGTGTAT 16408 ATGT AT  
 GTGCATTGT GTGA TACGT  
 ||||| ||| ||||  
 TATGTGACG TACT ATGTA  
 GTAT \_  
 GAM1381 DDM36 3' ATGTGATGTGCACATGTGTGAA 40568 G\_ A  
 GTGCAT ATT TATGTGTG ATTACGT  
 || ||||| |||||  
 TGA GTACACGT TAGTGTA  
 AGTGT G  
 GAM1381 DIS3 3' ATGTAAAAATATATAGTGC 30228 GTGAA  
 GCATTGTATGT TTACGT  
 ||||| ||||  
 CGTGATATATA AATGTA  
 AA\_  
 GAM1381 DJ473B4 3' GTGTGCACGTGTGTGCAAGTGC 38961 \_ TG AAT\_ GT  
 AC GTGCATT GTATG TG TAC  
 ||||| |||| || |||  
 CACGTGA CGTGT GC GTG  
 A GT ACGT  
 GAM1381 DJ79P11.1 3' TTACACATTTGTGGTGTAC 50915 TG\_  
 GTGCAT T ATGTGTGA  
 ||||| | |||||  
 CATGTG G TACACATT  
 GT TT  
 GAM1381 DKFZP434A043 5' ATGTAGTTCACTTAACAATGTA 31184 ATGT  
 TGCATTGT GTGAATTACGT  
 ||||| |||||  
 ATGTAACA CACTTGATGTA  
 ATT\_  
 GAM1381 DKFZP434A043 3' CAGGCATGCGTGTGTAT 31189 \_ G  
 GTGCAT TGTATGT TG  
 ||||| ||||| ||  
 TATGTG GCGTACG AC  
 T G  
 GAM1381 DKFZp434A1520 3' ATTCACATATGTGCAGTGT 61114 \_  
 GCATTGTAT GTGTGAAT  
 ||||| |||||  
 TGTGACGTG TACACTTA  
 TA  
 GAM1381 DKFZp434A2417 3' ATGTAATTATAGGATATAGTGT 66095 GTGTG  
 GCATTGTAT AATTACGT  
 ||||| |||||

		TGTGATATA	TTAATGTA		
		GGATA			
GAM1381	DKFZP434N093 3'	ATGTGAAGCATATGCAGTGTGC	79943	TG	GAA
		G CATTGTATGTGT	TTACGT		
		C GTGACGTATACG	AGTGTA		
		GT	A__		
GAM1381	DKFZP434P0721 3'	GTGTAATTCATACATATATAGA	63719	CAT_	GT
	TAC	TG	TGTATGTGTGAATTAC		
		AT	ATACATACTTAATG		
		AGAT	TG		
GAM1381	DKFZp547D155 3'	GTGTGGAGCACGTAGTGAC	70438	TG	GAAT
		GTGCAT	TATGTGT	TAC	
		CACGTG	ATGCACG	GTG	
		__	AGGT		
GAM1381	DKFZp547O146 5'	CCCCGTTTGCATATGCAATGC	39565	TG	TACGT
		GCATTGTATGTG	AAT		
		CGTAACGTATAC	TTG		
		GT	CCCCA		
GAM1381	DKFZP564C1940 5'	CGTGGGTGTGCGATGGGC	25900	G	TG GTGAA
		GT CATTGTA	T	TTACG	
		CG	GTAGCGT	G	GGTGC
		G	GT	_____	
GAM1381	DKFZP564L0864 3'	ATGTAGATAAATATATATAGTG	72553	GAA_	
		CATTGTATGTGT	TTACGT		
		GTGATATATATA	GATGTA		
		AATA			
GAM1381	DKFZP566F2124 3'	ATGTTAAATCCATATATGATGT	31573	TG	T A _
	AT	GTGCAT	TATGTG	GA	TTA CGT
		TATGTA	ATATAC	CT	AAT GTA
		GT	_	A	T
GAM1381	DKFZP586B0923 3'	ATGTGATTTGTATTTTAGATGC	93119	GTAT	TG
		GCATT	GTG	AATTACGT	
		CGTAG	TAT	TTAGTGTA	
		ATTT	GT		
GAM1381	DKFZP586D0623 3'	TACACATGCTGGTGTGT	71976	TG	_
		G CATT	GTATGTGTG		
		T	GTGG	CGTACACAT	
		GT	T		
GAM1381	DKFZP586I2223 3'	GTGTGCGCGGGTGTATGTGCGC	31272	TG_	G AAT
		GTGCAT	TAT	TGTG	TAC

CGCGTG GTG GCGC GTG  
TAT G GT\_  
GAM1381 DKFZP586I2223 3' GTGTGCGCGGGTGTATGTGCGC 54913 TG\_ G AAT  
GTGCAT TAT TGTG TAC  
||||| ||| ||| |||  
CGCGTG GTG GCGC GTG  
TAT G GT\_  
GAM1381 DKFZP586I2223 3' GTGTGCGCGGGTGTATGTGCGC 54922 TG\_ G AAT  
GTGCAT TAT TGTG TAC  
||||| ||| ||| |||  
CGCGTG GTG GCGC GTG  
TAT G GT\_  
GAM1381 DKFZp761J139 5' GTATCATGTGTGCAGTCGC 50115 C TG AT  
GTG ATTGTATG TGA TAC  
||| ||||| ||| |||  
CGC TGACGTGT ACT ATG  
— GT —  
GAM1381 DKFZp761K1423 3' ATGTATATGATACATGTAAATG 37329 G AAT\_\_  
TAC TGCATT TATGTGTG TACGT  
||||| ||||| |||||  
ATGTAA ATGTACAT ATGTA  
— AGTAT  
GAM1381 DKFZp761N0624 3' ATGTAATTTATTGAATATTGTA 50179 TT GT\_  
C GTGCA GTAT GTGAATTACGT  
||||| ||| |||||  
CATGT TATA TATTTAATGTA  
— AGT  
GAM1381 DKFZp762E1511 5' GTGTGTGTACATGGGGTGTGT 59515 TG G GT AAT  
G CATT TATGT G TAC  
| ||||| | |||  
T GTGG GTACA T GTG  
GT G TG GT\_  
GAM1381 DKFZp762L0311 3' GTTCACATATGATGTAC 38058 GT  
GTGCATT ATGTGTGAAT  
||||| |||||  
CATGTAG TATACACTTG  
—  
GAM1381 DKK2 3' GTGAAGTTGTGTATTTAATGCA 27019 T TG A\_ GT  
T GTGCATTG ATG TGA TTAC  
||||| ||| ||| |||  
TACGTAAT TAT GTT AGTG  
T GT GA  
GAM1381 DNAJC6 3' GTGTGCACATATACAATGTGC 28848 TG AAT  
G CATTGTATGTGTG TAC  
| ||||| |||  
C GTAACATATACAC GTG  
GT GT\_  
GAM1381 DNER 3' ACGTAACGTAGCATATGATGTA 57441 TG GTGAA  
T GTGCAT TATGT TTACGT  
||||| ||| |||||

			TATGTA ATACG AATGCA		
			GT ATGC_		
GAM1381 DREV1	3'	ATGTGATTTATGCAAAATTGTT 32069	T TTGTA		
A		G GCA TGTGTGAATTACGT			
		A TGT ACGTATTTAGTGTA			
		T TAAA_			
GAM1381 E2F5	3'	ATGTAGTTTGTGTTTTTAAAATGT 8708	TG GTATGT TG		
GC		G CATT G AATTACGT			
		C GTAA T TTGATGTA			
		GT AATTTT GT			
GAM1381 EAT2	3'	ATGTGGTTCTGTACAGTGATGT 79275	TG A GT_		
AT		GTGCAT T TGT GAATTACGT			
		TATGTA G ACA CTTGGTGTA			
		GT_ TGT			
GAM1381 EDG2	3'	ATGTAATGTATGTATGCAGTAT 7379	GC TG A		
GC		GT ATTGTATG TG ATTACGT			
		CG TGACGTAT AT TAATGTA			
		TA GT G			
GAM1381 EDG2	3'	ATGTAATGTATGTATGCAGTAT 54062	GC TG A		
GC		GT ATTGTATG TG ATTACGT			
		CG TGACGTAT AT TAATGTA			
		TA GT G			
GAM1381 EEF1E1	3'	ATGTAAATTAATATACAGTCAT 15001	C G A		
		GTG ATTGTATGT TGA TTACGT			
		TAC TGACATATA ATT AATGTA			
		_ _ A			
GAM1381 EFA6R	3'	GTGTGTGCGTGTGTGGGCAT 30987	A TG TG AAT		
		GTGC T TA TGTG TAC			
		TACG G GT GCGT GTG			
		_ GT GT GT_			
GAM1381 EFA6R	3'	GTGTGTGTGCGTGCGTGTGTGT 30988	TG _ TG AAT		
		G CAT TGTATG TG TAC			
		T GTG GCGTGC GT GTG			
		GT T GT GT_			
GAM1381 EFA6R	3'	TGTAGATTGCATATCAGTGTAT 30990	T TG A GT		
		GTGCATTG ATGTG A TTAC			
		TATGTGAC TATAC T GATG			
		_ GT A TG			
GAM1381 ENPP4	3'	TCAAACATACAGTGCG 30049	G		
		TGCATTGTATGT TGA			

GCGTGACATACA ACT  
 A  
 GAM1381 EPI64 3' ATGTAAGCTGCGTGCAGGCAC 95631 A TGAA  
 GTGC TTGTATGTG TTACGT  
 ||| ||||| |||||  
 CACG GACGTGCGT AATGTA  
 \_ CG\_  
 GAM1381 ERAP140 3' ATGTACATATACATATATATGA 75205 \_ A \_  
 GTGTAT AT TGTATGTGTG AT TACGT  
 || ||||| || |||||  
 TG ATATATACAT TA ATGTA  
 AGT A C  
 GAM1381 EREG 3' ATGTGAATAGGTTATATGCAAG 7491 A TGAA\_  
 CAC TGC TTGTATGTG TTACGT  
 ||| ||||| |||||  
 ACG AACGTATAT AGTGTA  
 \_ TGGATA  
 GAM1381 EREG 3' TGCATATTCAATGTAT 7514 T  
 GTGCATTG ATGTGTG  
 ||||| |||||  
 TATGTAAC TATACGT  
 T  
 GAM1381 FBP17 3' GTTCGTATGTGTGTTGCAC 72803 T GT  
 GTGCA T ATGTGTGAAT  
 ||||| |||||  
 CACGT G TGTATGCTTG  
 T TG  
 GAM1381 FBXO30 3' CATATATGCAAGCAC 49575 A  
 GTGC TTGTATGTGTG  
 ||| |||||  
 CACG AACGTATATAC  
 \_  
 GAM1381 FEM-2 3' TGTGAGCTGAGCAGGCAGTGCA 27585 A GTGAA GT  
 C GTGCATTGT TGT TTAC  
 ||||| ||| |||||  
 CACGTGACG ACG AGTG  
 G AGTCG TG  
 GAM1381 FLJ00001 3' GTGTGCACGCACATGCGTGTGT 81820 \_ AAT\_ GT  
 AT GTGCAT TGTATGTGTG TAC  
 ||||| ||||| |||  
 TATGTG GCGTACACGC GTG  
 T ACGT  
 GAM1381 FLJ10008 3' ATGTGAATATGTGTATATATGT 35724 \_ TG AA  
 AC GTGCAT TGTATG TG TTACGT  
 ||||| ||||| || |||||  
 CATGTA ATATGT AT AGTGTA  
 T GT A\_  
 GAM1381 FLJ10036 3' TGATAAGCATATGTTATGTGC 94952 TG TG GA  
 G CAT TATGTGT ATTA  
 | ||| ||||| |||||

			C GTA GTATACG TAGT		
			GT TT AA		
GAM1381	FLJ10094	3'	ACAGAGTTGTATATGTAATGTA 35806		TG ATTACGT
		T	GTGCATTGTATGTG A		
			TATGTAATGTATAT T		
			GT GAGACA		
GAM1381	FLJ10097	3'	ACGTAACATATACATATGTGT 68510 G _		AA_
		GTGT	CAT TGTATGTGTG TTACGT		
			GTG GTATACATAT AATGCA		
			T T ATC		
GAM1381	FLJ10097	3'	GTGTGTATATATATAATGTGT 68512 TG		AAT
			G CATTGTATGTGTG TAC		
			T GTAATATATATAT GTG		
			GT GT_		
GAM1381	FLJ10097	3'	GTGTGTGTATATATATAATGTG 68513 TG		AAT GT
		T	G CATTGTATGTGTG TAC		
			T GTAATATATATAT GTG		
			GT GT_ TGT		
GAM1381	FLJ10287	3'	TTTATATATGTAGGCAC 38847 A		
			GTGC TTGTATGTGTGAA		
			CACG GATGTATATATTT		
			-		
GAM1381	FLJ10477	3'	TATATATACATATGTAC 36154 _		
			GTGCAT TGTATGTGTG		
			CATGTA ACATATATAT		
			T		
GAM1381	FLJ10493	3'	ATCTTCATCTACATGTAATGTG 36187 TG		_ TTACGT
		T	G CATTGTATGT GTGAA		
			T GTAATGTACA TACTT		
			GT TC CTA		
GAM1381	FLJ10498	3'	GTGGACACACATATGTGTAT 36195 T		AA
			GTGCAT GTATGTGTG TTAC		
			TATGTG TATACACAC GGTG		
			- A_		
GAM1381	FLJ10539	3'	ACGTATCAAAAGTGTACAATGT 36255 TG		TG GTGAAT
		GT	G CATTGTA T TACGT		
			T GTAACAT G ATGCA		
			GT GT AAAACT		
GAM1381	FLJ10597	3'	GTTCCCATGTACATACATGCA 36319 T		_ AATT GT
		C	GTGCAT GTATGT GTG AC		

CACGTA CATACA TAC TG  
— TG CCCT  
GAM1381 FLJ10620 3' CATATATACATAATGTGC 36356 TG —  
G CAT TGTATGTGTG  
| ||| |||||  
C GTA ACATATATAC  
GT AT  
GAM1381 FLJ10713 3' CACATATTTAATGTAT 36465 T  
GTGCATTG ATGTGTG  
||||| |||||  
TATGTAAT TATACAC  
T  
GAM1381 FLJ10829 3' TGATATACACACATATGTGTAT 36715 T AATTACGT  
GTGCAT GTATGTGTG  
||||| |||||  
TATGTG TATACACAC  
— ATATAGTA  
GAM1381 FLJ10898 3' TTTACACATACGTGTAT 59440 T  
GTGCAT GTATGTGTGAA  
||||| |||||  
TATGTG CATAACACATTT  
—  
GAM1381 FLJ10904 3' ATGTAGTTCTTTGCAGTGT 36847 TGTGT  
GCATTGTA GAATTACGT  
||||| |||||  
TGTGACGT CTTGATGTA  
TT—  
GAM1381 FLJ10922 3' CGTAGCCATGTGCGATTGT 36875 — TGAA  
GCA TTGTATGTG TTACG  
||| ||||| |||||  
TGT AGCGTGTAC GATGC  
T C—  
GAM1381 FLJ10961 3' ATGTATAACATGCAATGATGCA 63485 TG A AAT  
C GTGCAT T TGTGTG TACGT  
||||| | ||||| |||||  
CACGTA A ACGTAC ATGTA  
GT\_ AAT  
GAM1381 FLJ10971 3' GTTTATACACAATGTAT 36927 AT  
GTGCATTGT GTGTGAAT  
||||| |||||  
TATGTAACA CATATTTG  
—  
GAM1381 FLJ11040 3' TATACATGCATATGCAC 37002 —  
GTGCAT TGTATGTGTG  
||||| |||||  
CACGTA ACGTACATAT  
T  
GAM1381 FLJ11042 3' ATGTAATGATGCTACAGTAATG 37005 — T GA  
TAT GCAT TGTA GTGT ATTACGT  
||| ||| ||| |||||



		TGTA ACAT CGTA TAATGTA		
		ATG _ G_		
GAM1381	FLJ11127	3' GTGTGTATATACATATGTAT 38715	_	AAT
		GTGCAT TGTATGTGTG TAC		
		TATGTA ACATATATAT GTG		
		T GT_		
GAM1381	FLJ11218	3' ATGTGGTATAAACATACAATGG 37168	G	G A
	GC	GT CATTGTATGT TG ATTACGT		
		CG GTAACATACA AT TGGTGTA		
		G A A		
GAM1381	FLJ11342	3' ATGACTCATATATATACATGTG 37248	___	A CGT
	TAT	GCAT TGTATGTGTGA TTA		
		TGTG ATATATATACT AGT		
		TAC C A		
GAM1381	FLJ11539	3' GCGTGATTCGCGTGTGGAA 45379	G TG	
		TT TA TGTGAATTACGT		
		AA GT GCGCTTAGTGCG		
		G GT		
GAM1381	FLJ11560	3' GTGAGTGTGCATGTATGCAC 47218	TTG	AA_
		GTGCA TATGTGTG TTAC		
		CACGT ATGTACGT AGTG		
		___ GTG		
GAM1381	FLJ11753	3' ATGTATCCCATATGTGGTGCC 45078	T TG	T AT
		G GCAT TATGTG GA TACGT		
		C CGTG GTATAC CT ATGTA		
		_ GT C _		
GAM1381	FLJ11996	3' TGCACATATAGGTAT 46446	A	
		GTGC TTGTATGTGTG		
		TATG GATATACACGT		
		-		
GAM1381	FLJ12547	5' GTGTGTGCACGTATGTATGTGT 46495	TG _	AAT
		G CAT TGTATGTGTG TAC		
		T GTA GTATGCACGT GTG		
		GT T GT_		
GAM1381	FLJ12547	5' TGTGTGCACGTATGTATGTGTG 46496	_____	AATTACGT
	CAC	CAT TGTATGTGTG		
		GTG GTATGCACGT		
		TGTAT GTG TG		
GAM1381	FLJ12549	3' ATGTGGTATCTTTGTATGGCAA 45810	A TG	_____
	TGTAT	ATTGT TGTG A ATTACGT		

			TAACG GTAT T TGGTGTA		
			_ GT TCTA		
GAM1381	FLJ12649	3'	ATGTACATACACGTATGTATGC 44775	_	AAT
	AC		GTGCAT TGTATGTGTG TACGT		
			CACGTA GTATGCACAT ATGTA		
			T AC_		
GAM1381	FLJ12681	3'	ACGCATCCCACACATGCAGGCA 42870	A	AATTA
	C		GTGC TTGTATGTGTG CGT		
			CACG GACGTACACAC GCA		
			_ CCTAC		
GAM1381	FLJ12750	3'	TTTCCTTTTGTGCAAGCAGTGC 45128	A	TG TTACGT
	AC		GTGCATTGT TGTG AA		
			CACGTGACG ACGT TT		
			A GT TCCTTTA		
GAM1381	FLJ12985	3'	CGTGATTCACACCTGGCAC 46239	ATTGTAT	
			GTGC GTGTGAATTACG		
			CACG CACACTTAGTGC		
			GTC_____		
GAM1381	FLJ12985	3'	GTGATTCACACCTGGCAC 46242	ATTGTAT	
			GTGC GTGTGAATTAC		
			CACG CACACTTAGTG		
			GTC_____		
GAM1381	FLJ12987	3'	ATGTATATATACATATATATGT 47192	_	AAT
	AT		GTGCAT TGTATGTGTG TACGT		
			TATGTA ATATACATAT ATGTA		
			T AT_		
GAM1381	FLJ12987	3'	CACACATATATGTAT 47193	T	
			GTGCAT GTATGTGTG		
			TATGTA TATACACAC		
			_		
GAM1381	FLJ12987	3'	TATATATACAGTCAT 47195	C	
			GTG ATTGTATGTGTG		
			TAC TGACATATATAT		
			_		
GAM1381	FLJ12994	3'	CACACATAGATGCGC 43126	G	
			GTGCATT TATGTGTG		
			CGCGTAG ATACACAC		
			_		
GAM1381	FLJ12994	3'	CACACATAGATGCGC 77476	G	
			GTGCATT TATGTGTG		

## CGCGTAG ATACACAC

—  
 GAM1381 FLJ13110 3' GTAAGTGTACATGTAGTGGTGT 43307 TG\_ AA\_  
 GCAT T ATGTGTG TTAC  
 |||| | ||||| ||||  
 TGTG G TGTACAT AATG  
 GT A GTG  
 GAM1381 FLJ13110 3' GTGTAATGCATGCAGTG 43308 GAAT  
 CATTGTATGTGT TAC  
 ||||| ||||| ||||  
 GTGACGTACGTA GTG  
 AT\_  
 GAM1381 FLJ13187 3' ATGTGGTTCATTAATAATGT 44842 ATGT  
 GCATTGT GTGAATTACGT  
 ||||| ||||| |||||  
 TGTAATA TACTTGGTGTA  
 AT\_  
 GAM1381 FLJ13231 3' TATTTTGATATGTGCATACAAT 43554 TG TG A CGT  
 GTGT G CATTGTATG TG ATTA  
 | ||||| || ||||  
 T GTAACATAC GT TAGT  
 GT GT A TTTATA  
 GAM1381 FLJ13441 3' TGAGACAGGCGTGCAGTGTGC 43673 TG G AA  
 G CATTGTATGT TG TTA  
 | ||||| || ||||  
 C GTGACGTGCG AC AGT  
 GT G AG  
 GAM1381 FLJ13614 3' TGATACATATATACATGTAT 57456 T A  
 GTGCAT GTATGTGTG ATTA  
 ||||| ||||| ||||  
 TATGTA CATATATAC TAGT  
 A  
 GAM1381 FLJ13659 3' CATGCGTAGTGGTGCAT 47245 TG\_  
 GTGCAT T ATGTGTG  
 ||||| | |||||  
 TACGTG G TCGGTAC  
 GT A  
 GAM1381 FLJ13920 3' GTAGTTCTATATGTAT 44655 \_  
 GTATGTGT GAATTAC  
 ||||| |||||  
 TATGTATA CTTGATG  
 T  
 GAM1381 FLJ14084 3' TGCATGTACATGTAT 41299 T  
 GTGCAT GTATGTGTG  
 ||||| |||||  
 TATGTA CATGTACGT  
 —  
 GAM1381 FLJ14213 3' GTTAAGCATATGTGCATGCAT 45797 T AATT  
 GTGCAT GTATGTGTG AC  
 ||||| ||||| || ||

			TACGTA CGTGTATAC	TG		
			— GAAT			
GAM1381	FLJ14281	3'	AATTACTATACATATACATGCA	46212	T	AATTACGT
		T	GTGCAT GTATGTGTG			
			TACGTA CATATACAT			
			— ATCATTAAG			
GAM1381	FLJ14326	3'	CCTAGATTACACACACGTGGTGT	49805	TG TG A	ACGT
		GT	G CAT T TGTGTGAATT			
			T GTG G ACACACTTAG			
			GT GT C ATCCA			
GAM1381	FLJ14566	5'	GTGGAAGCATGTGCGGCTGCG	51448	—	GAA
			TGCA TTGTATGTGT TTAC			
			GCGT GCGGTGTACG GGTG			
			C AA_			
GAM1381	FLJ14803	3'	TACACATGGGTGTAT	51619	G	
			GTGCATT TATGTGTG			
			TATGTGG GTACACAT			
			—			
GAM1381	FLJ20033	3'	GTGTGACATAAACAGATGTAAT	34348	G GAA_	GT
		GCAT	TGCATTGTAT TGT TTAC			
			ACGTAATGTA ACA AGTG			
			G AATAC TG			
GAM1381	FLJ20034	3'	TGCAGGTTTGCATGTATGTGCA	34389	T TG	ACGT
		T	GTGCAT GTATGTG AATT			
			TACGTG TATGTAC TTGG			
			— GT ACGTG			
GAM1381	FLJ20079	3'	TACACATATGTATGTAT	34499	—	
			GTGCAT TGTATGTGTG			
			TATGTA GTATACACAT			
			T			
GAM1381	FLJ20081	3'	GTGTAATTTGTTTTCTTCAGTG	34508	TATGT_ TG	GT
		TAT	GTGCATTG G AATTAC			
			TATGTGAC T TTAATG			
			TTCTTT GT TG			
GAM1381	FLJ20151	5'	GTGTGTTTGTGTGTGTGTGTC	77529	TG_ TG TG _	GT
		AC	GTGCAT TA TG AAT TAC			
			CACGTG GT GT TTG GTG			
			TGT GT GT T			
GAM1381	FLJ20174	3'	ACGTATAAATGTGCACATGCGT	34684	_ AAT_	
		ATGTAT	AT TGTATGTGTG TACGT			

			TA GCGTACACGT	ATGCA		
			T	GTAAAT		
GAM1381	FLJ20281	3'	ACGTAAATACATATATGCAGTG	90978	AA_	
		C	GCATTGTATGTGTG	TTACGT		
			CGTGACGTATATAC	AATGCA		
			ATA			
GAM1381	FLJ20296	3'	G TTCCTTGCACGTATAAAGCAC	34893	A	TG ATT
			GTGC TTGTATGTG	A AC		
			CACG AATATGCAC	T TG		
			A	GT CCT		
GAM1381	FLJ20337	3'	ATGATTTTATATTTATAATGTG	34962	TG	T TTACGT
		C	G CATTGTA	GTGTGAA		
			C	GTAATAT TATATTT		
			GT	T TAGTA		
GAM1381	FLJ20456	3'	GTTTATTGTTATAGTGCAT	35216	TGT	
			GTGCATTGTA	GTGAAT		
			TACGTGATAT	TATTTG		
			TGT			
GAM1381	FLJ20485	3'	ATGGAGTATACAACAATGCAT	38764	A	AATTA
			GTGCATTGT TGTGTG	CGT		
			TACGTAACA ACATAT	GTA		
			_	GAG__		
GAM1381	FLJ20487	3'	CATACATGTAAATGCAC	35246	GT_	
			GTGCATT	ATGTGTG		
			CACGTAA	TACATAC		
			ATG			
GAM1381	FLJ20502	3'	TCATTATGCAGTGTGT	35262	TG	T
			G CATTGTATG	GTGA		
			T	GTGACGTAT TACT		
			GT	_		
GAM1381	FLJ20533	3'	ATGTGATTTACGTTTTAATGTA	35357	TATG	
		T	GTGCATTG	TGTGAATTACGT		
			TATGTAAT	GCATTTAGTGTA		
			TTT_			
GAM1381	FLJ20666	3'	ATGTAAATTTCAAATGCAGTGT	35509	TG	G T A
		GT	G CATTGTAT	TG GA TTACGT		
			T	GTGACGTA AC TT AATGTA		
			GT	A T A		
GAM1381	FLJ20666	3'	ATGTAAATTTCAAATGCAGTGT	37088	TG	G T A
		GT	G CATTGTAT	TG GA TTACGT		

T GTGACGTA AC TT AATGTA  
 GT A T A  
 GAM1381 FLJ20701 3' GCGTTTGTGTGCGTGTACGTGT 35589 TG T TG AATT\_  
 GC G CAT GTA TGTG ACGT  
 I III III III  
 C GTG CAT GCGT TGCG  
 GT \_ GT GTGTT  
 GAM1381 FLJ21159 3' ATGTATATTTACATGAAATGCA 45716 GTAT \_  
 C GTGCATT GTGTGAAT TACGT  
 IIIII IIIII IIIII  
 CACGTAA TACATTTA ATGTA  
 AG\_ T  
 GAM1381 FLJ21276 3' ATGTGAGCATAGCATGTGTGAG 44916 A TG GAA\_  
 TAC TGC T TATGTGT TTACGT  
 III IIIII IIIII  
 ATG A GTGTACG AGTGTA  
 \_GT ATACG  
 GAM1381 FLJ21276 3' CACGCGTATGTGAGCAT 44917 AT\_  
 GTGC TGTATGTGTG  
 III IIIIIII  
 TACG GTATGCGCAC  
 AGT  
 GAM1381 FLJ21276 3' TGCGTTCACACTTGTGTGTGTA 44920 TGTAT\_ TACGT  
 T TGCAT GTGTGAAT  
 III IIIIIII  
 ATGTG CACACTTG  
 TGTGTT CG TG  
 GAM1381 FLJ21459 3' TGCACAATAAATGCAATGCAC 44521 \_\_\_\_\_  
 GTGCATTGTA TGTGTG  
 IIIIIII IIIII  
 CACGTAACGT ACACGT  
 AAATA  
 GAM1381 FLJ21477 3' TTACATGTGCATGTGT 47149 TG T  
 G CAT GTATGTGTGA  
 I III IIIIIII  
 T GTA CGTGTACATT  
 GT \_  
 GAM1381 FLJ22127 3' GTGCCGTGTGCTTGTGGTGCGC 42887 TG T TG AAT  
 GTGCAT TA G TG TAC  
 IIIII II I II III  
 CGCGTG GT C GT GTG  
 GT T GT GCC  
 GAM1381 FLJ22174 3' AATTTGTATGTAAATGTAC 41672 G TG  
 GTGCATT TATGTG AATT  
 IIIII IIIII IIIII  
 CATGTAA ATGTAT TTAA  
 \_ GT  
 GAM1381 FLJ22378 3' TGCACATGCAGTCTGC 46910 C  
 GTG ATTGTATGTGTG  
 III IIIIIIIII

		CGT TGACGTACACGT		
		C		
GAM1381	FLJ22390	5' ACGCCCACCACAAATGCAGTGC 42736	G	AATTA
		AC GTGCATTGTAT TGTG CGT		
		CACGTGACGTA ACAC GCA		
		A CACCC		
GAM1381	FLJ22479	3' TGTAGAAAATGCTTGTGGTGTA 46079	TG T	GAA GT
		C GTGCAT TA GTGT TTAC		
		CATGTG GT CGTA GATG		
		GT T AAA TG		
GAM1381	FLJ22479	3' TGTATGTACACATGCA 46080	AAT	T
		TGTATGTGTG TACG		
		ACGTACACAT ATGT		
		GT_ C		
GAM1381	FLJ23071	3' GCCCCACGCGCATGCTAATGCG 47264	_	AATTACGT
		TGCATT GTATGTGTG		
		GCGTAA CGTACGCGC		
		T ACCCCG		
GAM1381	FLJ23120	3' TAATATATACTACAATGTGC 85149	TG	T A
		G CATTGTA GTGTG ATTA		
		C GTAACAT CATAT TAAT		
		GT _ A		
GAM1381	FLJ23151	3' GTGGTATTGTACGGTGTAT 45478	TGTGA	
		GTGCATTGTATG ATTAC		
		TATGTGGCATGT TGGTG		
		TA__		
GAM1381	FLJ23259	3' TACATATATAATACAC 45309	C	
		GTG ATTGTATGTGTG		
		CAC TAATATATACAT		
		A		
GAM1381	FLJ23560	3' ATTTATGCTATATGATGCAT 45191	TG	_
		GTGCAT TAT GTGTGAAT		
		TACGTA ATA CGTATTTA		
		GT T		
GAM1381	FLJ23563	3' ATTTACCTATGCAGTGCAT 67588	T	
		GTGCATTGTATG GTGAAT		
		TACGTGACGTAT CATTTA		
		C		
GAM1381	FLJ23590	3' ATGTAAGTTTATATAATGTA 45017	TGTGAA	
		TGCATTGTATG TTACGT		

ATGTAATATAT AATGTA  
 TTG\_\_\_\_  
 GAM1381 FLJ23590 5' TCATGCAGCAGTGTGC 45022 TG A  
 G CATTGT TGTGTGA  
 | ||||| |||||  
 C GTGACG ACGTACT  
 GT \_  
 GAM1381 FLJ25193 3' GTGTGATTGATATATACAGTG 58701 G GT  
 CATTGTATGTGT AATTAC  
 ||||| |||||  
 GTGACATATATA TTAGTG  
 G TG  
 GAM1381 FLJ30567 3' ATTTGCATGTGTAATGGAC 58825 G TG  
 GT CATTGTATGTG AAT  
 || ||||| |||  
 CA GTAATGTGTAC TTA  
 G GT  
 GAM1381 FLJ30663 3' ACTTAACACATGTGCACATGTA 78654 \_ AATTACGT  
 C GTGCAT TGTATGTGTG  
 ||||| |||||  
 CATGTA ACGTGTACAC  
 C AATTCA  
 GAM1381 FLJ30663 3' ATGTACATTTATATGCAGTG 78655 TGAAT  
 CATTGTATGTG TACGT  
 ||||| |||||  
 GTGACGTATAT ATGTA  
 TTAC\_  
 GAM1381 FLJ31121 3' TGTGCATGCATGTGTAT 58539 \_ TG  
 GTGCAT TGTATG TG  
 ||||| ||||| ||  
 TATGTG ACGTAC GT  
 T GT  
 GAM1381 FLJ31952 3' GTGTATCAGATGTACGGTG 58387 G AT  
 CATTGTATGT TGA TAC  
 ||||| ||| |||  
 GTGGCATGTA ACT GTG  
 G AT  
 GAM1381 GAB3 3' TCACCTATACAGTGTGT 54634 TG T  
 G CATTGTATG GTGA  
 | ||||| |||||  
 T GTGACATAT CACT  
 GT C  
 GAM1381 GBTS1 3' GTGTGCACACGTGCGTGTGTGT 59060 TG \_ AAT  
 G CAT TGTATGTGTG TAC  
 | ||| ||||| |||  
 T GTG GCGTGCACAC GTG  
 GT T GT\_  
 GAM1381 GENX-3414 3' GTGTATGTGTGTATATATATGC 14149 \_ TG AAT\_ GT  
 AC GTGCAT TGTATG TG TAC  
 ||||| ||||| || |||



			CACGTA ATATAT GT GTG		
			T GT GTAT		
GAM1381	GPR88	3'	ATGTAGTTCATATATATTACCA 41876	CATT	
	C		GTG GTATGTGTGAATTACGT		
			CAC TATATATACTTGATGTA		
			CAT_		
GAM1381	GREAT	3'	ATGTGAATTCGTGTATAGTGGG 55481	G TG T A	
	C		GT CATTGTA TG GA TTACGT		
			CG GTGATAT GC TT AGTGTA		
			G GT _ A		
GAM1381	GS3955	3'	TCACATTGTGATGTAT 41320	TG T	
			GTGCAT TA GTGTGA		
			TATGTA GT TACACT		
			GT _		
GAM1381	GT650	3'	ATGTATAGCATATGTACATATG 53451	TG _ AAT	
	TGT		G CAT TGTATGTGTG TACGT		
			T GTA ACATGTATAC ATGTA		
			GT T GAT		
GAM1381	GTPBP1	3'	GTGTGTGTGTGTGTGGTGCA 15015	TG TG AAT	
			TGCAT TATG TG TAC		
			ACGTG GTGT GT GTG		
			GT GT GT_		
GAM1381	GTPBP2	3'	CACATATATATTGTAC 38868	T	
			GTGCA TGTATGTGTG		
			CATGT ATATATACAC		
			T		
GAM1381	GTPBP2	3'	TATATATACATATGTAT 38871	_	
			GTGCAT TGTATGTGTG		
			TATGTA ACATATATAT		
			T		
GAM1381	HCA127	3'	ATGTGGTTCAGGTGCTAAACAG 37949	AT_ _	
	TGTGT		CATTGT GTG TGAATTACGT		
			GTGACA CGT ACTTGGTGTA		
			AAT GG		
GAM1381	HCA4	3'	TACATATATAAGTAT 77593	A	
			GTGC TTGTATGTGTG		
			TATG AATATATACAT		
			_		
GAM1381	HELO1	3'	GTAGATCATGCATGTGATTGT 41497	_TG A	
			GCA T TATGTGTGA TTAC		

			TGT A GTACGTACT GATG		
			T GT A		
GAM1381	HERPUD1	3'	ATGTAGTTTAAATAAGCACTGTA 28017	T A G	
	C		GTGCA TGT TGT TGAATTACGT		
			CATGT ACG ATA ATTTGATGTA		
			C A _		
GAM1381	HEY2	3'	TTACATTTATATAGTGCAC 24321	__	
			GTGCATTGTAT GTGTGA		
			CACGTGATATA TACATT		
			TT		
GAM1381	HEYL	3'	GTGGCCCCATGTGATGGTGCGC 27399	TG _ TGAA	
			GTGCAT T ATGTG TTAC		
			CGCGTG A TGTAC GGTG		
			GT G CCC_		
GAM1381	HHGP	3'	ATGTCATGTATGCATGGATGTA 39509	__ TG ATTACGT	
	C		TGCAT TGTATG TGA		
			ATGTA ACGTAT ACT		
			GGT GT GTA T		
GAM1381	HIC2	3'	GTGTGTCTATGTGTGGTGTGT 65269	TG TG T AT	
			G CAT TATGTG GA TAC		
			T GTG GTGTAT CT GTG		
			GT GT _ GT		
GAM1381	HIF1AN	3'	GTGTGCATGCACACGCATGTAT 61978	_ A AAT GT	
			GTGCAT TGT TGTGTG TAC		
			TATGTA GCA ACGTAC GTG		
			C C GT_		
GAM1381	HIF1AN	3'	GTGTGCGTGTGTGTGCATGCAC 61979	T TG AAT_	
			GTGCAT GTATG TG TAC		
			CACGTA CGTGT GT GTG		
			_ GT GCGT		
GAM1381	HIF1AN	3'	GTGTGTGTGCGTGCGTGTGTGT 61980	TG _ TG AAT	
			G CAT TGTATG TG TAC		
			T GTG GCGTGC GT GTG		
			GT T GT GT_		
GAM1381	HIRIP3	3'	CCCTTGATACATGTACAAAGCA 13214	A AATTACGT	
	T		GTGC TTGTATGTGTG		
			TACG AACATGTACAT		
			A AGTTCCCA		
GAM1381	HNK-1ST	3'	TGTAGTTTATACATTTTCGAT 16773	T_ GT	
			ATTG ATGTGTGAATTAC		

			TAGC TACATATTGATG		
			TT TG		
GAM1381	HNRPA3	3'	GTGTGTATATATATATATGTAT 19258	_	AAT
			GTGCAT TGTATGTGTG TAC		
			TATGTA ATATATATAT GTG		
			T GT_		
GAM1381	HRMT1L3	3'	GCGGTGGTGTGCGTGTGCGTGC 39074	T TG A GT	
	AT		GTGCAT GTA TGTG ATTAC		
			TACGTG CGT GCGT TGGTG		
			_ GT G GCGT		
GAM1381	HRMT1L3	3'	GTGTGTGTGCGTGCGCGTGTGC 39077	TG _ TG AAT	
			G CAT TGTATG TG TAC		
			C GTG GCGTGC GT GTG		
			GT C GT GT_		
GAM1381	HRMT1L3	3'	GTGTGTGTGTGTGTGTGCGTGCGC 39078	T TG AAT_	
			GTGCAT GTATG TG TAC		
			CGCGTG CGTGT GT GTG		
			_ GT GTGT		
GAM1381	HSF2	3'	CGCAGATGTAATGCAC 15708	G	
			GTGCATTGTAT TGTG		
			CACGTAATGTA ACGC		
			G		
GAM1381	HSPC154	5'	ACGTGTCCGCCGCGCATGTGTAG 26350	AAT__	
	TG		CATTGTATGTGTG TACGT		
			GTGATGTGTACGC GTGCA		
			CGGCCT		
GAM1381	HSPC163	3'	TAACTACAGTGCAC 26365	T	
			GTGCATTGTA GTGTG		
			CACGTGACAT CACAT		
			-		
GAM1381	HTGN29	3'	ATGTTAAATACATGTACAATTG 39505	_	AATT
	C		GCA TTGTATGTGTG ACGT		
			CGT AACATGTACAT TGTA		
			T AAAT		
GAM1381	IDI1	5'	GTGTCGTCAAGCGCGTACGGGC 67046	A __ AT_ GT	
	GC		TGC TTGTATGTGT GA TAC		
			GCG GGCATGCGCG CT GTG		
			- AA GCT		
GAM1381	IL-23R	3'	TCACACATACAGGCAC 58457	A	
			GTGC TTGTATGTGTGA		

CACG GACATACACACT

GAM1381 IMPACT 3' GTGTAGTTACATCAATTTGATG 37394 TA\_ \_ AT\_ GT  
CAT GCATTG TG TGTGA TAC

||||| || ||||| |||  
CGTAGT AC ACATT GTG  
TTA T GAT

GAM1381 JDD1 3' TTTATGCATACGGTATAT 63222 C  
GTG ATTGTATGTGTGAA  
||| |||||  
TAT TGGCATACGTATTT  
A

GAM1381 KCNT1 3' GTGGCAGCGCATGTATGGGCGC 61839 A TG AA\_  
GTGC T TATGTGTG TTAC  
||||| ||||| |||||  
CGCG G ATGTACGC GGTG  
\_GT GAC

GAM1381 KIAA0089 3' TGTAATTCATATGTATTTG 69966 TT GT  
CA GTATGTGTGAATTAC  
|| |||||  
GT TATGTATACTTAATG  
T\_ TG

GAM1381 KIAA0090 3' TTACGTATATGAGCAC 88451 A TG  
GTGC T TATGTGTGA  
||||| |||||  
CACG A ATATGCATT  
\_GT

GAM1381 KIAA0101 3' ATGTAAATTTACATAAATGTGT 28423 TG GTA \_  
G CATT TGTGTGAATT ACGT  
| ||||| ||||| |||||  
T GTAA ATACATTTAA TGTA  
GT \_ A

GAM1381 KIAA0103 3' TCACATATACATGTAT 27929 T  
GTGCAT GTATGTGTGA  
||||| |||||  
TATGTA CATATACACT

GAM1381 KIAA0141 3' ATTTAGTTATATATTTAATGTA 28728 T ATTACGT  
T GTGCATTG ATGTGTGA  
||||| |||||  
TATGTAAT TATATATT  
T GATTTA

GAM1381 KIAA0155 3' TCACAAATGTATAATGTGT 27568 TG \_  
G CATTGTATG TGTGA  
| ||||| |||||  
T GTAATATGT ACACT  
GT AA

GAM1381 KIAA0173 3' ATGTGGTTTCTCTATAGTGCA 27667 TGTGT  
TGCATTGTA GAATTACGT  
||||| |||||

ACGTGATAT TTTGGTGTA  
 CTC\_\_  
 GAM1381 KIAA0189 3' CACACATATATATGTGT 28270 TG \_  
 G CAT TGTATGTGTG  
 I III IIIIIIIII  
 T GTA ATATACACAC  
 GT T  
 GAM1381 KIAA0189 3' CACACATATATATGTGT 28271 TG \_  
 G CAT TGTATGTGTG  
 I III IIIIIIIII  
 T GTA ATATACACAC  
 GT T  
 GAM1381 KIAA0189 3' CACATATATATGTGTGTAT 28272 \_\_\_\_  
 GTGCAT TGTATGTGTG  
 IIIII IIIIIIIII  
 TATGTG ATATACAC  
 TGT  
 GAM1381 KIAA0193 3' CATGCCTGTAGTGCAC 28651 T  
 GTGCATTGTA GTGTG  
 IIIIIII IIIII  
 CACGTGATGT CGTAC  
 C  
 GAM1381 KIAA0212 3' CACACATGCATGCAT 27932 T  
 GTGCAT GTATGTGTG  
 IIIII IIIIIIIII  
 TACGTA CGTACACAC  
 \_  
 GAM1381 KIAA0212 3' CATGCATGCATGCAC 27934 T  
 GTGCAT GTATGTGTG  
 IIIII IIIIIIIII  
 CACGTA CGTACGTAC  
 \_  
 GAM1381 KIAA0232 3' ATGTACAGTATATATGAATGCA 72745 G AAT  
 T GTGCATT TATGTGTG TACGT  
 IIIII IIIIIII IIIII  
 TACGTAA GTATATAT ATGTA  
 \_ GAC  
 GAM1381 KIAA0232 3' GTAAACACACATATAATTTAT 72756 C AA  
 GTG ATTGTATGTGTG TTAC  
 III IIIIIIIII IIIII  
 TAT TAATATACACAC AATG  
 T A\_  
 GAM1381 KIAA0237 3' GCGTGTGTGCGTGTGTGTGT 28526 TG \_ TG AAT  
 G CAT TGTATG TG TACGT  
 I III IIIII II IIIII  
 T GTG GCGTGC GT GTGCG  
 GT T GT \_\_\_\_  
 GAM1381 KIAA0237 3' GTGTGTGCGTGTGTGCGTGTGCG 28537 T TG AAT\_  
 TGCAT GTATG TG TAC  
 IIIII IIIII II IIIII

GCGTG CGTGT GC GTG  
 \_ GT GTGT  
 GAM1381 KIAA0240 3' CACACGTGCATGTAT 92433 T  
 GTGCAT GTATGTGTG  
 ||||| |||||  
 TATGTA CGTGCACAC  
 -  
 GAM1381 KIAA0240 3' TCAACATATAATGTAT 92440 G  
 GTGCATTGTATGT TGA  
 ||||| ||||| ||  
 TATGTAATATACA ACT  
 -  
 GAM1381 KIAA0247 3' GTTCTATGTATATAACTGCAT 28410 \_ TG\_  
 GTGCA TTGTATG T GAAT  
 ||||| ||||| | ||||  
 TACGT AATATAT A CTTG  
 C GT T  
 GAM1381 KIAA0252 3' TGGTCAGCATATATATTGTGC 62800 TG T GA  
 G CA TGTATGTGT ATTA  
 | || ||||| ||||  
 C GT ATATATACG TGGT  
 GT T AC  
 GAM1381 KIAA0275 3' CGTGGTGAGTGCAGCGTGT 28675 T A TG GA  
 GCAT GT TG T ATTACG  
 ||||| || || |||||  
 TGTG CG AC G TGGTGC  
 \_ \_ GT AG  
 GAM1381 KIAA0275 3' GTGCAGCGTGTGTGCGTGTGC 28686 TG T TG AAT  
 G CAT GTATG TG TAC  
 | ||| ||||| || ||||  
 C GTG CGTGT GC GTG  
 GT \_ GT GAC  
 GAM1381 KIAA0275 3' TGTGAGTGCATGTGTGCATGCA 28688 T TG AA\_ GT  
 T  
 GTGCAT GTATG TG TTAC  
 ||||| ||||| || ||||  
 TACGTA CGTGT AC AGTG  
 \_ GT GTG TG  
 GAM1381 KIAA0276 3' GTATGTATATACAGTGTGT 70967 TG TGAAT  
 G CATTGTATGTG TAC  
 | ||||| ||||| ||||  
 T GTGACATATAT ATG  
 GT GT\_  
 GAM1381 KIAA0276 3' TGTATGTATATACAGTGTGT 70970 TG TGAAT T  
 G CATTGTATGTG TACG  
 | ||||| ||||| ||||  
 T GTGACATATAT ATGT  
 GT GT\_ T  
 GAM1381 KIAA0295 3' TACATGTACATGTAT 68108 T  
 GTGCAT GTATGTGTG  
 ||||| ||||| ||||

TATGTA CATGTACAT

GAM1381 KIAA0318 3' GTATACTTTGTATGTGTCGTGC 68958 TG TG TTACGT  
AT GTGCAT TATGTG AA  
||||| ||||| ||  
TACGTG GTGTAT TT  
CT GT CATATGT

GAM1381 KIAA0318 3' GTGTGGGTGTGTGCATGTGCAC 68959 \_ TG GAAT  
GTGCAT TGTATG T TAC  
||||| ||||| | |||  
CACGTG ACGTGT G GTG  
T GT GGT\_

GAM1381 KIAA0319 3' ATGTACATAACATATGCAGTTT 29030 C GAAT  
AC GTG ATTGTATGTGT TACGT  
||| ||||| |||||  
CAT TGACGTATACA ATGTA  
T ATAC

GAM1381 KIAA0322 3' ATGCAATGCAATGCAT 92749 \_  
GTGCATTGTAT GTGT  
||||||| |||||  
TACGTAACGTA CGTA  
A

GAM1381 KIAA0323 3' ACGTGGTTTGCCTCAAGGGCAT 63253 A\_ TATGT TG  
GTGC TTG G AATTACGT  
||| ||| | |||||  
TACG AAC C TTGGTGCA  
GG TT\_\_GT

GAM1381 KIAA0332 3' GTTTGTGTGTATGCATGTGT 62703 TG T TG T\_  
G CAT GTATG TGAAT AC  
| ||| ||||| ||||| ||  
T GTA CGTAT GTTTG TG  
GT \_ GT TT

GAM1381 KIAA0365 3' ATTTACATGTGCAGGTGT 78664 \_  
GCAT TGTATGTGTGAAT  
||||| ||||| |||||  
TGTG ACGTGTACATTTA  
G

GAM1381 KIAA0417 3' GCGTGGTCCACTGTGTGTGATG 71244 TG TG\_ A  
T GCAT TA T GTG ATTACGT  
||||| ||| ||| |||||  
TGTA GT G CAC TGGTGCG  
GT GT T C

GAM1381 KIAA0420 3' GCGTCAAGGTGTGTGTGCACAT 63359 TG \_ TG AA \_  
GTGT CAT TGTATG TG TT ACGT  
||| ||||| || |||||  
GTA ACGTGT GT AA TGCG  
GT C GT GG C

GAM1381 KIAA0420 3' GTGTGTGCACATGTGTGCAT 63363 TGT AAT  
GTGCAT ATGTGTG TAC  
||||| ||||| |||

TACGTG TACACGT GTG  
 TG\_ GT\_  
 GAM1381 KIAA0444 3' TCCACATGCGTGTGTGTGC 62348 TG \_\_\_\_ T  
 G CAT TGTATGTG GA  
 | ||| ||||| ||  
 C GTG GCGTACAC CT  
 GT TTGT \_  
 GAM1381 KIAA0453 3' ACATGTATATATGTAC 69041 \_  
 GTGCAT TGTATGTGT  
 ||||| |||||  
 CATGTA ATATGTACA  
 T  
 GAM1381 KIAA0470 3' ATGTGATTTATATAACTTTGT 29054 TT A  
 GCA GT TGTGTGAATTACGT  
 ||| || ||||| |||||  
 TGT CA ATATATTTAGTGTA  
 TT \_  
 GAM1381 KIAA0513 3' ACGTGGTGTCTGATGCAT 28325 GT TGTGA  
 GTGCATT ATG ATTACGT  
 ||||| ||| |||||  
 TACGTAG TAC TGGTGCA  
 TC TG\_\_\_\_  
 GAM1381 KIAA0514 3' CACATGTGTGCAATGGAT 28078 G \_  
 GT CATTGTAT GTGTG  
 || ||||| |||||  
 TA GTAACGTG TACAC  
 G TG  
 GAM1381 KIAA0514 3' TGTAGTTCCCAGAGTGAC 28099 GTATG T  
 GTGCATT TG GAATTACG  
 ||||| || |||||  
 CACGTGA AC CTTGATGT  
 G\_\_\_\_ C  
 GAM1381 KIAA0544 3' ATGTTCCCATGCATGTGTGTGC 70887 TG\_ AATT  
 AC GTGCAT TATGTGTG ACGT  
 ||||| ||||| |||  
 CACGTG GTACGTAC TGTA  
 TGT CCT\_  
 GAM1381 KIAA0586 5' GCGGTCTTGTGCGGCAATGTGC 28545 TG A TG ATTA  
 G CATTGT TGTG A CGT  
 | ||||| ||| | |||  
 C GTAACG GCGT T GCG  
 GT \_ GT CTG\_  
 GAM1381 KIAA0596 3' CACGCATGCACGTGCAC 62826 \_  
 GTGCAT TGTATGTGTG  
 ||||| |||||  
 CACGTG ACGTACGCAC  
 C  
 GAM1381 KIAA0630 3' ATGTAGAGCAATTGCAATGCAT 89389 TGTG AA  
 GTGCATTGTA TG TTACGT  
 ||||| || |||||



		TACGTAACGT AC GATGTA	
		TA__ GA	
GAM1381 KIAA0649	3'	GCGTAGCCGTGCGTGTGTGTGA 29050	TG TG AA__
		TG CAT TATG TG TTACGT	
		GTA GTGT GC GATGCG	
		GT GT GTGCC	
GAM1381 KIAA0652	3'	ATGTGATGGCCACATGTAGTG 28457	TGA
		CATTGTATGTG ATTACGT	
		GTGATGTACAC TAGTGTA	
		CGG	
GAM1381 KIAA0660	3'	TTTGTACAGTATAGTGTAT 24519	_ TG
		GTGCATTGTA TGTG AA	
		TATGTGATAT ACAT TT	
		G GT	
GAM1381 KIAA0677	3'	CGTGCGTGCGTGCGTGCG 27826	T TG AAT
		TGCAT GTATG TG TACG	
		GCGTG CGTGC GC GTGC	
		_ GT _	
GAM1381 KIAA0677	3'	CGTGCGTGCGTGCGTGAT 27827	T TG AAT
		GTGCAT GTATG TG TACG	
		TATGTG CGTGC GC GTGC	
		_ GT _	
GAM1381 KIAA0677	3'	GTGTGCGTGCGTGCGTGCG 27831	T TG AAT
		TGCAT GTATG TG TAC	
		GCGTG CGTGC GC GTG	
		_ GT GT_	
GAM1381 KIAA0677	3'	GTGTGTGTGCGTGCGTGCG 27832	T TG AAT
		TGCAT GTATG TG TAC	
		GCGTG CGTGC GT GTG	
		_ GT GT_	
GAM1381 KIAA0705	3'	ACGTGGAGTCCCACGTGTCCGG 24531	_ T A_
		TGTGC CATTG TATGTG GA TTACGT	
		GTGGC GTGCAC CT GGTGCA	
		CT C GA	
GAM1381 KIAA0721	3'	GCGTATGATACTATAGATATAG 41342	G AAT__
		TGTAC CATTGTAT TGTG TACGT	
		GTGATATA ATAT ATGCG	
		G CATAGT	
GAM1381 KIAA0721	3'	GCGTATGATACTATAGATATAG 95970	G AAT__
		TGTAC CATTGTAT TGTG TACGT	

			GTGATATA ATAT	ATGCG		
			G	CATAGT		
GAM1381	KIAA0748	5'	ATTTTATATACGGTGTAT	28935	T	
			GTGCATTGTATGTG	GAAT		
			TATGTGGCATATAT	TTTA		
			T			
GAM1381	KIAA0757	3'	GTAGATCACATGTAGATGTAC	20135	G	A
			GTGCATT	TATGTGTGA	TTAC	
			CATGTAG	ATGTACACT	GATG	
			—	A		
GAM1381	KIAA0759	3'	ATGTGAGATATGCATATCATGT	67320	T	AA
	AT		GTGCAT	GTATGTGTG	TTACGT	
			TATGTA	TATACGTAT	AGTGTA	
			C	AG		
GAM1381	KIAA0798	3'	ATGTAGTTTACAAAAATGC	27717	GTATG	
			GCATT	TGTGAATTACGT		
			CGTAA	ACATTTGATGTA		
			AA			
GAM1381	KIAA0820	3'	TGTGATTGTATGTGCACTGTGT	69030	TG T	TG A GT
			G CA	TGTATGTG	A TTAC	
			T GT	ACGTGTAT	T AGTG	
			GT C	GT_	TG	
GAM1381	KIAA0825	3'	TTGCATGTGCAGTTCAC	61035	C	TG
			GTG	ATTGTATGTG	A	
			CAC	TGACGTGTAC	T	
			T	GT		
GAM1381	KIAA0844	3'	GTAATGTGTGTGCAATG	30204	TG GA	
			CATTGTATG	T ATTAC		
			GTAACGTGT	G TAATG		
			GT			
GAM1381	KIAA0853	3'	ATGTACAAAATACATATAATTG	30536	—	GAAT
	T		GCA	TTGTATGTGT	TACGT	
			TGT	AATATACATA	ATGTA	
			T	AAAC		
GAM1381	KIAA0870	3'	GTGTGCACACTGCGTATGTGTA	81470	—	T AAT GT
	C		TGCAT	TGTA GTGTG	TAC	
			ATGTG	GCGT CACAC	GTG	
			TAT	—	GT_	
GAM1381	KIAA0872	3'	GTATGTGTATTTATATGTATGT	30069	—	—
	ATGTAT		GCA	TGTATGTGTGAAT	TACGT	

			TGTA GTATGTATATTTA GTGTA		
			T T TGT		
GAM1381	KIAA0872	3'	GTGTATATATATATATATATGT 30070	_	A _ GT
	AT		GTGCAT TGTATGTGTG AT TAC		
			TATGTA ATATATATAT TA GTG		
			T A T		
GAM1381	KIAA0872	3'	GTGTATATATATATATATGTGT 30071	_	A _ GT
	AT		GTGCAT TGTATGTGTG AT TAC		
			TATGTG ATATATATAT TA GTG		
			T A T		
GAM1381	KIAA0872	3'	GTGTATTTATATGTATGTATGT 30072	_	_ GT
	AT		GCAT TGTATGTGTGAAT TAC		
			TGTA GTATGTATATTTA GTG		
			T T T		
GAM1381	KIAA0872	3'	TACATATACATATGTGT 30073	TG _	
			G CAT TGTATGTGTG		
			T GTA ACATATACAT		
			GT T		
GAM1381	KIAA0892	3'	ACGGGTGTGCATGTGGATGCAC 71007	G	AATTA
			GTGCATT TATGTGTG CGT		
			CACGTAG GTGTACGT GCA		
			_ GTGG_		
GAM1381	KIAA0924	3'	ATGTGATTCTTAAAGATGCAT 29714	GTATG T	
			GTGCATT TG GAATTACGT		
			TACGTAG AT CTTAGTGTA		
			AA__ T		
GAM1381	KIAA0931	3'	ATGTAATTTACTTCCGAGTAC 67413	A	TATGT
			GTGC TTG GTGAATTACGT		
			CATG AGC CATTTAATGTA		
			_ CTT_		
GAM1381	KIAA0931	3'	CAGATAATTTATGTATGTAATG 67415	TG	CGT
	TA		TGCATTGTATG TGAATTA		
			ATGTAATGTAT ATTTAAT		
			GT AGACA		
GAM1381	KIAA0937	3'	ACGTATATATATATATATATAT 91583	_	AAT__
	ATGCAT		AT TGTATGTGTG TACGT		
			TA ATATATATAT ATGCA		
			T ATATAT		
GAM1381	KIAA0964	3'	TATGTGTACATATGCAC 29768	_	TG
			GTGCAT TGTATG TG		

CACGTA ACATGT AT  
T GT  
GAM1381 KIAA0976 5' CATACATACATATGTGTAT 29889 \_\_\_\_  
GTGCAT TGTATGTGTG  
||||| |||||  
TATGTG ACATACATAC  
TAT  
GAM1381 KIAA0981 3' GTAACACAGGTGCAGTGTAT 61423 G AA  
GTGCATTGTAT TGTG TTAC  
||||||| ||| |||  
TATGTGACGTG ACAC AATG  
G \_\_\_\_  
GAM1381 KIAA0984 3' CATGCATGCATTGTAC 65527 T  
GTGCA TGTATGTGTG  
||||| |||||  
CATGT ACGTACGTAC  
T  
GAM1381 KIAA0984 3' TGTACCAATAACATGCATGCAT 65532 T GTGAAT GT  
GTGCAT GTATGT TAC  
||||| ||||| |||  
TACGTA CGTACA ATG  
\_ ATAACC TG  
GAM1381 KIAA0993 3' TCACACATACAAGTAC 64147 A  
GTGC TTGTATGTGTGA  
||| |||||  
CATG AACATACACACT  
\_  
GAM1381 KIAA0993 3' TGCACATATATGCAC 64148 T  
GTGCAT GTATGTGTG  
||||| |||||  
CACGTA TATACACGT  
\_  
GAM1381 KIAA0997 3' TTGATATATATATGTGCAC 30194 \_ G  
GTGCAT TGTATGTGT AA  
||||| ||||| |||  
CACGTG ATATATATA TT  
T G  
GAM1381 KIAA1001 3' ATGTATTTATATGTATATGTAT 30288 T T  
GTGCAT GTATGTGTGAAT ACGT  
||||| ||||| ||||| |||  
TATGTA TATGTATATTTA TGTA  
\_ \_ T  
GAM1381 KIAA1026 3' GCGTG GGGTGC GTGTGCACGTG 71197 TG \_ TG AA  
TGC G CAT TGTA TGTG TTACGT  
| ||| ||| |||||  
C GTG ACGT GCGT GGTGCG  
GT C GT GG  
GAM1381 KIAA1026 3' GCGTGTCTGTGCGTGTGGGCG 71198 A TG TG GA T  
TGC T TATG T AT ACGT  
||| | ||| | |||

GCG G GTGC G TG TGCG  
 \_GT GT TC \_  
 GAM1381 KIAA1026 3' GTGTGGCCGTGCGTGGGGTGCG 71204 G TG AAT\_ GT  
 TGCATT TATG TG TAC  
 ||||| ||| || |||  
 GCGTGG GTGC GC GTG  
 G GT CGGT  
 GAM1381 KIAA1052 5' ATTTATGCATATATGCAC 30248 T  
 GTGCAT GTATGTGTGAAT  
 ||||| |||||  
 CACGTA TATACGTATTTA  
 -  
 GAM1381 KIAA1077 3' TGTGAGCAAGCGGTGTGC 72911 TG A GTGAA  
 G CATTGT TGT TTACG  
 | ||||| ||| |||||  
 C GTGGCG ACG AGTGT  
 GT A \_\_\_\_\_  
 GAM1381 KIAA1078 3' TATACATATTGTGTAT 65123 T  
 GTGCAT GTATGTGTG  
 ||||| |||||  
 TATGTG TATACATAT  
 T  
 GAM1381 KIAA1085 3' GTGATAAATACATGTATAATTG 40358 \_ A\_\_ GT  
 T GCA TTGTATGTGTG ATTAC  
 ||| ||||| |||||  
 TGT AATATGTACAT TAGTG  
 T AAA  
 GAM1381 KIAA1096 3' CAGAATTTATATATAAATGTAT 68527 G ACGT  
 GTGCATT TATGTGTGAATT  
 ||||| |||||  
 TATGTAA ATATATATTAA  
 - GACT  
 GAM1381 KIAA1126 3' CGTGCGCGTGTGAGTGTGT 71926 TG G TG AAT  
 G CATT TA TGTG TACG  
 | ||||| ||| |||||  
 T GTGA GT GCGC GTGC  
 GT \_ GT \_\_\_\_  
 GAM1381 KIAA1128 3' CACATGTGCATGCAC 68474 T  
 GTGCAT GTATGTGTG  
 ||||| |||||  
 CACGTA CGTGTACAC  
 -  
 GAM1381 KIAA1165 3' GTTTTGCACATATGCATATGTG 67408 TG \_ AATT GT  
 C G CAT TGTATGTGTG AC  
 | ||| ||||| |||  
 C GTA ACGTATACAC TG  
 GT T GTTT  
 GAM1381 KIAA1203 3' CACATATGCATGCAT 71635 T  
 GTGCAT GTATGTGTG  
 ||||| |||||

TACGTA CGTATACAC

GAM1381 KIAA1209 3' ATG TAGTTCATATTATTGT 60749 TTGTAT  
GCA GTGTGAATTACGT  
||| |||||  
TGT TATACTTGATGTA  
TAT\_\_

GAM1381 KIAA1211 3' ATGCTCGCTCAATATGCAATGT 68891 TG \_\_ ATTACGT  
GC CATTGTATGT GTGA  
||| |||  
GTAACGTATA CGCT  
GT ACT CGTA

GAM1381 KIAA1223 3' ATGTGATAAAAAATGTGCATGT 71142 TG T GTGA\_  
GC G CAT GTATGT ATTACGT  
| ||| |||  
C GTA CGTGTA TAGTGTA  
GT \_ AAAAA

GAM1381 KIAA1228 3' TTCACGTGACAGTGCAT 65052 ATG  
GTGCATTGT TGTGAA  
||| |||  
TACGTGACA GCACTT  
GT\_

GAM1381 KIAA1238 3' GTGTGCACGCATGCATGTGTAT 71078 \_ AAT GT  
GTGCAT TGTATGTGTG TAC  
||| ||||| |||  
TATGTG ACGTACGCAC GTG  
T GT\_

GAM1381 KIAA1238 3' TGTAGTTCATGTTTGTGT 71081 TGTAT TG  
GCAT G TGAATTACG  
||| | |||||  
TGTG T ACTTGATGT  
TT\_\_ GT

GAM1381 KIAA1239 5' GCAGATTTATGTGAACAATGCA 71330 A TG ACGT  
T GTGCATTGT TG TGAATT  
||| || |||  
TACGTAACA GT ATTTAG  
A GT ACG

GAM1381 KIAA1254 3' ATTCTATATATACTATGCAT 70014 T \_  
GTGCAT GTATGTGT GAAT  
||| ||||| |||  
TACGTA CATATATA CTTA  
T T

GAM1381 KIAA1322 3' GTTAGTCATGCGTACATGTGTG 72740 TG \_ ATT GT  
C G CAT TGTATGTGTGA AC  
| ||| ||||| |||  
C GTG ACATGCGTACT TG  
GT T GAT

GAM1381 KIAA1354 3' AATTTATATATACATTGTGT 60913 TG T  
G CA TGTATGTGTGAATT  
| || |||||

T GT ACATATATATTAA  
 GT T  
 GAM1381 KIAA1354 3' ATGCACACATACATACATATGT 60915 \_ AATTACGT  
 AT GTGCAT TGTATGTGTG  
 ||||| |||||  
 TATGTA ACATACATAC  
 T ACACGTA  
 GAM1381 KIAA1354 3' CATACATGCATGCAC 60916 T  
 GTGCAT GTATGTGTG  
 ||||| |||||  
 CACGTA CGTACATAC  
 \_  
 GAM1381 KIAA1361 3' CACATATATTATGCAT 62196 T  
 GTGCAT GTATGTGTG  
 ||||| |||||  
 TACGTA TATATACAC  
 T  
 GAM1381 KIAA1363 3' TACAATATAATGTAT 69264 G  
 GTGCATTGTAT TGTG  
 ||||| |||||  
 TATGTAATATA ACAT  
 \_  
 GAM1381 KIAA1373 3' ATGTAGTTCGTGCTCCATGCAT 70930 T TAT TG  
 GTGCAT G G TGAATTACGT  
 ||||| | | |||||  
 TACGTA C C GCTTGATGTA  
 \_CT\_ GT  
 GAM1381 KIAA1383 3' TTTACACATCAGTGCAT 69786 T  
 GTGCATTG ATGTGTGAA  
 ||||| |||||  
 TACGTGAC TACACATTT  
 \_  
 GAM1381 KIAA1396 3' CACACATACAATACAC 62985 C  
 GTG ATTGTATGTGTG  
 || |||||  
 CAC TAACATACACAC  
 A  
 GAM1381 KIAA1396 3' GTGATTAGCACATGTAGTATGC 62992 GC G  
 GT ATTGTATGTGT AATTAC  
 || ||||| |||||  
 CG TGATGTACACG TTAGTG  
 TA A  
 GAM1381 KIAA1450 3' ATGTAGTTTGTAGCAGCAAAGT 65826 GTA\_ \_ TG  
 GTAC TGCATT TG TG AATTACGT  
 ||||| || |||||  
 ATGTGA AC AT TTGATGTA  
 AACG G GT  
 GAM1381 KIAA1462 3' TATACGTGCACATGTAT 91389 \_  
 GTGCAT TGTATGTGTG  
 ||||| |||||

TATGTA ACGTGCATAT  
 C  
 GAM1381 KIAA1484 3' ATGTGTGTCCGCGTGTAGTGTG 69975 TG T AT  
 T G CATTGTATGTG GA TACGT  
 I ||||| || ||||  
 T GTGATGTGCGC CT GTGTA  
 GT \_ GT  
 GAM1381 KIAA1484 3' GTGTGTCCGCGTGTAGTGTGT 69979 TG T AT  
 G CATTGTATGTG GA TAC  
 I ||||| || |||  
 T GTGATGTGCGC CT GTG  
 GT \_ GT  
 GAM1381 KIAA1492 3' TCTTTGCATATAATGCAC 64509 T\_  
 GTGCATTGTATGTG GA  
 ||||| ||  
 CACGTAATATACGT CT  
 TT  
 GAM1381 KIAA1497 5' TATACATACAAATGTAC 67518 \_  
 GTGCATT GTATGTGTG  
 ||||| |||||  
 CATGTAA CACATAT  
 A  
 GAM1381 KIAA1546 3' ACATGTATATGTGCAC 67901 \_  
 GTGCAT TGTATGTGT  
 ||||| |||||  
 CACGTG ATATGTACA  
 T  
 GAM1381 KIAA1546 3' ATGTGCACACACATGTATATGT 67903 TG\_ AAT  
 AT GTGCAT TATGTGTG TACGT  
 ||||| ||||| ||||  
 TATGTA GTACACAC GTGTA  
 TAT AC\_  
 GAM1381 KIAA1550 3' ACGTGTGTGTATGCGTATGTGT 66540 T AAT\_  
 GCAT GTATGTGTG TACGT  
 ||| ||||| ||||  
 TGTG TATGCGTAT GTGCA  
 \_ GTGT  
 GAM1381 KIAA1550 3' ATTCACACATGCGTGCAC 66546 T  
 GTGCAT GTATGTGTGAAT  
 ||||| |||||  
 CACGTG CGTACACACTTA  
 \_  
 GAM1381 KIAA1550 3' CACACATGCAGTCAT 66548 C  
 GTG ATTGTATGTGTG  
 ||| |||||  
 TAC TGACGTACACAC  
 \_  
 GAM1381 KIAA1550 3' CACACATGCATGCAC 66549 T  
 GTGCAT GTATGTGTG  
 ||||| |||||



CACGTA CGTACACAC

GAM1381 KIAA1550 3' CACACATGCATGCAC 66550 T  
GTGCAT GTATGTGTG  
||||| |||||||  
CACGTA CGTACACAC

GAM1381 KIAA1550 3' CATGCATACACATGCAC 66554 \_  
GTGCAT TGTATGTGTG  
||||| |||||||  
CACGTA ACATACGTAC  
C

GAM1381 KIAA1550 3' CGCACGTGTATGTGTAT 66556 TG\_  
GTGCAT TATGTGTG  
||||| |||||||  
TATGTG GTGCACGC  
TAT

GAM1381 KIAA1550 3' GTGTGAGCACGCACGTGTATGT 66564 TG\_ AA\_ GT  
GTAT TGCAT TATGTGTG TTAC  
||||| ||||||| |||  
ATGTG GTGCACGC AGTG  
TAT ACG TG

GAM1381 KIAA1550 3' GTGTGCACGTGTGTGTATGCG 66565 TG\_ TG AAT  
TGCAT TA TGTG TAC  
||||| || ||| |||  
GCGTA GT GCAC GTG  
TGT GT GT\_

GAM1381 KIAA1550 3' GTGTGCGCGTGTGTGTGTGTAT 66566 TG\_ TG AAT GT  
GTGCAT TA TGTG TAC  
||||| || ||| |||  
TATGTG GT GCGC GTG  
TGT GT GT\_

GAM1381 KIAA1550 3' GTGTGTGCACGTGTGTGTAT 66567 TGT AAT  
GTGCAT ATGTGTG TAC  
||||| ||||||| |||  
TATGTG TGCACGT GTG  
TG\_ GT\_

GAM1381 KIAA1550 3' GTGTGTGCGTGTGTCATGTGTGT 66568 TG \_ TG AAT  
G CAT TGTA TGTG TAC  
| ||| ||| ||| |||  
T GTG ACGT GCGT GTG  
GT T GT GT\_

GAM1381 KIAA1553 3' TTACATGTGTAGGGCAT 91922 A  
GTGC TTGTATGTGTGA  
||||| |||||||||||  
TACG GATGTGTACATT  
G

GAM1381 KIAA1577 3' ATGTATACATATATATATGTAT 64472 T AAT  
GTGCAT GTATGTGTG TACGT  
||||| ||||||| |||

TATGTA TATATATAC ATGTA  
 \_ AT\_  
 GAM1381 KIAA1582 3' GTGTGTGCATGTGTGGCGCG 65374 A TG AAT  
 TGC T TATGTGTG TAC  
 ||| | ||||| |||  
 GCG G GTGTACGT GTG  
 C GT GT\_  
 GAM1381 KIAA1600 3' ATGGTTCTATATATACAATTGC 71442 \_ \_ CGT  
 AC GTGCA TTGTATGTGT GAATTA  
 |||| | ||||| |||||  
 CACGT AACATATATA CTTGGT  
 T T A  
 GAM1381 KIAA1615 3' GTGTATATACACATATAGTGTA 68722 A \_ GT  
 T GTGCATTGTATGTGTG AT TAC  
 ||||| ||||| || |||  
 TATGTGATATACACAT TA GTG  
 A T  
 GAM1381 KIAA1615 3' GTGTGATGTATATGTGTGTGAT 68723 TG \_ A GT  
 GTAT GCAT TAT GTGTG ATTAC  
 ||| || ||||| |||||  
 TGTA GTG TATAT TAGTG  
 GT TG G TG  
 GAM1381 KIAA1615 3' TATACATATAGTGTAT 68726  
 GTGCATTGTATGTGTG  
 ||||| |||||  
 TATGTGATATACATAT  
  
 GAM1381 KIAA1615 3' TATATATATAGTGTGT 68727 TG  
 G CATTGTATGTGTG  
 | ||||| |||||  
 T GTGATATATATAT  
 GT  
 GAM1381 KIAA1634 3' ATGTGATTTATGATGAACAGTC 63386 C ATG\_  
 AC GTG ATTGT TGTGAATTACGT  
 || |||| | ||||| |||||  
 CAC TGACA GTATTTAGTGTA  
 \_ AGTA  
 GAM1381 KIAA1635 3' GTGTATTGCATATACTGTAT 67863 TT TG AT  
 GTGCA GTATGTG A TAC  
 |||| | |||| | |||  
 TATGT CATATAC T GTG  
 \_ GT AT  
 GAM1381 KIAA1673 3' ATTTTGTGCATGCACATAATGTA 70781 A ATTACGT  
 T GTGCATTGT TGTGTGA  
 ||||| |||||  
 TATGTAATA ACGTACT  
 C GTTTTA  
 GAM1381 KIAA1674 3' GCGTACGAGTGTGTGCATGTGT 68783 TG \_ TG GAAT  
 GC G CAT TGTATG T TACGT  
 | || |||| | |||||

C GTG ACGTGT G ATGCG  
 GT T GT AGC\_  
 GAM1381 KIAA1674 3' GTATGCATTCGTGCGTACGAGT 68788 TG \_ TG TACGT  
 GTGT CATT GTATG TGAAT  
 |||| |||| ||||  
 GTGA CATGC GCTTA  
 GT G GT CGTATGT  
 GAM1381 KIAA1674 3' GTGTGCACATGTGTGTATGCAT 68789 TG\_ AAT  
 GTGCAT TATGTGTG TAC  
 |||| |||| ||||  
 TACGTA GTGTACAC GTG  
 TGT GT\_  
 GAM1381 KIAA1674 3' GTGTGCGCCCGTGTGTATGTGC 68790 TG TG\_ T AAT GT  
 G CAT TATG GTG TAC  
 | || |||| || ||||  
 C GTA GTGC CGC GTG  
 GT TGT C GT\_  
 GAM1381 KIAA1674 3' GTGTGTGCACATGTGTGTAT 68791 TGT AAT  
 GTGCAT ATGTGTG TAC  
 |||| |||| ||||  
 TATGTG TACACGT GTG  
 TG\_ GT\_  
 GAM1381 KIAA1681 3' ATGTATACATATATGTATGTGT 61068 TG\_ AAT  
 AT TGCAT TATGTGTG TACGT  
 |||| |||| ||||  
 ATGTG GTATATAC ATGTA  
 TAT AT\_  
 GAM1381 KIAA1681 3' ATGTGTGTGTGTACACGTGCA 61069 AAT\_\_\_\_  
 TGTATGTGTG TACGT  
 |||| ||||  
 ACGTGCACAT GTGTA  
 GTGTGT  
 GAM1381 KIAA1681 3' GTGTATATATGTATACATATAT 61073 T AAT\_\_\_\_ GT  
 GTAT GCAT GTATGTGTG TAC  
 |||| |||| ||||  
 TGTA TATACATAT ATG  
 \_ GTATAT TG  
 GAM1381 KIAA1681 3' GTGTGTACACGTGCATGTAC 61074 T AAT  
 GTGCAT GTATGTGTG TAC  
 |||| |||| ||||  
 CATGTA CGTGCACAT GTG  
 \_ GT\_  
 GAM1381 KIAA1681 3' TAGCCTATTCGTGCATGTTGTG 61075 TG TG TACGT  
 TAT GTGCAT TATG TGAAT  
 |||| |||| ||||  
 TATGTG GTAC GCTTA  
 TT GT TCCGATG  
 GAM1381 KIAA1701 3' GCGTGTCTCTGTGTGTGCACGT 67819 \_ TG\_ AT  
 GCAC TGCAT TGTATG TGA TACGT  
 |||| |||| | || ||||

ACGTG ACGTGT G CT GTGCG  
 C GT T CT  
 GAM1381 KIAA1701 3' TACATTACAGTGTAC 67820 T  
 GTGCATTGTA GTGTG  
 ||||| ||||  
 CATGTGACAT TACAT  
 —  
 GAM1381 KIAA1719 3' ACGTAATTTGCCCAAGTCCAC 68153 C GTA T TG  
 GTG ATT TG G AATTACGT  
 ||| || || |||||  
 CAC TGA AC C TTAATGCA  
 C — C GT  
 GAM1381 KIAA1737 3' ACGTAATTGGCTATGAAGTAC 67344 A TG TGT G  
 GTGC T TA GT AATTACGT  
 |||| | || || |||||  
 CATG A AT CG TTAATGCA  
 A GT — G  
 GAM1381 KIAA1753 3' ATGAATATATATATATATGTGT 64878 — A A  
 AT GTGCAT TGTATGTGTG ATT CGT  
 ||||| ||||| ||| |||  
 TATGTG ATATATATAT TAA GTA  
 T A —  
 GAM1381 KIAA1762 3' TACACATACATGCAC 63790 T  
 GTGCAT GTATGTGTG  
 ||||| |||||  
 CACGTA CATAACAT  
 —  
 GAM1381 KIAA1795 3' GTGGTAGTCTATATAAGTGATG 72154 TG A A GT  
 TAT GTGCAT T TGTGTG ATTAC  
 ||||| | ||||| |||||  
 TATGTA G ATATAT TGATG  
 GT A C GTGT  
 GAM1381 KIAA1804 3' ATGTATGTTGGCGTGTGTGTGT 69787 G TG\_ TG G \_  
 GTGC CAT TA TGT AAT TACGT  
 ||| || ||| |||||  
 GTG GT GCG TTG ATGTA  
 T TGT GT G T  
 GAM1381 KIAA1804 3' GCGTGTGTGTGTGTGCATGCAT 69791 T TG AAT  
 GTGCAT GTATG TG TACGT  
 ||||| ||||| || |||||  
 TACGTA CGTGT GT GTGCG  
 — GT GT\_  
 GAM1381 KIAA1822 3' ATGTAATCCTCATATTAATGCA 67560 T TGA  
 C GTGCATTG ATGTG ATTACGT  
 ||||| ||||| |||||  
 CACGTAAT TATAC TAATGTA  
 — TCC  
 GAM1381 KIAA1822 3' GTGTGAGGCGCTGCAGTGCAT 67573 T GAAT  
 GTGCATTGTA GTGT TAC  
 ||||| ||||| |||

TACGTGACGT CGCG GTG  
\_ GAGT  
GAM1381 KIAA1826 3' TACTGTGCAATGCAT 67219 T  
GTGCATTGTATG GTG  
||||||| |||  
TACGTAACGTGT CAT  
  
GAM1381 KIAA1829 3' ATGTAGTTCATATTTTCAGTTCA 61945 C TAT  
T GTG ATTG GTGTGAATTACGT  
||| ||| |||||  
TAC TGAC TATACTTGATGTA  
T TT\_  
GAM1381 KIAA1838 3' CTTTCATTTCATATATATGATGC 64732 TG TACGT  
GCAT TATGTGTGAAT  
||| |||||  
CGTA ATATATACTTA  
GT CTTTCT  
GAM1381 KIAA1856 3' ACGTGCGTTGTGTGCATGCGAG 92659 A TG \_ \_  
CGC TGC TTGTATG TG AAT TACGT  
||| ||||| ||| |||  
GCG AGCGTAC GT TTG GTGCA  
\_ GT G C  
GAM1381 KIAA1856 3' GTGAGTGTGTGTGCATGCAC 92667 T TG GAA  
GTGCAT GTATG T TTAC  
||||| ||||| | |||  
CACGTA CGTGT G AGTG  
\_ GT TG\_  
GAM1381 KIAA1856 3' GTGTGCATGCACGTGTGTGCAC 92669 TGT GAAT\_  
GTGCAT ATGTGT TAC  
||||| ||||| |||  
CACGTG TGCACG GTG  
TG\_ TACGT  
GAM1381 KIAA1856 3' GTGTGTGTGCATGCACGTGTGT 92670 TG \_ TG AAT  
G CAT TGTATG TG TAC  
| ||| ||||| || |||  
T GTG ACGTAC GT GTG  
GT C GT GT\_  
GAM1381 KIAA1872 3' GTGTGGTTTGGCCAAAATGCAA 62945 GT\_\_ \_ GT  
TGGAC CATTGTAT GT GAATTAC  
||||||| || |||||  
GTAACGTA CG TTTGGTG  
AAAC G TG  
GAM1381 KIAA1910 5' TGCACAGGCAGTGCGC 73331 A  
GTGCATTGT TGTGTG  
||||||| |||||  
CGCGTGACG ACACGT  
G  
GAM1381 KIAA1918 3' CATACATACACATGCAC 73161 \_  
GTGCAT TGTATGTGTG  
||||| |||||

CACGTA ACATACATAC  
C  
GAM1381 KIAA1922 3' GGAATATCATACATCAATGTGT 73635 TG T ATTACGT  
G CATTG ATGTGTGA  
I IIII IIIIIII  
T GTAAC TACATACT  
GT \_ ATAAGGT  
GAM1381 KIAA1937 3' GTGTGCACATGTGTACCATGTG 73699 TG T \_ AAT GT  
C G CAT GTAT GTGTG TAC  
I III IIII IIII III  
C GTA CATG TACAC GTG  
GT C TG GT\_  
GAM1381 KIAA1944 3' TCTGCGTGTAGAATGTAC 75567 G TG \_  
GTGCATT TA TGT GA  
IIIIII II III II  
CATGTAA AT GCG CT  
G GT T  
GAM1381 KIAA1966 3' GTGTTTCTACATGTAGTTGCAC 55894 \_ T T  
GTGCA TTGTATGTG GAA TAC  
IIII IIIIIII III III  
CACGT GATGTACAT CTT GTG  
T \_ T  
GAM1381 KIAA1975 5' TACATGTGCACAATGTGC 73978 TG \_  
G CAT TGTATGTGTG  
I III IIIIIIIII  
C GTA ACGTGTACAT  
GT AC  
GAM1381 KIAA1979 3' CGTGATTACACCTGGGCAC 88277 ATTGTAT  
GTGC GTGTGAATTACG  
IIII IIIIIIIIIII  
CACG CACACTTAGTGC  
GTC\_\_\_\_  
GAM1381 KIAA1985 3' TTACATGTAAATAGTGTAT 44716 \_  
GTGCATTGT ATGTGTGA  
IIIIII IIIIIII  
TATGTGATA TGTACATT  
AA  
GAM1381 KLF12 5' TCTGCGTGTGCGTGTGCGC 23401 \_ TG \_  
GTGCAT TGTA TGT GA  
IIII IIII III II  
CGCGTG GCGT GCG CT  
T GT T  
GAM1381 KLF12 5' TCTGCGTGTGCGTGTGCGC 32806 \_ TG \_  
GTGCAT TGTA TGT GA  
IIII IIII III II  
CGCGTG GCGT GCG CT  
T GT T  
GAM1381 KLHL6 3' TTCATATGTATAGGTAT 55310 A  
GTGC TTGTATGTGTGAA  
IIII IIIIIIIIIII

TATG GATATGTATACTT

GAM1381 KOC1 3' ATTCCTCATGTATAATGTGC 91072 TG T\_  
G CATTGTATGTG GAAT  
I ||||| ||||  
C GTAATATGTAC CTTA  
GT TC

GAM1381 LANCL2 3' CATGCATGAATGTAT 37996 G  
GTGCATT TATGTGTG  
||||| |||||  
TATGTAA GTACGTAC

GAM1381 LEC3 3' TTGCACATATAGTCTGC 30865 C TG  
GTG ATTGTATGTG A  
||| ||||| I  
CGT TGATATACAC T  
C GT

GAM1381 LEPROTL1 3' TCAGTGCAGTGAC 31063 GTG  
GTGCATTGTAT TGA  
||||| |||  
CACGTGACGTG ACT

GAM1381 LIMK2 3' CACATGTGCAGGTAC 18724 A  
GTGC TTGTATGTGTG  
||| |||||  
CATG GACGTGTACAC

GAM1381 LIMK2 3' CACATGTGCAGGTAC 33622 A  
GTGC TTGTATGTGTG  
||| |||||  
CATG GACGTGTACAC

GAM1381 LRPPRC 3' ATGTACTTATGTATGTGTGATG 55704 TG TG\_ T  
CAT GTGCAT TATGTG AA TACGT  
||||| |||| || ||||  
TACGTA GTGTAT TT ATGTA  
GT GTA C

GAM1381 LTBP4 3' TTATGCGTATGTGCAC 13114 T  
GTGCAT GTATGTGTGA  
||||| |||||  
CACGTG TATGCGTATT

GAM1381 LUC7L 3' ATGTTCTGTGCATATAGTGTTG 35912 T TG\_ TACGT  
G GCATTGTATG T GAAT  
I ||||| I ||||  
G TGTGATATAC G CTTG  
T GTT TA

GAM1381 M96 5' CCTCGGTTTGTGCGTGCATATG 23737 TG \_ TG ACGT  
TGC G CAT TGTATGTG AATT  
I ||| ||||| ||||

			C GTA ACGTGCGT TTGG		
			GT T GT CTCCA		
GAM1381	M96	3'	GTGCAGTGTATATAATGC 23739	TG	GAAT
			GCATTGTATG T TAC		
			I		
			CGTAATATAT G GTG		
			GT AC__		
GAM1381	MAN1	3'	ATGAACTTGCACAGATAATGCA 26711	A	TG ATTACGT
	C		GTGCATTGT TGTG A		
			I		
			CACGTAATA ACAC T		
			G GT CAAGTA		
GAM1381	MAN1	3'	TATACATATGGCTGTAC 26714	_	TG
			GTGCA T TATGTGTG		
			I		
			CATGT G ATACATAT		
			C GT		
GAM1381	MAP4K3	3'	TAAGAAATTTATGTAGATAATGT 13243	A	TG ACGT
	AC		GTGCATTGT TG TGAATT		
			CATGTAATA AT ATTTAA		
			G GT GAATC		
GAM1381	MAPK11	3'	CGCATGTATGCATGCAC 10846	_	
			GTGCAT TGTATGTGTG		
			CACGTA GTATGTACGC		
			C		
GAM1381	MASA	3'	TATGTACACATATGTATGCA 64844	_	AATTACGT
			TGCAT TGTATGTGTG		
			ACGTA GTATACACAT		
			T GTA TG		
GAM1381	MAT2B	3'	GTGATATTTTCATATGTGTGGT 25225	TG	___ GT
			AT TATGTGTGA ATTAC		
			TG GTGTATACT TAGTG		
			GT TTA		
GAM1381	MATR3	3'	AACAGAAATTTGCATGTATAAT 38114	TG	ACGT
			ATTGTATGTG AATT		
			TAATATGTAC TTAA		
			GT AGACAAG		
GAM1381	MCAM	3'	GTGTATGCATACATATGTGTGT 21458	_	AAT_ GT
	AT		GTGCAT TGTATGTGTG TAC		
			TATGTG GTATACATAC GTG		
			T GTAT		
GAM1381	MCAM	3'	GTGTGTATGCATACATATGTGT 21459	TG	_ AAT
			G CAT TGTATGTGTG TAC		
			I		



T GTA ACATACGTAT GTG  
 GT T GT\_  
 GAM1381 MGC11115 3' GCGATCTGCACACGTGTGGGTG 50239 \_TG AATTA  
 T GCA T TATGTGTG CGT  
 ||| ||||| |||  
 TGT G GTGCACAC GCG  
 G GT GTCTA  
 GAM1381 MGC12518 3' ATGTGAAAGTATATATATGTGC 64078 \_ T AA\_  
 TGC GCAT GTATGTGTG TTACGT  
 ||| ||||| |||||  
 CGTG TATATATAT AGTGTA  
 T \_ GAA  
 GAM1381 MGC14798 3' ATGTAGTTGAAATCATACAGTA 54673 C TGTG\_  
 TAT GTG ATTGTATG AATTACGT  
 ||| ||||| |||||  
 TAT TGACATAC TTGATGTA  
 A TAAAG  
 GAM1381 MGC15397 3' ATGTGGACACTGTGCATCAATG 54678 G T \_ AA  
 TGC CATTG ATGT GTG TTACGT  
 |||| ||| ||| |||||  
 GTAAC TACG CAC GGTGTA  
 T \_ TGT A\_  
 GAM1381 MGC15631 3' ATGTGCCGGGTGTACTGGTGCA 51260 \_ TG G AAT  
 C GTGCATT GTA T TG TACGT  
 ||||| ||| || |||||  
 CACGTGG CAT G GC GTGTA  
 T GT G C\_  
 GAM1381 MGC16733 3' ATGTGGTAAATGTATAATGC 53210 GTGA  
 GCATTGTATGT ATTACGT  
 ||||| |||||  
 CGTAATATGTA TGGTGTA  
 AA\_  
 GAM1381 MGC17299 3' ACGTTGAGTACACATGAGTGCG 58234 G AATT  
 TGCATT TATGTGTG ACGT  
 ||||| ||||| |||  
 GCGTGA GTACACAT TGCA  
 \_ GAGT  
 GAM1381 MGC1842 3' ATGTGATTTAGACAGTGCAC 65644 TGTA G  
 GTGCAT TGT TGAATTACGT  
 ||||| ||| |||||  
 CACGTG ACA ATTTAGTGTA  
 \_ G  
 GAM1381 MGC22014 3' TACATATATAGATGCGC 64498 \_  
 GTGCAT TGTATGTGTG  
 ||||| |||||  
 CGCGTA ATATATACAT  
 G  
 GAM1381 MGC23280 3' AGGGAGTTTGCAATGTGATGCA 58392 TG G TG ACGT  
 C GTGCAT TAT TG AATT  
 ||||| ||| || |||||

CACGTA GTA AC TTGA  
GT \_ GT GGGAC  
GAM1381 MGC23918 3' GTGTCTGCACATGTGGATGTAC 58516 \_TG GA T  
GTGCA T TATGTGT AT AC  
||||| | ||||| || ||  
CATGT G GTACACG TG TG  
A GT TC \_  
GAM1381 MGC2463 3' ATGTGGTCTGTGTGCGTGTGTG 43957 A TG TG A\_\_\_\_  
GGCAC T TA TGTG ATTACGT  
| || ||| |||||  
G GT GCGT TGGTGTA  
\_GT GT GTGTC  
GAM1381 MGC2463 3' GTGTGGGCACAGGTGTGAGTGT 43958 TG \_TG G AAT\_ GT  
GT G CA T TAT TGTG TAC  
| || | || ||| |||  
T GT A GTG ACAC GTG  
GT G GT G GGGT  
GAM1381 MGC26641 3' TTCACATATATGTATGTAT 58660 \_  
GTGCAT TGTATGTGTGAA  
||||| |||||  
TATGTA GTATATACTT  
T  
GAM1381 MGC29937 3' ATGGGGGACATATATATATGTA 58112 T AA TA  
T GTGCAT GTATGTGTG T CGT  
||||| ||||| | |||  
TATGTA TATATATAC G GTA  
\_ AG GG  
GAM1381 MGC3040 3' ATGTTATATATACATATGTGGA 66843 \_ A T  
TGTAT CATT GTATGTGTG AT ACGT  
||| ||||| || |||  
GTAG TATACATAT TA TGTA  
GTG A T  
GAM1381 MGC3062 5' GCGTGGCGGCGCTGTGCGCGTG 43946 \_ \_ GAA  
CAC TGCAT TGTAT GTGT TTACGT  
||||| ||||| ||| |||||  
ACGTG GCGTG CGCG GGTGCG  
C T GC\_  
GAM1381 MGC33630 3' GTGTGTGTGCATGCACATGTGT 58344 TG \_ TG AAT  
G CAT TGTATG TG TAC  
| || ||||| || |||  
T GTA ACGTAC GT GTG  
GT C GT GT\_  
GAM1381 MGC35521 3' ATGCCCCGCATGCGTGCAATGC 59008 AATTA  
GCATTGTATGTGTG CGT  
||||| ||||| |||  
CGTAACGTGCGTAC GTA  
GCCCC  
GAM1381 MGC4268 3' GCGGCCAGTACCTGCGGTGTGC 48745 TG T \_ AATTA  
G CATTGTA GTG TG CGT  
| ||||| ||| || |||

C GTGGCGT CAT AC GCG  
 GT C G CG\_\_\_\_  
 GAM1381 MGC4400 5' GTGTGCGCTCTGCAGTGTGT 51057 TG TG AT  
 G CATTGTA TGTGA TAC  
 I ||||| |||| ||  
 T GTGACGT GCGCT GTG  
 GT CT \_\_\_\_  
 GAM1381 MGC4737 5' GCGTGCCGCCATGCAGTGCG 48849 T AA  
 TGCATTGTATG GTG TTACGT  
 ||||| |||| |||||  
 GCGTGACGTAC CGC GGTGCG  
 \_ C\_  
 GAM1381 MGC5309 3' GTAATATAATACAATGTGT 80816 TG GTGTGA  
 G CATTGTAT ATTAC  
 I ||||| ||||  
 T GTAACATA TAATG  
 GT ATA\_\_\_\_  
 GAM1381 MIG 3' TATACATACATGCAT 10039 T  
 GTGCAT GTATGTGTG  
 ||||| |||||  
 TACGTA CATACATAT  
 \_  
 GAM1381 MISS 3' ATGTATATGCACATGAATGCAT 58027 G AAT  
 GTGCATT TATGTGTG TACGT  
 ||||| ||||| ||||  
 TACGTAA GTACACGT ATGTA  
 \_ AT\_  
 GAM1381 MKP-7 3' GTTGTGCACAAATAATGTGC 66420 TG A AATT  
 G CATTGT TGTGTG AC  
 I ||||| ||||| ||  
 C GTAATA ACACGT TG  
 GT A GT\_\_\_\_  
 GAM1381 MKRN2 3' ACGTGCACTTACATGTGTGGTT 72411 C TG AT\_  
 CG TG AT TATGTGTGA TACGT  
 || || ||||| ||||  
 GC TG GTGTACATT GTGCA  
 T GT CAC  
 GAM1381 MRP64 5' CGTAGGTGGGCGGTGCGC 33241 ATGTGTGAA  
 GTGCATTGT TTACG  
 ||||| ||||  
 CGCGTGCGC GATGC  
 GGTG\_\_\_\_  
 GAM1381 MRPS35 3' GTATTCATGTATATACATGCAT 41525 \_ TG T  
 GTGCAT TGTATG TGAAT AC  
 ||||| ||||| |||| ||  
 TACGTA ATATAT ACTTA TG  
 C GT \_  
 GAM1381 MSP 3' GTGTGTGTGCATATGTGTGCAT 49420 \_ TG AAT  
 GTGCAT TGTATG TG TAC  
 ||||| ||||| || |||

TACGTG GTATAC GT GTG  
 T GT GT\_  
 GAM1381 MSRA 3' GTGATTCACAATCGTGGCAT 24684 AT TATG  
 GTGC TG TGTGAATTAC  
 |||| || ||||||||  
 TACG GC ACACTTAGTG  
 GT TA\_\_  
 GAM1381 MYO18B 3' ATGTATAAGTGTGTACAAGCAT 50886 A TG GAAT  
 GTGC TTGTATG T TACGT  
 |||| ||||| | ||||  
 TACG AACATGT G ATGTA  
 \_ GT AAT\_  
 GAM1381 NAPG 3' TACATATGCAGAGTAC 96729 A  
 GTGC TTGTATGTGTG  
 |||| ||||||||  
 CATG GACGTATACAT  
 A  
 GAM1381 NCK1 3' CATATATACTATGTAT 20471 T  
 GTGCAT GTATGTGTG  
 |||| ||||||||  
 TATGTA CATATATAC  
 T  
 GAM1381 NCK1 3' TATGTATGCAGTGCAT 20473 TG  
 GTGCATTGTATG TG  
 |||||||| ||  
 TACGTGACGTAT AT  
 GT  
 GAM1381 NIFU 3' CGCATATATATATATGTAT 67313 \_\_\_\_  
 GTGCAT TGTATGTGTG  
 |||| ||||||||  
 TATGTA ATATATACGC  
 TAT  
 GAM1381 NLP\_1 3' ATGTATATATGCATACATGTAT 23708 T AAT  
 GTGCAT GTATGTGTG TACGT  
 |||| |||||||| ||||  
 TATGTA CATACGTAT ATGTA  
 \_ AT\_  
 GAM1381 NMT1 3' GTAGCATGACGTGTGGTGTGC 40789 TG TG \_ AA  
 G CAT TATGT GTG TTAC  
 | ||| |||| ||| ||||  
 C GTG GTGCA TAC GATG  
 GT GT G \_\_\_\_  
 GAM1381 NNT 3' TATACATGGTGATGTAC 24715 TG\_  
 GTGCAT T ATGTGTG  
 |||| | ||||||  
 CATGTA G TACATAT  
 GT G  
 GAM1381 NOVA2 3' TGTGATATCTGTATATATTGCA 10251 T TGT \_ GT  
 T GTGCA TGTATG GA ATTAC  
 |||| ||||| || |||||

			TACGT ATATAT CT TAGTG		
			T GT_ A TG		
GAM1381	NRBF-2	3'	CTTCGTTTATTGTATAATGCAT 47760	T	TACGT
			GTGCATTGTATG GTGAAT		
			TACGTAATATGT TATTTG		
			_ CTTCA		
GAM1381	NSAP1	3'	TTATATATATTATGTAC 21043	T	
			GTGCAT GTATGTGTGA		
			CATGTA TATATATATT		
			T		
GAM1381	OBTP	5'	CACACATGCAGGCAT 34240	A	
			GTGC TTGTATGTGTG		
			TACG GACGTACACAC		
			-		
GAM1381	OLFM3	3'	TGTAATTCATTTCAAATGTCAC 82148	_	GTATGT GT
			GTG CATT GTGAATTAC		
			CAC GTAA TACTTAATG		
			T ACTT_ TG		
GAM1381	OR2C3	3'	ACTTATCTATGTATACAGTGTA 75444		TG AATTACGT
			GTGCATTGTATG TG		
			TATGTGACATAT AT		
			GT CTATTCA		
GAM1381	OSBPL11	3'	GTAAGTGAACGCGCATGTAAGG 42892	A	AATTACGT
			TAT GTGC TTGTATGTGTG		
			TATG AATGTACGCGC		
			G AAGTCAATGT		
GAM1381	OSBPL3	3'	TGTAGTTTCCACAGTGTG 31441	TGTA	TG
			CAT TGTG AATTACG		
			GTG ACAC TTGATGT		
			TG_ CT		
GAM1381	OSBPL5	3'	TCTGCGTGTGCGTGTGCGC 72693	_	TG _
			GTGCAT TGTA TGT GA		
			CGCGTG GCGT GCG CT		
			T GT T		
GAM1381	OSBPL7	3'	ATGTAGGAGAGTGTATGCGTGT 34806	_	TG GAA_
			GCGC TGCAT TGTATG T TTACGT		
			GCGTG GCGTAT G GATGTA		
			T GT AGAG		
GAM1381	PASK	3'	TCGCACATCAATGTAT 30728	T	
			GTGCATTG ATGTGTGA		

TATGTAAC TACACGCT

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      -
GAM1381 PDE10A 3' ATGTAAACGTATACATATGTGT 21858 T AA_
      AT      GTGCAT GTATGTGTG TTACGT
              ||||| ||||| |||||
              TATGTG TATACATAT AATGTA
                - GCA
GAM1381 PDE10A 3' ATGTAGCACACACACATAGATG 21859 G AA_
      TAT      TGCATT TATGTGTG TTACGT
              ||||| ||||| |||||
              ATGTAG ATACACAC GATGTA
                - ACAC
GAM1381 PDZD2 3' GTGAGTGTAAATGTATAATGTAC 80878 GTGAA
              GTGCATTGTATGT TTAC
              ||||| |||||
              CATGTAATATGTA AGTG
                ATGTG
GAM1381 PEGASUS 5' TGTGGTTTACTCCATGCAGTTG 42432 _ T_ GT
      T      GCA TTGTATG GTGAATTAC
              ||| ||||| |||||
              TGT GACGTAC CATTGGTG
                T CT TG
GAM1381 PELI2 3' ACGTAATTTATATGATTCTAAT 41177 TA_
      GTAC      TGCATTG TGTGTGAATTACGT
              ||||| |||||
              ATGTAAT GTATATTTAATGCA
                CTTA
GAM1381 PKNOX2 3' GCGTGAGACTTTTGCAATGTGC 90879 TG TGT GAA
              G CATTGTA GT TTACGT
              | ||||| || |||||
              C GTAACGT CA AGTGCG
              GT TTT G_
GAM1381 PLA2G3 3' GTGAACCAATACATATACAGTG 31686 AA_ GT
      C      GCATTGTATGTGTG TTAC
              ||||| |||||
              CGTGACATATACAT AGTG
                AACCA
GAM1381 PLU-1 5' TGTGATTAATCATGCGATGCA 21759 TGTG GT
              TGCATTGTATG AATTAC
              ||||| |||||
              ACGTAGCGTAC TTAGTG
                TAA_ TG
GAM1381 POLD3 3' ATCCCTTCCTATATACAGTGTG 91643 TG T TTACGT
      C      G CATTGTATGTG GAA
              | ||||| |||||
              C GTGACATATAT CTT
              GT C CCCTA
GAM1381 POMT2 3' GTGGGTGCGCGTGTGTGTAT 25396 TGT GAA
              GTGCAT ATGTGT TTAC
              ||||| ||||| |||||
```

TATGTG TGCGCG GGTG  
 TG\_ TG\_  
 GAM1381 PORIMIN 3' CATGCATATAATGTAC 53600  
 GTGCATTGTATGTGTG  
 |||||  
 CATGTAATATACGTAC

GAM1381 PPFIBP1 3' TATATATACAGTACAT 13254 C  
 GTG ATTGTATGTGTG  
 ||| |||||  
 TAC TGACATATATAT  
 A

GAM1381 PPP1R10 3' TGCGCATTGATGTAC 10739 T  
 GTGCATTG ATGTGTG  
 ||||| |||||  
 CATGTAGT TACGCGT

GAM1381 PPP1R13B 3' GTGTAATTTATGTAAAAATGTG 31011 TG GTA TG GT  
 T G CATT TG TGAATTAC  
 | ||| || |||||  
 T GTAA AT ATTTAATG  
 GT AA\_ GT TG

GAM1381 PRDM13 3' GTAGAATACAAATGTGGTGTGT 41240 TG TG G AA  
 G CAT TAT TGTG TTAC  
 | ||| ||| ||| |||  
 T GTG GTA ACAT GATG  
 GT GT A AA

GAM1381 PRDM7 3' ATGTGTTCCACGTGTGCTATGTG 53787 TG T TG T  
 T G CAT GTA TGTGAAT ACGT  
 | ||| ||| ||||| |||  
 T GTA CGT GCACTTG TGTA  
 GT T GT \_

GAM1381 PRDX2 5' GCGGGTCCACGCGTGTGATCGT 59882 \_ TG A A  
 GC AT TATGTGTG ATT CGT  
 || || ||||| ||| |||  
 TG TA GTGCGCAC TGG GCG  
 C GT C \_

GAM1381 PREI3 3' GTGTGTGTATGTATAGTGTAT 66324 GT AAT  
 GTGCATTGTATGT G TAC  
 ||||| ||| | |||  
 TATGTGATATGTA T GTG  
 TG GT\_

GAM1381 PRO0038 3' ATGTGCCTGCACGTGCAGTGCA 26091 AAT  
 TGCATTGTATGTGTG TACGT  
 ||||| |||||  
 ACGTGACGTGCACGT GTGTA  
 CC\_

GAM1381 PRO0365 5' ACGTATATATGCACATATATGT 26144 \_ AAT\_\_\_\_  
 GTGTAT AT TGTATGTGTG TACGT  
 || ||||| |||

			TG GTATATACAC	ATGCA		
			T	GTATAT		
GAM1381	PRO0365	5'	ACGTGTGTATATATACGTGTAT	26145	T	AAT
			GTGCAT GTATGTGTG	TACGT		
			TATGTG CATATATAT	GTGCA		
			_	GT_		
GAM1381	PRO0365	5'	CACACATATATACGTGTGT	26150	TG	___
			G CAT	TGTATGTGTG		
			T GTG	ATATACACAC		
			GT	CAT		
GAM1381	PRO0365	5'	CATATATACGTGTGTAT	26154	_	
			GTGCAT TGTATGTGTG			
			TATGTG	GCATATATAC		
			T			
GAM1381	PRO0365	5'	GTATATATATACACGTATATAT	26167	_	AATTACGT
			GCAC	TGCAT TGTATGTGTG		
			ACGTA ATATGCACAT			
			T	ATATATATGT		
GAM1381	PRO0461	3'	ACGTTGTTGTATGTATTGATGT	48376	_	TG ATT
			AC	GTGCATTG TATGTG A	ACGT	
			CATGTAGT ATGTAT	T TGCA		
			T	GT GT_		
GAM1381	PRO1257	5'	ATGTTCCCTGTACAAACAGTGCA	37708	A	T__ TACGT
			C	GTGCATTGT TGTG	GAAT	
			CACGTGACA ACAT	CTTG		
			A	GTC TA		
GAM1381	PRO1635	5'	GTGTAAATCAAAGTATATACAT	37730	T	___ A GT
			TGTGT	CA TGTATGTG TGA	TTAC	
			GT ACATATAT	ACT AATG		
			T	GAA A TG		
GAM1381	PRO2086	5'	ACGTAGAAAAATACATATAATG	26070	G	GAA_
			AGC	GT CATTGTATGTGT	TTACGT	
			CG GTAATATACATA	GATGCA		
			A	AAAA		
GAM1381	PRO2831	5'	TTATATGTATAAGCAT	37603	A	
			GTGC TTGTATGTGTGA			
			TACG AATATGTATATT			
			-			
GAM1381	PROL2	3'	GTGTTTTGTATATATACAATGG	22346	G	AAT__ GT
			AT	GT CATTGTATGTGTG	TAC	



TA GTAACATATATAT GTG  
 G GTTTT  
 GAM1381 PRRG1 3' ATGTAAGTGTATATATGTGTGT 6282 TGT AA\_  
 AT GTGCAT ATGTGTG TTACGT  
 ||||| ||||| |||||  
 TATGTG TATATAT AATGTA  
 TG\_ GTG  
 GAM1381 PRRG1 3' ATGTGATGAGACATACATGTAA 6283 GT\_ A\_\_\_\_  
 GTGTAT ATT ATGTGTG ATTACGT  
 ||| ||||| |||||  
 TGA TACATAC TAGTGTA  
 ATG AGAG  
 GAM1381 PRRG1 3' GTGTATAGGCATATATACGTGT 6285 \_ AAT\_ GT  
 GTAT TGCAT TGTATGTGTG TAC  
 ||||| ||||| |||  
 ATGTG GCATATATAC ATG  
 T GGAT TG  
 GAM1381 PSR 3' GTGGGAACGGTGTGCAATGTGC 65188 TG TG\_ GAA  
 G CATTGTA TGT TTAC  
 | ||||| | || ||||  
 C GTAACGT G CA GGTG  
 GT GT G AG\_  
 GAM1381 PTDSS2 3' ACGTGTGTACGTGTGTATGCG 47883 TGT TG AAT  
 TGCAT A TGTG TACGT  
 ||||| | |||| |||||  
 GCGTA T GCAT GTGCA  
 TG\_ GT GT\_  
 GAM1381 PTDSS2 3' GCGTGCGCCGCTGTGGTGTGC 47888 TG TG T TGAA  
 G CAT TA GTG TTACGT  
 | ||| || ||||| |||||  
 C GTG GT CGC GGTGCG  
 GT GT C C\_\_\_\_  
 GAM1381 PTP4A1 3' ATGTAATTGATAAAATGGTGAT 12935 TG TG ATG\_ G  
 GTGT CAT T TGT AATTACGT  
 ||| | ||| |||||  
 GTA G ATA TTAATGTA  
 GT GT GTAAA G  
 GAM1381 PTPN9 3' GTATGGGTCCATATGTACGTGT 11080 \_ A ACGT  
 GTAT TGCAT TGTATGTGTG ATT  
 ||||| ||||| ||||| |||  
 ATGTG GCATGTATAC TGG  
 T C GTATGT  
 GAM1381 R3HDM 3' GTGTAATTGCAAGGCTGTACA 31083 \_\_\_\_ TG GT  
 ATGTGT ATTGTATG TG AATTAC  
 ||||| || |||||  
 TAACATGT AC TTAATG  
 CGGA GT TG  
 GAM1381 Rab11-FIP2 3' TCATATATACATGTGT 29783 TG T  
 G CAT GTATGTGTGA  
 | ||| ||||| |||||

T GTA CATATATACT  
 GT \_  
 GAM1381 RAB21 3' ATGTAATGCAGATATAGTG 30381 G GA  
 CATTGTAT TGT ATTACGT  
 ||||| || |||||  
 GTGATATA ACG TAATGTA  
 G \_  
 GAM1381 RAB33B 3' ATGTAGTTCGCTATTAATAACA 48487 \_ GT\_\_\_\_  
 ATGCAT ATTGT AT GTGAATTACGT  
 |||| | |||||  
 TAACA TA CGCTTGATGTA  
 A ATTAT  
 GAM1381 RAB3GAP 3' ATTTGGTATATGTGCTAATGCA 66946 \_ AATTACGT  
 T GTGCATT GTATGTGTG  
 ||||| |||||  
 TACGTAA CGTGTATAT  
 T GGTTA  
 GAM1381 RAB9A 3' GTTTGCAGCAGTGTAT 14912 ATG TG  
 GTGCATTGT TG AAT  
 ||||| || |||  
 TATGTGACG AC TTG  
 \_ GT  
 GAM1381 RAI16 3' CGTGACATGTGGGTGCAC 42753 \_ TG GAATT  
 GTGCA T TATGTGT ACG  
 |||| | ||||| |||  
 CACGT G GTACACG TGC  
 G GT \_  
 GAM1381 RAI17 3' TCGTATGTACAATGCA 91287  
 TGCATTGTATGTGTGA  
 |||||  
 ACGTAACATGTATGCT  
  
 GAM1381 RALGPS1A 3' GCGTGCTGTACGTGTGTGTGTG 27606 TG TG\_ TG AAT  
 TGT CAT TA TGTG TACGT  
 || | ||| ||||  
 GTG GT GCAT GTGCG  
 GT TGT GT GTC  
 GAM1381 RAN 3' ATGTGGTTTGTACATATCAA 20904 \_ TG  
 TTG TATGTG AATTACGT  
 || |||| |||||  
 AAC ATACAT TTGGTGTA  
 T GT  
 GAM1381 RASSF2 3' GTGTGTGTACATGTGTGTGCAC 28441 TGT AAT\_  
 GTGCAT ATGTGTG TAC  
 |||| ||||| |||  
 CACGTG TGTACAT GTG  
 TG\_ GTGT  
 GAM1381 RI58 3' TATACTGCAGTGTAT 24848 T  
 GTGCATTGTA GTGTG  
 ||||| |||||

TATGTGACGT CATAT

GAM1381 RNF38 3' GTAATAAATGTATGATGTAC 42937 TG GTGA  
GTGCAT TATGT ATTAC  
||||| ||||| |||||  
CATGTA ATGTA TAATG  
GT AA\_\_

GAM1381 RNF38 3' GTGTAGTTTTTAATTATGCTGCA 42938 T \_\_\_\_\_ GT  
ATGTAT TTGTA GTGTGA ATTAC  
||||| ||||| |||||  
AACGT CGTATT TGATG

\_\_\_\_\_ AATTT TG  
GAM1381 RODH-4 5' CATGCATGTAGTGGGC 13530 G  
GT CATTGTATGTGTG  
|| ||||| |||||  
CG GTGATGTACGTAC  
G

GAM1381 RoXaN 3' ATGTGAGCACACACATGTGCAC 46634 \_ AA\_\_\_\_  
ATGCAC AT TGTATGTGTG TTACGT  
|| ||||| |||||  
TA ACGTGTACAC AGTGTA  
C ACACG

GAM1381 RoXaN 3' GGTACAGCACACATGTGAGCAC 46656 A TG AAT GT  
GTGC T TATGTGTG TAC  
||||| ||||| |||||  
CACG A GTACACAC ATG  
\_GT GAC GT

GAM1381 SART3 3' ATGTGCATTACATACAGATGT 28171 TG GTA \_  
GT G CATT TGTGTGAAT TACGT  
| ||||| ||||| |||||  
T GTAG ATACACTTA GTGTA  
GT AC\_ C

GAM1381 SCIN 3' TGCGCGTGGTGGTGCAC 52426 TG\_  
GTGCAT T ATGTGTG  
||||| |||||  
CACGTG G TGCGCGT  
GT G

GAM1381 SCYA18 3' TTCGTACATTCAATGCAT 11462 T  
GTGCATTG ATGTGTGAA  
||||| |||||  
TACGTAAC TACATGCTT  
T

GAM1381 SCYB10 3' ATGTAATTAAGTACTATGTAT 7797 T GTGTG  
GTGCAT GTAT AATTACGT  
||||| ||||| |||||  
TATGTA CATG TTAATGTA  
T AA\_\_\_\_

GAM1381 SCYB11 3' ATGTAATTCATAAAATGTAC 87439 GTATG  
GTGCATT TGTGAATTACGT  
||||| ||||| |||||

			CATGTAA ATACTTAATGTA	
			A_____	
GAM1381	SDCBP	3'	ATGTAAGCATTAAACAGTGTAT 18840	AT_ GAA
			GTGCATTGT GTGT TTACGT	
			TATGTGACA TACG AATGTA	
			AAT _____	
GAM1381	SDF1	3'	ACGTGTTTGTGCTGTGGTGTGT 90854	TG TG T TG T
			G CAT TA GTG AAT ACGT	
			T GTG GT CGT TTG TGCA	
			GT GT _ GT _	
GAM1381	SDFR1	3'	GCGTAATTGTAGATGCATGTAC 24866	T G TG A
			GTGCAT GTAT TG A TTACGT	
			CATGTA CGTA AT T AATGCG	
			_ G GT _	
GAM1381	SDFR1	3'	GCGTAATTGTAGATGCATGTAC 33916	T G TG A
			GTGCAT GTAT TG A TTACGT	
			CATGTA CGTA AT T AATGCG	
			_ G GT _	
GAM1381	SDS3	3'	TTACACATACGATGTGT 69237	TG
			G CATTGTATGTGTGA	
			T GTAGCATACACATT	
			GT	
GAM1381	SDS3	3'	TTCATATTTATAATGTGC 69238	TG T
			G CATTGTA GTGTGAA	
			C GTAATAT TATACTT	
			GT T	
GAM1381	SE57-1	3'	ATGTATGAAGGGCATGTATATG 47395	T GAAT_
	TAT		TGCAT GTATGTGT TACGT	
			ATGTA TATGTACG ATGTA	
			_ GGAAGT	
GAM1381	SE57-1	3'	TTCCTGCATATATATGTAT 47399	_ T
			GTGCAT TGTATGTG GAA	
			TATGTA ATATACGT CTT	
			T C	
GAM1381	SEC14L1	3'	ATGTGCTGTGTGTGTGCATGTG 11488	TG _ TG AAT
	TGC		G CAT TGTATG TG TACGT	
			C GTG ACGTGT GT GTGTA	
			GT T GT GTC	
GAM1381	SEC14L1	3'	GCGTGTGTGTGTGTGCATGTGC 11503	TG T TG AAT
			G CAT GTATG TG TACGT	

C GTA CGTGT GT GTGCG  
 GT \_ GT GT\_  
 GAM1381 SEC14L1 3' GTGGACTCATGCGTGTGTGTGT 11506 TG TG\_ A\_ GT  
 GT CAT TATGTGTGA TTAC  
 ||| ||||| |||  
 GTG GTGCGTACT GGTG  
 GT TGT CA  
 GAM1381 SEC14L1 3' GTGTGTGCATGTGCTGTGTGT 11508 TG T AAT  
 G CAT GTATGTGTG TAC  
 | ||| ||||| |||  
 T GTG CGTGTACGT GTG  
 GT T GT\_  
 GAM1381 SEC14L1 3' GTGTGTGTGCATGTGCTGTGT 11509 T AAT\_  
 GCAT GTATGTGTG TAC  
 |||| ||||| |||  
 TGTG CGTGTACGT GTG  
 T GTGT  
 GAM1381 SEC24B 3' TCTATATATAATGTAC 20899 T  
 GTGCATTGTATGTG GA  
 ||||| ||||| ||  
 CATGTAATATATAT CT  
 -  
 GAM1381 SEMA3E 3' TACATATATATGTAT 24885 T  
 GTGCAT GTATGTGTG  
 ||||| ||||| |||||  
 TATGTA TATATACAT  
 -  
 GAM1381 SEMA6B 3' GTGGGCCACGCGTGCGAGGGTGT 49492 TG A AA  
 G C TTGTATGTGTG TTAC  
 | | ||||| |||||  
 T G GACGTGCGCAC GGTG  
 GT G CG  
 GAM1381 SEMA6B 3' GTGTGGGTGTGCGTGCGTGTGC 49493 TG T TG AAT\_ GT  
 G CAT GTATG TG TAC  
 | ||| |||| || |||  
 C GTG CGTGC GT GTG  
 GT \_ GT GGGT  
 GAM1381 SERF1B 3' TCACATGTGAATGCAT 43421 G  
 GTGCATT TATGTGTGA  
 ||||| ||||| |||||  
 TACGTAA GTGTACACT  
 -  
 GAM1381 SERP1 3' GTAATTCACCAATTAAGTGC 27063 GTA\_ T  
 GCATT TG GTGAATTAC  
 |||| || ||||| |||||  
 CGTGA AC CACTTAATG  
 ATTA \_  
 GAM1381 SEZ6 3' GCCACTTTGTACATGTAATGTA 74364 TG TTACGT  
 T GTGCATTGTATGTG AA  
 ||||| ||||| ||||| ||

			TATGTAATGTACAT TT		
			GT CACCG		
GAM1381	SEZ6	3'	TTTGTACATGTAATGTAT 74368	TG	
			GTGCATTGTATGTG AA		
			TATGTAATGTACAT TT		
			GT		
GAM1381	SGP28	3'	ATGTGAGCCAAATGCAATGTGC 20228	TG	G TGAA
			G CATTGTAT TG TTACGT		
			C GTAACGTA AC AGTGTA		
			GT A CG__		
GAM1381	SH3BGL2	3'	ATGTATATACACATATAATATA 48884	C	AAT
	T		GTG ATTGTATGTGTG TACGT		
			TAT TAATATACACAT ATGTA		
			A AT_		
GAM1381	SHANK3	3'	GCGTGACCGTGTGCATGCG 65501	T TG _ AAT	
			TGCAT GTA TG TG TACGT		
			GCGTA CGT GC AC GTGCG		
			_ GT C _		
GAM1381	SHANK3	3'	GTGTGCATGCGTGGGGTGTAC 65504	G	AAT
			GTGCATT TATGTGTG TAC		
			CATGTGG GTGCGTAC GTG		
			G GT_		
GAM1381	SIAT8C	5'	ATGTGGTGGGCATACAAGGCGC 31877	A	GTGA
			GTGC TTGTATGT ATTACGT		
			CGCG AACATACG TGGTGTA		
			G GG_		
GAM1381	SLAC2-B	3'	TACATGTGCATGTGCAT 30514	_	
			GTGCAT TGTATGTGTG		
			TACGTG ACGTGTACAT		
			T		
GAM1381	SLC6A14	3'	GTGTGTACATGTACATGCAT 23356	T	AAT
			GTGCAT GTATGTGTG TAC		
			TACGTA CATGTACAT GTG		
			_ GT_		
GAM1381	SLK	3'	TATACATATTATGTAT 28228	T	
			GTGCAT GTATGTGTG		
			TATGTA TATACATAT		
			T		
GAM1381	SMOC2	5'	GCGTGCGGTATGAGTGCGTGCGT 72376	G T TG GAA__	
	GTGC		CAT GTATG T TTACGT		

			GTG CGTGC G GGTGCG		
			T _ GT AGTATG		
GAM1381	SNRK	3'	TGTGGTTCACATAGATAGTGAG 34774	G	A GT
	C		GT CATTGT TGTGTGAATTAC		
			CG GTGATA ATACACTTGGTG		
			A G TG		
GAM1381	SPIB	3'	GCGGGGACATGCGTGAGTGCG 11909	G	AATTA
			TGCATT TATGTGTG CGT		
			GCGTGA GTGCGTAC GCG		
			_ AGGG_		
GAM1381	SPIB	3'	GCGTGAGTGCGTGTGGTG 11910	TG	TG GAA
			CAT TATG T TTACGT		
			GTG GTGC G AGTGCG		
			GT GT__		
GAM1381	SPINLW1	3'	GTGAACATACACATGCATGTAT 39871	T	AA_
			GTGCAT GTATGTGTG TTAC		
			TATGTA CGTACACAT AGTG		
			_ ACA		
GAM1381	SRF	3'	ATGTAATTTGTACAGGGGCC 11941	T	ATTGTA TG
			G GC TGTG AATTACGT		
			C CG ACAT TTAATGTA		
			_ GGG__ GT		
GAM1381	SRP9	3'	ATGATCACTGTGCTATAATGTA 79190	T	__ ATTACGT
	C		TGCATTGTA GT GTGA		
			ATGTAATAT CG CACT		
			_ TGT AGTA		
GAM1381	SRP9	3'	TGCATTGTTATACATACTGTGT 79193	T	ATTACGT
	AC		GTGCAT GTATGTGTGA		
			CATGTG CATACATATT		
			T GTTACGTA		
GAM1381	SSBP2	3'	ATGTGATTCAAACAACTGTAC 59526	TT	A G
			GTGCA GT TGT TGAATTACGT		
			CATGT CA ACA ACTTAGTGTA		
			_ _ A		
GAM1381	SSFA2	3'	TACTGTATACAGTGTAC 73769	GT_	
			GTGCATTGTAT GTG		
			CATGTGACATA CAT		
			TGT		
GAM1381	STARD7	5'	ACGGGCCTGCGCGTGCGGCGCG 39328	A	GAATTA
	C		GTGC TTGTATGTGT CGT		

			CGCG GGC GTGCGCG	GCA		
			C	TCCGG_		
GAM1381	STARD7	5'	ACGGGCCTGCGCGTGCGGCGCG	57695	A	GAATTA
		C	GTGC TTGTATGTGT	CGT		
			CGCG GGC GTGCGCG	GCA		
			C	TCCGG_		
GAM1381	STRIN	3'	GTGTATATATACACATATGTGT	32769	_	AAT_ GT
		GTAT	TGCAT TGTATGTGTG	TAC		
			ATGTG GTATACACAT	ATG		
			T	ATAT TG		
GAM1381	STRIN	3'	TATACATATATTGTAT	32770	T	
			GTGCA TGTATGTGTG			
			TATGT ATATACATAT			
			T			
GAM1381	STX1B2	3'	GCGTGCGTGTGCGTGTGATGTG	53517	TG TG TG	AAT
		T	G CAT TATG TG	TACGT		
			T GTA GTGC GT	GTGCG		
			GT GT GT GC_			
GAM1381	STX1B2	3'	GCGTGTGATGTGTGTGATGCAC	53518	TG TG	GAAT
			GTGCAT TATG T	TACGT		
			CACGTA GTGT A	GTGCG		
			GT GT GT_			
GAM1381	STX3A	3'	ATGTATGTACACATAAGTGTGT	14802	TG G	AAT
			G CATT TATGTGTG	TACGT		
			T GTGA ATACACAT	ATGTA		
			GT _ GT_			
GAM1381	STXBP3	3'	TGTAATTTAAACAATGTA	23439	ATGTG	
			TGCATTGT TGAATTACG			
			ATGTAACA ATTTAATGT			
			A_			
GAM1381	SUCLA2	3'	ACGAAGCATGTATAATGCA	13891		GAATTA
			TGCATTGTATGTGT	CGT		
			ACGTAATATGTACG	GCA		
			AA_			
GAM1381	SV2	3'	ATGTATACTTACATATGTGTGT	29304	TG_	AT_
		GCAT	TGCAT TATGTGTGA	TACGT		
			ACGTG GTATACATT	ATGTA		
			TGT CAT			
GAM1381	SV2	3'	GCGTGTGCGTGTGTCATGTGTGT	29310	TG _ TG	AAT
			G CAT TGTA TGTG	TACGT		



			T GTG ACGT GCGT GTGCG		
			GT T GT ____		
GAM1381	SV2	3'	GTGTGTGCGTGTGCGTGTGCAT 29314	_	TG AAT
			GTGCAT TGTA TGTG TAC		
			TACGTG GCGT GCGT GTG		
			T GT GT_		
GAM1381	SV2	3'	TGTGTGCGTGTGCGTGTGCAT 29315	_	TG AATTACGT
			GTGCAT TGTA TGTG		
			TACGTG GCGT GCGT		
			T GT GTG TG		
GAM1381	SYNJ2	3'	ATGTTTAAGTGTGTACATGTGC 61764	TG T	TG GAATT
			G CAT GTATG T ACGT		
			C GTA CATGT G TGTA		
			GT _ GT AATT_		
GAM1381	SYPL	3'	CACACATATAGGTAT 92911	A	
			GTGC TTGTATGTGTG		
			TATG GATATACACAC		
			—		
GAM1381	SYPL	3'	TTTATATGTATGGGCAT 92913	A TG	
			GTGC T TATGTGTGAA		
			TACG G ATGTATATTT		
			_GT		
GAM1381	TAF5L	3'	GTGACCTCGCGCATGCGAGCAC 26967	A	A_
			GTGC TTGTATGTGTGA TTAC		
			CACG AGCGTACGCGCT AGTG		
			CC		
GAM1381	TBLR1	3'	AATATATACATACAGTGTAT 45096	A	
			GTGCATTGTATGTGTG ATT		
			TATGTGACATACATAT TAA		
			A		
GAM1381	TBLR1	3'	TATACATACAGTGTAT 45105		
			GTGCATTGTATGTGTG		
			TATGTGACATACATAT		
GAM1381	TCL6	3'	ATGTGTATGTGTATGCGTGCAT 40094	T	TG AAT
			GTGCAT GTATG TG TACGT		
			TACGTG CGTAT GT GTGTA		
			_ GT AT_		
GAM1381	TCL6	3'	GCGTGAGTATGTGTATGTGTAT 40105	T	TG AA
			GTGCAT GTATG TG TTACGT		

			TATGTG TATGT AT AGTGCG		
			_ GT G_		
GAM1381	TCL6	3'	ATGTGTATGTGTATGCGTGCAT 40125	T	TG AAT
			GTGCAT GTATG TG TACGT		
			TACGTG CGTAT GT GTGTA		
			_ GT AT_		
GAM1381	TCL6	3'	GCGTGAGTATGTGTATGTGTAT 40137	T	TG AA
			GTGCAT GTATG TG TTACGT		
			TATGTG TATGT AT AGTGCG		
			_ GT G_		
GAM1381	TERE1	3'	ATGTGATTTGGCAGTCAGGGTA 25260	A	TA G
	C		GTGC TTG TGT TGAATTACGT		
			CATG GAC ACG GTTTAGTGTA		
			G TG _		
GAM1381	TIAF1	3'	CGTGTTATGTGCAATG 54329	TGAAT	
			CATTGTATGTG TACG		
			GTAACGTGTAT GTGC		
			T_		
GAM1381	TIGD5	3'	ATGTACGGGGCATACAAGGCAC 51698	A	GTGAAT
			GTGC TTGTATGT TACGT		
			CACG AACATACG ATGTA		
			G GGGC_		
GAM1381	TIGD5	3'	CACATGTACGGGGCAT 51699	A	
			GTGC TTGTATGTGTG		
			TACG GGCATGTACAC		
			G		
GAM1381	TNFAIP3	3'	GTGTGTACATATATAATATAC 20826	C	AAT
			GTG ATTGTATGTGTG TAC		
			CAT TAATATATACAT GTG		
			A GT_		
GAM1381	TP53INP1	3'	GTGCTTACATGTATGGATGTGT 72954	TG _TG	AT
			G CA T TATGTGTGA TAC		
			T GT G ATGTACATT GTG		
			GT A GT C_		
GAM1381	TP53INP1	3'	GTGCTTACATGTATGGATGTGT 52727	TG _TG	AT
			G CA T TATGTGTGA TAC		
			T GT G ATGTACATT GTG		
			GT A GT C_		
GAM1381	TRAF3	3'	GTGTGCCCCACATGCGGTG 59744	TGAAT	
			CATTGTATGTG TAC		

GTGGCGTACAC GTG  
 CCGGT  
 GAM1381 TRIM4 3' ACGTGAGAACATGTGATGT 52249 TG GTGAA  
 GCAT TATGT TTACGT  
 |||| |||| ||||  
 TGTA GTACA AGTGCA  
 GT AG\_\_\_  
 GAM1381 TRIM4 3' TTGTATGTACAGTGTTA 52257 T TG  
 G GCATTGTATGTG A  
 | ||||| |||||  
 A TGTGACATGTAT T  
 T GT  
 GAM1381 TRIP-Br2 3' ATGTTTTATATGTGTATGGTGC 28577 TG TG AATT  
 A TGCAT TATG TG ACGT  
 |||| |||| || ||||  
 ACGTG ATGT AT TGTA  
 GT GT ATTT  
 GAM1381 TRIP3 3' ACGTGATTCTACTGTACATTGC 78218 T \_ T  
 AT GTGCA TGTAT GTG GAATTACGT  
 |||| |||| || |||||  
 TACGT ACATG CAT CTTAGTGCA  
 T T \_  
 GAM1381 TSPAN-2 3' CACACATATAATATAT 19163 C  
 GTG ATTGTATGTGTG  
 || |||||  
 TAT TAATATACACAC  
 A  
 GAM1381 TTTY9 3' ATGTATTGGTACTATAGTGTA 49183 T TG T  
 T GTGCATTGTA GTG AA TACGT  
 ||||| || || ||||  
 TATGTGATAT CAT TT ATGTA  
 \_ GG T  
 GAM1381 UCH37 3' TCATGTGCATGTAGTGCAT 32022 \_  
 GTGCATTGTATGT GTGA  
 ||||| ||||  
 TACGTGATGTACG TACT  
 TG  
 GAM1381 USP22 3' GTGCTGCAGCTCATACGGTGTG 68022 TG T GAAT\_ GT  
 T G CATTGTATG GT TAC  
 | ||||| || ||||  
 T GTGGCATAAC CG GTG  
 GT T ACGTC  
 GAM1381 VIT 3' TGGGGCACGCACGGTGCAT 53904 AT AA  
 GTGCATTGT GTGTG TTA  
 ||||| |||| ||||  
 TACGTGGCA CGCAC GGT  
 \_ GG  
 GAM1381 WAC 3' CATATGGGCAGTGTAC 33552 A  
 GTGCATTGT TGTGTG  
 ||||| |||||

			CATGTGACG GTATAC		
			G		
GAM1381	WAC	3'	CATATGGGCAGTGTAC	55186	A
			GTGCATTGT TGTGTG		
			CATGTGACG GTATAC		
			G		
GAM1381	WAC	3'	CATATGGGCAGTGTAC	55192	A
			GTGCATTGT TGTGTG		
			CATGTGACG GTATAC		
			G		
GAM1381	WBP4	3'	CATTGTAATACAGTGTAT	23230	GT__
			GTGCATTGTAT GTG		
			TATGTGACATA TAC		
			ATGT		
GAM1381	WBSCR17	3'	GTGTGCCTGCGTGCTGTGCG	81303	T GTGAAT
			TGCAT GTATGT TAC		
			GCGTG CGTGCG GTG		
			T TCCGT_		
GAM1381	WDR7	3'	TGCATGTACATTGTAT	30962	T
			GTGCA TGTATGTGTG		
			TATGT ACATGTACGT		
			T		
GAM1381	WWP1	3'	TTGCACAGATAGTGTAT	22813	A TG
			GTGCATTGT TGTG A		
			TATGTGATA ACAC T		
			G GT		
GAM1381	ZDHC7	3'	GTGTGCGCGCGTGTGTGCAT	34844	TGT AAT GT
			GTGCAT ATGTGTG TAC		
			TACGTG TCGCGCGC GTG		
			TG_ GT_		
GAM1381	ZFD25	3'	ATGTAATAAAATGCAATGTGT	32577	TG GTGTGA
			G CATTGTAT ATTACGT		
			T GTAACGTA TAATGTA		
			GT AAA__		
GAM1381	ZIM2	3'	GTGTAACGTATATATAGTGT	31087	AAT
			GCATTGTATGTGTG TAC		
			TGTGATATATATGC GTG		
			AAT		
GAM1381	ZNF-U69274	3'	ATGTGATAGCTGTGCATGCAT	26988	T T GA
			GTGCAT GTATG GT ATTACGT		

			TACGTA CGTGT CG TAGTGTA		
			— — A_		
GAM1381	ZNF222	3'	AAATTTGATACATGTATATAAT 25340	TG	TG A CGT
			GTGT G CATTGTATG TG ATTA		
			I		
			T GTAATATAT AC TAGT		
			GT GT A TTAAAG		
GAM1381	ZNF238	3'	TTAAAGATTTGCATGTGCAGTG 20971	TG	TG ACGT
			TGC G CATTGTATGTG AATT		
			I		
			C GTGACGTGTAC TTAG		
			GT GT AAATTC		
GAM1381	ZNF340	5'	ACGGTGTGTGCTGTGGTGCAC 84557	TG	T TG AATTA
			GTGCAT TA G TG CGT		
			CACGTG GT C GT GCA		
			GT _ GT GTG_		
GAM1381	ZNF363	3'	GTGACACTACGCGTGCAGTTCA 73453	C	AA_ GT
			T GTG ATTGTATGTGTG TTAC		
			TAC TGACGTGCGCAT AGTG		
			T CAC		
GAM1381	ZNF396	3'	GTGTTGTCAAGTACAGTGTGT 75670	TG	GTG AT_
			G CATTGTAT TGA TAC		
			I		
			T GTGACATG ACT GTG		
			GT A_ GTT		
GAM1381	LOC113763	3'	ACGTGGCTTTGTACATGTGATG 56576	TG	TG _
			C GCAT TATGTG AA TTACGT		
			CGTA GTACAT TT GGTGCA		
			GT GT C		
GAM1381	LOC116150	3'	GTGTGTGCGTGTGCACGTGCAC 56633	_	TG AAT
			GTGCAT TGTA TGTG TAC		
			CACGTG ACGT GCGT GTG		
			C GT GT_		
GAM1381	LOC116150	3'	GTGTGTGTGTGTGCGTGTGCAC 56634	_	TG AAT
			GTGCAT TGTATG TG TAC		
			CACGTG GCGTGT GT GTG		
			T GT GT_		
GAM1381	LOC116228	3'	CGTGTTACATATAGTGGAC 73797	G	TGAAT
			GT CATTGTATGTG TACG		
			CA GTGATATACAT GTGC		
			G T_		
GAM1381	LOC116441	3'	TGCACATGCAAGTAT 57090	A	
			GTGC TTGTATGTGTG		

TATG AACGTACACGT

GAM1381 LOC120425 5' CACGCATGCACATGTGT 74008 TG \_  
G CAT TGTATGTGTG  
I III IIIIIIIII  
T GTA ACGTACGCAC  
GT C

GAM1381 LOC120939 3' ACACATATATGTGCGC 76240 \_  
GTGCAT TGTATGTGT  
IIIIII IIIIIIIII  
CGCGTG ATATACACA  
T

GAM1381 LOC121441 3' TGTGGTTTATAGCATACATTTG 74068 T\_ \_ GT  
T GCA TGTATG TGTGAATTAC  
III IIIII IIIIIIIII  
TGT ACATAC ATATTTGGTG  
TT G TG

GAM1381 LOC122416 5' TGTGCAGTGCAGGTGCAC 74122 \_ TG  
GTGCATTGTA TG TG  
IIIIIIII II II  
CACGTGGCGT AC GT  
G GT

GAM1381 LOC122525 3' ATGTAATTTGAAATGCTCTAAT 76006 \_ GTG  
GTAT GCATT GTAT TGAATTACGT  
IIII III IIIIIIIII  
TGTA CGTA GTTTAATGTA  
TCT AA\_

GAM1381 LOC122553 3' TTCATATATACATTGTAT 74135 T  
GTGCA TGTATGTGTGAA  
IIII IIIIIIIIIII  
TATGT ACATATATACTT  
T

GAM1381 LOC122773 3' TTCATATATATGTAC 74173 TTG  
GTGCA TATGTGTGAA  
IIII IIIIIIIII  
CATGT ATATATACTT

GAM1381 LOC122786 3' AATTATATTCATGTTGTAATGC 74154 TAT TG TACGT  
AT GTGCATTG G TGAAT  
IIIIII I IIIII  
TACGTAAT T ACTTA  
GT\_ GT TATTAAG

GAM1381 LOC122786 3' TCATAATGCAGTGCAT 74161 G  
GTGCATTGTAT TGTGA  
IIIIIIII IIIII  
TACGTGACGTA ATACT

GAM1381 LOC123016 3' GTGTATGTATGTATATAGTGTA 58107 TG AAT\_ GT  
TGCATTGTATG TG TAC  
IIIIIIII II III

ATGTGATATAT AT GTG  
 GT GTAT  
 GAM1381 LOC123435 5' GTGTGCACGTGTGTGCGTGTGC 74209 \_ TG AAT\_ GT  
 AC GTGCAT TGTATG TG TAC  
 ||||| ||||| || |||  
 CACGTG GCGTGT GC GTG  
 T GT ACGT  
 GAM1381 LOC123435 5' GTGTGTGCACGTGTGTGC 74210 TG TGT AAT  
 G CAT ATGTGTG TAC  
 | ||| ||||| |||  
 C GTG TGCACGT GTG  
 GT \_ GT\_  
 GAM1381 LOC123435 5' GTGTGTGCGTGTGACGTGTGT 74211 TG \_ TG AAT  
 G CAT TGTA TGTG TAC  
 | ||| |||| |||  
 T GTG ACGT GCGT GTG  
 GT C GT GT\_  
 GAM1381 LOC124145 3' CATATATACAGTTCAT 74252 C  
 GTG ATTGTATGTGTG  
 ||| |||||  
 TAC TGACATATATAC  
 T  
 GAM1381 LOC124152 3' CACACATTAATGCAT 74256 T  
 GTGCATTG ATGTGTG  
 ||||| |||||  
 TACGTAAT TACACAC  
 \_  
 GAM1381 LOC124470 3' GTGAAATGTGCATGGTGCAC 75641 TG TG AA  
 GTGCAT TATG TG TTAC  
 ||||| |||| || ||||  
 CACGTG GTAC GT AGTG  
 \_ GT AA  
 GAM1381 LOC125434 3' ATGTAGTTTGTACAGAAAGTCAC 74407 C GTA TG  
 GTG ATT TGTG AATTACGT  
 ||| ||| ||||| |||||  
 CAC TGA ACAT TTGATGTA  
 \_ AG\_ GT  
 GAM1381 LOC125704 3' GTGTGCACAGGTGAGTGTGGTG 74411 TG \_ G AAT GT  
 TGC CAT T AT TGTG TAC  
 ||| | ||||| |||  
 GTG G TG ACAC GTG  
 GT TGAG G GT\_  
 GAM1381 LOC125704 3' GTGTGCATACAAATGATGTGT 74412 TG TG A AAT  
 G CAT T TGTGTG TAC  
 | ||| | ||||| |||  
 T GTA A ACATAC GTG  
 GT GT A GT\_  
 GAM1381 LOC125704 3' GTGTGTGCACATGAGTGCAC 74413 G AAT  
 GTGCATT TATGTGTG TAC  
 ||||| ||||| |||

CACGTGA GTACACGT GTG  
\_ GT\_  
GAM1381 LOC126037 3' GTGTGTATGTGTGCGCGTGCG 74434 \_ TG AAT  
TGCAT TGTATG TG TAC  
||||| |||  
GCGTG GCGTGT AT GTG  
C GT GT\_  
GAM1381 LOC126964 3' ATGTGCGTGCGTGCATATGTGT 74614 TG \_ TG AAT  
G CAT TGTATG TG TACGT  
| ||| ||| |||  
T GTA ACGTGC GC GTGTA  
GT T GT \_  
GAM1381 LOC126964 3' GCGTGCATGCATGTGCGTGCGT 74618 T \_ AAT\_  
GCAT GCAT GTATGT GTG TACGT  
||||| ||| |||  
CGTG CGTGCG TAC GTGCG  
\_ TG GTAC  
GAM1381 LOC126964 3' GCGTGCGTGCATATGTGTGTGT 74619 TG \_ TG AAT  
G CAT TGTATG TG TACGT  
| ||| ||| |||  
T GTG GTATAC GC GTGCG  
GT T GT \_  
GAM1381 LOC128989 3' CACATGTACGTGCAC 74804 T  
GTGCAT GTATGTGTG  
||||| |||  
CACGTG CATGTACAC  
\_  
GAM1381 LOC129888 5' CGTGAGGCCGTACAATGC 74905 T GAA  
GCATTGTATG GT TTACG  
||||| ||| |||  
CGTAACATGC CG AGTGC  
\_ G\_  
GAM1381 LOC130595 5' TACCATACGATGCAT 75752 T  
GTGCATTGTATG GTG  
||||| |||  
TACGTAGCATAC CAT  
\_  
GAM1381 LOC131118 3' GTATTAGTTTATGTATATGAGT 59165 A TG TG CGT  
AC GTGC T TATG TGAATTA  
||||| ||| |||  
CATG A ATAT ATTTGAT  
\_ GT GT TATGC  
GAM1381 LOC131308 3' TACAATACAGTGTAT 75007 G  
GTGCATTGTAT TGTG  
||||| |||  
TATGTGACATA ACAT  
\_  
GAM1381 LOC131873 3' TGAGCAATATTTACAATGTAT 75883 T GAA  
GTGCATTGTA GTGT TTA  
||||| ||| |||



	TATGTAACAT TATA AGT	
	T ACG	
GAM1381 LOC132660 5'	TGTGGGTTATGCAGTGC 75062	TGTGAA
	GCATTGTATG TTACG	
	CGTGACGTAT GGTGT	
	TG____	
GAM1381 LOC134957 3'	ATGTAGTGGCTATGCAGTGT 57662	T GA
	GCATTGTATG GT ATTACGT	
	TGTGACGTAT CG TGATGTA	
	_ G_	
GAM1381 LOC139231 3'	ATGTCAGTATACATACATGTGT 75373	TG T AATT
	G CAT GTATGTGTG ACGT	
	T GTA CATACATAT TGTA	
	GT _ GAC_	
GAM1381 LOC140275 5'	ATGTGACCATATCATAGATGAT 74795	TG A TGAA__
	GCAC TGCAT T TGTG TTACGT	
	ACGTA A ATAC AGTGTA	
	GT G TATACC	
GAM1381 LOC140275 5'	TAGAATTCGCATGTACAGTG 74796	ACGT
	CATTGTATGTGTGAATT	
	GTGACATGTACGCTTAA	
	GATA	
GAM1381 LOC142941 3'	ATGTGGTTTGCAGCAACATGGA 82882	G T A _ TG
	T GT CAT GT TG TG AATTACGT	
	TA GTA CA AC AC TTGGTGTA	
	G _ _ G GT	
GAM1381 LOC143162 3'	ATGTAATTTACGTGTCCCAAT 76494	T_ TG
	ATTG A TGTGAATTACGT	
	TAAC T GCATTTAATGTA	
	CC GT	
GAM1381 LOC143310 3'	ATGTGGTGTGCCAGGCGGTGTG 76526	TG A T A
	C G CATTGT TG GTG ATTACGT	
	C GTGGCG AC CGT TGGTGTA	
	GT G _ G	
GAM1381 LOC143465 5'	GTGTATATGTTATGTATACACA 82969	_ TG AT__ GT
	TGCAC CAT TGTATG TGA TAC	
	GTA ACATAT ATT ATG	
	C GT GTAT TG	
GAM1381 LOC143465 5'	TCAAACATGTCAATGTAT 82971	_ G
	GTGCATTG TATGT TGA	

TATGTAAC GTACA ACT  
 T A  
 GAM1381 LOC143680 3' ATGTGAACAAATATACTATGTA 82986 T G AA  
 T GTGCAT GTATGT TG TTACGT  
 ||||| ||||| || |||||  
 TATGTA CATATA AC AGTGTA  
 T A A\_  
 GAM1381 LOC143916 5' ATGTGCTTGTGTGTGTGCATGT 76637 TG T TG AAT\_  
 GC G CAT GTATG TG TACGT  
 | ||| ||||| || |||||  
 C GTA CGTGT GT GTGTA  
 GT \_ GT GTTC  
 GAM1381 LOC143916 5' GTGTGTGCATGTGCGTGTGTGT 76645 TG \_ AAT  
 G CAT TGTATGTGTG TAC  
 | ||| ||||| ||||| |||||  
 T GTG GCGTGTACGT GTG  
 GT T GT\_  
 GAM1381 LOC143916 5' GTGTGTGTGCATGTGCGTGTGT 76646 TG T AAT\_  
 G CAT GTATGTGTG TAC  
 | ||| ||||| ||||| |||||  
 T GTG CGTGTACGT GTG  
 GT \_ GTGT  
 GAM1381 LOC144017 3' ATGTAGTACTTTTACAGTGTAT 83002 TGT GA  
 GTGCATTGTA GT ATTACGT  
 ||||| || |||||  
 TATGTGACAT CA TGATGTA  
 TTT \_  
 GAM1381 LOC144203 3' ATTTGTACATATGTGTGTGT 76705 TG \_ TG  
 G CAT TGTATGTG AAT  
 | ||| ||||| ||||| |||||  
 T GTG GTATACAT TTA  
 GT T GT  
 GAM1381 LOC144231 3' ATGTTGTATATATACAATGC 83012 AATT  
 GCATTGTATGTGTG ACGT  
 ||||| ||||| ||||| |||||  
 CGTAACATATATAT TGTA  
 GT\_  
 GAM1381 LOC144486 3' ATGTAGTTTAGCAAGTACAGTG 83081 G \_  
 C GCATTGTAT TG TGAATTACGT  
 ||||| || ||||| ||||| |||||  
 CGTGACATG AC ATTTGATGTA  
 A G  
 GAM1381 LOC144486 3' ATTCTCATGTATGTGTGC 83082 TG T T  
 G CAT GTATGTG GAAT  
 | ||| ||||| ||||| |||||  
 C GTG TATGTAC CTTA  
 GT \_ T  
 GAM1381 LOC144845 3' CATGCATGGTGGTGCAT 56658 TG \_  
 GTGCAT T ATGTGTG  
 ||||| | |||||

TACGTG G TACGTAC  
GT G  
GAM1381 LOC145021 3' TTTTCTTTGCATGTACAATTGC 76986 \_ TG TTACGT  
GCA TTGTATGTG AA  
||| ||||| ||  
CGT AACATGTAC TT  
T GT CTTTTG  
GAM1381 LOC145384 3' CACATGTATACATGTGT 77196 TG \_  
G CAT TGTATGTGTG  
| ||| ||||| ||  
T GTA ATATGTACAC  
GT C  
GAM1381 LOC145439 5' ACGTAGTTTGGCCAGGCAGTTC 77206 C A T TG  
AC GTG ATTGT TG G AATTACGT  
||| ||||| ||| |||||  
CAC TGACG AC C TTGATGCA  
T G C GT  
GAM1381 LOC145547 3' TTCACATGTAGGTGTGT 77268 TG G  
G CATT TATGTGTGAA  
| ||| ||||| ||  
T GTGG ATGTACACTT  
GT \_  
GAM1381 LOC145566 5' ACGTGCACACATGTACAGTATG 77270 GC AAT  
C GT ATTGTATGTGTG TACGT  
|| ||||| ||||| |||||  
CG TGACATGTACAC GTGCA  
TA AC\_  
GAM1381 LOC145581 5' GTGTGTCTGTGTGTGCGTGCGC 77281 T TG\_ AT  
GTGCAT GTATG T GA TAC  
||||| ||||| | ||| |||  
CGCGTG CGTGT G CT GTG  
\_ GT T GT  
GAM1381 LOC145624 5' CACATATGTGTATGTAT 83406 TG\_  
GTGCAT TATGTGTG  
||||| ||||| ||  
TATGTA GTATACAC  
TGT  
GAM1381 LOC145678 3' ATGTAAACAGAAATGTATGCAA 83419 TG GAA\_\_\_\_  
TGT CATTGTATG T TTACGT  
||||| ||| |||||  
GTAACGTAT A AATGTA  
GT AAGACA  
GAM1381 LOC145693 5' GTGTATGCATGTGCGTGTGTGT 77353 \_\_\_\_\_ AAT GT  
GTGC T TGTATGTGTG TAC  
| ||||| ||| |||  
G GCGTGTACGT GTG  
TGTGT AT\_ T  
GAM1381 LOC145824 5' CTCTCCCTTACATATGCAATTT 77524 \_ ATTACGT  
GC GCA TTGTATGTGTGA  
||| ||||| |||||

	CGT AACGTATACATT	
	TT CCCTCTCA	
GAM1381 LOC145854 3'	ACAAATTTGAACATGTAGTGTA 77549	G ACGT
C	GTGCATTGTATGT TGAATT	
	CATGTGATGTACA GTTTAA	
	A ACA	
GAM1381 LOC145891 3'	CATATATATAGTCAC 77560 C	
	GTG ATTGTATGTGTG	
	CAC TGATATATATAC	
	—	
GAM1381 LOC145900 3'	ATGTGGTTTGCCCCAAGTGTGC 77564	TGTATGT TG
AC	GTGCAT G AATTACGT	
	CACGTG C TTGGTGTA	
	TGAACCC GT	
GAM1381 LOC146226 5'	GTGTGGGCACCTGTGCATGCAA 83624	___ AAT_ GT
TGC	TTGTATGT GTG TAC	
	AACGTACG CAC GTG	
	TGTC GGGT T	
GAM1381 LOC146237 3'	ATGTGAGCACACGTGTGTGTGT 83630	TG TG_ AA
GT	G CAT TATGTGTG TTACGT	
	T GTG GTGCACAC AGTGTA	
	GT TGT G_	
GAM1381 LOC146237 3'	GGCCTGTTTGTGCATGTGAGCA 83631	A TG TG TACGT
C	GTGC T TATGTG AAT	
	CACG A GTACGT TTG	
	_GT GT TCCGGG	
GAM1381 LOC146485 5'	GTGGGAACACATTTGGTGCAC 59789	T GAA
	GTGCATTG ATGTGT TTAC	
	CACGTGGT TACACA GGTG	
	T AG_	
GAM1381 LOC146520 5'	CATATGTAGGATGTAT 77952	G
	GTGCATT TATGTGTG	
	TATGTAG ATGTATAC	
	G	
GAM1381 LOC146652 5'	GTGAGCACGTGTGTGTGTGCAT 78079	TG_ TG AA
	GTGCAT TA TGTG TTAC	
	TACGTG GT GCAC AGTG	
	TGT GT G_	
GAM1381 LOC146667 5'	GTGTGCCTGCACATGTGTGCAC 83707	TGT GAAT_
	GTGCAT ATGTGT TAC	

CACGTG TACACG GTG  
TG\_ TCCGT  
GAM1381 LOC146850 3' CACACTGTAATGTAC 83820 T  
GTGCATTGTA GTGTG  
||||||| ||||  
CATGTAATGT CACAC  
  
GAM1381 LOC147040 3' CTTTCCTTCATGTGTGCGTGTCAT 78234 T TG TTACGT  
GTGCAT GTATG TGAA  
||||| |||| ||||  
TACGTG CGTGT ACTT  
\_ GT CTTTCC  
GAM1381 LOC147080 5' TCACGCATCGATGTGC 83937 TG T  
G CATTG ATGTGTGA  
| |||| |||||  
C GTAGC TACGCACT  
GT \_  
GAM1381 LOC147525 3' TACATGTATATGGTAC 78376 AT  
GTGC TGTATGTGTG  
||| |||||  
CATG ATATGTACAT  
GT  
GAM1381 LOC147990 3' TATATATATATATGCAC 84099 \_  
GTGCAT TGTATGTGTG  
||||| |||||  
CACGTA ATATATATAT  
T  
GAM1381 LOC148014 3' GTGTGCGTGTCATGTGTGCAC 78612 TGT TG AAT  
GTGCAT ATG TG TAC  
||||| ||| || |||  
CACGTG TAC GC GTG  
TG\_ GT GT\_  
GAM1381 LOC148014 3' GTGTGTGTGCGTGTCATGTGTGC 78613 TG \_ TG AAT  
G CAT TGTATG TG TAC  
| ||| ||||| || |||  
C GTG ACGTGC GT GTG  
GT T GT GT\_  
GAM1381 LOC148195 3' GCTTGATGTGTGTGCAATGTAC 84135 TG GA C  
GTGCATTGTATG T ATTA GT  
||||||| | ||| ||  
CATGTAACGTGT G TAGT CG  
GT\_ T  
GAM1381 LOC148343 5' CGTACAGCGTGCGGTGCA 78793 GTGAAT  
TGCATTGTATGT TACG  
||||||| ||||  
ACGTGGCGTGCG ATGC  
AC\_\_\_\_  
GAM1381 LOC148508 3' TATACAATATAATGCAT 84161 \_  
GTGCATTGTAT GTGTG  
||||||| ||||

TACGTAATATA CATAT

A

GAM1381 LOC148887 3' GCGTGGTTAGCTCATGTGCAGT 84241 C TG\_\_  
CAC TG ATTGTATGTG AATTACGT

|| ||||| |||||

AC TGACGTGTAC TTGGTGCG

\_ TCGA

GAM1381 LOC148932 3' TGTGATTTTCACTGTGGGGTGT 79115 G \_ T GT  
GCATT TAT GTG GAATTAC

|||| ||| ||| |||||

TGTGG GTG CAC TTTAGTG

G T T TG

GAM1381 LOC149076 3' CATGCGTGTCCGGTGTAT 79149 \_  
GTGCATTG TATGTGTG

||||| |||||

TATGTGGC GTGCGTAC

T

GAM1381 LOC149322 3' ATGTGATAGATGGATGCATGCA 59543 T G GA  
TGCAT GTAT TGT ATTACGT

|||| ||| ||| |||||

ACGTA CGTA GTA TAGTGTA

\_ G GA

GAM1381 LOC149684 5' ATGTTGTGTGTGTATACATGCA 84610 T TG AATT  
T GTGCAT GTATG TG ACGT

||||| |||| || |||

TACGTA CATAT GT TGTA

\_ GT GTGT

GAM1381 LOC149703 3' TTCTATGCGTGGAATGTAC 84663 G \_  
GTGCATT TATGTGT GAA

||||| ||||| |||

CATGTAA GTGCGTA CTT

G T

GAM1381 LOC149830 3' TTATACATGCATGCG 84726 T  
TGCAT GTATGTGTGA

|||| |||||

GCGTA CGTACATATT

-

GAM1381 LOC149839 5' GCGTAGTCAGCTGTGTGGTGCA 79536 TG T GA  
T GTGCAT TATG GT ATTACGT

||||| ||| || |||||

TACGTG GTGT CG TGATGCG

GT \_ AC

GAM1381 LOC150111 3' GTGGAGCGCGTGTGGGGCGC 84860 A TG GAAT  
GTGC T TATGTGT TAC

|||| | ||||| |||

CGCG G GTGCGCG GTG

G GT AG\_\_

GAM1381 LOC150111 3' GTGTGGGGCGCGTGTGGGGCGC 84861 A TG GAAT  
GTGC T TATGTGT TAC

|||| | ||||| |||

			CGCG G GTGCGCG GTG						
			G GT GGGT						
GAM1381	LOC150111	3'	GTGTGGGGCGCGTGTGGGGCGC	84862	A	TG		GAAT	
			GTGC T TATGTGT TAC						
			CGCG G GTGCGCG GTG						
			G GT GGGT						
GAM1381	LOC150225	5'	GTGCTGTTTATGCGTGTAGAGC	85010	A			__	GT
		AC	GTGC TTGTATGTGTGAAT TAC						
			CACG GATGTGCGTATTTG GTG						
			A TC						
GAM1381	LOC150606	3'	GTGTGTATGTGTAGAGTGTGC	85091	TG	G	TG	AAT	
			G CATT TATG TG TAC						
			C GTGA ATGT AT GTG						
			GT G GT GT_						
GAM1381	LOC150696	3'	TGCATACACAATGTAT	58489	A				
			GTGCATTGT TGTGTG						
			TATGTAACA ATACGT						
			C						
GAM1381	LOC150967	5'	GTCAGTCACATTGCAGTGTGT	80084	TG	T		ATT	
			G CATTGTA GTGTGA AC						
			T GTGACGT TACACT TG						
			GT _ GAC						
GAM1381	LOC151162	5'	CGTGTATGCATGTGCAC	85243	_		TG		
			GTGCAT TGTATG TG						
			CACGTG ACGTAT GC						
			T GT						
GAM1381	LOC151258	5'	ATGTGGGCCATTAGGTGATGCA	80196		TG	ATGT	AA	
		T	GTGCAT T GTG TTACGT						
			TACGTA G TAC GGTGTA						
			GT GAT_ CG						
GAM1381	LOC151405	5'	TACACATAAGTGCAT	85339	G				
			GTGCATT TATGTGTG						
			TACGTGA ATACACAT						
			-						
GAM1381	LOC151414	5'	GTGTGTTCTGAACACATATGATT	80241	_	TG		_	GT
		GC	GCA T TATGTGT GAAT TAC						
			CGT A ATACACA CTTG GTG						
			T GT AG T						
GAM1381	LOC151614	5'	GTGTATGCGCGTGCATGTGTGT	80308	TG	_		AAT	GT
			G CAT TGTATGTGTG TAC						

		T GTG ACGTGCGCGT GTG		
		GT T AT_		
GAM1381	LOC151614 5'	GTGTGTGTGTATGCGCGTGTCAT 80309	_	TG AAT
		GTGCAT TGTATG TG TAC		
		TACGTG GCGTAT GT GTG		
		C GT GT_		
GAM1381	LOC151979 3'	GTGTGAGCACATGTGTGATG 80425	TG	AAT_
		CAT TATGTGTG TAC		
		GTA GTGTACAC GTG		
		GT GAGT		
GAM1381	LOC151996 5'	GTGGGAACATGATAGTGTAT 85538	A	GAA
		GTGCATTGT TGTGT TTAC		
		TATGTGATA GTACA GGTG		
		_ AG_		
GAM1381	LOC152009 5'	TCTAATATATAATGTAT 85542	GT	
		GTGCATTGTATGT GA		
		TATGTAATATATA CT		
		AT		
GAM1381	LOC152059 5'	CATATGTGCAAGCAT 80444	A	
		GTGC TTGTATGTGTG		
		TACG AACGTGTATAC		
		-		
GAM1381	LOC152274 3'	ATGTATGTCATGTATACGAGCA 80499	A	TG AT
	T	GTGC TTGTATG TGA TACGT		
		TACG AGCATAT ACT ATGTA		
		GT GT		
GAM1381	LOC152316 3'	GTGCTTATGTGGGTGGTGAC 85616	TG A TG AT	
		GTGCAT T TG TGA TAC		
		CACGTG G GT ATT GTG		
		GT G GT C_		
GAM1381	LOC152328 3'	ATGTGCTTTATGGTGTGGTGCA 80522	TG G T	
	T	GTGCAT TAT TGTGAA TACGT		
		TACGTG GTG GTATTT GTGTA		
		GT _ C		
GAM1381	LOC152578 3'	GACTTATTTATATATATATGTA 85782	T	TACGT
	T	GTGCAT GTATGTGTGAAT		
		TATGTA TATATATATTTA		
		TTCAGT		
GAM1381	LOC152633 5'	ATGTACCTGTGTGTGTGCATGT 85803	_	TG AAT_
	GCAC	TGCAT TGTATG TG TACGT		



	ACGTG ACGTGT GT ATGTA		
	T GT GTCC		
GAM1381 LOC152633 5'	ATGTATGAGTGTATGAGTGCAT 85804	G	TG GAAT
	GTGCATT TATG T TACGT		
	TACGTGA GTAT G ATGTA		
	_ GT AGT_		
GAM1381 LOC152633 5'	ATGTGAGCTGTACATGTAGAGT 85805	G	AA__
	GTAC TGCATT TATGTGTG TTACGT		
	ATGTGA ATGTACAT AGTGTA		
	G GTCG		
GAM1381 LOC152633 5'	CACATGTGTATGGATGCAT 85806	G__	
	GTGCATT TATGTGTG		
	TACGTAG GTGTACAC		
	GTAT		
GAM1381 LOC152633 5'	GCGTGAGCACGTGTATAGATGT 85812	_	TG AA
	AC GTGCAT TGTA TGTG TTACGT		
	CATGTA ATAT GCAC AGTGCG		
	G GT G_		
GAM1381 LOC152633 5'	GCGTGAGCATGCATGTGCGTGT 85813	T	AA_
	AC GTGCAT GTATGTGTG TTACGT		
	CATGTG CGTGTACGT AGTGCG		
	_ ACG		
GAM1381 LOC152633 5'	GTGTACACGTGTATAGGTGTAC 85818	_	TG AAT
	GTGCAT TGTA TGTG TAC		
	CATGTG ATAT GCAC GTG		
	G GT AT_		
GAM1381 LOC152633 5'	GTGTAGTGTGAGCATGTGTGCA 85819	TGT	GTGA GT
	T GTGCAT ATGT ATTAC		
	TACGTG TACG TGATG		
	TG_ AGTG TG		
GAM1381 LOC152633 5'	GTGTATAGGTGTACATGTGCAT 85820	_	TG G AAT
	GTGCAT TGTA T TG TAC		
	TACGTG ACAT G AT GTG		
	T GT G AT_		
GAM1381 LOC152633 5'	GTGTATGAGTGCATACATATGC 85821	_	TG GA _ GT
	AT GTGCAT TGTATG T AT TAC		
	TACGTA ACATAC G TA GTG		
	T GT AG T		
GAM1381 LOC152633 5'	GTGTGAGCCTGTGCACGTGCAT 85822	_	T GAAT
	GTGCAT TGTATG GT TAC		

TACGTG ACGTGT CG GTG  
 C C AGT\_  
 GAM1381 LOC152633 5' GTGTGTGCGCATGTGTGC 85823 TG TGT AAT  
 G CAT ATGTGTG TAC  
 | ||| ||||| |||  
 C GTG TACGCGT GTG  
 GT \_\_\_\_ GT\_  
 GAM1381 LOC152633 5' TATGCATATGGTGTAC 85824 TG  
 GTGCAT TATGTGTG  
 ||||| |||||  
 CATGTG ATACGTAT  
 GT  
 GAM1381 LOC152633 5' TGCATACATATGCATATGGTGT 85827 TG AATTACGT  
 AC GTGCAT TATGTGTG  
 ||||| |||||  
 CATGTG ATACGTAT  
 GT ACATACGTG  
 GAM1381 LOC152633 5' TGCGTGTACACGTGTAT 85828 \_ TG  
 GTGCAT TGTA TGTG  
 ||||| ||| |||  
 TATGTG ACAT GCGT  
 C GT  
 GAM1381 LOC152793 3' GTGTTTGTGTGTTTATAATGCA 80667 T TG AAT\_ GT  
 C GTGCATTGTA G TG TAC  
 ||||| ||| |||  
 CACGTAATAT T GT GTG  
 T GT GTTT  
 GAM1381 LOC152925 3' TGTGATTCAATTAATACA 80738 GTG\_  
 TGTAT TGAATTACG  
 ||||| |||||  
 ACATA ACTTAGTGT  
 ATTA  
 GAM1381 LOC153139 5' GTAATTC AATTAGCAAGTAT 85927 A ATGTG  
 GTGC TTGT TGAATTAC  
 ||| ||| |||||  
 TATG AACG ACTTAATG  
 \_ ATTA\_  
 GAM1381 LOC153146 5' GTGTGTTTCGTGTGTGTGTGGTG 85932 G TG \_\_TG \_ GT  
 TGT CAT TAT G TGAAT TAC  
 ||| ||| | ||||| |||  
 GTG GTG T GCTTG GTG  
 T GT TG GT T  
 GAM1381 LOC153196 5' TATATATATAATGTGT 85976 TG  
 G CATTGTATGTGTG  
 | ||||| |||||  
 T GTAATATATATAT  
 GT  
 GAM1381 LOC153196 5' TATATATATAATGTGT 85977 TG  
 G CATTGTATGTGTG  
 | ||||| |||||

T GTAATATATATAT  
 GT  
 GAM1381 LOC153339 3' GTTCATATATGTCTAGTGTGT 86011 TG \_\_\_\_  
 G CATTG TATGTGTGAAT  
 | |||| |||||  
 T GTGAT GTATATACTTG  
 GT CT  
 GAM1381 LOC153387 5' ATGTGCATATATACATATAT 86036 \_\_\_\_ AAT  
 GTAT GCAT TGTATGTGTG TACGT  
 ||| ||||| |||  
 TGTA ACATATATAT GTGTA  
 TAT AC\_  
 GAM1381 LOC153387 5' CATATATATATGTGCAT 86037 \_  
 GTGCAT TGTATGTGTG  
 |||| |  
 TACGTG ATATATATAC  
 T  
 GAM1381 LOC153416 3' TCATGCATAAGTGTAT 60542 G  
 GTGCATT TATGTGTGA  
 |||| |  
 TATGTGA ATACGTA  
 -  
 GAM1381 LOC153454 3' ATGTATATATACACACATATAT 80831 \_ AAT\_\_\_\_  
 ATGTAT AT TGTATGTGTG TACGT  
 || ||||| |||  
 TA ATATACACAC ATGTA  
 T ATATAT  
 GAM1381 LOC153469 3' TTACTATGCAATGTGT 80842 TG T  
 G CATTGTATG GTGA  
 | ||||| |||  
 T GTAACGTAT CATT  
 GT -  
 GAM1381 LOC153516 5' TTACATGTCAGTGCAT 56713 T  
 GTGCATTG ATGTGTGA  
 |||| |  
 TACGTGAC TGTACATT  
 -  
 GAM1381 LOC153577 5' GTGTGTTTACGCGTGGGTGGTG 86060 TG \_\_\_\_ \_ GT  
 TAT GCAT T ATGTGTGAAT TAC  
 ||| | ||||| |||  
 TGTG G TGCGCATTTG GTG  
 GT GG T  
 GAM1381 LOC153711 5' CATACATACATATGCAC 86133 \_  
 GTGCAT TGTATGTGTG  
 |||| |  
 CACGTA ACATACATAC  
 T  
 GAM1381 LOC153894 3' ACGTATATATGCACATGAATGC 80972 G GAAT\_  
 AT GTGCATT TATGTGT TACGT  
 |||| | |||

TACGTAA GTACACG ATGCA  
\_ TATAT  
GAM1381 LOC154184 5' GTAATTCAATTAGCAAGTAT 86182 A ATGTG  
GTGC TTGT TGAATTAC  
||||| |||||  
TATG AACG ACTTAATG  
\_ ATTA\_  
GAM1381 LOC154214 5' GTGTAACCTGAAGCATATACAG 81057 GAA\_\_ GT  
TGT CATTGTATGTGT TTAC  
||||||| ||||  
GTGACATATACG AATG  
AAGTCC TG  
GAM1381 LOC154215 3' ATGTTTGTCCATACATACATGT 81054 T A T\_  
AT GTGCAT GTATGTGTG AT ACGT  
||||| ||||| || ||||  
TATGTA CATACATAC TG TGTA  
\_ C TT  
GAM1381 LOC154807 5' GTGGCCCGGTATGCAGTGTGC 86254 TG TGTGAA  
G CATTGTATG TTAC  
| ||||| ||||  
C GTGACGTAT GGTG  
GT GGCCC\_  
GAM1381 LOC157556 3' GCGTGGTTCCAGGTG 86487 G T  
TAT TG GAATTACGT  
||| || |||||  
GTG AC CTTGGTGCG  
G \_  
GAM1381 LOC157556 5' TGCATATACAGGCAT 86490 A  
GTGC TTGTATGTGTG  
||||| |||||  
TACG GACATATACGT  
\_  
GAM1381 LOC157624 5' TTATGCATTTAGTGCAT 86501 T  
GTGCATTG ATGTGTGA  
||||| |||||  
TACGTGAT TACGTATT  
T  
GAM1381 LOC157681 5' ACGTAAATTCCATGCAATGTGC 81541 TG TGT \_  
G CATTGTATG GAATT ACGT  
| ||||| |||||  
C GTAACGTAC CTAA TGCA  
GT \_ A  
GAM1381 LOC157918 3' CGTCTGTGTGCACGTGCG 86644 A T\_  
TGTATGTGTG AT ACG  
||||| || |||  
GCGTGACGT TG TGC  
G TC  
GAM1381 LOC157918 3' GCGTCTGTGTGCGCGTGTGTGT 86646 TG TGT A T\_  
GC G CAT ATGTGTG AT ACGT  
| ||| ||||| || ||||

	C GTG TGC	CGT TG TGC	
	GT TG_	G TC	
GAM1381 LOC157918 3'	GCGTGTCTGTGTATGTGTGCAC	86647	TGT TG GA T
	GTGCAT ATG T AT	ACGT	
	CACGTG TAT G TG	TGCG	
	TG_ GT TC	_	
GAM1381 LOC157918 3'	GTGTGCGCGTGTGTGTGCGC	86650	TGT TG AAT
	GTGCAT A TGTG	TAC	
	CGCGTG T GCGC	GTG	
	TG_ GT	GT_	
GAM1381 LOC158156 3'	TGTAATTTTATAGCAATGCA	81728	A T GT
	TGCATTGT TGTG	GAATTAC	
	ACGTAACG ATAT TTTAATG		
	_ T TG		
GAM1381 LOC158476 3'	GTGTTTTCAGTTGTATGCAGTG	86850	TG__ T_ GT
	TAC	GCATTGTATG TGAA TAC	
	TGTGACGTAT ACTT	GTG	
	GTTG	TT	
GAM1381 LOC158696 3'	GTGTGTGTGTGTGTGCGTGCAC	81974	T TG AAT_
	GTGCAT GTATG TG	TAC	
	CACGTG CGTGT GT	GTG	
	_ GT GTGT		
GAM1381 LOC158722 3'	ATGTAAAAGTGTATATGTATGC	81992	_ TG GAA
	AT	GTGCAT TGTATG T TTACGT	
	TACGTA GTATAT G AATGTA		
	T GT AA_		
GAM1381 LOC158722 3'	GTGTATATGTATGCATATGCAT	81995	_ TG AAT
	GTGCAT TGTATG TG	TAC	
	TACGTA ACGTAT AT	GTG	
	T GT AT_		
GAM1381 LOC158835 3'	ATGTGATGATTTGTATACAGTG	82008	GT TGA_
	CATTGTAT G	ATTACGT	
	GTGACATA T	TAGTGTA	
	TG TTAG		
GAM1381 LOC158956 3'	ACAAATTTGAACATGTAGTGTA	66640	G ACGT
	C	GTGCATTGTATGT TGAATT	
	CATGTGATGTACA GTTTAA		
	A ACA		
GAM1381 LOC159036 3'	GTGTGTATGCATGATGTAC	86974	GT AAT
	GTGCATT ATGTGTG	TAC	

		CATGTAG TACGTAT GTG		
		— GT—		
GAM1381	LOC160484 3'	TATAATGCGGTGCGC 82216	G	
		GTGCATTGTAT TGTG		
		CGCGTGCGCGTA ATAT		
		—		
GAM1381	LOC163882 3'	GTGTGTGTGCGTGCGCATGTGC 82167	TG _ TG AAT	
		G CAT TGTATG TG TAC		
		C GTA GCGTGC GT GTG		
		GT C GT GT—		
GAM1381	LOC163882 3'	GTGTGTTTGCGTGTGTGTGCGT 82168	___ GT TG TG _ GT	
		GCGC CAT T A TG AAT TAC		
		GTG G T GC TTG GTG		
		CGT TG GT GT T		
GAM1381	LOC164397 5'	TGTGGATTACATGATGCG 82533	GTAT A	
		TGCATT GTGTGA TTACG		
		GCGTAG TACATT GGTGT		
		— A		
GAM1381	LOC164945 5'	CGCACATATGTGCTGCAC 87184	T__	
		GTGCA TGTATGTGTG		
		CACGT GTATACACGC		
		CGT		
GAM1381	LOC169026 3'	TCATGGTGCAATGCAC 82730	G	
		GTGCATTGTAT TGTGA		
		CACGTAACGTG GTACT		
		—		
GAM1381	LOC169679 3'	TCACATATGAATGCAC 87288	G	
		GTGCATT TATGTGTGA		
		CACGTAA GTATACACT		
		—		
GAM1381	LOC196214 3'	ATGTGATTTTGCACAGTGC 89617	TGTA TG _	
		GCAT TGTG AA TTACGT		
		CGTG ACAC TT AGTGTA		
		— GT T		
GAM1381	LOC196411 3'	ATGTATATATACACATATATGT 87665	T AAT_	
		AT TGCAT GTATGTGTG TACGT		
		ATGTA TATACACAT ATGTA		
		— ATAT		
GAM1381	LOC196411 3'	ATGTGTGTATGTATACATGTAT 87666	T TG AAT	
		GTGCAT GTATG TG TACGT		

TATGTACATAT AT GTGTA  
 \_ GT GT\_  
 GAM1381 LOC196411 3' GTATGTATATACATGTGTGT 87678 \_\_\_\_ AATTACGT  
 AT GCAT TGTATGTGTG  
 |||| |||||  
 TGTG ACATATATAT  
 TGT GTA TGC  
 GAM1381 LOC196411 3' TACACATATATATGTAT 87680 \_  
 GTGCAT TGTATGTGTG  
 |||| |||||  
 TATGTA ATATACACAT  
 T  
 GAM1381 LOC196411 3' TACACATATATGTAT 87681 T  
 GTGCAT GTATGTGTG  
 |||| |||||  
 TATGTA TATACACAT  
 -  
 GAM1381 LOC196411 3' TACACATATATGTAT 87682 T  
 GTGCAT GTATGTGTG  
 |||| |||||  
 TATGTA TATACACAT  
 -  
 GAM1381 LOC196411 3' TACACATATATGTAT 87683 T  
 GTGCAT GTATGTGTG  
 |||| |||||  
 TATGTA TATACACAT  
 -  
 GAM1381 LOC196738 3' ATGTAATTTACGTGTCCCAAT 87502 T\_ TG  
 ATTG A TGTGAATTACGT  
 ||| | |||||  
 TAAC T GCATTTAATGTA  
 CC GT  
 GAM1381 LOC197131 3' GTGTCTCACATATGTGTGT 87888 TG TGT AT  
 G CAT ATGTGTGA TAC  
 | || ||||| ||  
 T GTG TATACT GTG  
 GT \_\_\_\_ CT  
 GAM1381 LOC197287 5' CACACATGCATGCAC 60860 T  
 GTGCAT GTATGTGTG  
 |||| |||||  
 CACGTA CGTACACAC  
 -  
 GAM1381 LOC197287 5' TCACATATGTACATGTAC 60864 \_  
 GTGCAT TGTATGTGTGA  
 |||| |||||  
 CATGTA ATGTATACT  
 C  
 GAM1381 LOC197287 5' TGTGATACACACATGCATGTAC 60866 T A GT  
 GTGCAT GTATGTGTG ATTAC  
 |||| ||||| ||||

CATGTA CGTACACAC TAGTG  
\_ A TG  
GAM1381 LOC199232 5' GCGTGGTCCGGTGCGTGGTGC 88972 TG AT G TGA  
G C TGTAT TG ATTACGT  
| | ||||| || |||||  
C G GCGTG GC TGGTGCG  
GT GT G \_  
GAM1381 LOC199675 3' GCGTGCGTGTGTGTGCGTGTGT 88263 TG \_ TG AAT  
GC G CAT TGTATG TG TACGT  
| ||| ||||| || |||||  
C GTG GCGTGT GT GTGCG  
GT T GT GC\_  
GAM1381 LOC199675 3' GCGTGTGTTCGTGTATGTGCG 88264 TGT TG \_  
TGCAT ATG TGAAT TACGT  
||||| ||| ||||| |||||  
GCGTG TAT GCTTG GTGCG  
\_ GT T  
GAM1381 LOC199675 3' GTGTACACCTGCGTGCGTGTGT 88265 \_ \_ AAT GT  
GTGC T TGTATGT GTG TAC  
| ||||| ||| |||  
G GCGTGCG CAC GTG  
TGT TC AT\_ T  
GAM1381 LOC199675 3' GTGTGCGTGCGCGTGTGTGTGC 88266 TG\_ AAT\_ GT  
AT GTGCAT TATGTGTG TAC  
||||| ||||| |||  
TACGTG GTGCGCGT GTG  
TGT GCGT  
GAM1381 LOC199675 3' GTGTGTTTCGTGTATGTGCGTGT 88267 \_ \_ \_ GT  
GTGC CAT TGTATGTG TGAAT TAC  
||| ||||| ||||| |||  
GTG GCGTGTAT GCTTG GTG  
T GT T  
GAM1381 LOC199675 3' TGTATGTGCGTGTGTGCGTGCG 88271 T TG AAT\_ GT  
C GTGCAT GTATG TG TAC  
||||| ||||| || |||  
CGCGTG CGTGT GC ATG  
\_ GT GTGT TG  
GAM1381 LOC199729 3' TTAAATATATGTATATGATGT 73034 TG TG A ACGT  
AT GTGCAT TATG TG ATT  
||||| ||||| ||| |||  
TATGTA ATAT AT TAA  
GT GT A ATTTA  
GAM1381 LOC199786 3' CAGGCGTGGCAGTGAC 88372 \_ G  
GTGCATTGT ATGT TG  
||||||| ||||| |||  
CACGTGACG TGCG AC  
G G  
GAM1381 LOC199907 3' AATTTATGTGTATGGTTCAC 88458 C TG TG  
GTG AT TATG TGAATT  
||| || ||||| |||||



CAC TG ATGT ATTTAA  
T GT GT  
GAM1381 LOC200059 3' TTCTATGCAATGATGCAT 88553 TG A \_  
GTGCAT T TGTGT GAA  
||||| | ||||| |||  
TACGTA A ACGTA CTT  
GT \_ T  
GAM1381 LOC200268 3' TTTACACATGGATGCAC 88694 G  
GTGCATT TATGTGTGAA  
||||| |||||  
CACGTAG GTACACATTT  
  
GAM1381 LOC200734 3' GTGTAAAAAATATATATACAAG 88866 \_ AA\_ GT  
TGTAT CATT GTATGTGTG TTAC  
||| ||||| |||  
GTGA CATATATAT AATG  
A AAAA TG  
GAM1381 LOC200853 3' GTAAACGTGTAGTGGTGCAC 88915 TG \_ TG GAA  
GTGCAT T A TGT TTAC  
||||| | | ||| |||  
CACGTG G T GCA AATG  
GT A GT \_  
GAM1381 LOC200853 3' GTGTTGTATGTACAGGCAC 88916 A TG AT  
GTGC TTGTATGTG A TAC  
||| ||||| | |||  
CACG GACATGTAT T GTG  
\_ GT \_  
GAM1381 LOC201116 5' GTGGTTCTGCGGGTGC 88105 G \_  
GTAT TGT GAATTAC  
|||| | |||||  
CGTG GCG CTTGGTG  
G T  
GAM1381 LOC201164 3' TGTGAGTGTGCGGTGCG 88127 TG GTGAA  
TGCATTGTA T TTACG  
|||||| | |||||  
GCGTGCGT G AGTGT  
GT \_  
GAM1381 LOC203078 3' CACACGTATATATGTGT 89273 TG \_  
G CAT TGTATGTGTG  
| ||| |||||  
T GTA ATATGCACAC  
GT T  
GAM1381 LOC203078 3' CACACGTATATATGTGT 89274 TG \_  
G CAT TGTATGTGTG  
| ||| |||||  
T GTA ATATGCACAC  
GT T  
GAM1381 LOC203100 3' ACGTGGTTTGTATTGGAGATGT 89279 TG GTAT TG  
GC G CATT GTG AATTACGT  
| ||| ||| |||||

C GTAG TAT TTGGTGCA  
 GT AGGT GT  
 GAM1381 LOC203276 3' CATGCATACAATGTGT 90479 TG  
 G CATTGTATGTGTG  
 | |||||  
 T GTAACATACGTAC  
 GT  
 GAM1381 LOC203276 3' TTTTGATACATGCATACAATGT 90491 TG A CGT  
 GT G CATTGTATGTGTG ATTA  
 | |||||  
 T GTAACATACGTAC TAGT  
 GT A TTTA  
 GAM1381 LOC203305 3' CATGCATACAATGTGT 90523 TG  
 G CATTGTATGTGTG  
 | |||||  
 T GTAACATACGTAC  
 GT  
 GAM1381 LOC203305 3' TTTTGATACATGCATACAATGT 90535 TG A CGT  
 GT G CATTGTATGTGTG ATTA  
 | |||||  
 T GTAACATACGTAC TAGT  
 GT A TTTA  
 GAM1381 LOC203369 3' GCATATATATATGTAT 89340 \_  
 GTGCAT TGTATGTGT  
 |||||  
 TATGTAATATATACG  
 T  
 GAM1381 LOC203377 5' CGTGTATGCATGTGCAC 90581 \_ TG  
 GTGCAT TGTATG TG  
 |||||  
 CACGTG ACGTAT GC  
 T GT  
 GAM1381 LOC203392 5' GTGAGTGCGCGTGAGTGTGC 89354 TG G GAA  
 G CATT TATGTGT TTAC  
 | |||||  
 C GTGA GTGCGCG AGTG  
 GT \_ TG\_  
 GAM1381 LOC203504 3' GTGATTCACTGTGTAC 90641 TGTATGT  
 GTGCAT GTGAATTAC  
 |||||  
 CATGTG CACTTAGTG  
 T\_\_\_\_\_  
 GAM1381 LOC203523 3' AGGGATTTGTACATATATGTGC 89374 TG T TG ACGT  
 G CAT GTATGTG AATT  
 | |||||  
 C GTA TATACAT TTAG  
 GT \_ GT GGAT  
 GAM1381 LOC204301 3' ATGTAGTTTGCCCCCAAGTGTG 89462 TG GTATGT TG  
 C G CATT G AATTACGT  
 | |||||

C GTGA C TTGATGTA  
 GT ACCCC\_GT  
 GAM1381 LOC205095 3' ACGTAGAGGCATGTGTGCGAGT 90695 TG \_ TG AA\_  
 GTGT CATT GTATG TG TTACGT  
 |||| |||| || ||||  
 GTGA CGTGT AC GATGCA  
 GT G GT GGA  
 GAM1381 LOC205327 3' ATGTAATTCATAGCTGCATTGT 89500 T TG  
 GCA TGTA TGTGAATTACGT  
 ||| ||| |||||  
 TGT ACGT ATACTTAATGTA  
 T CG  
 GAM1381 LOC205327 3' GTGGTTCACCATAATTGTGT 89503 TG\_ T  
 GCAT TATG GTGAATTAC  
 |||| ||| |||||  
 TGTG ATAC CACTTGGTG  
 TTA \_  
 GAM1381 LOC219445 3' ATGTGGTGGCGTCAGTAATGTA 91572 GTA \_ GA  
 C GTGCATT TG TGT ATTACGT  
 ||||| || ||| |||||  
 CATGTAA AC GCG TGGTGTA  
 TG\_ T G\_  
 GAM1381 LOC219505 3' TCGACACATGTAGTGT 91268 \_  
 GCATTGTATGTGT GA  
 ||||| ||| ||  
 TGTGATGTACACA CT  
 G  
 GAM1381 LOC219649 3' CGCATGTGCAGTGTGC 92954 TG  
 G CATTGTATGTGTG  
 | |||||  
 C GTGACGTGTACGC  
 GT  
 GAM1381 LOC219688 3' ACGTGACGCATACATACACATG 93049 \_ AA  
 TAT GTGCAT TGTATGTGTG TTACGT  
 ||||| ||||| |||||  
 TATGTA ACATACATAC AGTGCA  
 C GC  
 GAM1381 LOC219722 5' GCCACTAGTTTCTATATATGGT 93082 TG T CGT  
 GTAC GTGCAT TATGTG GAATTA  
 ||||| ||||| |||||  
 CATGTG ATATAT TTTGAT  
 GT C CACCGA  
 GAM1381 LOC219741 3' TTCAGATTCACGTGTAGATGTG 93130 TG G TG ACGT  
 T G CATT TA TGTGAATT  
 | |||| ||| |||||  
 T GTAG AT GCACTTAG  
 GT \_ GT ACTTT  
 GAM1381 LOC219988 3' TTTGCACATACATGTAT 91629 T TG  
 GTGCAT GTATGTG AA  
 ||||| ||||| ||

		TATGTA CATAAC TT		
		— GT		
GAM1381	LOC220534 3'	ATGTGGTTTGGCCCTCAAGTGCG 90721		GTATGT TG
	C	GTGCATT G AATTACGT		
		CGCGTGA C TTGGTGTA		
		ACTCC_ GT		
GAM1381	LOC220573 3'	GTAATTGTATATGGGGTGTAC 69604	G	TG A
		GTGCATT TATGTG A TTAC		
		CATGTGG GTATAT T AATG		
		G GT_		
GAM1381	LOC220635 3'	ATGTGATAGATGGATGCATGCA 90773	T	G GA
		TGCAT GTAT TGT ATTACGT		
		ACGTA CGTA GTA TAGTGTA		
		_ G GA		
GAM1381	LOC220753 3'	TGTAGTTCAGTCTTGCAGTATA 92946	C	TGTG GT
	C	GTG ATTGTA TGAATTAC		
		CAT TGACGT ACTTGATG		
		A TCTG TG		
GAM1381	LOC220766 3'	ATGTGATTTATATAACTTTGT 90793	TT	A
		GCA GT TGTGTGAATTACGT		
		TGT CAATATATTTAGTGTA		
		TT _		
GAM1381	LOC220963 3'	GTGTGTGTGTGTGCTATGCAT 91451	T	TG AAT
		GTGCAT GTATG TG TAC		
		TACGTA CGTGT GT GTG		
		T GT GT_		
GAM1381	LOC221061 3'	GTTTGTATATACGGTTAC 93221	C	TG
		GTG ATTGTATGTG AAT		
		CAT TGGCATATAT TTG		
		_ GT		
GAM1381	LOC221271 3'	GTAATTTACAGTGAGGCAT 91869	ATTG	G
		GTGC TAT TGTGAATTAC		
		TACG GTG ACATTTAATG		
		GA__ _		
GAM1381	LOC221288 5'	GGGTAAATTCATTGTGTAATGT 93617	T	_ GT
	AT	GTGCATTGTATG GTGAATT AC		
		TATGTAATGTGT TACTTAA TG		
		_ A GGT		
GAM1381	LOC221312 3'	GTGTGTTTGTGTGTGCATGTAT 91909	T	TG TG _ GT
		TGCAT GTA TG AAT TAC		

	ATGTA CGT GT TTG GTG		
	_ GT GT T T		
GAM1381 LOC221336 3'	ATGTGACCACTGTGCAATGCG 92270	T	AA
	TGCATTGTATG GTG TTACGT		
	GCGTAACGTGT CAC AGTGTA		
	_ C_		
GAM1381 LOC221337 3'	GTGTGTGTGTGTGCATGTGCAC 92114	_	TG AAT
	GTGCAT TGTATG TG TAC		
	CACGTG ACGTGT GT GTG		
	T GT GT_		
GAM1381 LOC221474 5'	GTGTGTGCGCGTGTGTGTAT 92385	TGT	AAT
	GTGCAT ATGTGTG TAC		
	TATGTG TGCGCGT GTG		
	TG_ GT_		
GAM1381 LOC221601 5'	GTAATTC AATTAGCAAGTAT 93650	A	ATGTG
	GTGC TTGT TGAATTAC		
	TATG AACG ACTTAATG		
	_ ATTA_		
GAM1381 LOC221656 5'	TCGTGCGTATTCGATGCG 92234	_	TG
	TGCATTG TATG TGA		
	GCGTAGC ATGC GCT		
	TT GT		
GAM1381 LOC221662 3'	TGTGGTTTATACTGTGC 92406	_	
	GTAT GTGTGAATTACG		
	CGTG CATATTTGGTGT		
	T		
GAM1381 LOC221662 3'	TTTAAATTCATATGTGCACTGT 92407	T	ACGT
AT	GTGCA TGTATGTGTGAATT		
	TATGT ACGTGTATACTTAA		
	C ATTTA		
GAM1381 LOC221687 3'	GTGATGCAGGTACAGTGCGC 92249	G	GA
	GTGCATTGTAT TGT ATTAC		
	CGCGTGACATG ACG TAGTG		
	G _		
GAM1381 LOC221751 3'	AATTTGTATGTAAATGTAC 92042	G	TG
	GTGCATT TATGTG AATT		
	CATGTAA ATGTAT TTAA		
	_ GT		
GAM1381 LOC221766 3'	TTATCTGTACAGTGTAC 93779	GT	
	GTGCATTGTAT GTGA		

		CATGTGACATG TATT		
		TC		
GAM1381	LOC221773 3'	ACGTAAAAGAAATGTATTAATG 91034	_	GTGAA
		TAT GTGCATTG TATGT TTACGT		
		TATGTAAT ATGTA AATGCA		
		T AAGAA		
GAM1381	LOC221814 3'	AATTTACATTGCAATGCAT 93940	T	
		GTGCATTGTA GTGTGAATT		
		TACGTAACGT TACATTAA		
		-		
GAM1381	LOC221895 3'	ATTTGCACATGTAATCAT 92522	C	TG
		GTG ATTGTATGTG AAT		
		TAC TAATGTACAC TTA		
		- GT		
GAM1381	LOC221981 3'	CATATATGCATGCAT 93990	T	
		GTGCAT GTATGTGTG		
		TACGTA CGTATATAC		
		-		
GAM1381	LOC222008 3'	ATGTAGAAATACATATAGGTAT 94005	A	GAA
		GTGC TTGTATGTGT TTACGT		
		TATG GATATACATA GATGTA		
		- AA-		
GAM1381	LOC222008 3'	ATGTGATTTGCAGATTTGTAGG 94006	ATTGT_ G TG	
		GCAC TGC AT TG AATTACGT		
		ACG TA AC TTAGTGTA		
		GGATGTT G GT		
GAM1381	LOC222029 3'	ATTTACATGTATATGTAT 94035	T	
		GTGCAT GTATGTGTGAAT		
		TATGTA TATGTACATTAA		
		-		
GAM1381	LOC222066 3'	CACACGTTAGTGACAC 92741	T	
		GTGCATTG ATGTGTG		
		CACGTGAT TGCACAC		
		-		
GAM1381	LOC222159 5'	CTCAATGCACATATCAGTGCGC 94077	T	A ACGT
		GTGCATTG ATGTGTG ATT		
		CGCGTGAC TATACAC TAA		
		- G CTCT		
GAM1381	LOC222223 3'	GTGTGATTTGGAAGGCACATGT 94217	TG	_____ GT
		GAGCAT T TATGTGT GAATTAC		

	A GTACACG TTTAGTG		
	GT GAAGG TG		
GAM1381 LOC245806 3'	TATATATATGTATGCAT 91892	—	
	GTGCAT TGTATGTGTG		
	TACGTA GTATATATAT		
	T		
GAM1381 LOC245806 3'	TTATATATATATATGTAT 91894	—	
	GTGCAT TGTATGTGTGA		
	TATGTA ATATATATATT		
	T		
GAM1381 LOC253012 5'	GCAAGATTTGCACAGTACAGTG 97272	—	TG ACGT
	TAT GTGCATTGTA TGTG AATT		
	TATGTGACAT ACAC TTAG		
	G GT AACG		
GAM1381 LOC253091 3'	TTTTCTTTACATGTACAATTGC 95599	—	TTACGT
	GCA TTGTATGTGTGAA		
	CGT AACATGTACATTT		
	T CTTTTG		
GAM1381 LOC253187 5'	ATGTGATGATTACTGTATTGTG 97112	T —	TGA
	CAT GTGCAT GTAT GTG ATTACGT		
	TACGTG TATG CAT TAGTGTA		
	T T TAG		
GAM1381 LOC253681 3'	CTTTCTTCATGTGTGCGTGCAT 95131	T TG	TTACGT
	GTGCAT GTATG TGAA		
	TACGTG CGTGT ACTT		
	— GT CTTTCC		
GAM1381 LOC253782 3'	TATGTGTTCTATTTATGTATAT 95699	— TG	—
	ATATGTAT TGTATG TGAAT TACGT A		
	ATATAT ATTTA GTGTA T		
	T GT TCTT		
GAM1381 LOC253907 3'	TTTTCTTTACATGTACAATTGC 94925	—	TTACGT
	GCA TTGTATGTGTGAA		
	CGT AACATGTACATTT		
	T CTTTTG		
GAM1381 LOC254028 3'	GCGTGCGGTTGGTATGTCAATG 96541	T TG	—
	CAT TGCATTG ATGTG AAT TACGT		
	ACGTAAC TGTAT TTG GTGCG		
	— GG GC		
GAM1381 LOC254057 5'	CGTGGGTGTGCCAGTGCAT 96999	TAT TG	GAA
	GTGCATTG G T TTACG		

TACGTGAC C G GGTGC  
\_\_\_\_ GT TG\_  
GAM1381 LOC254082 5' TACACATAACGGTGTAT 97204 \_  
GTGCATTGT ATGTGTG  
||||||| |||||  
TATGTGGCA TACACAT  
A  
GAM1381 LOC254170 3' GTAGATTTATATGCAATGCAC 94927 TGAA  
GTGCATTGTATGTG TTAC  
||||||| |||  
CACGTAACGTATAT GATG  
TTA\_  
GAM1381 LOC254228 3' TAGTATGTACATATATGTGT 95957 TG T AAT GT  
G CAT GTATGTGTG TAC  
| ||| ||||| |||  
T GTA TATATACAT ATG  
GT \_ GT\_ ATT  
GAM1381 LOC254228 3' TATGTACATATATATGTGTAT 95958 \_ AATTACGT  
GTGCAT TGTATGTGTG  
||||| |||||  
TATGTG ATATATACAT  
T GTA TG  
GAM1381 LOC254243 3' CATGCATACAATGTGT 97408 TG  
G CATTGTATGTGTG  
| |||||  
T GTAACATACGTAC  
GT  
GAM1381 LOC254243 3' TATTTTGATACATGCATACAAT 97420 TG A CGT  
GTGT G CATTGTATGTGTG ATTA  
| |||||  
T GTAACATACGTAC TAGT  
GT A TTTATA  
GAM1381 LOC254251 3' GTGTGTTTGCGTGTGTGTGTAT 95908 TG\_\_\_\_ TG TG \_ GT  
GTGCAC TA TG AAT TAC  
|| || |||  
GT GC TTG GTG  
TATGTGT GT GT T T  
GAM1381 LOC254251 3' TACACGACAGTGCAT 95910 A  
GTGCATTGT TGTGTG  
||||||| |||||  
TACGTGACA GCACAT  
-  
GAM1381 LOC254358 3' ATGTAGTTTGCCCCCAAGTGTG 94974 TG GTATGT TG  
C G CATT G AATTACGT  
| ||| | |||||  
C GTGA C TTGATGTA  
GT ACCCC\_GT  
GAM1381 LOC254423 3' GTGTCTCATTGTGTGATGTGC 97437 TG TG T AT  
G CAT TATG GTGA TAC  
| ||| ||| ||| |||



C GTA GTGT TACT GTG  
 GT GT \_ CT  
 GAM1381 LOC254559 5' GCGTGGTTCGGCGTGCCAGGCG 96597 ATT G  
 C GTGC GTATGT TGAATTACGT  
 ||| ||||| |||||  
 CGCG CGTGCG GCTTGGTGCG  
 GAC \_  
 GAM1381 LOC254755 3' CGTGCCACATGTGGGTGCAC 97366 \_TG GAATT  
 GTGCA T TATGTGT ACG  
 ||||| ||||| |||  
 CACGT G GTACACG TGC  
 G GT \_  
 GAM1381 LOC255624 3' CGTGATTACACCTGGGCAC 94522 ATTGTAT  
 GTGC GTGTGAATTACG  
 ||| |||||  
 CACG CACACTTAGTGC  
 GTC\_  
 GAM1381 LOC255624 3' GTGATTACACCTGGGCAC 94525 ATTGTAT  
 GTGC GTGTGAATTAC  
 ||| |||||  
 CACG CACACTTAGTG  
 GTC\_  
 GAM1381 LOC255650 3' GTGTGTGCGCGTGTGTGTGTAC 96718 TG\_ AAT  
 GTGCAT TATGTGTG TAC  
 ||||| ||||| |||  
 CATGTG GTGCGCGT GTG  
 TGT GT\_  
 GAM1381 LOC256158 5' CGTGTTTCGGGCAGTGGC 97664 ATTGTA G  
 GC TGT TGAATTACG  
 || ||| |||||  
 CG ACG GCTTGGTG  
 GTG\_ G  
 GAM1381 LOC256394 3' ATGTGGTTCAGTTAATCAGTGT 94940 TG TATGTG  
 GC G CATTG TGAATTACGT  
 | |||| |||||  
 C GTGAC ACTTGGTGTA  
 GT TAATTG  
 GAM1381 LOC257017 5' TTGTATATACATATGCAC 97380 \_ TG  
 GTGCAT TGTATGTG A  
 ||||| ||||| |  
 CACGTA ACATATAT T  
 T GT  
 GAM1381 LOC257130 3' TACGTATATGATGTAT 96392 TG  
 GTGCAT TATGTGTG  
 ||||| |||||  
 TATGTA ATATGCAT  
 GT  
 GAM1381 LOC257130 3' TGAGAATATACGTATATGATGT 96393 TG A ACGT  
 AT GTGCAT TATGTGTG ATT  
 ||||| ||||| |||

TATGTA ATATGCAT TAA  
 GT A GAGTA  
 GAM1381 LOC257319 3' GTGTGTGTGCGTGC GTGTGTAT 95775 \_ TG AAT  
 GTGCAT TGTATG TG TAC  
 ||||| ||||| || |||  
 TATGTG GCGTGC GT GTG  
 T GT GT\_  
 GAM1381 LOC257354 3' GCGTCAAGGTGTGTGTGCACAT 95092 TG \_ TG AA \_  
 GTGT CAT TGTATG TG TT ACGT  
 ||| ||||| || |||||  
 GTA ACGTGT GT AA TGCG  
 GT C GT GG C  
 GAM1381 LOC257354 3' GTGTGTGCACATGTGTGCAT 95096 TGT AAT  
 GTGCAT ATGTGTG TAC  
 ||||| ||||| |||  
 TACGTG TACACGT GTG  
 TG\_ GT\_  
 GAM1381 LOC257465 3' GTGTACGCACATGTGTGTGTAT 81599 TG\_ AAT GT  
 GTGCAT TATGTGTG TAC  
 ||||| ||||| |||  
 TATGTG GTACACGC GTG  
 TGT AT\_  
 GAM1381 LOC257484 3' TACATATATAGATGCGC 88817 \_  
 GTGCAT TGTATGTGTG  
 ||||| |||||  
 CGCGTA ATATATACAT  
 G  
 GAM1381 LOC51003 3' ACTTAATACATGTATATAATGT 32143 TG A C  
 AT GTGCATTGTATG TG ATTA GT  
 ||||| ||||| || ||||| ||  
 TATGTAATATAT AC TAAT CA  
 GT A T  
 GAM1381 LOC51003 3' CATGTATATAATGTAT 32144 TG  
 GTGCATTGTATG TG  
 ||||| ||||| ||  
 TATGTAATATAT AC  
 GT  
 GAM1381 LOC51014 3' TCATGGATGTGATGCAC 65851 TG G  
 GTGCAT TAT TGTGA  
 ||||| ||| |||||  
 CACGTA GTA GTACT  
 GT G  
 GAM1381 LOC51019 3' TTACATATGCATGCAT 32130 T  
 GTGCAT GTATGTGTGA  
 ||||| |||||  
 TACGTA CGTATACATT  
 \_  
 GAM1381 LOC51133 5' TTATACATATAGTTAC 32285 C  
 GTG ATTGTATGTGTGA  
 ||| |||||  
 ||| |||||

CAT TGATATACATATT

GAM1381 LOC51136 3' GTGTTTTAAAATATATATAATG 32324      T GT  
T GCATTGTATGTGT GAA TAC  
||||||| |||  
TGTAATATATATA TTT GTG  
AAA T

GAM1381 LOC51177 5' GCGTGCGTGTGTGTGCGAGTGC 32774 TG A TG AAT  
G C TTGTATG TG TACGT  
| | ||||| || ||||  
C G AGCGTGT GT GTGCG  
GT \_ GT GC\_

GAM1381 LOC51246 3' GCGTGAGTGGTGTGCAGGCGC 33217 A TG GTGAA  
GTGC TTGTA T TTACGT  
||| |||| | ||||  
CGCG GACGT G AGTGCG  
\_ GT GTG\_

GAM1381 LOC51580 3' CATACATGCAATGTAT 31861  
GTGCATTGTATGTGTG  
|||||||  
TATGTAACGTACATAC

GAM1381 LOC51696 3' TGATAATTCATGTATGATGTG 32561 TG TG T CGT  
C G CAT TATGTG GAATTA  
| ||| ||||| |||||  
C GTA ATGTAC TTTAAT  
GT GT \_ AGTT

GAM1381 LOC51705 3' GCTACTTTGTACATATAAGTAT 32693 A TG TTACGT  
GTGC TTGTATGTG AA  
||| ||||| ||  
TATG AATATACAT TT  
\_ GT CATCGT

GAM1381 LOC57086 3' TACATGTGCACAATGTGC 39780 TG \_  
G CAT TGTATGTGTG  
| ||| |||||  
C GTA ACGTGTACAT  
GT AC

GAM1381 LOC57116 3' ATGTAATTATTATACATTGTAT 39863 T TGTG  
GTGCA TGTATG AATTACGT  
||||| |||||  
TATGT ACATAT TTAATGTA  
T TA\_

GAM1381 LOC57826 3' ATGTGATTTATGGGTCAGCAT 41014 AT T G  
GTGC TG AT TGTGAATTACGT  
||| || |||||  
TACG AC TG GTATTTAGTGTA  
\_ \_ G

GAM1381 LOC86651 3' ATGTGATAGATGGATGCATGCA 68756 T G GA  
TGCAT GTAT TGT ATTACGT  
||||| ||| |||||

ACGTA CGTA GTA TAGTGTA  
 \_ G GA  
 GAM1381 LOC89958 3' GTGTGCAGGTACATACACATGC 60923 \_ \_ AAT GT  
 G TGCAT TGTATGTG TG TAC  
 ||||| ||||| || |||  
 GCGTA ACATACAT AC GTG  
 C GG GT\_  
 GAM1381 LOC89958 3' TACACATGCGTGCAC 60924 T  
 GTGCAT GTATGTGTG  
 ||||| |||||  
 CACGTG CGTACACAT  
 -  
 GAM1381 LOC90019 5' GTGTGTGCGCGTGCGTGTGTGT 56770 TG \_ AATTACGT  
 G CAT TGTATGTGTG  
 | ||| |||||  
 T GTG GCGTGCGCGT  
 GT T GTG TGC  
 GAM1381 LOC90038 3' CATGCATACAATGTGT 61152 TG  
 G CATTGTATGTGTG  
 | |||||  
 T GTAACATACGTAC  
 GT  
 GAM1381 LOC90038 3' TATTTTGATACATGCATACAAT 61162 TG A CGT  
 GTGT G CATTGTATGTGTG ATTA  
 | ||||| |||||  
 T GTAACATACGTAC TAGT  
 GT A TTTATA  
 GAM1381 LOC90288 3' ATGACCACAGTGTGCTGTGTATG 62081 \_ \_ AATTACGT  
 CAT CATT GTATG TGTG  
 |||| |||||  
 GTAG CGTGT ACAC  
 TGT G CAGTA T  
 GAM1381 LOC90333 3' GACAAGGTTTTTGCATATAATG 62289 T ACGT  
 CAT GTGCATTGTATGTG GAATT  
 ||||| |||||  
 TACGTAATATACGT TTTGG  
 T AACAGT  
 GAM1381 LOC90488 3' ACAGTTCCATATGTATAATGTG 63031 TG \_ ACGT  
 C G CATTGTATGTGTG AATT  
 | ||||| |||||  
 C GTAATATGTATAC TTGA  
 GT C CA  
 GAM1381 LOC90488 3' CATATGTATAATGTGC 63032 TG  
 G CATTGTATGTGTG  
 | |||||  
 C GTAATATGTATAC  
 GT  
 GAM1381 LOC90520 3' ACGTAATAAAATGCAATGTGT 63141 TG GTGTGA  
 G CATTGTAT ATTACGT  
 | ||||| |||||

T GTAACGTA TAATGCA  
 GT AAA\_\_\_\_  
 GAM1381 LOC90844 3' ACGTAATTCATATATCTATATG 64207 TGT\_  
 C GCAT ATGTGTGAATTACGT  
 |||| |||||  
 CGTA TATATACTTAATGCA  
 TATC  
 GAM1381 LOC90906 5' GTGGTGTGCATGTGGTGT 64311 TG TG GA  
 GCAT TATG T ATTAC  
 |||| ||| | ||||  
 TGTG GTAC G TGGTG  
 GT GT\_\_\_\_  
 GAM1381 LOC91064 5' ACGTGAGGCTGTGTGATGC 64759 TG T GAA  
 GCAT TATG GT TTACGT  
 |||| |||| || |||||  
 CGTA GTGT CG AGTGCA  
 GT \_ G\_\_\_\_  
 GAM1381 LOC91064 5' ATGTGCGACATACGTGTGCGC 64760 TGT AAT  
 GTGCAT ATGTGTG TACGT  
 ||||| ||||| ||||  
 CGCGTG TGCATAC GTGTA  
 \_\_\_\_ AGC  
 GAM1381 LOC91138 5' ATGTATATATGTGCATATGTATG 65028 TG AT\_\_\_\_  
 ATATAT AT TATGTGTGA TACGT  
 || ||||| ||||  
 TA ATGTATACT ATGTA  
 GT GTATAT  
 GAM1381 LOC91138 5' TATATGTATGATGTAT 65031 TG  
 GTGCAT TATGTGTG  
 ||||| |||||  
 TATGTA ATGTATAT  
 GT  
 GAM1381 LOC91421 3' GTGTTTGTGCACATATGTGTGT 65993 \_\_\_\_ AAT\_ GT  
 GTGC CAT TGTATGTGTG TAC  
 || ||||| ||||  
 GTG GTATACACGT GTG  
 TGT GTTT  
 GAM1381 LOC91496 5' TATGTAATTTATGTAATGCATT 66225 T \_\_\_\_  
 CAGTGCAC TG ATGT GTGAATTACGT A  
 || |||| ||||| ||  
 AC TACG TATTTAATGTA T  
 T TAATG  
 GAM1381 LOC91565 5' GTTCCCTTGTGTGACGTGCAC 66465 TGTGAATT  
 GTGCATTGTATG AC  
 ||||| ||||  
 CACGTGACGTGT TG  
 TGTTCCCT  
 GAM1381 LOC91694 3' GTGTGTGTGCGTGCATGTGTGC 66964 TG \_ TG AAT  
 G CAT TGTATG TG TAC  
 | ||| |||| || |||

C GTG GCGTGC GT GTG  
 GT T GT GT\_  
 GAM1381 LOC91974 5' GTGTATTTGTGCACGTGTGTGT 67759 TG\_ \_ \_ GT  
 GTAC CAT TATGTGT GAAT TAC  
 ||| ||||| ||| |||  
 GTG GTGCACG TTTA GTG  
 TGT TG T  
 GAM1381 LOC92080 3' GTGTGAGCCTGCATGCATACAT 68056 G T AA\_ GT  
 GTGT CAT GTATGTGTG TTAC  
 ||| ||||| |||  
 GTA CATACGTAC AGTG  
 T \_ GTCCG TG  
 GAM1381 LOC92080 3' TACATGTGTGGTGCAC 68057 TG  
 GTGCAT TATGTGTG  
 ||||| |||||  
 CACGTG GTGTACAT  
 GT  
 GAM1381 LOC92080 3' TACGTGATCTATACGTGTGTGT 68058 G TG\_ A  
 GTGT CAT TATGTGTG ATTACGT A  
 ||| ||||| ||||| |  
 GTG GTGCATAT TAGTGCA T  
 T TGT C  
 GAM1381 LOC92218 3' GTGTATACATATATGTGTGTAT 68508 \_ AAT  
 GTGCAT TGTATGTGTG TAC  
 ||||| ||||| |||  
 TATGTG GTATATACAT GTG  
 T AT\_  
 GAM1381 LOC92661 5' ACGGCCGAGCATGATGGTGCAT 70076 TG A GAATTA  
 GTGCAT T TGTGT CGT  
 ||||| | ||||| |||  
 TACGTG A GTACG GCA  
 GT\_ AGCCG\_  
 GAM1381 LOC93052 5' ACGTGCCTCCCGCGTACGTGCG 71255 T T AT  
 TGCAT GTATGTG GA TACGT  
 ||||| ||||| || |||||  
 GCGTG CATGCGC CT GTGCA  
 \_ C CC  
 GAM1381 LOC93052 5' CGTACGTGCGTGGTGTGC 71259 TG TG AAT  
 GCAT TATG TG TACG  
 ||||| ||||| || |||||  
 CGTG GTGC GC ATGC  
 TG GT \_  
 GAM1381 LOC93052 5' CGTGATGTCGTGAGTGC 71260 T TGTGA  
 TGCATTG ATG ATTACG  
 ||||| ||||| |||||  
 GCGTGAC TGC TAGTGC  
 \_ TG\_  
 GAM1381 LOC93052 5' GCGTGGTGTGCATACATGCG 71263 T TG GA  
 TGCAT GTATG T ATTACGT  
 ||||| ||||| | |||||

GCGTA CATA C G TGGTGCG  
 \_ GT \_  
 GAM1381 LOC93297 3' TGTGATTCATGAGTGCA 71950 G  
 TGTAT TGTGAATTACG  
 ||||| |||||  
 ACGTG GTACTTAGTGT  
 A  
 GAM1381 LOC93613 3' CACGCATGGTGATGCAC 72696 TG\_  
 GTGCAT T ATGTGTG  
 ||||| | |||||  
 CACGTA G TACGCAC  
 GT G  
 GAM1382 GOSR2 3' CTCAGAGCCAGTCCT 53962 GAAA  
 AGGACTGGT TGAAG  
 ||||| |||||  
 TCCTGACCG ACTTC  
 AG\_  
 GAM1382 JRK 3' CATCTCCATTTCACGGG 86525 G A  
 CT GTGAAATG AGATG  
 || ||||| |||||  
 GG CACTTTAC TCTAC  
 G C  
 GAM1382 MYD88 3' CATCTTCACCCTCAGTTTCCTC 10167 C \_ TGAAA  
 A A AGGA CTGG TGAAGATG  
 | |||| ||| |||||  
 A TCCT GACT ACTTCTAC  
 C TT CCC\_  
 GAM1382 NIPSNAP1 3' CATCTCAAGGCCACCAGTCC 13290 AAA\_ A  
 GGACTGGTG TGA GATG  
 ||||| ||| |||||  
 CCTGACCAC ACT CTAC  
 CGGA \_  
 GAM1382 PGK1 3' ATCTTCACTGCACCCTG 4301 ACTG AAA  
 CAGG GTG TGAAGAT  
 |||| ||| |||||  
 GTCC CAC ACTTCTA  
 \_ GTC  
 GAM1382 PRG2 5' ATCTTCATCTCTGTCT 10777 T T AA  
 GGAC GG GA TGAAGAT  
 |||| || || |||||  
 TCTG TC CT ACTTCTA  
 \_ T \_  
 GAM1382 TCFL4 3' CATCCTGCAGTCCCCACCAGTC 63460 AAA\_ AA\_  
 CTG CAGGACTGGTG TG GATG  
 ||||| || |||||  
 GTCCTGACCAC AC CTAC  
 CCCTG GTC  
 GAM1382 TZFP 5' ATCTTCACCCCCACCTCC 26889 CT AAA\_  
 GGA GGTG TGAAGAT  
 || |||| |||||

CCT CCAC ACTTCTA  
 \_ CCCC  
 GAM1382 WHN 3' CATCTTCATCCCAACAGCCC 13171 A G AA  
 GG CTG TG ATGAAGATG  
 || ||| || |||||  
 CC GAC AC TACTTCTAC  
 C A CC  
 GAM1382 AP1GBP1 3' CATCCCCACGGCCAGTCT 23391 GAAA AA  
 GGA CTG TG GATG  
 ||||| || |||  
 TCTGACCG AC CTAC  
 GC\_ CC  
 GAM1382 AP1GBP1 3' CATCCCCACGGCCAGTCT 54517 GAAA AA  
 GGA CTG TG GATG  
 ||||| || |||  
 TCTGACCG AC CTAC  
 GC\_ CC  
 GAM1382 BTN2A1 3' ATCTTCATCTGCCCTG 54339 ACTG GAA  
 CAGG GT ATGAAGAT  
 ||| || |||||  
 GTCC CG TACTTCTA  
 \_ TC\_  
 GAM1382 C20orf116 3' CATCTTCATCCCTCCCCACC 43737 AC T A\_  
 GG TGG GA ATGAAGATG  
 || ||| || |||||  
 CC ACC CT TACTTCTAC  
 \_ C CCC  
 GAM1382 CALN1 3' CATCTTCATCTCGGAATTCC 48858 CTGG A  
 GGA TGA ATGAAGATG  
 ||| ||| |||||  
 CCT GCT TACTTCTAC  
 TAAG C  
 GAM1382 DNAJA2 3' CATCTTCATTTTGAAGTTCC 59780 CT \_  
 GGA GGT GAAATGAAGATG  
 ||| ||| |||||  
 CCT TCA TTTTACTTCTAC  
 TG G  
 GAM1382 FLJ22055 3' CATCTTCACTCTCCACCCC 45493 AC T AA  
 GG TGG GA TGAAGATG  
 || ||| || |||||  
 CC ACC CT ACTTCTAC  
 CC T C\_  
 GAM1382 FLJ22167 5' CATCTTCATTATAATAACCCCC 44568 ACT GA\_\_\_\_  
 C GG GGT AATGAAGATG  
 || ||| |||||  
 CC CCA TTACTTCTAC  
 CC\_ ATAATA  
 GAM1382 HN1L 3' CTTCAATTTTACCCCC 57996 ACT  
 GG GGTGAAATGAAG  
 || |||||



CC CCATTTTACTTC  
 C\_  
 GAM1382 HSPC059 3' CATCTCCATTTACCATATCCT 33293 C\_ A  
 AGGA TGGTCAAATG AGATG  
 ||| ||||| |||  
 TCCT ACCACTTTAC TCTAC  
 AT C  
 GAM1382 KIAA0478 3' CATCTTCATCCCCTTCCT 29543 CT T AA  
 AGGA GG GA TGAAGATG  
 ||| || |||||  
 TCCT CC CT ACTTCTAC  
 TC \_ \_  
 GAM1382 KIAA1373 5' ATCCTCATTTTCACAG 70929 G A  
 CTG TGAAATGA GAT  
 || ||||| ||  
 GAC ACTTTACT CTA  
 \_ C  
 GAM1382 KRT6IRS 3' CATCTCCACCCTGCTGGTCCTG 53086 TG AAA A  
 CAGGAC GTG TG AGATG  
 ||||| || |||||  
 GTCCTG CGT AC TCTAC  
 GT CCC C  
 GAM1382 MGC15631 3' TCACACACCAAGTCCTGTG 51269 AAA  
 TACAGGACTGGTG TGA  
 ||||| ||||| ||  
 GTGTCCTGACCAC ACT  
 AC\_  
 GAM1382 MUC17 3' CATCTTCATGAAAAACACCTGT 94272 AC GTGAA\_  
 A TACAGG TG ATGAAGATG  
 ||||| || |||||  
 ATGTCC AC TACTTCTAC  
 \_ AAAAAG  
 GAM1382 NPC1L1 3' CATCTTCACCTCGGGCCTG 25412 A TGAAA  
 CAGG CTGG TGAAGATG  
 ||| ||| |||||  
 GTCC GGCT ACTTCTAC  
 G CC\_  
 GAM1382 OR7C1 5' CTGCAGTTCACCAGCC 82429 A A A  
 GG CTGGTGAA TG AG  
 || ||||| || ||  
 CC GACCACTT AC TC  
 \_ G G  
 GAM1382 PRPF8 3' CATCTTCATCTTCAACC 61185 \_ \_  
 GGT GAA ATGAAGATG  
 ||| || |||||  
 CCA CTT TACTTCTAC  
 A C  
 GAM1382 TIAF1 3' CATCTCCATCTTCACCCTTC 54326 CT \_ A  
 GA GGTGAA ATG AGATG  
 || ||||| || |||||

CT CCACTT TAC TCTAC  
 TC C C  
 GAM1382 LOC127428 3' CTATATTTCACCACCCTG 74665 AC A  
 CAGG TGGTCAAATG AG  
 ||| ||||| ||  
 GTCC ACCACTTTAT TC  
 C\_ A  
 GAM1382 LOC145264 5' TCTTCATCCTTCCTG 77050 CT TGAA  
 CAGGA GG ATGAAGA  
 ||| || |||||  
 GTCCT CC TACTTCT  
 T\_ \_\_\_\_  
 GAM1382 LOC145786 5' CATCTTCAAAGCCAGCCATGTA 83490 \_ A GAAA  
 TACA GG CTGGT TGAAGATG  
 ||| || |||| |  
 ATGT CC GACCG ACTTCTAC  
 A \_ AA\_  
 GAM1382 LOC146669 3' CATCCTCACCAATCCTG 78055 C A\_  
 CAGGA TGGTGA ATG  
 ||| |||| |  
 GTCCT ACCACT TAC  
 A CC  
 GAM1382 LOC152273 3' CATCTTCATGAATGGAATCCTT 80535 C CTGGTGAA  
 A A AGGA ATGAAGATG  
 | ||| |||||  
 A TCCT TACTTCTAC  
 T AAGGTAAG  
 GAM1382 LOC152274 3' CTTCAATTTTAACCCCC 80507 ACT \_  
 GG GGT GAAATGAAG  
 || ||| |||||  
 CC CCA TTTTACTTC  
 C\_ A  
 GAM1382 LOC158364 5' TCCCGCACCAACAGTCCTGTA 81877 \_\_\_\_ AAAT  
 TACAGGACT GGTG GA  
 ||||| ||| ||  
 ATGTCCTGA CCAC CT  
 CAA GCC\_  
 GAM1382 LOC203052 3' CATCTTGTGGGACCAGTCCTG 90451 GAA G  
 CAGGACTGGT AT AAGATG  
 ||||| || |||||  
 GTCCTGACCA TG TTCTAC  
 GGG \_  
 GAM1382 LOC221813 5' ATCTTCATCTCAGCTA 93935 \_ A  
 TGG TGA ATGAAGAT  
 ||| ||| |||||  
 ATC ACT TACTTCTA  
 G C  
 GAM1382 LOC222234 3' ATCTTCACTTCAAGCTC 94243 GA GG A  
 G CT TGAA TGAAGAT  
 | || |||| |||||

C GA ACTT ACTTCTA  
 TC \_ C  
 GAM1383 CHST6 3' GAGGTCTGTACATCACATACAT 41230 C CTT CC  
 A TGTG ATG TG ACAGACCTC  
 ||||| || |||||  
 ATAC TAC AC TGTCTGGAG  
 A ACT A\_  
 GAM1383 PCDH11X 3' TCTGTGGCTGTTTACA 27242 CAT TTT  
 TGTG GC GCCACAGA  
 ||||| || |||||  
 ACAC TG CGGTGTCT  
 T\_ T\_  
 GAM1383 SALL1 3' GTCTGTATATACATGTACA 11433 CTTTGCC  
 TGTGCATG ACAGAC  
 ||||| |||||  
 ACATGTAC TGTCTG  
 ATATA\_  
 GAM1383 SLC9A3R1 3' AGACCTGTGGCAGACAC 70420 CATGC AC  
 GTG TTTGCCACAG CT  
 ||| ||||| ||  
 CAC AGACGGTGTC GA  
 \_ CA  
 GAM1383 SORCS3 3' CTGCAGAAAGCATGCACA 30372 GCCA  
 TGTGCATGCTTT CAG  
 ||||| ||||| ||  
 ACACGTACGAAA GTC  
 GAC\_  
 GAM1383 DCOHM 3' AGTCTATGGAAATGCTCA 49591 T GCTTTG C C  
 TG GCAT CCA AGAC T  
 || |||| || |||| |  
 AC CGTA GGT TCTG A  
 T AA\_ A A  
 GAM1383 FLJ25416 3' TCTGTGGCTTACAATGCCA 58814 T GCTTT  
 TG GCAT GCCACAGA  
 || |||| |||||  
 AC CGTA CGGTGTCT  
 \_ ACATT  
 GAM1383 HSA250839 3' GAGACCTTAGGCAAAGCATGCA 37259 AC AC  
 TGCATGCTTTGCC AG CTC  
 ||||| || |||||  
 ACGTACGAAACGG TC GAG  
 AT CA  
 GAM1383 KIAA1643 3' GAGGCCTGTGGCTTCTGCAC 64551 TGCTTT A  
 GTGCA GCCACAG CCTC  
 ||||| ||||| |||||  
 CACGT CGGTGTC GGAG  
 CTT\_ C  
 GAM1383 KIAA1915 3' AGGTCTGTGACATGCA 73275 CTTTGC  
 TGCATG CACAGACCT  
 ||||| |||||

ACGTAC GTGTCTGGA  
 A\_\_\_\_  
 GAM1383 MGC13251 3' TGTGGCAAACACGCACA 51149 A C  
 TGTGC TG TTTGCCACA  
 ||||| || |||||  
 ACACG AC AAACGGTGT  
 C \_  
 GAM1383 MGC29891 5' AGGCCCCCAAACATGCACA 58199 C CCACAGA  
 TGTGCATG TTTG CCT  
 ||||| ||| |||  
 ACACGTAC AAAC GGA  
 A CCCC\_\_\_\_  
 GAM1383 MR 3' GTGCAGCAAAGCACAC 48324 CA \_  
 GTG TGCTTTGC CAC  
 ||| ||||| |||  
 CAC ACGAAACG GTG  
 \_ AC  
 GAM1383 PACSIN2 3' GAAGTCTGTGGCATTTCAGGCAC 23341 A CTT C  
 A TGTGC TG TGCCACAGAC TC  
 ||||| || ||||| |||  
 ACACG AC ACGGTGTCTG AG  
 G TT\_ A  
 GAM1383 ZFD25 3' GAAGTCTGTGGCAAAGC 32580 C  
 GCTTTGCCACAGAC TC  
 ||||| ||||| |||  
 CGAAACGGTGTCTG AG  
 A  
 GAM1383 LOC123691 5' TTGTGAAAAGCATGCACA 75620 GC  
 TGTGCATGCTTT CACAG  
 ||||| ||||| |||  
 ACACGTACGAAA GTGTT  
 A\_  
 GAM1383 LOC124538 3' AGATCATGGGCAATGCATGCAC 75648 T A \_ C  
 A TGTGCATGC TTGCC CA GA CT  
 ||||| ||||| ||| |||  
 ACACGTACG AACGG GT CT GA  
 T \_ A A  
 GAM1383 LOC125434 3' AGGTCTGTGTGAAACACACA 74406 CA C TG C  
 TGTG TG TT C ACAGACCT  
 ||| ||| | |||||  
 ACAC AC AA G TGTCTGGA  
 \_ A GT\_  
 GAM1383 LOC128582 5' GTTCACAGCAAAGCACGCAC 75784 A CACA  
 GTGC TGCTTTGC GAC  
 ||| ||||| |||  
 CACG ACGAAACG TTG  
 C ACAC  
 GAM1383 LOC150287 3' GTCACAGCAAAGCAACACA 79783 CA CACA  
 TGTG TGCTTTGC GAC  
 ||| ||||| |||

			ACAC ACGAAACG CTG		
			A_ ACA_		
GAM1383	LOC220514	3'	GAAGTCTGTGGCATTTCAGGCAC 60446	A CTT	C
		A	TGTGC TG TGCCACAGAC TC		
			ACACG AC ACGGTGTCTG AG		
			G TT_ A		
GAM1384	DRD4	3'	CCTGATGGCCAGGCCTCAGGGA 5846	AC AA	G G
			TCCCTGAG CCT CTA T AGG		
			AGGGACTC GGA GGT A TCC		
			C_ CC _G		
GAM1384	IL16	5'	CCCACTAGTTTACACCACAGG 15714	AGACCCT	A
			CCTG AACTAGTG GG		
			GGAC TTGATCAC CC		
			ACCACAT _		
GAM1384	ITPKB	3'	CGATTAGCAGCCTCAGGGA 9426	ACC AA	GA
			TCCCTGAG CT CTAGT G		
			AGGGACTC GA GATTA C		
			C_ C_ G_		
GAM1384	LFG	5'	CACCCGGGCCTCAGGGA 76714	A TAACTA	
			TCCCTGAG CCC GTG		
			AGGGACTC GGG CAC		
			C CC_		
GAM1384	MLC1	3'	CCTCACTGAGAAGGCCCCAGGG 30779	AGAC AAC	
			CCCTG CCT TAGTGAGG		
			GGGAC GGA GTCACTCC		
			CCC_ AGA		
GAM1384	MLC1	3'	CCTCACTGAGAAGGCCCCAGGG 57591	AGAC AAC	
			CCCTG CCT TAGTGAGG		
			GGGAC GGA GTCACTCC		
			CCC_ AGA		
GAM1384	REQ	3'	CCTCTGGCCCCAGGCCCTCAGG 20769	AC AACTAGT	
		GA	TCCCTGAG CCT GAGG		
			AGGGACTC GGA CTCC		
			CC CCCCCGT		
GAM1384	BMF	3'	CTCCAGCAGACCTCAGGGA 53155	ACC AA	AGT
			TCCCTGAG CT CT GAG		
			AGGGACTC GA GA CTC		
			CA_ C_ C_		
GAM1384	DKFZp434F1719	3'	CCTCACTAGCCAGGGTGTT 49998	G AA	
			GA ACCCT CTAGTGAGG		

TT TGGGA GATCACTCC  
 G CC  
 GAM1384 DKFZP434P211 3' CCGTGCTAGAGTCCTCAGGGA 27262 \_ CCTAA GA  
 TCCCTGAG AC CTAGT GG  
 ||||| || |||| ||  
 AGGGACTC TG GATCG CC  
 C A\_\_\_\_ TG  
 GAM1384 EZFIT 3' CTTACTGAGCCTCAG 41107 ACC AAC  
 CTGAG CT TAGTGAG  
 |||| || |||||  
 GACTC GA GTCATTC  
 C\_\_ \_\_  
 GAM1384 FLJ00024 5' CTCAAAGGGTCTCCAG 63759 \_ AACTAG  
 CTG AGACCCT TGAG  
 || ||||| |||  
 GAC TCTGGGA ACTC  
 C A\_\_\_\_  
 GAM1384 FLJ12934 3' CCTCTCTCAGGGTCTCA 43199 AACT T  
 TGAGACCCT AG GAGG  
 ||||| || |||  
 ACTCTGGGA TC CTCC  
 C\_\_ T  
 GAM1384 FLJ22635 3' CCTCCAGCCAGGCTCTCAGGGA 46980 C AA AGT  
 TCCCTGAGA CCT CT GAGG  
 ||||| ||| || |||  
 AGGGACTCT GGA GA CTCC  
 C CC C\_\_  
 GAM1384 FLJ25124 3' CCTCACTGTGTGCCCTCAGGGA 58452 ACCCTA \_  
 TCCCTGAG AC TAGTGAGG  
 ||||| || |||||  
 AGGGACTC TG GTCACTCC  
 CCG\_\_ T  
 GAM1384 FLJ32384 3' GCTGGGTCTCAAGGA 58160 C TAACT  
 TCC TGAGACCC AGT  
 || ||||| |||  
 AGG ACTCTGGG TCG  
 A \_\_\_\_  
 GAM1384 HSH2 3' CCTCAGAGCAAGGCCCTCAGGG 51674 AC AA AG  
 A TCCCTGAG CCT CT TGAGG  
 ||||| ||| || |||  
 AGGGACTC GGA GA ACTCC  
 CC AC G\_  
 GAM1384 HSJ1 3' CACAAATCAGGGCTCAGGGA 22126 A AACTA  
 TCCCTGAG CCCT GTG  
 ||||| ||| |||  
 AGGGACTC GGGA CAC  
 \_ CTA  
 GAM1384 KIAA0367 3' CCTCACTGTATAATTGAG 67296 ACCCTA T  
 CTGAG AC AGTGAGG  
 |||| || |||||

				GACTT	TG TCACTCC		
				AATA__ _			
GAM1384	KIAA0450	3'	CCCACCAGCTCTTCTCAGGGA	27626		CCCTAA A A	
			TCCCTGAGA	CT GTG GG			
			AGGGACTCT	GA CAC CC			
			TCTC__ C _				
GAM1384	KIAA0930	3'	CTCACTGAAGTCCCAGGG	70541	A	CCTAAC	
			CCCTG GAC	TAGTGAG			
			GGGAC CTG	GTCAC TC			
			C AA__				
GAM1384	KIAA1319	3'	CCTTAACCCTAAGGCTCAGGGA	40406	A C	ACTAG	
			TCCCTGAG CC TA	TGAGG			
			AGGGACTC GG AT	ATTCC			
			_ A CCCA_				
GAM1384	KIAA1656	3'	CCACACCTGGAGGCATCTCAGG	65785	C_ AA	_ A	
	GA		TCCCTGAGA CCT	CTAG TG GG			
			AGGGACTCT GGA	GGTC AC CC			
			AC _ C A				
GAM1384	P24B	3'	CCTCAGCAGCTGAAGGTCTCAG	23749	C	CTAA_ AG	
	AGA		TC CTGAGACC	CT TGAGG			
			AG GACTCTGG	GA ACTCC			
			A AAGTC CG				
GAM1384	PHRET1	5'	CCTTATCTCTAAGGCGCTCAGG	41056	AC	AACTA	
	GA		TCCCTGAG CCT	GTGAGG			
			AGGGACTC GGA	TATTCC			
			GC ATCTC				
GAM1384	RBT1	3'	CACTGGGGCCTCAGGGA	25350	A	AACT	
			TCCCTGAG CCCT	AGTG			
			AGGGACTC GGGG	TCAC			
			C _				
GAM1384	SLC4A3	3'	CCTCAGAGACCCCAAGACCTTA	17388	ACCCTAA__	AG	
	GGA		TCCCTGAG	CT TGAGG			
			AGGGATTC	GA ACTCC			
			CAGAACCCCA G_				
GAM1384	STK36	3'	TCACGGACCTTAGGGA	72106	AC	TAATA	
			TCCCTGAG CC	GTGA			
			AGGGATTC GG	CACT			
			CA _				
GAM1384	TU3A	3'	CTCCTAGGTCTCAGAGA	23188	C	CTAAC T	
			TC CTGAGACC	TAG GAG			

		AG GACTCTGG	ATC CTC	
		A _____		
GAM1384	UBCE7IP5 3'	TCATGGTCTCAGGGA	30160	CTAACTA
		TCCCTGAGACC	GTGA	
		AGGGACTCTGG	TACT	
		_____		
GAM1384	ZNF238 5'	CTGATTAAAATTCAGGGA	20960	ACCCTAAC G
		TCCCTGAG	TAGT AG	
		AGGGACTT	ATTA TC	
		AAA_____ G		
GAM1384	LOC112868 3'	CCTCCAAGGACCAGGTCTCAGA	72893	C CTAA_ AGT
	GA	TC CTGAGACC	CT GAGG	
		AG GACTCTGG	GA CTCC	
		A ACCAG AC_		
GAM1384	LOC116236 3'	CCTCACTGGAGAGATCCCAAGG	73810	GA_ CC AA
	G	CCCT GA CT CTAGTGAGG		
		GGGA CT GA GGTCACTCC		
		ACC A_ GA		
GAM1384	LOC146184 3'	CCTCACTAGCGTACTCTCA	83620	CCCTAA
		TGAGA CTAGTGAGG		
		ACTCT GATCACTCC		
		CATGC_		
GAM1384	LOC148183 5'	CCTGGGAGTCGGGGTCTCAGAG	84117	C TA AGTG
	A	TC CTGAGACCC ACT AGG		
		AG GACTCTGGG TGA TCC		
		A GC GGG_		
GAM1384	LOC149722 5'	CCTCACTATCTAGATCCCA	84598	A CC AC
		TG GA CTA TAGTGAGG		
		AC CT GAT ATCACTCC		
		C A_ CT		
GAM1384	LOC150174 3'	CCGTGCTAGAGTCCTCAGGGA	79606	_ CCTAA GA
		TCCCTGAG AC CTAGT GG		
		AGGGACTC TG GATCG CC		
		C A_____ TG		
GAM1384	LOC150213 3'	CCGTGCTAGAGTCCTCAGGGA	74853	_ CCTAA GA
		TCCCTGAG AC CTAGT GG		
		AGGGACTC TG GATCG CC		
		C A_____ TG		
GAM1384	LOC150236 5'	CCGTGCTAGAGTCCTCAGGGA	79686	_ CCTAA GA
		TCCCTGAG AC CTAGT GG		



AGGGACTC TG GATCG CC  
 C A\_\_\_\_\_ TG  
 GAM1384 LOC203292 3' CCTCACTAGCCAGGGTGT 90511 G AA  
 GA ACCCT CTAGTGAGG  
 || |||| |||||  
 TT TGGGA GATCACTCC  
 G CC  
 GAM1384 LOC219743 3' CCCACAGCCTGGGTCTCAGGGA 93126 TAA A A  
 TCCCTGAGACCC CT GTG GG  
 ||||| || |||  
 AGGGACTCTGGG GA CAC CC  
 TCC \_ \_  
 GAM1384 LOC221830 3' CTCCTAGTCACCAGTGA 92508 C AGACCCTA  
 TC CTG ACTAGTGAG  
 || || |||||  
 AG GAC TGATCACTC  
 T CAC\_\_\_\_\_  
 GAM1384 LOC222134 3' CTCCTTGGTTTCAGG 94137 CTA ACT  
 CCTGAGACC AGTGAG  
 ||||| |||||  
 GGACTTTGG TCACTC  
 T\_\_\_\_\_  
 GAM1384 LOC253650 3' CCTCACTAGCCAGGGTGT 96164 G AA  
 GA ACCCT CTAGTGAGG  
 || |||| |||||  
 TT TGGGA GATCACTCC  
 G CC  
 GAM1384 LOC90288 3' CTCTCTCAGAGCTCAGGGA 62093 ACC AACT T  
 TCCCTGAG CT AG GAG  
 ||||| || |||  
 AGGGACTC GA TC CTC  
 GA\_ C\_\_ T  
 GAM1385 ABCC12 3' CTTGGGGTTGGTTCTGGGTGGT 52646 G TAAGT\_  
 GAA TTCATCACT GG CTCCAAG  
 ||||| || |||||  
 AAGTGGTGG TC GGGGTTC  
 G TTGGTT  
 GAM1385 ADAMTS1 3' TTGAGATCACTTGTCTTGTGGT 22761 T GT C\_ \_ G  
 GG TCATCAC GG AAGT TC CAA  
 ||||| || ||| |||  
 GGTGGTG TC TTCA AG GTT  
 T TG CT A  
 GAM1385 AFG3L2 3' TTTGGAGATGTTTCGTTGGTGTG 96734 T TG GTAA\_  
 G TCA CAC G GTCTCCAAG  
 ||| || | |||||  
 GGTGTG T TAGAGGTTT  
 \_ GT GCTTG  
 GAM1385 AKAP13 5' CTTGGCTCTTCTTATTCGAGTG 58578 \_ TCT\_  
 ATGAG ATCACT GGGTAAG CCAAG  
 ||||| ||||| |||||

			TAGTGA CTTATTC GGTTC G TTCTC	
GAM1385 ARF4L	3'	CTTGGAGAATGTGTTTGGGATG 69813	A GG AG_	
AA		TTCATC CTG TA TCTCCAAG		
		AAGTAG GGT GT AGAGGTTC		
		_ TT GTA		
GAM1385 ARF4L	3'	TTGGGGGCGGGGGGATGGA 69818	A GGGTAA	
		TTCATC CT GTCTCCAA		
		AGGTAG GG CGGGGGTT		
		_ GGG_		
GAM1385 ARSD	3'	TTTGCTCATGGTGGGA 23800	C	
		TTCATCA TGGGTAAG		
		AGGTGGT ACTCGTTT		
		-		
GAM1385 C14orf1	3'	TTTGGGGGTGGGAAGAGATGG 23182	A GGGTAA	
		TCATC CT GTCTCCAAG		
		GGTAG GA TGGGGGTTT		
		A AGGG_		
GAM1385 C21orf2	3'	CTTGGGGAAGCCCAGGGTGAA 17011	A AAG	
		TTCATC CTGGGT TCTCCAAG		
		AAGTGG GACCCG AGGGGTTC		
		_ A_		
GAM1385 C5R1	3'	CTTGGAGGTGGAGGTTGTGGTG 8205	TGGGTAAG	
AG		TTCATCAC TCTCCAAG		
		GAGTGGTG GGAGGTTC		
		TTGGAGGT		
GAM1385 CCNA1	5'	TTTGGGGCCTCCTGTCTGGTGG 14036	A TG GT_ T	
GAG		TC TCAC G A AG CTCCAAG		
		AG GGTG C T TC GGGGTTT		
		_ GT TG CC C		
GAM1385 CDKN2A	5'	TTGGAGGTCCGGGTGGGAG 54232	A G TAAG	
		TTC TCACT GG TCTCCAA		
		GAG GGTGG CC GGAGGTT		
		_ G T_		
GAM1385 CENTD2	3'	TTGGGGACTTTTTGAT 57560	CTGGGT	
		ATCA AAGTCTCCAA		
		TAGT TTCAGGGGTT		
		TT_		
GAM1385 CENTD2	3'	TTGGGGACTTTTTGAT 30879	CTGGGT	
		ATCA AAGTCTCCAA		

		TAGT TTCAGGGGTT	
		TT____	
GAM1385 CHST6	3'	CAAGGGTTGTGTCCAGTGATGG 41223	GT AGT CAAG
A		TTCATCACTGG A CTC	
		AGGTAGTGACC T GGG	
		TG GTT AAC	
GAM1385 CNN3	3'	TTTATTCAGTGAGAA 59306 A	
		TTC TCACTGGGTAAG	
		AAG AGTGACTTATTT	
		—	
GAM1385 COL4A4	5'	TTTGGGGGTGTGCGGTGGGGAG 3630	AT GG AG
		TTC CACT GTA TCTCCAAG	
		GAG GTGG CGT GGGGGTTT	
		GG _ GT	
GAM1385 CPO	3'	TTTGGATGCTGTCACTGATGAA 3639	GTA C
		TTCATCACTGG AGT TCCAAG	
		AAGTAGTGACT TCG AGGTTT	
		G_ T	
GAM1385 DPYSL3	3'	TTTGGGGTGAGTGGGTGGTGG 7320	GGGTAAGT
		TCATCACT CTCCAAG	
		GGTGGTGG GGGGTTT	
		GTGAGT__	
GAM1385 DYRK1A	5'	TTGGGGGAGCGGTTGTGAG 55255	C GGTAAG
		TTCAT ACTG TCTCCA	
		GAGTG TGGC GGGGGTT	
		T GA__	
GAM1385 ED1	3'	TTTGGGGGTCAGCATCCAGTGT 7377	T AAG__
GAG		TCA CACTGGGT TCTCCAAG	
		AGT GTGACCTA GGGGGTTT	
		_ CGACT	
GAM1385 EEF1A1	3'	CTTAATCAGTGGTGGGA 7387	GG
		TTCATCACTG TAAG	
		AGGTGGTGAC ATTC	
		TA	
GAM1385 EGFL5	5'	CTTGCTCAGTGATGAG 86619	
		TTCATCACTGGGTAAG	
		GAGTAGTGACTCGTTC	
GAM1385 EGR3	3'	GATTTTTGGTGGTGGGA 59555	TG GT
		TTCATCAC G AAGTC	

AGGTGGTG T TTTAG  
 GT\_\_  
 GAM1385 EIF2C1 3' CTTGGATCTATCCTGATCTGGT 24175 TG A TC\_\_\_\_  
 GATGAA TCAC GGT AG TCCAAG  
 |||| ||| || |||||  
 AGTG CTA TC AGGTTC  
 GT G CTATCT  
 GAM1385 EIF4G1 5' TTGGGGACTGCTGGTGG 17072 TG GTA  
 TCAC G AGTCTCCAA  
 |||| | |||||  
 GGTG C TCAGGGGTT  
 GT G\_\_  
 GAM1385 EYA2 3' TTTGGGGGGGTGCCTGGTGATGA 17889 TG AG  
 G TTCATCAC GGTA TCTCCAAG  
 ||||| ||| |||||  
 GAGTAGTG CCGT GGGGGTTT  
 GT G\_  
 GAM1385 FGF2 3' CTTGGAGGCTTATCTA 8870  
 TGGGTAAGTCTCCAAG  
 |||||  
 ATCTATTCGGAGGTTC  
  
 GAM1385 FOSB 3' TTTGGGGACAGGGGGTGGGAA 22113 A GGGTAA  
 TTC TCACT GTCTCCAAG  
 ||| |||| |||||  
 AAG GGTGG CAGGGGTTT  
 \_ GGGA\_\_  
 GAM1385 FZD1 3' CTTGCTCGGCGGTGGA 13034 A  
 TTCATC CTGGGTAAG  
 ||||| |||||  
 AGGTGG GGCTCGTTC  
 C  
 GAM1385 FZD4 3' CTTGTATTTTGTCTGTGATGG 24140 T GG TCTC  
 A TTCATCAC G TAAG CAAG  
 ||||| | ||| |||  
 AGGTAGTG C GTTT GTTC  
 T TT TAT\_  
 GAM1385 GAB2 3' TTGGAGCTCGGGTGGTGG 24508 G GTA T  
 TTCATCACT G AG CTCCAA  
 ||||| | |||||  
 AGGTGGTGG C TC GAGGTT  
 G \_\_ \_  
 GAM1385 GAB2 3' TTGGGGGTGCAGGGTGG 24509 A G TAAG  
 TTCATC CTG G TCTCCAA  
 ||||| ||| | |||||  
 AGGTGG GAC T GGGGGTT  
 \_ G \_\_\_\_  
 GAM1385 GAB2 3' TTGGAGCTCGGGTGGTGG 54465 G GTA T  
 TTCATCACT G AG CTCCAA  
 ||||| | |||||

			AGGTGGTGG C TC GAGGTT		
			G _ _		
GAM1385	GAB2	3'	TTGGGGGTGCAGGGTGG 54466	A	G TAAG
			TTCATC CTG G TCTCAA		
			AGGTGG GAC T GGGGGTT		
			_ G _		
GAM1385	GHR	3'	TTTGGGGGAGTGACAGGATGG 3892	A	GG AG
			TCATC CTG TA TCTCCAAG		
			GGTAG GAC GT GGGGGTTT		
			_ A_ GA		
GAM1385	HIVEP3	3'	TTTGGGGAAAGGCTGATGGTGA 44441	CTG	AAG
	A		TTCATCA GGT TCTCCAAG		
			AAGTGGT TCG AGGGGTTT		
			AG_ GAA		
GAM1385	HOXC9	3'	GGAGGGTTTCAGTGTGAG 61265	T	GG AAG
			TTCA CACTG T TCTCC		
			GAGT GTGAC G GGAGG		
			T TT _		
GAM1385	HOXD3	3'	CTTGCTGTAGTGGTGG 22574	_	
			TCATCACTG GGTAAG		
			GGTGGTGAT TCGTTC		
			G		
GAM1385	INHBB	3'	TGGGGACGGGTGGGAA 9345	A	GGGTAA
			TTC TCACT GTCTCCA		
			AAG GGTGG CAGGGGT		
			_ G _		
GAM1385	ITGA1	3'	TTTATCTAGGATGGA 63539	A	
			TTCATC CTGGGTAAG		
			AGGTAG GATCTATTT		
			-		
GAM1385	ITGB7	3'	TGGAGGACAGTGGGAA 6089	A	GGTAAGT
			TTC TCACTG CTCCA		
			AAG GGTGAC GAGGT		
			_ AG _		
GAM1385	JTB	3'	TTGGAGCCTTGTGGTGG 21964	T	TAAGT
			TTCATCAC GGG CTCCA		
			AGGTGGTG TCC GAGGTT		
			T _		
GAM1385	KCNS2	3'	GGCTTACCCAGGATGGA 68313	A	
			TTCATC CTGGGTAAGTC		

AGGTAG GACCCATTCGG

GAM1385 KIF3B 3' TTTGGGACCTGCTCAGTGAGGA 16618 A A T  
A TTC TCACTGGGTA GTC CCAAG

||| ||||| ||| |||||  
AAG AGTGA CTCGT CAG GGTTT  
G C \_

GAM1385 LEP 3' CTTGGGGGGTTTTTACTCCAGT 4049 \_ \_  
GGTGAA TCACTGG GTAAG TCTCCAAG

||||| ||||| |||||  
GGTGACC CATTG GGGGGTTC  
T TTG

GAM1385 LMO2 3' TTTGGGGGGTTTGAGGGTGG 18742 GGG GT  
TCACT TAA CTCCAAG

||||| ||| |||||  
GGTGG GTT GGGGTTT  
GA\_ TG

GAM1385 LYAAT1 5' TTTGGGGGGTTTGCTCCAG 54350 \_ GT  
CTGG GTAA CTCCAAG

||||| ||| |||||  
GACC CGTT GGGGTTT  
T TG

GAM1385 MMP26 3' CTTGGGGACTGCTAGGATGAA 41438 A GTA  
TTCATC CTGG AGTCTCCAAG

||||| ||| |||||  
AAGTAG GATC TCAGGGGTTC  
\_ G\_

GAM1385 MUC4 3' CTTGCTCAGTGAAGAG 56326 A  
TTC TCACTGGGTAAG

||| |||||  
GAG AGTGA CTCGTT  
A

GAM1385 MUCDHL 3' GCTTCTCGGTGGTGGG 87303 T  
TTCATCACTGGG AAGT

||||||| |||  
AGGTGGTGGCTC TTCG

GAM1385 MUCDHL 3' GCTTCTCGGTGGTGGG 48373 T  
TTCATCACTGGG AAGT

||||||| |||  
AGGTGGTGGCTC TTCG

GAM1385 NFRKB 5' AGCCTTGTTTCAGTGGGGAG 20493 AT GG T  
TTC CACTG TAAG CT

||| ||||| ||| ||  
GAG GTGAC GTTC GA  
GG TT C

GAM1385 NLGN2 5' GCTTCCCGGTGGTGGG 88157 T  
TTCATCACTGGG AAGT

||||||| |||

AAGTGGTGGCCC TTCG

GAM1385 NR3C1 3' ACTTTTCAGTGATGG 3920 T  
TCATCACTGGG AAGT  
||||||| |||  
GGTAGTGACTT TTCA

GAM1385 PDE4D 3' TTTGGAAACTCTTGGTGAGAG 73585 A TG TA C  
TTC TCAC GG AGT TCCAAG  
||| ||| || ||| |||  
GAG AGTG TC TCA AGGTTT

GAM1385 PFN2 3' TTGGCTGTCTTGTGATGAA 53829 T GT AGTCT  
TTCATCAC GG A CCAA  
||||||| || | |||  
AAGTAGTG TC T GGTT  
T TG C\_\_\_\_

GAM1385 PFN2 3' TTGGCTGTCTTGTGATGAA 10530 T GT AGTCT  
TTCATCAC GG A CCAA  
||||||| || | |||  
AAGTAGTG TC T GGTT  
T TG C\_\_\_\_

GAM1385 PIWIL1 3' TTTGGAGATTTACTTA 72825  
TGGGTAAGTCTCCAAG  
|||||||  
ATTCATTTAGAGGTTT

GAM1385 PLAGL1 3' GGCTTATTCAGTGATGA 10614  
TCATCACTGGGTAAGTC  
|||||||  
AGTAGTGACTTATTCGG

GAM1385 PODXL 3' TTTGGAGGTGGGCAGGATGGA 18246 A GG AG  
TTCATC CTG TA TCTCCAAG  
||||| ||| || |||  
AGGTAG GAC GT GGAGGTTT  
\_ GG \_

GAM1385 PPP3CB 3' CTTGGGGCAATTTCCAGTGGAG 40899 AT TAAGT  
G TC CACTGGG CTCCAAG  
|| ||||| |||||  
GG GTGACCT GGGGTTC  
AG TTAAC

GAM1385 PRPS2 3' TTGGGGAAATGGTGGTGG 10904 GGTAAG  
TCATCACTG TCTCAA  
||||||| |||||  
GGTGGTGGT AGGGGTT  
AA\_\_\_\_

GAM1385 PTGFRN 3' CTTGGCCCCGGCCTGTGGTGG 67189 T AAGTCT  
TCATCAC GGGT CCAAG  
||||||| ||| |||||

		GGTGGTG TCCG    GTTC		
		— GGCCC—		
GAM1385 RBM8A	3'	CTTGCTGTGTTACCCAGGGTGG 17545	A	GTCTC
A		TTCATC CTGGGTAA CAAG		
		AGGTGG GACCCATT GTTC		
		— GTGTC		
GAM1385 RET	3'	TAAACAGCTGACCCAGTGATGG 4373	A	CTCCAAG
		TCATCACTGGGT AGT		
		GGTAGTGACCCA TCG		
		G ACAAATC		
GAM1385 RET	3'	TAAACAGCTGACCCAGTGATGG 40170	A	CTCCAAG
		TCATCACTGGGT AGT		
		GGTAGTGACCCA TCG		
		G ACAAATC		
GAM1385 RET	3'	TAAACAGCTGACCCAGTGATGG 40182	A	CTCCAAG
		TCATCACTGGGT AGT		
		GGTAGTGACCCA TCG		
		G ACAAATC		
GAM1385 RET	3'	TAAACAGCTGACCCAGTGATGG 40598	A	CTCCAAG
		TCATCACTGGGT AGT		
		GGTAGTGACCCA TCG		
		G ACAAATC		
GAM1385 RGR	3'	AGATTGCCTAGTGGTGAA 11321	G	
		TTCATCACTGGGTAA TCT		
		AAGTGGTGATCCGTT AGA		
		—		
GAM1385 RNASE1	3'	TTGGAGAACGGTGAATGGA 63877	—	GGTAAG
		TTCAT CACTG TCTCAA		
		AGGTA GTGGC AGAGGTT		
		A A—		
GAM1385 RRM2	3'	CTTGCCCCTGTTAAGTGGTGAA 6408	—	
		TTCATCACT GGGTAAG		
		AAGTGGTGA CCCGTTC		
		ATTGTC		
GAM1385 RXRA	3'	CTGGAGCAGGGGCTTCCTCAGT 11409	T	— AG
GGTGAG		CACTGGG AAGT CTCCA		
		GTGACTC TTCG GAGGT		
		C GGGAC C		
GAM1385 SCN8A	3'	TTGGAGATGGGTGGGGGA 26386	AT	GGGTAA
		TTC CACT GTCTCAA		



AGG GTGG TAGAGGTT  
 GG G\_\_\_\_  
 GAM1385 SERPINF2 3' TTGGGGAGTTTAGGGTGG 6261 A GGT G  
 TCATC CTG AA TCTCCAA  
 ||||| ||| || |||||  
 GGTGG GAT TT AGGGGTT  
 \_ \_ G  
 GAM1385 SIRT6 3' CTTGCTGTGTTGTCCAGAGGTG 33296 A GT GTCTC  
 AG TTCATC CTGG AA CAAG  
 ||||| ||||| || |||||  
 GAGTGG GACC TT GTTC  
 A TG GTGTC  
 GAM1385 SLC12A7 3' CTTGGCTGGATTTACCCAGTGG 21700 \_  
 T ATCACTGGGTAAGTCT CCAAG  
 ||||| ||||| |||||  
 TGGTGACCCATTTAGG GGTTTC  
 TC  
 GAM1385 SLC19A1 3' TGGGGGGGCTGCCTTTGTGGTG 11759 T\_ A AAG  
 G TCATCAC GGGTA GTCTCC  
 ||||| ||||| |||||  
 GGTGGTG TCCGT CGGGGG  
 TT \_ GGTT  
 GAM1385 SLC2A8 3' TTGGAGGTTGGGTGCTGG 27424 T G TAAG  
 TCA CACT GG TCTCCAA  
 ||| ||||| || |||||  
 GGT GTGG TT GGAGGTT  
 C G \_\_\_\_  
 GAM1385 SLC8A1 3' ACTTACCTGCTGATGGA 40838 CT  
 TTCATCA GGGTAAGT  
 ||||| |||||  
 AGGTAGT TCCATTCA  
 CG  
 GAM1385 SLC9A6 3' TTGGAGGGGCTGGGGTGG 21011 A TG GTAAG  
 TCATC C G TCTCCAA  
 ||||| | |||||  
 GGTGG G C GGAGGTT  
 \_GT GG\_\_\_\_  
 GAM1385 SMARCD2 3' TTGGAGCTTGGTGAGGAG 11828 A TG TAAGT  
 TTC TCAC GG CTCCAA  
 ||| ||||| || |||||  
 GAG AGTG TC GAGGTT  
 G GT \_\_\_\_  
 GAM1385 SPARC 3' TTTGGGACTAGAGGCTCAGTGG 11901 A\_\_ T  
 TGG CATCACTGGGT AGTC CCAAG  
 ||||| ||||| |||||  
 GTGGTGACTCG TCAG GGTTT  
 GAGA \_  
 GAM1385 SPON1 3' TTTGGAGACTTAAAACCAG 62460 G\_\_  
 CTGG TAAGTCTCCAAG  
 ||||| ||||| |||||

GACC ATTCAGAGGTTT  
 AAA  
 GAM1385 SSRP1 3' TTTGGGGAGAGATAGGGTGG 11985 GG AAG  
 TCACT GT TCTCCAAG  
 ||||| || |||||  
 GGTGG TA AGGGGTTT  
 GA GAG  
 GAM1385 SUFU 3' CTTGGAGACTTGCCTAGTTGT 32410 C  
 AT ACTGGGTAAGTCTCCAAG  
 || |||||  
 TG TGATCCGTTT CAGAGGTTT  
 T  
 GAM1385 SVIL 5' TCATGTGGATTGCCCAGTAAT 41411 C TC AG  
 GGA TTCAT ACTGGGTAAGTC CA  
 ||||| ||||| ||  
 AGGTA TGACCCGTTT TAG GT  
 A GT ACTT  
 GAM1385 TAP2 3' CTAGAGCTTTGCCTGGTGATGA 5027 TG T CAAG  
 G TTCATCAC GGTAAG CTC  
 ||||| ||||| ||  
 GAGTAGTG CCGTTT GAG  
 GT C ATC  
 GAM1385 TARDBP 3' TTGGTTTGTTCAGTGTGGA 23775 T GG TCT  
 TTCA CACTG TAAG CCAA  
 ||| |||| ||| ||  
 AGGT GTGAC GTTT GGTT  
 \_ TT \_  
 GAM1385 TBX6 5' TTTGGAGGCTTGGCTCGTGATG 16039 T G  
 GA TTCATCAC GG TAAGTCTCCAAG  
 ||||| || |||||  
 AGGTAGTG TC GTTCGGAGGTTT  
 C G  
 GAM1385 TBX6 5' TTTGGAGGCTTGGCTCGTGATG 54967 T G  
 GA TTCATCAC GG TAAGTCTCCAAG  
 ||||| || |||||  
 AGGTAGTG TC GTTCGGAGGTTT  
 C G  
 GAM1385 TEAD3 3' TTGGGGGAGCATGATGG 12212 C GGTAAG  
 TCATCA TG TCTCCA  
 ||||| || |||||  
 GGTAGT AC GGGGGTT  
 \_ GA \_  
 GAM1385 TFCEP2 5' TTGGGGGTGGCTGGTGG 18954 TG G AG  
 TCAC G TA TCTCCA  
 ||| || |||||  
 GGTG C GT GGGGGTT  
 GT G \_  
 GAM1385 TRAF5 3' GCTTACCTGGTGATGA 16084 TG  
 TCATCAC GGTAAGT  
 ||||| |||||

		AGTAGTG CCATTCTG		
		GT		
GAM1385 TRPC5	5'	TTGGAGACAGGGTGGGGAG 25004	AT	GGGTAA
		TTC CACT GTCTCCAA		
		GAG GTGG CAGAGGTT		
		GG GA__		
GAM1385 UBL3	3'	CTTGGAAGTGCCTGGTGGT 23032	TG	AGTC
		ATCAC GGTA TCCAAG		
		TGGTG CCGT AGGTTC		
		GT C__		
GAM1385 VDR	3'	TTTGGGGGTTCCGTGATG 4577	T	GTA GT
		CATCAC GG A CTCCAAG		
		GTAGTG CC T GGGGTTT		
		_ __TG		
GAM1385 XT3	3'	CTTGGGGGTCAAGTGGGTGGA 39523	_	GGGTAAG
		TTCATC ACT TCTCCAAG		
		AGGTGG TGG GGGGGTTC		
		G AACT__		
GAM1385 XYLB	3'	TTTGGAGGCATGGTGGATGAA 17562	_	GGTAA
		TTCATC ACTG GTCTCCAAG		
		AAGTAG TGGT CGGAGGTTT		
		G A__		
GAM1385 YES1	3'	TTTGCTCATGGTGAA 18361	C	
		TTCATCA TGGGTAAG		
		AAGTGGT ACTCGTTT		
		-		
GAM1385 YWHAG	3'	TAGCAGTTTCCTCAGTGATGGA 25022	T T	CCAAG
		TTCATCACTGGG AAG CT		
		AGGTAGTGAATC TTT GA		
		C _ CGATT		
GAM1385 ZNF144	3'	TTTGGGGGTGCCTGGAGATGAA 23084	A TG	AG
		TTCATC C GGTA TCTCCAAG		
		AAGTAG G CCGT GGGGGTTT		
		A GT _		
GAM1385 ZNF265	3'	CTTGGGGGCTTTTGTGTTATGG 18397	C	TGGGT
		TCAT AC AAGTCTCCAAG		
		GGTA TG TTCGGGGGTTC		
		T TTT__		
GAM1385 AD-020	3'	TTTGAGAATTATCTGTGTGATG 59389	_	G CAAG
AG		TTCATCAC TGGGTAA TCTC		

			GAGTAGTG GTCTATT AGAG		
			T A TTT		
GAM1385 AD-020	3'	TTTGAGAATTATCTGTGTGATG 39313		_	G CAAG
AG		TTCATCAC TGGGTAA TCTC			
		GAGTAGTG GTCTATT AGAG			
		T A TTT			
GAM1385 AKAP6	3'	TTTGTGATGTCTAGTGATG 14999		TAA	TC
		CATCACTGGG GTC CAAG			
		GTAGTGATCT TAG GTTT			
		G _ T _			
GAM1385 AKAP8	3'	CTTG GGGAGGCCGTGGTGAG 19602		TG	AAG
		TTCATCAC GGT TCTCCAAG			
		GAGTGGTG CCG AGGGGTTC			
		_ G _			
GAM1385 ALS2CR3	3'	TTTGAGG CAGGGTGGTGGG 30490		GGGTAA	
		TTCATCACT GTCTCCAAG			
		GGGTGGTGG CGGAGGTTT			
		GA _ _ _			
GAM1385 BLZF1	5'	CTTGAGTGCATTTTCAGTGGT 13369		TAA	_
		ATCACTGGG GT CTCCAAG			
		TGGTGA CTT CG GAGGTTC			
		TTA T			
GAM1385 BTN1A1	3'	CTTGAGGGAATATTATGATGG 8194		C	GTAAG
A		TTCATCA TGG TCTCCAAG			
		AGGTAGT ATT GGAGGTTC			
		_ ATAAG			
GAM1385 C1orf34	3'	CTTGAGATGAGCCTGGTGAAG 60670		A	TG AA
G		TC TCAC GGT GTCTCCAAG			
		GG AGTG CCG TAGAGGTTC			
		A GT AG			
GAM1385 C20orf188	3'	TTTGGGTACAGGCTTGGTGGGA 31582		A	TG AA CT
G		TTC TCAC GGT GT CCAAG			
		GAG GGTG TCG CA GGTTT			
		_ GT GA TG			
GAM1385 CDCA7	3'	ATTACTTG GTGTTGAA 49202		T	TG
		TTCA CAC GGTAAGT			
		AAGT GTG TCATTTA			
		T GT			
GAM1385 COQ7	3'	GATTTATTTAGGGTGGA 32332		A	
		TTCATC CTGGGTAAGTC			

AGGTGG GATTTATTTAG

GAM1385 COTL1 3' GGATTGCTCGGTGGTGAG 87957 GTC  
TTCATCACTGGGTAA TCC  
||||||| |||  
GAGTGGTGGCTCGTT AGG

GAM1385 CRTAM 3' CTTGGGGATCAGGGTCAGTGTG 38981 T GTAA\_  
AG TTCA CACTGG GTCTCCAAG  
||| ||| |||||  
GAGT GTGACT TAGGGGTTC  
GGGAC

GAM1385 D6S2654E 3' CTTGGGGGCCACAGTGAAGTGAAG 24049 \_ GGTA  
TTCA TCACTG GTCTCCAAG  
||| ||| |||||  
GAGT AGTGAC CGGGGGTTC  
C AC\_

GAM1385 DHRS2 3' TTTGGGGGCTTACTCA 19384  
TGGGTAAGTCTCCAAG  
|||||||  
ACTCATTCGGGGGTTT

GAM1385 Di-Ras2 3' CTTGGGGATAGGATGGTGGCTG 34188 \_ GGTA  
GA TTCA TCACTG GTCTCCAAG  
||| ||| |||||  
AGGT GGTGGT TAGGGGTTC  
C AGGA\_

GAM1385 DJ667H12.2 3' GGCTTGCCTGTGATGG 38987 T  
TCATCAC GGGTAAGTC  
||||| |||||  
GGTAGTG TCCGTTCGG

GAM1385 DKFZp761G2113 3' CTTGGACATAAGTTTGGTGGGG 69902 AT TG TAA C  
AG TTC CAC GG GT TCCAAG  
||| ||| || |||||  
GAG GTG TT TA AGGTTC  
GG GT GAA C

GAM1385 DNAJB5 3' TTGGAGGCTGTGTGGGGAA 24356 AT TGGGTA  
TTC CAC AGTCTCAA  
||| ||| |||||  
AAG GTG TCGGAGGTT  
GG TG\_

GAM1385 DUSP14 5' TTTGGATTCTTGGTGGAGGA 22836 AT TG T GTC  
TTC CAC GG AA TCCAAG  
||| ||| || |||||  
AGG GTG TC TT AGGTTT  
AG GT C \_

GAM1385 ELF4 3' GGGCTGACTTGGTGATGGA 7434 TG A  
TTCATCAC GGT AGTCT  
||||| ||| |||||

AGGTAGTG TCA TCGGG  
 GT G  
 GAM1385 FBXO26 3' TTTGGGGAAATCTCTGGTGTG 46096 T TG TAAG  
 G TCA CAC GG TCTCCAAG  
 ||| ||| || |||||  
 GGT GTG CT AGGGGTTT  
 T GT CTAA  
 GAM1385 FKBP14 3' TTTGGGGGGCCAAGGAGGGTGGA 35631 A GGGTAA  
 TTCATC CT GTCTCCAAG  
 ||||| || |||||  
 AGGTGG GA CGGGGGTTT  
 \_ GGAAC\_  
 GAM1385 FLJ10546 5' TTTGGCTTTGCTTAATGATGGA 59484 C TCT  
 TTCATCA TGGGTAAG CCAAG  
 ||||| ||||| |||||  
 AGGTAGT ATTCGTTT GGTTT  
 A C\_  
 GAM1385 FLJ10704 3' CTTCTGGCTGGTCCAGTGATGG 36454 TA TCCAAG  
 TCATCACTGGG AGTC  
 ||||| |||||  
 GGTAGTGACCT TCGG  
 GG TCTTC  
 GAM1385 FLJ10718 3' GCTTCTTGGTGGTGAA 36494 TG T  
 TTCATCAC GG AAGT  
 ||||| || |||||  
 AAGTGGTG TC TTCG  
 GT \_  
 GAM1385 FLJ11053 3' TAAAATGCTACTTGGTGATGAA 88732 TG A CTCCAAG  
 TTCATCAC GGTA GT  
 ||||| ||||| |||||  
 AAGTAGTG TCAT CG  
 GT \_ TAAAATT  
 GAM1385 FLJ11383 3' TTTGGAGAGGATCTAGTGCATG 46285 \_ AAG  
 GA TTCAT CACTGGGT TCTCCAAG  
 ||||| ||||| |||||  
 AGGTA GTGATCTA AGAGGTTT  
 C GG\_  
 GAM1385 FLJ12517 3' TGGCACTTGTCTAGGATGGA 43440 A GT CT  
 TTCATC CTGG AAGT CCA  
 ||||| ||||| |||||  
 AGGTAG GATC TTCA GGT  
 \_ TG C\_  
 GAM1385 FLJ12526 3' ACTTTCCCAGTGATGAG 45561 T  
 TTCATCACTGGG AAGT  
 ||||| ||||| |||||  
 GAGTAGTGACCC TTCA  
 T  
 GAM1385 FLJ12568 3' TTTGGGTTTTGCTCAGTGTGAA 46504 T T T  
 TTCA CACTGGGTAAG C CCAAG  
 ||||| ||||| ||||| |||||

AAGT GTGACTCGTTT G GGTTT  
 \_ T \_  
 GAM1385 FLJ12650 3' CTTGGGGGCAAGTAGAGGTGAG 44526 A GGTA  
 TTCATC CTG GTCTCCAAG  
 ||||| ||| |||||  
 GAGTGG GAT CGGGGGTTC  
 A GAA\_  
 GAM1385 FLJ12787 3' AGGTTTATCTGGGATGGA 49745 A TG GT  
 TTCATC C GGTA CT  
 ||||| | ||||| ||  
 AGGTAG G CTATT GA  
 \_GT TG  
 GAM1385 FLJ12875 3' TTTGGAGGAGCAGTGGTGGG 44611 GGTAAG  
 TTCATCACTG TCTCCAAG  
 ||||| |||||  
 GGGTGGTGAC GGAGGTTT  
 GA\_  
 GAM1385 FLJ12891 3' GAGTTGTCAGTGGTGAA 46340 G GT G  
 TTCATCACT G AA TC  
 ||||| | |||  
 AAGTGGTGAC TT AG  
 \_TG G  
 GAM1385 FLJ14326 3' GCTATTCTAGTGGTGGG 49810 TA  
 TTCATCACTGGG AGT  
 ||||| |||  
 AGGTGGTGATCT TCG  
 TA  
 GAM1385 FLJ14393 5' TTTGGAGGCTTAGCAAGGA 51322 A GGG  
 TC CT TAAGTCTCCAAG  
 || || |||||  
 AG GA ATTCGGAGGTTT  
 \_ ACG  
 GAM1385 FLJ14564 3' TTTGGTGACCTTTTACCAAGTG 76507 G \_ T  
 GTGAG ATCACT GGTA GTC CCAAG  
 ||||| |||| || |||||  
 TGGTGA CCATT CAG GGTTT  
 A TTC T  
 GAM1385 FLJ21477 3' TTTGGGTATATACCCAGTAATG 47150 C A CT  
 G TCAT ACTGGGTA GT CCAAG  
 ||| ||||| || |||||  
 GGTA TGACCCAT TA GGTTT  
 A A TG  
 GAM1385 FLJ21839 5' TTTGGGGGCCCCGGGTGGAGG 41550 AT G TAA  
 TC CACT GG GTCTCCAAG  
 || ||| || |||||  
 GG GTGG CC CGGGGGTTT  
 AG G \_  
 GAM1385 FLJ22031 3' ATTTGTTTCGGTGTGAA 46885 T GG  
 TTCA CACTG TAAGT  
 ||| ||||| |||||

AAGT GTGGC GTTTA  
 \_ TT  
 GAM1385 FLJ22055 3' TTTGGAGGCTGGAATGATGG 45502 CTGGGTA  
 TCATCA AGTCTCCAAG  
 ||||| |||||  
 GGTAGT TCGGAGGTTT  
 AAGG\_\_  
 GAM1385 FLJ22167 3' TTGGA CTCCAGAGGTGGA 44585 A TAAGTC  
 TTCATC CTGGG TCCAA  
 ||||| ||||| |||||  
 AGGTGG GACCT AGGTT  
 A C\_\_\_\_  
 GAM1385 FLJ31951 3' TTTGGAGTCTGCTTTAGTGAAG 58556 A TA T  
 GA TTC TCACTGGG AG CTCCAAG  
 ||| ||||| ||| |||||  
 AGG AGTGATTT TC GAGGTTT  
 A CG T  
 GAM1385 GMEB2 5' GGCTTATCCAGTGGGAA 24735 A  
 TTC TCACTGGGTAAGTC  
 ||| |||||  
 AAG GGTGACCTATTCGG  
 \_  
 GAM1385 GOLGA1 3' ATTTACCTGGTGGGAA 9086 A TG  
 TTC TCAC GGTAAGT  
 ||| ||||| |||||  
 AAG GGTG CCATTTA  
 \_ GT  
 GAM1385 GTPBP2 3' CTTGGCCATCTGGTGGTGG 38869 TG AAGTCT  
 TCATCAC GGT CCAAG  
 ||||| ||| |||||  
 GGTGGTG CTA GGTTT  
 GT CC\_\_\_\_  
 GAM1385 HCA66 3' ATTTGCTCAGTGATGG 71775  
 TCATCACTGGGTAAGT  
 |||||  
 GGTAGTGA CTGTTTA  
 \_  
 GAM1385 HSPC065 3' CTTTTCCTCAGTGGTGGGA 26300 T\_  
 TTCATCACTGGG AAG  
 ||||| ||||| |||  
 AGGTGGTGACCC TTC  
 TT  
 GAM1385 HUMNPIIY20 3' CTTGGCAACTGCGCGGTGATGG 83346 G A CT  
 TCATCACTG GTA GT CCAAG  
 ||||| ||| ||| |||||  
 GGTAGTGGC CGT CA GGTTT  
 G \_ AC  
 GAM1385 ITM3 3' TTGGGGAGTGGGGATGAG 48168 A GGG AG  
 TTCATC CT TA TCTCCA  
 ||||| || || |||||



GAGTAG GG GT AGGGGTT  
 \_ \_ \_ G\_  
 GAM1385 JIK 3' TTTGGGGACGGGGGTGGGTGG 32800 \_ GGGTAA  
 TCATC ACT GTCTCCAAG  
 ||||| ||| |||||  
 GGTGG TGG CAGGGGTTT  
 G GGG\_\_  
 GAM1385 KIAA0007 3' CTTGCCCAGTGGTGAG 80112  
 TTCATCACTGGGTAAAG  
 |||||  
 GAGTGGTGACCCGTTT  
  
 GAM1385 KIAA0057 3' CTTGGAGGTGCAGTGATGA 24425 G TAAG  
 TCATCACTG G TCTCCAAG  
 ||||| | |||||  
 AGTAGTGAC T GGAGGTTC  
 G \_\_\_\_  
 GAM1385 KIAA0057 3' GAGTGTTCATGTGATGAG 24428 \_ GG AGT  
 TTCATCAC TG TA CTC  
 ||||| || || |||  
 GAGTAGTG AC GT GAG  
 T TT \_\_\_\_  
 GAM1385 KIAA0061 3' TTTGGGGGTGATGAGGTGGGGA 68297 AT GG AAG  
 A TTC CACT GT TCTCCAAG  
 ||| ||| || |||||  
 AAG GTGG TA GGGGGTTT  
 GG AG GT\_  
 GAM1385 KIAA0275 3' CTTGGGGACACTGGGTGGTGG 28677 G AA  
 TCATCACT GGT GTCTCCAAG  
 ||||| ||| |||||  
 GGTGGTGG TCA CAGGGGTTC  
 G \_\_\_\_  
 GAM1385 KIAA0326 3' TTTACATCAGTGATGAG 64332 \_  
 TTCATCACTGG GTAAG  
 ||||| |||||  
 GAGTAGTGA CT CATT  
 A  
 GAM1385 KIAA0355 3' CTTGGGGACAAGGGTGGT 28026 GGGTAA  
 ATCACT GTCTCCAAG  
 ||||| |||||  
 TGGTGG CAGGGGTTC  
 GAA\_\_  
 GAM1385 KIAA0391 3' TTTGGAGGCTTATCAAGAGTTG 27928 TCA G  
 GA TTCA CT GGTAAGTCTCCAAG  
 ||| || |||||  
 AGGT GA CTATTCGGAGGTTT  
 TGA A  
 GAM1385 KIAA0418 3' TTTGGGGGCCTGGGTGGT 27566 G TAA  
 ATCACT GG GTCTCCAAG  
 ||||| || |||||

TGGTGG TC CGGGGGTTT  
 G \_\_\_\_  
 GAM1385 KIAA0451 3' CTTTTCCTAGTGGTGA 29107 T\_  
 TTCATCACTGGG AAG  
 ||||| ||  
 AGGTGGTGATCC TTC  
 TT  
 GAM1385 KIAA0478 5' TTTGGGGATGCCAGTTGGTGG 29565 \_ GTAA  
 TCATCA CTGG GTCTCCAAG  
 |||| || |||||  
 GGTGGT GACC TAGGGGTTT  
 T G\_\_\_\_  
 GAM1385 KIAA0672 3' CTTGGGGATTAGGGGAGTGAGA 29409 A GGGTA  
 A TTC TCACT AGTCTCCAAG  
 || |||| |||||  
 AAG AGTGA TTAGGGGTTC  
 \_ GGGGA  
 GAM1385 KIAA0802 3' CTTGGAGGAGCATGGTGGCGAG 62566 AT GG AAG  
 TTC CACT GT TCTCCAAG  
 || |||| || |||||  
 GAG GTGG CG GGAGGTTC  
 CG TA A\_\_\_\_  
 GAM1385 KIAA0819 3' TGGGGGACAGGATGAG 63583 A GGTAAGT  
 TTCATC CTG CTCCA  
 |||| || ||||  
 GAGTAG GAC GGGGT  
 \_ AG\_\_\_\_  
 GAM1385 KIAA0821 3' TTTGGGGGAAGTGTAGTGAGGA 29948 A G TAAG  
 G TTC TCACTG G TCTCCAAG  
 || |||| | |||||  
 GAG AGTGAT T GGGGGTTT  
 G G GAA\_  
 GAM1385 KIAA0831 3' TTGGAGCTTGGTGGTGA 29984 TG TAAGT  
 TTCATCAC GG CTCCA  
 |||| || ||||  
 AGGTGGTG TC GAGGTT  
 GT \_\_\_\_  
 GAM1385 KIAA0981 3' TTTGGAGACTTGTACTGT 61430 TGG  
 AC GTAAGTCTCCAAG  
 || |||||  
 TG TGTTCAAGGTTT  
 TCA  
 GAM1385 KIAA1238 3' TTTGGGGACTTATTTAGT 71083  
 ACTGGGTAAGTCTCCAAG  
 |||||  
 TGATTTATTCAGGGGTTT  
 GAM1385 KIAA1301 3' TTGGGGACTGGAGATGAG 66345 A GGGTA  
 TTCATC CT AGTCTCCA  
 |||| || |||||

GAGTAG GG TCAGGGGTT  
 A \_\_\_\_\_  
 GAM1385 KIAA1344 3' GATTTTGTTCAGTGATGG 72448 GG \_  
 TCATCACTG TAAG TC  
 ||||| ||| ||  
 GGTAGTGAC GTTT AG  
 TT T  
 GAM1385 KIAA1456 3' TTTGGGGGTTTATTGGAGGA 67012 A\_ TG G GT  
 TC C G TAA CTCCAAG  
 || | ||| |||||  
 AG G T ATT GGGGTTT  
 GA GT\_ TG  
 GAM1385 KIAA1464 3' GCTAATTTAGTGATGAA 68267 A  
 TTCATCACTGGGT AGT  
 ||||| |||  
 AAGTAGTGATTTA TCG  
 A  
 GAM1385 KIAA1536 3' TTGGAGGAACCGGGATGGA 40494 A GTAAG  
 TTCATC CTGG TCTCAA  
 |||| ||| |||||  
 AGGTAG GGCC GGAGGTT  
 \_ AA\_\_\_\_  
 GAM1385 KIAA1538 5' ACTGCCTGGTGGTGGA 71527 TG A  
 TTCATCAC GGTA GT  
 ||||| ||| ||  
 AGGTGGTG CCGT CA  
 GT \_  
 GAM1385 KIAA1553 3' TGGGATCTACTTAGTGGTGAA 91921 AG T  
 TTCATCACTGGGTA TC CCA  
 ||||| ||| |||  
 AAGTGGTGATTCAT AG GGT  
 CT \_  
 GAM1385 KIAA1655 3' CTTGGGGAAGTGGCTGGTGGGG 66608 AT TG G AG  
 AG TTC CAC G TA TCTCCAAG  
 ||| ||| | ||| |||||  
 GAG GTG C GT AGGGGTTC  
 GG GT G GA  
 GAM1385 KIAA1786 3' TTTGGGGGCTTGTGTCAATTGA 66045 CTG \_  
 TCA GG TAAGTCTCCAAG  
 ||| || ||||| |||||  
 AGT CT GTTCGGGGGTTT  
 TAA GT  
 GAM1385 KIAA1796 3' TTTGGCCACATCTTGCTTGCTG 91457 CT TCT\_\_\_\_  
 ATGAG ATCA GGGTAAG CCAAG  
 ||| ||||| |||||  
 TAGT TTCGTTT GGTTT  
 CG TACACC  
 GAM1385 KIAA1866 3' CTTGGAGGAAAGCCGCTGGTGG 60934 C GTAAG  
 TCATCA TGG TCTCCAAG  
 ||||| ||| |||||

GGTGGT GCC GGAGGTTC  
C GAAA\_  
GAM1385 KIAA1970 3' CTTGGGGTCTTCAGTGAAGAG 74297 A GTA T  
TTC TCACTGG AG CTCCAAG  
||| ||||| || |||||  
GAG AGTGACT TC GGGGTTC  
A \_\_\_\_ T  
GAM1385 KR18 3' GGCTGGGCTTAGTGGTG 52752 A\_  
CATCACTGGGT AGTC  
||||||| |||  
GTGGTGATTCTG TCGG  
GG  
GAM1385 KREMEN 3' TTTGGGACCTTTGGGGGTGAG 49410 A G TAA T  
TTCATC CT GG GTC CCAAG  
||||| || || ||| |||||  
GAGTGG GG TT CAG GGTTT  
\_ G TC\_ \_  
GAM1385 KRTAP1-5 3' GCATTGCTTGATGGA 49226 T \_  
TTCATCAC GGGTAA GT  
||||||| ||||| ||  
AGGTAGTG TTCGTT CG  
\_ A  
GAM1385 MGC1127 3' TTGGGGGGGTGGGTGGTGGGA 53219 GGG AG  
TTCATCACT TA TCTCCAA  
||||||| || |||||  
AGGTGGTGG GT GGGGGTT  
\_\_\_\_ G\_  
GAM1385 MGC14480 3' TTGGAGTGTCCAGTGGGGA 58752 AT GT AGT  
TC CACTGG A CTCCAA  
|| ||||| | |||||  
AG GTGACC T GAGGTT  
GG TG\_\_\_\_  
GAM1385 MGC15476 3' TTGGGGATTGCTTGG 58967 TG  
C GGTAAGTCTCCAA  
| |||||  
G TCGTTTAGGGGTT  
GT  
GAM1385 MGC16075 5' TTTGGAACTTACTCAGGGTGA 51288 A C  
A TTCATC CTGGGTAAGT TCCAAG  
||||| |||||  
AAGTGG GACTCATTCA AGGTTT  
\_ A  
GAM1385 MGC22776 5' CTTGTGTCCGGGTGGTGGGA 58620 G \_\_\_\_  
TTCATCACT GG TAAG  
||||||| || |||  
AGGTGGTGG CC GTTC  
G TGT  
GAM1385 MGC35558 3' ATTTGCTTAGGATGAA 58775 A  
TTCATC CTGGGTAAGT  
||||| |||||

AAGTAG GATTCGTTTA

GAM1385 MGC4730 3' CTGAACATTTGCTCAGTGGAGA 64258 AT CTCCAAG  
A TTC CACTGGGTAAGT

||| |||||

AAG GTGACTCGTTTA

AG CAAGTC

GAM1385 MGC8721 3' GAATCATTCACTGGTGGG 60357 AAG

TTCATCACTGGGT TC

||||||| ||

AGGTGGTGACTTA AG

CTA

GAM1385 MKRN4 3' TGGGACTTGTGTTTGTGATGAA 47757 T GG T

TTCATCAC G TAAGTC CCA

||||||| | ||||| |||

AAGTAGTG T GTTCAG GGT

T TT \_

GAM1385 NBL1 3' GGCTTGCCTGGTGGGGGA 59319 AT TG

TTC CAC GGTAAGTC

||| ||| |||||

AGG GTG CCGTTCGG

GG GT

GAM1385 OSBPL3 3' TTTGGGGAATGCAGTGAT 31444 G AAG

ATCACTG GT TCTCCAAG

||||||| || |||||

TAGTGAC TA AGGGGTTT

G \_

GAM1385 PAFAH2 5' GATTCACCCGGTGATGAA 4764 A

TTCATCACTGGGT AGTC

||||||| |||

AAGTAGTGGCCCA TTAG

C

GAM1385 PCDH19 3' CTTATTCAGTGCTGAA 63702 T

TTCA CACTGGGTAAG

||| |||||

AAGT GTGACTTATTC

C

GAM1385 PCDH19 3' GCTATGCTCAGTGGGAA 63703 A \_

TTC TCACTGGGTA AGT

||| ||||| |||

AAG GGTGACTCGT TCG

\_ A

GAM1385 PGR1 3' TTGGGGATGACAGTATGGA 52759 C GGTA

TTCAT ACTG GTCTCCAA

||||| ||| |||||

AGGTA TGAC TAGGGGTT

\_ AG \_

GAM1385 PIF1 3' CTTGGAGGGGACTGGTGGGGA 61022 AT TG GTAAG

TC CAC G TCTCCAAG

|| ||| | |||||

AG GTG C GGAGGTTC  
 GG GT AGG\_\_  
 GAM1385 PIG11 3' GCTTGCTTGGGATGAA 61613 A TG  
 TTCATC C GGTAAGT  
 ||||| | |||||  
 AAGTAG G TCGTTCG  
 \_GT  
 GAM1385 PIP5K2B 3' TTGGAGGCTTGATGTGG 13083 TGGG  
 TCAC TAAGTCTCCAA  
 ||| |||||  
 GGTG GTTCGGAGGTT  
 TA\_\_  
 GAM1385 PIWIL2 3' CTTGGAGATGGGCTGGTGAGAA 36056 A TG G AA  
 TTC TCAC G T GTCTCCAAG  
 ||| ||| | |||||  
 AAG AGTG C G TAGAGGTTC  
 \_ GT \_GG  
 GAM1385 PMAIP1 3' CTTAAGATTGTTTATTTAGTGG 40891 \_\_ CCAAG  
 T ATCACTGGGTAA GTCT  
 ||||| |||  
 TGGTGATTTATT TAGA  
 TGT ATTC  
 GAM1385 POU4F2 3' TTTGGAGGTTTGTGTGTAGA 15902 \_ T GG GT  
 TC AC G TAA CTCCAAG  
 || || | |||||  
 AG TG T GTT GAGGTTT  
 A \_TT TG  
 GAM1385 PP1628 5' CTTGGGGACTTGCTTGGGGAAG 47296 A A TG  
 G TC TC C GGTAAGTCTCCAAG  
 || || | |||||  
 GG AG G TCGTTCAGGGGTTC  
 A G GT  
 GAM1385 PRO0038 3' TTTACCCAGTGTGGA 26095 T  
 TTCA CACTGGGTAAG  
 ||| |||||  
 AGGT GTGACCCATTT  
 -  
 GAM1385 PRO2037 3' TTTGTAGCTTTTATTTATTGGT 37785 C T\_ C  
 GAA TTCATCA TGGGTAAG CT CAAG  
 ||||| ||||| || |||  
 AAGTGGT ATTTATTT GA GTTT  
 T TC T  
 GAM1385 PRO2730 3' TTGGGGATAAGGTGCTGAA 47424 T GGGTAA  
 TTCA CACT GTCTCCAA  
 ||| ||| |||||  
 AAGT GTGG TAGGGGTT  
 C AA\_\_  
 GAM1385 PTRF 3' TTTGGAGGCTGAGGTGGGGAG 63508 AT GGGTA  
 TTC CACT AGTCTCCAAG  
 || ||| |||||

			GAG GTGG TCGGAGGTTT		
			GG AG__		
GAM1385	RAB14	3'	TTTGAATAAAAACCTTGGTGG 32876	_	AAGTC_
	TGAA		TCATCACTG GGT TCCAAG		
			AGTGGTGGT CCA AGGTTT		
			T AAAATA		
GAM1385	RNF29	5'	CTTGGGGACAGCGAGGAGATGA 52340	A	GG AA
	G		TTCATC CT GT GTCTCCAAG		
			GAGTAG GG CG CAGGGGTTC		
			A AG A_		
GAM1385	RNPC1	3'	CTTGGGGGTTGGTGGAGGGTGG 33989	A	GG TA GT
	A		TTCATC CT G A CTCCAAG		
			AGGTGG GA T T GGGGTTC		
			_ GG GG TG		
GAM1385	RoXaN	3'	GTCTAAGTTTACCCAGTATGG 46657	C	T CCAAG
			TCAT ACTGGGTAAG CT		
			GGTA TGACCCATTT GA		
			_ _ ATCTGT		
GAM1385	SKD3	3'	CTTGGGGACTAGGCCAGTGTTG 47994	T	GTA
	G		TCA CACTGG AGTCTCCAAG		
			GGT GTGACC TCAGGGGTTC		
			T GGA		
GAM1385	SLC5A7	5'	CTTGAGACGCCGAGTGAGGAG 41512	A	G AA
			TTC TCACT GGT GTCTCCAAG		
			GAG AGTGA CCG CAGAGGTTC		
			G G _		
GAM1385	SMARCF1	3'	ATTTATTCAGTATGAA 37432	C	
			TTCAT ACTGGGTAAGT		
			AAGTA TGACTTATTTA		
			_		
GAM1385	SMARCF1	3'	ATTTATTCAGTATGAA 20036	C	
			TTCAT ACTGGGTAAGT		
			AAGTA TGACTTATTTA		
			_		
GAM1385	SMARCF1	3'	ATTTATTCAGTATGAA 57482	C	
			TTCAT ACTGGGTAAGT		
			AAGTA TGACTTATTTA		
			_		
GAM1385	TANK	3'	TTGGATTCTAGTGAGAG 14813	A	TAAGTC
			TTC TCACTGGG TCCAA		

GAG AGTGATCT AGGTT  
 \_ TT\_\_\_\_  
 GAM1385 TIGD5 3' CTTGGAGGAGCTCTGTTGGTGA 51701 \_ T AAG  
 G TTCATCA C GGGT TCTCCAAG  
 ||||| | ||| |||||  
 GAGTGGT G CTCG GGAGGTTC  
 TT A\_\_  
 GAM1385 TSCOT 3' ACTTTCCTGGTGATGGA 52333 TG T  
 TTCATCAC GG AAGT  
 ||||| || |||  
 AGGTAGTG CC TTCA  
 GT T  
 GAM1385 UBE2M 3' TGGGGGGCGGCCGGTGGGGGA 14266 AT GTAA AAG  
 TTC CACTGG GTCTCC  
 || ||||| |||||  
 AGG GTGGCC CGGGGG  
 GG GG\_\_ GTT  
 GAM1385 UPB1 3' TTTGGGGACTAGGTAGAGGTGA 32892 A GG A  
 A TTCATC CTG TA GTCTCCAAG  
 ||||| ||| || |||||  
 AAGTGG GAT AT CAGGGGTTT  
 A GG \_  
 GAM1385 YME1L1 3' TTTGGAGGCTGAGGCGGGTGGA 26534 A\_ GGGTA  
 TTCATC CT AGTCTCCAAG  
 ||||| || |||||  
 AGGTGG GG TCGGAGGTTT  
 GC AG\_\_  
 GAM1385 YME1L1 3' TTTGGAGGCTGAGGCGGGTGGA 57784 A\_ GGGTA  
 TTCATC CT AGTCTCCAAG  
 ||||| || |||||  
 AGGTGG GG TCGGAGGTTT  
 GC AG\_\_  
 GAM1385 ZIC5 3' ATTTATTCAGTATGAA 52439 C  
 TTCAT ACTGGGTAAGT  
 |||| |||||  
 AAGTA TGA CT TATTTA  
 \_  
 GAM1385 ZNF238 3' TATGAAGGTTTGCTTGGGATGA 20967 A TG GT C AG  
 A TTCATC C GGTA CT CA  
 ||||| | |||| || ||  
 AAGTAG G TCGTT GA GT  
 \_ GT TG A ATT  
 GAM1385 LOC114932 5' CTTGGAGGGTTCCGGTGAGAA 72712 A TA G  
 TTC TCACTGGG A TCTCCAAG  
 || ||||| | |||||  
 AAG AGTGGCCT T GGAGGTTC  
 \_ \_\_ G  
 GAM1385 LOC114932 3' CTTGGTTGAGCCTGGTGAAGAA 72713 A TG AAG T\_  
 TTC TCAC GGT TC CCAAG  
 || |||| || || |||||



	AAG AGTG CCG AG GGTTTC	
	A GT ____ TT	
GAM1385 LOC115110 5'	CTTG GGGGTTGGGGGTGGT 71716	GGGTA GT
	ATCACT A CTCCAAG	
	TGGTGG T GGGGTTC	
	GGG__TG	
GAM1385 LOC115399 5'	TTTGGGGGGATGCAGTGTGG 73440	T G AAG
	TCA CACTG GT TCTCCAAG	
	GGT GTGAC TA GGGGGTTT	
	T G G__	
GAM1385 LOC124044 3'	TTGGTGGGTCCAGTGGT 76029	TAAG T
	ATCACTGGG TC CCAA	
	TGGTGACCT GG GGTT	
	G__ T	
GAM1385 LOC124470 3'	TTTGGGGGAAATGGCTGGGATG 75646	A TG G AG__
AG	TTCATC C G TA TCTCCAAG	
	GAGTAG G C GT GGGGGTTT	
	_GT G AAA	
GAM1385 LOC124895 5'	TTTGGAACGTTTGGGGGTGA 74351	A G TAA C__
A	TTCATC CT GG GT TCCAAG	
	AAGTGG GG TT CA AGGTTT	
	_ G TG_ AA	
GAM1385 LOC128344 3'	TTGGAGGATATTGATGG 74739	CTGG AG
	TCATCA GTA TCTCCA	
	GGTAGT TAT GGAGGT	
	____ A_	
GAM1385 LOC129138 3'	CTTGAGAGCTGCACTTGTCTGGT 57121	TG GT ____
GAGGA	TCAC G AAGT CTCCAAG	
	AGTG C TTCA GAGGTTC	
	GT TG CGTC	
GAM1385 LOC130470 5'	TTGGGGACTTGTGCGGGA 74945	A G
	TC CTG GTAAGTCTCCA	
	AG GGC TGTTCAGGGGT	
	_ G	
GAM1385 LOC133121 3'	ACGTTACTCAGGATGAA 75081	A _
	TTCATC CTGGGTAA GT	
	AAGTAG GACTCATT CA	
	_ G	
GAM1385 LOC139065 3'	ATTTATTTAATGATGAA 75815	C
	TTCATCA TGGGTAAGT	

AAGTAGT ATTTATTTA

A

GAM1385 LOC139422 3' ATTTATTTAGTGATCGA 75838 \_

TC ATCACTGGGTAAGT

|| |||||

AG TAGTGATTTATTTA

C

GAM1385 LOC142927 3' GGGTTTACACAGTGGTGAG 76431 G GT

TTCATCACTG GTAA CT

||||||| ||| ||

GAGTGGTGAC CATT GG

A TG

GAM1385 LOC142948 3' GATTCTGCTTAGTGTTGG 82888 T \_

TCA CACTGGGTA AGTC

||| ||||| |||

GGT GTGATTCGT TTAG

T C

GAM1385 LOC143884 3' TGCAGTTTGCTCAGTGGTGGA 76657 T C

TTCATCACTGGGTAAG CT CA

||||||| ||| ||

AGGTGGTGACTCGTTT GA GT

\_ C

GAM1385 LOC144519 5' CTTGGGCCATCCGTTTGGTGAG 76869 C\_ AAGTC

TTCATCA TGGGT TCCAAG

||||| ||| |||||

GAGTGGT GCCTA GGGTTC

TT CC\_\_

GAM1385 LOC145333 3' TTTGGGGACTGAAGGTGAGTGG 83333 \_ GGGTA

TCA TCACT AGTCTCCAAG

||| ||| |||||

GGT AGTGG TCAGGGGTTT

G AAG\_\_

GAM1385 LOC145553 5' CTTGCCCTCTCCAGTGATGGA 56666 \_\_\_\_\_

TTCATCACT GGGTAAG

||||||| |||||

AGGTAGTGA CCCGTTC

CCTCT

GAM1385 LOC146268 3' TTTGGGGCTCGTGGTGGTGGA 77816 GG TA T

TTCATCACT G AGTC CCAAG

||||||| | ||| |||||

AGGTGGTGG T TCGG GGTTT

\_ GC \_

GAM1385 LOC146723 3' TGGGGACTTAGGGGA 78087 A GGG

TC CT TAAGTCTCCA

|| || |||||

AG GG ATTCAGGGGT

\_ G\_\_

GAM1385 LOC146823 3' ATTTACCTAGTGGAGG 83791 AT

TC CACTGGGTAAGT

|| |||||

	GG GTGATCCATTTA	
	AG	
GAM1385 LOC148371 3'	CTTAATCAGTGGTGA 78806	GG
	TTCATCACTG TAAG	
	AGGTGGTGAC ATTC	
	TA	
GAM1385 LOC148887 3'	CTTGCCAGGCCTGGTGATGG 84236	TG AAGTCT
	TCATCAC GGT CCAAG	
	GGTAGTG CCG GGTTT	
	GT GACC__	
GAM1385 LOC149076 3'	CTTGAGGCAGGGAGGTGA 79151	GGGTAA
	TCACT GTCTCCAAG	
	AGTGG CGGAGGTTC	
	AGGGA__	
GAM1385 LOC149175 3'	TTTGCAGTTTTACCTAGTGCTG 79213	T T C
G	TCA CACTGGGTAAG CT CAAG	
	GGT GTGATCCATTT GA GTTT	
	C T C	
GAM1385 LOC150197 3'	TTGGGGATTCGAGGTGG 79601	GGGTA
	TCACT AGTCTCCAA	
	GGTGG TTAGGGGTT	
	AGC__	
GAM1385 LOC150225 3'	CTTGAGGCTGAGGCGTGAGAA 84993	A TGGGTA
	TTC TCAC AGTCTCCAAG	
	AAG AGTG TCGGAGGTTC	
	_ CGGAG_	
GAM1385 LOC150481 3'	CTTGAGGCAGTGGGGCTTGGG 79885	A TG AA_____
GTGG	TC C GGT GTCTCCAAG	
	GG G TCG CGGAGGTTC	
	_GT GGGTGA	
GAM1385 LOC150848 5'	TGGAGGTAAGGGTGAA 85134	A GGGTAAG
	TTCATC CT TCTCCA	
	AAGTGG GA GGAGGT	
	_ AT_____	
GAM1385 LOC150935 3'	TTTGAAGTTATCTGGAGGTGAG 80041	A TG GT C
	TTCATC C GGTA CT CAAG	
	GAGTGG G CTATT GA GTTT	
	A GT _ A	
GAM1385 LOC151446 5'	TTGGAATTAAGTGATGAA 85380	GG AAGTC
	TTCATCACT GT TCCA	

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AAGTAGTGA TA AGGTT
AT _____
GAM1385 LOC151610 3' TTTGGGGATGGTGGGAGTGAAG 80292 A GGGTAA
G TC TCACT GTCTCCAAG
|| |||| |||||
GG AGTGA TAGGGGTTT
A GGGTGG
GAM1385 LOC152313 5' CCCCGGGCTTGTTCGGGATGAG 85660 A GG CCAAG
TTCATC CTG TAAGTCT
||||| ||| |||||
GAGTAG GGC GTTCGGG
_ TT CCCCT
GAM1385 LOC152794 5' TTTGGAGAAGACAGTGGCTGG 80686 _ GGTAAG
TCA TCACTG TCTCCAAG
||| ||||| |||||
GGT GGTGAC AGAGGTTT
C AGA_____
GAM1385 LOC152851 5' CTTGCTTGAGTGGTGG 80710 _
TCATCACT GGGTAAG
||||| |||||
GGTGGTGA TTCGTTT
G
GAM1385 LOC153232 5' TTTGGGGGAAGCCCTGCGTGGT 85987 T__ AAG
GAG TCATCAC GGGT TCTCCAAG
||||| ||| |||||
AGTGGTG CCCG GGGGGTTT
CGT AA_
GAM1385 LOC153769 3' TTGGGGACTTGAGCATGG 80929 C GG
TCA TG TAAGTCTCCAA
||| || |||||
GGT AC GTTCAGGGGTT
_ GA
GAM1385 LOC158287 3' TGGGGGCAAGTGGGAG 86724 A GGGTAA
TTC TCACT GTCTCCA
||| ||||| |||||
GAG GGTGA CGGGGGT
_ A_____
GAM1385 LOC158819 5' AGACTTATCTGGAGGTGAG 86900 A TG
TTCATC C GGTAAGTCT
||||| | |||||
GAGTGG G CTATTCAGA
A GT
GAM1385 LOC158969 5' GCTTGCTTTGTGATGGA 82062 TG
TTCATCAC GGTAAGT
||||| |||||
AGGTAGTG TCGTTTG
TT
GAM1385 LOC161356 5' TTTACCCAGGGTGAA 82270 A
TTCATC CTGGGTAAG
||||| |||||

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AAGTGG GACCCATTT

GAM1385 LOC169436 5' CTTGGGGGTGAACCTGGTGGTG 82740 TG AA  
GA TTCATCAC GGT GTCTCCAAG

||||||| ||| |||||||  
AGGTGGTG CCA TGGGGGTTC  
GT AG

GAM1385 LOC170082 3' TTTGGGGGTTTGTGTGTATG 82569 \_ TGGG GT  
CAT CAC TAA CTCCAAG

||| ||| ||| |||||||  
GTA GTG GTT GGGGTTT  
T T\_\_ TG

GAM1385 LOC196214 3' TGGAGGATGGTGGGAG 89622 A GGGTAAG  
TTC TCACT TCTCCA

||| ||||| |||||||  
GAG GGTGG GGAGGT  
\_ TA\_\_\_\_\_

GAM1385 LOC197136 3' TTGGTGGGTCCAGTGGT 89731 TAAG T  
ATCACTGGG TC CCAA

||||||| || |||||  
TGGTGACCT GG GGTT  
G\_\_ T

GAM1385 LOC199733 3' TTTGGAAAGACTGCCCGTGATG 89853 T A \_  
G TCATCAC GGGTA GTC TCCAAG

||||||| ||||| ||| |||||||  
GGTAGTG CCCGT CAG AGGTTT  
\_ \_ AA

GAM1385 LOC200014 3' TTTGGTACTACTTGGTGGGAA 88547 A TG A CT  
TTC TCAC GGTA GT CCAAG

||| ||||| ||||| || |||||  
AAG GGTG TCAT CA GGTTT  
\_ GT \_ T\_

GAM1385 LOC200301 5' TTTGGGGCCTGCTTGGTGGGAG 88757 A TG A T  
TTC TCAC GGTA GTC CCAAG

||| ||||| ||||| ||| |||||  
GAG GGTG TCGT CGG GGTTT  
\_ GT C \_

GAM1385 LOC200819 3' CTTGGGGAACCCTGGTGGTGGGA 90143 TG TAAG  
TTCATCAC GG TCTCCAAG

||||||| || |||||||  
AGGTGGTG CC AGGGGTTC  
GT CA\_\_

GAM1385 LOC201952 5' CTTGGAAGGTAGACCTGGTGGT 90273 TG AAG \_  
GAG TTCATCAC GGT TCT CCAAG

||||||| ||| ||| |||||  
GAGTGGTG CCA GGA GGTTT  
GT GAT A

GAM1385 LOC202108 3' CTTAATCAGTGGTGGGA 89154 GG  
TTCATCACTG TAAG

||||||| |||||

		AGGTGGTGAC ATTC		
		TA		
GAM1385	LOC203636 3'	CTTGGGTGAGTTCCAGTGGCGG 89425	AT	TA G _
	A	TTC CACTGGG A TC TCCAAG		
		AGG GTGACCT T AG GGGTTC		
		CG _ G T		
GAM1385	LOC219972 3'	TTTGGAGACAAGGAGTAATGAA 91639	C	GGGTAA
		TTCAT ACT GTCTCCAAG		
		AAGTA TGA CAGAGGTTT		
		A GGAA _		
GAM1385	LOC221271 3'	TTTGGAGATGGCGGTGGAGAA 91886	AT	GGTAA
		TTC CACTG GTCTCCAAG		
		AAG GTGGC TAGAGGTTT		
		AG GG _		
GAM1385	LOC221504 3'	ACTTGCCCATGGTGGG 92418	C	
		TTCATCA TGGGTAAGT		
		AGGTGGT ACCCGTTCA		
		-		
GAM1385	LOC221838 3'	CTTAATCAGTGGTGGG 92543	GG	
		TTCATCACTG TAAG		
		AGGTGGTGAC ATTC		
		TA		
GAM1385	LOC221839 3'	CTTAATCAGTGATGGG 92496	GG	
		TTCATCACTG TAAG		
		AGGTAGTGAC ATTC		
		TA		
GAM1385	LOC222182 3'	CTTGGGGGCTTGGACCTTGATG 94190	CT	G _
	G	TCATCA GG TAAGTCTCCAAG		
		GGTAGT CC GTTCGGGGGTTT		
		T _ AG		
GAM1385	LOC253805 3'	TTGGGGGCGCAGTTATGGA 96441	C	G AAGT
		TTCAT ACTG GT CTCCAA		
		AGGTA TGAC CG GGGGTT		
		T G _		
GAM1385	LOC253868 3'	TTGAGGGCTTATTCAGTGGGGG 95585	AT	TC G
	A	TTC CACTGGGTAAGTC CAA		
		AGG GTGACTTATTCGG GTT		
		GG GA		
GAM1385	LOC253926 3'	TCAATGGCTTGTTTGCTGATGA 94923	CT	GG TCCAAG
	G	TTCATCA G TAAGTC		

		GAGTAGT T GTTCGG		
		CG TT TAACTT		
GAM1385	LOC254622 5'	AAGGAGATTTGGAGGTGA	96292	GGG AAG
		TCACT TAAGTCTCC		
		AGTGG GTTTAGAGG		
		AG_ AAG		
GAM1385	LOC254826 3'	TTGGAGGCTGGGGGTGA	97244	GGGTA
		TCACT AGTCTCCA		
		AGTGG TCGGAGGTT		
		GGG_		
GAM1385	LOC254826 3'	TTTGGAGATTTGTGGAAAAGTG	97245	GGG_
	A	TCACT TAAGTCTCCAAG		
		AGTGA GTTTAGAGGTTT		
		AAAGGT		
GAM1385	LOC255004 3'	CTGCCCGCTGACCCGGTGGTGA	95550	A CTCCAAG
	G	TTCATCACTGGGT AGT		
		GAGTGGTGGCCCA TCG		
		G CCCGTC		
GAM1385	LOC255082 5'	CTTGGGCCTGGCCAGTGGCGG	96396	AT A T T
		TC CACTGGGT AG C CCAAG		
		GG GTGACCCG TC G GGTTT		
		CG G C _		
GAM1385	LOC255772 3'	TTGGTGTCTGTGATGAG	96011	T GT AGTCT
		TTCATCAC GG A CCA		
		GAGTAGTG CC T GGTT		
		T TG _		
GAM1385	LOC256867 5'	CTTGGGGGCAAGGTGGGGTGAG	94864	A GGGTAA
		TTCATC CT GTCTCCAAG		
		GAGTGG GG CGGGGGTTC		
		_ TGGAA_		
GAM1385	LOC257144 3'	TTTGGAGAGTATAGTGGTAGGA	95817	_ GGTAAG
		TTC ATCACTG TCTCCAAG		
		AGG TGGTGAT AGAGGTTT		
		A ATG_		
GAM1385	LOC257478 3'	TGGAGGGCGGGATGGA	73108	A GGTAAG
		TTCATC CTG TCTCCA		
		AGGTAG GGC GGAGGT		
		_ G_		
GAM1385	LOC55924 3'	CTTGGGGGCTAGCTGGTGGAGG	38874	AT TG G A
	A	TTC CAC G TA GTCTCCAAG		

AGG GTG C AT CGGGGGTTC  
 AG GT G \_  
 GAM1385 LOC63928 3' CTTTCCTAGTGATGGA 42034 T  
 TTCATCACTGGG AAG  
 |||||  
 AGGTAGTGATCC TTC  
 T  
 GAM1385 LOC83690 5' CTTGGAGATTTTCCTGGGGA 48815 A TG T  
 TC C GG AAGTCTCCAAG  
 || || |||||  
 AG G CC TTTAGAGGTTC  
 G GT T  
 GAM1385 LOC89985 5' GGCTTATTTGGGGGTGGA 61020 A TG  
 TTCATC C GGTAAGTC  
 ||||| | |||||  
 AGGTGG G TTATTCGG  
 G GT  
 GAM1385 LOC90120 3' TGGGGGCAAGTGGGAG 61544 A GGGTAA  
 TTC TCACT GTCTCCA  
 ||| ||||| |||||  
 GAG GGTGA CGGGGGT  
 \_ A \_  
 GAM1385 LOC90139 3' TTTGGTCTGGGCTCAGTGGGAG 55406 A AAGTCT  
 TTC TCACTGGGT CCAAG  
 ||| ||||| |||||  
 GAG GGTGACTCG GGTTT  
 \_ GGTCT\_  
 GAM1385 LOC90408 5' TTGGAGATCAGGTAGTGA 62673 GGTA  
 TCACTG GTCTCCA  
 ||||| |||||  
 AGTGAT TAGAGGTT  
 GGAC\_  
 GAM1385 LOC90499 3' GGACTTCAGTGATG 63065 GTA  
 CATCACTGG AGTCT  
 ||||| |||||  
 GTAGTGACT TCAGG  
 \_  
 GAM1385 LOC90639 5' TTTGGAGACTTGACTAGTGG 63667 G  
 TCACTGG TAAGTCTCCAAG  
 ||||| |||||  
 GGTGATC GTTCAGAGGTTT  
 A  
 GAM1385 LOC90841 3' CTTGGAGCCTCTCTCGGTGGGG 64198 AT TA T  
 A TC CACTGGG AG CTCCAAG  
 || ||||| || |||||  
 AG GTGGCTC TC GAGGTTC  
 GG TC C  
 GAM1385 LOC91547 3' TGGAGAACGTGGTGG 66407 G AAG  
 TCACTG GT TCTCCA  
 ||||| || |||||



		GGTGGT CA AGAGGT		
		G ____		
GAM1385	LOC91565	3' TTATCCATTTATCTGTTGATGG 66466	CT	CTCCAAG
	A	TTCATCA GGGTAAGT		
		AGGTAGT TCTATTTA		
		TG CCTATTT		
GAM1385	LOC91694	5' TTTGATTTTCATT CAGTGATGG 66967	__	TCCAAG
	A	TTCATCACTGGGT AAGTC		
		AGGTAGT GACTTA TTTAG		
		CT TTT		
GAM1385	LOC92140	3' AGAATATACTCAGTGATGGA 68281	AG_	
		TTCATCACTGGGTA TCT		
		AGGTAGT GACTCAT AGA		
		ATA		
GAM1385	LOC93268	3' AGATTTATCCAGTGGT 71875		
		ATCACTGGGTAAGTCT		
		TGGTGACCTATTTAGA		
GAM1385	LOC94468	3' CTTGGGGAGCGGTTTGGAGGTG 60431	A	GG AAG
	GA	TTCATC CTG T TCTCCAAG		
		AGGTGG GGT G AGGGGTTC		
		A TT GCG		
GAM1386	ACPT	3' GTGCCAGGGATCCTGCTGA 54990	T	ATTGA
		TCAGCAGG ATTT AC		
		AGTCGTCC TAGG TG		
		_ GACCG		
GAM1386	ADAMTS5	3' GTGTTCAATAGATACC 22894		
		GGTATTTATTGAACAC		
		CCATAGATAACTTGTG		
GAM1386	AGL	5' TGTTTACTATACTTGCT 5372	TTAT	
		AGCAGGTAT TGAACA		
		TCGTTCATA ATTTGT		
		TC__		
GAM1386	APOA4	3' TTCAATAAAGCTGCTGA 4907	GTA	
		TCAGCAG TTTATTGAA		
		AGTCGTC AAATAACTT		
		G__		
GAM1386	ARHGAP6	3' TTTACCGAGTACCTGCTGA 25519	AT	
		TCAGCAGGTATTT TGAA		

			AGTCGTCCATGAG ATTT		
			CC		
GAM1386	ARHGAP6	3'	TTTACCGAGTACCTGCTGA 20411	AT	
			TCAGCAGGTATTT TGAA		
			AGTCGTCCATGAG ATTT		
			CC		
GAM1386	C21orf33	3'	TTCAGACCTGCTGA 16199	ATTTA	
			TCAGCAGGT TTGAA		
			AGTCGTCCA GACTT		
			_____		
GAM1386	CLASP1	3'	TGTCTTGTACAGCCTGCTGA 65313	ATT TGA	
			TCAGCAGGT TAT ACA		
			AGTCGTCCG ATG TGT		
			AC_ TTC		
GAM1386	CYP46	3'	TGCTCAATAAATGTGTGTTGA 21898	GG A	
			TCAGCA TATTTATTGA CA		
			AGTTGT GTAAATAACT GT		
			GT C		
GAM1386	DVL3	3'	GTGCTCAATAAATGGTAGCT 15374	AGG A	
			AGC TATTTATTGA CAC		
			TCG GTAAATAACT GTG		
			ATG C		
GAM1386	EIF2B1	3'	CAAGAAACACTTGCTGA 59657	A A	
			TCAGCAGGT TTT TTG		
			AGTCGTTCA AAA AAC		
			C G		
GAM1386	GALK1	3'	GTGCTCAATAAACTTGT 3850	AT A	
			GCAGGT TTATTGA CAC		
			TGTTCA AATAACT GTG		
			_____ C		
GAM1386	GDI1	3'	GTGTTCTGTGGTACTTGCTGA 59980	TATT	
			TCAGCAGGTATT GAACAC		
			AGTCGTTTCATGG CTTGTG		
			TGT_		
GAM1386	GUCY1B3	3'	CAATAAATATTTGTTGA 5965		
			TCAGCAGGTATTTATTG		
			AGTTGTTTATAAATAAC		
GAM1386	IDH3B	3'	GTGTTCAATAAAGAACATG 22578	G A_	
			CA GT TTTATTGAACAC		

			GT CA AAATAACTTGTG			
			A AG			
GAM1386	MEF2D	3'	GTGCTCAATAAATGAATG	96916	GG	A
			CA TATTTATTGA CAC			
			GT GTAAATAACT GTG			
			AA C			
GAM1386	MEF2D	3'	TCAATAAATGCTGA	96918	GGTA	
			TCAGCA TTTATTGA			
			AGTCGT AAATAACT			
			—			
GAM1386	MKI67	3'	TCATAAATACTTGCTGA	10049		T
			TCAGCAGGTATTTAT GA			
			AGTCGTTCATAAATA CT			
			—			
GAM1386	MT3	3'	GTGTTCCCTTTCCCTGCTGA	19881		TATTTATT
			TCAGCAGG GAACAC			
			AGTCGTCC CTTGTG			
			CTTTCC__			
GAM1386	NCOA6	5'	TGCTCAATAAATATTAGCTG	25980	AG	A
			CAGC GTATTTATTGA CA			
			GTCG TATAAATAACT GT			
			AT C			
GAM1386	NCOA6	5'	TTCTGGAATACCTACTG	25983	C	ATT
			CAG AGGTATTT GAA			
			GTC TCCATAAG CTT			
			A GT_			
GAM1386	NKX2E	5'	GTGCTCAGCGCTACCTGCTG	15244		TTTA A
			CAGCAGGTA TTGA CAC			
			GTCGTCCAT GACT GTG			
			CGC_ C			
GAM1386	PLA2G2D	3'	GTGCTCAATTCATGCCTGT	24799	TT	A
			GCAGGTAT ATTGA CAC			
			TGTCCGTA TAACT GTG			
			CT C			
GAM1386	PLA2G4C	3'	GTGCTCAATAAATGCTTGCTGA	73416		A
			TCAGCAGGTATTTATTGA CAC			
			AGTCGTTTCGTAAATAACT GTG			
			C			
GAM1386	PTGFRN	3'	GTGTTTCAGAGAGCTGCTGA	67192	GTA	A
			TCAGCAG TTT TTGAACAC			

AGTCGTC GAG GACTTGTG  
 \_\_\_\_ A  
 GAM1386 PX19 3' TCAATAAATACTTGTGA 25088  
 TCAGCAGGTATTTATTGA  
 |||||  
 AGTTGTTCATAAATAACT

GAM1386 RABGGTB 3' TGTTC AATAACTGAGCT 15930 A\_ ATT  
 AGC GGT TATTGAACA  
 ||| ||| |||||  
 TCG TCA ATA ACTTGT  
 AG \_\_\_\_

GAM1386 RNMT 3' GTGTTCAATATGTATTGCTGA 13724 G T  
 TCAGCAG TAT TATTGAACAC  
 ||||| ||| |||||  
 AGTCGTT ATG ATA ACTTGTG  
 \_ T

GAM1386 RPLP1 3' TGTTC AATAAAAAGCTGA 6402 AGGTA  
 TCAGC TTTATTGAACA  
 |||| |||||  
 AGTCG AAATA ACTTGT  
 AA\_\_\_\_

GAM1386 SAA4 3' GTGTTCAATAAATGTTTGT 21493 GG  
 GCA TATTTATTGAACAC  
 ||| |||||  
 TGT GTAAATA ACTTGTG  
 TT

GAM1386 SLC17A5 3' GTGTTCAACACTACGTGT 24893 G TTTA  
 GCA GTA TTGAACAC  
 ||| ||| |||||  
 TGT CAT AACTTGTG  
 G CAC\_

GAM1386 SLC18A1 3' TGTTCACTACTTGCT 11751 TTTAT  
 AGCAGGTA TGAACA  
 ||||| |||||  
 TCGTTCAT ACTTGT

GAM1386 SLC1A4 3' TGTTTTTCCAATTACCTGCTGA 11719 TTTATT\_  
 TCAGCAGGTA GAACA  
 ||||| |||||  
 AGTCGTCCAT TTTGT  
 TAACCTT

GAM1386 SLC20A2 3' TTCAATAAATCTTGT 22177 T  
 GCAGG ATTTATTGAA  
 |||| |||||  
 TGTTC TAAATAACTT

GAM1386 SLC8A1 3' TGTTCACTTACCTGCTGA 40840 TTTAT  
 TCAGCAGGTA TGAACA  
 ||||| |||||

			AGTCGTCCAT	ACTTGT		
			TC__			
GAM1386	SOD3	5'	CAATAAACATTTGTTG	11860	A	
			CAGCAGGT TTTATTG			
			GTTGTTTA AAATAAC			
			C			
GAM1386	SPAG11	3'	GTGTTCAATAAATATTTGTTGA	33259		
			TCAGCAGGTATTTATTGAACAC			
			AGTTGTTTATAAATAACTTGTG			
GAM1386	SPAG11	3'	GTGTTCAATAAATATTTGTTGA	54244		
			TCAGCAGGTATTTATTGAACAC			
			AGTTGTTTATAAATAACTTGTG			
GAM1386	SPAG11	3'	GTGTTCAATAAATATTTGTTGA	54250		
			TCAGCAGGTATTTATTGAACAC			
			AGTTGTTTATAAATAACTTGTG			
GAM1386	SPAG11	3'	GTGTTCAATAAATATTTGTTGA	54252		
			TCAGCAGGTATTTATTGAACAC			
			AGTTGTTTATAAATAACTTGTG			
GAM1386	WDR8	3'	AATAAATACTTGCTGA	35158		
			TCAGCAGGTATTTATT			
			AGTCGTTCATAAATAA			
GAM1386	YWHAZ	3'	TGCTCAATAAATATTGATGA	12707	GCA	A
			TCA GGTATTTATTGA CA			
			AGT TTATAAATAACT GT			
			AG_ C			
GAM1386	Z39IG	3'	GTGCTCAATAAATATCT	23436	A	
			AGGTATTTATTGA CAC			
			TCTATAAATAACT GTG			
			C			
GAM1386	ZNF2	3'	GTGCTCAATAAATATTTATATG	40807	GC_	A
	A		TCA AGGTATTTATTGA CAC			
			AGT TTTATAAATAACT GTG			
			ATA C			
GAM1386	AFAP	3'	TGTTCAATAAATATAGTT	41310	AG	
			AGC GTATTTATTGAACA			

TTG TATAAATAACTTGT  
 A\_  
 GAM1386 AKAP6 3' TTCAATAAAAATTTACTGA 14998 C A  
 TCAG AGGT TTTATTGAA  
 |||| ||| |||||  
 AGTC TTTA AAATAACTT  
 A A  
 GAM1386 ARHGEF9 3' GTGTTCAATGGGACCTGCTG 30819 A  
 CAGCAGGT TTTATTGAACAC  
 ||||| |||||  
 GTCGTCCA GGGTAACTTGTG  
 —  
 GAM1386 cerk 3' TGTTCATAAGAAACC 42854 A\_  
 GGT TTTATTGAACA  
 ||| |||||  
 CCA GAATAACTTGT  
 AA  
 GAM1386 DCLRE1A 5' GTGTTTGGGATACCTGTT 69166 TA TG  
 AGCAGGTATT T AACAC  
 ||||| | ||||  
 TTGTCCATAG G TTGTG  
 — GT  
 GAM1386 DKFZp434E0519 5' GTAACATACCTGCTGA 49992 —  
 TCAGCAGGTAT TTAT  
 ||||| ||||  
 AGTCGTCCATA AATG  
 C  
 GAM1386 DKFZp547O146 3' GTGTTGCCAAAGATACCTGCTG 39567 A \_  
 A TCAGCAGGTATTT TTG AACAC  
 ||||| ||| ||||  
 AGTCGTCCATAGA AAC TTGTG  
 — CG  
 GAM1386 DKFZp761O17121 3' GTGTTCAACAGTGCATGT 50143 G TA  
 GCA GTATT TTGAACAC  
 ||| |||| |||||  
 TGT CGTGA AACTTGTG  
 A C\_  
 GAM1386 E2F6 3' GTGCTCAATAAATGTCTG 8716 GT A  
 CAG ATTTATTGA CAC  
 ||| ||||| |||  
 GTC TAAATAACT GTG  
 TG C  
 GAM1386 ERO1L 3' CAATAAATATTTGTTGG 27429  
 TCAGCAGGTATTTATTG  
 |||||  
 GGTTGTTTATAAATAAC  
 GAM1386 FLJ10314 5' GTGTTCAAGGCTACCCAGTGA 36015 GCA TTTA  
 TCA GGTA TTGAACAC  
 ||| ||| |||||

AGT CCAT AACTTGTG  
 GAC CGG\_  
 GAM1386 FLJ11164 3' CAGAAACTCCTGCTGA 37122 TA A  
 TCAGCAGG TTT TTG  
 ||||| ||| |||  
 AGTCGTCC AAA GAC  
 TC A  
 GAM1386 FLJ13340 3' GTTTTTTATCCTGCTGA 54110 TATT TT  
 TCAGCAGG TA GAAC  
 ||||| || |||  
 AGTCGTCC AT TTTG  
 T\_\_ TT  
 GAM1386 FLJ14050 3' GTGCTCAATAAACGATAACTGC 60328 G \_\_\_\_ A  
 GCAG TATT TATTGA CAC  
 ||| ||| ||||| |||  
 CGTC ATAG ATA ACT GTG  
 A CAA C  
 GAM1386 FLJ14437 3' TTCAATAAATATTTGCTGG 50831  
 TCAGCAGGTATTTATTGAA  
 ||||| ||||| |||||  
 GGTCGTTTATAAATAACTT  
  
 GAM1386 FLJ14675 3' CATTGGAACCTGCTGA 51518 A AT\_  
 TCAGCAGGT TTT TG  
 ||||| ||| ||  
 AGTCGTCCA AAG AC  
 A GTT  
 GAM1386 FLJ20132 3' GTGCTCAATAAATTGCT 34607 GGT A  
 AGCA ATTTATTGA CAC  
 ||| ||||| |||  
 TCGT TAAATAACT GTG  
 \_\_\_\_ C  
 GAM1386 GOA 3' TGCTCAATAAACACTTGTTGA 78077 A A  
 TCAGCAGGT TTTATTGA CA  
 ||||| ||||| ||  
 AGTTGTTCA AAATAACT GT  
 C C  
 GAM1386 GREAT 5' TCAGAACTCCTGCTGA 55484 TA AT  
 TCAGCAGG TTT TGA  
 ||||| ||| |||  
 AGTCGTCC AAG ACT  
 TC \_\_\_\_  
 GAM1386 KIAA0014 3' GTGCCCAGCTGGTTCCTGCTGA 27850 T TA AA  
 TCAGCAGG ATT TTG CAC  
 ||||| ||| ||| |||  
 AGTCGTCC TGG GAC GTG  
 T TC CC  
 GAM1386 KIAA0227 3' GTGTTCAACAAATGCTTGT 60701 A  
 GCAGGTATTT TTGAACAC  
 ||||| ||||| |||||

			TGTTTCGTAAA AACTTGTG		
			C		
GAM1386	KIAA0322	3'	CAAGAAAACACCTGCTG	92750	A A_
			CAGCAGGT TTT TTG		
			GTCGTCCA AAA AAC		
			C AG		
GAM1386	KIAA0377	3'	GTGCTCAATAAATATAAACT	27797	CAG A
			AG GTATTTATTGA CAC		
			TC TATAAATAACT GTG		
			AAA C		
GAM1386	KIAA0637	3'	GTTCAATGACACGCTGA	29239	AG ATT
			TCAGC GT TATTGAAC		
			AGTCG CA GTAACCTG		
			CA _		
GAM1386	KIAA1077	3'	GTTTTTAAATACCAGCT	72910	A TT
			AGC GGTATTTA GAAC		
			TCG CCATAAAT TTTG		
			A T_		
GAM1386	KIAA1077	5'	TGTTCTGAATACCTCTGA	72912	C TT
			TCAG AGGTATTTA GAACA		
			AGTC TCCATAAGT CTTGT		
			- -		
GAM1386	KIAA1524	5'	TTCAGTTGACCTACTGA	73456	C ATTT
			TCAG AGGT ATTGAA		
			AGTC TCCA TGACTT		
			A GT_		
GAM1386	MGC11316	3'	GTGCCATTAAATACCAACTGA	51942	CA T A_
			TCAG GGTATTTA TG AC		
			AGTC CCATAAAT AC TG		
			AA T CG		
GAM1386	MGC12679	3'	TCAATAAATATTGAATGA	51207	GCA
			TCA GGTATTTATTGA		
			AGT TTATAAATAACT		
			AAG		
GAM1386	MGC13071	3'	GTTCAATAAACATTAGC	51089	AG A
			GC GT TTTATTGAAC		
			CG TA AAATAACTTG		
			AT C		
GAM1386	MGC26590	3'	TGTTCAATAAAAGTTTTGC	56288	TA_
			GCAGG TTTATTGAACA		



			CGTTT AAATAACTTGT		
			TGA		
GAM1386	MGC2747	3'	TTCAGTGT TACTTGCTGA	44091	TT
			TCAGCAGGTA TATTGAA		
			AGTCGTT CAT GTGACTT		
			T_		
GAM1386	MGC3248	3'	GTGTTCAATAAAGAACC	50656	A_
			GGT TTTATTGAACAC		
			CCA AAATAACTTGTG		
			AG		
GAM1386	MGC4606	3'	TGTCCGTACCTGCTGG	44510	TTATT A
			TCAGCAGGTAT G ACA		
			GGTCGTCCATG C TGT		
			_____C		
GAM1386	MYT1	3'	GTGCTCAATGAGGGCCGCTGA	15781	A A A
			TCAGC GGT TTTATTGA CAC		
			AGTCG CCG GAGTAACT GTG		
			_ G C		
GAM1386	NTSR2	3'	TGCTCAATAAATTTTGTCTGG	24718	T A
			TCAGCAGG ATTTATTGA CA		
			GGTCGTTT TAAATAACT GT		
			T C		
GAM1386	NXP-2	3'	TGTTTTGAAATACCTGT	71110	ATT
			GCAGGTATTT GAACA		
			TGTCCATAAA TTTGT		
			GT_		
GAM1386	PELI1	5'	GTGTTCAAGAGGACTGCTGA	40279	GTA A
			TCAGCAG TTT TTGAACAC		
			AGTCGTC GAG AACTTGTG		
			AG_ _		
GAM1386	PRSC	3'	TGCTCAATCGTGCACTGC	21673	_ TT A
			GCAG GTAT ATTGA CA		
			CGTC CGTG TAACT GT		
			A C_ C		
GAM1386	SC65	3'	GTGCTCAATAAATGTTTGT	21295	GG A
			GCA TATTTATTGA CAC		
			TGT GTAAATAACT GTG		
			TT C		
GAM1386	SPAG7	3'	TTCAATAAATACTGTT	16885	G
			AGCAG TATTTATTGAA		

TTGTC ATAAATAACTT

GAM1386 TBDN100 3' GTTTTTTATCCTGCTGA 46959 TATT TT  
TCAGCAGG TA GAAC  
||||||| || ||||  
AGTCGTCC AT TTTG  
T\_\_ TT

GAM1386 TBX19 3' GTGCCCAATAAACATTTGCTGA 17652 A AA  
TCAGCAGGT TTTATTG CAC  
||||||| ||||| |||  
AGTCGTTTA AAATAAC GTG  
C CC

GAM1386 TIP-1 3' TCAATAAAAATGCTGG 27506 GGTA  
TCAGCA TTTATTGA  
||||| |||||  
GGTCGT AAATAACT  
AA\_\_

GAM1386 TRIM26 3' GTGCTCAATAAAGACTTGTTGA 12893 A A  
TCAGCAGGT TTTATTGA CAC  
||||||| ||||| |||  
AGTTGTTCA AAATAACT GTG  
G C

GAM1386 TRPC3 3' GTGCTCAATAAATGTTGA 12396 GGTA A  
TCAGCA TTTATTGA CAC  
||||| ||||| |||  
AGTTGT AAATAACT GTG  
\_\_\_\_ C

GAM1386 VPS33B 3' GTGTCCACCAACTACCTGCT 37906 T AT A  
AGCAGGTA TT TG ACAC  
||||||| || || ||||  
TCGTCCAT AA AC TGTG  
C CC C

GAM1386 ZFP95 3' TGCCCAATAAATATTTGTTGA 27382 AA  
TCAGCAGGTATTTATTG CA  
||||||| ||||| |||  
AGTTGTTTATAAATAAC GT  
CC

GAM1386 ZFP95 3' TGCCCAATAAATATTTGTTGA 59026 AA  
TCAGCAGGTATTTATTG CA  
||||||| ||||| |||  
AGTTGTTTATAAATAAC GT  
CC

GAM1386 LOC126364 3' GTGCTCAATAAATGCTT 75696 A  
AGGTATTTATTGA CAC  
||||||| ||||| |||  
TTCGTAAATAACT GTG  
C

GAM1386 LOC142893 5' GTGATTAAATACCTGT 82878 AT A  
GCAGGTATTT TGA CAC  
||||||| ||| |||

TGTCCATAAA ATT GTG  
 — A  
 GAM1386 LOC142955 5' GTGTTCAATAAATAATTTTGA 76448 CAGG  
 TCAG TATTTATTGAACAC  
 ||| |||||  
 AGTT ATAAATAACTTGTG  
 TTTA  
 GAM1386 LOC145622 5' TGCTCAATAGGATTACGCTGA 77317 AG — A  
 TCAGC GTA TTTATTGA CA  
 |||| || ||||| ||  
 AGTCG CAT GGATAACT GT  
 — TA C  
 GAM1386 LOC145660 5' GTGTTCAATAAACATCTCT 77324 C A  
 AG AGGT TTTATTGAACAC  
 || ||| |||||  
 TC TCTA AAATAACTTGTG  
 — C  
 GAM1386 LOC145739 3' TCAATAAATATTGCT 77442 G  
 AGCAG TATTTATTGA  
 |||| |||||  
 TCGTT ATAAATAACT  
 —  
 GAM1386 LOC146714 5' TTCATTGAGCACCTGCTG 83744 A T  
 CAGCAGGT TTTA TGAA  
 ||||| ||| |||  
 GTCGTCCA GAGT ACTT  
 C T  
 GAM1386 LOC146802 3' TGTTCAACACCTCTGA 78138 C ATT TA  
 TCAG AGGT TTGAACA  
 ||| ||| |||||  
 AGTC TCCA AACTTGT  
 — C —  
 GAM1386 LOC147040 3' GTGTCTGTGGTATACCTGT 78237 — T A  
 GCAGGTAT TTAT GA CAC  
 ||||| ||| |||  
 TGTCCATA GGTG CT GTG  
 T T —  
 GAM1386 LOC148936 3' TCAATAAATATTGGTT 84302 AG  
 AGC GTATTTATTGA  
 || |||||  
 TTG TATAAATAACT  
 GT  
 GAM1386 LOC148938 3' TCAATAAATATTGGTT 84283 AG  
 AGC GTATTTATTGA  
 || |||||  
 TTG TATAAATAACT  
 GT  
 GAM1386 LOC150035 5' GTGTCCAACCTGAAACCTGT 84810 A TA A  
 GCAGGT TT TTG ACAC  
 |||| || ||| |||

	TGTCCA AG AAC TGTG		
	A TC C		
GAM1386 LOC150142 5'	GTGTTGGAATAGCTGCTGA 79579	G	ATTG
	TCAGCAG TATTT AACAC		
	AGTCGTC ATAAG TTGTG		
	G G__		
GAM1386 LOC150630 3'	GTGCTCAATAAATACTGAGTGA 85110	GCA	A
	TCA GGTATTTATTGA CAC		
	AGT TCATAAATAACT GTG		
	GAG C		
GAM1386 LOC150978 3'	GTGTTCAATAAAAAGCTGA 80086	AGGTA	
	TCAGC TTTATTGAACAC		
	AGTCG AAATAACTTGTG		
	AA__		
GAM1386 LOC151465 3'	TGTTCAATGTCCTCTGA 62780	C	TATT
	TCAG AGG TATTGAACA		
	AGTC TCC GTAACCTGT		
	_ T__		
GAM1386 LOC152225 5'	GTGCTCAATAAAAGCTTGTT 85595	A	A
	AGCAGGT TTTATTGA CAC		
	TTGTTTCG AAATAACT GTG		
	A C		
GAM1386 LOC152453 3'	GTGTTGGTGCATACCTGT 80603	T	TG A
	GCAGGTAT TAT A CAC		
	TGTCCATA GTG T GTG		
	C GT_		
GAM1386 LOC154562 3'	TCAATAAATACTTGTT 81093		
	AGCAGGTATTTATTGA		
	TTGTTTCATAAATAACT		
GAM1386 LOC154739 5'	TCAGCGGGCCACTTGCTGA 86240	A_	TA
	TCAGCAGGT TT TTGA		
	AGTCGTTCA GG GACT		
	CC GC		
GAM1386 LOC157660 3'	TCAACAAATATTTGTTGA 86511	A	
	TCAGCAGGTATTT TTGA		
	AGTTGTTTATAAA AACT		
	C		
GAM1386 LOC158310 3'	GTGCTCAATAAATATCTGCCGA 86761	A	A
	TC GCAGGTATTTATTGA CAC		

	AG CGTCTATAAATAACT GTG	
	C C	
GAM1386 LOC163404 3'	GTGTTCAACAAAAATGTGATGA 82129	G G A A
	TCA CA GT TTT TTGAACAC	
	AGT GT TA AAA AACTTGTG	
	A G A C	
GAM1386 LOC197407 3'	CATTCAATACTTGTGTA 88058	TAT
	TCAGCAGGTATT TG	
	AGTTGTTCATAA AC	
	CTT	
GAM1386 LOC197408 5'	CATTCAATACTTGTGTA 89748	TAT
	TCAGCAGGTATT TG	
	AGTTGTTCATAA AC	
	CTT	
GAM1386 LOC203068 3'	TCAATAAATACTTGTT 89256	
	AGCAGGTATTTATTGA	
	TTGTTCATAAATAACT	
GAM1386 LOC203286 3'	TGTCCAAGTCCCTGCTGG 90505	TATTTA A
	TCAGCAGG TTG ACA	
	GGTCGTCC AAC TGT	
	CTG__ C	
GAM1386 LOC220430 5'	TTCAAAATACCTGC 94337	AT
	GCAGGTATTT TGAA	
	CGTCCATAAA ACTT	
GAM1386 LOC220930 5'	GTGCTCAATAAATTTATGCT 93133	GGT A
	AGCA ATTTATTGA CAC	
	TCGT TAAATAACT GTG	
	ATT C	
GAM1386 LOC222681 5'	TCTGTTGATCCTGCTGA 92854	T T T
	TCAGCAGG ATT AT GA	
	AGTCGTCC TAG TG CT	
	_ T T	
GAM1386 LOC253681 3'	GTGTCTGTGGTATACCTGT 95134	_ T A
	GCAGGTAT TTAT GA CAC	
	TGTCCATA GGTG CT GTG	
	T T _	
GAM1386 LOC253805 3'	GTGTTGAGATAATACCTGT 96434	TA G
	GCAGGTATT TT AACAC	

	TGTCCATAA GA TTGTG		
	TA G		
GAM1386 LOC255104 3'	TGGTGAATACATGCTGA 95400	G	
	TCAGCA GTATTTATTG		
	AGTCGT CATAAGTGGT		
	A		
GAM1386 LOC256087 3'	GTGTTCAATAAATGTTT 95116	GG	
	A TATTTATTGAACAC		
	T GTAAATAACTTGTG		
	TT		
GAM1386 LOC256338 3'	TCAATAAATAATTGTTGA 94611	G	
	TCAGCAG TATTTATTGA		
	AGTTGTT ATAAATAACT		
	A		
GAM1386 LOC257494 3'	GTGCTCAATAAAGACTTGTTGA 97797	A	A
	TCAGCAGGT TTTATTGA CAC		
	AGTTGTTCA AAATAACT GTG		
	G C		
GAM1386 LOC257507 5'	TCTGTTGATCCTGCTGA 97776	T	T T
	TCAGCAGG ATT AT GA		
	AGTCGTCC TAG TG CT		
	_ T T		
GAM1386 LOC257625 5'	TCTGTTGATCCTGCTGA 97907	T	T T
	TCAGCAGG ATT AT GA		
	AGTCGTCC TAG TG CT		
	_ T T		
GAM1386 LOC50999 3'	GTGCAAGTAATCCTGCTGA 32102	T	TA A
	TCAGCAGG ATT TTG AC		
	AGTCGTCC TAA AAC TG		
	_ TG G		
GAM1386 LOC91628 3'	GTGCTCAATAAATTGTAGCTG 66761	AGGT	A
	CAGC ATTTATTGA CAC		
	GTCG TAAATAACT GTG		
	ATGT C		
GAM1386 LOC91907 3'	GTGTGGCAATATCTGCTGA 67496	TATTGA	
	TCAGCAGGTATT ACAC		
	AGTCGTCTATAA TGTG		
	CGG__		
GAM1386 LOC92755 3'	TCAATAAATACTTGTT 70502		
	AGCAGGTATTTATTGA		

TTGTTTCATAAATAACT

GAM1387 AICDA	5'	GCCTGAGACTTGCAGGGAGGCA	40329	C	ATTTGC__
AGAA		TTC TGCCTCCCT	CAGGC		
		AAG ACGGAGGGA	GTCCG		
		A	CGTTCAGA		
GAM1387 ANK1	3'	GCCTCCGGCCCAGGGAGGCCAG	40027	CT	ATTT __
AA		TTC GCCTCCCT	GCC AGGC		
		AAG CGGAGGGA	CGG TCCG		
		AC	CC__ CC		
GAM1387 ANK1	3'	GCCTCCGGCCCAGGGAGGCCAG	3473	CT	ATTT __
AA		TTC GCCTCCCT	GCC AGGC		
		AAG CGGAGGGA	CGG TCCG		
		AC	CC__ CC		
GAM1387 EIF2C1	3'	CCCAAATCCAGAGGAAGCAAGG	24170	_ C _ _	CCA
A		TCCT GC TCC CT ATTTG	GG		
		AGGA CG AGG GA TAAAC	CC		
		A A A CC	__		
GAM1387 IKBKG	3'	CCCGGCACTGGGGAAGTCAAGA	13311	C _ C	TT A
A		TTC TG C TCCCTA	TGCC GG		
		AAG AC G AGGGGT	ACGG CC		
		A T A	C_ C		
GAM1387 IKBKG	3'	CCCGGCACTGGGGAAGTCAAGA	94663	C _ C	TT A
A		TTC TG C TCCCTA	TGCC GG		
		AAG AC G AGGGGT	ACGG CC		
		A T A	C_ C		
GAM1387 LY9	3'	AAATAAAAGGCAGGAA	71680	CCC	
		TTCTGCCT	TATTT		
		AAGGACGGA	ATAAA		
		AA_			
GAM1387 MAFF	3'	TGGCAAATAGGGAGACAAGGA	24655	GC_	
		TCCT	CTCCCTATTTGCCA		
		AGGA	GAGGGATAAACGGT		
		ACA			
GAM1387 MC1R	5'	GCCCAGATGGAAGGAGGCAGG	9954	__	CCA
		CCTGCCTCC	CTATTTG GGC		
		GGACGGAGG	GGTAGAC CCG		
		AA	__		
GAM1387 MYO15A	3'	GCCTGAGGGAGGAGGCAGGAG	32671	_	ATTTGC
		TTCTGCCTCC	CT CAGGC		

GAGGACGGAGG GG GTCCG  
 A GA\_\_\_\_  
 GAM1387 NRG1 3' GCAAATAGAAAACAGGAA 25646 CCTCC  
 TTCCTG CTATTTGC  
 ||||| |||||  
 AAGGAC GATAAACG  
 AAAA\_  
 GAM1387 NRG1 3' GCAAATAGAAAACAGGAA 25659 CCTCC  
 TTCCTG CTATTTGC  
 ||||| |||||  
 AAGGAC GATAAACG  
 AAAA\_  
 GAM1387 SEPN1 3' GCCTGGCAGAGGAAGAAGGAA 66369 GC C AT  
 TTCCT CT CCT TTGCCAGGC  
 |||| |||| |||||  
 AAGGA GA GGA GACGGTCCG  
 A\_ A \_  
 GAM1387 SMURF1 3' GCCTAACCCGCGGGAGGCGGAA 92453 T TATTTGCC  
 TTCC GCCTCCC AGGC  
 ||| ||||| |||  
 AAGG CGGAGGG TCCG  
 \_ CGCCCAA\_  
 GAM1387 STAT6 3' GCCTAGGACGGATAGGCAGGAA 12021 CCCT \_ \_  
 TTCCTGCCT ATTTG CC AGGC  
 ||||| |||| |||||  
 AAGGACGGA TAGGC GG TCCG  
 \_ A A  
 GAM1387 TFF3 3' GCCCAGGCCTCAAGGGCAGGAA 63566 CCCTATTT A\_  
 TTCCTGCCT GCC GGC  
 ||||| ||| |||  
 AAGGACGGG CGG CCG  
 AACTC\_ AC  
 GAM1387 TOP3B 5' GCCCGGCGGCTCAGAAAGGCGG 14129 CC AT\_ A  
 GAA TTCCTGCCT CT TTGCC GGC  
 ||||| || ||||| |||  
 AAGGGCGGA GA GGCGG CCG  
 AA CTC C  
 GAM1387 VAV1 3' GCCTTGGCAGAGAGACGAG 18305 C\_ A \_  
 CTC CT TTTGCCA GGC  
 ||| || ||||| |||  
 GAG GA AGACGGT CCG  
 CA G T  
 GAM1387 YWHAB 5' GCTGTGGATAGAGAAGCAGGAA 12692 C C TG CA  
 TTCCTGC TC CTATT C GGC  
 ||||| || |||| | |||  
 AAGGACG AG GATAG G TCG  
 A A GT\_  
 GAM1387 AF020591 3' GCCTGGCAAACATGGCA 27141 TCCCTA  
 TGCC TTTGCCAGGC  
 ||| |||||



ACGG AAACGGTCCG  
 TAC\_\_  
 GAM1387 BCL2L1 3' CCTCAGGCAGGAAGGGCAGGAA 56804 CC ATT \_\_  
 TTCCTGCCT CT TGCC AGG  
 ||||| || ||| ||  
 AAGGACGGG GG ACGG TCC  
 AA \_\_ AC  
 GAM1387 BNIP-S 5' TAAAGAAGGAGGCAGGAA 56263 CTA  
 TTCCTGCCTCC TTTG  
 ||||| |||  
 AAGGACGGAGG AAAT  
 AAG  
 GAM1387 BTBD3 5' GCAAATAAGAGAAACAGGAA 30311 C\_\_ CC  
 TTCCTG CTC TATTTG  
 |||| ||| |||||  
 AAGGAC GAG ATAAACG  
 AAA A\_  
 GAM1387 C20orf28 3' GCCTGAGACGGGAGGCAGGAA 31224 TAT GC  
 TTCCTGCCTCCC TT CAGGC  
 ||||| || |||||  
 AAGGACGGAGGG AG GTCCG  
 C\_\_ A\_  
 GAM1387 CHODL 5' CCCGGCAGGGAGGCAGGGA 46310 ATTT A  
 TTCCTGCCTCCCT GCC GG  
 ||||| ||| ||  
 AGGGACGGAGGGA CGG CC  
 \_\_ C  
 GAM1387 D2S448 3' CCTGAAGGGAAGCAGG 73519 C ATTTGC  
 CCTGC TCCCT CAGG  
 |||| ||| |||  
 GGACG AGGGA GTCC  
 A A\_\_  
 GAM1387 DKFZP434K1772 3' GCCTTACTCAGGAAGGCAGGAG 67714 C ATTTGCC  
 TTCCTGCCT CCT AGGC  
 ||||| ||| |||  
 GAGGACGGA GGA TCCG  
 A CTCAT\_\_  
 GAM1387 DKFZp547I094 3' CCTGGCAACCTGAGGGAGG 49637 AT\_\_  
 CCTCCCT TTGCCAGG  
 ||||| |||||  
 GGAGGGA AACGGTCC  
 GTCC  
 GAM1387 DKFZP547L112 3' CCTGGATATAGCAAGGCAGGAA 66529 CC TTG  
 TTCCTGCCT CTAT CCAGG  
 ||||| ||| |||||  
 AAGGACGGA GATA GGTCC  
 AC TA\_  
 GAM1387 FABP7 5' CAAATAAGAAGGCAGGAG 7542 CCC  
 TTCCTGCCT TATTTG  
 ||||| |||||

GAGGACGGA ATAAAC  
 AGA  
 GAM1387 FLJ14957 3' CCCAAAGTGGGAGGCAGGGA 51744 TA CCA  
 TTCCTGCCTCCC TTTG GG  
 ||||| ||| ||  
 AGGGACGGAGGG AAAC CC  
 TG \_\_\_\_  
 GAM1387 FLJ20343 3' CCTGGCAAACCTGACCAG 34998 CC CCTA  
 CTG TC TTTGCCAGG  
 ||| || |||||  
 GAC AG AAACGGTCC  
 C\_ TC\_\_  
 GAM1387 FLJ23185 3' CCTGGCAGGATGAGGCAGAGA 46830 \_ CCTA  
 TC CTGCCTC TTTGCCAGG  
 || ||||| |||||  
 AG GACGGAG GGACGGTCC  
 A TA\_\_  
 GAM1387 GGA2 3' GCCTGATGGGTGGGAGAAGGAA 56882 GC T GC  
 TTCCT CTCCC ATTT CAGGC  
 |||| |||| ||| ||||  
 AAGGA GAGGG TGGG GTCCG  
 A\_ \_ TA  
 GAM1387 GGA2 3' GCCTGATGGGTGGGAGAAGGAA 30468 GC T GC  
 TTCCT CTCCC ATTT CAGGC  
 |||| |||| ||| ||||  
 AAGGA GAGGG TGGG GTCCG  
 A\_ \_ TA  
 GAM1387 HDAC11 3' GCCCATAGGTCCAGGGAGGCAG 45718 ATTT A\_\_\_\_  
 G CCTGCCTCCCT GCC GGC  
 ||||| ||| |||  
 GGACGGAGGGA TGG CCG  
 CC\_\_ ATAC  
 GAM1387 IKKE 5' CACAAGGAGGCAGGGA 25746 CTAT CCA  
 TTCCTGCCTCC TTG G  
 ||||| ||| |  
 AGGGACGGAGG AAC C  
 \_\_\_\_ A\_  
 GAM1387 IL1F10 3' CAAGAAGGAGGCAGGAA 50771 CTA  
 TTCCTGCCTCC TTTG  
 ||||| |||  
 AAGGACGGAGG GAAC  
 AA\_  
 GAM1387 KIAA0370 5' GCCCAGCAAATAGGAGCCTGGA 73209 T\_ CTC CA  
 G TTCC GC CCTATTTGC GGC  
 ||| || ||||| |||  
 GAGG CG GGATAAACG CCG  
 TC A\_\_ AC  
 GAM1387 KIAA0551 3' GCCTGGTTGAGAAGGAGAG 66839 \_ A\_ T  
 CTC CCT TT GCCAGGC  
 ||| ||| || |||||

GAG GGA AG TGGTCCG  
 A AG T  
 GAM1387 KIAA1183 3' CCCGGATGGGAGGAGGAA 62530 G TATTTG A  
 TTCCT CCTCCC CC GG  
 |||| |||| ||  
 AAGGA GGAGGG GG CC  
 \_ TA\_\_ C  
 GAM1387 KIAA1464 3' CCTGACCCATGGAGGCAGGAG 68264 CTATTTGC  
 TTCCTGCCTCC CAGG  
 ||||| ||||  
 GAGGACGGAGG GTCC  
 TACCCA\_  
 GAM1387 MAPK8IP3 3' GCCTGGTAGATGAAGCAG 52987 C CCT  
 CTGC TC ATTTGCCAGGC  
 ||| || |||||  
 GACG AG TAGATGGTCCG  
 A \_  
 GAM1387 MGC2306 3' GCCTGGCAGGGGGTGAAGGCAG 50963 \_ AT  
 GAG TTCCTGCCT CCCT TTGCCAGGC  
 ||||| ||| |||||  
 GAGGACGGA GGGG GACGGTCCG  
 AGT \_  
 GAM1387 MGC2865 5' GCCTGGCAAACCGAAGCAAGAA 50451 C C CCTA  
 TTC TGC TC TTTGCCAGGC  
 ||| ||| || |||||  
 AAG ACG AG AAACGGTCCG  
 A A CC\_  
 GAM1387 MGC9753 3' GCCTGATTTTGGGGAGGAGGAA 53049 G TTTGC  
 TTCCT CCTCCCTA CAGGC  
 |||| ||||| ||||  
 AAGGA GGAGGGGT GTCCG  
 \_ TTTA\_  
 GAM1387 PALM 3' GCCTGGTAGGAGAGAGACAGGA 10414 C C A  
 TCCTG CTC CT TTTGCCAGGC  
 |||| ||| || |||||  
 AGGAC GAG GA GGATGGTCCG  
 A A \_  
 GAM1387 PDZD2 5' CCTGGCACGGAAGGAGGAA 80866 G C TATT  
 TTCCT CCT CC TGCCAGG  
 |||| ||| || |||||  
 AAGGA GGA GG ACGGTCC  
 \_ A C\_  
 GAM1387 PLPL 3' CCTGGAGGGGGAGGCAGGAG 39431 ATTTG  
 TTCCTGCCTCCCT CCAGG  
 ||||| ||||  
 GAGGACGGAGGGG GGTCC  
 GA\_  
 GAM1387 RABEX5 3' GCCTGGAATGGAAGGCGGGAA 27186 C TATTTG  
 TTCCTGCCT CC CCAGGC  
 ||||| || |||||

AAGGGCGGA GG GGTCCG  
 A TAA\_\_\_\_  
 GAM1387 SHANK3 5' GCCTGCTCGCAGGGAGGCAGAG 65500 \_ ATTT C  
 A TC CTGCCTCCCT GC AGGC  
 || ||||| || ||||  
 AG GACGGAGGGA CG TCCG  
 A CGCT \_  
 GAM1387 SRF 5' CCGGGCCACAGGGGCAGGAA 11944 CCTATTT A  
 TTCCTGCCTC GCC GG  
 ||||| || ||  
 AAGGACGGGG CGG CC  
 ACAC\_\_ G  
 GAM1387 TREX1 5' CCCAGCAGAGGGAGGCAG 53280 AT CA  
 CTGCCTCCCT TTGC GG  
 ||||| || ||  
 GACGGAGGGA GACG CC  
 \_ AC  
 GAM1387 TREX1 5' CCCAGCAGAGGGAGGCAG 53290 AT CA  
 CTGCCTCCCT TTGC GG  
 ||||| || ||  
 GACGGAGGGA GACG CC  
 \_ AC  
 GAM1387 URG4 3' GCCCCAGGGTAGGGAGACA 35506 C GCCA  
 TG CTCCCTATTT GGC  
 || ||||| ||  
 AC GAGGGATGGG CCG  
 A ACCC  
 GAM1387 LOC124222 3' CCTGACAAACAGGCAGGGA 74271 CCCTA C  
 TTCCTGCCT TTTG CAGG  
 ||||| || ||||  
 AGGGACGGA AAAC GTCC  
 C\_\_ A  
 GAM1387 LOC131873 5' CCCGGAGGAGAGGCAGGGA 75877 \_ ATTTG A  
 TTCCTGCCTC CCT CC GG  
 ||||| || ||  
 AGGGACGGAG GGA GG CC  
 A \_\_\_\_ C  
 GAM1387 LOC144348 5' CCTTCCGTAGAAAGACAGGCA 76806 CC A C\_\_  
 TGCCT CT TTTGC AGG  
 |||| ||||| ||  
 ACGGA GA AGATG TCC  
 CA A CCT  
 GAM1387 LOC146316 5' CTTGAGAGGCAGGAA 60872 CCTAT CC  
 TTCCTGCCTC TTG AG  
 ||||| || ||  
 AAGGACGGAG AGC TC  
 \_\_\_\_ T\_  
 GAM1387 LOC148529 5' CCTGGCAGACAGGAAGACA 84167 C C A  
 TG CT CCT TTTGCCAGG  
 || || || |||||

AC GA GGA AGACGGTCC  
 A A C  
 GAM1387 LOC149606 3' GCCCGCGGAGCAGGGAG 79454 A\_ CA  
 CTCCCT TTTGC GGC  
 ||||| ||||| ||  
 GAGGGA AGGCG CCG  
 CG C\_  
 GAM1387 LOC151057 3' CCAGGAAAGAAGGCAGGAA 85209 CCCTA G A  
 TTCCTGCCT TTT CC GG  
 ||||| || || ||  
 AAGGACGGA AAA GG CC  
 AG\_\_ \_ A  
 GAM1387 LOC153346 5' CCCAGATGGAAGGCA 86022 CC CCA  
 TGCCT CTATTTG GG  
 ||||| ||||| ||  
 ACGGA GGTAGAC CC  
 A\_ \_  
 GAM1387 LOC196418 5' CCTTCCGTAGAAAGACAGGCA 87696 CC A C\_  
 TGCCT CT TTTGC AGG  
 ||||| ||||| ||  
 ACGGA GA AGATG TCC  
 CA A CCT  
 GAM1387 LOC199786 3' GCCTGGCAGCTGAGGCAGAGA 88386 \_ CCTAT  
 TC CTGCCTC TTGCCAGGC  
 || ||||| |||||  
 AG GACGGAG GACGGTCCG  
 A TC\_  
 GAM1387 LOC200058 3' CCTGAAGGATGGGAAGCCAGGA 88556 C C GC  
 A  
 TTCCTG CT CCTATTT CAGG  
 ||||| || ||||| |||||  
 AAGGAC GA GGGTAGG GTCC  
 C A AA  
 GAM1387 LOC204579 5' CCCGGCTATGAGGCAGGAA 89465 CCTATTT A  
 TTCCTGCCTC GCC GG  
 ||||| || || ||  
 AAGGACGGAG CGG CC  
 TAT\_\_ C  
 GAM1387 LOC219700 5' GCCTGGCAGTCCAAAGACCAAG 93064 C CCTCCCTAT  
 AA  
 TTC TG TTGCCAGGC  
 ||| || |||||  
 AAG AC GACGGTCCG  
 A CAGAAACCT  
 GAM1387 LOC253181 5' GCCTGGCAAACAGCACAGGA 97558 CCTCC A  
 TCCTG CT TTTGCCAGGC  
 ||||| || |||||  
 AGGAC GA AAACGGTCCG  
 AC\_\_ C  
 GAM1387 LOC253296 3' GCCTGGGGCCACAGGAAAGGCA 94490 C\_ ATTTG\_  
 GGAA  
 TTCCTGCCT CCT CCAGGC  
 ||||| || |||||

		AAGGACGGA GGA GGTCCG	
		AA CACCGG	
GAM1387	LOC253298 5'	GCCTGGGGCCACAGGAAAGGCA 97215	C_ ATTTG_
		GGAA TTCCTGCCT CCT CCAGGC	
		AAGGACGGA GGA GGTCCG	
		AA CACCGG	
GAM1387	LOC254107 5'	CCCAGAGGGCAGGAA 94384	CCCTA CCA
		TTCCTGCCT TTTG G	
		AAGGACGGG AGAC C	
		_____ C_	
GAM1387	LOC255189 5'	CTGACCAAGGCAGGAA 96589	CCCTATT C_
		TTCCTGCCT TG CAG	
		AAGGACGGA AC GTC	
		_____ CA	
GAM1387	LOC257160 3'	CCTGACTGGGGAGGAAG 94846	G TTTGC
		CT CCTCCCTA CAGG	
		GA GGAGGGGT GTCC	
		A CA_	
GAM1387	LOC257570 3'	GCCTGGGGCCACAGGAAAGGCA 97833	C_ ATTTG_
		GGAA TTCCTGCCT CCT CCAGGC	
		AAGGACGGA GGA GGTCCG	
		AA CACCGG	
GAM1387	LOC257571 5'	GCCTGGGGCCACAGGAAAGGCA 97945	C_ ATTTG_
		GGAA TTCCTGCCT CCT CCAGGC	
		AAGGACGGA GGA GGTCCG	
		AA CACCGG	
GAM1388	ADAR 3'	GTTTTTTGGAGTCTTGGTTGTG 6627	_ ATACAA
		TACA CCAA TTCAGAAGAC	
		GTGT GGTT AGGTTTTTTG	
		T CTG_	
GAM1388	ADAR 3'	GTTTTTTGGAGTCTTGGTTGTG 31752	_ ATACAA
		TACA CCAA TTCAGAAGAC	
		GTGT GGTT AGGTTTTTTG	
		T CTG_	
GAM1388	ADAR 3'	GTTTTTTGGAGTCTTGGTTGTG 31762	_ ATACAA
		TACA CCAA TTCAGAAGAC	
		GTGT GGTT AGGTTTTTTG	
		T CTG_	
GAM1388	AGT 3'	CTTCGGTTTGTATTTAGTGT 3455	C TT A
		ACAC AAATACAA C GAAG	

			TGTG TTTATGTT G CTTC		
			A TG_		
GAM1388	C14orf1	3'	CTTCTGGTCAGCTGTATTTGTG 23179	C	AT___
		TA	TACAC AAATACA TCAGAAG		
			ATGTG TTTATGT GGTCTTC		
			_ CGACT		
GAM1388	CSPG3	3'	GTTTTTTGGGGGGTCTTGGT 15237	AT	AA
			ACCAA AC TTCAGAAGAC		
			TGGTT TG GGGTTTTTTG		
			C_ GG		
GAM1388	FBXW1B	3'	TCTCCTGATATTTGGT 24526	CAAT	A
			ACCAAATA TCAG AGA		
			TGGTTTAT AGTC TCT		
			___ C		
GAM1388	FBXW1B	3'	TCTCCTGATATTTGGT 53330	CAAT	A
			ACCAAATA TCAG AGA		
			TGGTTTAT AGTC TCT		
			___ C		
GAM1388	FBXW1B	3'	TCTCCTGATATTTGGT 53341	CAAT	A
			ACCAAATA TCAG AGA		
			TGGTTTAT AGTC TCT		
			___ C		
GAM1388	FGF13	3'	GTCTTCCTGTCATTGTATTTGG 53321	T_	_
			CCAAATACAAT CAG AAGAC		
			GGTTTATGTTA GTC TTCTG		
			CT C		
GAM1388	GRINL1A	3'	TCTCAAATGTATTTGGTTA 69520	C	A C
			A ACCAAATACA TT AGA		
			A TGGTTTATGT AA TCT		
			T A C		
GAM1388	HNRPA1	3'	GTCTTCGGAACCTTGGTGTA 48295	ATACAA	A
			TACACCAA TTC GAAGAC		
			ATGTGGTT AAG CTTCTG		
			CCA___ G		
GAM1388	KLK5	5'	TCTTCTGAATTCTATAGTG 24861	CAA	C
			CAC ATA AATTCAGAAGA		
			GTG TAT TTAAGTCTTCT		
			A___ C		
GAM1388	LEP	3'	GTTTTCTGAATAACATTTGTGT 4057	_	ACA
		G	CAC CAAAT ATTCAGAAGAC		

			GTG GTTTA TAAGTCTTTTG			
			T CAA			
GAM1388	MAP3K8	3'	TTTTGTGTATATTGGTGTA 17794	_	ATT	
			TACACCAA ATACA CAGAA			
			ATGTGGTT TATGT GTTTT			
			A _			
GAM1388	NCOA6	3'	TTTTGGATGTATTTGTTGTA 25984	C	A	
			TACA CAAATACA TTCAGAA			
			ATGT GTTTATGT AGGTTTT			
			T _			
GAM1388	NDP	3'	GTCTTCTGAACGTTTGGT 4243	ACAA		
			ACCAAAT TTCAGAAGAC			
			TGGTTG AAGTCTTCTG			
			C _			
GAM1388	PFKFB2	3'	GTCCCCTCTGGATTGTCCAGTG 20604	CAAAT	A _	
	TA		TACAC ACAATTCAGA GAC			
			ATGTG TGTTAGGTCT CTG			
			ACC _ CCC			
GAM1388	PLS1	5'	GTCTTCTGAATTGTTTT 10661	T		
			AAA ACAATTCAGAAGAC			
			TTT TGTTAAGTCTTCTG			
			T			
GAM1388	PPP2R4	3'	TTTTCTGAGTTCCCGTGTG 60564	CAAATAC		
			TACAC AATTCAGAAGA			
			GTGTG TTGAGTCTTT			
			CCC _			
GAM1388	PRKCM	3'	AGTTCTGTTTGGTGTG 10810	C		
			TACACCAAATA AATT			
			GTGTGGTTTGT TTGA			
			C			
GAM1388	PRPF18	3'	GTCTCTGAGTTCTACCTGATGT 13406	C AA C	A	
	A		TACA CA TA AATTCAGA GAC			
			ATGT GT AT TTGAGTCT CTG			
			A CC C _			
GAM1388	SNX13	3'	TCTTAAATGATTTGGTG 30701	A ATTCAG		
			CACCAAAT CA AAGA			
			GTGGTTTA GT TTCT			
			_ AAA _			
GAM1388	SPON1	3'	CTTCTGAAC TTTTGGT 62449	TACAA		
			ACCAAA TTCAGAAG			



			TGGTTT AAGTCTTC		
			TTC__		
GAM1388	STAU2	3'	CTTCAGACATTTGGTGT 26904	ACAAT A	
			ACACCAAAT TC GAAG		
			TGTGGTTTA AG CTTC		
			C__ A		
GAM1388	TMEM2	3'	GTTTTTTGTTATTGTTTTGTGT 25426	_ T T_	
	G		CAC CAAA ACAAT CAGAAGAC		
			GTG GTTT TGTTA GTTTTTTG		
			T _ TT		
GAM1388	ARFGEF2	3'	GTTTTCTGTTGTTTGAGTGTG 21200	_ CAATT	
			TACAC CAAATA CAGAAGAC		
			GTGTG GTTTGT GTCTTTTG		
			A T__		
GAM1388	BICD2	3'	TCTTCTCTTGCTTGGTGTA 70404	ATA TTC	
			TACACCAA CAA AGAAGA		
			ATGTGGTT GTT TCTTCT		
			C_ C_		
GAM1388	CAMKK2	3'	TCTGTGGGACCAATTTGGTGTA 21587	ACAATT__	
			TACACCAAAT CAGA		
			ATGTGGTTTA GTCT		
			ACCAGGGT		
GAM1388	CDK5RAP3	5'	GAATTGTGCTTGGTGTG 47283	A	
			TACACCAA TACAATTC		
			GTGTGGTT GTGTTAAG		
			C		
GAM1388	CHST3	3'	CTCCTGCTTTATTTGGTGT 14973	CAATT A	
			ACACCAAATA CAG AG		
			TGTGGTTTAT GTC TC		
			TTC_ C		
GAM1388	DDX33	3'	CTTCTGAATCCTGTCACGTGTA 39374	CAA CA	
			TACAC ATA ATTCAGAAG		
			ATGTG TGT TAAGTCTTC		
			CAC CC		
GAM1388	FLJ13154	3'	GTCTTCTGGATTCTGGTG 44800	AATAC	
			CACCA AATTCAGAAGAC		
			GTGGT TTAGGTCTTCTG		
			CT__		
GAM1388	FLJ20548	3'	TCTGAATTGGAGGGCAGTG 35380	A_ AAATA	
			TAC CC CAATTCAGA		

			GTG GG GTTAAGTCT		
			AC GAG__		
GAM1388	GMEB2	3'	GTTTTCTGTAGGTTTAGTGTG 24737	C	ACAATT
			TACAC AAAT CAGAAGAC		
			GTGTG TTTG GTCTTTTG		
			A GAT__		
GAM1388	GMFB	3'	TCTGCTTGCATTGGTGTA 14671	ATA	TT
			TACACCAA CAA CAGA		
			ATGTGGTT GTT GTCT		
			AC_ C_		
GAM1388	HRIHFB2072	3'	TCTTATGTATTGGTGTA 50726	A	ATTC
			TACACCAA TACA AGA		
			ATGTGGTT ATGT TCT		
			_ AT__		
GAM1388	IMP-2	3'	GTCTTTTTGCATTTTGGTGTA 21571	TA_	TTCA
			TACACCAAA CAA GAAGAC		
			ATGTGGTTT GTT TTTCTG		
			TAC ____		
GAM1388	IMP-2	3'	GTCTTTTTGCATTTTGGTGTA 21571	TA_	TTCA
			TACACCAAA CAA GAAGAC		
			ATGTGGTTT GTT TTTCTG		
			TAC ____		
GAM1388	KHDRBS1	3'	CTCCTGAATTGAGTTTGATG 21624	C	A A
			CA CAAAT CAATTCAG AG		
			GT GTTTG GTTAAGTC TC		
			A A C		
GAM1388	KIAA1026	3'	CTCTTGAATTGCATTTG 71194	A	GA
			CAAAT CAATTCA AG		
			GTTTA GTTAAGT TC		
			C TC		
GAM1388	KIAA1437	3'	GTTTTTTGGGTTTTTTTGGTGT 60592	TAC	
			ACACCAAA AATTCAGAAGAC		
			TGTGGTTT TTGGGTTTTTTG		
			TT_		
GAM1388	KOC1	3'	AATTGTGTTGGGTGTG 91069	A	
			TACACC AATACAATT		
			GTGTGG TTGTGTAA		
			G		
GAM1388	MGC10981	3'	GTCCGCTGGACCACTTTGGTGT 51023	TACAA	AA
	A		TACACCAAA TTCAG GAC		

			ATGTGGTTT	AGGTC CTG	
			CACC_	GC	
GAM1388	OSRF	3'	GTCTCCTTCAGTATTTGGT	59524	AATTC A
			ACCAAATAC	AG AGAC	
			TGGTTTATG	TC TCTG	
			ACT_	C	
GAM1388	PELI1	5'	GTTTTCTGGGTTTGGCTGGAGT	40280	A AA C
	G		TAC CCA	TA AATTCAGAAGAC	
			GTG GGT	GT TTGGGTCTTTTG	
			A CG	_	
GAM1388	PRKCBP1	3'	CTGTGCTTTTGGTGTA	24834	TA ATT
			TACACCAA	CA CAG	
			ATGTGGTTT	GT GTC	
			TC	___	
GAM1388	SIAT8D	3'	GTCTTCTGGAATCTCTTTTGGT	19031	TACAA_
			ACCAA	TTCAGAAGAC	
			TGGTTT	AGGTCTTCTG	
			TCTCTA		
GAM1388	SLC2A12	3'	CTTCTGAACGTGGATAGTG	59080	CAAA AA
			CAC	TAC TTCAGAAG	
			GTG	GTG AAGTCTTC	
			ATAG	C_	
GAM1388	SMC1L1	3'	CTCCTGGCCCTTTTGGTGTA	71959	TACAAT A
			TACACCAA	TCAG AG	
			ATGTGGTTT	GGTC TC	
			TTCCC_	C	
GAM1388	SYTL4	3'	GTTTTCAAAGATTGATTTGGTG	54943	A CA_
	TG		TACACCAAAT	CAATT GAAGAC	
			GTGTGGTTTA	GTTAG CTTTGT	
			_	AAA	
GAM1388	USP22	3'	TCTGCTTTACATTTGGTGTA	68029	AC TT
			TACACCAAAT	AA CAGA	
			ATGTGGTTTA	TT GTCT	
			CA	TC	
GAM1388	WAC	3'	TGAATTGTATCTGTTGTA	55189	C A
			TACA	CA ATACAATTCA	
			ATGT	GT TATGTTAAGT	
			T	C	
GAM1388	WAC	3'	TGAATTGTATCTGTTGTA	55195	C A
			TACA	CA ATACAATTCA	

		ATGT GT TATGTTAAGT		
		T C		
GAM1388 WAC	3'	TGAATTGTATCTGTTGTA 33555	C A	
		TACA CA ATACAATTCA		
		ATGT GT TATGTTAAGT		
		T C		
GAM1388 ZNF271	5'	CTTATTCTGTAAATTGGTGTA 95251	A	ATTCAG
		TACACCAA TACA AAG		
		ATGTGGTT ATGT TTC		
		A CCTTA_		
GAM1388 LOC135932	3'	GTCTTCTGGCAACATTTGGTG 76200	ACAAT	
		CACCAAAT TCAGAAGAC		
		GTGGTTTA GGTCTTCTG		
		CAAC_		
GAM1388 LOC135932	3'	GTCTTCTGGCAACATTTGGTG 76200	ACAAT	
		CACCAAAT TCAGAAGAC		
		GTGGTTTA GGTCTTCTG		
		CAAC_		
GAM1388 LOC139522	5'	AATTGCATTTGGTGTA 75849	A	
		TACACCAAAT CAATT		
		GTGTGGTTTA GTTAA		
		C		
GAM1388 LOC142973	3'	GTCTTCAGAAACCTTTGGTGTA 60280	TACAA A	
		TACACCAA TTC GAAGAC		
		ATGTGGTTT AAG CTTCTG		
		CCA_ A		
GAM1388 LOC147645	3'	TCTTCCTGTATTTGTG 78425	C	ATTCA
		CAC AAATACA GAAGA		
		GTG TTTATGT CTTCT		
		_ C_		
GAM1388 LOC151249	3'	GTCTTCGGAAACCTTGGTGTA 60062	ATACAA A	
		TACACCAA TTC GAAGAC		
		ATGTGGTT AAG CTTCTG		
		CCA_ G		
GAM1388 LOC153817	3'	GTCTTCAGAAACCTTGGTGTA 61044	ATACAA A	
		TACACCAA TTC GAAGAC		
		ATGTGGTT AAG CTTCTG		
		CCA_ A		
GAM1388 LOC153876	3'	GTCTTCTGAATCATTAAATGAGT 86156	_	AATACA
G		CAC CA ATTCAGAAGAC		

		GTG GT	TAAGTCTTCTG		
		A	AATTAC		
GAM1388	LOC157531 5'	TCTTGTGTGTTTGGGTG	86473	A	ATTC
		TAC CCAAATACA	AGA		
		GTG GGTTTGTGT	TCT		
		_	GT__		
GAM1388	LOC157739 3'	GTTTTCTGCTCACATGTTTGTG	81584	_	CAATT_
	TG	CAC CAAATA	CAGAAGAC		
		GTG GTTTGT	GTCTTTTG		
		T	ACACTC		
GAM1388	LOC157773 3'	GTCTTTGTTGTGTATTTGAGT	81608	_	ATTCA
		AC CAAATACA	GAAGAC		
		TG GTTTATGT	TTTCTG		
		A	GTTG_		
GAM1388	LOC220840 3'	GTCTTCGGAAACCTTGGTGTA	90809		ATACAA A
		TACACCAA	TTC GAAGAC		
		ATGTGGTT	AAG CTTCTG		
		CCA__	G		
GAM1388	LOC220929 5'	TCTTCTGAACATTTTGATG	91405	C	TACAA
		CA CAAA	TTCAGAAGA		
		GT GTTT	AAGTCTTCT		
		A	TAC__		
GAM1388	LOC254251 3'	GTTTTTACACTTGTGTTTGTGT	95909	_	TTCA
	G	CAC CAAATACAA	GAAGAC		
		GTG GTTTGTGTT	TTTTTG		
		T	CACA		
GAM1388	LOC51313 3'	TTGGATTGTGTTTGTGTG	33513	_	
		CAC CAAATACAATTCAG			
		GTG GTTTGTGTTAGGTT			
		T			
GAM1388	LOC90631 3'	GTCTCAGGAGCCGTATTTGGT	63638		AA_ A A
	GT	ACACCAAATAC	TTC GA GAC		
		TGTGGTTTATG	AGG CT CTG		
		CCG	A C		
GAM1388	LOC91263 3'	CTTCTCAATCACATTTGGTG	65379		ACA C
		CACCAAAT	ATT AGAAG		
		GTGGTTTA	TAA TCTTC		
		CAC	C		
GAM1388	LOC92979 5'	GTTTTCTGTGTCAAGTTTGGT	56438		TACAATT_
	GTG	TACACCAAA	CAGAAGAC		

		GTGTGGTTT	GTCTTTTG	
		TGAACTGT		
GAM1389	CSNK1D	5' CCGGAAGATCCGAGTCCATC	8550	CA AC TTCAC
		GA GA CG TCTTCCGG		
		CT CT GC AGAAGGCC		
		AC GA CT__		
GAM1389	CSNK1D	5' CCGGAAGATCCGAGTCCATC	57406	CA AC TTCAC
		GA GA CG TCTTCCGG		
		CT CT GC AGAAGGCC		
		AC GA CT__		
GAM1389	MEL	3' TGAAGCGATTCTGTCT	18122	C _
		AGACAGAA CGTT CA		
		TCTGTCTT GCGA GT		
		A A		
GAM1389	MYCL2	3' AAGCCTGACCATTCTGTCT	18168	CC T CT
		AGACAGAA GT CA CTT		
		TCTGTCTT CA GT GAA		
		AC _ CC		
GAM1389	C22orf3	5' CCGGAAGAATCTCCGTCCTTGT	24351	AAC TTCAC
	CT	AGACAG CG TCTTCCGG		
		TCTGTT GC AGAAGGCC		
		CCT CTCTA		
GAM1389	DGKD	5' CCGGAAGAGTGAAAGG	59401	G
		CC TTCACTCTTCCGG		
		GG AAGTGAGAAGGCC		
		A		
GAM1389	FLJ20457	5' CCGGAAGAGCACGCCAGTC	35220	AGAAC TCA
		GAC CGT CTCTTCCGG		
		CTG GCA GAGAAGGCC		
		ACCC_ C__		
GAM1389	FYCO1	5' CCAGAAAGTTTCGGTTCTG	44489	TTC C C
		CAGAACCG ACT TTC GG		
		GTCTTGGC TGA AAG CC		
		TT_ _ A		
GAM1389	KIAA0447	3' AGCAAACGGTTCTGTT	71664	CA
		GACAGAACCGTT CT		
		TTGTCTTGGCAA GA		
		AC		
GAM1389	MGC13170	3' CCGGAAGAGAAGGGTGTCTG	51146	_ G AC
		CAGA ACC TTC TCTTCCGG		

		GTCT TGG AAG AGAAGGCC		
		G G _		
GAM1389	RALGPS1A	3' CCGGGGAGTGAACGGT	27599	T
		ACCGTTCACTCT CCGG		
		TGGCAAGTGAGG GGCC		
		-		
GAM1389	SLI	5' CGGAAGGGCAGCTTC	78585	CC CA
		GAA GTT CTCTTCCG		
		CTT CGA GGGAAGGC		
		_ C_		
GAM1389	LOC90538	3' CCAGAGGAGTGAATGGTTCTGT	63188	C
	CT	AGACAGAACCGTTCACTCTTC GG		
		TCTGTCTTGGTAAGTGAGGAG CC		
		A		
GAM1390	NRAP	3' CCAGCTGCAGAGTGAT	20508	_
		ATCACTTTGCAG GG		
		TAGTGAGACGTC CC		
		GA		
GAM1390	SLC16A7	3' TAATCCTACAAAGTGA	16405	CA
		TCACTTTG GGGATTA		
		AGTGAAAC TCCTAAT		
		A_		
GAM1390	XYLB	3' ATCAGCTGAAAAGTGAT	17558	G G_
		ATCACTTT CAG GAT		
		TAGTGAAA GTC CTA		
		A GA		
GAM1390	C8orf13	3' CATTAGTAAAGGAGCAAAGTGA	81569	AGGGA
		TCACTTTGC TTACTAATG		
		AGTGAAACG AATGATTAC		
		AGGA_		
GAM1390	FLJ21477	3' CATCCGTGTCCCTGCAAAGGA	47146	A T TA
		TC CTTTGCAGGGAT AC ATG		
		AG GAAACGTCCCTG TG TAC		
		- _ CC		
GAM1390	HZFW1	3' CATCAGTATTGGTAAAGTGA	47458	AGGGAT A
		TCACTTTGC TACT ATG		
		AGTGAAATG ATGA TAC		
		GTT_ C		
GAM1390	LOC256021	3' ATTAAAACCCCAAAGTGAT	96514	CA A AC
		ATCACTTTG GGG TT TAAT		

[illegible]



		GG T CTGATGGTGTT	
		GT TTC__	
GAM1391 CALU	3'	CTGTGGTGGGAAGAGTTAGG 6886	AC GG TG
		CCTGACT CT C CCATAG	
		GGATTGA GA G GGTGTC	
		__ AG GT	
GAM1391 CLDN14	5'	GTGGGCAGGTGGTCAGG 57841	G TG
		CCTGACTACCTG C C	
		GGA CTGGTGGAC G G	
		G GT	
GAM1391 CLN5	5'	TTGTGGTGGTCATCTCCGGC 21435	T CTACC TG
		GCC GA TGGC CCATAG	
		CGG CT ACTG GGTGTT	
		C CT__ GT	
GAM1391 COX7A2	5'	TTGTGGCGGTTGCTGGTCAG 8519	CCT
		CTGACTA GGCTGCCATAG	
		GA CTGGT TTGGCGGTGTT	
		CG_	
GAM1391 DDEF2	5'	GCGGCTGGGTGGCGGGTA 13953	A TG
		TGCCTG CTACC GCTGC	
		ATGGGC GGTGG CGGCG	
		_ GT	
GAM1391 DLG4	3'	GGGGTCGGGGGTCGGGT 7255	A G
		GCCTGACT CCTGGCT CC	
		TGGGCTGG GGGCTGG GG	
		- -	
GAM1391 DYRK1A	3'	TTGTGGTGAAGTTTGT CAGGCA 7359	TAC GGCT
		TGCCTGAC CT GCCATAG	
		ACG GACTG GA TGGTGT	
		TTT AG__	
GAM1391 DYRK1A	3'	TTGTGGTGAAGTTTGT CAGGCA 55210	TAC GGCT
		TGCCTGAC CT GCCATAG	
		ACG GACTG GA TGGTGT	
		TTT AG__	
GAM1391 DYRK1A	3'	TTGTGGTGAAGTTTGT CAGGCA 55256	TAC GGCT
		TGCCTGAC CT GCCATAG	
		ACG GACTG GA TGGTGT	
		TTT AG__	
GAM1391 EPB41L2	3'	CTGTGGTGGTGTTCTGTTGGT 7482	T TACCTG TG
		GCC GAC GC CCATAG	

			TGG TTG    TG GGTGTC	
			_ TCTTG_ GT	
GAM1391 FCMD	3'	GTTGGTAGTTAGGCA	22096	T
		TGCCTGACTACC GGC		
		ACGGATTGATGG TTG		
GAM1391 FPGS	3'	CTGTGGCAGCTGCCCCCTGGCA	17085	TGACTACCT
		TGCC        GGCTGCCATAG		
		ACGG        TCGACGGTGTC		
		TCCCCG__		
GAM1391 GAB2	3'	TTATGGTGGCATGTGTTGTGTA	24506	C T CTG TG
		TGC TGAC AC GC CCATAG		
		ATG GTTG TG CG GGTATT		
		T _ TA_ GT		
GAM1391 GAB2	3'	TTATGGTGGCATGTGTTGTGTA	54463	C T CTG TG
		TGC TGAC AC GC CCATAG		
		ATG GTTG TG CG GGTATT		
		T _ TA_ GT		
GAM1391 HD	3'	TGTGGCAGTGGCCAGGCA	9195	A ACCTG
		TGCCTG CT GCTGCCATA		
		ACGGAC GG TGACGGTGT		
		C _____		
GAM1391 HIP1	3'	TATGGTGGTTGGTTGGGT	18066	TG CCTG TG
		GCC ACTA GC CCATA		
		TGG TGGT TG GGTAT		
		GT _____ GT		
GAM1391 IFNAR1	3'	TAGCCGGGTAGTAGGTA	5286	A
		TGCCTG CTACCTGGCTG		
		ATGGAT GATGGGCCGAT		
GAM1391 JMJ	3'	TTGTGGCAGCTGAAGGCGG	17135	TA _
		C CCT GGCTGCCATAG		
		G GGA TCGACGGTGTT		
		GC AG		
GAM1391 LAPTM5	3'	TGTGGCAGCTGGGGAGGTT	22205	A_ TG
		GA CT CC GCTGCCATA		
		TTGG GG CGACGGTGT		
		AG GT		
GAM1391 LENG4	5'	CTGTGGCGGGCCCCATTAGGTA	44165	CTACCT _
		TGCCTGA GGCT GCCATAG		

			ATGGATT	CCGG	CGGTGTC	
			ACC__	G		
GAM1391	MCM6	5'	TTGTGGCGGT	CGAGCGTGGCGC	19791	CT A _ _
	A		TGC	G CTAC CT GGCTGCCATAG		
			ACG	C GGTG GA CTGGCGGTGTT		
			__	C G		
GAM1391	NAPB	5'	CTGTGGCGGCCGCGCGGGCG	70181		ACTA _
			TGCCTG	CC TGGCTGCCATAG		
			GCGGGC	GG GCCGCGGTGTC		
			__	C		
GAM1391	NDUFA5	3'	TTATGGTAATATGGTCATGT	17196	C	CC GC
			GC TGA	CTA TG TGCCATAG		
			TG	ACTGGT AT ATGGTATT		
			T	__ A		
GAM1391	P3	3'	AGTTAGGTAGGTGGGC	39064	GA	
			GCCT	CTACCTGGCT		
			CGGG	GATGGATTGA		
			TG			
GAM1391	PCTP	3'	CTGTGGCAGCTAGCAAAAGCA	41097		CTGACTAC
			TGC	CTGGCTGCCATAG		
			ACG	GATCGACGGTGTC		
			AAAAC	__		
GAM1391	PPP1R12B	3'	TGTGGTAGCCACTCCAGG	49475		ACTACC
			CCTG	TGGCTGCCATA		
			GGAC	ACCGATGGTGT		
			CTC	__		
GAM1391	PPP1R12B	3'	TGTGGTAGCCACTCCAGG	49486		ACTACC
			CCTG	TGGCTGCCATA		
			GGAC	ACCGATGGTGT		
			CTC	__		
GAM1391	PTGFRN	3'	TGTGGTGGGAAGACGGGCA	67195		A A GGCT
			TGCCTG	CT CCT GCCATA		
			ACGGGC	GA GGG TGGTGT		
			A A	__		
GAM1391	PYGB	3'	GTGGCTGTGGTTGGCA	11178	T	CT TG
			TGCC	GACTAC GGC C		
			ACGG	TTGGTG TCG G		
			_	__ GT		
GAM1391	PYGO2	3'	TATGGCAGTTTCTTGGT	63991		CCT
			ACTA	GGCTGCCATA		

TGGT TTGACGGTAT  
 TCT  
 GAM1391 RAB27A 3' TTATGGTGGCAAATGTTTGGTA 15928 T TACCTG TG  
 TGCC GAC GC CCATAG  
 |||| || || ||||  
 ATGG TTG CG GGTATT  
 T TAAA\_\_ GT  
 GAM1391 RPL36AL 5' GCGAAGGGGCCAGGTGTCGGGC 6398 T GCCATAG  
 GCCTGAC ACCTGGCT  
 ||||| |||||  
 CGGGCTG TGGACCGG  
 \_ GAAGCGT  
 GAM1391 RPN1 3' CTGTGGCAGGCAGATTGGGT 11390 TG CTAC G  
 GCC A CTG CTGCCATAG  
 || | || |||||  
 TGG T GAC GACGGTGTC  
 GT A\_\_ G  
 GAM1391 SCN3A 3' TGTGGTGCATGTTTGGGCA 22633 TG CT CTG T  
 TGCC A AC GC GCCATA  
 ||| | || |||||  
 ACGG T TG CG TGGTGT  
 GT\_\_ TA\_\_  
 GAM1391 SDC4 3' GATGTTGCTGGGTGGTTGAGT 11479 CT TG TGC AG  
 GC GACTACC GC CAT  
 || ||||| || |||  
 TG TTGGTGG CG GTA  
 AG GT TT\_ GT  
 GAM1391 SF3B3 3' CTGTGGTGGGACTGGGTAGGGT 24857 TGA TG\_\_TG  
 A TGCC CTACC G C CCATAG  
 ||| |||| | | |||||  
 ATGG GATGG C G GGTGTC  
 \_ GT AG GT  
 GAM1391 SFRP4 3' CTGTACCATTAGGAGTTAGGTA 11577 A C CC  
 TGCCTGACT CCTGG TG ATAG  
 ||||| |||| || |||  
 ATGGATTGA GGATT AC TGTC  
 \_ \_ CA  
 GAM1391 SFTPA2 3' CTGTGGCAGGCCTGGTCAGGC 22647 CCT \_  
 GCCTGACTA GGC TGCCATAG  
 ||||| || |||||  
 CGGACTGGT CCG ACGGTGTC  
 \_ G  
 GAM1391 SLA 3' GTTAGGTGTCAGGCA 22172 T  
 TGCCTGAC ACCTGGC  
 ||||| |||||  
 ACGGACTG TGGATTG  
 \_  
 GAM1391 SLC12A2 5' GCCGGGGGTCGGGCA 6453 A  
 TGCCTGACT CCTGGC  
 ||||| |||||

ACGGGCTGG GGGCCG

GAM1391 TAF4B 3' CTGTGGTGA<sup>—</sup>CTTTGGTCGGC 87168 T CCT CT  
GCC GACTA GG GCCATAG  
||| ||| || |||||  
CGG CTGGT TC TGGTGTC  
— T— AG

GAM1391 TAGLN2 3' CTGTGGCAGCTGCTGCCCCAGC 13096 C ACTACCT  
CA TG CTG GGCTGCCATAG  
|| ||| |||||  
AC GAC TCGACGGTGTC  
C CCGTTCG

GAM1391 TSPY 5' TGTGGCGTGGGTCTGGGCA 82109 ACCTGGC  
TGCCTGACT TGCCATA  
||||| |||||  
ACGGGCTGG GCGGTGT  
GT—

GAM1391 UNC13 3' GTGCCTGGCTGGCTGGGTAGTC 21059 C TG \_ TAG  
AGC GC TGA<sup>—</sup>CTACC GCT GCCA  
|| ||||| ||| |||  
CG ACTGATGG CGG CCGT  
— GT T CCGTGT

GAM1391 VCP 3' CTATCCAACCTGGGTAGGTGGG 75369 GA TG CTGCC  
TA TGCCT CTACC G ATAG  
|||| |||| | |||  
ATGGG GATGG C TATC  
TG GT CAACC

GAM1391 VIPR2 3' GTTGATGGTCGGTGGTTGGGT 12615 TG T GC TAG  
GCC ACTACC GGCT CA  
||| ||||| ||| ||  
TGG TGGTGG CTGG GT  
GT \_ TA TGT

GAM1391 WFS1 3' CTGTCCAGCAGGTAGTGGGT 20009 G G CC  
GCCT ACTACCTG CTG ATAG  
|||| ||||| ||| |||  
TGGG TGATGGAC GAC TGTC  
— \_ C—

GAM1391 XKRY 3' GCAACCAAGGTGGTCGGGCA 16257 \_ C  
TGCCTGACTACCT GG TGC  
||||||| ||| |||  
ACGGGCTGGTGGGA CC ACG  
A A

GAM1391 XKRY 3' GCAACCAAGGTGGTCGGGCA 60019 \_ C  
TGCCTGACTACCT GG TGC  
||||||| ||| |||  
ACGGGCTGGTGGGA CC ACG  
A A

GAM1391 ZNF192 3' CTGTGGTACAGATAGTTGGCA 20855 T C GC  
TGCC GACTA CTG TGCCATAG  
|||| |||| ||| |||||

ACGG TTGAT GAC ATGGTGTG  
 \_ A \_  
 GAM1391 ATP6V0A1 5' TGTGGCGGTTGCTGTGGC 17733 TG TACC  
 GCC AC TGGCTGCCATA  
 ||| || |||||  
 CGG TG GTTGGCGGTGT  
 \_ TC\_  
 GAM1391 C1QTNF6 3' CTGTGTTCTGGGTGTTTCAGGT 49144 C TG CTGC  
 GCCTGA TACC G CATAG  
 ||||| |||| | ||||  
 TGGACT GTGG C GTGTC  
 T GT TT\_  
 GAM1391 CBX6 3' GTATGCAGGTAGTCAGCCA 26623 C G\_  
 TG CTGACTACCTG C TGC  
 || ||||| ||||  
 AC GACTGATGGAC G ATG  
 C \_T  
 GAM1391 CBX6 3' TGGGGCTGGGTAGTTGGG 26632 TG TG G  
 CC ACTACC GCT CCA  
 || ||||| ||||  
 GG TGATGG CGG GGT  
 GT GT \_  
 GAM1391 CCNI 5' CTACAGCAAGCTGGGTAGCAGG 22419 A TG \_ CA  
 CA TGCCTG CTACC GCT GC TAG  
 ||||| |||| ||||  
 ACGGAC GATGG CGA CG ATC  
 \_ GT A AC  
 GAM1391 CDT1 3' CTGTGGCAATATGGGGTTGGGT 77673 TG A TGGC  
 A TGCC ACT CC TGCCATAG  
 |||| |||| |||||  
 ATGG TGG GG ACGGTGTC  
 GT \_ TATA  
 GAM1391 COE2 3' TGTGCAGCTGGTTGGGCA 64257 TG ACCT \_  
 TGCC ACT GGCTGC CA  
 |||| || ||||| ||  
 ACGG TGG TCGACG GT  
 GT \_ T  
 GAM1391 CSEN 3' GTGGCTGGGTGGTCAGCA 25534 C TG TG  
 TGC TGA CTACC GC C  
 ||| ||||| || |  
 ACG ACTGGTGG CG G  
 \_ GT GT  
 GAM1391 dJ309H15.1 3' CTGTGGTAGTTAGCGGGCAGG 56796 A AC  
 CCTG CT CTGGCTGCCATAG  
 |||| || |||||  
 GGAC GG GATTGATGGTGTC  
 \_ GC  
 GAM1391 DKFZP434H204 5' GCCCTGCCAGGTGGTGGGCA 66429 G T\_  
 TGCCT ACTACCTGGC GC  
 ||||| ||||| || ||

ACGGG TGGTGGACCG CG  
 \_ TCC  
 GAM1391 DKFZP564O0423 3' TGTGGTGGCCATGTGGT 91705 C TG  
 ACTAC TGGC CCATA  
 ||||| |||| ||||  
 TGGTG ACCG GGTGT  
 T GT  
 GAM1391 DNAJC5 3' TGGTTTCTTGGGAGTCGGGCA 61457 A TG CT\_  
 TGCCTGACT CC G GCCA  
 ||||| || | ||||  
 ACGGGCTGA GG T TGGT  
 \_ GT CTT  
 GAM1391 DTX2 3' TGGCTGGGTGGCCAGGCA 71955 A TG  
 TGCCTG CTACC GCTG  
 ||||| |||| ||||  
 ACGGAC GGTGG CGGT  
 C GT  
 GAM1391 ERG-1 5' TGTGGCGGTTACCTGG 41845 CC  
 CTA TGGCTGCCATA  
 || ||||| ||||  
 GGT ATTGGCGGTGT  
 CC  
 GAM1391 FEM-2 3' GCACTGGGTGGCGGGCA 27582 A TG C  
 TGCCTG CTACC G TGC  
 ||||| |||| | ||||  
 ACGGGC GGTGG C ACG  
 \_ GT \_  
 GAM1391 FLJ00001 3' TGTGGTAGCTTTTAGGC 81823 CTACCT  
 GCCTGA GGCTGCCATA  
 ||||| ||||| |||||  
 CGGATT TCGATGGTGT  
 T\_\_\_\_\_  
 GAM1391 FLJ10468 3' TGTGGGAGGTGGTCAG 36150 GGCTG  
 CTGACTACCT CCATA  
 ||||| |||| ||||  
 GACTGGTGGA GGTGT  
 G\_\_\_\_\_  
 GAM1391 FLJ10853 3' CTGTGGCAGTTGTTGCCTGAGC 36767 CTGACT\_ CT  
 A TGC AC GGCTGCCATAG  
 || || ||||| |||||  
 ACG TG TTGACGGTGTC  
 AGTCCGT \_  
 GAM1391 FLJ10901 3' TTGTGGCATGTTCTGGTTGGG 36835 TG CCT \_  
 CC ACTA GGC TGCCATAG  
 || |||| || ||||| |||||  
 GG TGGT TTG ACGGTGTT  
 GT C\_\_ T  
 GAM1391 FLJ10989 5' TGTGGTGGCAGGCTGGGCA 36953 ACTA G TG  
 TGCCTG CCTG C CCATA  
 ||||| |||| | ||||

ACGGGT GGAC G GGTGT  
 C\_\_\_ \_GT  
 GAM1391 FLJ12428 3' CTATGGTTGGGGGTAGTTAGG 42944 GGCT  
 CCTGACTACCT GCCATAG  
 ||||| |||||  
 GGATTGATGGG TGGTATC  
 GGT\_  
 GAM1391 FLJ13193 3' TTATGTTAAGGAAGTCAGGTA 49776 A GGCTGC  
 TGCCTGACT CCT CATAG  
 ||||| || |||||  
 ATGGACTGA GGA GTATT  
 A ATT\_  
 GAM1391 FLJ14490 3' TTGTGGCAGCTGGTGCCGGGT 51401 AC T  
 GCCTG TACC GGCTGCCATAG  
 |||| ||| |||||  
 TGGGC GTGG TCGACGGTGTT  
 C\_ \_  
 GAM1391 FLJ20506 5' TATGGCGGCTACCAG 35268 ACTACC  
 CTG TGGCTGCCATA  
 ||| |||||  
 GAC ATCGGCGGTAT  
 C\_  
 GAM1391 FLJ20986 3' TTATGGTGGGAGGTGGTTGGG 44548 TG GG TG  
 CC ACTACCT C CCATAG  
 || ||||| | |||||  
 GG TGGTGGA G GGTATT  
 GT G\_ GT  
 GAM1391 FLJ22477 5' TTGTGGCAGCCAGATATCGGGC 45348 C C  
 GCCTGA TA CTGGCTGCCATAG  
 |||| || |||||  
 CGGGCT AT GACCGACGGTGTT  
 \_ A  
 GAM1391 FLJ22679 3' TTGTGGCGGGTAGAGTCAG 49926 AC G  
 CTGACT CTG CTGCCATAG  
 |||| ||| |||||  
 GACTGA GAT GGCGGTGTT  
 \_ G  
 GAM1391 FLJ22679 3' TTGTGGCGGGTAGAGTCAG 34682 AC G  
 CTGACT CTG CTGCCATAG  
 |||| ||| |||||  
 GACTGA GAT GGCGGTGTT  
 \_ G  
 GAM1391 FLJ23231 3' TTGGCCTTGGCTGGCTAGTTGG 46916 TG CTG \_ TAG  
 GCA CC ACTA C GCT GCCA  
 || |||| | ||| |||||  
 GG TGAT G CGG CGGT  
 GT C GT TTC T  
 GAM1391 GGA2 3' GGCCTGGTAGTCAGGT 30474 T  
 GCCTGACTACC GGCT  
 ||||| |||||



			TGGACTGATGG CCGG		
			T		
GAM1391	GGA2	3'	GGCCTGGTAGTCAGGT 56888	T	
			GCCTGACTACC GGCT		
			TGGACTGATGG CCGG		
			T		
GAM1391	GLP	3'	TATGGTAGTTCCTTAGG 37848	CTACCT	
			CCTGA GGCTGCCATA		
			GGATT TTGATGGTAT		
			CCC__		
GAM1391	H2-ALPHA	5'	CTGTGGCAGCCGGTTGAGGT 73010	GACT T	
			GCCT ACC GGCTGCCATAG		
			TGGA TGG CCGACGGTGTC		
			GT__ _		
GAM1391	IL-17RE	3'	TGGCTCCAGGTGGTCAGGACA 58297	_ CT	
			TG CCTGACTACCTGG GCCA		
			AC GGA CTGGTGGACC CGGT		
			A T_		
GAM1391	KIAA0212	3'	CTGTGGCGGCAGTGGTGGGTA 27939	G CTG	
			TGCCT ACTAC GCTGCCATAG		
			ATGGG TGGTG CGGCGGTGTC		
			_ A__		
GAM1391	KIAA0237	3'	TTGTGGTTCCCGGGTGGCAGGT 28540	A CT	
			GCCTG CTACCTGG GCCATAG		
			TGGAC GGTGGGCC TGGTGTT		
			_ CT		
GAM1391	KIAA0317	3'	TGTGGTGGTCCTTAGGCA 29091	CTACCT TG	
			TGCCTGA GGC CCATA		
			ACGGATT CTG GGTGT		
			C_____ GT		
GAM1391	KIAA0523	3'	CTATGGTGA CTGGGTTAGGTA 67735	ACT TG CT	
			TGCCTG ACC G GCCATAG		
			ATGGAT TGG C TGGTATC		
			_____ GT AG		
GAM1391	KIAA0544	3'	TGGTGGCTGGGTGTCAGGCA 70911	T TG TG	
			TGCCTGAC ACC GC CCA		
			ACGGA CTG TGG CG GGT		
			_ GT GT		
GAM1391	KIAA0547	3'	GTTAGGAGTCAGGTA 28916	A	
			TGCCTGA CT CCTGGC		

ATGGACTGA GGATTG

GAM1391 KIAA0721 3' TTATGGTAAGCTATTTGGGTA 41351 TG CTACC \_  
TGCC A TGGCT GCCATAG  
|||| | |||| |||||  
ATGG T ATCGA TGGTATT  
GT T\_\_\_\_ A

GAM1391 KIAA0721 3' TTATGGTAAGCTATTTGGGTA 95979 TG CTACC \_  
TGCC A TGGCT GCCATAG  
|||| | |||| |||||  
ATGG T ATCGA TGGTATT  
GT T\_\_\_\_ A

GAM1391 KIAA1023 3' TGTGGCGGTCAGAAGGC 34272 GACTAC  
GCCT CTGGCTGCCATA  
|||| |||||  
CGGA GACTGGCGGTGT  
A\_\_\_\_

GAM1391 KIAA1094 5' TGTGGGGGGTGGCCGGGC 29807 A GGCTG  
GCCTG CTACCT CCATA  
|||| |||| |  
CGGGC GGTGGG GGTGT  
C G\_\_\_\_

GAM1391 KIAA1257 3' CTGTGGTGGTTATCATAGTTA 62739 CC\_ TG  
TGACTA TGGC CCATAG  
|||| | ||||  
ATTGAT ATTG GGTGTC  
ACT GT

GAM1391 KIAA1280 5' TTGTGGTGGCTGTCTGTGGGG 69735 G TACCT TG  
CCT AC GGC CCATAG  
||| || |||||  
GGG TG TCG GGTGTT  
G TCTG\_ GT

GAM1391 KIAA1320 5' TTATGGCAGCTGGGTG 69314 TG  
TACC GCTGCCATAG  
|||| |||||  
GTGG CGACGGTATT  
GT

GAM1391 KIAA1414 3' GTATCATGTAGTCGGGCA 67991 C C  
TGCCTGACTAC TGG TGC  
||||||| ||| |||  
ACGGGCTGATG ACT ATG  
T \_

GAM1391 KIAA1553 5' CTGTGGCAGCACCGGGGCAGGC 91919 A A TG\_  
A TGCCCTG CT CC GCTGCCATAG  
|||| || |||||  
ACGGAC GG GG CGACGGTGTC  
\_ \_ CCA

GAM1391 KIAA1644 3' GTCTAGGTAGGTAGGTA 85031 A \_  
TGCCCTG CTACCTGG C  
|||| ||||| |

ATGGAT GATGGATC G  
 G T  
 GAM1391 KIAA1751 3' GTGGTGGAAAGTCAGG 71704 A TGGCT  
 CCTGACT CC GCCAT  
 ||||| || ||||  
 GGA CTG A GG TGGTG  
 A \_\_\_\_  
 GAM1391 KIAA1863 3' TGTGGCGATGGTGGGGT 64876 TGA TGGC  
 GCC CTACC TGCCATA  
 || |||| |||||  
 TGG GGTGG GCGGTGT  
 \_\_\_\_ TA\_\_  
 GAM1391 KIAA1951 3' CTGTGGTGGCCAGCTACTCAGG 73762 C C TG  
 CCTGA TA CTGGC CCATAG  
 |||| || |||| |||||  
 GGA CTG A GACCG GGTGTC  
 C C GT  
 GAM1391 MGC10701 3' CTGTGGTAAGGCTCTGTCTGGGC 51027 TACCT \_\_\_\_  
 A TGCCTGAC GGCT GCCATAG  
 ||||| || |||||  
 ACGGGCTG TCGG TGGTGTC  
 TC\_\_\_\_ AA  
 GAM1391 MGC10814 5' TTGTGGCTGCAGGTGTTAGGT 51044 T GT  
 GCCTGAC ACCTG C GCCATAG  
 ||||| |||| | |||||  
 TGGATTG TGGAC G CGGTGTT  
 \_ \_T  
 GAM1391 MGC16733 3' TTGTGGTAGCTGTTACAAGTA 53212 C ACT CT  
 TGC TG AC GGCTGCCATAG  
 || || || |||||  
 ATG AC TG TCGATGGTGTT  
 A AT\_ \_\_\_\_  
 GAM1391 MGC2452 5' CTGTGGCCTCTGTAGTTAGGGC 50982 \_ CT CT  
 A TGCC TGA CTAC GG GCCATAG  
 |||| |||| || |||||  
 ACGG ATTGATG TC CGGTGTC  
 G \_\_\_\_ TC  
 GAM1391 MGC2477 5' TTGTGGTGGAAATCCAGTGAGGT 44077 G ACCTGG TG  
 GCCT ACT C CCATAG  
 |||| || | |||||  
 TGGA TGA G GGTGTT  
 G CCTAA\_ GT  
 GAM1391 MGC26655 5' CTGCGGAGTGTGGGTGGTTGGG 56290 TG \_ G A  
 C GCC ACTACCTG GCT CC TAG  
 || ||||| || || ||||  
 CGG TGGTGGGT TGA GG GTC  
 GT G \_ C  
 GAM1391 MGC3195 5' CTGTGGCGGCTAGGCCCGCGTG 49123 C ACTA  
 C GC TG CCTGGCTGCCATAG  
 || || |||||

CG GC GGATCGGCGGTGTC  
 T GCCC  
 GAM1391 MGC4643 3' TTATGGTGTGTGTAGTCAGTG 51159 \_ C GC  
 TA TGC CTGACTAC TG TGCCATAG  
 ||| ||||| || |||||  
 ATG GACTGATG GT GTGGTATT  
 T T A\_  
 GAM1391 MIC2L1 3' CTGTGGTGGAGGGTGGTCAGTC 48823 C GG TG  
 G TG CTGACTACCT C CCATAG  
 || ||||| | |||||  
 GC GACTGGTGGG G GGTGTC  
 T A\_ GT  
 GAM1391 MKNK1 3' TGTGGCGGCTGGGGCTGCA 13481 CTGACTA TG  
 TGC CC GCTGCCATA  
 || || |||||  
 ACG GG CGGCGGTGT  
 TCG\_\_\_ GT  
 GAM1391 NAP1L2 5' CTGTGGTAGCCACCTTAGGC 41735 CTACC  
 GCCTGA TGGCTGCCATAG  
 ||||| |||||  
 CGGATT ACCGATGGTGTG  
 CC\_\_\_  
 GAM1391 NIBAN 5' CTGTGGCAGCCCTTCTTCAGAC 42001 C CTACCT  
 A TG CTGA GGCTGCCATAG  
 || ||| |||||  
 AC GACT CCGACGGTGTG  
 A TCTTC\_  
 GAM1391 PCF11 5' CTGTGGCGGCTGGAAGTGG 31891 \_\_\_TG  
 CTAC C GCTGCCATAG  
 |||| | |||||  
 GGTG G CGGCGGTGTC  
 AA GT  
 GAM1391 PRO0650 5' TTATGCACCTACCAGGGGTCAG 26216 A C\_\_\_ C  
 GCA CCTGACT CCTGG TGC ATAG  
 ||||| |||| | |||||  
 GGA CTGG GGACC ACG TATT  
 \_ ATCC \_  
 GAM1391 PRO2730 5' TGAGGCTAGGTGGTTGGGCA 47420 TG GC  
 TGCC ACTACCTGGCT CA  
 |||| ||||| ||  
 ACGG TGGTGGATCGG GT  
 GT A\_  
 GAM1391 RER1 3' GCCAGGTGGGCAGGCA 22864 A  
 TGCCTG CTACCTGGC  
 ||||| |||||  
 ACGGAC GGTGGACCG  
 G  
 GAM1391 SLC39A3 3' GTCCTCGGGCTGGTCAGGC 57978 \_ CT  
 GCCTGACTA CCTGG GC  
 ||||| |||| ||

		CGGACTGGT GGGCT TG	
		C CC	
GAM1391	SPEC1	3' TTATGGTAGTGGGGTCAGG 39614	CTA G
		CCTGA CCT GCTGCCATAG	
		GGA CT GGG TGATGGTATT	
		___ G	
GAM1391	STI2	3' TTGTGTAGCTTGGGAGTCAGGC 88969	A T _ TAG
	A	TGCCTGACT CC GGCTGC CA	
		ACGGACTGA GG TCGATG GT	
		G T T T	
GAM1391	STK25	3' TGTGGTGTGGATCAGGTA 21053	CTAC TG T
		TGCCTGA C GC GCCATA	
		ATGGACT G TG TGGTGT	
		A___GT _	
GAM1391	SYNCOILIN	3' CTGTGGTATAACTGTCAGGTA 47895	TACCTGGC
		TGCCTGAC TGCCATAG	
		ATGGACTG ATGGTGTC	
		TCAAT___	
GAM1391	TBX21	3' TTGTGGTGGTTGTGTGTGGGT 25329	G T C TG
		GCCT AC AC TGGC CCATAG	
		TGGG TG TG GTTG GGTGTT	
		_ _ T GT	
GAM1391	TRIP13	5' CTGTGGCGGCGACGCTGGGC 14895	GA CTACCTG
		GCCT GCTGCCATAG	
		CGGG CGGCGGTGTC	
		TCGCAG___	
GAM1391	VEZATIN	3' GTTAGGTGGTTGGCA 34227	T
		TGCC GACTACCTGGC	
		ACGG TTGGTGGATTG	
		—	
GAM1391	WFDC3	3' TGGATTGGGTA GTGGGT 96926	G TG CTG
		GCCT ACTACC G CCA	
		TGGG TGATGG T GGT	
		_ GT A__	
GAM1391	ZNF297	3' GGTCAGGGGTCAGGT 18392	A
		GCCTGACT CCTGGCT	
		TGGACTGG GGA CTGG	
		—	
GAM1391	LOC112714	5' CTGTGGCAGCCGGTTGAGGT 72872	GA CT T
		GCCT ACC GGCTGCCATAG	

TGGG TGG CCGACGGTGTC  
 GT\_\_ \_  
 GAM1391 LOC113675 5' TGGTCTGGGATAGTTGGGCA 56574 TG \_ TG CT  
 TGCC ACTA CC G GCCA  
 |||| ||| || | ||||  
 ACGG TGAT GG C TGGT  
 GT A GT \_\_  
 GAM1391 LOC121219 5' CTATGGTGGTTGGGCGGCTGGT 74044 \_ GA TA TG TG  
 GC GC CT C CC GC CCATAG  
 || || | || || |||||  
 CG GG G GG TG GGTATC  
 T TC GC GT GT  
 GAM1391 LOC124460 3' CAGCCAGGTGGTCAGG 76041  
 CCTGACTACCTGGCTG  
 |||||  
 GGA CTGGTGGACCGAC  
  
 GAM1391 LOC124997 5' TGTGGCAGCAGCTGGGC 74389 GA ACCTG  
 GCCT CT GCTGCCATA  
 |||| || |||||  
 CGGG GA CGACGGTGT  
 TC \_\_\_\_  
 GAM1391 LOC125929 3' TTGTGGTAGTGGTTGTAGTTAG 75675 CTG\_  
 CTGACTAC GCTGCCATAG  
 ||||| |||||  
 GATTGATG TGATGGTGTT  
 TTGG  
 GAM1391 LOC132720 5' CGGCCGGGGGTTGGGC 75064 TG A  
 GCC ACT CCTGGCTG  
 || || |||||  
 CGG TGG GGGCCGGC  
 GT \_  
 GAM1391 LOC139231 3' TATGGCGGTGAAGTGGGC 75378 G ACCTG  
 GCCT ACT GCTGCCATA  
 |||| || |||||  
 CGGG TGA TGGCGGTAT  
 \_ AG\_\_  
 GAM1391 LOC144347 3' AGCCAGGAGGTTGGGCA 76810 TG A  
 TGCC ACT CCTGGCT  
 |||| || |||||  
 ACGG TGG GGACCGA  
 GT A  
 GAM1391 LOC145497 3' TGTGGCAGGGGCTGGGCA 77220 ACTA GG  
 TGCCTG CCT CTGCCATA  
 |||| || |||||  
 ACGGGT GGG GACGGTGT  
 C\_\_ \_  
 GAM1391 LOC145761 5' CTGCATTCCCAGGAGGTTAGGC 83475 A C\_\_ CATAG  
 A TGCCTGACT CCTGG TGC  
 ||||| |||| |||

ACGGATTGG GGACC ACG  
 A CTT TC  
 GAM1391 LOC146599 5' GCCCACCAGGGGTCAGGT 78025 A CT\_  
 GCCTGACT CCTGG GC  
 ||||| ||| ||  
 TGGACTGG GGACC CG  
 \_ ACC  
 GAM1391 LOC147299 3' CTGTGGCGTCCCTCGTCGGGTA 78346 TACCT C  
 TGCCTGAC GG TGCCATAG  
 ||||| || |||||  
 ATGGGCTG CC GCGGTGTC  
 CTC\_ T  
 GAM1391 LOC147622 5' CTGTGGCGCACTTGGTTGGG 84050 TG CCTG T  
 CC ACTA GC GCCATAG  
 || ||| || |||||  
 GG TGGT CG CGGTGTC  
 GT TCA\_ \_  
 GAM1391 LOC147976 5' TGTGGCATTGTGGTAGGCA 78590 ACTAC TG C  
 TGCCTG C G TGCCATA  
 ||||| | | |||||  
 ACGGAT G T ACGGTGT  
 \_ \_ GT T  
 GAM1391 LOC150005 5' TGTGGTGGTGTGTCAGGT 84823 TACCTG TG  
 GCCTGAC GC CCATA  
 ||||| || |||||  
 TGGACTG TG GGTGT  
 \_ \_ GT  
 GAM1391 LOC151273 5' CTGTGGCAGTTCAGTCAG 67016 ACCT  
 CTGACT GGCTGCCATAG  
 ||||| |||||  
 GACTGA TTGACGGTGTC  
 C\_  
 GAM1391 LOC151429 5' TGTGGTGA CTGTT CAGGT 85362 CT CT CT  
 GCCTGA AC GG GCCATA  
 ||||| || || |||||  
 TGGACT TG TC TGGTGT  
 \_ \_ AG  
 GAM1391 LOC152805 5' CTGTGGCGGGGCCAAGTGAGGC 80688 G ACC \_  
 GCCT ACT TGGCT GCCATAG  
 ||| || |||| |||||  
 CGGA TGA ACCGG CGGTGTC  
 G \_ GG  
 GAM1391 LOC152845 5' GCCGGGTAGCAGGCA 60333 A  
 TGCCTG CTACCTGGC  
 ||||| |||||  
 ACGGAC GATGGGCCG  
 \_  
 GAM1391 LOC153222 3' CTATGGCAGTTTTGCAATCAGG 80784 CTACCT  
 T GCCTGA GGCTGCCATAG  
 ||||| |||||

	TGGACT	TTGACGGTATC	
	AACGTT		
GAM1391 LOC153339 5'	CTATGGCAGTTAAAAGTGGT	86006	C__
	ACTAC TGGCTGCCATAG		
	TGGTG ATTGACGGTATC		
	AAA		
GAM1391 LOC153454 3'	AGTTAGATGGTTAGGT	80830	C
	GCCTGACTA CTGGCT		
	TGGATTGGT GATTGA		
	A		
GAM1391 LOC155060 3'	TTATGGTGGCCGGCCAGTTTGG	86334	T AC TG
	CC GACT CTGGC CCATAG		
	GG TTGA GGCCG GGTATT		
	T CC GT		
GAM1391 LOC155179 3'	TGTGGCGGTCAGAAGGC	81326	GA CTAC
	GCCT CTGGCTGCCATA		
	CGGA GACTGGCGGTGT		
	A_____		
GAM1391 LOC168966 5'	TGTGGTGGTTGCTCAGACA	87278	C CTACC TG
	TG CTGA TGGC CCATA		
	AC GACT GTTG GGTGT		
	A C_____ GT		
GAM1391 LOC196812 3'	CTGTGGCACCCCTGTTTGGGT	89569	TG CT CT C
	GCC A AC GG TGCCATAG		
	TGG T TG CC ACGGTGTC		
	GT__ T_ C		
GAM1391 LOC197342 3'	CTGTGGTAGCTGGAAGTGGGGC	88000	G A T
A	TGCCT ACT CC GGCTGCCATAG		
	ACGGG TGA GG TCGATGGTGTC		
	G A _		
GAM1391 LOC199870 3'	TTGTGGTGGTCACTGCTCAGTG	88433	_ CTACC TG
TA	TGC CTGA TGGC CCATAG		
	ATG GACT ACTG GGTGTT		
	T CGTC_ GT		
GAM1391 LOC201736 5'	TAGCTGGGCTGGTTGGGTA	89053	TG _ TG
	TGCC ACTA CC GCTG		
	ATGG TGGT GG CGAT		
	GT C GT		
GAM1391 LOC202934 3'	TGGGCCAGGTGGGCAGGT	90432	A TG
	GCCTG CTACCTGGC CCA		



	TGGAC GGTGGACCG GGT	
	G     —	
GAM1391 LOC203365 3'	CTGTGGTAGTTTTTTTGAGCA 89348	CT CTACCT
	TGC GA   GGCTGCCATAG	
	ACG TT   TTGATGGTGTC	
	AG TTT—	
GAM1391 LOC205418 3'	CTGTGGCGGCTCCCATTGAG 90684	CTACCT
	CTGA   GGCTGCCATAG	
	GACT   TCGGCGGTGTC	
	TACCC—	
GAM1391 LOC206480 5'	CTGTGGCAGCCTCAGTTGGC 90718	T ACCT
	GCC GACT   GGCTGCCATAG	
	CGG TTGA   CCGACGGTGTC	
	— CT—	
GAM1391 LOC220534 3'	TATGGTAGTTCCCTTAGG 90722	CTACCT
	CCTGA   GGCTGCCATA	
	GGATT   TTGATGGTAT	
	CCC—	
GAM1391 LOC220538 3'	TATGGTAGTTCCCTTAGG 90734	CTACCT
	CCTGA   GGCTGCCATA	
	GGATT   TTGATGGTAT	
	CCC—	
GAM1391 LOC220662 3'	TCAGGTAGTTGAGGCA 91183	—
	TGCCT GACTACCTGG	
	ACGGA TTGATGGACT	
	G	
GAM1391 LOC220827 3'	CTGCATTCCCAGGAGGTTAGGC 91242	A C— CATAG
A	TGCCTGACT CCTGG TGC	
	ACGGATTGG GGACC ACG	
	A CTT TC	
GAM1391 LOC221143 3'	CTGTGGTAGCTGAAATTTGGG 93567	TG CTACCT
	CC A   GGCTGCCATAG	
	GG T   TCGATGGTGTC	
	GT TAAAG—	
GAM1391 LOC253216 5'	GCCCTGCCAGGTGGTGGGCA 94960	G T—
	TGCCT ACTACCTGGC GC	
	ACGGG TGGTGGACCG CG	
	— TCC	
GAM1391 LOC254528 3'	TTATGGTGGAGGTGGTCTGGGT 95056	— GG TG
	GCCT GACTACCT C CCATAG	

TGGG CTGGTGGA G GGTATT  
 T \_ GT  
 GAM1391 LOC255426 5' TGGGAGCCGGGCGGTCGGGC 97161 TA G  
 GCCTGAC CCTGGCT CCA  
 ||||| ||||| ||  
 CGGGCTG GGGCCGA GGT  
 GC G  
 GAM1391 LOC256041 5' GCTGTGCGGTATCAGGCA 97606 C T  
 TGCCTGA TACCTGGC GC  
 ||||| ||||| ||  
 ACGGACT ATGGGCTG CG  
 \_ T  
 GAM1391 LOC257054 5' CTGTGTGCATGCAGCTGGTCGG 95660 C G \_ \_  
 GC GCCTGACTA CTG C TGC CATAG  
 ||||| || | || ||||  
 CGGGCTGGT GAC G ACG GTGTC  
 C \_ T T  
 GAM1391 LOC257286 3' TATGGTAGTTCCCTTAGG 94556 CTACCT  
 CCTGA GGCTGCCATA  
 |||| |||||  
 GGATT TTGATGGTAT  
 CCC\_  
 GAM1391 LOC257451 3' TATGGCAGTTTCTTGGT 95561 CCT  
 ACTA GGCTGCCATA  
 ||| |||||  
 TGGT TTGACGGTAT  
 TCT  
 GAM1391 LOC63923 3' GTGGCAGCTTGGGGC 67123 TGA CTA T  
 GCC CC GGCTGCCAT  
 ||| || |||||  
 CGG GG TCGACGGTG  
 \_ T  
 GAM1391 LOC91301 5' TATGGTGGCCGGGGAGGC 65547 GACTA TG  
 GCCT CCTGGC CCATA  
 ||| ||||| ||||  
 CGGA GGGCCG GGTAT  
 G\_ GT  
 GAM1391 LOC91516 5' TTGTGGTGGCCCTGCTCATGT 66306 C C CCT TG  
 GC TGA TA GGC CCATAG  
 || ||| || |||||  
 TG ACT GT CCG GGTGTT  
 T C C\_ GT  
 GAM1391 LOC91759 5' TGGCACCTAGGAGTCAGGCA 67091 A C  
 TGCCTGACT CCTGG TGCCA  
 ||||| ||||| ||||  
 ACGGACTGA GGATC ACGGT  
 \_ C  
 GAM1391 LOC91963 5' AGACTAGGCTAGTTGGGT 67688 TG \_ \_  
 GCC ACTA CCTGG CT  
 ||| |||| ||||| ||

			TGG TGAT GGATC GA		
			GT C A		
GAM1391	LOC93622	3'	TGTGCACAGGTGGTTGGGT 56932	TG	GC _
			GCC ACTACCTG TGC CA		
			TGG TGGTGGAC ACG GT		
			GT _ T		
GAM1392	BACE	3'	CCCCCAAATCTTCCTCTGGAGC 23977	G TT _ C	
	TT		AAGCT CCA GGA GAT TGGGGG		
			TTCGA GGT CCT CTA ACCCCC		
			_ CT T A		
GAM1392	BACE	3'	CCCCCAAATCTTCCTCTGGAGC 57287	G TT _ C	
	TT		AAGCT CCA GGA GAT TGGGGG		
			TTCGA GGT CCT CTA ACCCCC		
			_ CT T A		
GAM1392	C5R1	3'	CCCAGCCTCCCCCAATGGCA 8202	A_ T_	
			TGCCATTGG GA CTGGG		
			ACGGTAACC CT GACCC		
			CC CC		
GAM1392	CHRNA4	3'	CCCCCAGACCCCATCCAGC 5615	CCAT AGA	
			GCTG TGG TCTGGGGG		
			CGAC ACC AGACCCCC		
			CT_ CC_		
GAM1392	EZH1	3'	CCCAGGCCCCAACGGCAGC 8816	A AGA	
			GCTGCC TTGG TCTGGG		
			CGACGG AACC GGACCC		
			C CC_		
GAM1392	GORASP1	3'	CCTGTATCCCCAGTGGCAACT 49109	C A CT	
			AG TGCCATTGG GAT GGG		
			TC ACGGTGACC CTA TCC		
			A C TG		
GAM1392	GPR62	5'	CCCCCAAGAGGATGGCAGC 89519	GGAGA _	
			GCTGCCATT TCT GGGGG		
			CGACGGTAG AGA CCCCC		
			G_ A		
GAM1392	MOCS1	3'	CCCCCAGACCCCTCCTCTAGC 92034	CCATT A_	
			GCTG GGAG TCTGGGGG		
			CGAT CCTC AGACCCCC		
			CT_ CCC		
GAM1392	PLAB	5'	CCCCCAGACCCCGCCCAGCT 65853	CCAT AGA	
			AGCTG TGG TCTGGGGG		

		TCGAC	GCC	AGACCCCC		
		CC__	CC__			
GAM1392	PSCD4	3'	CCCCCAGAAGGA	ACCGCAGCT	25404	CATT AGA__
			AGCTGC	GG TCTGGGGG		
			TCGACG	CC AGACCCCC		
			__	AAGGA		
GAM1392	RPA2	5'	CCCAGACCCG	CACCTT	11378	C CATT AGA
			AAG TGC	GG TCTGGG		
			TTC ACG	CC AGACCC		
			C __	C__		
GAM1392	SLC1A5	5'	CCCCAGATTCT	GGCA	18845	TTGGA
			TGCCA	GATCTGGGG		
			ACGGT	TTAGACCCC		
			C__			
GAM1392	SLC1A5	5'	CCCCAGATTCT	GGCA	78536	TTGGA
			TGCCA	GATCTGGGG		
			ACGGT	TTAGACCCC		
			C__			
GAM1392	SORCS2	3'	CCCAGACCCAA	AGCT	40415	GCCA AGA
			AGCT	TTGG TCTGGG		
			TCGA	AACC AGACCC		
			__	C__		
GAM1392	ABLM	3'	CCTCCTGCAAT	GGCAGC	9764	G ATCT
			GCTGCCATTG	AG GGGG		
			CGACGGTAAC	TC CTCC		
			G __			
GAM1392	ABLM	3'	CCTCCTGCAAT	GGCAGC	22025	G ATCT
			GCTGCCATTG	AG GGGG		
			CGACGGTAAC	TC CTCC		
			G __			
GAM1392	C11orf9	3'	CCCCCAGATGG	TATTGCAGCTT	25210	C TGGAG
			AAGCTGC	AT ATCTGGGGG		
			TTCGACG	TA TAGACCCCC		
			T TGG__			
GAM1392	C16orf5	3'	CCCCTGGGACCA	AACAGCAGC	25446	CA AGA TG
			GCTGC	TTGG TC GGGG		
			CGACG	AACC GG CCCC		
			AC	A__ GT		
GAM1392	CLSTN3	3'	CCTTTCTACCCCA	AATGGCAGC	28209	AGATCT_
			AGCTGCCATTG	GGGG		

		TCGACGGTAACC	TTCC	
		CCCATCT		
GAM1392 DEPP	5'	CCCCCAGACCTCCTCAGCT	22821	CCATT A
		AGCTG GGAG TCTGGGGG		
		TCGAC CCTC AGACCCCC		
		T___ C		
GAM1392 FLJ12788	3'	CCCCCAGATTACTCACAGCT	42543	CCATT A
		AGCTG GG GATCTGGGGG		
		TCGAC TC TTAGACCCCC		
		AC___ A		
GAM1392 FREQ	3'	CCCCCAGACCCTTGAGCGCT	26572	T _ TT AGA
		AGC GC CA GG TCTGGGGG		
		TCG CG GT CC AGACCCCC		
		_ A TC _		
GAM1392 KIAA0321	5'	CCCCCAGAGAGACTGGCAGC	62392	TTGGAGA
		GCTGCCA TCTGGGGG		
		CGACGGT AGACCCCC		
		CAGAG_		
GAM1392 KIAA0346	3'	CCCTTCCACCCCATTGGCAGCT	68362	T AGATCT
		AGCTGCCA TGG GGGG		
		TCGACGGT ACC TCCC		
		T CCACCT		
GAM1392 KIAA0773	3'	CCCCCAGACCACGGTGGACAGC	28052	_ GAGA
T		AGCTG CCATTG TCTGGGGG		
		TCGAC GGTGGC AGACCCCC		
		A ACC_		
GAM1392 KIAA1538	3'	CCCCAAATCCAGTGAGCT	71536	GC GATC
		AGCT CATTGGA TGGGG		
		TCGA GTGACCT ACCCC		
		_ AA_		
GAM1392 MGC2941	3'	CCCCAAATCTGGAGAGC	44158	G_ TTGGA C
		GCT CCA GAT TGGGG		
		CGA GGT CTA ACCCC		
		GA _ _ _ A		
GAM1392 MGC4737	3'	CCCCCAGACCCCTCCAGC	48846	CCATT A_
		GCTG GGAG TCTGGGGG		
		CGAC CCTC AGACCCCC		
		_ _ _ CCC		
GAM1392 PALM	3'	CCCCATGTCACGGCAGCTT	10411	ATT GA C
		AAGCTGCC G GAT TGGGG		

TTCGACGG C CTG ACCCC  
 \_\_\_\_A\_ T  
 GAM1392 PRO1489 3' CCTATCATCTTCAATAACA 37723 CC CTG  
 TG ATTGGAGAT GGG  
 || ||||| ||  
 AC TAACTTCTA TCC  
 AA CTA  
 GAM1392 RIN3 3' CCCCAGACCCCGCAGCT 45743 CATT AGA  
 AGCTGC GG TCTGGGG  
 ||||| || |||||  
 TCGACG CC AGACCCC  
 \_\_\_\_CC\_  
 GAM1392 TRIAD3 3' CCCCAGGCCACCAACGGCAGT 94502 A A AGA  
 CC A GCTGCC TTGG TCTGGGGG  
 | ||||| ||| |||||  
 C TGACGG AACC GGACCCCC  
 C C ACC  
 GAM1392 LOC136442 3' CCCCAGACGCTGGCGCT 54284 T T GAGA  
 AGC GCCA TG TCTGGGG  
 ||| ||| || |||||  
 TCG CGGT GC AGACCCC  
 \_ C \_  
 GAM1392 LOC138835 5' CCATCTCCACGGCAGCTT 75954 AT TC  
 AAGCTGCC TGGAGA TGG  
 ||||| ||||| |||  
 TTCGACGG ACCTCT ACC  
 C\_ \_  
 GAM1392 LOC143451 3' CCCCAGAATCACAGCAG 76562 CAT \_ GA  
 CTGC TG GA TCTGGGGG  
 ||| ||| || |||||  
 GACG AC CT AGACCCCC  
 \_\_\_\_A A\_  
 GAM1392 LOC145125 3' CCCCAGAATCACAGCAG 77004 CAT \_ GA  
 CTGC TG GA TCTGGGGG  
 ||| ||| || |||||  
 GACG AC CT AGACCCCC  
 \_\_\_\_A A\_  
 GAM1392 LOC147136 5' CCCCAGAGCAAAAGGCA 78261 A GGAGA  
 TGCC TT TCTGGGGG  
 ||| || |||||  
 ACGG AA AGACCCCC  
 A ACG\_  
 GAM1392 LOC147700 3' CCCCAGACCCACCAG 59196 CCAT AGA  
 CTG TGG TCTGGGGG  
 ||| ||| |||||  
 GAC ACC AGACCCCC  
 C\_\_ C\_\_  
 GAM1392 LOC149113 3' CCCCAGAAGGAATGCAGC 79163 C GGAGA  
 GCTGC ATT TCTGGGGG  
 ||||| ||| |||||

		CGACG TAA AGACCCCC		
		_ GGA_		
GAM1392	LOC154992 3'	CCCCCAGAAGGAATGCAGC 81213	C	GGAGA
		GCTGC ATT TCTGGGGG		
		CGACG TAA AGACCCCC		
		_ GGA_		
GAM1392	LOC161244 3'	CCCCCAGATCTCCCCGTCAGC 87083	CCATT	
		GCTG GGAGATCTGGGGG		
		CGAC CCTCTAGACCCCC		
		TGCC_		
GAM1392	LOC161244 3'	CCCCCAGATCTCCCCGTCAGC 87084	CCATT	
		GCTG GGAGATCTGGGGG		
		CGAC CCTCTAGACCCCC		
		TGCC_		
GAM1392	LOC201868 3'	CCCCCAGAAGGAATGCAGCT 89076	C	GGAGA
		AGCTGC ATT TCTGGGGG		
		TCGACG TAA AGACCCCC		
		_ GGA_		
GAM1392	LOC221405 5'	CCCAAGGCCCCACTGGCAGCTT 93881	T	AGA G
		AAGCTGCCA TGG TCT GGG		
		TTCGACGGT ACC GGA CCC		
		C CC_ A		
GAM1392	LOC254440 3'	CCCCCAGAATCACAGCAG 97064	CAT _	GA
		CTGC TG GA TCTGGGGG		
		GACG AC CT AGACCCCC		
		_ A A_		
GAM1392	LOC92340 3'	CCCCCAGACCCCGCCGCCCGCT 68990	T_	CAT AGA
		AGC GC TGG TCTGGGGG		
		TCG CG GCC AGACCCCC		
		CC CC_ CC_		
GAM1393	ADH1B 3'	CTTAGACATAAAGTAAAAT 72644	C	CAC
		ATTT ACTTT TGTCTGAG		
		TAAA TGAAA ACAGATTC		
		A T_		
GAM1393	ADH1B 3'	CTTAGACATAAAGTAAAAT 72644	C	CAC
		ATTT ACTTT TGTCTGAG		
		TAAA TGAAA ACAGATTC		
		A T_		
GAM1393	AHR 3'	ATCTCAGATGTTAAAATAAATG 7875	CAC C	T
		CATTT TTT AC GTCTGAGAT		

			GTAAA AAA TG TAGACTCTA		
			TA_ T _		
GAM1393	AHR	3'	ATCTCAGATGTTAAATAAATG 7875	CAC C T	
			CATTT TTT AC GTCTGAGAT		
			GTAAA AAA TG TAGACTCTA		
			TA_ T _		
GAM1393	FDFT1	3'	TAGGAAAGTGAAATG 15518	A	
			CATTTCACTTTC CTG		
			GTAAAGTGAAAG GAT		
			—		
GAM1393	FDFT1	3'	TAGGAAAGTGAAATG 15518	A	
			CATTTCACTTTC CTG		
			GTAAAGTGAAAG GAT		
			—		
GAM1393	JTB	3'	ATCTCAGACAGTGAAAGTGAAA 21959		
	TG		CATTTCACTTTCACTGTCTGAGAT		
			GTAAAGTGAAAGTGACAGACTCTA		
			—		
GAM1393	JTB	3'	ATCTCAGACAGTGAAAGTGAAA 21959		
	TG		CATTTCACTTTCACTGTCTGAGAT		
			GTAAAGTGAAAGTGACAGACTCTA		
			—		
GAM1393	KLF4	3'	TCCCAGACAGTGGATATG 14891	CT A	
			CA TTCACTGTCTG GA		
			GT AGGTGACAGAC CT		
			AT C		
GAM1393	KLF4	3'	TCCCAGACAGTGGATATG 14891	CT A	
			CA TTCACTGTCTG GA		
			GT AGGTGACAGAC CT		
			AT C		
GAM1393	PHYH	3'	ACAGTAAAAGTGAAAT 20608	C	
			ATTTCACTTT ACTGT		
			TAAAGTGAAA TGACA		
			A		
GAM1393	PHYH	3'	ACAGTAAAAGTGAAAT 20608	C	
			ATTTCACTTT ACTGT		
			TAAAGTGAAA TGACA		
			A		
GAM1393	PKD2	3'	TCCAGGTTGAAAGTGAAA 60096	CTG A	
			TTTCACTTTCA TCTG GA		



			AAAGTGAAAGT GGAC CT		
			T__ _		
GAM1393	PKD2	3'	TCCAGGTTGAAAGTGAAA 60096	CTG	A
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T__ _		
GAM1393	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1393	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1393	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA	CTG
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1393	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA	CTG
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1393	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT	CT
			TTCAC TTTCA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1393	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT	CT
			TTCAC TTTCA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1393	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G	T_
			CTTTCACT TC GAGAT		
			GAAAGTGA AG TTCTA		
			G TC		
GAM1393	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G	T_
			CTTTCACT TC GAGAT		
			GAAAGTGA AG TTCTA		
			G TC		
GAM1393	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT 45802	ACTTTCACT	
			G CATTTC GTCTGAGAT		

			GTAAAG	CAGACTCTA		
			AAACATTT_			
GAM1393	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT	45802	ACTTTC	ACT
		G	CATTT	GTCTGAGAT		
			GTAAAG	CAGACTCTA		
			AAACATTT_			
GAM1393	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG	45281	CTT	
			CATTTCA	TCACTGTCTGAGAT		
			GTAAAGT	AGTGACAGACTCTA		
			C_			
GAM1393	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG	45281	CTT	
			CATTTCA	TCACTGTCTGAGAT		
			GTAAAGT	AGTGACAGACTCTA		
			C_			
GAM1393	KIAA0984	3'	TTTGTCCAGTGAAAATGAA	65534	C	TC
			TTCA	TTTCACTG	TGAG	
			AAGT	AAAGTGAC	GTTT	
			A	CT		
GAM1393	KIAA0984	3'	TTTGTCCAGTGAAAATGAA	65534	C	TC
			TTCA	TTTCACTG	TGAG	
			AAGT	AAAGTGAC	GTTT	
			A	CT		
GAM1393	KLHL6	3'	ATCTCAGAGCAGGAAA	55299	A	_
			TTTC	CTG	TCTGAGAT	
			AAAG	GAC	AGACTCTA	
			_	G		
GAM1393	KLHL6	3'	ATCTCAGAGCAGGAAA	55299	A	_
			TTTC	CTG	TCTGAGAT	
			AAAG	GAC	AGACTCTA	
			_	G		
GAM1393	NIR3	3'	GCAGTGAAAGTGCAAT	66242	T	
			ATT	CACTTTCACTGT		
			TAA	GTGAAAGTGACG		
			C			
GAM1393	NIR3	3'	GCAGTGAAAGTGCAAT	66242	T	
			ATT	CACTTTCACTGT		
			TAA	GTGAAAGTGACG		
			C			
GAM1393	PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA	53598	CA	G
			TTCACTTT	CT	TCTGAGAT	

		AAGTGAAA GG AGACTCTA	
		CC G	
GAM1393	PORIMIN	3' ATCTCAGAGGGCCAAAGTGAA 53598	CA G
		TTCACTTT CT TCTGAGAT	
		AAGTGAAA GG AGACTCTA	
		CC G	
GAM1393	PP35	3' ATCTCAGACTGAAA 22814 CT	
		TTTCA GTCTGAGAT	
		AAAGT CAGACTCTA	
		—	
GAM1393	PP35	3' ATCTCAGACTGAAA 22814 CT	
		TTTCA GTCTGAGAT	
		AAAGT CAGACTCTA	
		—	
GAM1393	PRTD-NY3	3' CTCATTGCAATAAGTGAAATG 48148	TCAC C_
		CATTTCAC TT TGT TGAG	
		GTAAAGTGAA ACG ACTC	
		TA__ TT	
GAM1393	PRTD-NY3	3' CTCATTGCAATAAGTGAAATG 48148	TCAC C_
		CATTTCAC TT TGT TGAG	
		GTAAAGTGAA ACG ACTC	
		TA__ TT	
GAM1393	SEP15	3' TCCTACAGTAAGAGTGAAA 14934	C CT
		TTTCACTTT ACTGT GA	
		AAAGTGAGA TGACA CT	
		A TC	
GAM1393	SEP15	3' TCCTACAGTAAGAGTGAAA 14934	C CT
		TTTCACTTT ACTGT GA	
		AAAGTGAGA TGACA CT	
		A TC	
GAM1393	SFXN2	3' CTCAGGGGAAAAAAGTGAAA 73941	CACTG
		TTTCACTTT TCTGAG	
		AAAGTGAAA GGA CTC	
		AAAGG	
GAM1393	SFXN2	3' CTCAGGGGAAAAAAGTGAAA 73941	CACTG
		TTTCACTTT TCTGAG	
		AAAGTGAAA GGA CTC	
		AAAGG	
GAM1393	LOC149703	3' ATCTCAGACAGCCGTTTGAAA 84647	ACTTTCA
		TTTC CTGTCTGAGAT	

	AAAG GACAGACTCTA		
	GTTTGCC		
GAM1393 LOC149703 3'	ATCTCAGACAGCCGTTTGGAAA 84647	ACTTTCA	
	TTTC CTGTCTGAGAT		
	AAAG GACAGACTCTA		
	GTTTGCC		
GAM1393 LOC154007 3'	ATCTCAAACCCTTTAGTGAAA 81015	TTCACT C	
	TTTCACT GT TGAGAT		
	AAAGTGA CA ACTCTA		
	TTTCC_ A		
GAM1393 LOC154007 3'	ATCTCAAACCCTTTAGTGAAA 81015	TTCACT C	
	TTTCACT GT TGAGAT		
	AAAGTGA CA ACTCTA		
	TTTCC_ A		
GAM1393 LOC155004 3'	TCATTTAAGTGAAAGGAAA 81226	A GTC_	
	TTTC CTTTCACT TGA		
	AAAG GAAAGTGA ACT		
	_ ATTT		
GAM1393 LOC155004 3'	TCATTTAAGTGAAAGGAAA 81226	A GTC_	
	TTTC CTTTCACT TGA		
	AAAG GAAAGTGA ACT		
	_ ATTT		
GAM1393 LOC222134 5'	ACAGTGAAGTGAAATG 94136	T	
	CATTTCACTT CACTGT		
	GTAAAGTGAA GTGACA		
	-		
GAM1393 LOC222134 5'	ACAGTGAAGTGAAATG 94136	T	
	CATTTCACTT CACTGT		
	GTAAAGTGAA GTGACA		
	-		
GAM1394 ABCC12 3'	GACTGGGTGACAAGTGGTAATG 52647	_ GTG CG TG	
	TATTGC AC GTC GCC GTT		
	GTAATG TG CAG TGG CAG		
	G AA_ _ GT		
GAM1394 ABCC12 3'	GACTGGGTGACAAGTGGTAATG 52647	_ GTG CG TG	
	TATTGC AC GTC GCC GTT		
	GTAATG TG CAG TGG CAG		
	G AA_ _ GT		
GAM1394 ABCC8 5'	GCCGGGCCGGGCGGCG 4458	G	
	CGT GTCCGGCCTGGT		

			GCG CGGGCCGGGCCG			
			G			
GAM1394	ABCC8	5'	GCCGGGCGGGCGGCG	4458	G	
			CGT GTCCGGCCTGGT			
			GCG CGGGCCGGGCCG			
			G			
GAM1394	ACK1	3'	AACCAGGCTGGACCTGGGCAG	19340	A T	
			TTGC CG GGTCCGGCCTGGTT			
			GACG GT CCAGGTCGGACCAA			
			G _			
GAM1394	ACK1	3'	AACCAGGCTGGACCTGGGCAG	19340	A T	
			TTGC CG GGTCCGGCCTGGTT			
			GACG GT CCAGGTCGGACCAA			
			G _			
GAM1394	ADM	3'	GTTGTTCCGCCGCTGGAATG	6664	G	C__
			TATT CACGTGGT CGGC			
			GTAA GTGCGCCG GTTG			
			G CTT			
GAM1394	ADM	3'	GTTGTTCCGCCGCTGGAATG	6664	G	C__
			TATT CACGTGGT CGGC			
			GTAA GTGCGCCG GTTG			
			G CTT			
GAM1394	ADORA1	5'	GGCCGGGCTGGGAGCGCTGCGG	5427	_	GG
			TTGCA CGT TCCGGCCTGGTT			
			GGCGT GCG GGGTCGGGCCGG			
			C A_			
GAM1394	ADORA1	5'	GGCCGGGCTGGGAGCGCTGCGG	5427	_	GG
			TTGCA CGT TCCGGCCTGGTT			
			GGCGT GCG GGGTCGGGCCGG			
			C A_			
GAM1394	ADORA3	3'	AGTTGGGCTGAACATGTGTGTG	5438	TG	TG_ C GG
	GTG		TAT CACG GT CGGCCT TT			
			GTG GTGT CA GTCGGG GA			
			GT GTA A TT			
GAM1394	ADORA3	3'	AGTTGGGCTGAACATGTGTGTG	5438	TG	TG_ C GG
	GTG		TAT CACG GT CGGCCT TT			
			GTG GTGT CA GTCGGG GA			
			GT GTA A TT			
GAM1394	ADORA1A	3'	AATCATCAGCCACGTGTAG	52783	CC	CC
			TTGCACGTGGT GG TGGTT			

			GATGTGCACCG CT ACTAA		
			A_ _		
GAM1394	ADRA1A	3'	AATCATCAGCCACGTGTAG 52783	CC	CC
			TTGCACGTGGT GG TGGTT		
			GATGTGCACCG CT ACTAA		
			A_ _		
GAM1394	ADRA1D	3'	AGCTAGGCCGCGGAGTGTGC 5445	TGG	_
			GCACG TC CGGCCTGGTT		
			CGTGT GG GCCGGATCGA		
			GA_ C		
GAM1394	ADRA1D	3'	AGCTAGGCCGCGGAGTGTGC 5445	TGG	_
			GCACG TC CGGCCTGGTT		
			CGTGT GG GCCGGATCGA		
			GA_ C		
GAM1394	ADRA2A	5'	GGCCGGGCGCGGCCAGAACCGC 5455	ACG	_
	AG		TTGC TGGTCCGGCCTGGTT		
			GACG ACCGGGCGGGCCGG		
			CCAAG		
GAM1394	ADRA2A	5'	GGCCGGGCGCGGCCAGAACCGC 5455	ACG	_
	AG		TTGC TGGTCCGGCCTGGTT		
			GACG ACCGGGCGGGCCGG		
			CCAAG		
GAM1394	AGL	5'	GGCCAGGTTGGGTACCGGGTG 5350	G	_
			CAC TGGT CCGGCCTGGTT		
			GTG GCCA GGTTGGACCGG		
			G TG		
GAM1394	AGL	5'	GGCCAGGTTGGGTACCGGGTG 5350	G	_
			CAC TGGT CCGGCCTGGTT		
			GTG GCCA GGTTGGACCGG		
			G TG		
GAM1394	AGTR1	5'	AGCTCTGCCGGGCCGCGCGGT 5470	A	CT
	G		TATTGC CGTGGTCCGGC GGTT		
			GTGGCG GCGCCGGGCCG TCGA		
			_ TC		
GAM1394	AGTR1	5'	AGCTCTGCCGGGCCGCGCGGT 5470	A	CT
	G		TATTGC CGTGGTCCGGC GGTT		
			GTGGCG GCGCCGGGCCG TCGA		
			_ TC		
GAM1394	AGTR1	5'	AGCTCTGCCGGGCCGCGCGGT 16706	A	CT
	G		TATTGC CGTGGTCCGGC GGTT		

			GTGGCG GCGCCGGGCCG TCGA		
			— TC		
GAM1394	AGTR1	5'	AGCTCTGCCGGGCCGCGCGGT 23776	A	CT
	G		TATTGC CGTGGTCCGGC GGTT		
			GTGGCG GCGCCGGGCCG TCGA		
			— TC		
GAM1394	AGTR1	5'	AGCTCTGCCGGGCCGCGCGGT 23776	A	CT
	G		TATTGC CGTGGTCCGGC GGTT		
			GTGGCG GCGCCGGGCCG TCGA		
			— TC		
GAM1394	AGTR1	5'	AGCTCTGCCGGGCCGCGCGGT 49005	A	CT
	G		TATTGC CGTGGTCCGGC GGTT		
			GTGGCG GCGCCGGGCCG TCGA		
			— TC		
GAM1394	AGTR1	5'	AGCTCTGCCGGGCCGCGCGGT 49005	A	CT
	G		TATTGC CGTGGTCCGGC GGTT		
			GTGGCG GCGCCGGGCCG TCGA		
			— TC		
GAM1394	AGTR1	5'	AGCTCTGCCGGGCCGCGCGGT 16706	A	CT
	G		TATTGC CGTGGTCCGGC GGTT		
			GTGGCG GCGCCGGGCCG TCGA		
			— TC		
GAM1394	ANGPT2	3'	AACCAAGAATGTTATGTGCAA 6704	TC GC	—
			TTGCACGTGG CG CT GGTT		
			AACGTGTATT GT GA CCAA		
			— AA A		
GAM1394	ANGPT2	3'	AACCAAGAATGTTATGTGCAA 6704	TC GC	—
			TTGCACGTGG CG CT GGTT		
			AACGTGTATT GT GA CCAA		
			— AA A		
GAM1394	ANXA7	5'	AGCCGGGTTGGGCTGTGACGCT 6718	—	—
	GC		GCA CGT GGTCCGGCCTGGTT		
			CGT GCA TCGGGTTGGGCCGA		
			C GTG		
GAM1394	ANXA7	5'	AGCCGGGTTGGGCTGTGACGCT 6718	—	—
	GC		GCA CGT GGTCCGGCCTGGTT		
			CGT GCA TCGGGTTGGGCCGA		
			C GTG		
GAM1394	ANXA7	3'	TCTGATTCTGTGTAATA 6721	TG C	
			TATTGCACG GTC GG		

			ATAATGTGT TAG CT		
			CT T		
GAM1394 ANXA7	3'	TCTGATTCTGTGTAATA	6721	TG C	
		TATTGCACG GTC GG			
		ATAATGTGT TAG CT			
		CT T			
GAM1394 ANXA7	5'	AGCCGGGTTGGGCTGTGACGCT	14450	_ _	
GC		GCA CGT GGTCCGGCCTGGTT			
		CGT GCA TCGGGTTGGGCCGA			
		C GTG			
GAM1394 ANXA7	5'	AGCCGGGTTGGGCTGTGACGCT	14450	_ _	
GC		GCA CGT GGTCCGGCCTGGTT			
		CGT GCA TCGGGTTGGGCCGA			
		C GTG			
GAM1394 ANXA7	3'	TCTGATTCTGTGTAATA	14453	TG C	
		TATTGCACG GTC GG			
		ATAATGTGT TAG CT			
		CT T			
GAM1394 ANXA7	3'	TCTGATTCTGTGTAATA	14453	TG C	
		TATTGCACG GTC GG			
		ATAATGTGT TAG CT			
		CT T			
GAM1394 AP1S1	3'	GGCCGGGGTGTGGCGATG	7068	A GT G	
		TATTGC C G TCCGGCC			
		GTAGCG G T GGGCCGG			
		_ TG G			
GAM1394 AP1S1	3'	GGCCGGGGTGTGGCGATG	7068	A GT G	
		TATTGC C G TCCGGCC			
		GTAGCG G T GGGCCGG			
		_ TG G			
GAM1394 APAF1	3'	AATTAGGAGCCAGGTGCGGTG	6725	G CCGG	
		TATTGCAC TGGT CCTGGTT			
		GTGGCGTG ACCG GGATTAA			
		G A__			
GAM1394 APAF1	3'	AATTAGGAGCCAGGTGCGGTG	6725	G CCGG	
		TATTGCAC TGGT CCTGGTT			
		GTGGCGTG ACCG GGATTAA			
		G A__			
GAM1394 APAF1	3'	AATTAGGAGCCAGGTGCGGTG	25034	G CCGG	
		TATTGCAC TGGT CCTGGTT			



			GTGGCGTG ACCG GGATTAA		
			G A__		
GAM1394	APAF1	3'	AATTAGGAGCCAGGTGCGGTG 25034	G	CCGG
			TATTGCAC TGGT CCTGGTT		
			GTGGCGTG ACCG GGATTAA		
			G A__		
GAM1394	APLP1	5'	GGCCGGGCGCGGGCGGGAGTGCA 17705	GTG_	
	G		TTGCAC GTCCGGCCTGGTT		
			GACGTG CGGGCCGGGCCGG		
			AGGG		
GAM1394	APLP1	5'	GGCCGGGCGCGGGCGGGAGTGCA 17705	GTG_	
	G		TTGCAC GTCCGGCCTGGTT		
			GACGTG CGGGCCGGGCCGG		
			AGGG		
GAM1394	ARHD	3'	GCTGGGCTGGACCCGGT 27419	A T	TG
			GC CG GGTCCGGCC GT		
			TG GC CCAGGTCGG CG		
			— — GT		
GAM1394	ARHD	3'	GCTGGGCTGGACCCGGT 27419	A T	TG
			GC CG GGTCCGGCC GT		
			TG GC CCAGGTCGG CG		
			— — GT		
GAM1394	ARHGAP6	3'	GCCAGGTCGGAGCAGT 6762	G G	
			AC TG TCCGGCCTGGT		
			TG AC AGGCTGGACCG		
			— G		
GAM1394	ARHGAP6	3'	GCCAGGTCGGAGCAGT 6762	G G	
			AC TG TCCGGCCTGGT		
			TG AC AGGCTGGACCG		
			— G		
GAM1394	ATP10C	5'	CCGGGCCGCGAGTGATG 44408	TG A	
			TAT C CGTGGTCCGG		
			GTA G GCGCCGGGCC		
			GT A		
GAM1394	ATP10C	5'	CCGGGCCGCGAGTGATG 44408	TG A	
			TAT C CGTGGTCCGG		
			GTA G GCGCCGGGCC		
			GT A		
GAM1394	ATP2B2	5'	GGCCGGGCGGGCGCGCACCAG 8069	AC__ _	
	C		GC GTG GTCCGGCCTGGTT		

			CG CGC CGGGCCGGGCCGG		
			ACCA G		
GAM1394	ATP2B2	5'	GGCCGGGCGGGCCGGGCGCGC 8068	A	__
	A		TGC CGT GGTCCGGCCTGGTT		
			ACG GCG CCGGGCCGGGCCGG		
			C GG		
GAM1394	ATP2B2	5'	GGCCGGGCGGGCCGGGCGCGC 8068	A	__
	A		TGC CGT GGTCCGGCCTGGTT		
			ACG GCG CCGGGCCGGGCCGG		
			C GG		
GAM1394	ATP2B2	5'	GGCCGGGCGGGCGCGCACCAG 8069	AC__	_
	C		GC GTG GTCCGGCCTGGTT		
			CG CGC CGGGCCGGGCCGG		
			ACCA G		
GAM1394	ATP6V1A1	3'	GACTAGTGCCTATGTGT 8076	GTCC	_
			GCACGTG GGC CTGGTT		
			TGTGTAT CCG GATCAG		
			____ T		
GAM1394	ATP6V1A1	3'	GACTAGTGCCTATGTGT 8076	GTCC	_
			GCACGTG GGC CTGGTT		
			TGTGTAT CCG GATCAG		
			____ T		
GAM1394	ATP6V1C1	3'	GATCAGGTCTGTAAATGTGTA 8091	GGTCC	
			TGCACGT GGCCTGGTT		
			ATGTGTA CTGGACTAG		
			AATGT		
GAM1394	ATP6V1C1	3'	GATCAGGTCTGTAAATGTGTA 8091	GGTCC	
			TGCACGT GGCCTGGTT		
			ATGTGTA CTGGACTAG		
			AATGT		
GAM1394	ATP8A2	3'	GCTGTCACTACGTGTGATG 93513	TG	C_
			TAT CACGTGGT CGGC		
			GTA GTGCATCA GTCG		
			GT CT		
GAM1394	ATP8A2	3'	GCTGTCACTACGTGTGATG 93513	TG	C_
			TAT CACGTGGT CGGC		
			GTA GTGCATCA GTCG		
			GT CT		
GAM1394	ATRX	3'	GACACAGAATTGTGTGCAATA 4916	TG CCGGC	_
			TATTGCACG GT CTG GTT		

		ATAACGTGT TA GAC CAG	
		GT A____ A	
GAM1394 ATRX	3'	GACACAGAATTGTGTGCAATA 4916	TG CCGGC _
		TATTGCACG GT CTG GTT	
		ATAACGTGT TA GAC CAG	
		GT A____ A	
GAM1394 ATRX	3'	GACACAGAATTGTGTGCAATA 56247	TG CCGGC _
		TATTGCACG GT CTG GTT	
		ATAACGTGT TA GAC CAG	
		GT A____ A	
GAM1394 ATRX	3'	GACACAGAATTGTGTGCAATA 56247	TG CCGGC _
		TATTGCACG GT CTG GTT	
		ATAACGTGT TA GAC CAG	
		GT A____ A	
GAM1394 B4GALT2	3'	GGCATTGGGTCAGTGCGGTA 47583	G GT _
		TATTGCAC TG CCG GCC	
		ATGGCGTG AC GGT CGG	
		_ TG TA	
GAM1394 B4GALT2	3'	GGCATTGGGTCAGTGCGGTA 47583	G GT _
		TATTGCAC TG CCG GCC	
		ATGGCGTG AC GGT CGG	
		_ TG TA	
GAM1394 B4GALT5	3'	TAGCTGGTGACACTTGTGTGCT 16512	T ____ GT_ CTGGTT
	GTG	GCAC GTG CCGGC	
		CGTG CAC GGTCG	
		T TGTT AGT A TT	
GAM1394 B4GALT5	3'	TAGCTGGTGACACTTGTGTGCT 16512	T ____ GT_ CTGGTT
	GTG	GCAC GTG CCGGC	
		CGTG CAC GGTCG	
		T TGTT AGT A TT	
GAM1394 B4GALT7	3'	GGCTGGGCCAGGACACGTGGGG 23415	G G _ TG
	TG	TATT CACGTG TCC GGCC GTT	
		GTGG GTGCAC AGG CCGG CGG	
		G _ A GT	
GAM1394 B4GALT7	3'	GGCTGGGCCAGGACACGTGGGG 23415	G G _ TG
	TG	TATT CACGTG TCC GGCC GTT	
		GTGG GTGCAC AGG CCGG CGG	
		G _ A GT	
GAM1394 BCL7A	3'	GATCAGGCTGGGCACTCGCTGT 40641	_ TG_
		GCA CG GTCCGGCCTGGTT	

			TGT GC CGGGTCGGACTAG		
			C TCA		
GAM1394 BCL7A	3'	GATCAGGCTGGGCACTCGCTGT 40641	_ TG_		
		GCA CG GTCCGGCCTGGTT			
		TGT GC CGGGTCGGACTAG			
		C TCA			
GAM1394 BRF1	3'	GGCCGGGTGTGTGCAG 7713	TGG		
		TTGCACG TCCGGCC			
		GACGTGT GGGCCGG			
		GT_			
GAM1394 BRF1	3'	GGCCGGGTGTGTGCAG 7713	TGG		
		TTGCACG TCCGGCC			
		GACGTGT GGGCCGG			
		GT_			
GAM1394 BSN	3'	GGCCAGGCTTCCCGTGCG 12925	T TCC		
		TGCACG GG GGCCTGGTT			
		GCGTGC CC TCGGACCGG			
		_ T_			
GAM1394 BSN	3'	GGCCAGGCTTCCCGTGCG 12925	T TCC		
		TGCACG GG GGCCTGGTT			
		GCGTGC CC TCGGACCGG			
		_ T_			
GAM1394 BST2	3'	GATTGGGCATGGGGTGCGGTG 15085	GTGG _ TG		
		TATTGCAC TCCG GCC GTT			
		GTGGCGTG GGGT CGG TAG			
		_____ A GT			
GAM1394 BST2	3'	GATTGGGCATGGGGTGCGGTG 15085	GTGG _ TG		
		TATTGCAC TCCG GCC GTT			
		GTGGCGTG GGGT CGG TAG			
		_____ A GT			
GAM1394 BTEB1	5'	TGGCCGTGGATGCTGCGTGCGG 6852	TG ____ TGGTT		
		TTGCACG GT C CGGCC			
		GGCGTGC CG G GCCGG			
		GT TAG T TT			
GAM1394 BTEB1	5'	TGGCCGTGGATGCTGCGTGCGG 6852	TG ____ TGGTT		
		TTGCACG GT C CGGCC			
		GGCGTGC CG G GCCGG			
		GT TAG T TT			
GAM1394 C1orf1	3'	GCCGGGCATGGTGGTG 6861	TG A G		
		TAT C CGTG TCCGGC			

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GTG G GTAC GGGCCG
GT _ _
GAM1394 C1orf1 3' GCCGGGCATGGTGGTG 6861 TG A G
TAT C CGTG TCCGGC
||| | ||| |||||
GTG G GTAC GGGCCG
GT _ _
GAM1394 C21orf5 3' TCAGGCTAGGTGCGGTG 17613 G GGTCC
TATTGCAC T GGCCTGG
||||||| | |||||
GTGGCGTG A TCGGACT
G _ _
GAM1394 C21orf5 3' TCAGGCTAGGTGCGGTG 17613 G GGTCC
TATTGCAC T GGCCTGG
||||||| | |||||
GTGGCGTG A TCGGACT
G _ _
GAM1394 C5R1 3' ATTAGGCTGAGAGCAGTG 8200 G G _
CAC TG TC CGGCCTGGT
||| || |||||
GTG AC AG GTCGGATTA
_ G A
GAM1394 C5R1 3' ATTAGGCTGAGAGCAGTG 8200 G G _
CAC TG TC CGGCCTGGT
||| || |||||
GTG AC AG GTCGGATTA
_ G A
GAM1394 CACNA1A 3' GCCAGGCCGGGCCGGGCG 3561 ACGT
TGC GGTCCGGCCTGGT
||| |||||
GCG CCGGGCCGGACCG
GG _
GAM1394 CACNA1A 3' GCCAGGCCGGGCCGGGCG 3561 ACGT
TGC GGTCCGGCCTGGT
||| |||||
GCG CCGGGCCGGACCG
GG _
GAM1394 CALD1 3' TGCCTGCGGAATGTGTGCAGTA 52470 TGG G CT T
TATTGCACG TCCG C GGT
||||||| ||| | |||
ATGACGTGT AGGC G CCG
GTA _ T_ TT
GAM1394 CALD1 3' TGCCTGCGGAATGTGTGCAGTA 52470 TGG G CT T
TATTGCACG TCCG C GGT
||||||| ||| | |||
ATGACGTGT AGGC G CCG
GTA _ T_ TT
GAM1394 CAPN10 3' GGCTGGCACCGCGTGCCATG 43596 T _
TAT GCACGTGGT CCGGCC
||| ||||| |||||

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			GTA CGTGCGCCA GGTCCG			
			C C			
GAM1394	CAPN10	3'	GGCTGGCACCGCGTGCCATG 43596	T	—	
			TAT GCACGTGGT CCGGCC			
			GTA CGTGCGCCA GGTCCG			
			C C			
GAM1394	CAPN10	3'	GGCTGGCACCGCGTGCCATG 43603	T	—	
			TAT GCACGTGGT CCGGCC			
			GTA CGTGCGCCA GGTCCG			
			C C			
GAM1394	CAPN10	3'	GGCTGGCACCGCGTGCCATG 43603	T	—	
			TAT GCACGTGGT CCGGCC			
			GTA CGTGCGCCA GGTCCG			
			C C			
GAM1394	CAPNS1	5'	GACACGAGGGCCGCGGTGCAGT 8251	—	GGCCTG	
	G		TATTGCAC GTGGTCC GTT			
			GTGACGTG CGCCGGG CAG			
			G AGCA__			
GAM1394	CAPNS1	5'	GACACGAGGGCCGCGGTGCAGT 8251	—	GGCCTG	
	G		TATTGCAC GTGGTCC GTT			
			GTGACGTG CGCCGGG CAG			
			G AGCA__			
GAM1394	CASP10	3'	TTGGA CTGGGTGCGGTG 52125	G		
			TATTGCAC TGGTCCGG			
			GTGGCGTG GTCAGGTT			
			G			
GAM1394	CASP10	3'	TTGGA CTGGGTGCGGTG 52125	G		
			TATTGCAC TGGTCCGG			
			GTGGCGTG GTCAGGTT			
			G			
GAM1394	CASP10	3'	TTGGA CTGGGTGCGGTG 52109	G		
			TATTGCAC TGGTCCGG			
			GTGGCGTG GTCAGGTT			
			G			
GAM1394	CASP10	3'	TTGGA CTGGGTGCGGTG 52109	G		
			TATTGCAC TGGTCCGG			
			GTGGCGTG GTCAGGTT			
			G			
GAM1394	CASP2	5'	TGGTTTGT TGGGCTGTGGGCG 52147	A TG	_____	TGGTT
	GTG		TGC CG GTCCG GCC			

			GCG GT CGGGT TGG			
			G GT TTGTT TT			
GAM1394	CASP2	5'	TGGTTTGTGTTGGGCTGTGGGCG	52147	A TG	_____ TGGTT
	GTG		TGC CG GTCCG GCC			
			GCG GT CGGGT TGG			
			G GT TTGTT TT			
GAM1394	CASP2	5'	TGGTTTGTGTTGGGCTGTGGGCG	52161	A TG	_____ TGGTT
	GTG		TGC CG GTCCG GCC			
			GCG GT CGGGT TGG			
			G GT TTGTT TT			
GAM1394	CASP2	5'	TGGTTTGTGTTGGGCTGTGGGCG	52161	A TG	_____ TGGTT
	GTG		TGC CG GTCCG GCC			
			GCG GT CGGGT TGG			
			G GT TTGTT TT			
GAM1394	CASP3	3'	CCAGGTAATGTGAATA	52194	G	GGTCCG
			TATT CACGT GCCTGG			
			ATAA GTGTA TGGACC			
			- A_____			
GAM1394	CASP3	3'	CCAGGTAATGTGAATA	52194	G	GGTCCG
			TATT CACGT GCCTGG			
			ATAA GTGTA TGGACC			
			- A_____			
GAM1394	CASP3	3'	CCAGGTAATGTGAATA	15098	G	GGTCCG
			TATT CACGT GCCTGG			
			ATAA GTGTA TGGACC			
			- A_____			
GAM1394	CASP3	3'	CCAGGTAATGTGAATA	15098	G	GGTCCG
			TATT CACGT GCCTGG			
			ATAA GTGTA TGGACC			
			- A_____			
GAM1394	CASP7	5'	AGCTGGGCTGCTGGGTG	52900	G	CC TG
			CAC TGGT GGCC GTT			
			GTG GTCG TCGG CGA			
			G _ GT			
GAM1394	CASP7	5'	AGCTGGGCTGCTGGGTG	52900	G	CC TG
			CAC TGGT GGCC GTT			
			GTG GTCG TCGG CGA			
			G _ GT			
GAM1394	CASQ2	3'	GACCATCAAGGGTCATGGCAGT	6937	A	GT GGCC
	G		TATTGC CGTG CC TGGTT			

			GTGACG GTAC GG ACCAG		
			_ TG AACT		
GAM1394	CASQ2	3'	GACCATCAAGGGTCATGGCAGT 6937	A	GT GGCC
	G		TATTGC CGTG CC TGGTT		
			GTGACG GTAC GG ACCAG		
			_ TG AACT		
GAM1394	CBFA2T2	3'	AGCCAGGCTGGAGGCGGCAG 17457	A	GG
			TTGC CGT TCCGGCCTGGTT		
			GACG GCG AGGTCGGACCGA		
			_ G_		
GAM1394	CBFA2T2	3'	AGCCAGGCTGGAGGCGGCAG 17457	A	GG
			TTGC CGT TCCGGCCTGGTT		
			GACG GCG AGGTCGGACCGA		
			_ G_		
GAM1394	CCND1	3'	GGCCCCGAGGCCGCGTGCG 53890	_	CCT
			TGCACGTGGTC CGG GGTT		
			GCGTGCGCCGG GCC CCGG		
			A _		
GAM1394	CCND1	3'	GGCCCCGAGGCCGCGTGCG 53890	_	CCT
			TGCACGTGGTC CGG GGTT		
			GCGTGCGCCGG GCC CCGG		
			A _		
GAM1394	CCND1	3'	AGTGTGGGCCACTGTGGTG 53883	TG C	GC
			TAT CA GTGGTCCG CT		
			GTG GT CACCGGGT GA		
			GT _ GT		
GAM1394	CCND1	3'	AGTGTGGGCCACTGTGGTG 53883	TG C	GC
			TAT CA GTGGTCCG CT		
			GTG GT CACCGGGT GA		
			GT _ GT		
GAM1394	CCR2	3'	AACCTCAGGGCTGTGTGTA 5385	TG	GGCCT
			TGCACG GTCC GGTT		
			ATGTGT CGGG CCAA		
			GT ACT_		
GAM1394	CCR2	3'	AACCTCAGGGCTGTGTGTA 5385	TG	GGCCT
			TGCACG GTCC GGTT		
			ATGTGT CGGG CCAA		
			GT ACT_		
GAM1394	CDH16	3'	AACTGGGCTGGGCCCTATGGGA 14494	G CGT	TG
			TT CA GGTCCGGCC GTT		



			AG GT CCGGGTCGG CAA		
			G ATC GT		
GAM1394	CDH16	3'	AACTGGGCTGGGCCCTATGGGA 14494	G CGT	TG
			TT CA GGTCCGGCC GTT		
			AG GT CCGGGTCGG CAA		
			G ATC GT		
GAM1394	CDS1	5'	GGTGGGGCCGCGTTAGTG 7005	C	G
			TATTG ACGTGGTCC GCC		
			GTGAT TGC GCCGGG TGG		
			— G		
GAM1394	CDS1	5'	GGTGGGGCCGCGTTAGTG 7005	C	G
			TATTG ACGTGGTCC GCC		
			GTGAT TGC GCCGGG TGG		
			— G		
GAM1394	CHRNA1	3'	AGTTTGTGGCCATGGTAGTG 60533	A	— GC
			TATTGC CGTGGTC CG CT		
			GTGATG GTACCGG GT GA		
			— T TT		
GAM1394	CHRNA1	3'	AGTTTGTGGCCATGGTAGTG 60533	A	— GC
			TATTGC CGTGGTC CG CT		
			GTGATG GTACCGG GT GA		
			— T TT		
GAM1394	CIT	3'	TTGGTTGGGAAGTCCTTAGGTG 69751	G	_____ TGGTT
			CAGTG CAC TGG TCCGGCC		
			GTG ATT GGGTTGG		
			G CCTGAA TTG		
GAM1394	CIT	3'	TTGGTTGGGAAGTCCTTAGGTG 69751	G	_____ TGGTT
			CAGTG CAC TGG TCCGGCC		
			GTG ATT GGGTTGG		
			G CCTGAA TTG		
GAM1394	CNN1	3'	GA CTGGCATACTATGTG 7114	CCG	T
			CACGTGGT GCC GGTT		
			GTGTATCA CGG TCAG		
			TA_ _		
GAM1394	CNN1	3'	GA CTGGCATACTATGTG 7114	CCG	T
			CACGTGGT GCC GGTT		
			GTGTATCA CGG TCAG		
			TA_ _		
GAM1394	COL18A1	3'	CAGGCAGGGTGCAGTA 55292	GTGGT	G
			TATTGCAC CC GCCTG		

			ATGACGTG GG CGGAC	
			_____ A	
GAM1394	COL18A1	3'	CAGGCAGGGTGCAGTA 55288	GTGGT G
			TATTGCAC CC GCCTG	
			ATGACGTG GG CGGAC	
			_____ A	
GAM1394	COL18A1	3'	CAGGCAGGGTGCAGTA 55288	GTGGT G
			TATTGCAC CC GCCTG	
			ATGACGTG GG CGGAC	
			_____ A	
GAM1394	COL18A1	3'	CAGGCAGGGTGCAGTA 47576	GTGGT G
			TATTGCAC CC GCCTG	
			ATGACGTG GG CGGAC	
			_____ A	
GAM1394	COL18A1	3'	CAGGCAGGGTGCAGTA 47576	GTGGT G
			TATTGCAC CC GCCTG	
			ATGACGTG GG CGGAC	
			_____ A	
GAM1394	COL18A1	3'	CAGGCAGGGTGCAGTA 55292	GTGGT G
			TATTGCAC CC GCCTG	
			ATGACGTG GG CGGAC	
			_____ A	
GAM1394	COX10	3'	AATTAGCCTCCACATGTGCAAT 7120	GTCC C
	G		TATTGCACGTG GGC TGGTT	
			GTAACGTGTAC CCG ATTAA	
			ACCT _	
GAM1394	COX10	3'	AATTAGCCTCCACATGTGCAAT 7120	GTCC C
	G		TATTGCACGTG GGC TGGTT	
			GTAACGTGTAC CCG ATTAA	
			ACCT _	
GAM1394	CRHR1	5'	GGCCGGGCGGGCCGCGGGGC 15213	A_
			GC CGTGGTCCGGCCTGGTT	
			CG GCGCCGGGCGGGCCGG	
			GG	
GAM1394	CRHR1	5'	GGCCGGGCGGGCCGCGGGGC 15213	A_
			GC CGTGGTCCGGCCTGGTT	
			CG GCGCCGGGCGGGCCGG	
			GG	
GAM1394	CRHR1	5'	GGCCGGGCGGGCCGGG 15214	G
			C TGGTCCGGCCTGGTT	

			G GCCGGGCCGGGCCGG			
			G			
GAM1394	CRHR1	5'	GGCCGGGCCGGGCCGGG	15214	G	
			C TGGTCCGGCCTGGTT			
			G GCCGGGCCGGGCCGG			
			G			
GAM1394	CRHR1	5'	GGCCGGGCCGGGCCGG	15212		
			CGTGGTCCGGCCTGGTT			
			GCGCCGGGCCGGGCCGG			
GAM1394	CRHR1	5'	GGCCGGGCCGGGCCGG	15212		
			CGTGGTCCGGCCTGGTT			
			GCGCCGGGCCGGGCCGG			
GAM1394	CRK	3'	ATCATGCACCGTGTGAATA	59853	G	CCG C
			TATT CACGTGGT GC TGGT			
			ATAA GTGTGCCA CG ACTA			
			— — T			
GAM1394	CRK	3'	ATCATGCACCGTGTGAATA	59853	G	CCG C
			TATT CACGTGGT GC TGGT			
			ATAA GTGTGCCA CG ACTA			
			— — T			
GAM1394	CROT	3'	AACTTTTTTGGGCTGGGTGCAG	40947	G	CCT
	TG		TATTGCAC TGGTCCGG GGTT			
			GTGACGTG GTCGGGTT TCAA			
			G TTT			
GAM1394	CROT	3'	AACTTTTTTGGGCTGGGTGCAG	40947	G	CCT
	TG		TATTGCAC TGGTCCGG GGTT			
			GTGACGTG GTCGGGTT TCAA			
			G TTT			
GAM1394	CROT	3'	GCCGGGTATGGTGGTG	40949	TG A	G
			TAT C CGTG TCCGGC			
			GTG G GTAT GGGCCG			
			GT _ _			
GAM1394	CROT	3'	GCCGGGTATGGTGGTG	40949	TG A	G
			TAT C CGTG TCCGGC			
			GTG G GTAT GGGCCG			
			GT _ _			
GAM1394	CSPG4	3'	GGCCGAGGCCACTGTAGTG	8572	C	_
			TATTGCA GTGGTC CGGCC			

			GTGATGT CACCGG GCCGG		
			— A		
GAM1394	CSPG4	3'	GGCCGAGGCCACTGTAGTG 8572	C	—
			TATTGCA GTGGTC CGGCC		
			GTGATGT CACCGG GCCGG		
			— A		
GAM1394	CTSB	5'	GCTGCAGCGCTGGGCTGGTGTG 64729	GT_	— GTT
			CAGTG TTGCAC GGTCCGGC CTG		
			GACGTG TCGGGTCG GAC		
			TGG C GTCGG		
GAM1394	CTSB	5'	GCTGCAGCGCTGGGCTGGTGTG 64729	GT_	— GTT
			CAGTG TTGCAC GGTCCGGC CTG		
			GACGTG TCGGGTCG GAC		
			TGG C GTCGG		
GAM1394	CYP1B1	3'	AACCAGGTCCAGATGTGCTATA 3650	T	GGTCC
			TAT GCACGT GGCCTGGTT		
			ATA CGTGTA CTGGACCAA		
			T GAC__		
GAM1394	CYP1B1	3'	AACCAGGTCCAGATGTGCTATA 3650	T	GGTCC
			TAT GCACGT GGCCTGGTT		
			ATA CGTGTA CTGGACCAA		
			T GAC__		
GAM1394	DBH	3'	AACCAGGCTGATGCCGTGCGG 5789	TG	C
			TTGCACG GTC GGCCTGGTT		
			GGCGTGC TAG TCGGACCAA		
			CG _		
GAM1394	DBH	3'	AACCAGGCTGATGCCGTGCGG 5789	TG	C
			TTGCACG GTC GGCCTGGTT		
			GGCGTGC TAG TCGGACCAA		
			CG _		
GAM1394	DBT	3'	AACCAAAAAGCCAAGTGTGGTG 8605	TG	G CCGGCC
			TAT CAC TGGT TGGTT		
			GTG GTG ACCG ACCAA		
			GT A AAAA__		
GAM1394	DBT	3'	AACCAAAAAGCCAAGTGTGGTG 8605	TG	G CCGGCC
			TAT CAC TGGT TGGTT		
			GTG GTG ACCG ACCAA		
			GT A AAAA__		
GAM1394	DBT	3'	ATTAGGCCGGGCATGGTG 8607	GTG	
			CAC GTCCGGCCTGGT		

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GTG CGGGCCGGATTA
GTA
GAM1394 DBT 3' ATTAGGCCGGGCATGGTG 8607 GTG
CAC GTCCGGCCTGGT
||| |||||
GTG CGGGCCGGATTA
GTA
GAM1394 DCLRE1C 3' ACCTGGTTGGGTGTGGTG 42523 TG GTGGT T
TAT CAC CCGGCC GGT
||| ||| ||||| |||
GTG GTG GGTGGA CCA
GT ____ T
GAM1394 DCLRE1C 3' ACCTGGTTGGGTGTGGTG 42523 TG GTGGT T
TAT CAC CCGGCC GGT
||| ||| ||||| |||
GTG GTG GGTGGA CCA
GT ____ T
GAM1394 DDX11 3' AACCTAGGCCGGTGTGTGGTG 47645 TG TGGT _
TAT CACG CCGGCCT GTT
||| ||| ||||| |||
GTG GTGT GGCCGA CCAA
GT ____ T
GAM1394 DDX11 3' AACCTAGGCCGGTGTGTGGTG 47645 TG TGGT _
TAT CACG CCGGCCT GTT
||| ||| ||||| |||
GTG GTGT GGCCGA CCAA
GT ____ T
GAM1394 DIO3 5' GCCGGGCCGGAGGTGGAG 7244 G GTGG
TT CAC TCCGGCCTGGT
|| ||| |||||
GA GTG AGGCCGGGCCG
G G__
GAM1394 DIO3 5' GCCGGGCCGGAGGTGGAG 7244 G GTGG
TT CAC TCCGGCCTGGT
|| ||| |||||
GA GTG AGGCCGGGCCG
G G__
GAM1394 DIRC1 3' GGTTGGGTAAATATTTGCAATA 53667 C G__
TATTGCA GTG TCCGGCC
||||| ||| |||||
ATAACGT TAT GGGTTGG
T AAAT
GAM1394 DIRC1 3' GGTTGGGTAAATATTTGCAATA 53667 C G__
TATTGCA GTG TCCGGCC
||||| ||| |||||
ATAACGT TAT GGGTTGG
T AAAT
GAM1394 DLEU1 3' AACTGGGAACCTTCATATGTGC 19693 GTCC __ TG
AGTA ATTGCACGTG GG CC GTT
||||||| || |||

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			TGACGTGTAT	CC GG CAA		
			ACTT AA GT			
GAM1394	DLEU1	3'	AACTGGGAACCTTCATATGTGC	19693	GTCC _	TG
		AGTA	ATTGCACGTG	GG CC GTT		
			TGACGTGTAT	CC GG CAA		
			ACTT AA GT			
GAM1394	DLG5	3'	GGCCACGGCTGCGTGCGAT	82917	TG C_	
			ATTGCACG	GTC GGCC		
			TAGCGTGC	CGG CCGG		
			GT CA			
GAM1394	DLG5	3'	GGCCACGGCTGCGTGCGAT	82917	TG C_	
			ATTGCACG	GTC GGCC		
			TAGCGTGC	CGG CCGG		
			GT CA			
GAM1394	DMP1	3'	ATCAGTTTGCGTGCAATG	15318	TG TCCGGC	
			TATTGCACG	G CTGGT		
			GTAACGTGC	T GACTA		
			GT T_____			
GAM1394	DMP1	3'	ATCAGTTTGCGTGCAATG	15318	TG TCCGGC	
			TATTGCACG	G CTGGT		
			GTAACGTGC	T GACTA		
			GT T_____			
GAM1394	DNASE1L1	5'	GGCCAGATCATGTGTGG	22078	TG	C
			T CACGTGGTC	GGCC		
			G GTGTACTAG	CCGG		
			GT	A		
GAM1394	DNASE1L1	5'	GGCCAGATCATGTGTGG	22078	TG	C
			T CACGTGGTC	GGCC		
			G GTGTACTAG	CCGG		
			GT	A		
GAM1394	DNLC2A	3'	CCAGTGACCGTGTGTGG	26361	TG	CGGC
			T CACGTGGTC	CTGG		
			G GTGTGCCAG	GACC		
			GT	T_____		
GAM1394	DNLC2A	3'	CCAGTGACCGTGTGTGG	26361	TG	CGGC
			T CACGTGGTC	CTGG		
			G GTGTGCCAG	GACC		
			GT	T_____		
GAM1394	DNM2	3'	GGCTGGGCTTGGGCTATGTG	17058	_	TG
			CACGTGGTCCG	GCC GTT		

			GTGTATCGGGT CGG CGG		
			T GT		
GAM1394	DNM2	3'	GGCTGGGCTTGGGCTATGTG 17058	_	TG
			CACGTGGTCCG GCC GTT		
			GTGTATCGGGT CGG CGG		
			T GT		
GAM1394	DRD3	3'	GACATGGCTGGGCTACGTGAAT 53356	G	TG
	A		TATT CACGTGGTCCGGCC GTT		
			ATAA GTGCATCGGGTCGG CAG		
			TA		
GAM1394	DRD3	3'	GACATGGCTGGGCTACGTGAAT 53356	G	TG
	A		TATT CACGTGGTCCGGCC GTT		
			ATAA GTGCATCGGGTCGG CAG		
			TA		
GAM1394	DRD5	3'	GGTTGTGTGTGTGTGCAGTG 5848	TG_TC	
			TATTGCACG G CGGCC		
			GTGACGTGT T GTTGG		
			GTG GT		
GAM1394	DRD5	3'	GGTTGTGTGTGTGTGCAGTG 5848	TG_TC	
			TATTGCACG G CGGCC		
			GTGACGTGT T GTTGG		
			GTG GT		
GAM1394	DSC3	3'	AGCTGGTTCTGTGGGCTGCTGC 44337	C TG	___ GC TG
	AGTG		TTGCA G GTCC G C GTT		
			GACGT C CGGG C G CGA		
			_GT TGT TT GT		
GAM1394	DSC3	3'	AGCTGGTTCTGTGGGCTGCTGC 44337	C TG	___ GC TG
	AGTG		TTGCA G GTCC G C GTT		
			GACGT C CGGG C G CGA		
			_GT TGT TT GT		
GAM1394	DSCAM	5'	AGCCGGGCCGGGCGGAGCGCG 7324	___	
			CGTG GTCCGGCCTGGTT		
			GCGC CGGGCCGGGCCGA		
			GAGG		
GAM1394	DSCAM	5'	AGCCGGGCCGGGCGGAGCGCG 7324	___	
			CGTG GTCCGGCCTGGTT		
			GCGC CGGGCCGGGCCGA		
			GAGG		
GAM1394	DSCR3	3'	TGGA CTATTGCAATA 20197	C	
			TATTGCA GTGGTCCG		

ATAACGT TATCAGGT

GAM1394	DSCR3	3'	TGGACTATTGCAATA	20197	C	
			TATTGCA GTGGTCCG			
			ATAACGT TATCAGGT			
GAM1394	DSCR3	5'	AGCTAGGGAGTGTGTGCGA	20169	GT G	GGC
			TTGCAC G TCC CTGGTT			
			AGCGTG T AGG GATCGA			
			TG G ____			
GAM1394	DSCR3	5'	AGCTAGGGAGTGTGTGCGA	20169	GT G	GGC
			TTGCAC G TCC CTGGTT			
			AGCGTG T AGG GATCGA			
			TG G ____			
GAM1394	DTNB	5'	GGCTGGGCCGAGCGTGCGG	52498	GG	TG
			TTGCACGT TCCGGCC GTT			
			GGCGTGCG AGGCCGG CGG			
			____ GT			
GAM1394	DTNB	5'	GGCTGGGCCGAGCGTGCGG	52498	GG	TG
			TTGCACGT TCCGGCC GTT			
			GGCGTGCG AGGCCGG CGG			
			____ GT			
GAM1394	DTNB	5'	GGCTGGGCCGAGCGTGCGG	52503	GG	TG
			TTGCACGT TCCGGCC GTT			
			GGCGTGCG AGGCCGG CGG			
			____ GT			
GAM1394	DTNB	5'	GGCTGGGCCGAGCGTGCGG	52503	GG	TG
			TTGCACGT TCCGGCC GTT			
			GGCGTGCG AGGCCGG CGG			
			____ GT			
GAM1394	DTNB	5'	GGCTGGGCCGAGCGTGCGG	41581	GG	TG
			TTGCACGT TCCGGCC GTT			
			GGCGTGCG AGGCCGG CGG			
			____ GT			
GAM1394	DTNB	5'	GGCTGGGCCGAGCGTGCGG	41581	GG	TG
			TTGCACGT TCCGGCC GTT			
			GGCGTGCG AGGCCGG CGG			
			____ GT			
GAM1394	DUOX1	3'	CAGTCACCATGTGTGG	33828	TG	CC C
			T CACGTGGT GGC TG			



			G GTGTACCA CTG AC			
			GT    — —			
GAM1394	DUOX1	3'	CAGTCACCATGTGTGG    33828	TG	CC	C
			T CACGTGGT GGC TG			
			G GTGTACCA CTG AC			
			GT    — —			
GAM1394	ED1	3'	AACCAGCCAACCATCATGTGTA 7360		CC__	C
	G		TTGCACGTGGT    GGC TGGTT			
			GATGTGTACTA    CCG ACCAA			
			CCAA —			
GAM1394	ED1	3'	AACCAGCCAACCATCATGTGTA 7360		CC__	C
	G		TTGCACGTGGT    GGC TGGTT			
			GATGTGTACTA    CCG ACCAA			
			CCAA —			
GAM1394	EDAR	3'	TTGGATGTGTGCAGTA    42271	GTG		
			TATTGCAC    GTCCGG			
			ATGACGTG    TAGGTT			
			TG_			
GAM1394	EDAR	3'	TTGGATGTGTGCAGTA    42271	GTG		
			TATTGCAC    GTCCGG			
			ATGACGTG    TAGGTT			
			TG_			
GAM1394	EFNA1	3'	AGCTGGAAGGGGCCACGTG    15388		GGC	TG
			CACGTGGTCC    C GTT			
			GTGCACCGGG    G CGA			
			GAA GT			
GAM1394	EFNA1	3'	AGCTGGAAGGGGCCACGTG    15388		GGC	TG
			CACGTGGTCC    C GTT			
			GTGCACCGGG    G CGA			
			GAA GT			
GAM1394	EGFL4	3'	AGAGGGTCGGGTGCGGTG    61807	GTGGT		GGTT
			TATTGCAC    CCGGCCT			
			GTGGCGTG    GGCTGGG			
			_____ AGAA			
GAM1394	EGFL4	3'	AGAGGGTCGGGTGCGGTG    61807	GTGGT		GGTT
			TATTGCAC    CCGGCCT			
			GTGGCGTG    GGCTGGG			
			_____ AGAA			
GAM1394	EGFL4	5'	GGCCATGGTGTGTGCAGTG    61817	TGGT	__	
			TATTGCACG    CC GGCC			

			GTGACGTGT GG CCGG		
			GT__ TA		
GAM1394 EGFL4	5'	GGCCATGGTGTGTGCAGTG 61817	TGGT __		
		TATTGCACG CC GGCC			
		GTGACGTGT GG CCGG			
		GT__ TA			
GAM1394 EGFL5	3'	TTGGGCCGGGTGCGGTG 86630	GTGGT TG		
		TATTGCAC CCGGCC G			
		GTGGCGTG GGCCGG T			
		_____ GT			
GAM1394 EGFL5	3'	TTGGGCCGGGTGCGGTG 86630	GTGGT TG		
		TATTGCAC CCGGCC G			
		GTGGCGTG GGCCGG T			
		_____ GT			
GAM1394 EGLN1	5'	TGGCCGGGCCGAGGGCGTGGGG 41898	G _____ TGGTT		
TG		TT CACGT GGTCCGGCC			
		GG GTGCG CCGGGCCGG			
		G GGAG TT			
GAM1394 EGLN1	5'	TGGCCGGGCCGAGGGCGTGGGG 41898	G _____ TGGTT		
TG		TT CACGT GGTCCGGCC			
		GG GTGCG CCGGGCCGG			
		G GGAG TT			
GAM1394 EML1	5'	GCCGGGCCGGGGAGCG 59729	GG		
		CGT TCCGGCCTGGT			
		GCG GGGCCGGGCCG			
		AG			
GAM1394 EML1	5'	GCCGGGCCGGGGAGCG 59729	GG		
		CGT TCCGGCCTGGT			
		GCG GGGCCGGGCCG			
		AG			
GAM1394 EMP2	3'	AGCTGGGTTGCTTCTGCTGCAG 7447	C TG TC_ TG		
TA		TATTGCA G G CGGCC GTT			
		ATGACGT C C GTTGG CGA			
		_GT TTC GT			
GAM1394 EMP2	3'	AGCTGGGTTGCTTCTGCTGCAG 7447	C TG TC_ TG		
TA		TATTGCA G G CGGCC GTT			
		ATGACGT C C GTTGG CGA			
		_GT TTC GT			
GAM1394 EMX2	5'	GGTTGGGCGCGTTTGGTG 87567	C G		
		TATTG ACGTG TCCGGCC			

		GTGGT TGCGC GGGTTGG			
		T _			
GAM1394	EMX2	5' GGTTGGGCGCGTTTGGTG 87567	C	G	
		TATTG ACGTG TCCGGCC			
		GTGGT TGCGC GGGTTGG			
		T _			
GAM1394	ENG	5' GGCCGGGCTGGATGAGC 3690	G_		
		GT GTCCGGCCTGGTT			
		CG TAGGTCGGGCCGG			
		AG			
GAM1394	ENG	5' GGCCGGGCTGGATGAGC 3690	G_		
		GT GTCCGGCCTGGTT			
		CG TAGGTCGGGCCGG			
		AG			
GAM1394	EP300	5' AGTCGGGTCGGAGAGAGGCGGC 7474	A	GG__	GT
	A	TGC CGT TCCGGCCTG T			
		ACG GCG AGGCTGGGC A			
		_ GAGAG TG			
GAM1394	EP300	5' AGTCGGGTCGGAGAGAGGCGGC 7474	A	GG__	GT
	A	TGC CGT TCCGGCCTG T			
		ACG GCG AGGCTGGGC A			
		_ GAGAG TG			
GAM1394	EXTL3	3' AGCCGGGGCCGTCTGTGTGGTG 7525	TG	T TC	_
		TAT CACG GG CGGCCT GGTT			
		GTG GTGT CT GCCGGG CCGA			
		GT _ _ G			
GAM1394	EXTL3	3' AGCCGGGGCCGTCTGTGTGGTG 7525	TG	T TC	_
		TAT CACG GG CGGCCT GGTT			
		GTG GTGT CT GCCGGG CCGA			
		GT _ _ G			
GAM1394	EXTL3	3' AGCTGGGGCCGTCTGTGTGGTG 7526	TG	T TC	_ TG
		TAT CACG GG CGGC C GTT			
		GTG GTGT CT GCCG G CGA			
		GT _ _ G GT			
GAM1394	EXTL3	3' AGCTGGGGCCGTCTGTGTGGTG 7526	TG	T TC	_ TG
		TAT CACG GG CGGC C GTT			
		GTG GTGT CT GCCG G CGA			
		GT _ _ G GT			
GAM1394	EZH1	3' GGCTGGCACCCCGTGT 8822	T	_	
		GCACG GGT CCGGCC			

			TGTGC CCA GGTCGG		
			C C		
GAM1394 EZH1	3'	GGCTGGCACCCCGTGT	8822	T _	
		GCACG GGT CCGGCC			
		TGTGC CCA GGTCGG			
		C C			
GAM1394 F2RL3	3'	GACCGGGCCGGGCCGGGGGTGC	14180	G__	
GG		TTGCAC TGGTCCGGCCTGGTT			
		GGCGTG GCCGGGCCGGGCCAG			
		GGG			
GAM1394 F2RL3	3'	GACCGGGCCGGGCCGGGGGTGC	14180	G__	
GG		TTGCAC TGGTCCGGCCTGGTT			
		GGCGTG GCCGGGCCGGGCCAG			
		GGG			
GAM1394 FADD	3'	GTCAGGCGGGGTGCTGTGGTG	13798	TG C G G GT	
		TAT CA GTG TCCG CCTG T			
		GTG GT CGT GGGC GGAC G			
		GT _ G _ TG			
GAM1394 FADD	3'	GTCAGGCGGGGTGCTGTGGTG	13798	TG C G G GT	
		TAT CA GTG TCCG CCTG T			
		GTG GT CGT GGGC GGAC G			
		GT _ G _ TG			
GAM1394 FANCC	3'	AATTGGCCTGGCTGGGTGCAGT	70516	G C TGGTT	
G		TATTGCAC TGGTC GGCC			
		GTGACGTG GTCGG CCGG			
		G T TTAA			
GAM1394 FANCC	3'	AATTGGCCTGGCTGGGTGCAGT	70516	G C TGGTT	
G		TATTGCAC TGGTC GGCC			
		GTGACGTG GTCGG CCGG			
		G T TTAA			
GAM1394 FASN	3'	ACTGGGCTGGGCCTCGTG	14630	T TG	
		CACG GGTCCGGCC GT			
		GTGC CCGGGTCCG CA			
		T GT			
GAM1394 FASN	3'	ACTGGGCTGGGCCTCGTG	14630	T TG	
		CACG GGTCCGGCC GT			
		GTGC CCGGGTCCG CA			
		T GT			
GAM1394 FCMD	3'	GTTGGGTTCTGTGGAGTG	22095	G T GT	
		TATT CACG G CCGGC			

			GTGA GTGT T GGTTG		
			G C TG		
GAM1394 FCMD	3'	GCTGGGCATGGTGGTG	22093	TG A G	
		TAT C CGTG TCCGGC			
		GTG G GTAC GGGTCG			
		GT _ _			
GAM1394 FCMD	3'	GCTGGGCATGGTGGTG	22093	TG A G	
		TAT C CGTG TCCGGC			
		GTG G GTAC GGGTCG			
		GT _ _			
GAM1394 FCMD	3'	GTTGGGTTCTGTGGAGTG	22095	G T GT	
		TATT CACG G CCGGC			
		GTGA GTGT T GGTTG			
		G C TG			
GAM1394 FGF2	3'	CTAGGCCGGGTGCAGTG	8869	GTGGT	
		TATTGCAC CCGGCCTGG			
		GTGACGTG GGCCGGATC			
GAM1394 FGF2	3'	CTAGGCCGGGTGCAGTG	8869	GTGGT	
		TATTGCAC CCGGCCTGG			
		GTGACGTG GGCCGGATC			
GAM1394 FGFR1	3'	GGCCAGGTTGGGGGCAGTGTTG	5206	T GTGG	
TG		TAT GCAC TCCGGCCTGGTT			
		GTG TGTG GGGTTGGACCGG			
		T ACGG			
GAM1394 FGFR1	3'	GGCCAGGTTGGGGGCAGTGTTG	5206	T GTGG	
TG		TAT GCAC TCCGGCCTGGTT			
		GTG TGTG GGGTTGGACCGG			
		T ACGG			
GAM1394 FGFR1	3'	GGCCAGGTTGGGGGCAGTGTTG	31799	T GTGG	
TG		TAT GCAC TCCGGCCTGGTT			
		GTG TGTG GGGTTGGACCGG			
		T ACGG			
GAM1394 FGFR1	3'	GGCCAGGTTGGGGGCAGTGTTG	31799	T GTGG	
TG		TAT GCAC TCCGGCCTGGTT			
		GTG TGTG GGGTTGGACCGG			
		T ACGG			
GAM1394 FGFR1	3'	GGCCAGGTTGGGGGCAGTGTTG	43634	T GTGG	
TG		TAT GCAC TCCGGCCTGGTT			

			GTG TGTG GGGTTGGACCGG	
			T ACGG	
GAM1394 FGFR1	3'	GGCCAGGTTGGGGGCAGTGTTG 43634	T GTGG	
TG		TAT GCAC TCCGGCCTGGTT		
		GTG TGTG GGGTTGGACCGG		
		T ACGG		
GAM1394 FGFR3	3'	GGCCGGCCCTGTGTGCAG 3773	TG T_	
		TTGCACG G CCGGCC		
		GACGTGT C GGCCGG		
		GT CC		
GAM1394 FGFR3	3'	GGCCGGCCCTGTGTGCAG 3773	TG T_	
		TTGCACG G CCGGCC		
		GACGTGT C GGCCGG		
		GT CC		
GAM1394 FLT1	3'	GGCTGAAACCATGTGCAA 8920	C_	
		TTGCACGTGGT CGGCC		
		AACGTGTACCA GTCGG		
		AA		
GAM1394 FLT1	3'	GGCTGAAACCATGTGCAA 8920	C_	
		TTGCACGTGGT CGGCC		
		AACGTGTACCA GTCGG		
		AA		
GAM1394 FMO2	3'	GGTTGGGCCTGGGCAATG 7586	A T	
		TATTGC CG GGTCCGGCC		
		GTAACG GT CCGGGTTGG		
		G _		
GAM1394 FMO2	3'	GGTTGGGCCTGGGCAATG 7586	A T	
		TATTGC CG GGTCCGGCC		
		GTAACG GT CCGGGTTGG		
		G _		
GAM1394 FPGS	3'	GGCCGGGCCCGACGCAGGTGC 17090	G _	
		GCAC TG GTCCGGCCTGGTT		
		CGTG AC CAGGCCGGGCCGG		
		G G		
GAM1394 FPGS	3'	GGCCGGGCCCGACGCAGGTGC 17090	G _	
		GCAC TG GTCCGGCCTGGTT		
		CGTG AC CAGGCCGGGCCGG		
		G G		
GAM1394 FUS1	3'	GGTTGGGTGTTGGTTTGTGTGT 23450	TG TG T _ GG	
GG		T CACG G CCG GCCT TT		

			G GTGT T GGT TGGG GG			
			GT GT T TG TT			
GAM1394	FUS1	3'	GGTTGGGTGTTGGTTTGTGTGT 23450	TG	TG T	__ GG
	GG		T CACG G CCG GCCT TT			
			G GTGT T GGT TGGG GG			
			GT GT T TG TT			
GAM1394	FUS1	5'	TGGCTGGGGCAGGTTATGGTAG 23454	__	G G	TGGTT
	TG		TTGC AC TG TCCGGCC			
			GATG TG AC GGGTCGG			
			GTAT G G TT			
GAM1394	FUS1	5'	TGGCTGGGGCAGGTTATGGTAG 23454	__	G G	TGGTT
	TG		TTGC AC TG TCCGGCC			
			GATG TG AC GGGTCGG			
			GTAT G G TT			
GAM1394	FZD10	5'	GCCAGGCCGGGCGGGCA 23239	ACGTG		
			TGC GTCCGGCCTGGT			
			ACG CGGGCCGGACCG			
			GG__			
GAM1394	FZD10	5'	GCTGGGCCCGGCCTCGGT 23240	A T T	TG	
			GC CG GG CCGGCC GT			
			TG GC CC GGCCGG CG			
			_ T _ GT			
GAM1394	FZD10	5'	GCTGGGCCCGGCCTCGGT 23240	A T T	TG	
			GC CG GG CCGGCC GT			
			TG GC CC GGCCGG CG			
			_ T _ GT			
GAM1394	FZD10	5'	GCCAGGCCCGGCGGGCA 23239	ACGTG		
			TGC GTCCGGCCTGGT			
			ACG CGGGCCGGACCG			
			GG__			
GAM1394	FZD4	3'	ATCGGGCTGGATGCTCTGTG 24127	T	__	GT
			CACG GGT CCGGCCTG T			
			GTGT TCG GGTCGGGC A			
			C TA TG			
GAM1394	FZD4	3'	ATCGGGCTGGATGCTCTGTG 24127	T	__	GT
			CACG GGT CCGGCCTG T			
			GTGT TCG GGTCGGGC A			
			C TA TG			
GAM1394	GAA	5'	AGCCGGGCGCGGGGCTGCG 3838	TG	_	
			CG GTCC GGCCTGGTT			

			GC CGGG CCGGGCCGA		
			GT G		
GAM1394	GAA	5'	AGCCGGGCGCGGGGCTGCG 3838	TG	_
			CG GTCC GGCCTGGTT		
			GC CGGG CCGGGCCGA		
			GT G		
GAM1394	GABPB1	3'	TGGTTAGGCCAAATGTTGTGTA 17907	_____	CG TGGTT
	ATA		TGCACG TGGTC GCC		
			ATGTGT ACCGG TGG		
			TGTAA AT TT		
GAM1394	GABPB1	3'	TGGTTAGGCCAAATGTTGTGTA 17907	_____	CG TGGTT
	ATA		TGCACG TGGTC GCC		
			ATGTGT ACCGG TGG		
			TGTAA AT TT		
GAM1394	GJA4	3'	GACTGGGCTGGGGAAGCAGGTG 59368	G G_____	TG
			CAC TG TCCGGCC GTT		
			GTG AC GGGTCGG CAG		
			G GAAG GT		
GAM1394	GJA4	3'	GACTGGGCTGGGGAAGCAGGTG 59368	G G_____	TG
			CAC TG TCCGGCC GTT		
			GTG AC GGGTCGG CAG		
			G GAAG GT		
GAM1394	GNAI2	5'	AGCCGGGCCGTGGGCCGTGTG 67545	_____	
			CACGTGGTCC GGCCTGGTT		
			GTGTGCCGGG CCGGGCCGA		
			TG		
GAM1394	GNAI2	5'	AGCCGGGCCGTGGGCCGTGTG 67545	_____	
			CACGTGGTCC GGCCTGGTT		
			GTGTGCCGGG CCGGGCCGA		
			TG		
GAM1394	GNPI	3'	GGCCTAAGGGCTATGTTTGGTA 18447	C _____	
			TATTG ACGTGGTCC GGCC		
			ATGGT TGTATCGGG CCGG		
			T AAT		
GAM1394	GNPI	3'	GGCCTAAGGGCTATGTTTGGTA 18447	C _____	
			TATTG ACGTGGTCC GGCC		
			ATGGT TGTATCGGG CCGG		
			T AAT		
GAM1394	GP6	3'	GTACCACTGGGCCAAGTGCAGT 33032	G	CC T
	G		TATTGCAC TGGTCCGG TGGT		



			GTGACGTG ACCGGGTC ACCA		
			A _ TGT		
GAM1394	GP6	3'	GTACCACTGGGCCAAGTGCAGT 33032	G	CC T
	G		TATTGCAC TGGTCCGG TGGT		
			GTGACGTG ACCGGGTC ACCA		
			A _ TGT		
GAM1394	GPRK6	3'	GGCCAGAGATTGGGCTGCCTGT 9114	TG C TG	C_
	GATA		AT CA G GTCCGG CTGGTT		
			TA GT C CGGGTT GACCGG		
			GT C GT AGA		
GAM1394	GPRK6	3'	GGCCAGAGATTGGGCTGCCTGT 9114	TG C TG	C_
	GATA		AT CA G GTCCGG CTGGTT		
			TA GT C CGGGTT GACCGG		
			GT C GT AGA		
GAM1394	GPRK7	3'	AACAGGCCAGGTGCGGTG 57624	G GGTCC	GTT
			TATTGCAC T GGCCTG		
			GTGGCGTG A CCGGAC		
			G _ AAG		
GAM1394	GPRK7	3'	AACAGGCCAGGTGCGGTG 57624	G GGTCC	GTT
			TATTGCAC T GGCCTG		
			GTGGCGTG A CCGGAC		
			G _ AAG		
GAM1394	GPT	3'	GGCCAGGCTGGGTCGC 17965	GT	
			GTG CCGGCCTGGTT		
			CGC GGTCGGACCGG		
			TG		
GAM1394	GPT	3'	GGCCAGGCTGGGTCGC 17965	GT	
			GTG CCGGCCTGGTT		
			CGC GGTCGGACCGG		
			TG		
GAM1394	GRAP2	3'	AATTGGGCTGGTAATTAGTTGA 16675	C GTGGT_	TG
	TG		TATTG AC CCGGCC GTT		
			GTAGT TG GGTCGG TAA		
			_ ATTAAT GT		
GAM1394	GRAP2	3'	AATTGGGCTGGTAATTAGTTGA 16675	C GTGGT_	TG
	TG		TATTG AC CCGGCC GTT		
			GTAGT TG GGTCGG TAA		
			_ ATTAAT GT		
GAM1394	GSR	3'	AACCAGGAGACACGTGTGG 94513	TG	GTCCGG
			T CACGTG CCTGGTT		

			G GTGCAC GGACCAA		
			GT AGA__		
GAM1394	GSR	3'	AACCAGGAGACACGTGTGG 94513	TG	GTCCGG
			T CACGTG CCTGGTT		
			G GTGCAC GGACCAA		
			GT AGA__		
GAM1394	GYG2	3'	AGCTGGTGGGCGTTGTGTGTAG 14046		TG _ G T
	T		ATTGCACG GT CC GCC GGTT		
			TGATGTGT TG GG TGG TCGA		
			GT C G _		
GAM1394	GYG2	3'	AGCTGGTGGGCGTTGTGTGTAG 14046		TG _ G T
	T		ATTGCACG GT CC GCC GGTT		
			TGATGTGT TG GG TGG TCGA		
			GT C G _		
GAM1394	H4FL	3'	GGCCAGGCCTTTCTTGCAATA 13051		CGT TCC
			TATTGCA GG GGCCTGGTT		
			ATAACGT CC CCGGACCGG		
			T__ TTT		
GAM1394	H4FL	3'	GGCCAGGCCTTTCTTGCAATA 13051		CGT TCC
			TATTGCA GG GGCCTGGTT		
			ATAACGT CC CCGGACCGG		
			T__ TTT		
GAM1394	HAGH	5'	AGCCCGGCCCGGGTCATGGTGG 18028		TG A GT _ T
	TG		TAT C CGTG CCGG CC GGTT		
			GTG G GTAC GGCC GG CCGA		
			GT_ TG C C		
GAM1394	HAGH	5'	AGCCCGGCCCGGGTCATGGTGG 18028		TG A GT _ T
	TG		TAT C CGTG CCGG CC GGTT		
			GTG G GTAC GGCC GG CCGA		
			GT_ TG C C		
GAM1394	HAL	3'	GGTTAGGCTGATGGCAGTA 9172	A _ CG	
			TATTGC CGT GGTC GCC		
			ATGACG GTA TCGG TGG		
			_ G AT		
GAM1394	HAL	3'	GGTTAGGCTGATGGCAGTA 9172	A _ CG	
			TATTGC CGT GGTC GCC		
			ATGACG GTA TCGG TGG		
			_ G AT		
GAM1394	HAS3	3'	AGCTGGGCGCGTTAGTGTA 18036	G T TG	
			TGCAC TGG CCGGCC GTT		

			ATGTG ATT GGCCGG CGA		
			— — GT		
GAM1394 HAS3	3'	AGCTGGGCCGGTTAGTGTA	18036	G T	TG
		TGCAC TGG CCGGCC GTT			
		ATGTG ATT GGCCGG CGA			
		— — GT			
GAM1394 HCFC1	3'	GGCCAGGTTCGGGGGCAGGCA	70996	AC	GG
		TGC GT TCCGGCCTGGTT			
		ACG CG GGGCTGGACCGG			
		GA G_			
GAM1394 HCFC1	3'	GGCCAGGTTCGGGGGCAGGCA	70996	AC	GG
		TGC GT TCCGGCCTGGTT			
		ACG CG GGGCTGGACCGG			
		GA G_			
GAM1394 HCS	3'	AGTGTGGTTTATGTGTAATA	38458	T	GC
		TATTGCACGTGG CCG CT			
		ATAATGTGTATT GGT GA			
		T GT			
GAM1394 HCS	3'	AGTGTGGTTTATGTGTAATA	38458	T	GC
		TATTGCACGTGG CCG CT			
		ATAATGTGTATT GGT GA			
		T GT			
GAM1394 HD	3'	GGCCAGGCAACGTGCG	9189	G	C
		TGCACGT GTC GGCC			
		GCGTGCA CGG CCGG			
		A A			
GAM1394 HD	3'	GGCCAGGCAACGTGCG	9189	G	C
		TGCACGT GTC GGCC			
		GCGTGCA CGG CCGG			
		A A			
GAM1394 HEXA	3'	GCCAGGCTGGAGTCAGTG	4976	G	_
		CAC TGG TCCGGCCTGGT			
		GTG ACT AGGTCGGACCG			
		_ G			
GAM1394 HEXA	3'	GCCAGGCTGGAGTCAGTG	4976	G	_
		CAC TGG TCCGGCCTGGT			
		GTG ACT AGGTCGGACCG			
		_ G			
GAM1394 HIP1	3'	GACCAGGCTGGGCATCATAGCA	18060	ACGTG_	
A		TTGC GTCCGGCCTGGTT			

			AACG CGGGTCGGACCAG	
			ATACTA	
GAM1394	HIP1	3'	GACCAGGCTGGGCATCATAGCA 18060	ACGTG_
	A		TTGC GTCCGGCCTGGTT	
			AACG CGGGTCGGACCAG	
			ATACTA	
GAM1394	HIP12	3'	GGTCCTGGGCCATGTG 66231	_ _
			CACGTGGTCC GG CC	
			GTGTACCGGG CC GG	
			T T	
GAM1394	HIP12	3'	GGTCCTGGGCCATGTG 66231	_ _
			CACGTGGTCC GG CC	
			GTGTACCGGG CC GG	
			T T	
GAM1394	HNF3G	3'	GGTTGGGAACATGGTGGTG 72344	TG A G_
			TAT C CGTG TCCGGCC	
			GTG G GTAC GGGTTGG	
			GT_ AA	
GAM1394	HNF3G	3'	GGTTGGCCCTTTGGGTGTGATG 72343	TG G___ T
			TAT CAC T GG CCGGCC	
			GTA GTG G CC GGTTGG	
			GT G TTT C	
GAM1394	HNF3G	3'	GGTTGGGAACATGGTGGTG 72344	TG A G_
			TAT C CGTG TCCGGCC	
			GTG G GTAC GGGTTGG	
			GT_ AA	
GAM1394	HNF3G	3'	GGTTGGCCCTTTGGGTGTGATG 72343	TG G___ T
			TAT CAC T GG CCGGCC	
			GTA GTG G CC GGTTGG	
			GT G TTT C	
GAM1394	HNRPA2B1	3'	GCCAGGATCATGGTGTAAATA 9241	_ _
			TATTGCAC GTGGTCC GGC	
			ATAATGTG TACTAGG CCG	
			G A	
GAM1394	HNRPA2B1	3'	GCCAGGATCATGGTGTAAATA 9241	_ _
			TATTGCAC GTGGTCC GGC	
			ATAATGTG TACTAGG CCG	
			G A	
GAM1394	HNRPA2B1	3'	GCCAGGATCATGGTGTAAATA 48354	_ _
			TATTGCAC GTGGTCC GGC	

			ATAATGTG TACTAGG CCG			
			G A			
GAM1394	HNRPA2B1	3'	GCCAGGATCATGGTGTAAATA 48354		—	—
			TATTGCAC GTGGTCC GGC			
			ATAATGTG TACTAGG CCG			
			G A			
GAM1394	HOXD13	5'	GGCCAGGCCGGGCCATGAGC 4978	A		
			GC CGTGGTCCGGCCTGGTT			
			CG GTACCGGGCCGGACCGG			
			A			
GAM1394	HOXD13	5'	GGCCAGGCCGGGCCATGAGC 4978	A		
			GC CGTGGTCCGGCCTGGTT			
			CG GTACCGGGCCGGACCGG			
			A			
GAM1394	HPCAL1	3'	GCCTGGCTGTTGTGTGGTA 9269	TG	TGGTC	T
			TAT CACG CGGCC GGT			
			ATG GTGT GTCGG CCG			
			GT T____ T			
GAM1394	HPCAL1	3'	GCCTGGCTGTTGTGTGGTA 9269	TG	TGGTC	T
			TAT CACG CGGCC GGT			
			ATG GTGT GTCGG CCG			
			GT T____ T			
GAM1394	HPCAL1	3'	GCCTGGCTGTTGTGTGGTA 56187	TG	TGGTC	T
			TAT CACG CGGCC GGT			
			ATG GTGT GTCGG CCG			
			GT T____ T			
GAM1394	HPCAL1	3'	GCCTGGCTGTTGTGTGGTA 56187	TG	TGGTC	T
			TAT CACG CGGCC GGT			
			ATG GTGT GTCGG CCG			
			GT T____ T			
GAM1394	HPS1	3'	GATCAGATGGCCGTGTGCTGTG 3966	T	T GC	
			TAT GCACGTGG CCG CTGGTT			
			GTG CGTGTGCC GGT GACTAG			
			T _ A_			
GAM1394	HPS1	3'	GATCAGATGGCCGTGTGCTGTG 3966	T	T GC	
			TAT GCACGTGG CCG CTGGTT			
			GTG CGTGTGCC GGT GACTAG			
			T _ A_			
GAM1394	HPS4	3'	CTGGGCTTGTGTGGTA 41986	TG	T	
			TAT CACG GGTCCGG			

			ATG GTGT TCGGGTC			
			GT _			
GAM1394	HPS4	3'	CTGGGCTTGTGTGGTA	41986	TG T	
			TAT CACG GGTCCGG			
			ATG GTGT TCGGGTC			
			GT _			
GAM1394	HTLF	5'	TCGCGGCCGCGTCCAGTA	9283	C _	
			TATTG ACGTGGTC CGG			
			ATGAC TGCGCCGG GCT			
			C C			
GAM1394	HTLF	5'	TCGCGGCCGCGTCCAGTA	9283	C _	
			TATTG ACGTGGTC CGG			
			ATGAC TGCGCCGG GCT			
			C C			
GAM1394	HTR3B	3'	AGCTTTCTGGGTCGGGTGTGGT	20071	TG G GT CCT	
	G		TAT CAC TG CCGG GGTT			
			GTG GTG GC GGTC TCGA			
			GT G TG TT_			
GAM1394	HTR3B	3'	AGCTTTCTGGGTCGGGTGTGGT	20071	TG G GT CCT	
	G		TAT CAC TG CCGG GGTT			
			GTG GTG GC GGTC TCGA			
			GT G TG TT_			
GAM1394	HUNK	3'	GCTTTTAGGCCAGGTGTGGTG	27457	TG G C__	
			TAT CAC TGGTC GGC			
			GTG GTG ACCGG TCG			
			GT G ATTT			
GAM1394	HUNK	3'	GCTTTTAGGCCAGGTGTGGTG	27457	TG G C__	
			TAT CAC TGGTC GGC			
			GTG GTG ACCGG TCG			
			GT G ATTT			
GAM1394	HYAL2	5'	GGCTGGGCTGGGCCCGGGATGG	52532	A ____ TG	
	CGGTG		GC CGT GGTCCGGCC GTT			
			CG GTA CCGGGTCGG CGG			
			_ GGGC GT			
GAM1394	HYAL2	5'	GGCTGGGCTGGGCCCGGGATGG	52532	A ____ TG	
	CGGTG		GC CGT GGTCCGGCC GTT			
			CG GTA CCGGGTCGG CGG			
			_ GGGC GT			
GAM1394	IFNAR2	3'	GACTTTAGGATCACGTGT	6041	GGCCT	
			GCACGTGGTCC GGTT			

			TGTGCACTAGG	TCAG	
			ATT__		
GAM1394	IFNAR2	3'	GACTTTAGGATCACGTGT	6041	GGCCT
			GCACGTGGTCC	GGTT	
			TGTGCACTAGG	TCAG	
			ATT__		
GAM1394	IL1RL1LG	3'	GCCAGGTTGAGGTCTGGTA	22470	A T GT _
			TGC CG G C CGGCCTGGT		
			ATG GT C G GTTGGACCG		
			_ _ TG A		
GAM1394	IL1RL1LG	3'	GCCAGGTTGAGGTCTGGTA	22470	A T GT _
			TGC CG G C CGGCCTGGT		
			ATG GT C G GTTGGACCG		
			_ _ TG A		
GAM1394	IL2RB	3'	AGCCAGGAAGTGTGTGT	6067	TG CCGG
			GCACG GT CCTGGTT		
			TGTGT CA GGACCGA		
			GT A__		
GAM1394	IL2RB	3'	AGCCAGGAAGTGTGTGT	6067	TG CCGG
			GCACG GT CCTGGTT		
			TGTGT CA GGACCGA		
			GT A__		
GAM1394	IL8	5'	AACCATCTCACTGTGTGTAA	94476	TG CC CC
			TTGCACG GT GG TGGTT		
			AATGTGT CA CT ACCAA		
			GT _ CT		
GAM1394	IL8	5'	AACCATCTCACTGTGTGTAA	94476	TG CC CC
			TTGCACG GT GG TGGTT		
			AATGTGT CA CT ACCAA		
			GT _ CT		
GAM1394	INPP5A	3'	AGCTGGGTGTTTGTGTGGGATA	18657	G TG TCCG TG
			TATT CACG G GCC GTT		
			ATAG GTGT T TGG CGA		
			G GT TG__ GT		
GAM1394	INPP5A	3'	AGCTGGGTGTTTGTGTGGGATA	18657	G TG TCCG TG
			TATT CACG G GCC GTT		
			ATAG GTGT T TGG CGA		
			G GT TG__ GT		
GAM1394	JAG2	5'	AGCCGGGCGCGGCAGCCG	9467	TG_
			CG GTCCGGCCTGGTT		

			GC CGGGCCGGGCCGA		
			CGA		
GAM1394	JAG2	3'	CCATGGCTGTGTTGGTG 9468	G TC	_
			CAC TGG CGGCC TGG		
			GTG GTT GTCGG ACC		
			_ GT T		
GAM1394	JAG2	3'	CCATGGCTGTGTTGGTG 9468	G TC	_
			CAC TGG CGGCC TGG		
			GTG GTT GTCGG ACC		
			_ GT T		
GAM1394	JAG2	5'	AGCCGGGCGCGGCAGCCG 9467	TG_	
			CG GTCCGGCCTGGTT		
			GC CGGGCCGGGCCGA		
			CGA		
GAM1394	JAG2	3'	GGCCGAGGCCATGTGCA 9471		_
			TGCACGTGGTC CGGCC		
			ACGTGTACCGG GCCGG		
			A		
GAM1394	JAG2	3'	GGCCGAGGCCATGTGCA 9471		_
			TGCACGTGGTC CGGCC		
			ACGTGTACCGG GCCGG		
			A		
GAM1394	JRK	3'	GACCAGGCTGGAGTGAAGTGGT 86527	TG ACG G	
	G		TAT C TG TCCGGCCTGGTT		
			GTG G GT AGGTCCGACCAG		
			GT AA_ G		
GAM1394	JRK	3'	GACCAGGCTGGAGTGAAGTGGT 86527	TG ACG G	
	G		TAT C TG TCCGGCCTGGTT		
			GTG G GT AGGTCCGACCAG		
			GT AA_ G		
GAM1394	KCNA6	5'	GGCTGGGCGAGGGGTGTGATG 9515	TG GTG__	
			TAT CAC GTCCGGCC		
			GTA GTG CGGGTCCG		
			GT GGGAG		
GAM1394	KCNA6	5'	GGCTGGGCGAGGGGTGTGATG 9515	TG GTG__	
			TAT CAC GTCCGGCC		
			GTA GTG CGGGTCCG		
			GT GGGAG		
GAM1394	KCNH1	5'	GCCGGGACTGCGTGCGG 9524	TG _	
			TTGCACG GTCC GGC		



			GGCGTGC CAGG CCG		
			GT G		
GAM1394 KCNH1	5'	GCCGGGACTGCGTGCGG	9524	TG	_
		TTGCACG GTCC GGC			
		GGCGTGC CAGG CCG			
		GT G			
GAM1394 KCNJ1	5'	GTAGGATCTGTGCAATA	4026	T	G
		TATTGCACG GGTCC GC			
		ATAACGTGT CTAGG TG			
		_ A			
GAM1394 KCNJ1	5'	GTAGGATCTGTGCAATA	4026	T	G
		TATTGCACG GGTCC GC			
		ATAACGTGT CTAGG TG			
		_ A			
GAM1394 KCNK3	3'	GGTGGGGGCTGGGTGCAGTG	9553	G	_ G
		TATTGCAC TGGTC C GCC			
		GTGACGTG GTCGG G TGG			
		G G G			
GAM1394 KCNK3	3'	GGTGGGGGCTGGGTGCAGTG	9553	G	_ G
		TATTGCAC TGGTC C GCC			
		GTGACGTG GTCGG G TGG			
		G G G			
GAM1394 KCNK6	3'	TCAGGCTGAGTGTGGTG	16696	TG	GTGGTC
		TAT CAC CGGCCTGG			
		GTG GTG GTCGGA			
		GT A_____			
GAM1394 KCNK6	3'	TCAGGCTGAGTGTGGTG	16696	TG	GTGGTC
		TAT CAC CGGCCTGG			
		GTG GTG GTCGGA			
		GT A_____			
GAM1394 KCNS2	3'	GGCCAGGCTTTGATATCTGTGA	68312	TG	C GTCC
TG		TAT CA GTG GGCCTGGTT			
		GTA GT TAT TCGGACCGG			
		GT C AGTT			
GAM1394 KCNS2	3'	GGCCAGGCTTTGATATCTGTGA	68312	TG	C GTCC
TG		TAT CA GTG GGCCTGGTT			
		GTA GT TAT TCGGACCGG			
		GT C AGTT			
GAM1394 KIFC3	5'	GGCCGGGCGCGGCGGAGC	18688	ACG	
		GC TGGTCCGGCCTGGTT			

		CG GCCGGGCGGGGCCGG			
		A__			
GAM1394 KIFC3	5'	GGCCGGGCGGGGCCGAGC	18688	ACG	
		GC TGGTCCGGCCTGGTT			
		CG GCCGGGCGGGGCCGG			
		A__			
GAM1394 KLHL3	3'	ATGGGGTCGTGTGTGAT	87453	TG TGGTC	G
		AT CACG CGGCCT GT			
		TA GTGT GCTGGG TA			
		GT _____ G			
GAM1394 KLHL3	3'	ATGGGGTCGTGTGTGAT	87453	TG TGGTC	G
		AT CACG CGGCCT GT			
		TA GTGT GCTGGG TA			
		GT _____ G			
GAM1394 KLKB1	3'	GATCTCCATGACTGTGTGTTGT	6099	T TG C_ CCT	
G		TAT GCACG GTC GG GGTT			
		GTG TGTGT CAG CC CTAG			
		T GT TA T__			
GAM1394 KLKB1	3'	GATCTCCATGACTGTGTGTTGT	6099	T TG C_ CCT	
G		TAT GCACG GTC GG GGTT			
		GTG TGTGT CAG CC CTAG			
		T GT TA T__			
GAM1394 KNS2	5'	GGCTGGGCTGCTGGTGCGA	18692	__ TG	
		TTGCAC G GTCCGGCC			
		AGCGTG C CGGGTCGG			
		GT GT			
GAM1394 KNS2	5'	GGCTGGGCTGCTGGTGCGA	18692	__ TG	
		TTGCAC G GTCCGGCC			
		AGCGTG C CGGGTCGG			
		GT GT			
GAM1394 LAMC2	3'	GCCATGTCATGTGAGTG	18712	G TCC	
		TATT CACGTGG GGC			
		GTGA GTGTACT CCG			
		____ GTA			
GAM1394 LAMC2	3'	GCCATGTCATGTGAGTG	18712	G TCC	
		TATT CACGTGG GGC			
		GTGA GTGTACT CCG			
		____ GTA			
GAM1394 LAMP1	5'	GGCCGGGCTCTTGCGTCTGGTA	18705	C ____	
		TATTG ACGT GGTCCGGCC			

			ATGGT TGCG TCGGGCCGG		
			C TTC		
GAM1394 LAMP1	5'	GGCCGGGCTCTTGCGTCTGGTA 18705	C ____		
		TATTG ACGT GGTCCGGCC			
		ATGGT TGCG TCGGGCCGG			
		C TTC			
GAM1394 LAMP2	3'	GCTGGGCATGGTGGTG 25714	TG A G		
		TAT C CGTG TCCGGC			
		GTG G GTAC GGGTCG			
		GT _ _			
GAM1394 LAMP2	3'	GCTGGGCATGGTGGTG 25714	TG A G		
		TAT C CGTG TCCGGC			
		GTG G GTAC GGGTCG			
		GT _ _			
GAM1394 LDB1	5'	AGCCGGCGGGGCGCTGCGTGT 13981	TG _ G T		
		GCACG GT CC GCC GGTT			
		TGTGC CG GG CGG CCGA			
		GT C G _			
GAM1394 LDB1	5'	AGCCGGCGGGGCGCTGCGTGT 13981	TG _ G T		
		GCACG GT CC GCC GGTT			
		TGTGC CG GG CGG CCGA			
		GT C G _			
GAM1394 LDLR	3'	GCCGGGCGCGGTGGTG 4989	TG A G		
		TAT C CGTG TCCGGC			
		GTG G GCGC GGGCCG			
		GT _ _			
GAM1394 LDLR	3'	GCCGGGCGCGGTGGTG 4989	TG A G		
		TAT C CGTG TCCGGC			
		GTG G GCGC GGGCCG			
		GT _ _			
GAM1394 LEP	3'	GTTTGGCCGGGTGCGGTG 4056	G CG		
		TATTGCAC TGGTC GC			
		GTGGCGTG GCCGG TG			
		G TT			
GAM1394 LEP	3'	GTTTGGCCGGGTGCGGTG 4056	G CG		
		TATTGCAC TGGTC GC			
		GTGGCGTG GCCGG TG			
		G TT			
GAM1394 LETM1	3'	AGCTGGGCCGGGCCAAGGCAG 24619	ACG TG		
		TTGC TGGTCCGGCC GTT			

			GACG ACCGGGCCGG CGA		
			GA_ GT		
GAM1394 LETM1	3'	AGCTGGGCCGGGCCAAGGCAG	24619	ACG	TG
		TTGC TGGTCCGGCC GTT			
		GACG ACCGGGCCGG CGA			
		GA_ GT			
GAM1394 LHX3	3'	GGCTGGCCTGTGTGTAA	27375	TG T	
		TTGCACG G CCGGCC			
		AATGTGT C GGTCGG			
		GT C			
GAM1394 LHX3	3'	GGCTGGCCTGTGTGTAA	27375	TG T	
		TTGCACG G CCGGCC			
		AATGTGT C GGTCGG			
		GT C			
GAM1394 LMO1	3'	GGCCAGGCCGGGCCTGTACAGT	9792	C T	
		ATTG ACG GGTCCGGCCTGGTT			
		TGAC TGT CCGGGCCGGACCGG			
		A _			
GAM1394 LMO1	3'	GGCCAGGCCGGGCCTGTACAGT	9792	C T	
		ATTG ACG GGTCCGGCCTGGTT			
		TGAC TGT CCGGGCCGGACCGG			
		A _			
GAM1394 LOH11CR2A	3'	AGTCAGGCCCTGATCTAGTGCA	27537	GT C_ GT	
GTA		TATTGCAC GGTC GGCCTG T			
		ATGACGTG CTAG CCGGAC A			
		AT TC TG			
GAM1394 LOH11CR2A	3'	AGTCAGGCCCTGATCTAGTGCA	27537	GT C_ GT	
GTA		TATTGCAC GGTC GGCCTG T			
		ATGACGTG CTAG CCGGAC A			
		AT TC TG			
GAM1394 LSS	3'	GGCCAGGCTGGAGGCAG	9819	ACGTGG	
		TTGC TCCGGCCTGGTT			
		GACG AGGTCCGACCGG			
		G_____			
GAM1394 LSS	3'	GGCCAGGCTGGAGGCAG	9819	ACGTGG	
		TTGC TCCGGCCTGGTT			
		GACG AGGTCCGACCGG			
		G_____			
GAM1394 LTB4R	5'	GGCCAGGCCTTTGGCAGTG	5651	ACGT C	
		TATTGC GGTC GGCC			

			GTGACG	CCGG	CCGG		
			GTTT	A			
GAM1394	LTB4R	5'	GGCCAGGCCTTTGGCAGTG	5651	ACGT	C	
			TATTGC	GGTC	GGCC		
			GTGACG	CCGG	CCGG		
			GTTT	A			
GAM1394	MAPK8IP1	5'	CCCGCGGGCCGTGCGCGGTG	18402	A	GCC	TT
			TATTGC	CGTGGTCCG	TGG		
			GTGGCG	GTGCCGGGC	GCC		
			C	___	CT		
GAM1394	MAPK8IP1	5'	CCCGCGGGCCGTGCGCGGTG	18402	A	GCC	TT
			TATTGC	CGTGGTCCG	TGG		
			GTGGCG	GTGCCGGGC	GCC		
			C	___	CT		
GAM1394	MAPRE3	3'	GGCCGGGTGCTTTGTGTCAGTG	24667	_	T	_
			TATTG	CACG	GGT	CCGGCC	
			GTGAC	GTGT	TCG	GGCCGG	
			T	T	TG		
GAM1394	MAPRE3	3'	GGCCGGGTGCTTTGTGTCAGTG	24667	_	T	_
			TATTG	CACG	GGT	CCGGCC	
			GTGAC	GTGT	TCG	GGCCGG	
			T	T	TG		
GAM1394	MAT2A	3'	GACTTGGCTGGTGTGGTA	19786	TG	CGTGGT	T
			TAT	CA	CCGGCC	GGTT	
			ATG	GT	GGTCGG	TCAG	
			GT	___	T		
GAM1394	MAT2A	3'	GACTTGGCTGGTGTGGTA	19786	TG	CGTGGT	T
			TAT	CA	CCGGCC	GGTT	
			ATG	GT	GGTCGG	TCAG	
			GT	___	T		
GAM1394	MATN1	5'	GGCTGGGCCGGGCCATTG	9924	C	TG	
			CA	GTGGTCCGGCC	GTT		
			GT	TACCGGGCCGG	CGG		
			___	GT			
GAM1394	MATN1	5'	GGCTGGGCCGGGCCATTG	9924	C	TG	
			CA	GTGGTCCGGCC	GTT		
			GT	TACCGGGCCGG	CGG		
			___	GT			
GAM1394	MBD3	3'	GTCGGGTCCTGGCAGTG	14098	A	T	GT
			TATTGC	CG	G	CCGGC	

			GTGACG GT C GGCTG		
			_ C TG		
GAM1394	MBD3	3'	GTCGGGTCCTGGCAGTG 14098	A T GT	
			TATTGC CG G CCGGC		
			GTGACG GT C GGCTG		
			_ C TG		
GAM1394	MEF2D	5'	AGCCGGGCTGGAGGCTGTGCAG 19797	TGG	
			TTGCACG TCCGGCCTGGTT		
			GACGTGT AGGTCGGGCCGA		
			CGG		
GAM1394	MEF2D	5'	AGCCGGGCTGGAGGCTGTGCAG 19797	TGG	
			TTGCACG TCCGGCCTGGTT		
			GACGTGT AGGTCGGGCCGA		
			CGG		
GAM1394	MGAT3	5'	GGCCGGGCGGGGCGCG 10018	_	
			CGTGGTCC GGCCTGGTT		
			GCGCCGGG CCGGGCCGG		
			G		
GAM1394	MGAT3	5'	GGCCGGGCGGGGCGCG 10018	_	
			CGTGGTCC GGCCTGGTT		
			GCGCCGGG CCGGGCCGG		
			G		
GAM1394	MGAT4A	5'	AACATATGGACCAGTGTGATG 24208	TG G GCCTG	
			TAT CAC TGGTCCG GTT		
			GTA GTG ACCAGGT CAA		
			GT _ ATA_		
GAM1394	MGAT4A	5'	AACATATGGACCAGTGTGATG 24208	TG G GCCTG	
			TAT CAC TGGTCCG GTT		
			GTA GTG ACCAGGT CAA		
			GT _ ATA_		
GAM1394	MLLT7	3'	GGCCAGTGATGTGCGGTG 19862	G TCC	
			TATTGCACGT G GGCC		
			GTGGCGTGTA T CCGG		
			G GA_		
GAM1394	MLLT7	3'	GGCCAGTGATGTGCGGTG 19862	G TCC	
			TATTGCACGT G GGCC		
			GTGGCGTGTA T CCGG		
			G GA_		
GAM1394	MOG	3'	GGCCGGGTGCGGTG 10104	GTGGT	
			TATTGCAC CCGGCC		

GTGGCGTG GGCCGG

GAM1394 MOG 3' GGCCGGGTGCGGTG 10104 GTGGT  
TATTGCAC CCGGCC  
||||| |||||  
GTGGCGTG GGCCGG

GAM1394 MOV10L1 3' AGCCAGGCAGGGTCGTGTGTGG 38636 TG GT G  
T CACGTG CC GCCTGGTT  
| ||||| || |||||  
G GTGTGC GG CGGACCGA  
GT TG A

GAM1394 MOV10L1 3' AGCCAGGCAGGGTCGTGTGTGG 38636 TG GT G  
T CACGTG CC GCCTGGTT  
| ||||| || |||||  
G GTGTGC GG CGGACCGA  
GT TG A

GAM1394 MPP2 3' GGCTGGGTTGGAACAGGTGT 59825 G G TG  
GCAC TG TCCGGCC GTT  
||| || ||||| |||  
TGTG AC AGGTTGG CGG  
G A GT

GAM1394 MPP2 3' GGCTGGGTTGGAACAGGTGT 59825 G G TG  
GCAC TG TCCGGCC GTT  
||| || ||||| |||  
TGTG AC AGGTTGG CGG  
G A GT

GAM1394 MSF 3' GACCAGGGAAGTGTGT 88084 TGG GGC  
GCACG TCC CTGGTT  
|||| ||| |||||  
TGTGT AGG GACCAG  
GA\_ \_

GAM1394 MSF 3' GACCAGGGAAGTGTGT 88084 TGG GGC  
GCACG TCC CTGGTT  
|||| ||| |||||  
TGTGT AGG GACCAG  
GA\_ \_

GAM1394 MYCBP 3' GACTAAGTGCTGGGTGTGATA 24695 TG GTGGT \_ \_  
TAT CAC CCGGC CT GGTT  
||| ||| ||||| ||| |||  
ATA GTG GGTCG GA TCAG  
GT \_ \_ T A

GAM1394 MYCBP 3' GACTAAGTGCTGGGTGTGATA 24695 TG GTGGT \_ \_  
TAT CAC CCGGC CT GGTT  
||| ||| ||||| ||| |||  
ATA GTG GGTCG GA TCAG  
GT \_ \_ T A

GAM1394 MYL4 3' GGCCAGGCTGGGCTCTG 10176 T  
CG GGTCCGGCCTGGTT  
|| ||||| |||||

			GT TCGGGTCGGACCGG			
			C			
GAM1394	MYL4	3'	GGCCAGGCTGGGCTCTG	10176	T	
			CG GGTCCGGCCTGGTT			
			GT TCGGGTCGGACCGG			
			C			
GAM1394	MYO1C	3'	GCCGGGCATGGTGGTG	61207	TG A	G
			TAT C CGTG TCCGGC			
			GTG G GTAC GGGCCG			
			GT _ _			
GAM1394	MYO1C	3'	GGCCAGGCCGGGCCACAGCAAT	61210		AC
	A		TATTGC GTGGTCCGGCCTGGTT			
			ATAACG CACCGGGCCGGACCGG			
			A _			
GAM1394	MYO1C	3'	GGCCAGGCCGGGCCACAGCAAT	61210		AC
	A		TATTGC GTGGTCCGGCCTGGTT			
			ATAACG CACCGGGCCGGACCGG			
			A _			
GAM1394	MYO1C	3'	GCCGGGCATGGTGGTG	61207	TG A	G
			TAT C CGTG TCCGGC			
			GTG G GTAC GGGCCG			
			GT _ _			
GAM1394	MYOG	3'	GGCTGGGCTGGGCCTGC	59345	CGT	TG
			GCA GGTCCGGCC GTT			
			CGT CCGGGTCGG CGG			
			_____ GT			
GAM1394	MYOG	3'	GGCTGGGCTGGGCCTGC	59345	CGT	TG
			GCA GGTCCGGCC GTT			
			CGT CCGGGTCGG CGG			
			_____ GT			
GAM1394	NAPB	3'	GTCGTGACCGTGTGTGGTG	70189	TG	_
			TAT CACGTGGTC CGGC			
			GTG GTGTGCCAG GCTG			
			GT T			
GAM1394	NAPB	3'	GTCGTGACCGTGTGTGGTG	70189	TG	_
			TAT CACGTGGTC CGGC			
			GTG GTGTGCCAG GCTG			
			GT T			
GAM1394	NDRG1	3'	GCTGGGCTGGAACGTG	59568	GG	TG
			CACGT TCCGGCC GT			



			GTGCA AGGTCGG CG		
			— GT		
GAM1394	NDRG1	3'	GCTGGGCTGGAACGTG 59568	GG	TG
			CACGT TCCGGCC GT		
			GTGCA AGGTCGG CG		
			— GT		
GAM1394	NDUFA5	3'	GGTGATTATGGTAATA 17195	A	CG
			TATTGC CGTGGTC GCC		
			ATAATG GTATTAG TGG		
			— —		
GAM1394	NDUFA5	3'	GGTGATTATGGTAATA 17195	A	CG
			TATTGC CGTGGTC GCC		
			ATAATG GTATTAG TGG		
			— —		
GAM1394	NEK6	3'	AGCCAGGCTGGGCCAT 26930		
			GTGGTCCGGCCTGGTT		
			TACCGGGTCGGACCGA		
			— —		
GAM1394	NEK6	3'	AGCCAGGCTGGGCCAT 26930		
			GTGGTCCGGCCTGGTT		
			TACCGGGTCGGACCGA		
			— —		
GAM1394	NEK6	3'	GACCGTGTGATTTGTGTAGTG 26931	T	CG C
			TATTGCACG GGTC GC TGGTT		
			GTGATGTGT TTAG TG GCCAG		
			— — T		
GAM1394	NEK6	3'	GACCGTGTGATTTGTGTAGTG 26931	T	CG C
			TATTGCACG GGTC GC TGGTT		
			GTGATGTGT TTAG TG GCCAG		
			— — T		
GAM1394	NEO1	5'	GGCCGGGCCGGGCTGGGC 10204	ACGT	
			GC GGTCCGGCCTGGTT		
			CG TCGGGCCGGGCCGG		
			GG—		
GAM1394	NEO1	5'	GGCCGGGCCGGGCTGGGC 10204	ACGT	
			GC GGTCCGGCCTGGTT		
			CG TCGGGCCGGGCCGG		
			GG—		
GAM1394	NEU1	5'	AGCTGCCAGGGTCGCGGCAGTG 4739	A	GT _ CT
			TATTGC CGTG CC GGC GGTT		

		GTGACG GCGC GG CCG TCGA		
		— TG A —		
GAM1394 NEU1	5'	AGCTGCCAGGGTCGCGGCAGTG 4739	A	GT _ CT
		TATTGC CGTG CC GGC GGTT		
		GTGACG GCGC GG CCG TCGA		
		— TG A —		
GAM1394 NEU3	3'	AATCAGGCCTATTTGTGTAG 21844	TGGTCC	
		TTGCACG GGCCTGGTT		
		GATGTGT CCGGACTAA		
		TTAT_		
GAM1394 NEU3	3'	AATCAGGCCTATTTGTGTAG 21844	TGGTCC	
		TTGCACG GGCCTGGTT		
		GATGTGT CCGGACTAA		
		TTAT_		
GAM1394 NFYC	3'	AATTAGGTGAATGTGTGTAG 26438	TGG CG	
		TTGCACG TC GCCTGGTT		
		GATGTGT AG TGGATTAA		
		GTA _		
GAM1394 NFYC	3'	AATTAGGTGAATGTGTGTAG 26438	TGG CG	
		TTGCACG TC GCCTGGTT		
		GATGTGT AG TGGATTAA		
		GTA _		
GAM1394 NOS1	5'	AGTCGGGTTGGACGTCACTGC 5241	C _	GT
		GCA GTG GTCCGGCCTG T		
		CGT CAC CAGGTTGGGC A		
		_ TG TG		
GAM1394 NOS1	5'	AGTCGGGTTGGACGTCACTGC 5241	C _	GT
		GCA GTG GTCCGGCCTG T		
		CGT CAC CAGGTTGGGC A		
		_ TG TG		
GAM1394 NPM3	3'	GGTCAGCTCCATGTGCCATG 22768	T	TCC_
		TAT GCACGTGG GGCC		
		GTA CGTGTACC CTGG		
		C TCGA		
GAM1394 NPM3	3'	GGTCAGCTCCATGTGCCATG 22768	T	TCC_
		TAT GCACGTGG GGCC		
		GTA CGTGTACC CTGG		
		C TCGA		
GAM1394 NR3C1	3'	GGCCAAATTATTTGTGTAATA 3924	_	CC
		TATTGCAC GTGGT GGCC		

		ATAATGTG TATTA CCGG		
		TT AA		
GAM1394 NR3C1	3'	GGCCAAATTATTTGTGTAATA 3924	___	CC
		TATTGCAC GTGGT GGCC		
		ATAATGTG TATTA CCGG		
		TT AA		
GAM1394 NRL	3'	TTGGTTGGGAGAGAGCTGTGTG 20516	TG _____	TGGTT
	CAG	CACG GT CCGGCC		
		GTGT CG GGTGG		
		GT AGAGAG TTG		
GAM1394 NRL	3'	TTGGTTGGGAGAGAGCTGTGTG 20516	TG _____	TGGTT
	CAG	CACG GT CCGGCC		
		GTGT CG GGTGG		
		GT AGAGAG TTG		
GAM1394 NTSR1	3'	GCTGGCCCTGCGTGCCATG 10296	T _ T	
		TAT GCACGT GG CCGGC		
		GTA CGTGCG CC GGTCG		
		C T C		
GAM1394 NTSR1	3'	GCTGGCCCTGCGTGCCATG 10296	T _ T	
		TAT GCACGT GG CCGGC		
		GTA CGTGCG CC GGTCG		
		C T C		
GAM1394 NUMA1	5'	CTGGACTTTGTGTGCAGT 93439	T__	
		ATTGCACG GGTCCGG		
		TGACGTGT TCAGGTC		
		GTT		
GAM1394 NUMA1	5'	CTGGACTTTGTGTGCAGT 93439	T__	
		ATTGCACG GGTCCGG		
		TGACGTGT TCAGGTC		
		GTT		
GAM1394 OCLN	3'	CGGGTTCCTGCAATG 10315	CGT TCC TG	
		TATTGCA GG GGCC G		
		GTAACGT CC TTGG C		
		___ ___ GT		
GAM1394 OCLN	3'	CGGGTTCCTGCAATG 10315	CGT TCC TG	
		TATTGCA GG GGCC G		
		GTAACGT CC TTGG C		
		___ ___ GT		
GAM1394 OPRD1	5'	GGCTGGGCCCGGTGCGG 6192	G	
		TTGCAC TGGTCCGGCC		

GGCGTG GCCGGGTCCG

GAM1394	OPRD1	5'	GGCTGGG <sup>—</sup> CCGGTGCGG	6192	G	
			TTGCAC TGGTCCGGCC			
			GGCGTG GCCGGGTCCG			
GAM1394	OSR1	5'	GGCTGGG <sup>—</sup> CCGGGCAGTGC	17568	GTG	TG
			GCAC GTCCGGCC GTT			
			CGTG CGGGCCGG CGG			
			A <sup>—</sup> GT			
GAM1394	OSR1	5'	GGCTGGG <sup>—</sup> CCGGGCAGTGC	17568	GTG	TG
			GCAC GTCCGGCC GTT			
			CGTG CGGGCCGG CGG			
			A <sup>—</sup> GT			
GAM1394	OXTR	5'	CGGACCCGTGCGATA	6207	T	
			TATTGCACG GGTCCG			
			ATAGCGTGC CCAGGC			
GAM1394	OXTR	5'	CGGACCCGTGCGATA	6207	T	
			TATTGCACG GGTCCG			
			ATAGCGTGC CCAGGC			
GAM1394	PABPN1	5'	CTGGGCC <sup>—</sup> ACTGCGGTG	16179	C	
			TATTGCA GTGGTCCGG			
			GTGGCGT CACCGGGTC			
GAM1394	PABPN1	5'	CTGGGCC <sup>—</sup> ACTGCGGTG	16179	C	
			TATTGCA GTGGTCCGG			
			GTGGCGT CACCGGGTC			
GAM1394	PAFAH1B1	3'	ACTGGGT <sup>—</sup> CCACATGTAATG	4726	C	TCCG TG
			TATTGCA GTGG GCC GT			
			GTAATGT CACC TGG CA			
			A <sup>—</sup> GT			
GAM1394	PAFAH1B1	3'	ACTGGGT <sup>—</sup> CCACATGTAATG	4726	C	TCCG TG
			TATTGCA GTGG GCC GT			
			GTAATGT CACC TGG CA			
			A <sup>—</sup> GT			
GAM1394	PCDH11X	3'	GGTTAGTGCTATTGTGTAATG	52049	_	CC_
			TATTGCACG TGGT GGCC			

		GTAATGTGT ATCG TTGG	
		T TGA	
GAM1394	PCDH11X	3' GGTTAGTGCTATTGTGTAATG 52027	_ CC_
		TATTGCACG TGGT GGCC	
		GTAATGTGT ATCG TTGG	
		T TGA	
GAM1394	PCDH11X	3' GGTTAGTGCTATTGTGTAATG 52049	_ CC_
		TATTGCACG TGGT GGCC	
		GTAATGTGT ATCG TTGG	
		T TGA	
GAM1394	PCDH11X	3' GGTTAGTGCTATTGTGTAATG 52027	_ CC_
		TATTGCACG TGGT GGCC	
		GTAATGTGT ATCG TTGG	
		T TGA	
GAM1394	PCDH11Y	3' GGTTAGTGCTATTGTGTAATG 52083	_ CC_
		TATTGCACG TGGT GGCC	
		GTAATGTGT ATCG TTGG	
		T TGA	
GAM1394	PCDH11Y	3' GGTTAGTGCTATTGTGTAATG 52083	_ CC_
		TATTGCACG TGGT GGCC	
		GTAATGTGT ATCG TTGG	
		T TGA	
GAM1394	PCSK2	3' AACCAAAGGACATTATGTGT 10462	_ GGCC
		GCACGTG GTCC TGGTT	
		TGTGTAT CAGG ACCAA	
		TA AA_	
GAM1394	PCSK2	3' AACCAAAGGACATTATGTGT 10462	_ GGCC
		GCACGTG GTCC TGGTT	
		TGTGTAT CAGG ACCAA	
		TA AA_	
GAM1394	PCTP	3' GATTAGGCTGGGATTTGAGGT 41098	A_ TGG
		GC CG TCCGGCCTGGTT	
		TG GT GGGTCGGATTAG	
		GA TTA	
GAM1394	PCTP	3' GATTAGGCTGGGATTTGAGGT 41098	A_ TGG
		GC CG TCCGGCCTGGTT	
		TG GT GGGTCGGATTAG	
		GA TTA	
GAM1394	PDZK1	3' AACCATTACCATGTGTGAT 10505	TG CCGGCC
		AT CACGTGGT TGGTT	

		TA GTGTACCA	ACCAA			
		GT	CTT__			
GAM1394	PDZK1	3'	AACCATTACCATGTGTGAT	10505	TG	CCGGCC
			AT CACGTGGT	TGGTT		
			TA GTGTACCA	ACCAA		
			GT	CTT__		
GAM1394	PES1	3'	TGGCCAGAGGACCTAAGTGTGA	26674	TG	GT_ _ TGGTT
	TG		T CAC	GGTCC GGCC		
			A GTG	CCAGG CCGG		
			GT AAT	AGA TT		
GAM1394	PES1	3'	TGGCCAGAGGACCTAAGTGTGA	26674	TG	GT_ _ TGGTT
	TG		T CAC	GGTCC GGCC		
			A GTG	CCAGG CCGG		
			GT AAT	AGA TT		
GAM1394	PFKFB1	5'	GGCCAGGTACCTTGTGGGCAGT	10514	_	T CCG
	G		TATTGC	ACG GGT GCCTGGTT		
			GTGACG	TGT CCA TGGACCGG		
			GG	T _		
GAM1394	PFKFB1	5'	GGCCAGGTACCTTGTGGGCAGT	10514	_	T CCG
	G		TATTGC	ACG GGT GCCTGGTT		
			GTGACG	TGT CCA TGGACCGG		
			GG	T _		
GAM1394	PGD	3'	GACCAGGAGCTGCTCATGTGCG	78798	_	CCGG
			TGCACGTG	GT CCTGGTT		
			GCGTGTAC	CG GGACCAG		
			T	TCGA		
GAM1394	PGD	3'	GACCAGGAGCTGCTCATGTGCG	78798	_	CCGG
			TGCACGTG	GT CCTGGTT		
			GCGTGTAC	CG GGACCAG		
			T	TCGA		
GAM1394	PHF1	3'	GGCCTGATGGCTCTGTGCAGTA	10544	_	G C
			TATTGCAC	GT GTC GGCC		
			ATGACGTG	CG TAG CCGG		
			TCT	G T		
GAM1394	PHF1	3'	GGCCTGATGGCTCTGTGCAGTA	10544	_	G C
			TATTGCAC	GT GTC GGCC		
			ATGACGTG	CG TAG CCGG		
			TCT	G T		
GAM1394	PHLDA3	5'	GGTCGGGCTGGGCCAGCTGGGG	24766	G	CG GT
	TA		TATT	CA TGGTCCGGCCTG T		

		ATGG GT ACCGGGTCGGGC G			
		G CG TG			
GAM1394	PHLDA3	5' GGTCGGGCTGGGCCAGCTGGGG 24766	G CG		GT
	TA	TATT CA TGGTCCGGCCTG T			
		ATGG GT ACCGGGTCGGGC G			
		G CG TG			
GAM1394	PIGR	3' TGGCCTTAGGGGTCATGTATGA 72611	GC	GT ____	TGGTT
	TG	TT ACGTG CC GGCC			
		AG TGTAC GG CCGG			
		TA TG GATT TT			
GAM1394	PIGR	3' TGGCCTTAGGGGTCATGTATGA 72611	GC	GT ____	TGGTT
	TG	TT ACGTG CC GGCC			
		AG TGTAC GG CCGG			
		TA TG GATT TT			
GAM1394	PITPN	5' GGCCGGGCCGGGCCACG 20628			
		CGTGGTCCGGCCTGGTT			
		GCACCGGGCCGGGCCGG			
GAM1394	PITPN	5' GGCCGGGCCGGGCCACG 20628			
		CGTGGTCCGGCCTGGTT			
		GCACCGGGCCGGGCCGG			
GAM1394	PITPN	5' GGCCGGGCCGGGCCACG 20629			
		CGTGGTCCGGCCTGGTT			
		GCACCGGGCCGGGCCGG			
GAM1394	PITPN	5' GGCCGGGCCGGGCCACG 20629			
		CGTGGTCCGGCCTGGTT			
		GCACCGGGCCGGGCCGG			
GAM1394	PITPNB	3' AGTCTGGCCTGCGTGCGGTG 24778	TG T	C	
		TATTGCACG G CCGG CT			
		GTGGCGTGC C GGTC GA			
		GT C T			
GAM1394	PITPNB	3' AGTCTGGCCTGCGTGCGGTG 24778	TG T	C	
		TATTGCACG G CCGG CT			
		GTGGCGTGC C GGTC GA			
		GT C T			
GAM1394	PKD2L1	5' GGCTAGGCTGGGCTGTGC 32265	GT		
		GCAC GGTCCGGCCTGGTT			

CGTG TCGGGTCGGATCGG

GAM1394 PKD2L1 5' GGCTAGGCTGGGCTGTGC 32265 GT  
GCAC GGTCCGGCCTGGTT  
|||||  
CGTG TCGGGTCGGATCGG

GAM1394 PLA2G7 5' AGCGCTTGGGTCGCGTTGGTG 17437 C GT \_ \_  
TATTG ACGTG CCG GC CT  
||||| ||| ||  
GTGGT TGCGC GGT CG GA

\_ TG T C  
GAM1394 PLA2G7 5' AGCGCTTGGGTCGCGTTGGTG 17437 C GT \_ \_  
TATTG ACGTG CCG GC CT  
||||| ||| ||  
GTGGT TGCGC GGT CG GA

\_ TG T C  
GAM1394 PODXL 3' ATCAGGCTCCGGCTGTAGTA 18229 CG TCC GT  
TATTGCA TGG GGCCTG T  
||||| ||| ||||| |  
ATGATGT GCC TCGGAC A  
CG \_ TG

GAM1394 PODXL 3' ATCAGGCTCCGGCTGTAGTA 18229 CG TCC GT  
TATTGCA TGG GGCCTG T  
||||| ||| ||||| |  
ATGATGT GCC TCGGAC A  
CG \_ TG

GAM1394 POLA 3' GTTACGGTGAGGATCATGTGTT 33738 T G\_ TGGTT  
GTA TAT GCACGTGGTCC GCC  
||| ||||| |||  
ATG TGTGTACTAGG TGG  
T AG CATTGG

GAM1394 POLA 3' GTTACGGTGAGGATCATGTGTT 33738 T G\_ TGGTT  
GTA TAT GCACGTGGTCC GCC  
||| ||||| |||  
ATG TGTGTACTAGG TGG  
T AG CATTGG

GAM1394 PP 5' GTCGGCGCCGCGTGCGG 40896 \_  
TTGCACGTGGT CCGGC  
||||||| ||||  
GGCGTGCGCCG GGCTG  
C

GAM1394 PP 5' GTCGGCGCCGCGTGCGG 40896 \_  
TTGCACGTGGT CCGGC  
||||||| ||||  
GGCGTGCGCCG GGCTG  
C

GAM1394 PPEF1 3' ATTAGGTTAAATGTCAGTA 20681 C GGTCC  
TATTG ACGT GGCCTGGT  
||||| ||| |||||



		ATGAC TGTA TTGGATTA			
		— AA—			
GAM1394 PPEF1	3'	ATTAGGTTAAATGTCAGTA 20681	C	GGTCC	
		TATTG ACGT GGCCTGGT			
		ATGAC TGTA TTGGATTA			
		— AA—			
GAM1394 PPEF1	3'	AACTGGGTTGGACCTAGTG 20680	GT	TG	
		CAC GGTCCGGCC GTT			
		GTG CCAGGTTGG CAA			
		AT GT			
GAM1394 PPEF1	3'	AACTGGGTTGGACCTAGTG 20680	GT	TG	
		CAC GGTCCGGCC GTT			
		GTG CCAGGTTGG CAA			
		AT GT			
GAM1394 PRCC G	3'	AGCTAGCAAAGACTTGTGTGAT 19930	TG	T CG_ C	
		TAT CACG GGTC GC TGGTT			
		GTA GTGT TCAG CG ATCGA			
		GT _ AAA _			
GAM1394 PRCC G	3'	AGCTAGCAAAGACTTGTGTGAT 19930	TG	T CG_ C	
		TAT CACG GGTC GC TGGTT			
		GTA GTGT TCAG CG ATCGA			
		GT _ AAA _			
GAM1394 PROC TG	3'	TGGCTGGGCTTTTGCATGGCAA 4344	A	_____	TGGTT
		TGC CGTG GTCCGGCC			
		ACG GTAC CGGGTCGG			
		_ GTTTT TT			
GAM1394 PROC TG	3'	TGGCTGGGCTTTTGCATGGCAA 4344	A	_____	TGGTT
		TGC CGTG GTCCGGCC			
		ACG GTAC CGGGTCGG			
		_ GTTTT TT			
GAM1394 PRV1	3'	TCGGACCTGTGCAATA 73534	T		
		TATTGCACG GGTCCGG			
		ATAACGTGT CCAGGCT			
		—			
GAM1394 PRV1	3'	TCGGACCTGTGCAATA 73534	T		
		TATTGCACG GGTCCGG			
		ATAACGTGT CCAGGCT			
		—			
GAM1394 PRX2	3'	GTGGGCCGGAAGGTGGAA 32840	G	GTGG	GG
		TT CAC TCCGGCCT T			

		AA GTG AGGCCGGG G			
		G GA__ TT			
GAM1394 PRX2	3'	GTGGGCCGGAAGGTGGAA 32840	G	GTGG	GG
		TT CAC TCCGGCCT T			
		AA GTG AGGCCGGG G			
		G GA__ TT			
GAM1394 PTGIS	3'	AATCAGGCTGGGTTGTCACTG 6322	C	__	
		CA GTGG TCCGGCCTGGTT			
		GT CACT GGGTCGGAATAA			
		_ GTT			
GAM1394 PTGIS	3'	AATCAGGCTGGGTTGTCACTG 6322	C	__	
		CA GTGG TCCGGCCTGGTT			
		GT CACT GGGTCGGAATAA			
		_ GTT			
GAM1394 PTPN11	5'	AGCCGGGCCGGGGGGCAGC 11084	AC	GG	
		GC GT TCCGGCCTGGTT			
		CG CG GGGCCGGGCCGA			
		A_ GG			
GAM1394 PTPN11	5'	AGCCGGGCCGGGGGGCAGC 54594	AC	GG	
		GC GT TCCGGCCTGGTT			
		CG CG GGGCCGGGCCGA			
		A_ GG			
GAM1394 PTPN11	5'	AGCCGGGCCGGGGGGCAGC 54594	AC	GG	
		GC GT TCCGGCCTGGTT			
		CG CG GGGCCGGGCCGA			
		A_ GG			
GAM1394 PTPN11	5'	AGCCGGGCCGGGGGGCAGC 11084	AC	GG	
		GC GT TCCGGCCTGGTT			
		CG CG GGGCCGGGCCGA			
		A_ GG			
GAM1394 PTPN18	5'	GCCGGGCTGGACCTTGC 26867	CGT		
		GCA GGTCCGGCCTGGT			
		CGT CCAGGTCGGGCCG			
		T__			
GAM1394 PTPN18	5'	GCCGGGCTGGACCTTGC 26867	CGT		
		GCA GGTCCGGCCTGGT			
		CGT CCAGGTCGGGCCG			
		T__			
GAM1394 PTPRA	3'	AATTGGGCTGGATTGTGCTTTG 55078	TT	TG	TG
		TA GCACG GTCCGGCC GTT			

		GT CGTGT TAGGTCGG TAA			
		TT _ GT			
GAM1394	PTPRA	3' AATTGGGCTGGATTGTGCTTTG 11087	TT	TG	TG
		TA GCACG GTCCGGCC GTT			
		GT CGTGT TAGGTCGG TAA			
		TT _ GT			
GAM1394	PTPRA	3' AATTGGGCTGGATTGTGCTTTG 11087	TT	TG	TG
		TA GCACG GTCCGGCC GTT			
		GT CGTGT TAGGTCGG TAA			
		TT _ GT			
GAM1394	PTPRA	3' AATTGGGCTGGATTGTGCTTTG 55078	TT	TG	TG
		TA GCACG GTCCGGCC GTT			
		GT CGTGT TAGGTCGG TAA			
		TT _ GT			
GAM1394	PTPRA	3' AATTGGGCTGGATTGTGCTTTG 55086	TT	TG	TG
		TA GCACG GTCCGGCC GTT			
		GT CGTGT TAGGTCGG TAA			
		TT _ GT			
GAM1394	PTPRA	3' AATTGGGCTGGATTGTGCTTTG 55086	TT	TG	TG
		TA GCACG GTCCGGCC GTT			
		GT CGTGT TAGGTCGG TAA			
		TT _ GT			
GAM1394	RAB23	3' GCTGAAGGTATGTGCAGTA 32784		GTC_	
		TATTGCACGTG CGGC			
		ATGACGTGTAT GTCG			
		GGAA			
GAM1394	RAB23	3' GCTGAAGGTATGTGCAGTA 32784		GTC_	
		TATTGCACGTG CGGC			
		ATGACGTGTAT GTCG			
		GGAA			
GAM1394	RAP1GA1	3' AGCCCCTGTGGCCGTGTG 11249	_	CCT	
		CACGTGGTC CGG GGTT			
		GTGTGCCGG GTC CCGA			
		T C_			
GAM1394	RAP1GA1	3' AGCCCCTGTGGCCGTGTG 11249	_	CCT	
		CACGTGGTC CGG GGTT			
		GTGTGCCGG GTC CCGA			
		T C_			
GAM1394	RET	3' GGCCAAGGCTTGGATGCGTGTG 4370	_	-	-
	TAATA	TGCACGTG GTCCG GCCT GGTT			

			ATGTGTGC TAGGT CGGA CCGG			
			G T A			
GAM1394	RET	3'	GGCCAAGGCTTGGATGCGTGTG 4370	-	-	-
		TAATA	TGCACGTG GTCCG GCCT GGTT			
			ATGTGTGC TAGGT CGGA CCGG			
			G T A			
GAM1394	RET	3'	GGCCAAGGCTTGGATGCGTGTG 40168	-	-	-
		TAATA	TGCACGTG GTCCG GCCT GGTT			
			ATGTGTGC TAGGT CGGA CCGG			
			G T A			
GAM1394	RET	3'	GGCCAAGGCTTGGATGCGTGTG 40178	-	-	-
		TAATA	TGCACGTG GTCCG GCCT GGTT			
			ATGTGTGC TAGGT CGGA CCGG			
			G T A			
GAM1394	RET	3'	GGCCAAGGCTTGGATGCGTGTG 40594	-	-	-
		TAATA	TGCACGTG GTCCG GCCT GGTT			
			ATGTGTGC TAGGT CGGA CCGG			
			G T A			
GAM1394	RET	3'	GGCCAAGGCTTGGATGCGTGTG 40594	-	-	-
		TAATA	TGCACGTG GTCCG GCCT GGTT			
			ATGTGTGC TAGGT CGGA CCGG			
			G T A			
GAM1394	RET	3'	GGCCAAGGCTTGGATGCGTGTG 40168	-	-	-
		TAATA	TGCACGTG GTCCG GCCT GGTT			
			ATGTGTGC TAGGT CGGA CCGG			
			G T A			
GAM1394	RET	3'	GGCCAAGGCTTGGATGCGTGTG 40178	-	-	-
		TAATA	TGCACGTG GTCCG GCCT GGTT			
			ATGTGTGC TAGGT CGGA CCGG			
			G T A			
GAM1394	RFC1	3'	AACCAGGCTGGGTCAGGC 11299	ACG	GT	
			GC TG CCGGCCTGGTT			
			CG AC GGTCCGACCAA			
			G__ TG			
GAM1394	RFC1	3'	AACCAGGCTGGGTCAGGC 11299	ACG	GT	
			GC TG CCGGCCTGGTT			
			CG AC GGTCCGACCAA			
			G__ TG			
GAM1394	RFNG	3'	CCCTGGTGGGCTGCGGTGATG 88174	TG A	TG	G T TT
			TAT C CG GTCCG CC GG			

		GTA G GC CGGGT GG CC		
		GT _ GT _ T CC		
GAM1394 RFNG	3'	CCCTGGTGGGCTGCGGTGATG 88174	TG A TG	G T TT
		TAT C CG GTCCG CC GG		
		GTA G GC CGGGT GG CC		
		GT _ GT _ T CC		
GAM1394 RNASE4	3'	GGCTGGGCTTTTCTGTAATA 11355	CGT_	
		TATTGCA GGTCCGGCC		
		ATAATGT TCGGGTCGG		
		CTTT		
GAM1394 RNASE4	3'	GGCTGGGCTTTTCTGTAATA 11355	CGT_	
		TATTGCA GGTCCGGCC		
		ATAATGT TCGGGTCGG		
		CTTT		
GAM1394 RNH	5'	TGGCCGGGCGCCCAGGCGTGTG 11371	TG _ _	TGGTT
G		CACGT GGT CCGGCC		
		GTGCG CCG GGCCGG		
		GT GAC CG TT		
GAM1394 RNH	5'	TGGCCGGGCGCCCAGGCGTGTG 11371	TG _ _	TGGTT
G		CACGT GGT CCGGCC		
		GTGCG CCG GGCCGG		
		GT GAC CG TT		
GAM1394 RNH	5'	TGGCCGGGCGCCCAGGCGTGTG 59626	TG _ _	TGGTT
G		CACGT GGT CCGGCC		
		GTGCG CCG GGCCGG		
		GT GAC CG TT		
GAM1394 RNH	5'	TGGCCGGGCGCCCAGGCGTGTG 59626	TG _ _	TGGTT
G		CACGT GGT CCGGCC		
		GTGCG CCG GGCCGG		
		GT GAC CG TT		
GAM1394 RNMT	3'	GGCTACTACACTTGTGTAATG 13723	_ _	CC
		TATTGCAC GTGGT GGCC		
		GTAATGTG CATCA TCGG		
		TTCA _		
GAM1394 RNMT	3'	GGCTACTACACTTGTGTAATG 13723	_ _	CC
		TATTGCAC GTGGT GGCC		
		GTAATGTG CATCA TCGG		
		TTCA _		
GAM1394 ROCK2	5'	GGCCGGGCTGGGCGGGC 66014	ACGT	
		GC GGTCCGGCCTGGTT		

			CG CCGGGTCGGGCCGG		
			GG__		
GAM1394	ROCK2	5'	GGCCGGGCTGGGCCGGGCCG 66015	ACGT	
			TTGC GGTCCGGCCTGGTT		
			GGCG CCGGGTCGGGCCGG		
			GG__		
GAM1394	ROCK2	3'	GCCGGGCATGATGGTGGTG 66011	TG A G CCG	
			TAT C CGT GT GCCTGGT		
			GTG G GTA TA CGGGCCG		
			GT_ G __		
GAM1394	ROCK2	3'	GCCGGGCATGATGGTGGTG 66011	TG A G CCG	
			TAT C CGT GT GCCTGGT		
			GTG G GTA TA CGGGCCG		
			GT_ G __		
GAM1394	ROCK2	5'	GGCCGGGCTGGGCCGGG 66012	G	
			C TGGTCCGGCCTGGTT		
			G GCCGGGTCGGGCCGG		
			G		
GAM1394	ROCK2	5'	GGCCGGGCTGGGCCGGG 66012	G	
			C TGGTCCGGCCTGGTT		
			G GCCGGGTCGGGCCGG		
			G		
GAM1394	ROCK2	5'	GGCCGGGCTGGGCCGGG 66013	G	
			C TGGTCCGGCCTGGTT		
			G GCCGGGTCGGGCCGG		
			G		
GAM1394	ROCK2	5'	GGCCGGGCTGGGCCGGGC 66014	ACGT	
			GC GGTCCGGCCTGGTT		
			CG CCGGGTCGGGCCGG		
			GG__		
GAM1394	ROCK2	5'	GGCCGGGCTGGGCCGGG 66013	G	
			C TGGTCCGGCCTGGTT		
			G GCCGGGTCGGGCCGG		
			G		
GAM1394	ROCK2	5'	GGTCCGGGCCGCGCGGTG 66016	A	_
			TATTGC CGTGGTCCGG CC		
			GTGGCG GCGCCGGGCC GG		
			_ T		
GAM1394	ROCK2	5'	GGCCGGGCTGGGCCGGGCCG 66015	ACGT	
			TTGC GGTCCGGCCTGGTT		

			GGCG CCGGGTCGGGCCGG			
			GG__			
GAM1394	ROCK2	5'	GGTCCGGGCCGCGGCGGTG 66016	A		—
			TATTGC CGTGGTCCGG CC			
			GTGGCG GCGCCGGGCC GG			
			— T			
GAM1394	ROM1	5'	AGCCGGGCCGGGCTGACTCAGC 4382	AC_ _		
	A		TGC GT GGTCCGGCCTGGTT			
			ACG CA TCGGGCCGGGCCGA			
			ACT G			
GAM1394	ROM1	5'	AGCCGGGCCGGGCTGACTCAGC 4382	AC_ _		
	A		TGC GT GGTCCGGCCTGGTT			
			ACG CA TCGGGCCGGGCCGA			
			ACT G			
GAM1394	RRAS2	5'	ATCAGGCTGGGCTCTGTAGC 24290	_ T		GT
			GC ACG GGTCCGGCCTG T			
			CG TGT TCGGGTCGGAC A			
			A C TG			
GAM1394	RRAS2	5'	ATCAGGCTGGGCTCTGTAGC 24290	_ T		GT
			GC ACG GGTCCGGCCTG T			
			CG TGT TCGGGTCGGAC A			
			A C TG			
GAM1394	S100A11	5'	GGCTGGGCCCGGAAGGGCGTG 18837	GG_		TG
			CACGT TCCGGCC GTT			
			GTGCG GGGCCGG CGG			
			GGAA GT			
GAM1394	S100A11	5'	GGCTGGGCCCGGAAGGGCGTG 18837	GG_		TG
			CACGT TCCGGCC GTT			
			GTGCG GGGCCGG CGG			
			GGAA GT			
GAM1394	SDHC	3'	GGCCGGGTTGGGGGGTG 69384	GTGG		
			CAC TCCGGCCTGGTT			
			GTG GGGTTGGGCCGG			
			GG_			
GAM1394	SDHC	3'	GGCCGGGTTGGGGGGTG 69384	GTGG		
			CAC TCCGGCCTGGTT			
			GTG GGGTTGGGCCGG			
			GG_			
GAM1394	SECTM1	3'	GGCCGGGCTGGGAGGCGGCGG 11529	A GG		
			TTGC CGT TCCGGCCTGGTT			

			GGCG GCG GGGTCGGGCCGG		
			— GA		
GAM1394	SECTM1	3'	GGCCGGGCTGGGAGGCGGCGG 11529	A	GG
			TTGC CGT TCCGGCCTGGTT		
			GGCG GCG GGGTCGGGCCGG		
			— GA		
GAM1394	SERPINB9	3'	GACCAGGTTGGACTGTTTAATG 14755	C	GT
			TATTG AC GGTCCGGCCTGGTT		
			GTAAT TG TCAGGTTGGACCAG		
			T —		
GAM1394	SERPINB9	3'	GACCAGGTTGGACTGTTTAATG 14755	C	GT
			TATTG AC GGTCCGGCCTGGTT		
			GTAAT TG TCAGGTTGGACCAG		
			T —		
GAM1394	SFRS2IP	5'	GCTGGGCATGGTAGTG 16356	A	G
			TATTGC CGTG TCCGGC		
			GTGATG GTAC GGGTCG		
			— —		
GAM1394	SFRS2IP	5'	GCTGGGCATGGTAGTG 16356	A	G
			TATTGC CGTG TCCGGC		
			GTGATG GTAC GGGTCG		
			— —		
GAM1394	SFRS7	3'	TGGTTGGTATAAAGTTATGTGT 59448	GG	_____ TGGTT
	A		GCACGT T CCGGCC		
			TGTGTA G GGTG		
			TT AAATAT TT		
GAM1394	SFRS7	3'	TGGTTGGTATAAAGTTATGTGT 59448	GG	_____ TGGTT
	A		GCACGT T CCGGCC		
			TGTGTA G GGTG		
			TT AAATAT TT		
GAM1394	SH3GL2	3'	TGGATCATGTGGAGTG 11630	G	
			TATT CACGTGGTCCG		
			GTGA GTGTACTAGGT		
			G		
GAM1394	SH3GL2	3'	TGGATCATGTGGAGTG 11630	G	
			TATT CACGTGGTCCG		
			GTGA GTGTACTAGGT		
			G		
GAM1394	SIM2	3'	GTTGGGCATGGTGGTG 23787	TG A	G
			TAT C CGTG TCCGGC		



			GTG G GTAC GGGTTG		
			GT _ _		
GAM1394	SIM2	3'	GTTGGGCATGGTGGTG 23787	TG A G	
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGTTG		
			GT _ _		
GAM1394	SLC16A1	5'	GACTGGCTAGCTGCGTG 11741	TG CC T	
			CACG GT GGCC GGTT		
			GTGC CG TCGG TCAG		
			GT A _ _		
GAM1394	SLC16A1	5'	GACTGGCTAGCTGCGTG 11741	TG CC T	
			CACG GT GGCC GGTT		
			GTGC CG TCGG TCAG		
			GT A _ _		
GAM1394	SLC25A12	3'	GACCAGGCTAATGACTTGTGTG 13525	T__ C__	
			TGC CACG GGTC GGCCTGGTT		
			GTGT TCAG TCGGACCAG		
			GTGT TAA		
GAM1394	SLC25A12	3'	GACCAGGCTAATGACTTGTGTG 13525	T__ C__	
			TGC CACG GGTC GGCCTGGTT		
			GTGT TCAG TCGGACCAG		
			GTGT TAA		
GAM1394	SLC31A1	3'	GCCGGGCATGGTGGTG 8512	TG A G	
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGCCG		
			GT _ _		
GAM1394	SLC31A1	3'	GCCGGGCATGGTGGTG 8512	TG A G	
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGCCG		
			GT _ _		
GAM1394	SLC4A10	3'	AACTGCTTGGATCATGTATGGT 41909	GC _ CT	
			A TATT ACGTGGTCCG GC GGTT		
			ATGG TGTACTAGGT CG TCAA		
			TA T _		
GAM1394	SLC4A10	3'	AACTGCTTGGATCATGTATGGT 41909	GC _ CT	
			A TATT ACGTGGTCCG GC GGTT		
			ATGG TGTACTAGGT CG TCAA		
			TA T _		
GAM1394	SLC4A4	3'	TGGCTGGTGTATATGTGCAA 13644	GT__ TGTT	
			TG TTGCACGTG CCGGCC		

			AACGTGTAT	GGTCGG		
			ATATGT	TT		
GAM1394	SLC4A4	3'	TGGCTGGTGTATATATGTGCAA	13644	GT_____	TGGTT
	TG		TTGCACGTG	CCGGCC		
			AACGTGTAT	GGTCGG		
			ATATGT	TT		
GAM1394	SLC7A5	3'	GGCTGGGTTGGGTAGGGTG	13012	GC G GG	
			TATT AC T	TCCGGCC		
			GTGG TG G	GGGTCGG		
			GA G TT			
GAM1394	SLC7A5	3'	GGCTGGGTTGGGTAGGGTG	13012	GC G GG	
			TATT AC T	TCCGGCC		
			GTGG TG G	GGGTCGG		
			GA G TT			
GAM1394	SMURF1	5'	GGCCGGGCGCGGCGCGGC	92454	ACGT	
			GC GGTCCGGCCTGGTT			
			CG CCGGGCCGGGCCGG			
			GG__			
GAM1394	SMURF1	5'	GGCCGGGCGCGGCGCGGC	92454	ACGT	
			GC GGTCCGGCCTGGTT			
			CG CCGGGCCGGGCCGG			
			GG__			
GAM1394	SMURF1	5'	GGCCGGGCGCGGCTGGGGGGCG	92455	ACGT_	
	GTG		TATTGC GGTCCGGCCTGGTT			
			GTGGCG TCGGGCCGGGCCGG			
			GGGGG			
GAM1394	SMURF1	5'	GGCCGGGCGCGGCTGGGGGGCG	92455	ACGT_	
	GTG		TATTGC GGTCCGGCCTGGTT			
			GTGGCG TCGGGCCGGGCCGG			
			GGGGG			
GAM1394	SMURF1	5'	GGCCGGGCTGGGGGGCGGTGG	92456	TG A GG	
			T C CGT TCCGGCCTGGTT			
			G G GCG GGGTCGGGCCGG			
			GT_ GG			
GAM1394	SMURF1	5'	GGCCGGGCTGGGGGGCGGTGG	92456	TG A GG	
			T C CGT TCCGGCCTGGTT			
			G G GCG GGGTCGGGCCGG			
			GT_ GG			
GAM1394	SP3	3'	AATTAGGTTAACTATGTACAAT	82492	C CC	
	A		TATTG ACGTGGT	GGCCTGGTT		

			ATAAC TGTATCA TTGGATTAA		
			A A_		
GAM1394	SP3	3'	AATTAGGTTAACTATGTACAAT 82492	C	CC
	A		TATTG ACGTGGT GGCCTGGTT		
			ATAAC TGTATCA TTGGATTAA		
			A A_		
GAM1394	SPG3A	3'	AGCCAGGCTGGATTTAATCTGT 31913	CGT__	
	A		TGCA GGTCCGGCCTGGTT		
			ATGT TTAGGTCGGACCGA		
			CTAAT		
GAM1394	SPG3A	3'	AGCCAGGCTGGATTTAATCTGT 31913	CGT__	
	A		TGCA GGTCCGGCCTGGTT		
			ATGT TTAGGTCGGACCGA		
			CTAAT		
GAM1394	SPTBN4	5'	GGCCGGGCGCGGCGGG 47389	G	
			C TGGTCCGGCCTGGTT		
			G GCCGGGCGCGGCGGG		
			G		
GAM1394	SPTBN4	5'	GGCCGGGCGCGGCGGG 47390	G	
			C TGGTCCGGCCTGGTT		
			G GCCGGGCGCGGCGGG		
			G		
GAM1394	SPTBN4	5'	AGCCGGGCTGGGCGGGC 47385	ACGT	
			GC GGTCCGGCCTGGTT		
			CG CCGGGTCGGGCCGA		
			GG__		
GAM1394	SPTBN4	5'	AGCCGGGCTGGGCGGGC 47385	ACGT	
			GC GGTCCGGCCTGGTT		
			CG CCGGGTCGGGCCGA		
			GG__		
GAM1394	SPTBN4	5'	GGCCGGGCGCGGCGGGCAG 47391	ACGT	
			TTGC GGTCCGGCCTGGTT		
			GACG CCGGGCCGGGCCGG		
			GG__		
GAM1394	SPTBN4	5'	GGCCGGGCGCGGCGGGCAG 47391	ACGT	
			TTGC GGTCCGGCCTGGTT		
			GACG CCGGGCCGGGCCGG		
			GG__		
GAM1394	SPTBN4	5'	GGCCGGGCGCGGCGGG 47389	G	
			C TGGTCCGGCCTGGTT		

			G GCCGGGCCGGGCCGG		
			G		
GAM1394	SPTBN4	5'	GGCCGGGCCGGGCCGGG	47390	G
			C TGGTCCGGCCTGGTT		
			G GCCGGGCCGGGCCGG		
			G		
GAM1394	STK31	5'	TGGTACGTGCAGTG	51963	GT
			TATTGCACGTG CCG		
			GTGACGTGCAT GGT		
			—		
GAM1394	STK31	5'	TGGTACGTGCAGTG	51963	GT
			TATTGCACGTG CCG		
			GTGACGTGCAT GGT		
			—		
GAM1394	STS	3'	ATCAGGTCGATTTGTGGTA	4447	A TG TC
			TGC CG G CGGCCTGGT		
			ATG GT T GCTGGACTA		
			_ GT TA		
GAM1394	STS	3'	ATCAGGTCGATTTGTGGTA	4447	A TG TC
			TGC CG G CGGCCTGGT		
			ATG GT T GCTGGACTA		
			_ GT TA		
GAM1394	SULT2A1	3'	GCCGGGCATGGTGGTG	71753	TG A G
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGCCG		
			GT _ _		
GAM1394	SULT2A1	3'	GCCGGGCATGGTGGTG	71753	TG A G
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGCCG		
			GT _ _		
GAM1394	SUOX	5'	AATCGGGCTGGTTAATG	4850	GGT
			CGT CCGGCCTGGTT		
			GTA GGTCGGGCTAA		
			ATT		
GAM1394	SUOX	5'	AATCGGGCTGGTTAATG	4850	GGT
			CGT CCGGCCTGGTT		
			GTA GGTCGGGCTAA		
			ATT		
GAM1394	SUPT6H	3'	GACCAGGCTGGGAGGGGAGTG	60395	GTGG__
			CAC TCCGGCCTGGTT		

			GTG	GGGTCGGACCAG		
			AGGGGA			
GAM1394	SUPT6H	3'	GACCAGGCTGGGAGGGGAGTG	60395	GTGG__	
			CAC	TCCGGCCTGGTT		
			GTG	GGGTCGGACCAG		
			AGGGGA			
GAM1394	SUV39H2	3'	GGCCAGGCCTGTGTGGTG	45139	TG T C	
			TAT	CACG GGTC GGCC		
			GTG	GTGT CCGG CCGG		
			GT	_ A		
GAM1394	SUV39H2	3'	GGCCAGGCCTGTGTGGTG	45139	TG T C	
			TAT	CACG GGTC GGCC		
			GTG	GTGT CCGG CCGG		
			GT	_ A		
GAM1394	SYT4	3'	CAGGTTTTGTGTCAGTA	62436	C TG TCC	
			TATTG	ACG G GGCCTG		
			ATGAC	TGT T TTGGAC		
			_ GT	__		
GAM1394	SYT4	3'	CAGGTTTTGTGTCAGTA	62436	C TG TCC	
			TATTG	ACG G GGCCTG		
			ATGAC	TGT T TTGGAC		
			_ GT	__		
GAM1394	TACSTD2	3'	CTGGGCCTATGTAGTA	9857	CGT	
			TATTGCA	GGTCCGG		
			ATGATGT	CCGGGTC		
			AT	_		
GAM1394	TACSTD2	3'	CTGGGCCTATGTAGTA	9857	CGT	
			TATTGCA	GGTCCGG		
			ATGATGT	CCGGGTC		
			AT	_		
GAM1394	TBL2	5'	GGCCAGGCCGCGCCCCGCGTG	52187	TC__	
	CG		TGCACGTGG	CGGCCTGGTT		
			GCGTGCGCC	GCCGGACCGG		
			CCCGC			
GAM1394	TBL2	5'	GGCCAGGCCGCGCCCCGCGTG	52187	TC__	
	CG		TGCACGTGG	CGGCCTGGTT		
			GCGTGCGCC	GCCGGACCGG		
			CCCGC			
GAM1394	TBL2	5'	GGCCAGGCCGCGCCCCGCGTG	24929	TC__	
	CG		TGCACGTGG	CGGCCTGGTT		

		GCGTGCGCC GCCGGACCGG		
		CCCGC		
GAM1394	TBL2	5' GGCCAGGCCGCGCCCCGCGTG 24929	TC__	
	CG	TGCACGTGG CGGCCTGGTT		
		GCGTGCGCC GCCGGACCGG		
		CCCGC		
GAM1394	TCF19	3' AACTGGGCTGGCCTGGTTCAGT 97731	C GT T	TG
	G	TATTG AC GG CCGGCC GTT		
		GTGAC TG CC GGTCGG CAA		
		T GT _ GT		
GAM1394	TCF19	3' AACTGGGCTGGCCTGGTTCAGT 97731	C GT T	TG
	G	TATTG AC GG CCGGCC GTT		
		GTGAC TG CC GGTCGG CAA		
		T GT _ GT		
GAM1394	TCF19	3' AACTGGGCTGGCCTGGTTCAGT 97861	C GT T	TG
	G	TATTG AC GG CCGGCC GTT		
		GTGAC TG CC GGTCGG CAA		
		T GT _ GT		
GAM1394	TCF19	3' AACTGGGCTGGCCTGGTTCAGT 97861	C GT T	TG
	G	TATTG AC GG CCGGCC GTT		
		GTGAC TG CC GGTCGG CAA		
		T GT _ GT		
GAM1394	TEM7	3' GGTCCTTGGCCAGGTGCAGTG 39893	G C__	
		TATTGCAC TGGTC GGCC		
		GTGACGTG ACCGG CTGG		
		G TTC		
GAM1394	TEM7	3' GGTCCTTGGCCAGGTGCAGTG 39893	G C__	
		TATTGCAC TGGTC GGCC		
		GTGACGTG ACCGG CTGG		
		G TTC		
GAM1394	TEM8	3' TCAGTTGTGTGCAATA 49856	TG TCCGGC	
		TATTGCACG G CTGG		
		ATAACGTGT T GACT		
		GT _____		
GAM1394	TEM8	3' TCAGTTGTGTGCAATA 49856	TG TCCGGC	
		TATTGCACG G CTGG		
		ATAACGTGT T GACT		
		GT _____		
GAM1394	TESK1	5' GATCGGGCTGGGCCCGCGC 20806	A T	
		GC CG GGTCGGCCTGGTT		

			CG GC CCGGGTCGGGCTAG		
			C _		
GAM1394	TESK1	5'	GATCGGGCTGGGCCCGCGC	20806	A T
			GC CG GGTCCGGCCTGGTT		
			CG GC CCGGGTCGGGCTAG		
			C _		
GAM1394	TGFBR1	5'	GGCCGGGCGCGGCCAC	16049	
			GTGGTCCGGCCTGGTT		
			CACCGGGCGGGCCGG		
GAM1394	TGFBR1	5'	GGCCGGGCGCGGCCAC	16049	
			GTGGTCCGGCCTGGTT		
			CACCGGGCGGGCCGG		
GAM1394	TGFBR1	5'	GGCCGGGCGCGGCCACAGGCGG	16050	AC
	TG		TATTGC GTGGTCCGGCCTGGTT		
			GTGGCG CACCGGGCGGGCCGG		
			GA		
GAM1394	TGFBR1	5'	GGCCGGGCGCGGCCACAGGCGG	16050	AC
	TG		TATTGC GTGGTCCGGCCTGGTT		
			GTGGCG CACCGGGCGGGCCGG		
			GA		
GAM1394	TK2	3'	TGGTCACACAGCCTGTGTGCAG	16062	TG TCC_____ TGGTT
	TG		TTGCACG G GGCC		
			GACGTGT C CTGG		
			GT CGACACA TT		
GAM1394	TK2	3'	TGGTCACACAGCCTGTGTGCAG	16062	TG TCC_____ TGGTT
	TG		TTGCACG G GGCC		
			GACGTGT C CTGG		
			GT CGACACA TT		
GAM1394	TM4SF2	3'	GCCCACGTCACGTGTAGTG	16064	TCC_
			TATTGCACGTGG GGC		
			GTGATGTGCACT CCG		
			GCAC		
GAM1394	TM4SF2	3'	GCCCACGTCACGTGTAGTG	16064	TCC_
			TATTGCACGTGG GGC		
			GTGATGTGCACT CCG		
			GCAC		
GAM1394	TMEM2	3'	GTTGGGTCGGGTGGCAGT	25425	_ G GT
			ATTGC AC TG CCGGC		

			TGACG TG GC GGTG		
			G G TG		
GAM1394	TMEM2	3'	GTTGGGTCGGGTGGCAGT 25425	_ G GT	
			ATTGC AC TG CCGGC		
			TGACG TG GC GGTG		
			G G TG		
GAM1394	TMEPAI	3'	GCCGGGCTGGGGCTGCGT 39447	TG _	
			ACG GTCC GGCCTGGT		
			TGC CGGG TCGGGCCG		
			GT G		
GAM1394	TMEPAI	3'	GCCGGGCTGGGGCTGCGT 39447	TG _	
			ACG GTCC GGCCTGGT		
			TGC CGGG TCGGGCCG		
			GT G		
GAM1394	TNFAIP6	3'	AACCAGGCTGGGCAACATAGCA 59464	AC_ G	
	A		TTGC GT GTCCGGCCTGGTT		
			AACG CA CGGGTCGGACCAA		
			ATA A		
GAM1394	TNFAIP6	3'	AACCAGGCTGGGCAACATAGCA 59464	AC_ G	
	A		TTGC GT GTCCGGCCTGGTT		
			AACG CA CGGGTCGGACCAA		
			ATA A		
GAM1394	TNFRSF14	3'	GACTGGGTTGGCTGCAGTGTGG 13783	TG _ TG T TG	
	TG		TAT CAC G G CCGGCC GTT		
			GTG GTG C C GGTG CAG		
			GT A GT_ GT		
GAM1394	TNFRSF14	3'	GACTGGGTTGGCTGCAGTGTGG 13783	TG _ TG T TG	
	TG		TAT CAC G G CCGGCC GTT		
			GTG GTG C C GGTG CAG		
			GT A GT_ GT		
GAM1394	TRH	3'	GACTGAAGCGTTGTGTGCAA 23054	TG TCCG CT_	
			TTGCACG G GC GGTT		
			AACGTGT T CG TCAG		
			GT G__ AAG		
GAM1394	TRH	3'	GACTGAAGCGTTGTGTGCAA 23054	TG TCCG CT_	
			TTGCACG G GC GGTT		
			AACGTGT T CG TCAG		
			GT G__ AAG		
GAM1394	TRIM34	5'	AGCCAGGGAAGCAGTGCAATG 55223	_ GG GGC	
			TATTGCAC GT TCC CTGGTT		



			GTAACGTG CG AGG GACCGA	
			A A_ _	
GAM1394	TRIM34	5'	AGCCAGGGAAGCAGTGCAATG 55223	_ GG GGC
			TATTGCAC GT TCC CTGGTT	
			GTAACGTG CG AGG GACCGA	
			A A_ _	
GAM1394	TRPM2	3'	GGCTGGGCCTGTGCAG 12405	T
			TTGCACG GGTCCGGCC	
			GACGTGT CCGGGTCGG	
			-	
GAM1394	TRPM2	5'	GCTGGGAACATGTGCAG 12404	G_
			TTGCACGTG TCCGGC	
			GACGTGTAC GGGTCG	
			AA	
GAM1394	TRPM2	5'	GCTGGGAACATGTGCAG 12404	G_
			TTGCACGTG TCCGGC	
			GACGTGTAC GGGTCG	
			AA	
GAM1394	TRPM2	3'	GGCTGGGCCTGTGCAG 12405	T
			TTGCACG GGTCCGGCC	
			GACGTGT CCGGGTCGG	
			-	
GAM1394	TSG101	5'	GGCCGGGTTGGGGGTGTGCGAT 20839	TGG
			ATTGCACG TCCGGCCTGGTT	
			TAGCGTGT GGGTTGGGCCGG	
			GG_	
GAM1394	TSG101	5'	GGCCGGGTTGGGGGTGTGCGAT 20839	TGG
			ATTGCACG TCCGGCCTGGTT	
			TAGCGTGT GGGTTGGGCCGG	
			GG_	
GAM1394	UBE2G2	3'	TTGGCCAGGTGCGGTG 64866	G T
			TATTGCAC TGG CCGG	
			GTGGCGTG ACC GGTT	
			G _	
GAM1394	UBE2G2	3'	TTGGCCAGGTGCGGTG 64866	G T
			TATTGCAC TGG CCGG	
			GTGGCGTG ACC GGTT	
			G _	
GAM1394	UBQLN2	3'	AGCCTGAAGGATCAGTGTAGTA 25564	G GGCCT
			TATTGCAC TGGTCC GGTT	

		ATGATGTG ACTAGG CCGA		
		_  AAGT_		
GAM1394	UBQLN2	3' AGCCTGAAGGATCAGTGTAGTA 25564	G	GGCCT
		TATTGCAC TGGTCC GGT		
		ATGATGTG ACTAGG CCGA		
		_  AAGT_		
GAM1394	UCHL1	3' GTCCACTGGGCCATTGTGGTG 14816	TG C	CC TT
		TAT CA GTGGTCCGG TGG		
		GTG GT TACCGGGTC ACC		
		GT _ _ TGT		
GAM1394	UCHL1	3' GTCCACTGGGCCATTGTGGTG 14816	TG C	CC TT
		TAT CA GTGGTCCGG TGG		
		GTG GT TACCGGGTC ACC		
		GT _ _ TGT		
GAM1394	UNC5C	3' AGTTGGGCTGTATGCTGTGTGG 13575	TG	TG C GG
	TA	TAT CACG GT CGGCCT TT		
		ATG GTGT TA GTCGGG GA		
		GT CG T TT		
GAM1394	UNC5C	3' AGTTGGGCTGTATGCTGTGTGG 13575	TG	TG C GG
	TA	TAT CACG GT CGGCCT TT		
		ATG GTGT TA GTCGGG GA		
		GT CG T TT		
GAM1394	USP9Y	5' TTCTGGTGGCTGTGTGGAGTA 64040	G	TG CG T TT
		TATT CACG GTC GCC GG		
		ATGA GTGT CGG TGG CT		
		G GT _ T TA		
GAM1394	USP9Y	5' TTCTGGTGGCTGTGTGGAGTA 64040	G	TG CG T TT
		TATT CACG GTC GCC GG		
		ATGA GTGT CGG TGG CT		
		G GT _ T TA		
GAM1394	VCAM1	3' GACTGGGTTTCTCTGTATAGTA 54770	C T TCC	TG
		TATTG ACG GG GGCC GTT		
		ATGAT TGT TC TTGG CAG		
		A C T_ GT		
GAM1394	VCAM1	3' GACTGGGTTTCTCTGTATAGTA 54770	C T TCC	TG
		TATTG ACG GG GGCC GTT		
		ATGAT TGT TC TTGG CAG		
		A C T_ GT		
GAM1394	VCAM1	3' GACTGGGTTTCTCTGTATAGTA 6546	C T TCC	TG
		TATTG ACG GG GGCC GTT		

		ATGAT TGT TC TTGG CAG	
		A C T__ GT	
GAM1394	VCAM1	3' GACTGGGTTTCTCTGTATAGTA 6546	C T TCC TG
		TATTG ACG GG GGCC GTT	
		ATGAT TGT TC TTGG CAG	
		A C T__ GT	
GAM1394	VDAC2	3' AACTGTGCAATTGTGTGCA 12584	TG CCG C
		TGCACG GT GC TGGTT	
		ACGTGT TA CG GTCAA	
		GT A__ T	
GAM1394	VDAC2	3' AACTGTGCAATTGTGTGCA 12584	TG CCG C
		TGCACG GT GC TGGTT	
		ACGTGT TA CG GTCAA	
		GT A__ T	
GAM1394	VENTX2	3' ACTCCTGACTGCGTGCA 27102	TG C CCT
		TGCACG GTC GG GGT	
		ACGTGC CAG CC TCA	
		GT T ____	
GAM1394	VENTX2	3' ACTCCTGACTGCGTGCA 27102	TG C CCT
		TGCACG GTC GG GGT	
		ACGTGC CAG CC TCA	
		GT T ____	
GAM1394	VHL	3' AATTAGGCGGGCGTGGTGGTG 5048	TG_ TG GT G
		TAT C ACG CC GCCTGGTT	
		GTG G TGC GG CGGATTAA	
		GT G ____ G	
GAM1394	VHL	3' AATTAGGCGGGCGTGGTGGTG 5048	TG_ TG GT G
		TAT C ACG CC GCCTGGTT	
		GTG G TGC GG CGGATTAA	
		GT G ____ G	
GAM1394	VIL2	3' GCTAAGATGCCATGTGCAG 12598	CC__
		TTGCACGTGGT GGC	
		GACGTGTACCG TCG	
		TAGAA	
GAM1394	VIL2	3' GCTAAGATGCCATGTGCAG 12598	CC__
		TTGCACGTGGT GGC	
		GACGTGTACCG TCG	
		TAGAA	
GAM1394	WASF3	3' TTGGCCGGCGGAGAGGCCGCGT 21830	_____ TG GTT
	GTGG	ACGTGGT CCGGCC	

			TGCGCCG	GGCCGG		
			GAGAGGC	TTG		
GAM1394	WASF3	3'	TTGGCCGGCGGAGAGGCCGCGT	21830	_____	TGGTT
			GTGG	ACGTGGT		CCGGCC
			TGCGCCG	GGCCGG		
			GAGAGGC	TTG		
GAM1394	WFS1	3'	GCCTGACTGTGTTCAAGT	20011	C TG C	
			TATTG	ACG GTC GGC		
			GTGAC	TGT CAG CCG		
			T	GT T		
GAM1394	WFS1	3'	GCCTGACTGTGTTCAAGT	20011	C TG C	
			TATTG	ACG GTC GGC		
			GTGAC	TGT CAG CCG		
			T	GT T		
GAM1394	WFS1	3'	GACCTTGCGACCATGTGTAG	20010	CG CT	
			TTGCACGTGGTC	GC GGTT		
			GATGTGTACCAG	CG CCAG		
			—	TT		
GAM1394	WFS1	3'	GACCTTGCGACCATGTGTAG	20010	CG CT	
			TTGCACGTGGTC	GC GGTT		
			GATGTGTACCAG	CG CCAG		
			—	TT		
GAM1394	WNT14	3'	GACCAGCCCAGCTGCGTG	GGGGT 12677	G TG CC C	
	A		TATT	CACG GT GGC TGGTT		
			ATGG	GTGC CG CCG ACCAG		
			G	GT AC —		
GAM1394	WNT14	3'	GACCAGCCCAGCTGCGTG	GGGGT 12677	G TG CC C	
	A		TATT	CACG GT GGC TGGTT		
			ATGG	GTGC CG CCG ACCAG		
			G	GT AC —		
GAM1394	WRN	5'	GCCGGGCCGGGGGCG	5096	GG	
			CGT	TCCGGCCTGGT		
			GCG	GGGCCGGGCCG		
			G_			
GAM1394	WRN	5'	GCCGGGCCGGGGGCG	5096	GG	
			CGT	TCCGGCCTGGT		
			GCG	GGGCCGGGCCG		
			G_			
GAM1394	WT1	3'	GGCCAGGGCATGTGTA	44355	G _	
			TGCACGTG	TCC GGCC		

		ATGTGTAC GGG CCGG		
		— A		
GAM1394 WT1	3'	GGCCAGGGCATGTGTA 44355	G	_
		TGCACGTG TCC GGCC		
		ATGTGTAC GGG CCGG		
		— A		
GAM1394 WT1	3'	GGCCAGGGCATGTGTA 44365	G	_
		TGCACGTG TCC GGCC		
		ATGTGTAC GGG CCGG		
		— A		
GAM1394 WT1	3'	GGCCAGGGCATGTGTA 44365	G	_
		TGCACGTG TCC GGCC		
		ATGTGTAC GGG CCGG		
		— A		
GAM1394 WT1	3'	GGCCAGGGCATGTGTA 44375	G	_
		TGCACGTG TCC GGCC		
		ATGTGTAC GGG CCGG		
		— A		
GAM1394 WT1	3'	GGCCAGGGCATGTGTA 4590	G	_
		TGCACGTG TCC GGCC		
		ATGTGTAC GGG CCGG		
		— A		
GAM1394 WT1	3'	GGCCAGGGCATGTGTA 4590	G	_
		TGCACGTG TCC GGCC		
		ATGTGTAC GGG CCGG		
		— A		
GAM1394 WT1	3'	GGCCAGGGCATGTGTA 44375	G	_
		TGCACGTG TCC GGCC		
		ATGTGTAC GGG CCGG		
		— A		
GAM1394 XPO1	3'	TGCAGCAAGATCATGTGCA 12684	CG C GTT	
		TGCACGTGGTC GC TG		
		ACGTGTACTAG CG AC		
		AA _ GTT		
GAM1394 XPO1	3'	TGCAGCAAGATCATGTGCA 12684	CG C GTT	
		TGCACGTGGTC GC TG		
		ACGTGTACTAG CG AC		
		AA _ GTT		
GAM1394 XRCC2	3'	GCTGGGCATGGTGGTG 18327	TG A G	
		TAT C CGTG TCCGGC		

			GTG G GTAC GGGTCG		
			GT _ _		
GAM1394	XRCC2	3'	GCTGGGCATGGTGGTG 18327	TG A G	
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGTCG		
			GT _ _		
GAM1394	YWHAG	3'	ATCAGGCTAGCTGTGC 25015	GT CC GT	
			GCAC GGT GGCCTG T		
			CGTG TCG TCGGAC A		
			_ A_ TG		
GAM1394	YWHAG	3'	ATCAGGCTAGCTGTGC 25015	GT CC GT	
			GCAC GGT GGCCTG T		
			CGTG TCG TCGGAC A		
			_ A_ TG		
GAM1394	ZNF136	3'	GGCTCTGGCTGGGTGTGGTG 59890	TG G C_	
			TAT CAC TGGTC G GCC		
			GTG GTG GTCGG C CGG		
			GT G T T		
GAM1394	ZNF136	3'	GGCTCTGGCTGGGTGTGGTG 59890	TG G C_	
			TAT CAC TGGTC G GCC		
			GTG GTG GTCGG C CGG		
			GT G T T		
GAM1394	ZNF219	5'	GCCGGGCGCGGGGGCG 33134	GG	
			CGT TCCGGCCTGGT		
			GCG GGGCCGGGCGG		
			G_		
GAM1394	ZNF219	5'	GCCGGGCGCGGGGGCG 33134	GG	
			CGT TCCGGCCTGGT		
			GCG GGGCCGGGCGG		
			G_		
GAM1394	ZNF36	3'	CTGAGGCCAGGTGCGGTG 93961	G _	
			TATTGCAC TGGTC CGG		
			GTGGCGTG ACCGG GTC		
			G A		
GAM1394	ZNF36	3'	CTGAGGCCAGGTGCGGTG 93961	G _	
			TATTGCAC TGGTC CGG		
			GTGGCGTG ACCGG GTC		
			G A		
GAM1394	ZNF36	5'	GGCCTAAGTCCGTGTGCGGTG 93965	TCC__	
			TATTGCACGTGG GGCC		

			GTGGCGTGTGCC	CCGG		
			TGAAT			
GAM1394	ZNF36	5'	GGCCTAAGTCCGTGTGCGGTG	93965	TCC__	
			TATTGCACGTGG	GGCC		
			GTGGCGTGTGCC	CCGG		
			TGAAT			
GAM1394	ZNF83	5'	AACCCGGAAGCGGATTATGTGG	36980	G	G__ T
		AGTG	ATT CACGTGGTCCG	CC GGTT		
			TGA GTGTATTAGGC	GG CCAA		
			G	GAA C		
GAM1394	ZNF83	5'	AACCCGGAAGCGGATTATGTGG	36980	G	G__ T
		AGTG	ATT CACGTGGTCCG	CC GGTT		
			TGA GTGTATTAGGC	GG CCAA		
			G	GAA C		
GAM1394	A	5'	GCTGGGTCCATCATGCAATG	39096	C_ _	
			TATTGCA	GTGG TCCGGC		
			GTAACGT	TACC GGGTCG		
			AC	T		
GAM1394	A	5'	GCTGGGTCCATCATGCAATG	39096	C_ _	
			TATTGCA	GTGG TCCGGC		
			GTAACGT	TACC GGGTCG		
			AC	T		
GAM1394	ADRM1	3'	CTGGGCGCTTGCAGTG	22797	C	G
			TATTGCA	GTG TCCGG		
			GTGACGT	CGC GGGTC		
			T	_		
GAM1394	ADRM1	3'	CTGGGCGCTTGCAGTG	22797	C	G
			TATTGCA	GTG TCCGG		
			GTGACGT	CGC GGGTC		
			T	_		
GAM1394	AFAP	3'	TGGCTGGGTTCATACTGTGAAA	41309	G	_ _ _ GT
		TA	TT CAC GT	G CCGGCC		TGGTT
			AA GTG CA	T GGTCGG		
			A	T TAC TG TT		
GAM1394	AFAP	3'	TGGCTGGGTTCATACTGTGAAA	41309	G	_ _ _ GT
		TA	TT CAC GT	G CCGGCC		TGGTT
			AA GTG CA	T GGTCGG		
			A	T TAC TG TT		
GAM1394	ALTE	3'	AGCTGGGCTGGGGAGGACGGT	16387	A	GG_ TG
			GC CGT	TCCGGCC GTT		

			TG GCA GGGTCGG CGA		
			_ GGAG GT		
GAM1394	ALTE	3'	AGCTGGGCTGGGGAGGACGGT 16387	A GG__	TG
			GC CGT TCCGGCC GTT		
			TG GCA GGGTCGG CGA		
			_ GGAG GT		
GAM1394	ALY	3'	GACCAGCAAATCCGCGTGCGG 19350	TCCG	C
			TTGCACGTGG GC TGGTT		
			GGCGTGCGCC CG ACCAG		
			TAAA _		
GAM1394	ALY	3'	GACCAGCAAATCCGCGTGCGG 19350	TCCG	C
			TTGCACGTGG GC TGGTT		
			GGCGTGCGCC CG ACCAG		
			TAAA _		
GAM1394	ANXA13	3'	AGCCAGGCCAAGCTGTGTAA 15040	GT	CC
			TTGCAC GGT GGCCTGGTT		
			AATGTG TCG CCGGACCGA		
			_ AA		
GAM1394	ANXA13	3'	AGCCAGGCCAAGCTGTGTAA 15040	GT	CC
			TTGCAC GGT GGCCTGGTT		
			AATGTG TCG CCGGACCGA		
			_ AA		
GAM1394	AP1GBP1	3'	GCCACTGCAGTGTGCAGTG 23396	TG	CC_
			TATTGCACG GT GGC		
			GTGACGTGT CG CCG		
			GA TCA		
GAM1394	AP1GBP1	3'	GCCACTGCAGTGTGCAGTG 54521	TG	CC_
			TATTGCACG GT GGC		
			GTGACGTGT CG CCG		
			GA TCA		
GAM1394	AP1GBP1	3'	GCCACTGCAGTGTGCAGTG 23396	TG	CC_
			TATTGCACG GT GGC		
			GTGACGTGT CG CCG		
			GA TCA		
GAM1394	AP1GBP1	3'	GCCACTGCAGTGTGCAGTG 54521	TG	CC_
			TATTGCACG GT GGC		
			GTGACGTGT CG CCG		
			GA TCA		
GAM1394	AP3S2	3'	GGCTAGATCTCAGGTGTGGTG 19521	TG	G _ CG
			TAT CAC TG GTC GCC		



		GTG GTG AC TAG CGG	
		GT G TC AT	
GAM1394 AP3S2	3'	GGCTAGATCTCAGGTGTGGTG 19521	TG G __ CG
		TAT CAC TG GTC GCC	
		GTG GTG AC TAG CGG	
		GT G TC AT	
GAM1394 APCL	3'	AGCTGGGCCTCCTGCGTGGGGT 19661	G TG TCC TG
G		TATT CACG G GGCC GTT	
		GTGG GTGC C CCGG CGA	
		G GT CT_ GT	
GAM1394 APCL	3'	AGCTGGGCCTCCTGCGTGGGGT 19661	G TG TCC TG
G		TATT CACG G GGCC GTT	
		GTGG GTGC C CCGG CGA	
		G GT CT_ GT	
GAM1394 APCL	3'	GGCAGCGGGCTGCGTACGATG 19679	C TG __
		TATTG ACG GTCCG GCC	
		GTAGC TGC CGGGC CGG	
		A GT GA	
GAM1394 APCL	3'	GGCAGCGGGCTGCGTACGATG 19679	C TG __
		TATTG ACG GTCCG GCC	
		GTAGC TGC CGGGC CGG	
		A GT GA	
GAM1394 APOF	3'	GCTATTAGCCAGGTGCGGTG 7910	G CC__
		TATTGCAC TGGT GGC	
		GTGGCGTG ACCG TCG	
		G ATTA	
GAM1394 APOF	3'	GCTATTAGCCAGGTGCGGTG 7910	G CC__
		TATTGCAC TGGT GGC	
		GTGGCGTG ACCG TCG	
		G ATTA	
GAM1394 ARHGAP5	3'	GGTTATATTTTGTGTAGTA 77078	TG CC
		TATTGCACG GT GGCC	
		ATGATGTGT TA TTGG	
		TT TA	
GAM1394 ARHGAP5	3'	GGTTATATTTTGTGTAGTA 77078	TG CC
		TATTGCACG GT GGCC	
		ATGATGTGT TA TTGG	
		TT TA	
GAM1394 ARHGAP8	5'	GGCTGCTGTGCTGGGTGCAGTG 31089	G TC CT
		TATTGCAC TGG CGGC GGTT	

			GTGACGTG GTC GTCG TCGG		
			G GT _		
GAM1394	ARHGAP8	5'	GGCTGCTGTGCTGGGTGCAGTG 31089	G TC CT	
			TATTGCAC TGG CGGC GGTT		
			GTGACGTG GTC GTCG TCGG		
			G GT _		
GAM1394	ARHU	5'	CGGGCCGGGCCCTGC 41073 CGT		
			GCA GGTCCGGCCTG		
			CGT CCGGGCCGGGC		
			C_		
GAM1394	ARHU	5'	CGGGCCGGGCCCTGC 41073 CGT		
			GCA GGTCCGGCCTG		
			CGT CCGGGCCGGGC		
			C_		
GAM1394	ARNTL2	3'	CCAGACCATGTTTAGTA 39459 C C		
			TATTG ACGTGGTC GG		
			ATGAT TGTACCAG CC		
			T A		
GAM1394	ARNTL2	3'	CCAGACCATGTTTAGTA 39459 C C		
			TATTG ACGTGGTC GG		
			ATGAT TGTACCAG CC		
			T A		
GAM1394	ASB10	3'	GCCGGGTGATGTCTGATG 55127 C GG		
			TATTG ACGT TCCGGC		
			GTAGT TGTA GGGCCG		
			C GT		
GAM1394	ASB10	3'	GCCGGGTGATGTCTGATG 55127 C GG		
			TATTG ACGT TCCGGC		
			GTAGT TGTA GGGCCG		
			C GT		
GAM1394	ATF3	3'	GGCTGTCACCACGTGCAGTA 14434 C_		
			TATTGCACGTGGT CGGCC		
			ATGACGTGCACCA GTCGG		
			CT		
GAM1394	ATF3	3'	GGCTGTCACCACGTGCAGTA 14434 C_		
			TATTGCACGTGGT CGGCC		
			ATGACGTGCACCA GTCGG		
			CT		
GAM1394	ATP5L	3'	GTGTTGTTGGACCATGTGTGAT 21357 TG CTGGTT		
			AT CACGTGGTCCGGC		

			TA GTGTACCAGGTTG		
			GT TTGTGA		
GAM1394	ATP5L	3'	GTGTTGTTGGACCATGTGTGAT 21357	TG	CTGGTT
			AT CACGTGGTCCGGC		
			TA GTGTACCAGGTTG		
			GT TTGTGA		
GAM1394	ATP9A	3'	ATATAGCTGGGCCATGTCAGTG 62036	C	CTGGTT
			TATTG ACGTGGTCCGGC		
			GTGAC TGTACCGGGTCG		
			— ATATAA		
GAM1394	ATP9A	3'	ATATAGCTGGGCCATGTCAGTG 62036	C	CTGGTT
			TATTG ACGTGGTCCGGC		
			GTGAC TGTACCGGGTCG		
			— ATATAA		
GAM1394	ATP9A	3'	GGCTGGGCATGCGTGCG 62046	—	
			TGCACGTG GTCCGGCC		
			GCGTGCGT CGGGTCGG		
			A		
GAM1394	ATP9A	3'	GGCTGGGCATGCGTGCG 62046	—	
			TGCACGTG GTCCGGCC		
			GCGTGCGT CGGGTCGG		
			A		
GAM1394	B3GNT6	3'	CGGGCTGGGTATGTG 22505	G	TG
			CACGTG TCCGGCC G		
			GTGTAT GGGTCGG C		
			— GT		
GAM1394	B3GNT6	3'	CGGGCTGGGTATGTG 22505	G	TG
			CACGTG TCCGGCC G		
			GTGTAT GGGTCGG C		
			— GT		
GAM1394	BA108L7.2	3'	AGCTAGGCCCCGAATGTACAAT 48253	C	GGTCC
	G		TATTG ACGT GGCCTGGTT		
			GTAAC TGTA CCGGATCGA		
			A AGCC_		
GAM1394	BA108L7.2	3'	AGCTAGGCCCCGAATGTACAAT 48253	C	GGTCC
	G		TATTG ACGT GGCCTGGTT		
			GTAAC TGTA CCGGATCGA		
			A AGCC_		
GAM1394	BANP	3'	GCCGGGCATGGTGGTG 66217	TG A	G
			TAT C CGTG TCCGGC		

			GTG G GTAC GGGCCG		
			GT _ _		
GAM1394 BANP	3'	GCCGGGCATGGTGGTG	66217	TG A G	
		TAT C CGTG TCCGGC			
		GTG G GTAC GGGCCG			
		GT _ _			
GAM1394 BIA2	3'	GACCTTAAGGCTGGGTGCAGTG	71282	GTGGT	___
		TATTGCAC CCGGCCT GGTT			
		GTGACGTG GGTCGGA CCAG			
		ATT			
GAM1394 BIA2	3'	GACCTTAAGGCTGGGTGCAGTG	71282	GTGGT	___
		TATTGCAC CCGGCCT GGTT			
		GTGACGTG GGTCGGA CCAG			
		ATT			
GAM1394 BICD2	3'	GGCTGGGTTGGACACCCACAGG	70398	AC	___ TG
T		GC GTGG TCCGGCC GTT			
		TG CACC AGGTTGG CGG			
		GA CAC GT			
GAM1394 BICD2	3'	GGCTGGGTTGGACACCCACAGG	70398	AC	___ TG
T		GC GTGG TCCGGCC GTT			
		TG CACC AGGTTGG CGG			
		GA CAC GT			
GAM1394 BIRC1	3'	AACCACTTATGACTGGGTGCGG	15784	G	CGGCC
TG		TATTGCAC TGGTC TGGTT			
		GTGGCGTG GTCAG ACCAA			
		G TATTC			
GAM1394 BIRC1	3'	AACCACTTATGACTGGGTGCGG	15784	G	CGGCC
TG		TATTGCAC TGGTC TGGTT			
		GTGGCGTG GTCAG ACCAA			
		G TATTC			
GAM1394 BPESC1	3'	ATTGGGCTGATGTGTAG	41469	GGTC	TG
		TTGCACGT CGGCC GT			
		GATGTGTA GTCGG TA			
		GT			
GAM1394 BPESC1	3'	ATTGGGCTGATGTGTAG	41469	GGTC	TG
		TTGCACGT CGGCC GT			
		GATGTGTA GTCGG TA			
		GT			
GAM1394 BRD3	3'	GACCAGGCTGGGCCTAAGCGA	23759	ACGT	
		TTGC GGTCCGGCCTGGTT			

			AGCG CCGGGTCGGACCAG	
			AAT_	
GAM1394 BRD3	3'	GACCAGGCTGGGCCTAAGCGA	23759	ACGT
		TTGC GGTCCGGCCTGGTT		
		AGCG CCGGGTCGGACCAG		
		AAT_		
GAM1394 BY55	5'	ACCAGGCCAGAGTGCAGTG	59343	GTGG C
		TATTGCAC TC GGCCTGGT		
		GTGACGTG AG CCGGACCA		
		_____ A		
GAM1394 BY55	5'	ACCAGGCCAGAGTGCAGTG	59343	GTGG C
		TATTGCAC TC GGCCTGGT		
		GTGACGTG AG CCGGACCA		
		_____ A		
GAM1394 C19orf7	3'	AGCTCCAGGATCCGTGCAGTG	61125	T _ CCT
		TATTGCACG GGTCC GG GGTT		
		GTGACGTGC CTAGG CC TCGA		
		_____ A _____		
GAM1394 C19orf7	3'	AGCTCCAGGATCCGTGCAGTG	61125	T _ CCT
		TATTGCACG GGTCC GG GGTT		
		GTGACGTGC CTAGG CC TCGA		
		_____ A _____		
GAM1394 C1orf16	3'	CTGGTTTTGTGTAGTA	29231	TG T
		TATTGCACG G CCGG		
		ATGATGTGT T GGTC		
		TT_		
GAM1394 C1orf16	3'	CTGGTTTTGTGTAGTA	29231	TG T
		TATTGCACG G CCGG		
		ATGATGTGT T GGTC		
		TT_		
GAM1394 C1orf17	3'	GACCAGTTTGCCATGTGGATA	68213	G CCGGC
		TATT CACGTGGT CTGGTT		
		ATAG GTGTACCG GACCAG		
		_____ TTT_		
GAM1394 C1orf17	3'	GACCAGTTTGCCATGTGGATA	68213	G CCGGC
		TATT CACGTGGT CTGGTT		
		ATAG GTGTACCG GACCAG		
		_____ TTT_		
GAM1394 C1orf24	3'	AATTAGGCTTAGACTGTGCAA	53700	GT C_
		TTGCAC GGTC GGCCTGGTT		

			AACGTG TCAG TCGGATTAA			
			___ AT			
GAM1394	C1orf24	3'	AATTAGGCTTAGACTGTGCAA 53700	GT	C_	
			TTGCAC GGTC GGCCTGGTT			
			AACGTG TCAG TCGGATTAA			
			___ AT			
GAM1394	C1orf34	3'	ATTAGGCTGGAGTCTGGTA 60662	A T	_	
			TGC CG GG TCCGGCCTGGT			
			ATG GT CT AGGTCGGATTA			
			_ _ G			
GAM1394	C1orf34	3'	ATTAGGCTGGAGTCTGGTA 60662	A T	_	
			TGC CG GG TCCGGCCTGGT			
			ATG GT CT AGGTCGGATTA			
			_ _ G			
GAM1394	C20orf139	3'	GGCTGGACCCACTGTAGTA 84758	C	_	
			TATTGCA GTGG TCCGGCC			
			ATGATGT CACC AGGTCGG			
			_ C			
GAM1394	C20orf139	3'	GGCTGGACCCACTGTAGTA 84758	C	_	
			TATTGCA GTGG TCCGGCC			
			ATGATGT CACC AGGTCGG			
			_ C			
GAM1394	C20orf142	3'	CTGGGCCAGGTGTAGTG 74774	G		
			TATTGCAC TGGTCCGG			
			GTGATGTG ACCGGGTC			
			G			
GAM1394	C20orf142	3'	CTGGGCCAGGTGTAGTG 74774	G		
			TATTGCAC TGGTCCGG			
			GTGATGTG ACCGGGTC			
			G			
GAM1394	C20orf161	3'	TGGCTGGGGTTGCCCTTGTGTA 53072	T_	____	TGGTT
	GTA		TGCACG GGT CCGGCC			
			ATGTGT CCG GGTCGG			
			TC TTGG TT			
GAM1394	C20orf161	3'	TGGCTGGGGTTGCCCTTGTGTA 53072	T_	____	TGGTT
	GTA		TGCACG GGT CCGGCC			
			ATGTGT CCG GGTCGG			
			TC TTGG TT			
GAM1394	C20orf21	3'	GATTGGGCTGGATGGTGT 35114	GTG	TG	
			GCAC GTCCGGCC GTT			

			TGTG TAGGTCGG TAG		
			G__ GT		
GAM1394	C20orf21	3'	GATTGGGCTGGATGGTGT 35114	GTG	TG
			GCAC GTCCGGCC GTT		
			TGTG TAGGTCGG TAG		
			G__ GT		
GAM1394	C22orf19	3'	GGCTGGGCATGGTGGTG 13428	TG A	G
			TAT C CGTG TCCGGCC		
			GTG G GTAC GGGTCGG		
			GT _ _		
GAM1394	C22orf19	3'	GGCTGGGCATGGTGGTG 13428	TG A	G
			TAT C CGTG TCCGGCC		
			GTG G GTAC GGGTCGG		
			GT _ _		
GAM1394	C22orf20	3'	GGCTGGCCCATGTGTGAT 47434	TG	T
			AT CACGTGG CCGGCC		
			TA GTGTACC GGTCGG		
			GT C		
GAM1394	C22orf20	3'	GGCTGGCCCATGTGTGAT 47434	TG	T
			AT CACGTGG CCGGCC		
			TA GTGTACC GGTCGG		
			GT C		
GAM1394	C3IP1	3'	CAGGCACCAGTGCAGTG 41281	G	CCG
			TATTGCAC TGGT GCCTG		
			GTGACGTG ACCA CGGAC		
			- -		
GAM1394	C3IP1	3'	CAGGCACCAGTGCAGTG 41281	G	CCG
			TATTGCAC TGGT GCCTG		
			GTGACGTG ACCA CGGAC		
			- -		
GAM1394	C6orf33	5'	GGCCGGGCTGGGCTACG 55883		
			CGTGGTCCGGCCTGGTT		
			GCATCGGGTCGGGCCGG		
			- -		
GAM1394	C6orf33	5'	GGCCGGGCTGGGCTACG 55883		
			CGTGGTCCGGCCTGGTT		
			GCATCGGGTCGGGCCGG		
			- -		
GAM1394	C6orf33	5'	GGCCGGGCTGGGCTACGCGCA 55884	A	
			TGC CGTGGTCCGGCCTGGTT		

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ACG GCATCGGGTCGGGCCGG
C
GAM1394 C6orf33 5' GGCCGGGCTGGGCTACGCGCA 55884 A
TGC CGTGGTCCGGCCTGGTT
||| |||||
ACG GCATCGGGTCGGGCCGG
C
GAM1394 C6orf5 3' GCCGGGCATGGTGGTG 31348 TG A G
TAT C CGTG TCCGGC
||| | ||| |||||
GTG G GTAC GGGCCG
GT _ _
GAM1394 C6orf5 3' GCCGGGCATGGTGGTG 31348 TG A G
TAT C CGTG TCCGGC
||| | ||| |||||
GTG G GTAC GGGCCG
GT _ _
GAM1394 C9orf12 3' GCCGGGCTGGGCAGTGTG 42792 TG
CACG GTCCGGCCTGGT
|||| |||||
GTGT CGGGTCGGGCCG
GA
GAM1394 C9orf12 3' GCCGGGCTGGGCAGTGTG 42792 TG
CACG GTCCGGCCTGGT
|||| |||||
GTGT CGGGTCGGGCCG
GA
GAM1394 C9orf5 3' GCCAGGCTGTAGGTG 49277 G GTC
CAC TG CGGCCTGGT
||| || |||||
GTG AT GTCGGACCG
G _ _
GAM1394 C9orf5 3' GCCAGGCTGTAGGTG 49277 G GTC
CAC TG CGGCCTGGT
||| || |||||
GTG AT GTCGGACCG
G _ _
GAM1394 C9orf5 3' GCTGGGCACGGTGGTG 49278 TG A G
TAT C CGTG TCCGGC
||| | ||| |||||
GTG G GCAC GGGTCG
GT _ _
GAM1394 C9orf5 3' GCTGGGCACGGTGGTG 49278 TG A G
TAT C CGTG TCCGGC
||| | ||| |||||
GTG G GCAC GGGTCG
GT _ _
GAM1394 CALN1 3' GGCTGGCCTGGCCACGTGTGGT 48873 TG C T
AT CACGTGGTC GGCC GGTT
|| ||||| ||| |||

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			TG GTGCACCGG CCGG TCGG		
			GT T _		
GAM1394	CALN1	3'	AGCATTAAAGGACCAGGTGCGGT 48852	G	GGCCTG
	G		TATTGCAC TGGTCC GTT		
			GTGGCGTG ACCAGG CGA		
			G AATTA_		
GAM1394	CALN1	3'	AGCATTAAAGGACCAGGTGCGGT 48852	G	GGCCTG
	G		TATTGCAC TGGTCC GTT		
			GTGGCGTG ACCAGG CGA		
			G AATTA_		
GAM1394	CALN1	3'	GGCTGGCCTGGCCACGTGTGGT 48873	TG	C T
			AT CACGTGGTC GGCC GGTT		
			TG GTGCACCGG CCGG TCGG		
			GT T _		
GAM1394	CARD6	3'	AGTGTGTTGGGATTACGTGT 50853	- -	
			GCACGTGGTCC GGC CT		
			TGTGCATTAGG TTG GA		
			G T		
GAM1394	CARD6	3'	AGTGTGTTGGGATTACGTGT 50853	- -	
			GCACGTGGTCC GGC CT		
			TGTGCATTAGG TTG GA		
			G T		
GAM1394	CAS1	3'	GCTATACCAAGTGTAATA 43204	G	CC
			TATTGCAC TGGT GGC		
			ATAATGTG ACCA TCG		
			_ TA		
GAM1394	CAS1	3'	GCTATACCAAGTGTAATA 43204	G	CC
			TATTGCAC TGGT GGC		
			ATAATGTG ACCA TCG		
			_ TA		
GAM1394	CCNA2	5'	GGCCGGGTCGGTGCGA 6945	G	GT
			TTGCAC TG CCGGCC		
			AGCGTG GC GGCCGG		
			_ TG		
GAM1394	CCNA2	5'	GGCCGGGTCGGTGCGA 6945	G	GT
			TTGCAC TG CCGGCC		
			AGCGTG GC GGCCGG		
			_ TG		
GAM1394	CDK5RAP3	5'	AACTGTGTTTGGGTTGGGTGTA 47277	G GG	_ C
	GTA		TATTGCAC T TCCGG C TGTT		

			ATGATGTG G GGGTT G GTCAA		
			G TT T T		
GAM1394	CDK5RAP3	5'	AACTGTGTTTGGGTTGGGTGTA 47277	G GG _ C	
			GTA TATTGCAC T TCCGG C TGGTT		
			ATGATGTG G GGGTT G GTCAA		
			G TT T T		
GAM1394	CGI-142	3'	TTGAGGCCATGTGTAA 32177	_	
			TTGCACGTGGTC CGG		
			AATGTGTACCGG GTT		
			A		
GAM1394	CGI-142	3'	TTGAGGCCATGTGTAA 32177	_	
			TTGCACGTGGTC CGG		
			AATGTGTACCGG GTT		
			A		
GAM1394	CGI-57	3'	GGCATGGGCCTGTGTGATG 73880	TG T _	
			TAT CACG GGTCCG GCC		
			GTA GTGT CCGGGT CGG		
			GT _ A		
GAM1394	CGI-57	3'	GGCATGGGCCTGTGTGATG 73880	TG T _	
			TAT CACG GGTCCG GCC		
			GTA GTGT CCGGGT CGG		
			GT _ A		
GAM1394	CGI-96	3'	TAGCTGGGCTGGGAGCATGTGT 31664	G_ TG	
			GCACGTG TCCGGCC GTT A		
			TGTGTAC GGGTCGG CGA T		
			GA GT		
GAM1394	CGI-96	3'	TAGCTGGGCTGGGAGCATGTGT 31664	G_ TG	
			GCACGTG TCCGGCC GTT A		
			TGTGTAC GGGTCGG CGA T		
			GA GT		
GAM1394	CHK	3'	GCCAGTCACTGCGTGCAA 7050	TG CC C T	
			TTGCACG GT GGC TGGT		
			AACGTGC CA CTG ACCG		
			GT _ _ C		
GAM1394	CHK	3'	GCCAGTCACTGCGTGCAA 7050	TG CC C T	
			TTGCACG GT GGC TGGT		
			AACGTGC CA CTG ACCG		
			GT _ _ C		
GAM1394	CHL1	3'	GATTGGGTTTGTATCTGTGGT 21748	TG C TCC TG	
	A		TAT CA GTGG GGCC GTT		

			ATG GT TATT TTGG TAG	
			GT C GT_ GT	
GAM1394	CHL1	3'	GATTGGGTTTGTATCTGTGGT 21748	TG C TCC TG
	A		TAT CA GTGG GGCC GTT	
			ATG GT TATT TTGG TAG	
			GT C GT_ GT	
GAM1394	CHST3	3'	GACCGTAGAGGCCAGGTGCGGT 14975	G T GGCC
	G		TATTGCAC TGG CC TGGTT	
			GTGGCGTG ACC GG GCCAG	
			G _ AGAT	
GAM1394	CHST3	3'	GACCGTAGAGGCCAGGTGCGGT 14975	G T GGCC
	G		TATTGCAC TGG CC TGGTT	
			GTGGCGTG ACC GG GCCAG	
			G _ AGAT	
GAM1394	CHUK	3'	AATCATGTTGTTGTGTGTA 7052	TG TC C
			TGCACG G CGGC TGGTT	
			ATGTGT T GTTG ACTAA	
			GT__ T	
GAM1394	CHUK	3'	AATCATGTTGTTGTGTGTA 7052	TG TC C
			TGCACG G CGGC TGGTT	
			ATGTGT T GTTG ACTAA	
			GT__ T	
GAM1394	CIC	3'	CATGTTGATCATGTGCAATA 30674	C C
			TATTGCACGTGGTC GGC TG	
			ATAACGTGTACTAG TTG AC	
			_ T	
GAM1394	CIC	3'	CATGTTGATCATGTGCAATA 30674	C C
			TATTGCACGTGGTC GGC TG	
			ATAACGTGTACTAG TTG AC	
			_ T	
GAM1394	CLPTM1	3'	GATCAGGCCCGGGCGGTGGGA 7100	G G G
			TT CAC TG TCCGGCCTGGTT	
			AG GTG GC GGGCCGGA CTAG	
			G _ G	
GAM1394	CLPTM1	3'	GATCAGGCCCGGGCGGTGGGA 7100	G G G
			TT CAC TG TCCGGCCTGGTT	
			AG GTG GC GGGCCGGA CTAG	
			G _ G	
GAM1394	CLSTN3	3'	CGGGGGGTTGGGTGTGGTG 28210	TG G GG GG
			TAT CAC T TCC CCTG	

			GTG GTG G GGG GGGC		
			GT G TT _		
GAM1394	CLSTN3	3'	CGGGGGGTTGGGTGTGGTG 28210	TG G GG GG	
			TAT CAC T TCC CCTG		
			GTG GTG G GGG GGGC		
			GT G TT _		
GAM1394	CNK2	3'	AACTGGGAAAGGGCTCTGTGTG 75960	TG T GG_ TG	
	GTA		TAT CACG GGTCC CC GTT		
			ATG GTGT TCGGG GG CAA		
			GT C AAA GT		
GAM1394	CNK2	3'	AACTGGGAAAGGGCTCTGTGTG 75960	TG T GG_ TG	
	GTA		TAT CACG GGTCC CC GTT		
			ATG GTGT TCGGG GG CAA		
			GT C AAA GT		
GAM1394	COQ7	3'	AGCCTCTAGGACTGTGAGCAAT 32328	A TG GGCCT	
	A		TATTGC CG GTCC GGTT		
			ATAACG GT CAGG CCGA		
			A GT ATCT_		
GAM1394	COQ7	3'	AGCCTCTAGGACTGTGAGCAAT 32328	A TG GGCCT	
	A		TATTGC CG GTCC GGTT		
			ATAACG GT CAGG CCGA		
			A GT ATCT_		
GAM1394	CPR2	3'	ATTAGGCCAGGTGTGGTG 48091	TG G GGTCC	
			TAT CAC T GGCCTGGT		
			GTG GTG A CCGGATTA		
			GT G _		
GAM1394	CPR2	3'	ATTAGGCCAGGTGTGGTG 48091	TG G GGTCC	
			TAT CAC T GGCCTGGT		
			GTG GTG A CCGGATTA		
			GT G _		
GAM1394	CPR2	3'	GTCGGCCAGGTGTGGTG 48102	TG G T	
			TAT CAC TGG CCGGC		
			GTG GTG ACC GGCTG		
			GT G _		
GAM1394	CPR2	3'	GTCGGCCAGGTGTGGTG 48102	TG G T	
			TAT CAC TGG CCGGC		
			GTG GTG ACC GGCTG		
			GT G _		
GAM1394	CSMD1	5'	AGCCATCGGTGTCGCGTGCG 52640	GT_ CC	
			TGCACGTG CCGG TGGTT		

			GCGTGCGC GGCT ACCGA		
			TGT _		
GAM1394 CSMD1	5'	AGCCATCGGTGTCGCGTGCG	52640	GT_ CC	
		TGCACGTG CCGG TGGTT			
		GCGTGCGC GGCT ACCGA			
		TGT _			
GAM1394 CSMD1	5'	AGCCATCGGTGTCGCGTGCG	73117	GT_ CC	
		TGCACGTG CCGG TGGTT			
		GCGTGCGC GGCT ACCGA			
		TGT _			
GAM1394 CSMD1	5'	AGCCATCGGTGTCGCGTGCG	73117	GT_ CC	
		TGCACGTG CCGG TGGTT			
		GCGTGCGC GGCT ACCGA			
		TGT _			
GAM1394 CTNNBIP1	5'	GGCCGGGTCGGGCGGC	39666	G	
		GT GTCCGGCCTGGTT			
		CG CGGGCTGGGCCGG			
		G			
GAM1394 CTNNBIP1	5'	GGCCGGGTCGGGCGGC	39666	G	
		GT GTCCGGCCTGGTT			
		CG CGGGCTGGGCCGG			
		G			
GAM1394 CYGB	5'	AGCCGGGCTGGGCTTGGAGC	56152	ACGT	
		GC GGTCCGGCCTGGTT			
		CG TCGGGTCGGGCCGA			
		AGGT			
GAM1394 CYGB	5'	AGCCGGGCTGGGCTTGGAGC	56152	ACGT	
		GC GGTCCGGCCTGGTT			
		CG TCGGGTCGGGCCGA			
		AGGT			
GAM1394 DCNP1	3'	GGTTTTGGGATTCTGTGTGGTG	55625	TG TG _	
		TAT CACG GTCC GGCC			
		GTG GTGT TAGG TTGG			
		GT CT GTT			
GAM1394 DCNP1	3'	GGTTTTGGGATTCTGTGTGGTG	55625	TG TG _	
		TAT CACG GTCC GGCC			
		GTG GTGT TAGG TTGG			
		GT CT GTT			
GAM1394 DDM36	3'	GGCTGGGTTGGGTGCAA	40574	G GG	
		TTGCAC T TCCGGCC			

			AACGTG G GGGTCGG		
			G TT		
GAM1394 DDM36	3'	GGCTGGGTTGGGTGCAA	40574	G GG	
		TTGCAC T TCCGGCC			
		AACGTG G GGGTCGG			
		G TT			
GAM1394 DDX12	3'	AACCTAGGCCGGTGTGTGGTG	59692	TG TGGT	_
		TAT CACG CCGGCCT GGTT			
		GTG GTGT GGCCGGA CCAA			
		GT _ T			
GAM1394 DDX12	3'	AACCTAGGCCGGTGTGTGGTG	59692	TG TGGT	_
		TAT CACG CCGGCCT GGTT			
		GTG GTGT GGCCGGA CCAA			
		GT _ T			
GAM1394 DDX17	5'	GCTGGGCTTGGTAGTA	48041	ACGT	
		TATTGC GGTCCGGC			
		ATGATG TCGGGTCG			
		GT_			
GAM1394 DDX17	5'	GCTGGGCTTGGTAGTA	48041	ACGT	
		TATTGC GGTCCGGC			
		ATGATG TCGGGTCG			
		GT_			
GAM1394 DDX35	3'	GGCCAAAACACCATGTGGGGTG	41640	G CC_	
		TATT CACGTGGT GGCC			
		GTGG GTGTACCA CCGG			
		G CAAAA			
GAM1394 DDX35	3'	GGCCAAAACACCATGTGGGGTG	41640	G CC_	
		TATT CACGTGGT GGCC			
		GTGG GTGTACCA CCGG			
		G CAAAA			
GAM1394 DGKD	3'	GACCGGGCTGGGTCTGCAG	59407	CGT GT	
		TTGCA G CCGGCCTGGTT			
		GACGT C GGTCGGGCCAG			
		_ TG			
GAM1394 DGKD	3'	CCATGGACCGTGTGTA	59399	GCC	
		TGCACGTGGTCCG TGG			
		ATGTGTGCCAGGT ACC			
		_			
GAM1394 DGKD	3'	CCATGGACCGTGTGTA	59399	GCC	
		TGCACGTGGTCCG TGG			

ATGTGTGCCAGGT ACC

GAM1394 DGKD 3' GACCGGGCTGGGTCTGCAG 59407 CGT GT  
TTGCA G CCGGCCTGGT  
|||| | |||||  
GACGT C GGTCGGGCCAG  
\_\_\_ TG

GAM1394 DIO2 3' TTAGGCTGAGGCAGTG 5837 GTG \_  
CAC GTC CGGCCTGG  
||| ||| |||||  
GTG CGG GTCGGATT  
A\_\_ A

GAM1394 DIO2 3' TTAGGCTGAGGCAGTG 25689 GTG \_  
CAC GTC CGGCCTGG  
||| ||| |||||  
GTG CGG GTCGGATT  
A\_\_ A

GAM1394 DIO2 3' TTAGGCTGAGGCAGTG 25689 GTG \_  
CAC GTC CGGCCTGG  
||| ||| |||||  
GTG CGG GTCGGATT  
A\_\_ A

GAM1394 DIO2 3' TTAGGCTGAGGCAGTG 5837 GTG \_  
CAC GTC CGGCCTGG  
||| ||| |||||  
GTG CGG GTCGGATT  
A\_\_ A

GAM1394 DJ102H19.4 5' ACTAGTGTGTGTAGTG 42005 TGGTCC \_  
TATTGCACG GGC CTGGT  
||||||| ||| |||||  
GTGATGTGT TTG GATCA  
\_\_\_\_\_ T

GAM1394 DJ102H19.4 5' ACTAGTGTGTGTAGTG 42005 TGGTCC \_  
TATTGCACG GGC CTGGT  
||||||| ||| |||||  
GTGATGTGT TTG GATCA  
\_\_\_\_\_ T

GAM1394 DJ122O8.2 3' TATGAGGTCGGGTGTAGTG 39994 GTGGT G T  
TATTGCAC CCGGCCT GT  
||||||| ||||| ||  
GTGATGTG GGCTGGA TA  
\_\_\_\_\_ G TC

GAM1394 DJ122O8.2 3' TATGAGGTCGGGTGTAGTG 39994 GTGGT G T  
TATTGCAC CCGGCCT GT  
||||||| ||||| ||  
GTGATGTG GGCTGGA TA  
\_\_\_\_\_ G TC

GAM1394 DJ667H12.2 5' GGCCGGGCCGGGACCCGCGAGT 38986 A \_  
GC CGTGG TCCGGCCTGGT  
|| ||||| |||||

		TG GCGCC GGGCCGGGCCGG		
		A CA		
GAM1394	DJ667H12.2 5'	GGCCGGGCGGGACCCGCGAGT	38986	A _
		GC CGTGG TCCGGCCTGGTT		
		TG GCGCC GGGCCGGGCCGG		
		A CA		
GAM1394	DKFZp434C0923 3'	GGTTGGGTCCCGTGTA	34218	T GT
		TTGCACG G CCGGCC		
		AATGTGC C GGTTGG		
		C TG		
GAM1394	DKFZp434C0923 3'	GGTTGGGTCCCGTGTA	34218	T GT
		TTGCACG G CCGGCC		
		AATGTGC C GGTTGG		
		C TG		
GAM1394	DKFZP434H0820 3'	AGCCAGGCTGGGGGTGC	63844	GTGG
		GCAC TCCGGCCTGGTT		
		CGTG GGGTCGGACCGA		
		G_		
GAM1394	DKFZP434H0820 3'	AGCCAGGCTGGGGGTGC	63844	GTGG
		GCAC TCCGGCCTGGTT		
		CGTG GGGTCGGACCGA		
		G_		
GAM1394	DKFZP434H132 3'	GCCAGTGCTGTGTGTA	31320	TGGTC _
		TGCACG CGGC CTGGT		
		ATGTGT GTCG GACCG		
		_ T		
GAM1394	DKFZP434H132 3'	GCCAGTGCTGTGTGTA	31320	TGGTC _
		TGCACG CGGC CTGGT		
		ATGTGT GTCG GACCG		
		_ T		
GAM1394	DKFZP434H132 3'	GCCAGTGCTGTGTGTA	73606	TGGTC _
		TGCACG CGGC CTGGT		
		ATGTGT GTCG GACCG		
		_ T		
GAM1394	DKFZP434H132 3'	GCCAGTGCTGTGTGTA	73606	TGGTC _
		TGCACG CGGC CTGGT		
		ATGTGT GTCG GACCG		
		_ T		
GAM1394	DKFZP434K046 3'	AACCGGGTTAATGATGCAATG	91757	_ GGTCCG
		TATTGCA CGT GCCTGGTT		



		GTAACGT GTA	TGGGCCAA	
		A AT____		
GAM1394	DKFZP434K046 3'	AACCGGGTTAATGATGCAATG	91757	_ GGTCCG
		TATTGCA CGT	GCCTGGTT	
		GTAACGT GTA	TGGGCCAA	
		A AT____		
GAM1394	DKFZP434K1772 3'	TTGGTCAGGCCCATGTGGTGGT	67718	TG _ T _ TGGTT
	G	AT C ACGTGG CC GGCC		
		TG G TGTACC GG CTGG		
		GT G C A TTG		
GAM1394	DKFZP434K1772 5'	GCCAGTGCTCCGTGCGGTG	67713	T GTCC _
		TATTGCACG G	GGC CTGGT	
		GTGGCGTGC C	TCG GACCG	
		_ _ _ _ T		
GAM1394	DKFZP434K1772 5'	GCCAGTGCTCCGTGCGGTG	67713	T GTCC _
		TATTGCACG G	GGC CTGGT	
		GTGGCGTGC C	TCG GACCG	
		_ _ _ _ T		
GAM1394	DKFZP434K1772 3'	TTGGTCAGGCCCATGTGGTGGT	67718	TG _ T _ TGGTT
	G	AT C ACGTGG CC GGCC		
		TG G TGTACC GG CTGG		
		GT G C A TTG		
GAM1394	DKFZP434P211 3'	ACCAGGTCCTCTGTGCA	27258	T TCC
		TGCACG GG	GGCCTGGT	
		ACGTGT TC	CTGGACCA	
		C _ _		
GAM1394	DKFZP434P211 3'	ACCAGGTCCTCTGTGCA	27258	T TCC
		TGCACG GG	GGCCTGGT	
		ACGTGT TC	CTGGACCA	
		C _ _		
GAM1394	DKFZP547E1010 5'	GCCAGGTCGGGGTATG	31542	G
		CGTG TCCGGCCTGGT		
		GTAT GGGCTGGACCG		
		G		
GAM1394	DKFZP547E1010 5'	GCCAGGTCGGGGTATG	31542	G
		CGTG TCCGGCCTGGT		
		GTAT GGGCTGGACCG		
		G		
GAM1394	DKFZP547E1010 5'	GCCAGGTCGGGGTATG	66935	G
		CGTG TCCGGCCTGGT		

		GTAT GGGCTGGACCG			
		G			
GAM1394	DKFZP547E1010 5'	GCCAGGTCGGGGTATG	66935	G	
		CGTG TCCGGCCTGGT			
		GTAT GGGCTGGACCG			
		G			
GAM1394	DKFZP564B1023 3'	ATTAGGCTGGGTGTGGTG	48537	TG	GTGGT
		TAT CAC CCGGCCTGGT			
		GTG GTG GGTCGGATTA			
		GT			
GAM1394	DKFZP564B1023 3'	ATTAGGCTGGGTGTGGTG	48537	TG	GTGGT
		TAT CAC CCGGCCTGGT			
		GTG GTG GGTCGGATTA			
		GT			
GAM1394	DKFZP564C186 3'	TGGGCTGGGCTGGGCTGGTGTG	72410	TG	G TG
	G	T CAC TGGTCCGGCC GTT			
		G GTG GTCGGGTCGG CGG			
		GT _ GT GTC			
GAM1394	DKFZP564C186 3'	TGGGCTGGGCTGGGCTGGTGTG	72410	TG	G TG
	G	T CAC TGGTCCGGCC GTT			
		G GTG GTCGGGTCGG CGG			
		GT _ GT GTC			
GAM1394	DKFZP564D0462 5'	TGTGATGGCGTGTCAGTA	70500	G	_
		TATTGCACGT GTC CG			
		ATGACGTGCG TAG GT			
		G T			
GAM1394	DKFZP564D0462 5'	TGTGATGGCGTGTCAGTA	70500	G	_
		TATTGCACGT GTC CG			
		ATGACGTGCG TAG GT			
		G T			
GAM1394	DKFZP566C243 3'	GCTGTAGCTGCGTGAGTA	31171	G	TG C_
		TATT CACG GT CGGC			
		ATGA GTGC CG GTCG			
		_ GT AT			
GAM1394	DKFZP566C243 3'	GCTGTAGCTGCGTGAGTA	31171	G	TG C_
		TATT CACG GT CGGC			
		ATGA GTGC CG GTCG			
		_ GT AT			
GAM1394	DKFZP566F2124 3'	TTAGATACGTGTAGTG	31575	G	CG
		TATTGCACGTG TC G			

		GTGATGTGCAT AG T		
		_ AT		
GAM1394	DKFZP566F2124 3'	TTAGATACGTGTAGTG	31575	G CG
		TATTGCACGTG TC G		
		GTGATGTGCAT AG T		
		_ AT		
GAM1394	DKFZp566H0824 3'	GGCCGGGTGCGGTG	34055	GTGGT
		TATTGCAC CCGGCC		
		GTGGCGTG GGCCGG		
		_____		
GAM1394	DKFZp566H0824 5'	AGCCGGGCATCCATTGTGTGTA	34044	TG CCG_
	A	TTGCACG GT GCCTGGTT		
		AATGTGT TA CGGGCCGA		
		GT CCTA		
GAM1394	DKFZp566H0824 5'	AGCCGGGCATCCATTGTGTGTA	34044	TG CCG_
	A	TTGCACG GT GCCTGGTT		
		AATGTGT TA CGGGCCGA		
		GT CCTA		
GAM1394	DKFZp566H0824 3'	GGCCGGGTGCGGTG	34055	GTGGT
		TATTGCAC CCGGCC		
		GTGGCGTG GGCCGG		
		_____		
GAM1394	DKFZP586D2223 3'	ACCTAGGCCCTGTGCAATG	37677	T TCCG _
		TATTGCACG GG GCCT GGT		
		GTAACGTGT CC CGGA CCA		
		_ _ _ T		
GAM1394	DKFZP586D2223 3'	ACCTAGGCCCTGTGCAATG	37677	T TCCG _
		TATTGCACG GG GCCT GGT		
		GTAACGTGT CC CGGA CCA		
		_ _ _ T		
GAM1394	DKFZP586D2223 3'	ATTGGGTTGGGCGCCGTG	37679	TG TG
		CACG GTCCGGCC GT		
		GTGC CGGGTTGG TA		
		CG GT		
GAM1394	DKFZP586D2223 3'	ATTGGGTTGGGCGCCGTG	37679	TG TG
		CACG GTCCGGCC GT		
		GTGC CGGGTTGG TA		
		CG GT		
GAM1394	DKFZp586H0623 3'	GCCAGCCAGGTGTAATA	34071	G CC
		TATTGCAC TGGT GGC		

		ATAATGTG ACCG CCG		
		G A_		
GAM1394	DKFZp586H0623 3'	GCCAGCCAGGTGTAATA	34071	G CC
		TATTGCAC TGGT GGC		
		ATAATGTG ACCG CCG		
		G A_		
GAM1394	DKFZP586N0721 5'	AGTCAACACGACCGCGTGT	31200	C GCC GT
		GCACGTGGTC G TG T		
		TGTGCGCCAG C AC A		
		_ACA TG		
GAM1394	DKFZP586N0721 5'	AGTCAACACGACCGCGTGT	31200	C GCC GT
		GCACGTGGTC G TG T		
		TGTGCGCCAG C AC A		
		_ACA TG		
GAM1394	DKFZP667O116 3'	GGTCAGGCGTGTGCA	94285	G C
		TGCACGTG TC GGCC		
		ACGTGTGC GG CTGG		
		_ A		
GAM1394	DKFZP667O116 3'	GGTCAGGCGTGTGCA	94285	G C
		TGCACGTG TC GGCC		
		ACGTGTGC GG CTGG		
		_ A		
GAM1394	DKFZP761E1824 3'	CCAGTTCTGTGCAATG	66437	TGGTCC GC
		TATTGCACG G CTGG		
		GTAACGTGT C GACC		
		_____ TT		
GAM1394	DKFZP761E1824 3'	CCAGTTCTGTGCAATG	66437	TGGTCC GC
		TATTGCACG G CTGG		
		GTAACGTGT C GACC		
		_____ TT		
GAM1394	DKFZP761I2123 3'	GCCCAGCCGTGTGTGGTG	48767	TG CC
		TAT CACGTGGT GGC		
		GTG GTGTGCCG CCG		
		GT AC		
GAM1394	DKFZP761I2123 3'	GCCCAGCCGTGTGTGGTG	48767	TG CC
		TAT CACGTGGT GGC		
		GTG GTGTGCCG CCG		
		GT AC		
GAM1394	DKFZp761K1423 5'	AATTGGTTCTTGACGTGCAGTG	37328	GGTCC GC TG
		TATTGCACGT G C GTT		

		GTGACGTGCA C G TAA	
		GTT__ TT GT	
GAM1394	DKFZp761K1423 5'	AATTGGTTCTTGACGTGCAGTG 37328	GGTCC GC TG
		TATTGCACGT G C GTT	
		GTGACGTGCA C G TAA	
		GTT__ TT GT	
GAM1394	DKFZp761K1824 3'	ACCAGCAATGTGTAGTA 34204	GGTCCGGC
		TATTGCACGT CTGGT	
		ATGATGTGTA GACCA	
		AC_____	
GAM1394	DKFZp761K1824 3'	ACCAGCAATGTGTAGTA 34204	GGTCCGGC
		TATTGCACGT CTGGT	
		ATGATGTGTA GACCA	
		AC_____	
GAM1394	DKFZp762K2015 3'	GATCGAATTGAGTTGTGTGCAA 72477	TG TC CC
	TG	TATTGCACG G CGG TGGT	
		GTAACGTGT T GTT GCTAG	
		GT GA AA	
GAM1394	DKFZp762K2015 3'	GATCGAATTGAGTTGTGTGCAA 72477	TG TC CC
	TG	TATTGCACG G CGG TGGT	
		GTAACGTGT T GTT GCTAG	
		GT GA AA	
GAM1394	DKFZp762L0311 3'	ACCAGGGTTGCTGTGGTG 38052	TG C GG CCGG
		TAT CA GT T CCTGGT	
		GTG GT CG G GGACCA	
		GT _ TT _____	
GAM1394	DKFZp762L0311 3'	ACCAGGGTTGCTGTGGTG 38052	TG C GG CCGG
		TAT CA GT T CCTGGT	
		GTG GT CG G GGACCA	
		GT _ TT _____	
GAM1394	DMWD 5'	TCTCAGCGGGTCAAGTGCAGTA 60882	G GT GC TT
		TATTGCAC TG CCG CTGG	
		ATGACGTG AC GGC GACT	
		A TG _ CTT	
GAM1394	DMWD 5'	TCTCAGCGGGTCAAGTGCAGTA 60882	G GT GC TT
		TATTGCAC TG CCG CTGG	
		ATGACGTG AC GGC GACT	
		A TG _ CTT	
GAM1394	DNAJA3 3'	ACTAGGCCGGGAAGCAGCA 60483	AC GG
		TGC GT TCCGGCCTGGT	

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ACG CG GGGCCGGATCA
A_ AA
GAM1394 DNAJA3 3' ACTAGGCCGGAAGCAGCA 60483 AC GG
TGC GT TCCGGCCTGGT
||| || |||||
ACG CG GGGCCGGATCA
A_ AA
GAM1394 DNAJC5 3' AGCTGAGGAGGAGGCTGTGTGT 61445 TG TG CGG_ _
GATG AT CACG GTC CCT GGTT
|| ||| || |||
TA GTGT CGG GGA TCGA
GT GT AGGA G
GAM1394 DNAJC5 3' AGCTGAGGAGGAGGCTGTGTGT 61445 TG TG CGG_ _
GATG AT CACG GTC CCT GGTT
|| ||| || |||
TA GTGT CGG GGA TCGA
GT GT AGGA G
GAM1394 DNAJC5 3' CAGGTTGGTCCAGTG 61449 G T
CAC TGG CCGGCCTG
||| ||| |||||
GTG ACC GGTTGGAC
_ T
GAM1394 DNAJC5 3' CAGGTTGGTCCAGTG 61449 G T
CAC TGG CCGGCCTG
||| ||| |||||
GTG ACC GGTTGGAC
_ T
GAM1394 DRCTNNB1A 5' GGCTGGGTTGTCAGTCAGTG 50842 C GT__ GT
TATTG AC G CCGGCC
||||| || | |||||
GTGAC TG T GGTCGG
_ ACTG TG
GAM1394 DRCTNNB1A 5' GGCTGGGTTGTCAGTCAGTG 50842 C GT__ GT
TATTG AC G CCGGCC
||||| || | |||||
GTGAC TG T GGTCGG
_ ACTG TG
GAM1394 DRF1 3' CTAGGCTGGGTGTGGTG 47029 TG GTGGT
TAT CAC CCGGCCTGG
||| ||| |||||
GTG GTG GGTCGGATC
GT ____
GAM1394 DRF1 3' CTAGGCTGGGTGTGGTG 47029 TG GTGGT
TAT CAC CCGGCCTGG
||| ||| |||||
GTG GTG GGTCGGATC
GT ____
GAM1394 DSCAML1 3' CCAGCGCCGTGTGCAATA 40359 TGGTC _
TATTGCACG CGGC CTGG
||||| ||| |||

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			ATAACGTGT	GCCG GACC		
			_____ C			
GAM1394	DSCAML1	3'	CCAGCGCCGTGTGCAATA	40359	TGGTC	_
			TATTGCACG	CGGC CTGG		
			ATAACGTGT	GCCG GACC		
			_____ C			
GAM1394	DVL2	3'	GCCAGGCTGGGCCGGGC	15360	ACGT	
			GC	GGTCCGGCCTGGT		
			CG	CCGGGTCGGACCG		
			GG__			
GAM1394	DVL2	3'	GCCAGGCTGGGCCGGGC	15360	ACGT	
			GC	GGTCCGGCCTGGT		
			CG	CCGGGTCGGACCG		
			GG__			
GAM1394	E1B-AP5	5'	GCCGGGCCGGGCTCG	22901	T	
			CG	GGTCCGGCCTGGT		
			GC	TCGGGCCGGGCCG		
			—			
GAM1394	E1B-AP5	5'	GCCGGGCCGGGCTCG	22901	T	
			CG	GGTCCGGCCTGGT		
			GC	TCGGGCCGGGCCG		
			—			
GAM1394	EDG2	5'	GGTTGGGGGCGCGCGTGCGA	7384		_ _
			TTGCACGTG	GTCC GGCC		
			AGCGTGCGC	CGGG TTGG		
			G	GG		
GAM1394	EDG2	5'	GGTTGGGGGCGCGCGTGCGA	7384		_ _
			TTGCACGTG	GTCC GGCC		
			AGCGTGCGC	CGGG TTGG		
			G	GG		
GAM1394	ELKS	5'	GGCTGGGCTGGGCAGGGCAA	30505	ACGTG	TG
			TTGC	GTCCGGCC GTT		
			AACG	CGGGTCGG CGG		
			GGA__	GT		
GAM1394	ELKS	5'	GGCTGGGCTGGGCAGGGCAA	30505	ACGTG	TG
			TTGC	GTCCGGCC GTT		
			AACG	CGGGTCGG CGG		
			GGA__	GT		
GAM1394	ELOVL1	3'	AACCACGGAGGCTGTGTGTA	43057	TG T GG	_
			TGCACG	G CC CC TGGTT		

		ATGTGT C GG GG ACCAA		
		GT _ A _ C		
GAM1394	ELOVL1	3' AACCACGGAGGCTGTGTGTA 43057	TG T GG _	
		TGCACG G CC CC TGGTT		
		ATGTGT C GG GG ACCAA		
		GT _ A _ C		
GAM1394	ENDO180	3' AACCAGGGCACGGGTGTGGTG 20139	TG GTGGT _ _	
		TAT CAC CCG GCC TGGTT		
		GTG GTG GGC CGG ACCAA		
		GT _ _ _ A G		
GAM1394	ENDO180	3' AACCAGGGCACGGGTGTGGTG 20139	TG GTGGT _ _	
		TAT CAC CCG GCC TGGTT		
		GTG GTG GGC CGG ACCAA		
		GT _ _ _ A G		
GAM1394	ENDO180	3' AGCTGGGCCGGGCTGGGATGTC 20140	C _ _ TG	
	A	TG ACGT GGTCCGCC GTT		
		AC TGTA TCGGGCCGG CGA		
		_ GGG GT		
GAM1394	ENDO180	3' AGCTGGGCCGGGCTGGGATGTC 20140	C _ _ TG	
	A	TG ACGT GGTCCGCC GTT		
		AC TGTA TCGGGCCGG CGA		
		_ GGG GT		
GAM1394	ERG-1	5' AGCTGGCTTATTGTGTGTGG 41841	TG TG CC T	
		T CACG GT GGCC GGTT		
		G GTGT TA TCGG TCGA		
		GT GT T _ _		
GAM1394	ERG-1	5' AGCTGGCTTATTGTGTGTGG 41841	TG TG CC T	
		T CACG GT GGCC GGTT		
		G GTGT TA TCGG TCGA		
		GT GT T _ _		
GAM1394	ERO1L	3' GATTGGGTTGTTTTTGTGTGTA 27431	TG TC_ TG	
	G	TTGCACG G CGGCC GTT		
		GATGTGT T GTTGG TAG		
		GT TTT GT		
GAM1394	ERO1L	3' GATTGGGTTGTTTTTGTGTGTA 27431	TG TC_ TG	
	G	TTGCACG G CGGCC GTT		
		GATGTGT T GTTGG TAG		
		GT TTT GT		
GAM1394	ESDN	3' GATCGTGCACCTTGTGTGGTA 55173	TG T CCG C	
		TAT CACG GGT GC TGGTT		



		ATG GTGT TCA CG GCTAG	
		GT T _ _ T	
GAM1394 ESDN	3'	GATCGTGCAC TTTGTGTGGTA 55173	TG T CCG C
		TAT CACG GGT GC TGGTT	
		ATG GTGT TCA CG GCTAG	
		GT T _ _ T	
GAM1394 ETAA16	5'	ACCGCCGCCCTGTGCAGTA 38650	T TC CT
		TATTGCACG GG CGGC GGT	
		ATGACGTGT CC GCCG CCA	
		_ C _ _	
GAM1394 ETAA16	5'	ACCGCCGCCCTGTGCAGTA 38650	T TC CT
		TATTGCACG GG CGGC GGT	
		ATGACGTGT CC GCCG CCA	
		_ C _ _	
GAM1394 FBXO9	3'	GTTGGCCAGGTGTGGTG 53105	TG G T
		TAT CAC TGG CCGGC	
		GTG GTG ACC GGTG	
		GT G _	
GAM1394 FBXO9	3'	GTTGGCCAGGTGTGGTG 53105	TG G T
		TAT CAC TGG CCGGC	
		GTG GTG ACC GGTG	
		GT G _	
GAM1394 FER1L4	3'	GGCCGGGCGGAGGTGCAAT 47358	G_
		ATTGCAC TGGTCCGGCC	
		TAACGTG GCCGGGCGCG	
		GA	
GAM1394 FER1L4	3'	GGCCGGGCGGAGGTGCAAT 47358	G_
		ATTGCAC TGGTCCGGCC	
		TAACGTG GCCGGGCGCG	
		GA	
GAM1394 FGD3	5'	ACCATCTACCGTGTGCAA 72895	CC CC
		TTGCACGTGGT GG TGGT	
		AACGTGTGCCA TC ACCA	
		_ T _	
GAM1394 FGD3	5'	ACCATCTACCGTGTGCAA 72895	CC CC
		TTGCACGTGGT GG TGGT	
		AACGTGTGCCA TC ACCA	
		_ T _	
GAM1394 FHOD2	5'	AGCCAGGTTACTGCGGCAGTA 73822	A TG CC
		TATTGC CG GT GGCCTGGTT	

		ATGACG GC CA TTGGACCGA		
		_ GT _		
GAM1394 FHOD2	5'	AGCCAGGTTACTGCGGCAGTA 73822	A TG CC	
		TATTGC CG GT GGCCTGGTT		
		ATGACG GC CA TTGGACCGA		
		_ GT _		
GAM1394 FKSG17	3'	GCTGGGCATGGTGGTG 49330	TG A G	
		TAT C CGTG TCCGGC		
		GTG G GTAC GGGTCG		
		GT _ _		
GAM1394 FKSG17	3'	GCTGGGCATGGTGGTG 49330	TG A G	
		TAT C CGTG TCCGGC		
		GTG G GTAC GGGTCG		
		GT _ _		
GAM1394 FLJ00001	3'	ACCAGGCCACTGTGCAGTG 81809	GT CC T	
		TATTGCAC GGT GGCCTGGT		
		GTGACGTG TCA CCGGACCA		
		_ _ C		
GAM1394 FLJ00001	3'	ACCAGGCCACTGTGCAGTG 81809	GT CC T	
		TATTGCAC GGT GGCCTGGT		
		GTGACGTG TCA CCGGACCA		
		_ _ C		
GAM1394 FLJ10043	3'	GCCGGGCATGGTAGTG 35760	A G	
		TATTGC CGTG TCCGGC		
		GTGATG GTAC GGGCCG		
		_ _		
GAM1394 FLJ10043	3'	GCCGGGCATGGTAGTG 35760	A G	
		TATTGC CGTG TCCGGC		
		GTGATG GTAC GGGCCG		
		_ _		
GAM1394 FLJ10060	3'	GACCTTTGTGGGATTTGTGCAA 35788	T G CT_	
TA		TATTGCACG GGTCC GC GGTT		
		ATAACGTGT TTAGG TG CCAG		
		_ G TTT		
GAM1394 FLJ10060	3'	GACCTTTGTGGGATTTGTGCAA 35788	T G CT_	
TA		TATTGCACG GGTCC GC GGTT		
		ATAACGTGT TTAGG TG CCAG		
		_ G TTT		
GAM1394 FLJ10350	5'	GGCCGGGCGGCGGCGGCGTG 95508	_	
		CACGT GGTCCGGCCTGGTT		

		GTGCG CCGGGCCGGGCCGG		
		GG		
GAM1394	FLJ10350	5' GGCCGGGCGCGGCCGGCGTG 95508	___	
		CACGT GGTCCGGCCTGGT		
		GTGCG CCGGGCCGGGCCGG		
		GG		
GAM1394	FLJ10460	3' ATTAGGCCGGGCGCAGTG 36125	G _	
		CAC TG GTCCGGCCTGGT		
		GTG AC CGGGCCGGATTA		
		_ G		
GAM1394	FLJ10460	3' ATTAGGCCGGGCGCAGTG 36125	G _	
		CAC TG GTCCGGCCTGGT		
		GTG AC CGGGCCGGATTA		
		_ G		
GAM1394	FLJ10597	3' GATCAAAGGCCGCGTGTAAAT 36316	T GGCC	
		ATTGCACGTGG CC TGGTT		
		TAATGTGCGCC GG ACTAG		
		_ AA__		
GAM1394	FLJ10597	3' GATCAAAGGCCGCGTGTAAAT 36316	T GGCC	
		ATTGCACGTGG CC TGGTT		
		TAATGTGCGCC GG ACTAG		
		_ AA__		
GAM1394	FLJ10713	3' GGTCAGAATTATTGTGTAATA 36469	TGG__ C	
		TATTGCACG TC GGCC		
		ATAATGTGT AG CTGG		
		TATTA A		
GAM1394	FLJ10713	3' GGTCAGAATTATTGTGTAATA 36469	TGG__ C	
		TATTGCACG TC GGCC		
		ATAATGTGT AG CTGG		
		TATTA A		
GAM1394	FLJ10715	5' GACTGGGTCGGAGGCCTGCGG 36476	C GG TG	
		TTGCA GT TCCGGCC GTT		
		GGCGT CG AGGCTGG CAG		
		C G_ GT		
GAM1394	FLJ10715	5' GACTGGGTCGGAGGCCTGCGG 36476	C GG TG	
		TTGCA GT TCCGGCC GTT		
		GGCGT CG AGGCTGG CAG		
		C G_ GT		
GAM1394	FLJ10748	3' TCCTTGATGGGCATGTGTGATG 36560	TG G GCCT TT	
		TAT CACGTG TCCG GG		

GTA GTGTAC GGGT CC  
 GT \_ AGTT TG  
 GAM1394 FLJ10748 3' TCCTTGATGGGCATGTGTGATG 36560 TG G GCCT TT  
 TAT CACGTG TCCG GG  
 ||| ||||| ||| ||  
 GTA GTGTAC GGGT CC  
 GT \_ AGTT TG  
 GAM1394 FLJ10811 3' GGGGGCCAGGTGTGGTG 36684 TG G GG  
 TAT CAC TGGTCC CC  
 ||| ||| ||||| ||  
 GTG GTG ACCGGG GG  
 GT G \_  
 GAM1394 FLJ10811 3' GGGGGCCAGGTGTGGTG 36684 TG G GG  
 TAT CAC TGGTCC CC  
 ||| ||| ||||| ||  
 GTG GTG ACCGGG GG  
 GT G \_  
 GAM1394 FLJ10847 3' TAGCTGGTGAAACTGCGTGCTG 36756 T TG \_\_\_\_ CTGGTT  
 TA T GCACG GT CCGGC  
 | ||||| || |||||  
 G CGTGC CA GGTCG  
 T GT AAGT A TT  
 GAM1394 FLJ10847 3' TAGCTGGTGAAACTGCGTGCTG 36756 T TG \_\_\_\_ CTGGTT  
 TA T GCACG GT CCGGC  
 | ||||| || |||||  
 G CGTGC CA GGTCG  
 T GT AAGT A TT  
 GAM1394 FLJ10932 3' GGCTGTGAACTTACGTGTGATG 36895 TG \_ \_  
 TAT CACGTGG TC CGGCC  
 ||| ||||| || |||||  
 GTA GTGCATT AG GTCGG  
 GT CA T  
 GAM1394 FLJ10932 3' GGCTGTGAACTTACGTGTGATG 36895 TG \_ \_  
 TAT CACGTGG TC CGGCC  
 ||| ||||| || |||||  
 GTA GTGCATT AG GTCGG  
 GT CA T  
 GAM1394 FLJ10986 5' GACATCTGGGCTGCGTGCTGTG 36943 T TG CCTG  
 TAT GCACG GTCCGG GTT  
 ||| ||||| ||||| |||  
 GTG CGTGC CGGGTC CAG  
 T GT TA\_\_  
 GAM1394 FLJ10986 5' GACATCTGGGCTGCGTGCTGTG 36943 T TG CCTG  
 TAT GCACG GTCCGG GTT  
 ||| ||||| ||||| |||  
 GTG CGTGC CGGGTC CAG  
 T GT TA\_\_  
 GAM1394 FLJ10989 3' TTAGGCTGGGTGCAGTG 36954 GTGGT  
 TATTGCAC CCGGCCTGG  
 ||||| |||||

GTGACGTG GGTCGGATT

GAM1394 FLJ10989 3' TTAGGCTGGGTGCAGTG 36954 GTGGT  
TATTGCAC CCGGCCTGG  
||||| |||||  
GTGACGTG GGTCGGATT

GAM1394 FLJ11088 3' AACTAAAGGGGTGTGTGTGGTG 37037 TG GT G GGCC  
TAT CAC G TCC TGGTT  
||| ||| ||| |||||  
GTG GTG T GGG ATCAA  
GT TG G AA\_\_

GAM1394 FLJ11088 3' AACTAAAGGGGTGTGTGTGGTG 37037 TG GT G GGCC  
TAT CAC G TCC TGGTT  
||| ||| ||| |||||  
GTG GTG T GGG ATCAA  
GT TG G AA\_\_

GAM1394 FLJ11101 3' AATCAGGCTGGATTTTAATGC 37048 CGT\_  
GCA GGTCCGGCCTGGTT  
||| |||||  
CGT TTAGGTCGGACTAA  
AATT

GAM1394 FLJ11101 3' AATCAGGCTGGATTTTAATGC 37048 CGT\_  
GCA GGTCCGGCCTGGTT  
||| |||||  
CGT TTAGGTCGGACTAA  
AATT

GAM1394 FLJ11274 5' GGCCCGGTGCGAGTGCAGTA 37200 G GT C  
TATTGCAC TG C GGCC  
||||| || |||  
ATGACGTG GC G CCGG  
A TG C

GAM1394 FLJ11274 5' GGCCCGGTGCGAGTGCAGTA 37200 G GT C  
TATTGCAC TG C GGCC  
||||| || |||  
ATGACGTG GC G CCGG  
A TG C

GAM1394 FLJ11370 3' AATTGGGTTGTGTGTGCA 46367 TGGTC TG  
TGCACG CGGCC GTT  
||||| ||||| |||  
ACGTGT GTTGG TAA  
GT\_\_ GT

GAM1394 FLJ11370 3' AATTGGGTTGTGTGTGCA 46367 TGGTC TG  
TGCACG CGGCC GTT  
||||| ||||| |||  
ACGTGT GTTGG TAA  
GT\_\_ GT

GAM1394 FLJ11577 3' GCTGGAAGTCATGTGTGA 47178 TG \_\_  
T CACGTGG TCCGGC  
| ||||| |||||

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      A GTGTACT AGGTCG
      GT   GA
GAM1394 FLJ11577 3' GCTGGAAGTCATGTGTGA 47178 TG   __
      T CACGTGG TCCGGC
      | ||||| |||||
      A GTGTACT AGGTCG
      GT   GA
GAM1394 FLJ11715 5' GGCCGGGCTGGATGCAG 44676   CG
      TTGCA TGGTCCGGCC
      |||| |||||
      GACGT GTCGGGCCGG
      AG
GAM1394 FLJ11715 5' GGCCGGGCTGGATGCAG 44676   CG
      TTGCA TGGTCCGGCC
      |||| |||||
      GACGT GTCGGGCCGG
      AG
GAM1394 FLJ11715 3' GCTGGGCATGGTGGTG 44675   TG A  G
      TAT C CGTG TCCGGC
      || | ||| |||||
      GTG G GTAC GGGTCG
      GT _ _
GAM1394 FLJ11715 3' GACTGGGGTTCGCTTTGTGTGA 44671   TG  T  CCGG TG
      TA      TAT CACG GGT  CC GTT
      || ||||| || |||
      ATA GTGT TCG  GG CAG
      GT  T  CTTG GT
GAM1394 FLJ11715 3' GACTGGGGTTCGCTTTGTGTGA 44671   TG  T  CCGG TG
      TA      TAT CACG GGT  CC GTT
      || ||||| || |||
      ATA GTGT TCG  GG CAG
      GT  T  CTTG GT
GAM1394 FLJ11715 3' GCTGGGCATGGTGGTG 44675   TG A  G
      TAT C CGTG TCCGGC
      || | ||| |||||
      GTG G GTAC GGGTCG
      GT _ _
GAM1394 FLJ12056 3' AGTCAGGAATCCACATGGTGTA 46250   __  TCCGG  GT
      ATA      TTGCAC GTGG  CCTG T
      ||||| |||  ||| |
      AATGTG CACC  GGAC A
      GTA  TAA__ TG
GAM1394 FLJ12056 3' AGTCAGGAATCCACATGGTGTA 46250   __  TCCGG  GT
      ATA      TTGCAC GTGG  CCTG T
      ||||| |||  ||| |
      AATGTG CACC  GGAC A
      GTA  TAA__ TG
GAM1394 FLJ12078 5' GTTGGGCATGGTAATG 46453   A  G
      TATTGC CGTG TCCGGC
      ||||| ||| |||||

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GTAATG GTAC GGGTTG

GAM1394 FLJ12078 5' GTTGGGCATGGTAATG 46453 A G  
TATTGC CGTG TCCGGC  
||||| ||| |||||  
GTAATG GTAC GGGTTG

GAM1394 FLJ12121 5' GCTGGGCCGACGACTGT 46457 C G TG  
GCA GT GTCCGGCC GT  
||| || ||||| ||  
TGT CA CAGGCCGG CG

GAM1394 FLJ12121 5' GCTGGGCCGACGACTGT 46457 C G TG  
GCA GT GTCCGGCC GT  
||| || ||||| ||  
TGT CA CAGGCCGG CG

GAM1394 FLJ12221 5' GGTCGGGGGTGGGTGCGGTA 62553 G G \_  
TATTGCAC TG TCC GGCC  
||||| || ||| ||||  
ATGGCGTG GT GGG CTGG  
G G G

GAM1394 FLJ12221 5' GGTCGGGGGTGGGTGCGGTA 62553 G G \_  
TATTGCAC TG TCC GGCC  
||||| || ||| ||||  
ATGGCGTG GT GGG CTGG  
G G G

GAM1394 FLJ12298 3' GCCGGGCATGGTGGTG 49665 TG A G  
TAT C CGTG TCCGGC  
||| | ||| |||||  
GTG G GTAC GGGCCG  
GT \_ \_

GAM1394 FLJ12298 3' GCCGGGCATGGTGGTG 49665 TG A G  
TAT C CGTG TCCGGC  
||| | ||| |||||  
GTG G GTAC GGGCCG  
GT \_ \_

GAM1394 FLJ12448 3' AGCTTGTGGCCGGGTGCAGTG 43175 GTGGT T\_\_  
TATTGCAC CCGGCC GGTT  
||||| ||||| ||||  
GTGACGTG GGCCGG TCGA  
TGT

GAM1394 FLJ12448 3' AGCTTGTGGCCGGGTGCAGTG 43175 GTGGT T\_\_  
TATTGCAC CCGGCC GGTT  
||||| ||||| ||||  
GTGACGTG GGCCGG TCGA  
TGT

GAM1394 FLJ12568 3' GATCACTTACAGGATCATGTTA 46499 C GGCC\_\_  
GTG ATTG ACGTGGTCC TGGTT  
||| ||||| ||||

			TGAT TGTACTAGG	ACTAG		
			—	ACATTC		
GAM1394	FLJ12568	3'	GATCACTTACAGGATCATGTTA	46499	C	GGCC__
			GTG	ATTG ACGTGGTCC	TGGTT	
			TGAT TGTACTAGG	ACTAG		
			—	ACATTC		
GAM1394	FLJ12610	3'	GGTTAAACTACCACGTGGGGTA	45516	G	CC__
			TATT CACGTGGT	GGCC		
			ATGG GTGCACCA	TTGG		
			G	TCAA		
GAM1394	FLJ12610	3'	GGTTAAACTACCACGTGGGGTA	45516	G	CC__
			TATT CACGTGGT	GGCC		
			ATGG GTGCACCA	TTGG		
			G	TCAA		
GAM1394	FLJ12783	3'	GGCCAGGTTGGGTTAACCCACT	48681	C	_____
			G	CA GTGG	TCCGGCCTGGTT	
			GT CACC	GGGTTGGACCGG		
			—	CAATT		
GAM1394	FLJ12783	3'	GGCCAGGTTGGGTTAACCCACT	48681	C	_____
			G	CA GTGG	TCCGGCCTGGTT	
			GT CACC	GGGTTGGACCGG		
			—	CAATT		
GAM1394	FLJ12816	3'	GACATGGCTGGACCATGGTGAT	41934	TG A	TG
			A	TAT C CGTGGTCCGGCC	GTT	
			ATA G GTACCAGGTCGG	CAG		
			GT_	TA		
GAM1394	FLJ12816	3'	GACATGGCTGGACCATGGTGAT	41934	TG A	TG
			A	TAT C CGTGGTCCGGCC	GTT	
			ATA G GTACCAGGTCGG	CAG		
			GT_	TA		
GAM1394	FLJ12875	5'	GGTTAGGCCGGGGGGGTGCGGT	44610	GTGG	GG
			ATTGCAC	TCCGGCCT TT		
			TGGCGTG	GGGCCGGA GG		
			GGG_	TT		
GAM1394	FLJ12875	5'	GGTTAGGCCGGGGGGGTGCGGT	44610	GTGG	GG
			ATTGCAC	TCCGGCCT TT		
			TGGCGTG	GGGCCGGA GG		
			GGG_	TT		
GAM1394	FLJ12985	3'	ATTAGGCCAGGTGCGGTG	46237	G GGTCC	
			TATTGCAC T	GGCCTGGT		



			GTGGCGTG A	CCGGATTA		
			G _____			
GAM1394	FLJ12985	3'	ATTAGGCCAGGTGCGGTG	46237	G GGTCC	
			TATTGCAC T	GGCCTGGT		
			GTGGCGTG A	CCGGATTA		
			G _____			
GAM1394	FLJ13072	3'	ACCAGGCCGCCGTCCAGTG	89797	G TC__	
			CAC TGG	CGGCCTGGT		
			GTG ACC	GCCGGACCA		
			_ TGCC			
GAM1394	FLJ13072	3'	ACCAGGCCGCCGTCCAGTG	89797	G TC__	
			CAC TGG	CGGCCTGGT		
			GTG ACC	GCCGGACCA		
			_ TGCC			
GAM1394	FLJ13089	5'	GCGGGGCCATGTGCAG	70862	G	
			TTGCACGTGGTCC GC			
			GACGTGTACCGGG CG			
			G			
GAM1394	FLJ13089	5'	GCGGGGCCATGTGCAG	70862	G	
			TTGCACGTGGTCC GC			
			GACGTGTACCGGG CG			
			G			
GAM1394	FLJ13110	3'	GGCCACCGAAACCACGTGAGTG	43304	G C_ CC	
			TATT CACGTGGT	CGG TGGTT		
			GTGA GTGCACCA	GCC ACCGG		
			_ AA _			
GAM1394	FLJ13110	3'	GGCCACCGAAACCACGTGAGTG	43304	G C_ CC	
			TATT CACGTGGT	CGG TGGTT		
			GTGA GTGCACCA	GCC ACCGG		
			_ AA _			
GAM1394	FLJ13181	5'	TGGTCGGCGCTTGTGCGGTGTG	47242	TG ____ _ TGGTT	
		G	CACGTG	GT CCGGCC		
			GTGCGC	CG GGCTGG		
			GT TGTT C	TT		
GAM1394	FLJ13181	5'	TGGTCGGCGCTTGTGCGGTGTG	47242	TG ____ _ TGGTT	
		G	CACGTG	GT CCGGCC		
			GTGCGC	CG GGCTGG		
			GT TGTT C	TT		
GAM1394	FLJ13197	3'	GACCCTCGCGGACCGTGTGTGA	44853	TG GCCT	
			T CACGTGGTCCG	GTTT		

		A GTGTGCCAGGC CCAG		
		GT GCTC		
GAM1394	FLJ13197	3' GACCCTCGCGGACCGTGTGTGA 44853	TG	GCCT
		T CACGTGGTCCG GGTT		
		A GTGTGCCAGGC CCAG		
		GT GCTC		
GAM1394	FLJ13224	5' AGCCGGGCGCTGCCTACGTGCA 45620	_	CCG
	G	TTGCACGT GGT GCCTGGTT		
		GACGTGCA CCG CGGGCCGA		
		T TCG		
GAM1394	FLJ13224	5' AGCCGGGCGCTGCCTACGTGCA 45620	_	CCG
	G	TTGCACGT GGT GCCTGGTT		
		GACGTGCA CCG CGGGCCGA		
		T TCG		
GAM1394	FLJ13265	3' GCCGGGTCGTCGTGCGG 45927	_	GT
		TTGCACG TG CCGGC		
		GGCGTGC GC GGCCG		
		T TG		
GAM1394	FLJ13265	3' GCCGGGTCGTCGTGCGG 45927	_	GT
		TTGCACG TG CCGGC		
		GGCGTGC GC GGCCG		
		T TG		
GAM1394	FLJ13544	3' AGCCCTCTGGCTGGGTGCGGTG 46574	G T	CCT
		TATTGCAC TGG CCGG GGTT		
		GTGGCGTG GTC GGTC CCGA		
		G _ TC_		
GAM1394	FLJ13544	3' AGCCCTCTGGCTGGGTGCGGTG 46574	G T	CCT
		TATTGCAC TGG CCGG GGTT		
		GTGGCGTG GTC GGTC CCGA		
		G _ TC_		
GAM1394	FLJ13590	5' ATCAGGCTTGAGTGCAGTG 45783	GTGG	C
		TATTGCAC TC GGCCTGGT		
		GTGACGTG AG TCGGACTA		
		_____ T		
GAM1394	FLJ13590	5' ATCAGGCTTGAGTGCAGTG 45783	GTGG	C
		TATTGCAC TC GGCCTGGT		
		GTGACGTG AG TCGGACTA		
		_____ T		
GAM1394	FLJ13659	3' TCTGGCTGGGTGCGGTG 47250	GTGGT	T
		TATTGCAC CCGGCC GG		

			GTGGCGTG	GGTCGG CT	
			_____ T		
GAM1394	FLJ13659	3'	TCTGGCTGGGTGCGGTG	47250	GTGGT T
			TATTGCAC	CCGGCC GG	
			GTGGCGTG	GGTCGG CT	
			_____ T		
GAM1394	FLJ13693	3'	AGCTGGAGGACTTGTGCAGTG	45646	T GG T
			TATTGCACG	GGTCC CC GGTT	
			GTGACGTGT	TCAGG GG TCGA	
			_____ A_		
GAM1394	FLJ13693	3'	AGCTGGAGGACTTGTGCAGTG	45646	T GG T
			TATTGCACG	GGTCC CC GGTT	
			GTGACGTGT	TCAGG GG TCGA	
			_____ A_		
GAM1394	FLJ13852	3'	GGCCAGGTCTGCGGCAGTG	43578	A TG T _
			TATTGC CG	G CC GGCC	
			GTGACG GC	C GG CCGG	
			_____ GT T A		
GAM1394	FLJ13852	3'	GGCCAGGTCTGCGGCAGTG	43578	A TG T _
			TATTGC CG	G CC GGCC	
			GTGACG GC	C GG CCGG	
			_____ GT T A		
GAM1394	FLJ13952	3'	GCCGGGCATTGTGGTGGTG	45616	TG A TG CCG
			TAT C CG	GT GCCTGGT	
			GTG G GT	TA CGGGCCG	
			GT_ GT	_____	
GAM1394	FLJ13952	3'	GCCGGGCATTGTGGTGGTG	45616	TG A TG CCG
			TAT C CG	GT GCCTGGT	
			GTG G GT	TA CGGGCCG	
			GT_ GT	_____	
GAM1394	FLJ13984	3'	GTTAGGCCAGGTGCAATG	45454	G CG
			TATTGCAC	TGGTC GC	
			GTAACGTG	ACCGG TG	
			G	AT	
GAM1394	FLJ13984	3'	GTTAGGCCAGGTGCAATG	45454	G CG
			TATTGCAC	TGGTC GC	
			GTAACGTG	ACCGG TG	
			G	AT	
GAM1394	FLJ14009	3'	GACTGGTCGCCATCACGTGTAA	45411	C_ T
	TA		TATTGCACGTGGT	CGGCC GGTT	

ATAATGTGCACTA GCTGG TCAG  
 CC \_  
 GAM1394 FLJ14009 3' GACTGGTCGCCATCACGTGTAA 45411 C\_ T  
 TA TATTGCACGTGGT CGGCC GGTT  
 ||||| |||| ||||  
 ATAATGTGCACTA GCTGG TCAG  
 CC \_  
 GAM1394 FLJ14084 3' GACTGTGAGATTGTGTGTGG 41298 TG TG CG CT  
 T CACG GTC GC GGTT  
 | ||| || || ||||  
 G GTGT TAG TG TCAG  
 GT GT AG \_  
 GAM1394 FLJ14084 3' GACTGTGAGATTGTGTGTGG 41298 TG TG CG CT  
 T CACG GTC GC GGTT  
 | ||| || || ||||  
 G GTGT TAG TG TCAG  
 GT GT AG \_  
 GAM1394 FLJ14107 3' TGGGCCGTGCGCGGTG 46701 A  
 TATTGC CGTGGTCCG  
 ||||| |||||  
 GTGGCG GTGCCGGGT  
 C  
 GAM1394 FLJ14107 3' TGGGCCGTGCGCGGTG 46701 A  
 TATTGC CGTGGTCCG  
 ||||| |||||  
 GTGGCG GTGCCGGGT  
 C  
 GAM1394 FLJ14129 3' ACTTGCCGGGTGCGGTG 48063 GTGGT T  
 TATTGCAC CCGGCC GGT  
 ||||| ||||| |||  
 GTGGCGTG GGCCGG TCA  
 \_ T  
 GAM1394 FLJ14129 3' ACTTGCCGGGTGCGGTG 48063 GTGGT T  
 TATTGCAC CCGGCC GGT  
 ||||| ||||| |||  
 GTGGCGTG GGCCGG TCA  
 \_ T  
 GAM1394 FLJ14490 3' GCTGGGCCGGGCCCCCGT 51400 T\_ TG  
 ACG GGTCCGGCC GT  
 || ||||| ||  
 TGC CCGGGCCGG CG  
 CC GT  
 GAM1394 FLJ14490 3' GCTGGGCCGGGCCCCCGT 51400 T\_ TG  
 ACG GGTCCGGCC GT  
 || ||||| ||  
 TGC CCGGGCCGG CG  
 CC GT  
 GAM1394 FLJ14668 3' TGGCCCCTGAGGCTGTGTGTAA 51515 TG \_ TGTT  
 TTGCACG GTC C GGCC  
 ||||| ||| |||

		AATGTGT CGG G CCGG		
		GT A TCC TT		
GAM1394	FLJ14668	3' TGGCCCCTGAGGCTGTGTGTAA 51515	TG _ _ _	TGGTT
		TTGCACG GTC C GGCC		
		AATGTGT CGG G CCGG		
		GT A TCC TT		
GAM1394	FLJ14906	3' TTGAGCTTTGTGTAATA 51693	T TC	
		TATTGCACG GG CGG		
		ATAATGTGT TC GTT		
		T GA		
GAM1394	FLJ14906	3' TTGAGCTTTGTGTAATA 51693	T TC	
		TATTGCACG GG CGG		
		ATAATGTGT TC GTT		
		T GA		
GAM1394	FLJ14950	3' GGCCAAGCTGGGTGTGGTA 51724	TG G CC	
		TAT CAC TGGT GGCC		
		ATG GTG GTCG CCGG		
		GT G AA		
GAM1394	FLJ14950	3' GGCCAAGCTGGGTGTGGTA 51724	TG G CC	
		TAT CAC TGGT GGCC		
		ATG GTG GTCG CCGG		
		GT G AA		
GAM1394	FLJ20004	3' GCTGGGCCTGGTGGTG 95296	TG A T	
		TAT C CG GGTCCGGC		
		GTG G GT CCGGGTCG		
		GT _ _		
GAM1394	FLJ20004	3' GCTGGGCCTGGTGGTG 95296	TG A T	
		TAT C CG GGTCCGGC		
		GTG G GT CCGGGTCG		
		GT _ _		
GAM1394	FLJ20034	3' GTCAGGCTGGGACAGTG 34381	G GT	GT
		CAC TG CCGGCCTG T		
		GTG AC GGTCGGAC G		
		_ AG TG		
GAM1394	FLJ20034	3' GTCAGGCTGGGACAGTG 34381	G GT	GT
		CAC TG CCGGCCTG T		
		GTG AC GGTCGGAC G		
		_ AG TG		
GAM1394	FLJ20034	3' GGCTGTGTCATGTGCGG 34379	TC	
		TTGCACGTGG CGGCC		

		GGCGTGTACT GTCGG	
		GT	
GAM1394	FLJ20034	3' GGCTGTGTCATGTGCGG 34379	TC
		TTGCACGTGG CGGCC	
		GGCGTGTACT GTCGG	
		GT	
GAM1394	FLJ20055	3' AATTAGCAGCCAGGTGCAGTG 34438	G CCG C
		TATTGCAC TGGT GC TGGTT	
		GTGACGTG ACCG CG ATTAA	
		G A__ _	
GAM1394	FLJ20055	3' AATTAGCAGCCAGGTGCAGTG 34438	G CCG C
		TATTGCAC TGGT GC TGGTT	
		GTGACGTG ACCG CG ATTAA	
		G A__ _	
GAM1394	FLJ20139	3' AATCTCTTGACTGGGTGCGGTG 34619	G C CCT
		TATTGCAC TGGTC GG GGTT	
		GTGGCGTG GTCAG TC CTAA	
		G T T__	
GAM1394	FLJ20139	3' AATCTCTTGACTGGGTGCGGTG 34619	G C CCT
		TATTGCAC TGGTC GG GGTT	
		GTGGCGTG GTCAG TC CTAA	
		G T T__	
GAM1394	FLJ20170	3' AATCAGTTGAGGTCAGTGTGAT 34670	TG G GT_ C
	A	TAT CAC TG C CGGC TGGTT	
		ATA GTG AC G GTTG ACTAA	
		GT _ TG A _	
GAM1394	FLJ20170	3' AATCAGTTGAGGTCAGTGTGAT 34670	TG G GT_ C
	A	TAT CAC TG C CGGC TGGTT	
		ATA GTG AC G GTTG ACTAA	
		GT _ TG A _	
GAM1394	FLJ20202	3' GGTTGAGCTCTGTGCAGTA 34730	T TC
		TATTGCACG GG CGGCC	
		ATGACGTGT TC GTTGG	
		C GA	
GAM1394	FLJ20202	3' GGTTGAGCTCTGTGCAGTA 34730	T TC
		TATTGCACG GG CGGCC	
		ATGACGTGT TC GTTGG	
		C GA	
GAM1394	FLJ20308	3' TGGCTGCTGAGGGGCTAGTGCA 66858	G _____ TGGTT
	GTG	GCAC TGGTCC GGCC	

			CGTG ATCGGG	TCGG		
			—	GAGTCG	TT	
GAM1394	FLJ20308	3'	TGGCTGCTGAGGGGCTAGTGCA	66858	G	_____ TGGTT
			GTG	GCAC TGGTCC	GGCC	
			CGTG ATCGGG	TCGG		
			—	GAGTCG	TT	
GAM1394	FLJ20452	3'	AATCACTAAAGGCCAGGTGCAG	35194	G	CGGCC
			TG	TATTGCAC TGGTC	TGGTT	
			GTGACGTG ACCGG	ACTAA		
			G	AAATC		
GAM1394	FLJ20452	3'	AATCACTAAAGGCCAGGTGCAG	35194	G	CGGCC
			TG	TATTGCAC TGGTC	TGGTT	
			GTGACGTG ACCGG	ACTAA		
			G	AAATC		
GAM1394	FLJ20464	3'	ACTAGGCCGGGCGCAGTG	35226	G	_
			CAC TG GTCCGGCCTGGT			
			GTG AC CGGGCCGGATCA			
			_	G		
GAM1394	FLJ20464	3'	ACTAGGCCGGGCGCAGTG	35226	G	_
			CAC TG GTCCGGCCTGGT			
			GTG AC CGGGCCGGATCA			
			_	G		
GAM1394	FLJ20489	3'	GGCCAGGTTGGGCACCTG	35252	C	G
			CA GTG TCCGGCCTGGTT			
			GT CAC GGGTTGGACCGG			
			C	_		
GAM1394	FLJ20489	3'	GGCCAGGTTGGGCACCTG	35252	C	G
			CA GTG TCCGGCCTGGTT			
			GT CAC GGGTTGGACCGG			
			C	_		
GAM1394	FLJ20546	3'	GCTGGGCATGGTGGTG	35369	TG A	G
			TAT C CGTG TCCGGC			
			GTG G GTAC GGGTCG			
			GT	_ _		
GAM1394	FLJ20546	3'	GCTGGGCATGGTGGTG	35369	TG A	G
			TAT C CGTG TCCGGC			
			GTG G GTAC GGGTCG			
			GT	_ _		
GAM1394	FLJ20546	3'	AGGCTGGGTGCGGTG	35364		GTGGT
			TATTGCAC	CCGGCCT		

GTGGCGTG GGTCGGA

GAM1394 FLJ20546 3' AGGCTGGGTGCGGTG 35364 GTGGT  
TATTGCAC CCGGCCT  
||||| |||||  
GTGGCGTG GGTCGGA

GAM1394 FLJ20584 5' GACTGGGCCGGGGTCTGCAG 35427 CGTGG TG  
TTGCA TCCGGCC GTT  
|||| ||||| ||  
GACGT GGGCCGG CAG  
CTG\_\_ GT

GAM1394 FLJ20584 5' GACTGGGCCGGGGTCTGCAG 35427 CGTGG TG  
TTGCA TCCGGCC GTT  
|||| ||||| ||  
GACGT GGGCCGG CAG  
CTG\_\_ GT

GAM1394 FLJ20666 3' ACTGCAAATCATGTCAGTG 35507 C CCG CT  
TATTG ACGTGGT GC GGT  
|||| ||||| || ||  
GTGAC TGACTA CG TCA  
\_ AA\_ \_

GAM1394 FLJ20666 3' ACTGCAAATCATGTCAGTG 35507 C CCG CT  
TATTG ACGTGGT GC GGT  
|||| ||||| || ||  
GTGAC TGACTA CG TCA  
\_ AA\_ \_

GAM1394 FLJ20666 3' ACTGCAAATCATGTCAGTG 37087 C CCG CT  
TATTG ACGTGGT GC GGT  
|||| ||||| || ||  
GTGAC TGACTA CG TCA  
\_ AA\_ \_

GAM1394 FLJ20666 3' ACTGCAAATCATGTCAGTG 37087 C CCG CT  
TATTG ACGTGGT GC GGT  
|||| ||||| || ||  
GTGAC TGACTA CG TCA  
\_ AA\_ \_

GAM1394 FLJ20695 3' TAGCTGGGCCTACAGTGT 35560 \_ \_ CTGGTT  
GCAC GT GGTCCGGC  
||| || |||||  
TGTG CA CCGGGTCG  
A T A TT

GAM1394 FLJ20695 3' TAGCTGGGCCTACAGTGT 35560 \_ \_ CTGGTT  
GCAC GT GGTCCGGC  
||| || |||||  
TGTG CA CCGGGTCG  
A T A TT

GAM1394 FLJ20700 3' ATTAGGCCGGGTGCCGTG 35571 TG  
CACG GTCCGGCCTGGT  
||| |||||



			GTGC TGGGCCGGATTA			
			CG			
GAM1394	FLJ20700	3'	ATTAGGCCGGGTGCCGTG 35571	TG		
			CACG GTCCGGCCTGGT			
			GTGC TGGGCCGGATTA			
			CG			
GAM1394	FLJ20793	3'	AGTCAGGTAGAAGATACATGTG 91802	TG	_	CG__ GT
			TGATA CACGTG GTC GCCTG T			
			GTGTAC TAG TGGAC A			
			GT A AAGA TG			
GAM1394	FLJ20793	3'	AGTCAGGTAGAAGATACATGTG 91802	TG	_	CG__ GT
			TGATA CACGTG GTC GCCTG T			
			GTGTAC TAG TGGAC A			
			GT A AAGA TG			
GAM1394	FLJ21162	3'	TTGGGCTGGGTGCAGTG 45899	GTGGT		TG
			TATTGCAC CCGGCC G			
			GTGACGTG GGTCGG T			
			_____ GT			
GAM1394	FLJ21162	3'	TTGGGCTGGGTGCAGTG 45899	GTGGT		TG
			TATTGCAC CCGGCC G			
			GTGACGTG GGTCGG T			
			_____ GT			
GAM1394	FLJ21272	3'	ACTGTGGCTGGGTGTGGTG 46732	TG	GTGGT	_
			TAT CAC CCGGCC TGGT			
			GTG GTG GGTCGG GTCA			
			GT _____ T			
GAM1394	FLJ21272	3'	ACTGTGGCTGGGTGTGGTG 46732	TG	GTGGT	_
			TAT CAC CCGGCC TGGT			
			GTG GTG GGTCGG GTCA			
			GT _____ T			
GAM1394	FLJ21313	3'	TGTAGGTGGACTATGTTAGTA 43693	C	G	GTT
			TATTG ACGTGGTCCG CCTG			
			ATGAT TGTATCAGGT GGAT			
			_____ GTC			
GAM1394	FLJ21313	3'	TGTAGGTGGACTATGTTAGTA 43693	C	G	GTT
			TATTG ACGTGGTCCG CCTG			
			ATGAT TGTATCAGGT GGAT			
			_____ GTC			
GAM1394	FLJ21415	3'	GGCCGGGCTCACGGTGGTG 45356	TG	A	_
			TAT C CGTG GTCCGGCC			

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GTG G GCAC CGGGCCGG
GT _ T
GAM1394 FLJ21415 3' GGCCGGGCTCACGGTGGTG 45356 TG A _
TAT C CGTG GTCCGGCC
||| | ||| |||||
GTG G GCAC CGGGCCGG
GT _ T
GAM1394 FLJ21438 3' GGCTGGGCCGGGCACTGAGATA 61525 TG C G TG
TAT CA GTG TCCGGCC GTT
||| || ||| ||||| |||
ATA GT CAC GGGCCGG CGG
GA _ _ GT
GAM1394 FLJ21438 3' GGCTGGGCCGGGCACTGAGATA 61525 TG C G TG
TAT CA GTG TCCGGCC GTT
||| || ||| ||||| |||
ATA GT CAC GGGCCGG CGG
GA _ _ GT
GAM1394 FLJ21817 3' CTGGGCACGTGTTGTG 42387 T G
TAT GCACGTG TCCGG
||| ||||| |||||
GTG TGTGCAC GGGTC
T _
GAM1394 FLJ21817 3' CTGGGCACGTGTTGTG 42387 T G
TAT GCACGTG TCCGG
||| ||||| |||||
GTG TGTGCAC GGGTC
T _
GAM1394 FLJ22104 3' CTGGATCACTGTAGTG 43350 C
TATTGCA GTGGTCCGG
||||| |||||
GTGATGT CACTAGGTC
_
GAM1394 FLJ22104 3' CTGGATCACTGTAGTG 43350 C
TATTGCA GTGGTCCGG
||||| |||||
GTGATGT CACTAGGTC
_
GAM1394 FLJ22215 3' GGTCAGACTCCCACGTGTGA 43094 TG _ C
T CACGTGG TC GGCC
| ||||| || |||
A GTGCACC AG CTGG
GT CTC A
GAM1394 FLJ22215 3' GGTCAGACTCCCACGTGTGA 43094 TG _ C
T CACGTGG TC GGCC
| ||||| || |||
A GTGCACC AG CTGG
GT CTC A
GAM1394 FLJ22215 5' GGTCAGACTCCCACGTGTGA 96838 TG _ C
T CACGTGG TC GGCC
| ||||| || |||

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A GTGCACC AG CTGG  
 GT CTC A  
 GAM1394 FLJ22215 5' GGTCAGACTCCCACGTGTGA 96838 TG \_\_\_\_ C  
 T CACGTGG TC GGCC  
 | ||||| || |||  
 A GTGCACC AG CTGG  
 GT CTC A  
 GAM1394 FLJ22378 3' GGCCGGGCTGAGGCTGTGCA 46903 GT \_  
 TGCAC GGTC CGGCCTGGTT  
 |||| ||| |||||  
 ACGTG TCGG GTCGGGCCGG  
 \_\_\_\_ A  
 GAM1394 FLJ22378 3' GGCCGGGCTGAGGCTGTGCA 46903 GT \_  
 TGCAC GGTC CGGCCTGGTT  
 |||| ||| |||||  
 ACGTG TCGG GTCGGGCCGG  
 \_\_\_\_ A  
 GAM1394 FLJ22477 3' GATAGACTGGGTCGTGTGTGA 45344 TG GT C GTT  
 T CACGTG CCGG CTG  
 | ||||| ||| |||  
 A GTGTGC GGTC GAT  
 GT TG A AG  
 GAM1394 FLJ22477 3' GATAGACTGGGTCGTGTGTGA 45344 TG GT C GTT  
 T CACGTG CCGG CTG  
 | ||||| ||| |||  
 A GTGTGC GGTC GAT  
 GT TG A AG  
 GAM1394 FLJ22615 3' GGTGCAGGGCTGCGTGCA 68518 TG G \_  
 TGCACG GTCC GC CT  
 ||||| ||| || ||  
 ACGTGC CGGG CG GG  
 GT A T  
 GAM1394 FLJ22615 3' GGTGCAGGGCTGCGTGCA 68518 TG G \_  
 TGCACG GTCC GC CT  
 ||||| ||| || ||  
 ACGTGC CGGG CG GG  
 GT A T  
 GAM1394 FLJ22944 5' CTGTACTGCAGTGTAGTA 47123 \_TG C  
 TATTGCAC G GT CGG  
 ||||| | || |||  
 ATGATGTG C CA GTC  
 A GT T  
 GAM1394 FLJ22944 5' CTGTACTGCAGTGTAGTA 47123 \_TG C  
 TATTGCAC G GT CGG  
 ||||| | || |||  
 ATGATGTG C CA GTC  
 A GT T  
 GAM1394 FLJ23017 3' AGCCAGGTTGGA CTAGTTGGGG 43121 A\_ \_  
 CA TGC CG TGGTCCGGCCTGGTT  
 ||| || |||||

ACG GT ATCAGGTTGGACCGA  
 GG TG  
 GAM1394 FLJ23017 3' AGCCAGGTTGGA TAGTTGGGG 43121 A\_ \_\_  
 CA TGC CG TGGTCCGGCCTGGTT  
 ||| || |||||  
 ACG GT ATCAGGTTGGACCGA  
 GG TG  
 GAM1394 FLJ23022 3' GGCTGTGGTCTGTGCAGTG 46812 T GT\_  
 TATTGCACG G C CGGCC  
 ||||| | ||||  
 GTGACGTGT C G GTCGG  
 \_TG T  
 GAM1394 FLJ23022 3' GGCTGTGGTCTGTGCAGTG 46812 T GT\_  
 TATTGCACG G C CGGCC  
 ||||| | ||||  
 GTGACGTGT C G GTCGG  
 \_TG T  
 GAM1394 FLJ23042 3' AACTTTATGCCGGGCCAGGTGT 47165 TG G CT\_  
 GGTG AT CAC TGGTCCGGC GGTT  
 || ||||| ||||  
 TG GTG ACCGGGCCG TCAA  
 GT G TATT  
 GAM1394 FLJ23042 3' AACTTTATGCCGGGCCAGGTGT 47165 TG G CT\_  
 GGTG AT CAC TGGTCCGGC GGTT  
 || ||||| ||||  
 TG GTG ACCGGGCCG TCAA  
 GT G TATT  
 GAM1394 FLJ23042 3' AGCCAGAGCTTCCATGTGCCAT 47168 T TCC \_  
 G TAT GCACGTGG GGC CTGGTT  
 ||| ||||| ||| |||||  
 GTA CGTGTACC TCG GACCGA  
 C T\_\_ A  
 GAM1394 FLJ23042 3' AGCCAGAGCTTCCATGTGCCAT 47168 T TCC \_  
 G TAT GCACGTGG GGC CTGGTT  
 ||| ||||| ||| |||||  
 GTA CGTGTACC TCG GACCGA  
 C T\_\_ A  
 GAM1394 FLJ23047 3' GGCTGGCTCTGTTGGTGCGGTG 44624 \_\_TG T\_  
 TATTGCAC G G CCGGCC  
 ||||| | | |||||  
 GTGGCGTG T C GGTCCG  
 GT GT TC  
 GAM1394 FLJ23047 3' GGCTGGCTCTGTTGGTGCGGTG 44624 \_\_TG T\_  
 TATTGCAC G G CCGGCC  
 ||||| | | |||||  
 GTGGCGTG T C GGTCCG  
 GT GT TC  
 GAM1394 FLJ23056 3' GACTAGGTTGGGTCAC 44722 GT  
 GTG CCGGCCTGGTT  
 ||| |||||

		CAC GGTGGATCAG			
		TG			
GAM1394	FLJ23056	3' GACTAGGTTGGGTCAC	44722	GT	
		GTG CCGGCCTGGTT			
		CAC GGTGGATCAG			
		TG			
GAM1394	FLJ23323	3' AGCTGGGGTTCTGCTGTGTGT	45049	TG CC _TG	
		GCACG GT GGC C GTT			
		TGTGT CG TTG G CGA			
		GT TC G GT			
GAM1394	FLJ23323	3' AGCTGGGGTTCTGCTGTGTGT	45049	TG CC _TG	
		GCACG GT GGC C GTT			
		TGTGT CG TTG G CGA			
		GT TC G GT			
GAM1394	FLJ23416	3' GCTGGGACCACATGTGTAA	49952	— —	
		TTGCAC GTGGTCC GGC			
		AATGTG CACCAGG TCG			
		TA G			
GAM1394	FLJ23416	3' GCTGGGACCACATGTGTAA	49952	— —	
		TTGCAC GTGGTCC GGC			
		AATGTG CACCAGG TCG			
		TA G			
GAM1394	FLJ23476	3' CTCAGGTGGCTGCGTGTGGTG	44960	TG TG CG TT	
		TAT CACG GTC GCCTGG			
		GTG GTGC CGG TGGACT			
		GT GT _ CT			
GAM1394	FLJ23476	3' CTCAGGTGGCTGCGTGTGGTG	44960	TG TG CG TT	
		TAT CACG GTC GCCTGG			
		GTG GTGC CGG TGGACT			
		GT GT _ CT			
GAM1394	FLJ23510	3' GGCTGGCTAATGTGCAGTG	45285	_ T	
		TATTGCACGT GG CCGGCC			
		GTGACGTGTA TC GGTCGG			
		A _			
GAM1394	FLJ23510	3' GGCTGGCTAATGTGCAGTG	45285	_ T	
		TATTGCACGT GG CCGGCC			
		GTGACGTGTA TC GGTCGG			
		A _			
GAM1394	FLJ23519	5' TGGCCGGGCGCCAGGCGTGTG	69210	TG _ _ TGGTT	
	G	CACGT GGT CCGGCC			

		GTGCG CCG GGCCGG		
		GT GAC CG TT		
GAM1394	FLJ23519	5' TGGCCGGGCGCCCAGGCGTGTG 69210	TG	___ _ TGGTT
	G	CACGT GGT CCGGCC		
		GTGCG CCG GGCCGG		
		GT GAC CG TT		
GAM1394	FLJ23537	3' AATCAGGCTGGACGTGGTG 46020	GTG	
		CAC GTCCGGCCTGGTT		
		GTG CAGGTCGGAATA		
		GTG		
GAM1394	FLJ23537	3' AATCAGGCTGGACGTGGTG 46020	GTG	
		CAC GTCCGGCCTGGTT		
		GTG CAGGTCGGAATA		
		GTG		
GAM1394	FLJ23556	3' GACTAGGCTGGGCAACAAAGCA 45949	AC_ G	
	A	TTGC GTGTCCGGCCTGGTT		
		AACG CA CGGGTCGGATCAG		
		AAA A		
GAM1394	FLJ23556	3' GACTAGGCTGGGCAACAAAGCA 45949	AC_ G	
	A	TTGC GTGTCCGGCCTGGTT		
		AACG CA CGGGTCGGATCAG		
		AAA A		
GAM1394	FLJ25359	5' AACTCAGAGGCCAGTGTGATG 58074	TG G CGGC _	
		TAT CAC TGGTC CTG GTT		
		GTA GTG ACCGG GAC CAA		
		GT _ A_ T		
GAM1394	FLJ25359	5' AACTCAGAGGCCAGTGTGATG 58074	TG G CGGC _	
		TAT CAC TGGTC CTG GTT		
		GTA GTG ACCGG GAC CAA		
		GT _ A_ T		
GAM1394	FLJ25461	3' GCTGTATCAGTGCAATG 58635	G C	
		TATTGCAC TGGT CGGC		
		GTAACGTG ACTA GTCG		
		_ T		
GAM1394	FLJ25461	3' GCTGTATCAGTGCAATG 58635	G C	
		TATTGCAC TGGT CGGC		
		GTAACGTG ACTA GTCG		
		_ T		
GAM1394	FLJ30567	3' CTGGAATATTGCAGTG 58826	C	
		TATTGCA GTGGTCCGG		

GTGACGT TATCAGGTC

GAM1394 FLJ30567 3' CTGGACTATTGCAGTG 58826 C  
TATTGCA GTGGTCCGG  
||||| |||||||  
GTGACGT TATCAGGTC

GAM1394 FLJ30655 5' GGCTGTAGATGCCGCGTGAGTA 58308 G C\_\_\_\_  
TATT CACGTGGT CGGCC  
||| ||||||| ||||  
ATGA GTGCGCCG GTCGG

— TAGAT  
GAM1394 FLJ30655 5' GGCTGTAGATGCCGCGTGAGTA 58308 G C\_\_\_\_  
TATT CACGTGGT CGGCC  
||| ||||||| ||||  
ATGA GTGCGCCG GTCGG

— TAGAT  
GAM1394 FLJ31455 3' GCTGGGCATGGTGGTG 58626 TG A G  
TAT C CGTG TCCGGC  
||| | ||| |||||||  
GTG G GTAC GGGTCG  
GT \_ \_

GAM1394 FLJ31455 3' GCTGGGCATGGTGGTG 58626 TG A G  
TAT C CGTG TCCGGC  
||| | ||| |||||||  
GTG G GTAC GGGTCG  
GT \_ \_

GAM1394 FLJ32784 3' GCTGTGGGCCACGGTGGTG 58228 TG A \_\_\_\_  
TAT C CGTGGTCC GGC  
||| | ||||||| |||  
GTG G GCACCGGG TCG  
GT \_ TG

GAM1394 FLJ32784 3' GCTGTGGGCCACGGTGGTG 58228 TG A \_\_\_\_  
TAT C CGTGGTCC GGC  
||| | ||||||| |||  
GTG G GCACCGGG TCG  
GT \_ TG

GAM1394 FLJ32978 3' GACTGTCAGAACATGTGCAGTA 58230 G C CT  
TATTGCACGTG TC GGC GGTT  
||||||||| || ||| ||||  
ATGACGTGTAC AG CTG TCAG  
A A \_\_\_\_

GAM1394 FLJ32978 3' GACTGTCAGAACATGTGCAGTA 58230 G C CT  
TATTGCACGTG TC GGC GGTT  
||||||||| || ||| ||||  
ATGACGTGTAC AG CTG TCAG  
A A \_\_\_\_

GAM1394 FLJ32978 3' GTCATGCTATGTGTTGTA 58233 T CC  
TAT GCACGTGGT GGC  
||| ||||||| |||

			ATG TGTGTATCG CTG		
			T TA		
GAM1394	FLJ32978	3'	GTCATGCTATGTGTTGTA 58233	T	CC
			TAT GCACGTGGT GGC		
			ATG TGTGTATCG CTG		
			T TA		
GAM1394	FLN29	3'	GATTGGGCCCCAGGTGT 21983	G	TCC TG
			GCAC TGG GGCC GTT		
			TGTG ACC CCGG TAG		
			G _ GT		
GAM1394	FLN29	3'	GATTGGGCCCCAGGTGT 21983	G	TCC TG
			GCAC TGG GGCC GTT		
			TGTG ACC CCGG TAG		
			G _ GT		
GAM1394	FUSIP1	3'	CTGGTTTATTGTGCAGTG 21774	_	T
			TATTGCACG TGG CCGG		
			GTGACGTGT ATT GGTC		
			T T		
GAM1394	FUSIP1	3'	CTGGTTTATTGTGCAGTG 21774	_	T
			TATTGCACG TGG CCGG		
			GTGACGTGT ATT GGTC		
			T T		
GAM1394	GBL	3'	GGCCAGGCTGGGCCAGGTCGG 42337	C	G
			TTG AC TGGTCCGGCCTGGTT		
			GGC TG ACCGGGTCGGACCGG		
			_ G		
GAM1394	GBL	3'	GGCCAGGCTGGGCCAGGTCGG 42337	C	G
			TTG AC TGGTCCGGCCTGGTT		
			GGC TG ACCGGGTCGGACCGG		
			_ G		
GAM1394	GCHFR	5'	GCCAGGCCGGGACGCGTG 17923		GT
			CACGTG CCGGCCTGGT		
			GTGCGC GGCCGGACCG		
			AG		
GAM1394	GCHFR	5'	GCCAGGCCGGGACGCGTG 17923		GT
			CACGTG CCGGCCTGGT		
			GTGCGC GGCCGGACCG		
			AG		
GAM1394	GDF10	5'	AGCCGGGCCGGGCGCGCAGTG 17113	_	_
			CAC GTG GTCCGGCCTGGTT		



			GTG CGC CGGGCCGGGCCGA		
			A G		
GAM1394	GDF10	5'	AGCCGGGCGGCGCGCAGTG 17113	_ _	
			CAC GTG GTCCGGCCTGGTT		
			GTG CGC CGGGCCGGGCCGA		
			A G		
GAM1394	GDF11	3'	ACCAAGCCGTGTGCAATA 19439	TGGTC C	
			TATTGCACG CGGC TGGT		
			ATAACGTGT GCCG ACCA		
			_____ A		
GAM1394	GDF11	3'	ACCAAGCCGTGTGCAATA 19439	TGGTC C	
			TATTGCACG CGGC TGGT		
			ATAACGTGT GCCG ACCA		
			_____ A		
GAM1394	GIT1	3'	GGCCAGGCCCTACCTGTGTGGT 25868	TG T CC	
	G		TAT CACG GGT GGCCTGGTT		
			GTG GTGT CCA CCGGACCGG		
			GT _ TC		
GAM1394	GIT1	3'	GGCCAGGCCCTACCTGTGTGGT 25868	TG T CC	
	G		TAT CACG GGT GGCCTGGTT		
			GTG GTGT CCA CCGGACCGG		
			GT _ TC		
GAM1394	GMPPA	3'	AGCCAGGCTGGATCGTCACATG 72195	C ____	
	C		GCA GTG GTCCGGCCTGGTT		
			CGT CAC TAGGTCGGACCGA		
			A TGC		
GAM1394	GMPPA	3'	AGCCAGGCTGGATCGTCACATG 72195	C ____	
	C		GCA GTG GTCCGGCCTGGTT		
			CGT CAC TAGGTCGGACCGA		
			A TGC		
GAM1394	GP5	3'	CCAGGCTGGCGTGCAAGTG 15640	TGGT	
			TATTGCACG CCGGCCTGG		
			GTGACGTGC GGTCGGACC		
			_____		
GAM1394	GP5	3'	CCAGGCTGGCGTGCAAGTG 15640	TGGT	
			TATTGCACG CCGGCCTGG		
			GTGACGTGC GGTCGGACC		
			_____		
GAM1394	GPR107	3'	GATTGGAGATGGCTATGTGTAA 40563	T GC_TG	
			TTGCACGTGG CCG C GTT		

			AATGTGTATC GGT G TAG		
			_ AGA GT		
GAM1394	GPR107	3'	GATTGGAGATGGCTATGTGTAA 40563	T GC_TG	
			TTGCACGTGG CCG C GTT		
			AATGTGTATC GGT G TAG		
			_ AGA GT		
GAM1394	GREB1	3'	GCCAGGCTGGTCTTGTG 27872	T T	
			CACG GG CCGGCCTGGT		
			GTGT TC GGTCGGACCG		
			_ T		
GAM1394	GREB1	3'	GCCAGGCTGGTCTTGTG 27872	T T	
			CACG GG CCGGCCTGGT		
			GTGT TC GGTCGGACCG		
			_ T		
GAM1394	GW112	3'	GTTAATCAGTGCAGTA 21192	G CC	
			TATTGCAC TGGT GGC		
			ATGACGTG ACTA TTG		
			_ A_		
GAM1394	GW112	3'	GTTAATCAGTGCAGTA 21192	G CC	
			TATTGCAC TGGT GGC		
			ATGACGTG ACTA TTG		
			_ A_		
GAM1394	HARS2	3'	AATCACTTCACTATGTGTA 55030	CC CC	
			TGCACGTGGT GG TGGTT		
			ATGTGTATCA CT ACTAA		
			_ TC		
GAM1394	HARS2	3'	AATCACTTCACTATGTGTA 55030	CC CC	
			TGCACGTGGT GG TGGTT		
			ATGTGTATCA CT ACTAA		
			_ TC		
GAM1394	HEY1	3'	AGCTGGGCTGGACTGTTGC 91248	C TG TG	
			GCA G GTCCGGCC GTT		
			CGT T CAGGTCGG CGA		
			_ GT GT		
GAM1394	HEY1	3'	AGCTGGGCTGGACTGTTGC 91248	C TG TG	
			GCA G GTCCGGCC GTT		
			CGT T CAGGTCGG CGA		
			_ GT GT		
GAM1394	HIC	3'	GCTGGGCTTGGCGGTG 67451	ACGT	
			TATTGC GGTCCGGC		

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GTGGCG TCGGGTCG
GT__
GAM1394 HIC 3' GCTGGGCTTGGCGGTG 67451 ACGT
TATTGC GGTCCGGC
||||| |||||
GTGGCG TCGGGTCG
GT__
GAM1394 HNK-1ST 3' GGTTTCCTGATTGTGTCAATG 16771 C TG C __
TATTG ACG GTC GG CC
||||| ||| || ||
GTAAC TGT TAG CC GG
_ GT T TTT
GAM1394 HNK-1ST 3' GGTTTCCTGATTGTGTCAATG 16771 C TG C __
TATTG ACG GTC GG CC
||||| ||| || ||
GTAAC TGT TAG CC GG
_ GT T TTT
GAM1394 HNRPA0 5' TGGCTGGGCCCAAGCTGTGTAG 22324 _ __ TGTT
TTGCAC GT GGTCCGGCC
||||| || |||||
GATGTG CG CCGGGTCGG
T AAC TT
GAM1394 HNRPA0 5' TGGCTGGGCCCAAGCTGTGTAG 22324 _ __ TGTT
TTGCAC GT GGTCCGGCC
||||| || |||||
GATGTG CG CCGGGTCGG
T AAC TT
GAM1394 HOMER-3 3' GGCCGGGCCGGGCTGGGCTGGG 16716 G C __
GTG ATT CA GT GGTCCGGCCTGGTT
||| || |||||
TGG GT CG TCGGGCCGGGCCGG
G _ GG
GAM1394 HOMER-3 3' GGCCGGGCCGGGCTGGGCTGGG 16716 G C __
GTG ATT CA GT GGTCCGGCCTGGTT
||| || |||||
TGG GT CG TCGGGCCGGGCCGG
G _ GG
GAM1394 HOMER-3 3' GGCCGGGCTGGGCTGGGGTG 16717 GT_
CAC GGTCCGGCCTGGTT
||| |||||
GTG TCGGGTCGGGCCGG
GGG
GAM1394 HOMER-3 3' GGCCGGGCTGGGCTGGGGTG 16717 GT_
CAC GGTCCGGCCTGGTT
||| |||||
GTG TCGGGTCGGGCCGG
GGG
GAM1394 HRH3 3' GGCCGCTTCGCCATGTGCTGTG 23369 T C__
TAT GCACGTGGT CGGCC
||| ||||| |||

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			GTG CGTGTACCG	GCCGG	
			T	CTTC	
GAM1394	HRH3	3'	GGCCGCTTCGCCATGTGCTGTG	23369	T C__
			TAT GCACGTGGT	CGGCC	
			GTG CGTGTACCG	GCCGG	
			T	CTTC	
GAM1394	HS6ST1	5'	GGCCGGGCGGAGCGCG	16661	G
			CGTG TCCGGCCTGGTT		
			GCGC AGGCCGGGCCGG		
			G		
GAM1394	HS6ST1	5'	GGCCGGGCGGAGCGCG	16661	G
			CGTG TCCGGCCTGGTT		
			GCGC AGGCCGGGCCGG		
			G		
GAM1394	HSA011916	3'	GGCTGGGCTGTGGGTGGGATA	60272	G __ TG
			TATT CAC G GTCCGGCC		
			ATAG GTG T CGGGTCGG		
			G GG GT		
GAM1394	HSA011916	3'	GGCTGGGCTGTGGGTGGGATA	60272	G __ TG
			TATT CAC G GTCCGGCC		
			ATAG GTG T CGGGTCGG		
			G GG GT		
GAM1394	HSA011916	3'	GGCTGGGCTGTGGGTGGGATA	31060	G __ TG
			TATT CAC G GTCCGGCC		
			ATAG GTG T CGGGTCGG		
			G GG GT		
GAM1394	HSA011916	3'	GGCTGGGCTGTGGGTGGGATA	31060	G __ TG
			TATT CAC G GTCCGGCC		
			ATAG GTG T CGGGTCGG		
			G GG GT		
GAM1394	HSBP1	3'	GCTAACTACTATGTGTAG	7738	CC__
			TTGCACGTGGT	GGC	
			GATGTGTATCA	TCG	
			TCAA		
GAM1394	HSBP1	3'	GCTAACTACTATGTGTAG	7738	CC__
			TTGCACGTGGT	GGC	
			GATGTGTATCA	TCG	
			TCAA		
GAM1394	HSGP25L2G	5'	ACCGGGCTGGGTAGAGTG	62164	GTG
			CAC GTCCGGCCTGGT		

		GTG TGGGTCGGGCCA			
		AGA			
GAM1394	HSGP25L2G 5'	ACCGGGCTGGGTAGAGTG	62164	GTG	
		CAC GTCCGGCCTGGT			
		GTG TGGGTCGGGCCA			
		AGA			
GAM1394	HSPBP1 5'	GGCGGGGCCGAGTGCAGTA	24362	G	G
		TATTGCAC TGGTCC GCC			
		ATGACGTG GCCGGG CGG			
		A G			
GAM1394	HSPBP1 5'	GGCGGGGCCGAGTGCAGTA	24362	G	G
		TATTGCAC TGGTCC GCC			
		ATGACGTG GCCGGG CGG			
		A G			
GAM1394	HSPC055 5'	AATTGGGAATAATTATGTGTGA	26265	TG	CCGG TG
	TG	TAT CACGTGGT CC GTT			
		GTA GTGTATTA GG TAA			
		GT ATAA GT			
GAM1394	HSPC055 5'	AATTGGGAATAATTATGTGTGA	26265	TG	CCGG TG
	TG	TAT CACGTGGT CC GTT			
		GTA GTGTATTA GG TAA			
		GT ATAA GT			
GAM1394	HSU79275 3'	CCAGGCTGTGTGCAG	66316	TGGTC	
		TTGCACG CGGCCTGG			
		GACGTGT GTCGGACC			
		_____			
GAM1394	HSU79275 3'	CCAGGCTGTGTGCAG	66316	TGGTC	
		TTGCACG CGGCCTGG			
		GACGTGT GTCGGACC			
		_____			
GAM1394	HT014 3'	GCCTCCGATTGTGTAGTA	39796	C TG	CCT T
		TATTG ACG GTCCGG GGT			
		ATGAT TGT TAGGCC CCG			
		_ GT T__ T			
GAM1394	HT014 3'	GCCTCCGATTGTGTAGTA	39796	C TG	CCT T
		TATTG ACG GTCCGG GGT			
		ATGAT TGT TAGGCC CCG			
		_ GT T__ T			
GAM1394	HTATIP 3'	AGCCAGGCAGCTGTGTACAGTG	21104	C TG	CCG
		TATTG ACG GT GCCTGGTT			

		GTGAC TGT CG CGGACCGA	
		A GT A__	
GAM1394 HTATIP	3'	AGCCAGGCAGCTGTGTACAGTG 21104	C TG CCG
		TATTG ACG GT GCCTGGTT	
		GTGAC TGT CG CGGACCGA	
		A GT A__	
GAM1394 HYA22	3'	GGTCTGTGACTGCTGTGTGATA 19428	TG _TG _ _
		TAT CAC G GTC CGG CC	
		ATA GTG C CAG GTC GG	
		GT TGT T T	
GAM1394 HYA22	3'	GGTCTGTGACTGCTGTGTGATA 19428	TG _TG _ _
		TAT CAC G GTC CGG CC	
		ATA GTG C CAG GTC GG	
		GT TGT T T	
GAM1394 HYPK	3'	GCTGGGCATGGTGGTG 33078	TG A G
		TAT C CGTG TCCGGC	
		GTG G GTAC GGGTCG	
		GT _ _	
GAM1394 HYPK	3'	GCTGGGCATGGTGGTG 33078	TG A G
		TAT C CGTG TCCGGC	
		GTG G GTAC GGGTCG	
		GT _ _	
GAM1394 IDI2	3'	GTCAGCCATGTGTAATG 52696	CC
		TATTGCACGTGGT GGC	
		GTAATGTGTACCG CTG	
		A_	
GAM1394 IDI2	3'	GTCAGCCATGTGTAATG 52696	CC
		TATTGCACGTGGT GGC	
		GTAATGTGTACCG CTG	
		A_	
GAM1394 INE1	3'	GGTGTTTGGGCCAGGTGCGGTG 13375	G ____
		TATTGCAC TGGTCCG GCC	
		GTGGCGTG ACCGGGT TGG	
		G TTG	
GAM1394 INE1	3'	GGTGTTTGGGCCAGGTGCGGTG 13375	G ____
		TATTGCAC TGGTCCG GCC	
		GTGGCGTG ACCGGGT TGG	
		G TTG	
GAM1394 IPLA2(GAMMA)	3'	AACTAGGCTTTTAAGATGTAA 60689	C GGTCC_
TA		TATTG ACGT GGCCTGGTT	

			ATAAT TGTA	TCGGATCAA		
			— GAATTT			
GAM1394	IPLA2(GAMMA)	3'	AACTAGGCTTTTAAAGATGTTAA	60689	C	GGTCC_
		TA	TATTG ACGT	GGCCTGGTT		
			ATAAT TGTA	TCGGATCAA		
			— GAATTT			
GAM1394	JDD1	5'	GGCCGGGCGGAGCCGGCG	63220	—	—
			CGT GG TCCGGCCTGGTT			
			GCG CC AGGCCGGGCCGG			
			G G			
GAM1394	JDD1	5'	GGCCGGGCGGAGCCGGCG	63220	—	—
			CGT GG TCCGGCCTGGTT			
			GCG CC AGGCCGGGCCGG			
			G G			
GAM1394	KATII	3'	ACTAGGTTGGGCATGGTGC	32642	GTG	
			GCAC GTCCGGCCTGGT			
			CGTG CGGGTTGGATCA			
			GTA			
GAM1394	KATII	3'	ACTAGGTTGGGCATGGTGC	32642	GTG	
			GCAC GTCCGGCCTGGT			
			CGTG CGGGTTGGATCA			
			GTA			
GAM1394	KCNJ9	3'	GATTGGGTGCCATGTGGAGTG	17154	G	CCG TG
			TATT CACGTGGT GCC GTT			
			GTGA GTGTACCG TGG TAG			
			G — GT			
GAM1394	KCNJ9	3'	GATTGGGTGCCATGTGGAGTG	17154	G	CCG TG
			TATT CACGTGGT GCC GTT			
			GTGA GTGTACCG TGG TAG			
			G — GT			
GAM1394	KCNS1	3'	GATCAGAAGGGCTGCGTGTAG	9575	TG	GGC
			TTGCACG GTCC CTGGTT			
			GATGTGC CGGG GACTAG			
			GT AA_			
GAM1394	KCNS1	3'	GATCAGAAGGGCTGCGTGTAG	9575	TG	GGC
			TTGCACG GTCC CTGGTT			
			GATGTGC CGGG GACTAG			
			GT AA_			
GAM1394	KIAA0036	5'	GCTGGGCCGGACCCGGTGG	27677	TG A T	TG
			T C CG GGTCCGGCC GT			

		G G GC CCAGGCCGG CG		
		GT _ _ GT		
GAM1394 KIAA0036	5'	GCTGGGCCGGACCCGGTGG 27677	TG A T	TG
		T C CG GGTCCGGCC GT		
		G G GC CCAGGCCGG CG		
		GT _ _ GT		
GAM1394 KIAA0040	3'	ACTGTGTACCTGTGCAATG 27773	T CCG C	
		TATTGCACG GGT GC TGGT		
		GTAACGTGT CCA TG GTCA		
		_ _ _ T		
GAM1394 KIAA0040	3'	ACTGTGTACCTGTGCAATG 27773	T CCG C	
		TATTGCACG GGT GC TGGT		
		GTAACGTGT CCA TG GTCA		
		_ _ _ T		
GAM1394 KIAA0089	3'	AGCCAGGAGTCAAGTGCAGTG 69962	G TCCGG	
		TATTGCAC TGG CCTGGTT		
		GTGACGTG ACT GGACCGA		
		A GA_ _		
GAM1394 KIAA0089	3'	AGCCAGGAGTCAAGTGCAGTG 69962	G TCCGG	
		TATTGCAC TGG CCTGGTT		
		GTGACGTG ACT GGACCGA		
		A GA_ _		
GAM1394 KIAA0090	3'	AACTGGCATACTGTGTGTA 88435	TG CCG T	
		TGCACG GT GCC GGTT		
		ATGTGT CA CGG TCAA		
		GT TA_ _		
GAM1394 KIAA0090	3'	AACTGGCATACTGTGTGTA 88435	TG CCG T	
		TGCACG GT GCC GGTT		
		ATGTGT CA CGG TCAA		
		GT TA_ _		
GAM1394 KIAA0100	3'	AGTCCTGATCAAGTGTGATA 27971	TG G C C	
		TAT CAC TGGTC GG CT		
		ATA GTG ACTAG CC GA		
		GT A T T		
GAM1394 KIAA0100	3'	AGTCCTGATCAAGTGTGATA 27971	TG G C C	
		TAT CAC TGGTC GG CT		
		ATA GTG ACTAG CC GA		
		GT A T T		
GAM1394 KIAA0152	3'	ATCAGGTTCTTGGTGTGATG 28293	TG GT TCC	GT
		TAT CAC GG GGCCTG T		



			GTA GTG TC TTGGAC A		
			GT GT ____ TG		
GAM1394	KIAA0152	3'	ATCAGGTTCTTGGTGTGATG 28293	TG GT TCC	GT
			TAT CAC GG GGCCTG T		
			GTA GTG TC TTGGAC A		
			GT GT ____ TG		
GAM1394	KIAA0210	3'	CAGTGGGTCATGGGTAGTA 28472	A GT GC	
			TATTGC CGTG CCG CTG		
			ATGATG GTAC GGT GAC		
			G TG ____		
GAM1394	KIAA0210	3'	CAGTGGGTCATGGGTAGTA 28472	A GT GC	
			TATTGC CGTG CCG CTG		
			ATGATG GTAC GGT GAC		
			G TG ____		
GAM1394	KIAA0237	3'	GGCTGACACGTCTGTGTGATG 28530	TG ____ C	
			TAT CACG TG GTC GGCC		
			GTA GTGT GC CAG TCGG		
			GT CT A _		
GAM1394	KIAA0237	3'	GGCTGACACGTCTGTGTGATG 28530	TG ____ C	
			TAT CACG TG GTC GGCC		
			GTA GTGT GC CAG TCGG		
			GT CT A _		
GAM1394	KIAA0252	3'	GCCGGGCATGGTGGTG 62793	TG A G	
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGCCG		
			GT _ _		
GAM1394	KIAA0252	3'	GCCGGGCATGGTGGTG 62793	TG A G	
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGCCG		
			GT _ _		
GAM1394	KIAA0252	3'	GGTTACGCCGGGTGCAGTA 62797	G CC	
			TATTGCAC TGGT GGCC		
			ATGACGTG GCCG TTGG		
			G CA		
GAM1394	KIAA0252	3'	GGTTACGCCGGGTGCAGTA 62797	G CC	
			TATTGCAC TGGT GGCC		
			ATGACGTG GCCG TTGG		
			G CA		
GAM1394	KIAA0266	3'	AGCCAAAGTGCTGGGTGCGGTG 41325	GTGGT _ _	
			TATTGCAC CCGGC CT GGTT		

		GTGGCGTG	GGTCG GA	CCGA	
		_____	T AA		
GAM1394	KIAA0266	3'	AGCCAAAGTGCTGGGTGCGGTG	41325	GTGGT _ _
			TATTGCAC	CCGGC CT	GGTT
			GTGGCGTG	GGTCG GA	CCGA
			_____	T AA	
GAM1394	KIAA0266	3'	GGGCTGGGTGCGGTG	41333	GTGGT
			TATTGCAC	CCGGCCT	
			GTGGCGTG	GGTCGGG	
			_____		
GAM1394	KIAA0266	3'	GGGCTGGGTGCGGTG	41333	GTGGT
			TATTGCAC	CCGGCCT	
			GTGGCGTG	GGTCGGG	
			_____		
GAM1394	KIAA0275	3'	AACTGGGCCGATGTGGTGTGA	28669	TG GTG C TG
			T CAC	GTC GGCC	GTT
			A GTG	TAG CCGG	CAA
			GT GTG	_ GT	
GAM1394	KIAA0275	3'	AACTGGGCCGATGTGGTGTGA	28669	TG GTG C TG
			T CAC	GTC GGCC	GTT
			A GTG	TAG CCGG	CAA
			GT GTG	_ GT	
GAM1394	KIAA0275	3'	CTGTGTGATGTGCAATA	28676	G TC
			TATTGCACGT	G CGG	
			ATAACGTGTA	T GTC	
			G GT		
GAM1394	KIAA0275	3'	CTGTGTGATGTGCAATA	28676	G TC
			TATTGCACGT	G CGG	
			ATAACGTGTA	T GTC	
			G GT		
GAM1394	KIAA0318	3'	CTACCTTAACCGGGCCAGTGTG	68952	TG G CCT_ T
	GTA		AT CAC	TGGTCCGG	GGT
			TG GTG	ACCGGGCC	CCA
			GT _	AATT TCG	
GAM1394	KIAA0318	3'	CTACCTTAACCGGGCCAGTGTG	68952	TG G CCT_ T
	GTA		AT CAC	TGGTCCGG	GGT
			TG GTG	ACCGGGCC	CCA
			GT _	AATT TCG	
GAM1394	KIAA0337	3'	GGCTGGGGAGGGCCATGTGCAA	28834	GG TG
	TA		TATTGCACGTGGTCC	CC GTT	

		ATAACGTGTACCGGG GG CGG	
		AG GT	
GAM1394 KIAA0337	3'	GGCTGGGGAGGGCCATGTGCAA 28834	GG TG
	TA	TATTGCACGTGGTCC CC GTT	
		ATAACGTGTACCGGG GG CGG	
		AG GT	
GAM1394 KIAA0410	3'	AATCAGGTGATAAGTGGTGTA 28771	GTG__ CG
	TG	TATTGCAC GTC GCCTGGTT	
		GTAATGTG TAG TGGACTAA	
		GTGAA _	
GAM1394 KIAA0410	3'	GGCTGGACCCATGTGAATA 28776	G _
		TATT CACGTGG TCCGGCC	
		ATAA GTGTACC AGGTCGG	
		_ C	
GAM1394 KIAA0410	3'	GGCTGGACCCATGTGAATA 28776	G _
		TATT CACGTGG TCCGGCC	
		ATAA GTGTACC AGGTCGG	
		_ C	
GAM1394 KIAA0410	3'	AATCAGGTGATAAGTGGTGTA 28771	GTG__ CG
	TG	TATTGCAC GTC GCCTGGTT	
		GTAATGTG TAG TGGACTAA	
		GTGAA _	
GAM1394 KIAA0419	5'	GATCAGTGCCTGCTGTGTGCTG 28189	_ TG CC _
	ATA	ATT GCACG GT GGC CTGGTT	
		TAG CGTGT CG CCG GACTAG	
		T GT T_ T	
GAM1394 KIAA0419	5'	GATCAGTGCCTGCTGTGTGCTG 28189	_ TG CC _
	ATA	ATT GCACG GT GGC CTGGTT	
		TAG CGTGT CG CCG GACTAG	
		T GT T_ T	
GAM1394 KIAA0427	3'	GATCAGGCCGGGGCAGCTGTAG 28720	CG G
		TTGCA TG TCCGGCCTGGTT	
		GATGT AC GGGCCGACTAG	
		CG G	
GAM1394 KIAA0427	3'	GATCAGGCCGGGGCAGCTGTAG 28720	CG G
		TTGCA TG TCCGGCCTGGTT	
		GATGT AC GGGCCGACTAG	
		CG G	
GAM1394 KIAA0431	3'	CAGCGGGCCAGGTGTGGTG 30888	TG G GC
		TAT CAC TGGTCCG CTG	

		GTG GTG ACCGGGC GAC			
		GT G _			
GAM1394 KIAA0431	3'	CAGCGGGCCAGGTGTGGTG	30888	TG G GC	
		TAT CAC TGGTCCG CTG			
		GTG GTG ACCGGGC GAC			
		GT G _			
GAM1394 KIAA0447	3'	AACTAATAGAAGACTGGGTGTG	71660	TG G CGGCC_	
		GTG TAT CAC TGGTC TGGTT			
		GTG GTG GTCAG ATCAA			
		GT G AAGATA			
GAM1394 KIAA0447	3'	AACTAATAGAAGACTGGGTGTG	71660	TG G CGGCC_	
		GTG TAT CAC TGGTC TGGTT			
		GTG GTG GTCAG ATCAA			
		GT G AAGATA			
GAM1394 KIAA0476	3'	GGTCCTGACCTGTGCAATA	29379	T C _	
		TATTGCACG GGTC GG CC			
		ATAACGTGT CCAG CC GG			
		_ T T			
GAM1394 KIAA0476	3'	GGTCCTGACCTGTGCAATA	29379	T C _	
		TATTGCACG GGTC GG CC			
		ATAACGTGT CCAG CC GG			
		_ T T			
GAM1394 KIAA0478	5'	CAGCGTGGCTGTGTGCAGTG	29542	TG _ GC	
		TATTGCACG GTC CG CTG			
		GTGACGTGT CGG GC GAC			
		GT T _			
GAM1394 KIAA0478	3'	TGGTTGGAGTCTGCTGGTGCGG	29564	_ TG _ TGGTT	
		TG TTGCAC G G TCCGGCC			
		GGCGTG C C AGGTTGG			
		GT GT TG TT			
GAM1394 KIAA0478	3'	TGGTTGGAGTCTGCTGGTGCGG	29564	_ TG _ TGGTT	
		TG TTGCAC G G TCCGGCC			
		GGCGTG C C AGGTTGG			
		GT GT TG TT			
GAM1394 KIAA0478	5'	CAGCGTGGCTGTGTGCAGTG	29542	TG _ GC	
		TATTGCACG GTC CG CTG			
		GTGACGTGT CGG GC GAC			
		GT T _			
GAM1394 KIAA0493	5'	AATCAGGTTGTCCTGTACAGTA	64267	C T TC	
		TATTG ACG GG CGGCCTGGTT			

		ATGAC TGT CC GTTGGACTAA	
		A _ T_	
GAM1394 KIAA0493	5'	AATCAGGTTGTCCTGTACAGTA 64267	C T TC
		TATTG ACG GG CGGCCTGGTT	
		ATGAC TGT CC GTTGGACTAA	
		A _ T_	
GAM1394 KIAA0495	3'	GCCGGGTTGATTGTGTG 62590	TG C
		CACG GTC GGCCTGGT	
		GTGT TAG TTGGGCCG	
		GT _	
GAM1394 KIAA0495	3'	GCCGGGTTGATTGTGCGG 62589	TGGTC
		TTGCACG CGGCCTGGT	
		GGCGTGT GTTGGGCCG	
		TA__	
GAM1394 KIAA0495	3'	GCCGGGTTGATTGTGCGG 62588	TGGTC
		TTGCACG CGGCCTGGT	
		GGCGTGT GTTGGGCCG	
		TA__	
GAM1394 KIAA0495	3'	GCCGGGTTGATTGTGCGG 62588	TGGTC
		TTGCACG CGGCCTGGT	
		GGCGTGT GTTGGGCCG	
		TA__	
GAM1394 KIAA0495	3'	GCCGGGTTGATTGTGCGG 62589	TGGTC
		TTGCACG CGGCCTGGT	
		GGCGTGT GTTGGGCCG	
		TA__	
GAM1394 KIAA0495	3'	GCCGGGTTGATTGTGTG 62590	TG C
		CACG GTC GGCCTGGT	
		GTGT TAG TTGGGCCG	
		GT _	
GAM1394 KIAA0513	3'	GCTGGGCTGTGGTGCAG 28364	_TG
		TTGCAC G GTCCGGC	
		GACGTG T CGGGTCG	
		G GT	
GAM1394 KIAA0513	3'	GCTGGGCTGTGGTGCAG 28364	_TG
		TTGCAC G GTCCGGC	
		GACGTG T CGGGTCG	
		G GT	
GAM1394 KIAA0514	3'	GGCCGGGCTGGGCTCAGC 28090	ACGT
		GC GGTCCGGCCTGGTT	

		CG	TCGGGTCGGGCCGG		
		AC__			
GAM1394	KIAA0514	3'	GGCCGGGCTGGGCTCAGC	28090	ACGT
			GC GGTCCGGCCTGGTT		
			CG TCGGGTCGGGCCGG		
			AC__		
GAM1394	KIAA0514	3'	GCTGGGCATGGTGGTG	28087	TG A G
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGTCG		
			GT _ _		
GAM1394	KIAA0514	3'	GCTGGGCATGGTGGTG	28087	TG A G
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGTCG		
			GT _ _		
GAM1394	KIAA0545	3'	GGCCAGGCCGGGGCGGTGGAG	63148	G G G
			TT CAC TG TCCGGCCTGGTT		
			GA GTG GC GGGCCGGACCGG		
			G _ G		
GAM1394	KIAA0545	3'	GGCCAGGCCGGGGCGGTGGAG	63148	G G G
			TT CAC TG TCCGGCCTGGTT		
			GA GTG GC GGGCCGGACCGG		
			G _ G		
GAM1394	KIAA0545	3'	GGCCATGCCGGTGTGGTA	63149	TG G CC
			TAT CAC TGGT GGCC		
			ATG GTG GCCG CCGG		
			GT _ TA		
GAM1394	KIAA0545	3'	GGCCATGCCGGTGTGGTA	63149	TG G CC
			TAT CAC TGGT GGCC		
			ATG GTG GCCG CCGG		
			GT _ TA		
GAM1394	KIAA0546	3'	GGTCAAATATTATGTGCAAT	71311	CC__
			ATTGCACGTGGT GGCC		
			TAACGTGTATTA CTGG		
			TAAA		
GAM1394	KIAA0546	3'	GGTCAAATATTATGTGCAAT	71311	CC__
			ATTGCACGTGGT GGCC		
			TAACGTGTATTA CTGG		
			TAAA		
GAM1394	KIAA0547	3'	GTCCATATTGGGCCAGGTGCGG	28914	G CC TT
			TATTGCAC TGGTCCGG TGG		

			GTGGCGTG ACCGGGTT ACC		
			G AT TGA		
GAM1394	KIAA0547	3'	GTCCATATTGGGCCAGGTGCGG 28914	G	CC TT
		TG	TATTGCAC TGGTCCGG TGG		
			GTGGCGTG ACCGGGTT ACC		
			G AT TGA		
GAM1394	KIAA0552	5'	GCTGGGGGCTATGTGCA 28316	GGC	TG
			TGCACGTGGTCC C GT		
			ACGTGTATCGGG G CG		
			___ GT		
GAM1394	KIAA0552	5'	GCTGGGGGCTATGTGCA 28316	GGC	TG
			TGCACGTGGTCC C GT		
			ACGTGTATCGGG G CG		
			___ GT		
GAM1394	KIAA0565	3'	GCTGGGCATGGTGGTG 66892	TG A	G
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGTCG		
			GT _ _		
GAM1394	KIAA0565	3'	GCTGGGCATGGTGGTG 66892	TG A	G
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGTCG		
			GT _ _		
GAM1394	KIAA0596	3'	GGTTCTGGGCCAGGTGTGGTG 62836	TG G	___
			TAT CAC TGGTCCGG CC		
			GTG GTG ACCGGGTC GG		
			GT G TT		
GAM1394	KIAA0596	3'	GGTTCTGGGCCAGGTGTGGTG 62836	TG G	___
			TAT CAC TGGTCCGG CC		
			GTG GTG ACCGGGTC GG		
			GT G TT		
GAM1394	KIAA0599	3'	GACCAACCCACTATGTGTGA 77178	TG	CC CC
			T CACGTGGT GG TGGTT		
			A GTGTATCA CC ACCAG		
			GT ___ CA		
GAM1394	KIAA0599	3'	GACCAACCCACTATGTGTGA 77178	TG	CC CC
			T CACGTGGT GG TGGTT		
			A GTGTATCA CC ACCAG		
			GT ___ CA		
GAM1394	KIAA0618	3'	GGCTGGGCTGGGTGTGCG 29173	TGG	TG
			TGCACG TCCGGCC GTT		

			GCGTGT GGGTCGG CGG		
			____ GT		
GAM1394	KIAA0618	3'	GGCTGGGCTGGGTGTGCG 29173	TGG	TG
			TGCACG TCCGGCC GTT		
			GCGTGT GGGTCGG CGG		
			____ GT		
GAM1394	KIAA0637	5'	GGCCGGGCGCGAGGTAATG 29238	ACG	
			TATTGC TGGTCCGGCC		
			GTAATG GCCGGGCCGG		
			GA_		
GAM1394	KIAA0637	5'	GGCCGGGCGCGAGGTAATG 29238	ACG	
			TATTGC TGGTCCGGCC		
			GTAATG GCCGGGCCGG		
			GA_		
GAM1394	KIAA0677	3'	GACTAGGCTGAGGTGC 27828	GTGGTC	
			GCAC CGGCCTGGTT		
			CGTG GTCGGATCAG		
			GA_____		
GAM1394	KIAA0677	3'	GACTAGGCTGAGGTGC 27828	GTGGTC	
			GCAC CGGCCTGGTT		
			CGTG GTCGGATCAG		
			GA_____		
GAM1394	KIAA0685	5'	GGCCGGGCCCCATGTGT 27964	_	
			GCACGTGG TCCGGCC		
			TGTGTACC GGGCCGG		
			C		
GAM1394	KIAA0685	5'	GGCCGGGCCCCATGTGT 27964	_	
			GCACGTGG TCCGGCC		
			TGTGTACC GGGCCGG		
			C		
GAM1394	KIAA0721	3'	GTTATGATCATGTGTGGTG 95972	TG	C_
			TAT CACGTGGTC GGC		
			GTG GTGTACTAG TTG		
			GT TA		
GAM1394	KIAA0721	3'	GTTATGATCATGTGTGGTG 41344	TG	C_
			TAT CACGTGGTC GGC		
			GTG GTGTACTAG TTG		
			GT TA		
GAM1394	KIAA0721	3'	GTTATGATCATGTGTGGTG 41344	TG	C_
			TAT CACGTGGTC GGC		



		GTG GTGTACTAG TTG		
		GT TA		
GAM1394 KIAA0721	3'	GTTATGATCATGTGTGGTG	95972	TG C_
		TAT CACGTGGTC GGC		
		GTG GTGTACTAG TTG		
		GT TA		
GAM1394 KIAA0737	3'	GCTGGGCTTCTGGTAGTG	29143	ACGT
		TATTGC GGTCCGGC		
		GTGATG TCGGGTCG		
		GTCT		
GAM1394 KIAA0737	3'	GCTGGGCTTCTGGTAGTG	29143	ACGT
		TATTGC GGTCCGGC		
		GTGATG TCGGGTCG		
		GTCT		
GAM1394 KIAA0746	3'	TCAGGCAGTGGTAATA	69456	A TGGTCCG
		TATTGC CG GCCTGG		
		ATAATG GT CGGACT		
		_ GA_____		
GAM1394 KIAA0746	3'	TCAGGCAGTGGTAATA	69456	A TGGTCCG
		TATTGC CG GCCTGG		
		ATAATG GT CGGACT		
		_ GA_____		
GAM1394 KIAA0773	3'	GGCTACAGGCTGTGTTCAATG	28058	C TG C_
		TATTG ACG GTC GGCC		
		GTAAC TGT CGG TCGG		
		T GT ACA		
GAM1394 KIAA0773	3'	GGCTACAGGCTGTGTTCAATG	28058	C TG C_
		TATTG ACG GTC GGCC		
		GTAAC TGT CGG TCGG		
		T GT ACA		
GAM1394 KIAA0789	3'	GGTCACATGCCATGTGCAG	63686	CC_
		TTGCACGTGGT GGCC		
		GACGTGTACCG CTGG		
		TACA		
GAM1394 KIAA0789	3'	GGTCACATGCCATGTGCAG	63686	CC_
		TTGCACGTGGT GGCC		
		GACGTGTACCG CTGG		
		TACA		
GAM1394 KIAA0800	5'	GACCTGAGGCTGTGTGTGTGT	28147	TGGTC _
		GCACG CGGCCT GGTT		

TGTGT GTCGGA CCAG  
 GTGT\_ GT  
 GAM1394 KIAA0800 5' GACCTGAGGCTGTGTGTGTGT 28147 TGGTC \_  
 GCACG CGGCCT GGTT  
 |||| |||| ||||  
 TGTGT GTCGGA CCAG  
 GTGT\_ GT  
 GAM1394 KIAA0830 3' TAGTTGGATTTGGCATGTGTGA 69702 TG \_ CTGGTT  
 TG T CACGTG GTCCGGC  
 | |||| |||||  
 A GTGTAC TAGGTTG  
 GT GGTT A TT  
 GAM1394 KIAA0830 3' TAGTTGGATTTGGCATGTGTGA 69702 TG \_ CTGGTT  
 TG T CACGTG GTCCGGC  
 | |||| |||||  
 A GTGTAC TAGGTTG  
 GT GGTT A TT  
 GAM1394 KIAA0855 3' AGTCAGGGACATACTTTGTGCA 30402 T CCGG\_ GT  
 ATA TATTGCACG GGT CCTG T  
 ||||||| || ||| |  
 ATAACGTGT TCA GGAC A  
 T TACAG TG  
 GAM1394 KIAA0855 3' AGTCAGGGACATACTTTGTGCA 30402 T CCGG\_ GT  
 ATA TATTGCACG GGT CCTG T  
 ||||||| || ||| |  
 ATAACGTGT TCA GGAC A  
 T TACAG TG  
 GAM1394 KIAA0872 3' GCCGGGCACGGTGGTG 30064 TG A G  
 TAT C CGTG TCCGGC  
 || | |||| |||||  
 GTG G GCAC GGGCCG  
 GT \_ \_  
 GAM1394 KIAA0872 3' GCCGGGCACGGTGGTG 30064 TG A G  
 TAT C CGTG TCCGGC  
 || | |||| |||||  
 GTG G GCAC GGGCCG  
 GT \_ \_  
 GAM1394 KIAA0884 3' ATCAGGCTGGGCACCGTG 70199 TG  
 CACG GTCCGGCCTGGT  
 |||| |||||||||  
 GTGC CGGGTCGGA  
 CA  
 GAM1394 KIAA0884 3' ATCAGGCTGGGCACCGTG 70199 TG  
 CACG GTCCGGCCTGGT  
 |||| |||||||||  
 GTGC CGGGTCGGA  
 CA  
 GAM1394 KIAA0907 3' GCTGGGCATGGTGGTG 30178 TG A G  
 TAT C CGTG TCCGGC  
 || | |||| |||||

			GTG G GTAC GGGTCG		
			GT _ _		
GAM1394	KIAA0907	3'	GCTGGGCATGGTGGTG 30178	TG A	G
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGTCG		
			GT _ _		
GAM1394	KIAA0939	3'	AGCTGGGCTGGGCTGGCTGGCA 62003	ACGT_	TG
			TGC GGTCCGGCC GTT		
			ACG TCGGGTCGG CGA		
			GTCGG GT		
GAM1394	KIAA0939	3'	AGCTGGGCTGGGCTGGCTGGCA 62003	ACGT_	TG
			TGC GGTCCGGCC GTT		
			ACG TCGGGTCGG CGA		
			GTCGG GT		
GAM1394	KIAA0940	3'	AATCAGGTTGCTGCATGCAATA 29862	C TG	CC
			TATTGCA G GT GGCCTGGTT		
			ATAACGT C CG TTGGAATA		
			A GT _		
GAM1394	KIAA0940	3'	AATCAGGTTGCTGCATGCAATA 29862	C TG	CC
			TATTGCA G GT GGCCTGGTT		
			ATAACGT C CG TTGGAATA		
			A GT _		
GAM1394	KIAA0992	3'	GTTGTGCTGGTGTAATG 32208	G TC	
			TATTGCAC TGG CGGC		
			GTAATGTG GTC GTTG		
			_ GT		
GAM1394	KIAA0992	3'	GTTGTGCTGGTGTAATG 32208	G TC	
			TATTGCAC TGG CGGC		
			GTAATGTG GTC GTTG		
			_ GT		
GAM1394	KIAA0993	3'	GGTCAGATGACCAGTGTAGTG 64146	G C_	
			TATTGCAC TGGTC GGCC		
			GTGATGTG ACCAG CTGG		
			_ TAGA		
GAM1394	KIAA0993	3'	GGTCAGATGACCAGTGTAGTG 64146	G C_	
			TATTGCAC TGGTC GGCC		
			GTGATGTG ACCAG CTGG		
			_ TAGA		
GAM1394	KIAA0997	5'	GGCCGGCTCAGTGCGGTG 30192	G GT	
			TATTGCAC TG CCGGCC		

			GTGGCGTG AC GGCCGG			
			_ TC			
GAM1394	KIAA0997	5'	GGCCGGCTCAGTGCGGTG	30192	G	GT
			TATTGCAC TG CCGGCC			
			GTGGCGTG AC GGCCGG			
			_ TC			
GAM1394	KIAA1000	3'	GCTGGATTTGTGCAGTA	65280	T	
			TATTGCACG GGTCCGGC			
			ATGACGTGT TTAGGTCG			
			-			
GAM1394	KIAA1000	3'	GCTGGATTTGTGCAGTA	65280	T	
			TATTGCACG GGTCCGGC			
			ATGACGTGT TTAGGTCG			
			-			
GAM1394	KIAA1023	3'	GGCTGGGCTGGGCTGGGC	34268	ACGT	TG
			GC GGTCCGGCC GTT			
			CG TCGGGTCGG CGG			
			GG_ GT			
GAM1394	KIAA1023	3'	GGCTGGGCTGGGCCGGG	34265	G	TG
			C TGGTCCGGCC GTT			
			G GCCGGGTCGG CGG			
			G GT			
GAM1394	KIAA1023	3'	GGCTGGGCTGGGCCGGGCGTGC	34266	__	TG
	GG		TTGCACGT GGTCCGGCC GTT			
			GGCGTGCG CCGGGTCGG CGG			
			GG GT			
GAM1394	KIAA1023	3'	GGCTGGGCTGGGCCGGGCGTGC	34266	__	TG
	GG		TTGCACGT GGTCCGGCC GTT			
			GGCGTGCG CCGGGTCGG CGG			
			GG GT			
GAM1394	KIAA1023	3'	GGCTGGGCTGGGCTGGGC	34267	ACGT	TG
			GC GGTCCGGCC GTT			
			CG TCGGGTCGG CGG			
			GG_ GT			
GAM1394	KIAA1023	3'	GGCTGGGCTGGGCTGGGC	34267	ACGT	TG
			GC GGTCCGGCC GTT			
			CG TCGGGTCGG CGG			
			GG_ GT			
GAM1394	KIAA1023	3'	GGCTGGGCTGGGCTGGGC	34268	ACGT	TG
			GC GGTCCGGCC GTT			

CG TCGGGTCGG CGG  
 GG\_\_ GT  
 GAM1394 KIAA1023 3' GGCTGGGCTGGGCTGGGC 34269 ACGT TG  
 GC GGTCCGGCC GTT  
 || ||||| ||  
 CG TCGGGTCGG CGG  
 GG\_\_ GT  
 GAM1394 KIAA1023 3' GGCTGGGCTGGGCTGGGC 34269 ACGT TG  
 GC GGTCCGGCC GTT  
 || ||||| ||  
 CG TCGGGTCGG CGG  
 GG\_\_ GT  
 GAM1394 KIAA1023 3' GGCTGGGCTGGGCCGGG 34265 G TG  
 C TGGTCCGGCC GTT  
 | ||||| ||  
 G GCCGGGTCGG CGG  
 G GT  
 GAM1394 KIAA1024 3' GGTCAATTGTGTGAATA 69063 G TG CC  
 TATT CACG GT GGCC  
 ||| ||| || |||  
 ATAA GTGT TA CTGG  
 \_ GT A\_  
 GAM1394 KIAA1024 3' GGTCAATTGTGTGAATA 69063 G TG CC  
 TATT CACG GT GGCC  
 ||| ||| || |||  
 ATAA GTGT TA CTGG  
 \_ GT A\_  
 GAM1394 KIAA1036 3' GACCAGGTTGGGGGGGTG 29820 GTGG  
 CAC TCCGGCCTGGTT  
 ||| ||||| ||  
 GTG GGGTTGGACCAG  
 GGG\_  
 GAM1394 KIAA1036 3' GACCAGGTTGGGGGGGTG 29820 GTGG  
 CAC TCCGGCCTGGTT  
 ||| ||||| ||  
 GTG GGGTTGGACCAG  
 GGG\_  
 GAM1394 KIAA1036 3' GACCAGAGGCCTGTGTGA 29819 TG T CGGC  
 T CACG GGTC CTGGTT  
 | ||| ||| |||||  
 A GTGT CCGG GACCAG  
 GT \_ A\_\_  
 GAM1394 KIAA1036 3' GTTGACCACGTGTGAT 29829 TG C  
 AT CACGTGGTC GGC  
 || ||||| ||  
 TA GTGCACCAG TTG  
 GT \_  
 GAM1394 KIAA1036 3' AGCTGGGCTGGGCTGGGGTAG 29811 ACG TG  
 TTGC TGGTCCGGCC GTT  
 ||| ||||| ||

			GATG	GTCGGGTCGG	CGA		
			GG_	GT			
GAM1394	KIAA1036	3'	AGCTGGGCTGGGCTGGGGTAG	29811	ACG	TG	
			TTGC	TGGTCCGGCC	GTT		
			GATG	GTCGGGTCGG	CGA		
			GG_	GT			
GAM1394	KIAA1036	3'	GACCAGAGGCCTGTGTGA	29819	TG	T	CGGC
			T	CACG	GGTC	CTGGTT	
			A	GTGT	CCGG	GACCAG	
			GT	_	A__		
GAM1394	KIAA1036	3'	GTTGACCACGTGTGAT	29829	TG	C	
			AT	CACGTGGTC	GGC		
			TA	GTGCACCAG	TTG		
			GT	_			
GAM1394	KIAA1037	3'	AGCTCTGAGGGCCAGGTGCAGT	30432	G		GGCCT
			TATTGCAC	TGGTCC	GGTT		
			GTGACGTG	ACCGGG	TCGA		
			G	AGTC_			
GAM1394	KIAA1037	3'	AGCTCTGAGGGCCAGGTGCAGT	30432	G		GGCCT
			TATTGCAC	TGGTCC	GGTT		
			GTGACGTG	ACCGGG	TCGA		
			G	AGTC_			
GAM1394	KIAA1049	5'	GGCTAGGTAGCGAGGCCGCGTG	30366	TG	_	_
			TGA	T	CACGTGGTC	CG	GCCTGGTT
			A	GTGCGCCGG	GC	TGGATCGG	
			GT	A	GA		
GAM1394	KIAA1049	5'	GGCTAGGTAGCGAGGCCGCGTG	30366	TG	_	_
			TGA	T	CACGTGGTC	CG	GCCTGGTT
			A	GTGCGCCGG	GC	TGGATCGG	
			GT	A	GA		
GAM1394	KIAA1052	3'	GCTGATGGCGTGCGGTG	30251	G	C	
			TATTGCACGT	GTC	GGC		
			GTGGCGTGCG	TAG	TCG		
			G	_			
GAM1394	KIAA1052	3'	GCTGATGGCGTGCGGTG	30251	G	C	
			TATTGCACGT	GTC	GGC		
			GTGGCGTGCG	TAG	TCG		
			G	_			
GAM1394	KIAA1100	3'	GGCTGGGCTGGGCGGCCGGCGG	29756	AC	G	TG
			T	ATTGC	GT	GTCCGGCC	GTT

		TGGCG CG CGGGTCGG CGG		
		GC G GT		
GAM1394 KIAA1100	3'	GGCTGGGCTGGGCGGCCGGCGG 29756	AC G	TG
	T	ATTGC GT GTCCGGCC GTT		
		TGGCG CG CGGGTCGG CGG		
		GC G GT		
GAM1394 KIAA1110	3'	GCTGGGCCGGCCGGCAGTG 61847	ACG T	TG
		TATTGC TGG CCGGCC GT		
		GTGACG GCC GGCCGG CG		
		— — GT		
GAM1394 KIAA1110	3'	GCTGGGCCGGCCGGCAGTG 61847	ACG T	TG
		TATTGC TGG CCGGCC GT		
		GTGACG GCC GGCCGG CG		
		— — GT		
GAM1394 KIAA1126	3'	GGTTGGTCGAGTCTTGTGTAAT 71936	T TC	TGGTT
	G	TATTGCACG GG CGGCC		
		GTAATGTGT CT GCTGG		
		T GA TTGG		
GAM1394 KIAA1126	3'	GGTTGGTCGAGTCTTGTGTAAT 71936	T TC	TGGTT
	G	TATTGCACG GG CGGCC		
		GTAATGTGT CT GCTGG		
		T GA TTGG		
GAM1394 KIAA1130	3'	GTGGGGCTGGTGCAAGTG 62427	G G	
		TATTGCAC TGGTCC GC		
		GTGACGTG GTCGGG TG		
		— G		
GAM1394 KIAA1130	3'	GTGGGGCTGGTGCAAGTG 62427	G G	
		TATTGCAC TGGTCC GC		
		GTGACGTG GTCGGG TG		
		— G		
GAM1394 KIAA1143	3'	AGCCATGTGCTTTGGGTCATGT 68667	C GT — C—	
	TAGTA	G ACGTG CC GGC TGGTT		
		T TGTAC GG TCG ACCGA		
		— TG TT TGT		
GAM1394 KIAA1143	3'	AGCCATGTGCTTTGGGTCATGT 68667	C GT — C—	
	TAGTA	G ACGTG CC GGC TGGTT		
		T TGTAC GG TCG ACCGA		
		— TG TT TGT		
GAM1394 KIAA1155	3'	TAGGCTGGGTGTGGTG 62241	TG GTGGT	
		TAT CAC CCGGCCTG		

		GTG GTG GGTCTGGAT		
		GT _____		
GAM1394 KIAA1155	3'	TAGGCTGGGTGTGGTG 62241	TG	GTGGT
		TAT CAC CCGGCCTG		
		GTG GTG GGTCTGGAT		
		GT _____		
GAM1394 KIAA1165	3'	AATTAGGTTGGGGTTGCAA 67401	CGTGG	
		TTGCA TCCGGCCTGGTT		
		AACGT GGGTTGGATTAA		
		TG____		
GAM1394 KIAA1165	3'	AATTAGGTTGGGGTTGCAA 67401	CGTGG	
		TTGCA TCCGGCCTGGTT		
		AACGT GGGTTGGATTAA		
		TG____		
GAM1394 KIAA1183	3'	GACTGGGCCCTGGGTCTGTG 62534	T GT _	TG
		CACG G CC GGCC GTT		
		GTGT C GG CCGG CAG		
		_TG TC GT		
GAM1394 KIAA1183	3'	GACTGGGCCCTGGGTCTGTG 62534	T GT _	TG
		CACG G CC GGCC GTT		
		GTGT C GG CCGG CAG		
		_TG TC GT		
GAM1394 KIAA1196	3'	GGCTGGGCTGGACCGGGCGTG 61473	_____	TG
		CACGT GGTCCGGCC GTT		
		GTGCG CCAGGTCGG CGG		
		GGA GT		
GAM1394 KIAA1196	3'	GGCTGGGCTGGACCGGGCGTG 61473	_____	TG
		CACGT GGTCCGGCC GTT		
		GTGCG CCAGGTCGG CGG		
		GGA GT		
GAM1394 KIAA1199	3'	CAGGTCCATGTGCA 72511	TCCG	
		TGCACGTGG GCCTG		
		ACGTGTACC TGGAC		
		_____		
GAM1394 KIAA1199	3'	CAGGTCCATGTGCA 72511	TCCG	
		TGCACGTGG GCCTG		
		ACGTGTACC TGGAC		
		_____		
GAM1394 KIAA1204	3'	TTGAGGCCAGGTGCGGTG 69221	G _	
		TATTGCAC TGGTC CGG		



		GTGGCGTG ACCGG GTT	
		G A	
GAM1394 KIAA1204	3'	TTGAGGCCAGGTGCGGTG 69221	G _
		TATTGCAC TGGTC CGG	
		GTGGCGTG ACCGG GTT	
		G A	
GAM1394 KIAA1228	3'	GCTGGCCGGGTGCGGTG 65044	G T
		TATTGCAC TGG CCGGC	
		GTGGCGTG GCC GGTCG	
		G _	
GAM1394 KIAA1228	3'	GCTGGCCGGGTGCGGTG 65044	G T
		TATTGCAC TGG CCGGC	
		GTGGCGTG GCC GGTCG	
		G _	
GAM1394 KIAA1238	5'	ACTGGGCGAGTGTGCGA 71076	TGG CG TG
		TTGCACG TC GCC GT	
		AGCGTGT AG CGG CA	
		G _ _ GT	
GAM1394 KIAA1238	5'	ACTGGGCGAGTGTGCGA 71076	TGG CG TG
		TTGCACG TC GCC GT	
		AGCGTGT AG CGG CA	
		G _ _ GT	
GAM1394 KIAA1244	3'	GACCAGGCTGGACAACATGGTG 71991	TG A _
A		T C CGTG GTCCGGCCTGGTT	
		A G GTAC CAGGTCGGACCAG	
		GT _ AA	
GAM1394 KIAA1244	3'	GACCAGGCTGGACAACATGGTG 71991	TG A _
A		T C CGTG GTCCGGCCTGGTT	
		A G GTAC CAGGTCGGACCAG	
		GT _ AA	
GAM1394 KIAA1257	3'	AGCATTCTGGGCTGGGTGTGGT 62725	TG G CC GTT
G		TAT CAC TGGTCCGG TG	
		GTG GTG GTCGGGTC AC	
		GT G TT GA	
GAM1394 KIAA1257	3'	AGCATTCTGGGCTGGGTGTGGT 62725	TG G CC GTT
G		TAT CAC TGGTCCGG TG	
		GTG GTG GTCGGGTC AC	
		GT G TT GA	
GAM1394 KIAA1276	5'	GCCAGGCCCTGTGGCAGTG 66431	A TG TCC
		TATTGC CG G GGCCTGGT	

			GTGACG GT C CCGGACCG		
			_ GT _		
GAM1394	KIAA1276	5'	GCCAGGCCCTGTGGCAGTG 66431	A	TG TCC
			TATTGC CG G GGCCTGGT		
			GTGACG GT C CCGGACCG		
			_ GT _		
GAM1394	KIAA1322	3'	GGCAAAGGGCCTCGTGCAGTG 72738	T	G _
			TATTGCACG GGTCC GCC		
			GTGACGTGC CCGGG CGG		
			T AAA		
GAM1394	KIAA1322	3'	GGCAAAGGGCCTCGTGCAGTG 72738	T	G _
			TATTGCACG GGTCC GCC		
			GTGACGTGC CCGGG CGG		
			T AAA		
GAM1394	KIAA1332	3'	ACCAGGGTTCATGTCAGTG 71158	C	TCCGG
			TATTG ACGTGG CCTGGT		
			GTGAC TGTACT GGACCA		
			_ TG _		
GAM1394	KIAA1332	3'	ACCAGGGTTCATGTCAGTG 71158	C	TCCGG
			TATTG ACGTGG CCTGGT		
			GTGAC TGTACT GGACCA		
			_ TG _		
GAM1394	KIAA1340	3'	AACCAGGTTTGAGGTTGTGTGT 69177	TG T	_
			GCACG G CC GGCCTGGTT		
			TGTGT T GG TTGGACCAA		
			GT _ AGT		
GAM1394	KIAA1340	3'	AACCAGGTTTGAGGTTGTGTGT 69177	TG T	_
			GCACG G CC GGCCTGGTT		
			TGTGT T GG TTGGACCAA		
			GT _ AGT		
GAM1394	KIAA1364	3'	GCTGGGCATGGTGGTG 63594	TG A	G
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGTCG		
			GT _ _		
GAM1394	KIAA1364	3'	GCTGGGCATGGTGGTG 63594	TG A	G
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGTCG		
			GT _ _		
GAM1394	KIAA1399	3'	GGCCAGGACATGTGCAATG 70252	G	_
			TATTGCACGTG TCC GGCC		

			GTAACGTGTAC AGG CCGG		
			— A		
GAM1394	KIAA1399	3'	GGCCAGGACATGTGCAATG 70252	G	—
			TATTGCACGTG TCC GGCC		
			GTAACGTGTAC AGG CCGG		
			— A		
GAM1394	KIAA1423	3'	AGCTAAATGAGGGGCCAGGTGC 61722	G	GGCC__
			AGTG ATTGCAC TGGTCC TGGTT		
			TGACGTG ACCGGG ATCGA		
			G GAGTAA		
GAM1394	KIAA1423	3'	AGCTAAATGAGGGGCCAGGTGC 61722	G	GGCC__
			AGTG ATTGCAC TGGTCC TGGTT		
			TGACGTG ACCGGG ATCGA		
			G GAGTAA		
GAM1394	KIAA1437	3'	GGCTGGGCTCTGCGGTG 60589	CGT	
			TATTGCA GGTCCGGCC		
			GTGGCGT TCGGGTCGG		
			C__		
GAM1394	KIAA1437	3'	GGCTGGGCTCTGCGGTG 60589	CGT	
			TATTGCA GGTCCGGCC		
			GTGGCGT TCGGGTCGG		
			C__		
GAM1394	KIAA1449	3'	ACCAGTCTCCATGTGTAG 40447	TCC	C
			TTGCACGTGG GG CTGGT		
			GATGTGTACC TC GACCA		
			— T		
GAM1394	KIAA1449	3'	ACCAGTCTCCATGTGTAG 40447	TCC	C
			TTGCACGTGG GG CTGGT		
			GATGTGTACC TC GACCA		
			— T		
GAM1394	KIAA1508	3'	CTGGCTTGTGCAATG 61883	T	T
			TATTGCACG GG CCGG		
			GTAACGTGT TC GGTC		
			— —		
GAM1394	KIAA1508	3'	CTGGCTTGTGCAATG 61883	T	T
			TATTGCACG GG CCGG		
			GTAACGTGT TC GGTC		
			— —		
GAM1394	KIAA1538	3'	GGTCAGGCTGCTTTGTGTGAGA 71553	TG	TG TC GT
			TG TAT CACG G CGGCCTG T		

		GTA GTGT T GTCGGAC G	
		GA GT TC TG	
GAM1394 KIAA1538	3'	GGTCAGGCTGCTTTGTGTGAGA 71553	TG TG TC GT
		TG TAT CACG G CGGCCTG T	
		GTA GTGT T GTCGGAC G	
		GA GT TC TG	
GAM1394 KIAA1550	3'	GGCCAGGCAACTGTGAGCAGTG 66558	A TG CCG
		TATTGC CG GT GCCTGGTT	
		GTGACG GT CA CGGACCGG	
		A GT A__	
GAM1394 KIAA1550	3'	GGCCAGGCAACTGTGAGCAGTG 66558	A TG CCG
		TATTGC CG GT GCCTGGTT	
		GTGACG GT CA CGGACCGG	
		A GT A__	
GAM1394 KIAA1550	3'	GGCCAGGCAGCTGTGAGCAGTG 66559	A TG CCG
		TATTGC CG GT GCCTGGTT	
		GTGACG GT CG CGGACCGG	
		A GT A__	
GAM1394 KIAA1550	3'	GGCCAGGCAGCTGTGAGCAGTG 66559	A TG CCG
		TATTGC CG GT GCCTGGTT	
		GTGACG GT CG CGGACCGG	
		A GT A__	
GAM1394 KIAA1550	3'	GGCCAGGCAGCTGTGAGCAGTG 66560	A TG CCG
		TATTGC CG GT GCCTGGTT	
		GTGACG GT CG CGGACCGG	
		A GT A__	
GAM1394 KIAA1550	3'	GGCCAGGCAGCTGTGAGCAGTG 66560	A TG CCG
		TATTGC CG GT GCCTGGTT	
		GTGACG GT CG CGGACCGG	
		A GT A__	
GAM1394 KIAA1550	3'	GGCCAGGCAGCTGTGGGCAATG 66561	A TG CCG
		TATTGC CG GT GCCTGGTT	
		GTAACG GT CG CGGACCGG	
		G GT A__	
GAM1394 KIAA1550	3'	GGCCAGGCAGCTGTGGGCAATG 66561	A TG CCG
		TATTGC CG GT GCCTGGTT	
		GTAACG GT CG CGGACCGG	
		G GT A__	
GAM1394 KIAA1550	3'	GGCCAGGCAGCTGTGGGCAGTG 66562	A TG CCG
		TATTGC CG GT GCCTGGTT	

		GTGACG GT CG CGGACCGG	
		G GT A__	
GAM1394 KIAA1550	3'	GGCCAGGCAGCTGTGGGCAGTG 66562	A TG CCG
		TATTGC CG GT GCCTGGTT	
		GTGACG GT CG CGGACCGG	
		G GT A__	
GAM1394 KIAA1550	3'	GGCCAGGCAGCTGTGGGCAGTG 66563	A TG CCG
		TATTGC CG GT GCCTGGTT	
		GTGACG GT CG CGGACCGG	
		G GT A__	
GAM1394 KIAA1550	3'	GGCCAGGCAGCTGTGGGCAGTG 66563	A TG CCG
		TATTGC CG GT GCCTGGTT	
		GTGACG GT CG CGGACCGG	
		G GT A__	
GAM1394 KIAA1559	3'	AGCCAAGTGGCCAGGTGCGGTG 73056	G CG C
		TATTGCAC TGGTC GC TGGTT	
		GTGGCGTG ACCGG TG ACCGA	
		G __ A	
GAM1394 KIAA1559	3'	AGCCAAGTGGCCAGGTGCGGTG 73056	G CG C
		TATTGCAC TGGTC GC TGGTT	
		GTGGCGTG ACCGG TG ACCGA	
		G __ A	
GAM1394 KIAA1559	3'	GGTTAGGGATTATGTCAAGTG 73071	C __
		TATTG ACGTGGTCC GGCC	
		GTGAC TGTATTAGG TTGG	
		GA	
GAM1394 KIAA1559	3'	GGTTAGGGATTATGTCAAGTG 73071	C __
		TATTG ACGTGGTCC GGCC	
		GTGAC TGTATTAGG TTGG	
		GA	
GAM1394 KIAA1600	3'	AATTGGGTATGTATGTGAATG 71440	G GTCCG TG
		TATT CACGTG GCC GTT	
		GTAA GTGTAT TGG TAA	
		GA__ GT	
GAM1394 KIAA1600	3'	AATTGGGTATGTATGTGAATG 71440	G GTCCG TG
		TATT CACGTG GCC GTT	
		GTAA GTGTAT TGG TAA	
		GA__ GT	
GAM1394 KIAA1671	3'	GGCCAGGCTGGAATGCAGTG 65684	CGTGG
		TATTGCA TCCGGCCTGGTT	

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GTGACGT  AGGTCGGACCGG
A____
GAM1394 KIAA1671 3' GGCCAGGCTGGAATGCAGTG 65684      CGTGG
TATTGCA  TCCGGCCTGGTT
|||||  |||||
GTGACGT  AGGTCGGACCGG
A____
GAM1394 KIAA1691 5' AGCCGGGCGCGGCGGCGC 92551  ACGT
GC  GGTCCGGCCTGGTT
||  |||||
CG  CCGGGCCGGGCCGA
GG__
GAM1394 KIAA1691 5' AGCCGGGCGCGGCGGCGC 92551  ACGT
GC  GGTCCGGCCTGGTT
||  |||||
CG  CCGGGCCGGGCCGA
GG__
GAM1394 KIAA1691 3' AGCTGGATGGCCACGTGCAG 92552      T  GC TG
TTGCACGTGG CCG C GTT
||||| ||| | |||
GACGTGCACC GGT G CGA
_ A_ GT
GAM1394 KIAA1691 5' GGCCGGGCGCGGCCAGGAGC 92559  ACGT_
GC  GGTCCGGCCTGGTT
||  |||||
CG  CCGGGCCGGGCCGG
AGGAC
GAM1394 KIAA1691 5' GGCCGGGCGCGGCCAGGAGC 92559  ACGT_
GC  GGTCCGGCCTGGTT
||  |||||
CG  CCGGGCCGGGCCGG
AGGAC
GAM1394 KIAA1691 3' GGCTGGGCCCTGCAGTG 92561      CGT
TATTGCA  GGTCCGGCC
|||||  |||||
GTGACGT  CCGGGTCGG
C__
GAM1394 KIAA1691 3' GGCTGGGCCCTGCAGTG 92561      CGT
TATTGCA  GGTCCGGCC
|||||  |||||
GTGACGT  CCGGGTCGG
C__
GAM1394 KIAA1691 3' AGCTGGATGGCCACGTGCAG 92552      T  GC TG
TTGCACGTGG CCG C GTT
||||| ||| | |||
GACGTGCACC GGT G CGA
_ A_ GT
GAM1394 KIAA1719 3' GACTAGGTTGGAGGTAGCAG 68161  _ GTGG
TTGC AC  TCCGGCCTGGTT
||| ||  |||||

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		GACG TG AGGTTGGATCAG	
		A G__	
GAM1394 KIAA1719	3'	GACTAGGTTGGAGGTAGCAG 68161	_ GTGG
		TTGC AC TCCGGCCTGGTT	
		GACG TG AGGTTGGATCAG	
		A G__	
GAM1394 KIAA1729	5'	AGCCAGGCAAATACTATTGTGA 89124	TG C CCG_
	TA	TAT CA GTGGT GCCTGGTT	
		ATA GT TATCA CGGACCGA	
		GT _ TAAA	
GAM1394 KIAA1729	5'	AGCCAGGCAAATACTATTGTGA 89124	TG C CCG_
	TA	TAT CA GTGGT GCCTGGTT	
		ATA GT TATCA CGGACCGA	
		GT _ TAAA	
GAM1394 KIAA1786	3'	TTAAGGCCACAGTGTGTGATA 66043	TG TG CC GGTT
		TAT CACG GT GGCCT	
		ATA GTGT CA CCGGA	
		GT GA _ ATTG	
GAM1394 KIAA1786	3'	TTAAGGCCACAGTGTGTGATA 66043	TG TG CC GGTT
		TAT CACG GT GGCCT	
		ATA GTGT CA CCGGA	
		GT GA _ ATTG	
GAM1394 KIAA1813	5'	GGCTGGGGTGTGTGGGGTG 70306	G GT G
		TATT CAC G TCCGGCC	
		GTGG GTG T GGGTCGG	
		G TG G	
GAM1394 KIAA1813	5'	GGCTGGGGTGTGTGGGGTG 70306	G GT G
		TATT CAC G TCCGGCC	
		GTGG GTG T GGGTCGG	
		G TG G	
GAM1394 KIAA1854	3'	AGCCAGGTTGGAGGTGGAGTA 71736	G GTGG
		TATT CAC TCCGGCCTGGTT	
		ATGA GTG AGGTTGGACCGA	
		G G__	
GAM1394 KIAA1854	3'	AGCCAGGTTGGAGGTGGAGTA 71736	G GTGG
		TATT CAC TCCGGCCTGGTT	
		ATGA GTG AGGTTGGACCGA	
		G G__	
GAM1394 KIAA1856	3'	GGCCAGGTGTGCACGTG 92665	GTCCG
		CACGTG GCCTGGTT	

			GTGCAC	TGGACCGG		
			GTG__			
GAM1394	KIAA1856	3'	GGCCAGGTGTGCACGTG	92665	GTCCG	
			CACGTG	GCCTGGTT		
			GTGCAC	TGGACCGG		
			GTG__			
GAM1394	KIAA1872	3'	GCCGGGCATGGTGGTG	62934	TG A G	
			TAT C	CGTG TCCGGC		
			GTG G	GTAC GGGCCG		
			GT _ _			
GAM1394	KIAA1872	3'	GCCGGGCATGGTGGTG	62934	TG A G	
			TAT C	CGTG TCCGGC		
			GTG G	GTAC GGGCCG		
			GT _ _			
GAM1394	KIAA1879	3'	ACCAGGCCAAGTGTGGTG	73559	TG GTGGTCC	
			TAT CAC	GGCCTGGT		
			GTG GTG	CCGGACCA		
			GT AA_____			
GAM1394	KIAA1879	3'	ACCAGGCCAAGTGTGGTG	73559	TG GTGGTCC	
			TAT CAC	GGCCTGGT		
			GTG GTG	CCGGACCA		
			GT AA_____			
GAM1394	KIAA1881	3'	GGTTGGGCTGGGCCCAGAGTGC	95343	GT__ GG	
			GCAC	GGTCCGGCCT TT		
			CGTG	CCGGGTCGGG GG		
			AGAC	TT		
GAM1394	KIAA1881	3'	GGTTGGGCTGGGCCCAGAGTGC	95343	GT__ GG	
			GCAC	GGTCCGGCCT TT		
			CGTG	CCGGGTCGGG GG		
			AGAC	TT		
GAM1394	KIAA1887	5'	TGGCTGGCAGCGCTGTGTGCGA	76780	TG ____ TGGTT	
			TTGCACG	GT CCGGCC		
			AGCGTGT	CG GGTCGG		
			GT	CGAC TT		
GAM1394	KIAA1887	5'	TGGCTGGCAGCGCTGTGTGCGA	76780	TG ____ TGGTT	
			TTGCACG	GT CCGGCC		
			AGCGTGT	CG GGTCGG		
			GT	CGAC TT		
GAM1394	KIAA1908	5'	GGCTGGAGCCCCAGGTGCAGTG	73401	G ____	
			TATTGCAC	TGG TCCGGCC		



			GTGACGTG ACC AGGTCGG		
			G CCG		
GAM1394	KIAA1908	5'	GGCTGGAGCCCCAGGTGCAGTG 73401	G	___
			TATTGCAC TGG TCCGGCC		
			GTGACGTG ACC AGGTCGG		
			G CCG		
GAM1394	KIAA1910	5'	GACTGGCGTCTGGGCTATTGCA 73326	C	__ TG
			GTG ATTGCA GTGGTCCGG C C GTT		
			TGACGT TATCGGGTC G G CAG		
			— T C GT		
GAM1394	KIAA1910	5'	GACTGGCGTCTGGGCTATTGCA 73326	C	__ TG
			GTG ATTGCA GTGGTCCGG C C GTT		
			TGACGT TATCGGGTC G G CAG		
			— T C GT		
GAM1394	KIAA1922	5'	GCTGGGCCTGGCAGTG 73633	A	T
			TATTGC CG GGTCCGGC		
			GTGACG GT CCGGGTCG		
			— —		
GAM1394	KIAA1922	5'	GCTGGGCCTGGCAGTG 73633	A	T
			TATTGC CG GGTCCGGC		
			GTGACG GT CCGGGTCG		
			— —		
GAM1394	KIAA1951	3'	CTGGCCAGGTGCGGTG 73760	G	T
			TATTGCAC TGG CCGG		
			GTGGCGTG ACC GGTC		
			G —		
GAM1394	KIAA1951	3'	CTGGCCAGGTGCGGTG 73760	G	T
			TATTGCAC TGG CCGG		
			GTGGCGTG ACC GGTC		
			G —		
GAM1394	KIAA1957	3'	GGCTGGGCTGGGCGCTGATGCT 75719	T	_ TG TG
			GTA TAT GCA CG GTCCGGCC GTT		
			ATG CGT GT CGGGTCGG CGG		
			T A CG GT		
GAM1394	KIAA1957	3'	GGCTGGGCTGGGCGCTGATGCT 75719	T	_ TG TG
			GTA TAT GCA CG GTCCGGCC GTT		
			ATG CGT GT CGGGTCGG CGG		
			T A CG GT		
GAM1394	KIAA1975	5'	GCCAGCTATGTGTAG 73973	CC	
			TTGCACGTGGT GGC		

			GATGTGTATCG CCG	
			A_	
GAM1394	KIAA1975	5'	GCCAGCTATGTGTAG 73973	CC
			TTGCACGTGGT GGC	
			GATGTGTATCG CCG	
			A_	
GAM1394	KIAA1979	3'	GGTTGGCTGTGTTTCAGTA 88288	C TG T
			TATTG ACG G CCGGCC	
			ATGAC TGT C GGTTGG	
			T GT_	
GAM1394	KIAA1979	3'	GGTTGGCTGTGTTTCAGTA 88288	C TG T
			TATTG ACG G CCGGCC	
			ATGAC TGT C GGTTGG	
			T GT_	
GAM1394	KIF13B	3'	GGCTGGGCTGGTGCAG 30913	G
			TTGCAC TGGTCCGGCC	
			GACGTG GTCGGGTCGG	
			—	
GAM1394	KIF13B	3'	GGCTGGGCTGGTGCAG 82826	G
			TTGCAC TGGTCCGGCC	
			GACGTG GTCGGGTCGG	
			—	
GAM1394	KIF13B	3'	GGCTGGGCTGGTGCAG 82826	G
			TTGCAC TGGTCCGGCC	
			GACGTG GTCGGGTCGG	
			—	
GAM1394	KIF13B	3'	GGCTGGGCTGGTGCAG 30913	G
			TTGCAC TGGTCCGGCC	
			GACGTG GTCGGGTCGG	
			—	
GAM1394	KLK6	5'	GGCGGGGGCCAGTGTGGTG 10921	TG G G_
			TAT CAC TGGTCC GCC	
			GTG GTG ACCGGG CGG	
			GT _ GG	
GAM1394	KLK6	5'	GGCGGGGGCCAGTGTGGTG 10921	TG G G_
			TAT CAC TGGTCC GCC	
			GTG GTG ACCGGG CGG	
			GT _ GG	
GAM1394	KPNB3	3'	GATCGGTAGTGTGTGTGTAG 9634	TG TCCG T
			TTGCACG G GCC GGTT	

			GATGTGT T TGG CTAG		
			GT GTGA _		
GAM1394	KPNB3	3'	GATCGGTAGTGTGTGTGTAG 9634	TG TCCG T	
			TTGCACG G GCC GGTT		
			GATGTGT T TGG CTAG		
			GT GTGA _		
GAM1394	L3MBTL2	3'	GGCGACCTGTGTGGTG 88759	TG T CG	
			TAT CACG GGTC GCC		
			GTG GTGT CCAG CGG		
			GT _ _		
GAM1394	L3MBTL2	3'	GGCGACCTGTGTGGTG 88759	TG T CG	
			TAT CACG GGTC GCC		
			GTG GTGT CCAG CGG		
			GT _ _		
GAM1394	LASP1	3'	GGCTGGGCTGGGCTGAGC 20458	A GT TG	
			GC C GGTCCGGCC GTT		
			CG G TCGGGTCGG CGG		
			A _ GT		
GAM1394	LASP1	3'	GGCTGGGCTGGGCTGAGC 20458	A GT TG	
			GC C GGTCCGGCC GTT		
			CG G TCGGGTCGG CGG		
			A _ GT		
GAM1394	LASP1	3'	GGCTGGGCTGGGCTGGGC 20459	ACGT TG	
			GC GGTCCGGCC GTT		
			CG TCGGGTCGG CGG		
			GG _ GT		
GAM1394	LASP1	3'	GGCTGGGCTGGGCTGGGC 20459	ACGT TG	
			GC GGTCCGGCC GTT		
			CG TCGGGTCGG CGG		
			GG _ GT		
GAM1394	LENG9	5'	GCTAGGCCGGAGCGCG 74520	G	
			CGTG TCCGGCCTGGT		
			GCGC AGGCCGGATCG		
			G		
GAM1394	LENG9	5'	GCTAGGCCGGAGCGCG 74520	G	
			CGTG TCCGGCCTGGT		
			GCGC AGGCCGGATCG		
			G		
GAM1394	LIG-1	3'	CCTAGGCTGCTGTGCGGTG 63895	TGGTC TT	
			TATTGCACG CGGCCTGG		

		GTGGCGTGT GTCGGATC C_____ CC		
GAM1394	LIG-1	3' CCTAGGCTGCTGTGCGGTG 63895 TATTGCACG CGGCCTGG               GTGGCGTGT GTCGGATC C_____ CC	TGGTC	TT
GAM1394	LUC7L	3' TGCTGAGGGCCGTGTCTGGTG 35914 CAC GG CGGCCT GGT                  GTG CT GCCGGG TCG GT GT AG TC	GT TC	__ T
GAM1394	LUC7L	3' TGCTGAGGGCCGTGTCTGGTG 35914 CAC GG CGGCCT GGT                  GTG CT GCCGGG TCG GT GT AG TC	GT TC	__ T
GAM1394	LW-1 G	5' CTGCATGGCGACGGCGTGTGGT 60259 TAT CACGT GTC GCC TG                      GTG GTGCG CAG CGG AC GT G __ T GTCA	TG G CG	_ GTT
GAM1394	LW-1 G	5' CTGCATGGCGACGGCGTGTGGT 60259 TAT CACGT GTC GCC TG                      GTG GTGCG CAG CGG AC GT G __ T GTCA	TG G CG	_ GTT
GAM1394	LW-1 G	5' CTGCATGGCGACGGCGTGTGGT 32368 TAT CACGT GTC GCC TG                      GTG GTGCG CAG CGG AC GT G __ T GTCA	TG G CG	_ GTT
GAM1394	LW-1 G	5' CTGCATGGCGACGGCGTGTGGT 32368 TAT CACGT GTC GCC TG                      GTG GTGCG CAG CGG AC GT G __ T GTCA	TG G CG	_ GTT
GAM1394	MAC30	5' AACCAGGCGCTGCGTGGAGTG 62677 TATT CACG GT GCCTGGTT                    GTGA GTGC CG CGGACCAA G GT ____	G TG CCG	
GAM1394	MAC30	5' AACCAGGCGCTGCGTGGAGTG 62677 TATT CACG GT GCCTGGTT                    GTGA GTGC CG CGGACCAA G GT ____	G TG CCG	
GAM1394	MAD4	3' AGCAAGGCGGGCCGTGTGTAA 21268 TTGCACGTGGTCCG CCT GTT 	G G	

			AATGTGTGCCGGGC GGA CGA		
			— A		
GAM1394	MAD4	3'	AGCAAGGCGGGCCGTGTGTAA 21268	G	G
			TTGCACGTGGTCCG CCT GTT		
			AATGTGTGCCGGGC GGA CGA		
			— A		
GAM1394	MAFB	3'	TCCGGCGGCTGCGTGCGG 18417	TG T	G T TT
			TTGCACG G CCG CC GG		
			GGCGTGC C GGC GG CC		
			GT _ _ _ TC		
GAM1394	MAFB	3'	TCCGGCGGCTGCGTGCGG 18417	TG T	G T TT
			TTGCACG G CCG CC GG		
			GGCGTGC C GGC GG CC		
			GT _ _ _ TC		
GAM1394	MAPK8IP3	3'	GGCTGGGTTGGGCTGGTG 52990	G	TG
			CAC TGGTCCGGCC GTT		
			GTG GTCGGGTTGG CGG		
			— GT		
GAM1394	MAPK8IP3	3'	GGCTGGGTTGGGCTGGTG 52990	G	TG
			CAC TGGTCCGGCC GTT		
			GTG GTCGGGTTGG CGG		
			— GT		
GAM1394	MGC:5244	5'	GGCCAGGCCGGGCGGCGTTGT 48328	_	G
			GCA CGT GTCCGGCCTGGTT		
			TGT GCG CGGGCCGGACCGG		
			T G		
GAM1394	MGC:5244	5'	GGCCAGGCCGGGCGGCGTTGT 48328	_	G
			GCA CGT GTCCGGCCTGGTT		
			TGT GCG CGGGCCGGACCGG		
			T G		
GAM1394	MGC10067	3'	AGTTAGGCCTGTATGTGT 58935	GTCC	GG
			GCACGTG GGCCT TT		
			TGTGTAT CCGGA GA		
			GT _ TT		
GAM1394	MGC10067	3'	AGTTAGGCCTGTATGTGT 58935	GTCC	GG
			GCACGTG GGCCT TT		
			TGTGTAT CCGGA GA		
			GT _ TT		
GAM1394	MGC10471	5'	GGTCAGGACAGTGCAGTG 48017	GTG	_
			TATTGCAC GTCC GGCC		

		GTGACGTG CAGG CTGG	
		A__ A	
GAM1394	MGC10471	5' GGTCAGGACAGTGCAGTG 48017	GTG _
		TATTGCAC GTCC GGCC	
		GTGACGTG CAGG CTGG	
		A__ A	
GAM1394	MGC10814	5' GCTGGGCATGGTGATG 51040	TG A G
		TAT C CGTG TCCGGC	
		GTA G GTAC GGGTCG	
		GT _ _	
GAM1394	MGC10814	5' GCTGGGCATGGTGATG 51040	TG A G
		TAT C CGTG TCCGGC	
		GTA G GTAC GGGTCG	
		GT _ _	
GAM1394	MGC11296	5' GGCCGGGCTGGGCGCCGGTAGT 50378	A TG
	G	TATTGC CG GTCCGGCCTGGTT	
		GTGATG GC CGGGTCGGGCCGG	
		_ CG	
GAM1394	MGC11296	5' GGCCGGGCTGGGCGCCGGTAGT 50378	A TG
	G	TATTGC CG GTCCGGCCTGGTT	
		GTGATG GC CGGGTCGGGCCGG	
		_ CG	
GAM1394	MGC1136	3' GGTTGGGCAGTGTGGTG 43804	TG GTG
		TAT CAC GTCCGGCC	
		GTG GTG CGGGTTGG	
		GT A__	
GAM1394	MGC1136	3' GGTTGGGCAGTGTGGTG 43804	TG GTG
		TAT CAC GTCCGGCC	
		GTG GTG CGGGTTGG	
		GT A__	
GAM1394	MGC12466	3' AGCTAGGCTGAAGTGTAGTG 79031	GTGGTC
		TATTGCAC CGGCCTGGTT	
		GTGATGTG GTCGGATCGA	
		AA_____	
GAM1394	MGC12466	3' AGCTAGGCTGAAGTGTAGTG 79031	GTGGTC
		TATTGCAC CGGCCTGGTT	
		GTGATGTG GTCGGATCGA	
		AA_____	
GAM1394	MGC12837	5' AGCCAGGCTGGGCTTCCTG 51181	CGT
		CA GGTCCGGCCTGGTT	

		GT TCGGGTCGGACCGA		
		CCT		
GAM1394	MGC12837	5' AGCCAGGCTGGGCTTCCTG	51181	CGT
		CA GGTCCGGCCTGGTT		
		GT TCGGGTCGGACCGA		
		CCT		
GAM1394	MGC12992	3' GGCAGGACCATGTGGATA	50345	G G
		TATT CACGTGGTCC GCC		
		ATAG GTGTACCAGG CGG		
		— A		
GAM1394	MGC12992	3' GGCAGGACCATGTGGATA	50345	G G
		TATT CACGTGGTCC GCC		
		ATAG GTGTACCAGG CGG		
		— A		
GAM1394	MGC13010	5' AGCCCGGTGTGTGCAGTG	51082	TGGT C
		TATTGCACG CCGG CT		
		GTGACGTGT GGCC GA		
		GT__ C		
GAM1394	MGC13010	5' AGCCCGGTGTGTGCAGTG	51082	TGGT C
		TATTGCACG CCGG CT		
		GTGACGTGT GGCC GA		
		GT__ C		
GAM1394	MGC13090	3' AGCCAGGGGAGGTTGTGTGT	51136	TG T GG_
		GCACG G CC CCTGGTT		
		TGTGT T GG GGACCGA		
		GT_ AGG		
GAM1394	MGC13090	3' AGCCAGGGGAGGTTGTGTGT	51136	TG T GG_
		GCACG G CC CCTGGTT		
		TGTGT T GG GGACCGA		
		GT_ AGG		
GAM1394	MGC13125	3' GGCTGGGCTGTGGTAGTG	51179	A TG
		TATTGC CG GTCCGGCC		
		GTGATG GT CGGGTCGG		
		_ GT		
GAM1394	MGC13125	3' GGCTGGGCTGTGGTAGTG	51179	A TG
		TATTGC CG GTCCGGCC		
		GTGATG GT CGGGTCGG		
		_ GT		
GAM1394	MGC14126	3' ATCATGCCGGGTGCGGTG	51853	GTGGT C
		TATTGCAC CCGGC TGGT		

		GTGGCGTG GGCCG ACTA	
		_____ T	
GAM1394	MGC14126	3' ATCATGCCGGGTGCGGTG 51853	GTGGT C
		TATTGCAC CCGGC TGGT	
		GTGGCGTG GGCCG ACTA	
		_____ T	
GAM1394	MGC14376	3' AGTTGGGTGATATGTGTCATG 51845	T G CG GG
		TAT GCACGTG TC GCCT TT	
		GTA TGTGTAT AG TGGG GA	
		C _ _ TT	
GAM1394	MGC14376	3' AGTTGGGTGATATGTGTCATG 51845	T G CG GG
		TAT GCACGTG TC GCCT TT	
		GTA TGTGTAT AG TGGG GA	
		C _ _ TT	
GAM1394	MGC14839	3' GGTTAGGTGGAGTGTGCAG 54698	TGG G GG
		TTGCACG TCCG CCT TT	
		GACGTGT AGGT GGA GG	
		G _ _ TT	
GAM1394	MGC14839	3' GGTTAGGTGGAGTGTGCAG 54698	TGG G GG
		TTGCACG TCCG CCT TT	
		GACGTGT AGGT GGA GG	
		G _ _ TT	
GAM1394	MGC15416	3' GGCCAAGGCCTGTGCAGTA 56543	T C_
		TATTGCACG GGTC GGCC	
		ATGACGTGT CCGG CCGG	
		_ AA	
GAM1394	MGC15416	3' GGCCAAGGCCTGTGCAGTA 50427	T C_
		TATTGCACG GGTC GGCC	
		ATGACGTGT CCGG CCGG	
		_ AA	
GAM1394	MGC15416	3' GGCCAAGGCCTGTGCAGTA 56543	T C_
		TATTGCACG GGTC GGCC	
		ATGACGTGT CCGG CCGG	
		_ AA	
GAM1394	MGC15416	3' GGCCAAGGCCTGTGCAGTA 50427	T C_
		TATTGCACG GGTC GGCC	
		ATGACGTGT CCGG CCGG	
		_ AA	
GAM1394	MGC15438	5' AGCCAGGCTGGGAGCTGGGA 51787	G C GG
		TT CA GT TCCGGCCTGGTT	



				AG GT CG GGGTCGGACCGA			
				G _ A_			
GAM1394	MGC15438	5'	AGCCAGGCTGGGAGCTGGGA	51787	G C GG		
			TT CA GT TCCGGCCTGGTT				
			AG GT CG GGGTCGGACCGA				
			G _ A_				
GAM1394	MGC15606	5'	TGGCTGGAGTACATTGGTGTGA	58881	TG ____ G	TGGTT	
	TG		T CAC GTG TCCGGCC				
			A GTG CAT AGGTCGG				
			GT GTTA G TT				
GAM1394	MGC15606	5'	TGGCTGGAGTACATTGGTGTGA	58881	TG ____ G	TGGTT	
	TG		T CAC GTG TCCGGCC				
			A GTG CAT AGGTCGG				
			GT GTTA G TT				
GAM1394	MGC15631	3'	ACCAGGCCAGGTGCGGTG	51257	G GGTCC		
			TATTGCAC T GGCCTGGT				
			GTGGCGTG A CCGGACCA				
			G ____				
GAM1394	MGC15631	3'	ACCAGGCCAGGTGCGGTG	51257	G GGTCC		
			TATTGCAC T GGCCTGGT				
			GTGGCGTG A CCGGACCA				
			G ____				
GAM1394	MGC16025	3'	GGCCAGGTGCCTGCGTTGTGAT	51923	TG _ _ CCG		
	G		TAT CA CGT GGT GCCTGGTT				
			GTA GT GCG CCG TGGACCGG				
			GT T T ____				
GAM1394	MGC16025	3'	GGCCAGGTGCCTGCGTTGTGAT	51923	TG _ _ CCG		
	G		TAT CA CGT GGT GCCTGGTT				
			GTA GT GCG CCG TGGACCGG				
			GT T T ____				
GAM1394	MGC16063	5'	GGCTAGGTTGTTTCTGTG	53861	T TC		
			CACG GG CGGCCTGGTT				
			GTGT CT GTTGGATCGG				
			_ TT				
GAM1394	MGC16063	5'	GGCTAGGTTGTTTCTGTG	53861	T TC		
			CACG GG CGGCCTGGTT				
			GTGT CT GTTGGATCGG				
			_ TT				
GAM1394	MGC16332	3'	GCTGGGACGCGGTGGTG	56777	TG A G		
			TAT C CGTG TCCGGC				

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GTG G GCAC GGGTCG
GT _ _
GAM1394 MGC16332 3' GCTGGGCACGGTGGTG 56777 TG A G
TAT C CGTG TCCGGC
||| | ||| |||||
GTG G GCAC GGGTCG
GT _ _
GAM1394 MGC16384 3' GTCAGGTCAAGGCTGCAGTG 53868 _TG C_ GT
CAC G GTC GGCCTG T
||| | ||| ||||| |
GTG C CGG CTGGAC G
A GT AA TG
GAM1394 MGC16384 3' GTCAGGTCAAGGCTGCAGTG 53868 _TG C_ GT
CAC G GTC GGCCTG T
||| | ||| ||||| |
GTG C CGG CTGGAC G
A GT AA TG
GAM1394 MGC16491 3' GATCAGGCTGGGCCAC 53638
GTGGTCCGGCCTGGTT
|||||||
CACCGGGTCGGA TAG
GAM1394 MGC16491 3' GATCAGGCTGGGCCAC 53638
GTGGTCCGGCCTGGTT
|||||||
CACCGGGTCGGA TAG
GAM1394 MGC17299 5' GCTGAGGCCATGTGAGTA 58238 G _
TATT CACGTGGTC CGGC
||| ||||| |||
ATGA GTGTACCGG GTCG
_ A
GAM1394 MGC17299 5' GCTGAGGCCATGTGAGTA 58238 G _
TATT CACGTGGTC CGGC
||| ||||| |||
ATGA GTGTACCGG GTCG
_ A
GAM1394 MGC20496 3' GGCTGGAGCCGTGTGT 53433 _
GCACGTGG TCCGGCC
||||| |||||
TGTGTGCC AGGTCCG
G
GAM1394 MGC20496 3' GGCTGGAGCCGTGTGT 53433 _
GCACGTGG TCCGGCC
||||| |||||
TGTGTGCC AGGTCCG
G
GAM1394 MGC21688 3' GCTGGGCTCGTGCTGTG 58267 T T
TAT GCACG GGTCCGGC
||| ||||| |||||

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			GTG CGTGC TCGGGTCG		
			T _		
GAM1394	MGC21688	3'	GCTGGGCTCGTGCTGTG	58267	T T
			TAT GCACG GGTCCGGC		
			GTG CGTGC TCGGGTCG		
			T _		
GAM1394	MGC22014	3'	AGCCATGTGGATGTGTGTGTGG	64484	TG TG_ G C
		TG	TAT CACG GTCCG C TGGTT		
			GTG GTGT TAGGT G ACCGA		
			GT GTG _ T		
GAM1394	MGC22014	3'	AGCCATGTGGATGTGTGTGTGG	64484	TG TG_ G C
		TG	TAT CACG GTCCG C TGGTT		
			GTG GTGT TAGGT G ACCGA		
			GT GTG _ T		
GAM1394	MGC23427	5'	GACCGGGCGCGGGCGCCCGCAG	58325	AC G
			TTGC GTG TCCGGCCTGGTT		
			GACG CGC GGGCCGGGCCAG		
			CC _		
GAM1394	MGC23427	5'	GACCGGGCGCGGGCGCCCGCAG	58325	AC G
			TTGC GTG TCCGGCCTGGTT		
			GACG CGC GGGCCGGGCCAG		
			CC _		
GAM1394	MGC2477	5'	GCCAGGCTGGGCTTG	44065	T
			CG GGTCCGGCCTGGT		
			GT TCGGGTCGGACCG		
			_		
GAM1394	MGC2477	5'	GCCAGGCTGGGCTTG	44065	T
			CG GGTCCGGCCTGGT		
			GT TCGGGTCGGACCG		
			_		
GAM1394	MGC2508	5'	ACCGGGCTGGTGCGAC	44253	G _
			GT GT CCGGCCTGGT		
			CA CG GGTCGGGCCA		
			G T		
GAM1394	MGC2508	5'	ACCGGGCTGGTGCGAC	44253	G _
			GT GT CCGGCCTGGT		
			CA CG GGTCGGGCCA		
			G T		
GAM1394	MGC2562	3'	GATTATTCTGGCCAGGTGCGGT	50439	G T CC
		G	TATTGCAC TGG CCGG TGGTT		

			GTGGCGTG ACC GGTC ATTAG		
			G _ TT		
GAM1394	MGC2562	3'	GATTATTCTGGCCAGGTGCGGT 50439	G T CC	
	G		TATTGCAC TGG CCGG TGGTT		
			GTGGCGTG ACC GGTC ATTAG		
			G _ TT		
GAM1394	MGC2714	5'	GGCCGGGCTGGGCGCGCCGGT 50201	_____	
	GCGG		GCAC GTGGTCCGGCCTGGTT		
			CGTG CGCCGGGTCTGGGCCGG		
			GCCG		
GAM1394	MGC2714	5'	GGCCGGGCTGGGCGCGCCGGT 50201	_____	
	GCGG		GCAC GTGGTCCGGCCTGGTT		
			CGTG CGCCGGGTCTGGGCCGG		
			GCCG		
GAM1394	MGC4248	3'	GCCAGGCTGGGTGCAGTG 50330	GTGGT	
			TATTGCAC CCGGCCTGGT		
			GTGACGTG GGTCGGACCG		
			_____		
GAM1394	MGC4248	3'	GCCAGGCTGGGTGCAGTG 50330	GTGGT	
			TATTGCAC CCGGCCTGGT		
			GTGACGTG GGTCGGACCG		
			_____		
GAM1394	MGC4251	3'	CTAGGCTCTGCAGTG 50459	CGTGGTCC	
			TATTGCA GGCCTGG		
			GTGACGT TCGGATC		
			C_____		
GAM1394	MGC4251	3'	CTAGGCTCTGCAGTG 50459	CGTGGTCC	
			TATTGCA GGCCTGG		
			GTGACGT TCGGATC		
			C_____		
GAM1394	MGC4549	3'	TGGCTGTACAGCCGTGTGT 50467	C_____ TGGTT	
			GCACGTGGT CGGCC		
			TGTGTGCCG GTCGG		
			AACT TT		
GAM1394	MGC4549	3'	TGGCTGTACAGCCGTGTGT 50467	C_____ TGGTT	
			GCACGTGGT CGGCC		
			TGTGTGCCG GTCGG		
			AACT TT		
GAM1394	MGC4655	3'	AACCAGTTGAAACCCGTGTAAT 52797	T C_ C	
	G		TATTGCACG GGT CGGC TGGTT		

			GTAATGTGC CCA GTTG ACCAA	
			_ AA _	
GAM1394	MGC4655	3'	AACCAGTTGAAACCCGTGTAAT 52797	T C_ C
	G		TATTGCACG GGT CGGC TGGTT	
			GTAATGTGC CCA GTTG ACCAA	
			_ AA _	
GAM1394	MGC4796	3'	GGCTGGGCCCTGTAGTG 61493	CGT
			TATTGCA GGTCCGGCC	
			GTGATGT CCGGGTCGG	
			C_	
GAM1394	MGC4796	3'	GGCTGGGCCCTGTAGTG 61493	CGT
			TATTGCA GGTCCGGCC	
			GTGATGT CCGGGTCGG	
			C_	
GAM1394	MGC9564	3'	AACCAGGTTCCCAACACGTGTA 54739	GTCC_
	G		TTGCACGTG GGCCTGGTT	
			GATGTGCAC TTGGACCAA	
			AACCC	
GAM1394	MGC9564	3'	AACCAGGTTCCCAACACGTGTA 54739	GTCC_
	G		TTGCACGTG GGCCTGGTT	
			GATGTGCAC TTGGACCAA	
			AACCC	
GAM1394	MGC9753	3'	GGCCAGGCTGCCTGTGTGCA 53055	TG TC
			TGCACG G CGGCCTGGTT	
			ACGTGT C GTCGGACCGG	
			GT C_	
GAM1394	MGC9753	3'	GGCCAGGCTGCCTGTGTGCA 53055	TG TC
			TGCACG G CGGCCTGGTT	
			ACGTGT C GTCGGACCGG	
			GT C_	
GAM1394	MMD	3'	GGTTGTAAAAGTCAGTGCAATA 59810	G TC_____
			TATTGCAC TGG CGGCC	
			ATAACGTG ACT GTTGG	
			_ GAAAAT	
GAM1394	MMD	3'	GGTTGTAAAAGTCAGTGCAATA 59810	G TC_____
			TATTGCAC TGG CGGCC	
			ATAACGTG ACT GTTGG	
			_ GAAAAT	
GAM1394	MOST2	5'	GTCAGGGCTACGGTGATG 39689	TG A _
			TAT C CGTGGTCC GGC	

			GTA G GCATCGGG CTG		
			GT _ A		
GAM1394	MOST2	5'	GTCAGGGCTACGGTGATG 39689	TG A	_
			TAT C CGTGGTCC GGC		
			GTA G GCATCGGG CTG		
			GT _ A		
GAM1394	MRPL56	3'	GACATTCAGGGCCGGGTGCAGT 51689	G	GGCCTG
	G		TATTGCAC TGGTCC GTT		
			GTGACGTG GCCGGG CAG		
			G ACTTA_		
GAM1394	MRPL56	3'	GACATTCAGGGCCGGGTGCAGT 51689	G	GGCCTG
	G		TATTGCAC TGGTCC GTT		
			GTGACGTG GCCGGG CAG		
			G ACTTA_		
GAM1394	MRPS21	5'	AACCCCTTTTGAAGTATGTGT 38640	TG	_ CCT_
	GGTG		AT CACGTGGT CCGG GGTT		
			TG GTGTATCA GGTT CCAA		
			GT A TTCC		
GAM1394	MRPS21	5'	AACCCCTTTTGAAGTATGTGT 38640	TG	_ CCT_
	GGTG		AT CACGTGGT CCGG GGTT		
			TG GTGTATCA GGTT CCAA		
			GT A TTCC		
GAM1394	MY014	5'	GGCCAAGAACCACGTGAATG 48140	G	_ C_
			TATT CACGTGGT C GGCC		
			GTAA GTGCACCA G CCGG		
			_ A AA		
GAM1394	MY014	5'	GGCCAAGAACCACGTGAATG 48140	G	_ C_
			TATT CACGTGGT C GGCC		
			GTAA GTGCACCA G CCGG		
			_ A AA		
GAM1394	NFAT5	5'	GGCCGGGCTGGGTCGAGCTGC 21711	CG_ GT	
			GCA TG CCGGCCTGGTT		
			CGT GC GGTCGGGCCGG		
			CGA TG		
GAM1394	NFAT5	5'	GGCCGGGCTGGGTCGAGCTGCG 56945	CG_ GT	
	ATG		TATTGCA TG CCGGCCTGGTT		
			GTAGCGT GC GGTCGGGCCGG		
			CGA TG		
GAM1394	NFAT5	5'	GGCCGGGCTGGGTCGAGCTGCG 56945	CG_ GT	
	ATG		TATTGCA TG CCGGCCTGGTT		

		GTAGCGT GC GGTCGGGCCGG		
		CGA TG		
GAM1394 NFAT5	5'	GGCCGGGCTGGGTCGAGCTGC 21711	CG_	GT
		GCA TG CCGGCCTGGTT		
		CGT GC GGTCGGGCCGG		
		CGA TG		
GAM1394 NIBAN	3'	AATTAGGCTTAGACTGTGCAA 41998	GT	C_
		TTGCAC GGTC GGCCTGGTT		
		AACGTG TCAG TCGGATTAA		
		__ AT		
GAM1394 NIBAN	3'	AATTAGGCTTAGACTGTGCAA 41998	GT	C_
		TTGCAC GGTC GGCCTGGTT		
		AACGTG TCAG TCGGATTAA		
		__ AT		
GAM1394 NPEPL1	5'	GGCCGGGCGCGGGCCGGGCAG 45090	ACGT	
		TTGC GGTCCGGCCTGGTT		
		GACG CCGGGCCGGGCCGG		
		GG__		
GAM1394 NPEPL1	5'	GGCCGGGCGCGGGCCGGGCAG 45090	ACGT	
		TTGC GGTCCGGCCTGGTT		
		GACG CCGGGCCGGGCCGG		
		GG__		
GAM1394 NYD-SP16	3'	AGCCAGGTTGTGCAGTGCTGTG 49217	T	GTG TC
		TAT GCAC G CGGCCTGGTT		
		GTG CGTG C GTTGGACCGA		
		T A__ GT		
GAM1394 NYD-SP16	3'	AGCCAGGTTGTGCAGTGCTGTG 49217	T	GTG TC
		TAT GCAC G CGGCCTGGTT		
		GTG CGTG C GTTGGACCGA		
		T A__ GT		
GAM1394 p25	3'	AACCTGGCTGGACCGCGTGTGA 22842	TG	T
		T CACGTGGTCCGGCC GGTT		
		A GTGCGCCAGGTCGG CCAA		
		GT T		
GAM1394 p25	3'	AACCTGGCTGGACCGCGTGTGA 22842	TG	T
		T CACGTGGTCCGGCC GGTT		
		A GTGCGCCAGGTCGG CCAA		
		GT T		
GAM1394 P450RAI-2	3'	CTGGTACCGTGTGAGTG 39103	G	_
		TATT CACGTGGT CCGG		

		GTGA GTGTGCCA GGTC		
		— T		
GAM1394	P450RAI-2 3'	CTGGTACCGTGTGAGTG	39103	G —
		TATT CACGTGGT CCGG		
		GTGA GTGTGCCA GGTC		
		— T		
GAM1394	p47 5'	GGCTGGGCCTGTGCGG	32343	T
		TTGCACG GGTCCGGCC		
		GGCGTGT CCGGGTCGG		
		—		
GAM1394	p47 5'	GGCTGGGCCTGTGCGG	32343	T
		TTGCACG GGTCCGGCC		
		GGCGTGT CCGGGTCGG		
		—		
GAM1394	PACSIN2 3'	CCACGCCGTGTGTAG	23339	TGGTC C
		TTGCACG CGGC TGG		
		GATGTGT GCCG ACC		
		— C		
GAM1394	PACSIN2 3'	CCACGCCGTGTGTAG	23339	TGGTC C
		TTGCACG CGGC TGG		
		GATGTGT GCCG ACC		
		— C		
GAM1394	PAI-RBP1 3'	GATTTGGCCAATGTGTAATA	31584	GGTCC TG
		TATTGCACGT GGCC GTT		
		ATAATGTGTA CCGG TAG		
		A — TT		
GAM1394	PAI-RBP1 3'	GATTTGGCCAATGTGTAATA	31584	GGTCC TG
		TATTGCACGT GGCC GTT		
		ATAATGTGTA CCGG TAG		
		A — TT		
GAM1394	PANK 3'	GGTTTACTGATCAGTGTGGTG	56334	TG G C —
		TAT CAC TGGTC GGCC		
		GTG GTG ACTAG TTGG		
		GT — TCAT		
GAM1394	PANK 3'	GGTTTACTGATCAGTGTGGTG	56334	TG G C —
		TAT CAC TGGTC GGCC		
		GTG GTG ACTAG TTGG		
		GT — TCAT		
GAM1394	PASK 5'	GGCTGCACTGCGTGCAG	30721	TG C
		TTGCACG GT CGGCC		



		GACGTGC CA GTCGG		
		GT C		
GAM1394 PASK	5'	GGCTGCACTGCGTGCAG 30721	TG C	
		TTGCACG GT CGGCC		
		GACGTGC CA GTCGG		
		GT C		
GAM1394 PB1	3'	AACTGGGTGATTGCCATTGTGG 36365	TG C	CCG_ TG
TA		TAT CA GTGGT GCC GTT		
		ATG GT TACCG TGG CAA		
		GT _ TTAG GT		
GAM1394 PB1	3'	AACTGGGTGATTGCCATTGTGG 36365	TG C	CCG_ TG
TA		TAT CA GTGGT GCC GTT		
		ATG GT TACCG TGG CAA		
		GT _ TTAG GT		
GAM1394 PBEF	3'	GACTGGGTGTGTGTTGTGTGTA 19234	TG TC _ TG	
		TGCACG G CG GCC GTT		
		ATGTGT T GT TGG CAG		
		GT GT G GT		
GAM1394 PBEF	3'	GACTGGGTGTGTGTTGTGTGTA 19234	TG TC _ TG	
		TGCACG G CG GCC GTT		
		ATGTGT T GT TGG CAG		
		GT GT G GT		
GAM1394 PDE4DIP	3'	AGTCAGGCTGGGTTTTGGTCTG 95437	___ T GT	GT
CA		TGCA CG G CCGGCCTG T		
		ACGT GT T GGTCGGAC A		
		CTG T TG TG		
GAM1394 PDE4DIP	3'	AGTCAGGCTGGGTTTTGGTCTG 95437	___ T GT	GT
CA		TGCA CG G CCGGCCTG T		
		ACGT GT T GGTCGGAC A		
		CTG T TG TG		
GAM1394 PEG10	3'	AGCCAAAATTATCGGTGCAGTG 30517	G	CCGGCC
		TATTGCAC TGGT TGGTT		
		GTGACGTG GCTA ACCGA		
		_ TAAA_		
GAM1394 PEG10	3'	AGCCAAAATTATCGGTGCAGTG 30517	G	CCGGCC
		TATTGCAC TGGT TGGTT		
		GTGACGTG GCTA ACCGA		
		_ TAAA_		
GAM1394 PEPP3	3'	CCAGGCTGGGGCCATG 30038	_	
		CGTGGTCC GGCCTGG		

			GTACCGGG TCGGACC		
			G		
GAM1394	PEPP3	3'	CCAGGCTGGGGCCATG 30038	—	
			CGTGGTCC GGCCTGG		
			GTACCGGG TCGGACC		
			G		
GAM1394	PEPP3	3'	GGTTAGTGCCCAGTGCAGTG 30043	GT CC_	
			TATTGCAC GGT GGCC		
			GTGACGTG CCG TTGG		
			AC TGA		
GAM1394	PEPP3	3'	GGTTAGTGCCCAGTGCAGTG 30043	GT CC_	
			TATTGCAC GGT GGCC		
			GTGACGTG CCG TTGG		
			AC TGA		
GAM1394	PHYHIP	3'	AGCTGGGCTGGACTTCTGGAG 28605	G CGT TG	
			TT CA GGTCCGGCC GTT		
			GA GT TCAGGTCGG CGA		
			G CT_ GT		
GAM1394	PHYHIP	3'	AGCTGGGCTGGACTTCTGGAG 28605	G CGT TG	
			TT CA GGTCCGGCC GTT		
			GA GT TCAGGTCGG CGA		
			G CT_ GT		
GAM1394	PIWIL2	3'	GACCTCCAGACCGGGTGCGGTG 36057	G C CCT	
			TATTGCAC TGGTC GG GGTT		
			GTGGCGTG GCCAG CC CCAG		
			G A T__		
GAM1394	PIWIL2	3'	GACCTCCAGACCGGGTGCGGTG 36057	G C CCT	
			TATTGCAC TGGTC GG GGTT		
			GTGGCGTG GCCAG CC CCAG		
			G A T__		
GAM1394	PIWIL2	3'	GCCGGGTGTGGCGGTG 36058	_ TGG	
			TATTGC ACG TCCGGC		
			GTGGCG TGT GGGCCG		
			G _		
GAM1394	PIWIL2	3'	GCCGGGTGTGGCGGTG 36058	_ TGG	
			TATTGC ACG TCCGGC		
			GTGGCG TGT GGGCCG		
			G _		
GAM1394	PLCL2	5'	CGCCCATGGCTGGATTGCGTGC 68135	TG _ TT	
	G		TGCACG GTCCGGCC TGG		

		GCGTGC TAGGTCGG ACC	
		GT T CGCG	
GAM1394 PLCL2	5'	CGCCCATGGCTGGATTGCGTGC 68135	TG _ TT
G		TGCACG GTCCGGCC TGG	
		GCGTGC TAGGTCGG ACC	
		GT T CGCG	
GAM1394 PMX2B	5'	AACTAGGCTCTGCTGGTAGTA 14076	AC TG TCC
		TATTGC G G GGCCTGGTT	
		ATGATG C C C TCGGATCAA	
		GT GT _	
GAM1394 PMX2B	5'	AACTAGGCTCTGCTGGTAGTA 14076	AC TG TCC
		TATTGC G G GGCCTGGTT	
		ATGATG C C C TCGGATCAA	
		GT GT _	
GAM1394 POLE3	3'	GATCGGCCTGCTGGTGTGGTA 33856	TG G CC T
		TAT CAC TGGT GGCC GGTT	
		ATG GTG GTCG CCGG CTAG	
		GT _ T_ _	
GAM1394 POLE3	3'	GATCGGCCTGCTGGTGTGGTA 33856	TG G CC T
		TAT CAC TGGT GGCC GGTT	
		ATG GTG GTCG CCGG CTAG	
		GT _ T_ _	
GAM1394 POLR3F	5'	AACCAGGCTTGTGCGTCCGATG 59938	C GTCC
		TATTG ACGTG GGCCTGGTT	
		GTAGC TGCGT TCGGACCAA	
		C GT_	
GAM1394 POLR3F	5'	AACCAGGCTTGTGCGTCCGATG 59938	C GTCC
		TATTG ACGTG GGCCTGGTT	
		GTAGC TGCGT TCGGACCAA	
		C GT_	
GAM1394 PPFIBP1	5'	GGCCGGGCGCGAGTGC 13253	G_
		GCAC TGGTCCGGCC	
		CGTG GCCGGGCGCG	
		AG	
GAM1394 PPFIBP1	5'	GGCCGGGCGCGAGTGC 13253	G_
		GCAC TGGTCCGGCC	
		CGTG GCCGGGCGCG	
		AG	
GAM1394 PPP1R10	3'	GGTTGGGTTTTGTGCAG 10737	T GT
		TTGCACG G CCGGCC	

		GACGTGT T GGTGG		
		T TG		
GAM1394 PPP1R10	3'	GGTTGGGTTTGTGCAG 10737	T GT	
		TTGCACG G CCGGCC		
		I		
		GACGTGT T GGTGG		
		T TG		
GAM1394 PPP1R14A	5'	GGCCAGGCTGGGTCCAGCAG 52688	ACG _	
		TTGC TGG TCCGGCCTGGTT		
		GACG ACC GGGTCGGACCGG		
		_ T		
GAM1394 PPP1R14A	5'	GGCCAGGCTGGGTCCAGCAG 52688	ACG _	
		TTGC TGG TCCGGCCTGGTT		
		GACG ACC GGGTCGGACCGG		
		_ T		
GAM1394 PPP1R3B	3'	GACCTCTGGGGCCGAGTGTGGT 44818	TG G GGCCT	
G		TAT CAC TGGTCC GGTT		
		GTG GTG GCCGGG CCAG		
		GT A GTCT_		
GAM1394 PPP1R3B	3'	GACCTCTGGGGCCGAGTGTGGT 44818	TG G GGCCT	
G		TAT CAC TGGTCC GGTT		
		GTG GTG GCCGGG CCAG		
		GT A GTCT_		
GAM1394 PRKAG3	3'	GACTGGGTCGGATGGCCCCCAG 33827	CAC G TG	
TG		TATTG GT GTCCGGCC GTT		
		GTGAC CG TAGGCTGG CAG		
		CCC G GT		
GAM1394 PRKAG3	3'	GACTGGGTCGGATGGCCCCCAG 33827	CAC G TG	
TG		TATTG GT GTCCGGCC GTT		
		GTGAC CG TAGGCTGG CAG		
		CCC G GT		
GAM1394 PRMT3	3'	ACCAGATTTATGTGCAA 65024	TCCGGC	
		TTGCACGTGG CTGGT		
		AACGTGTATT GACCA		
		TA_		
GAM1394 PRMT3	3'	ACCAGATTTATGTGCAA 65024	TCCGGC	
		TTGCACGTGG CTGGT		
		AACGTGTATT GACCA		
		TA_		
GAM1394 PRO0456	3'	TTAGGCTGGGTGCAGTG 26180	GTGGT	
		TATTGCAC CCGGCCTGG		

GTGACGTG GGTCCGATT

GAM1394 PRO0456 3' TTAGGCTGGGTGCAGTG 26180 GTGGT  
TATTGCAC CCGGCCTGG  
||||||| |||||||  
GTGACGTG GGTCCGATT

GAM1394 PRO0478 5' AACTGGGTGCGGTGGTGTAGTG 26181 GTGGT \_ TG  
TATTGCAC CCG GCC GTT  
||||||| ||| ||| |||  
GTGATGTG GGC TGG CAA  
GT\_\_ G GT

GAM1394 PRO0478 5' AACTGGGTGCGGTGGTGTAGTG 26181 GTGGT \_ TG  
TATTGCAC CCG GCC GTT  
||||||| ||| ||| |||  
GTGATGTG GGC TGG CAA  
GT\_\_ G GT

GAM1394 PRO0529 3' CCAGTGACCGTGTGTGG 25989 TG CGGC  
T CACGTGGTC CTGG  
| ||||||| ||||  
G GTGTGCCAG GACC  
GT T\_\_

GAM1394 PRO0529 3' CCAGTGACCGTGTGTGG 25989 TG CGGC  
T CACGTGGTC CTGG  
| ||||||| ||||  
G GTGTGCCAG GACC  
GT T\_\_

GAM1394 PRO0618 3' GCTGGGCACGGTGGTG 26202 TG A G  
TAT C CGTG TCCGGC  
||| | ||| |||||||  
GTG G GCAC GGGTCG  
GT \_ \_

GAM1394 PRO0618 3' GCTGGGCACGGTGGTG 26202 TG A G  
TAT C CGTG TCCGGC  
||| | ||| |||||||  
GTG G GCAC GGGTCG  
GT \_ \_

GAM1394 PRO0899 3' AGTTGGGCTGGGCGTCCTGGCA 37691 ACGTG\_ GG  
TGC GTCCGGCCT TT  
||| ||||||| ||  
ACG CGGGTCGGG GA  
GTCCTG TT

GAM1394 PRO0899 3' AGTTGGGCTGGGCGTCCTGGCA 37691 ACGTG\_ GG  
TGC GTCCGGCCT TT  
||| ||||||| ||  
ACG CGGGTCGGG GA  
GTCCTG TT

GAM1394 PRO1257 3' GACTGTATTATCATGTGCGATG 37709 CCG CT  
TATTGCACGTGGT GC GGTT  
||||||||| || ||||

			GTAGCGTGTACTA TG TCAG		
			TTA _		
GAM1394	PRO1257	3'	GACTGTATTATCATGTGCGATG 37709		CCG CT
			TATTGCACGTGGT GC GGTT		
			GTAGCGTGTACTA TG TCAG		
			TTA _		
GAM1394	PRO1386	3'	CTGGCCAGGTGCAGTG 48381	G T	
			TATTGCAC TGG CCGG		
			GTGACGTG ACC GGTC		
			G _		
GAM1394	PRO1386	3'	CTGGCCAGGTGCAGTG 48381	G T	
			TATTGCAC TGG CCGG		
			GTGACGTG ACC GGTC		
			G _		
GAM1394	PRO1386	3'	GCTGGGCACTGTGGTA 48382	TG C G	
			TAT CA GTG TCCGGC		
			ATG GT CAC GGGTCG		
			GT _ _		
GAM1394	PRO1386	3'	GCTGGGCACTGTGGTA 48382	TG C G	
			TAT CA GTG TCCGGC		
			ATG GT CAC GGGTCG		
			GT _ _		
GAM1394	PRO1853	3'	GCCGGGTATGGTGGTA 37772	TG A G	
			TAT C CGTG TCCGGC		
			ATG G GTAT GGGCCG		
			GT _ _		
GAM1394	PRO1853	3'	GCCGGGTATGGTGGTA 37772	TG A G	
			TAT C CGTG TCCGGC		
			ATG G GTAT GGGCCG		
			GT _ _		
GAM1394	PRO2015	5'	GTTAGACGATGTGTAATG 37562	G CG	
			TATTGCACGT GTC GC		
			GTAATGTGTA CAG TG		
			G AT		
GAM1394	PRO2015	5'	GTTAGACGATGTGTAATG 37562	G CG	
			TATTGCACGT GTC GC		
			GTAATGTGTA CAG TG		
			G AT		
GAM1394	PRO2325	5'	TGGCCAAGATGGCCGCGTGCGG 96304	C_____ TGGTT	
			TTGCACGTGGTC GGCC		

		GGCGTGCGCCGG CCGG		
		TAGAA TT		
GAM1394	PRO2325	5' TGGCCAAGATGGCCGCGTGCCG 96304	C_____	TGGTT
		TTGCACGTGGTC GGCC		
		GGCGTGCGCCGG CCGG		
		TAGAA TT		
GAM1394	PSR	3' AGCCACCAAGGCCAGGTGCAGT 65172	G	C_ CC
	G	TATTGCAC TGGTC GG TGGTT		
		GTGACGTG ACCGG CC ACCGA		
		G AA _		
GAM1394	PSR	3' AGCCACCAAGGCCAGGTGCAGT 65172	G	C_ CC
	G	TATTGCAC TGGTC GG TGGTT		
		GTGACGTG ACCGG CC ACCGA		
		G AA _		
GAM1394	PTP4A1	3' TTGGATTATTTGTGATA 12946	TG C	
		TAT CA GTGGTCCGG		
		ATA GT TATTAGGTT		
		GT T		
GAM1394	PTP4A1	3' TTGGATTATTTGTGATA 12946	TG C	
		TAT CA GTGGTCCGG		
		ATA GT TATTAGGTT		
		GT T		
GAM1394	PTPN9	3' AACTGGGTGGGTTCTGTGTCAA 11074	_	T GT G TG
	TA	TATTG CACG G CC GCC GTT		
		ATAAC GTGT C GG TGG CAA		
		T _TT G GT		
GAM1394	PTPN9	3' AACTGGGTGGGTTCTGTGTCAA 11074	_	T GT G TG
	TA	TATTG CACG G CC GCC GTT		
		ATAAC GTGT C GG TGG CAA		
		T _TT G GT		
GAM1394	PYY	3' GGCTGGAGGGCTGTGTGTGGT 14778	TG TG	_____
		AT CACG GTCC GGCC		
		TG GTGT CGGG TCGG		
		GT GT AGG		
GAM1394	PYY	3' GGCTGGAGGGCTGTGTGTGGT 14778	TG TG	_____
		AT CACG GTCC GGCC		
		TG GTGT CGGG TCGG		
		GT GT AGG		
GAM1394	PYY2	3' AGCTGCAGGGCTGTGTGTGGT 40823	TG TG	G CT
		AT CACG GTCC GC GGTT		

			TG GTGT CGGG CG TCGA		
			GT GT A _		
GAM1394	PYY2	3'	AGCTGCAGGGCTGTGTGTGGT 40823	TG	TG G CT
			AT CACG GTCC GC GGTT		
			TG GTGT CGGG CG TCGA		
			GT GT A _		
GAM1394	RAB24	3'	GGCAGAGGATTACGTCAGTG 55391	C	G_
			TATTG ACGTGGTCC GCC		
			GTGAC TGCATTAGG CGG		
			_ AGA		
GAM1394	RAB24	3'	GGCAGAGGATTACGTCAGTG 55391	C	G_
			TATTG ACGTGGTCC GCC		
			GTGAC TGCATTAGG CGG		
			_ AGA		
GAM1394	RALGPS1A	3'	GGCTGGGCCTGGTGGTG 27608	TG A T	
			TAT C CG GGTCCGGCC		
			GTG G GT CCGGGTCGG		
			GT _ _		
GAM1394	RALGPS1A	3'	GGCTGGGCCTGGTGGTG 27608	TG A T	
			TAT C CG GGTCCGGCC		
			GTG G GT CCGGGTCGG		
			GT _ _		
GAM1394	RBT1	3'	AACCAGGCCGGACCACGTGCAA 25348		
	TA		TATTGCACGTGGTCCGGCCTGGTT		
			ATAACGTGCACCAGGCCGGACCAA		
GAM1394	RBT1	3'	AACCAGGCCGGACCACGTGCAA 25348		
	TA		TATTGCACGTGGTCCGGCCTGGTT		
			ATAACGTGCACCAGGCCGGACCAA		
GAM1394	RNF24	5'	GGCCGGGCGCGGTGTGCAG 23320	TGGT	_
			TTGCACG CCG GCCTGGTT		
			GACGTGT GGC CGGGCCGG		
			_ G		
GAM1394	RNF24	5'	GGCCGGGCGCGGTGTGCAG 23320	TGGT	_
			TTGCACG CCG GCCTGGTT		
			GACGTGT GGC CGGGCCGG		
			_ G		
GAM1394	RSP3	3'	AATCAGGTAATGATGTGCGA 49172	G CCG	
			TTGCACGT GT GCCTGGTT		



			AGCGTGTA TA TGGACTAA		
			G A__		
GAM1394	RSP3	3'	AATCAGGTAATGATGTGCGA 49172	G CCG	
			TTGCACGT GT GCCTGGTT		
			AGCGTGTA TA TGGACTAA		
			G A__		
GAM1394	RTCD1	3'	GGTGGATATGTGTGATA 13576	TG G G	
			TAT CACGTG TCCG CC		
			ATA GTGTAT AGGT GG		
			GT _ _		
GAM1394	RTCD1	3'	GGTGGATATGTGTGATA 13576	TG G G	
			TAT CACGTG TCCG CC		
			ATA GTGTAT AGGT GG		
			GT _ _		
GAM1394	S164	5'	GGCGGACTGCTGCAGTA 60782	C TG G	
			TATTGCA G GTCCG CC		
			ATGACGT C CAGGC GG		
			_GT _		
GAM1394	S164	5'	GGCGGACTGCTGCAGTA 60782	C TG G	
			TATTGCA G GTCCG CC		
			ATGACGT C CAGGC GG		
			_GT _		
GAM1394	SARM	3'	GACCAGGCAGCCCCCATGGCAG 30607	A TCCG_	
	TA		TATTGC CGTGG GCCTGGTT		
			ATGACG GTACC CGGACCAG		
			_ CCCGA		
GAM1394	SARM	3'	GACCAGGCAGCCCCCATGGCAG 30607	A TCCG_	
	TA		TATTGC CGTGG GCCTGGTT		
			ATGACG GTACC CGGACCAG		
			_ CCCGA		
GAM1394	SC65	3'	AACTTAAGATGGGCCAGGTGCG 21286	G GCCT_	
	GTG		TATTGCAC TGGTCCG GGTT		
			GTGGCGTG ACCGGGT TCAA		
			G AGAAT		
GAM1394	SC65	3'	AACTTAAGATGGGCCAGGTGCG 21286	G GCCT_	
	GTG		TATTGCAC TGGTCCG GGTT		
			GTGGCGTG ACCGGGT TCAA		
			G AGAAT		
GAM1394	SDC3	3'	AGCTAGGCTCTCCCAGGTGCAA 27739	G TCC	
	TG		TATTGCAC TGG GGCCTGGTT		

			GTAACGTG ACC TCGGATCGA		
			G CTC		
GAM1394	SDC3	3'	AGCTAGGCTCTCCCAGGTGCAA 27739	G TCC	
	TG		TATTGCAC TGG GGCCTGGTT		
			GTAACGTG ACC TCGGATCGA		
			G CTC		
GAM1394	SEC31B-1	3'	GGCTAGGTTGGATGGAAGGTGA 31313	TG ACGTG	
			T C GTCCGGCCTGGTT		
			A G TAGGTTGGATCGG		
			GT GAAGG		
GAM1394	SEC31B-1	3'	GGCTAGGTTGGATGGAAGGTGA 31313	TG ACGTG	
			T C GTCCGGCCTGGTT		
			A G TAGGTTGGATCGG		
			GT GAAGG		
GAM1394	SEC61A1	3'	GGTGCATGGGCTGTGGTGGTG 25311	TG A TG _ _	
			TAT C CG GTCCG GC CT		
			GTG G GT CGGGT CG GG		
			GT _ GT A T		
GAM1394	SEC61A1	3'	GGTGCATGGGCTGTGGTGGTG 25311	TG A TG _ _	
			TAT C CG GTCCG GC CT		
			GTG G GT CGGGT CG GG		
			GT _ GT A T		
GAM1394	SEMA5B	3'	GGGCTGGGCCATTGTGGTG 63127	TG C	
			TAT CA GTGGTCCGGCCT		
			GTG GT TACCGGGTCGGG		
			GT _		
GAM1394	SEMA5B	3'	GGGCTGGGCCATTGTGGTG 63127	TG C	
			TAT CA GTGGTCCGGCCT		
			GTG GT TACCGGGTCGGG		
			GT _		
GAM1394	SFRS5	3'	GGTTGGGCTGGATATCTTTGTA 22644	CGTG_ GG	
	G		TTGCA GTCCGGCCT TT		
			GATGT TAGGTCGGG GG		
			TTCTA TT		
GAM1394	SFRS5	3'	GGTTGGGCTGGATATCTTTGTA 22644	CGTG_ GG	
	G		TTGCA GTCCGGCCT TT		
			GATGT TAGGTCGGG GG		
			TTCTA TT		
GAM1394	SLC11A2	3'	AACCAGTACTCTGGGTGCAATA 5231	G TCCGGC	
			TATTGCAC TGG CTGGTT		

			ATAACGTG GTC	GACCAA		
			G TCAT__			
GAM1394	SLC11A2	3'	AACCAGTACTCTGGGTGCAATA	5231	G	TCCGGC
			TATTGCAC TGG	CTGGTT		
			ATAACGTG GTC	GACCAA		
			G TCAT__			
GAM1394	SLC1A7	5'	TGGCCGGGCTCTCATGCGTGGA	21910	G	_____ TGGTT
	ATG		T CACGT	GGTCCGGCC		
			A GTGCG	TCGGGCCGG		
			G TACTC	TT		
GAM1394	SLC1A7	5'	TGGCCGGGCTCTCATGCGTGGA	21910	G	_____ TGGTT
	ATG		T CACGT	GGTCCGGCC		
			A GTGCG	TCGGGCCGG		
			G TACTC	TT		
GAM1394	SLC21A12	3'	CCCGATCGTGTGTGGTG	33015	TG	C
			TAT CACGTGGTC	GG		
			GTG GTGTGCTAG	CC		
			GT	C		
GAM1394	SLC21A12	3'	CCCGATCGTGTGTGGTG	33015	TG	C
			TAT CACGTGGTC	GG		
			GTG GTGTGCTAG	CC		
			GT	C		
GAM1394	SLC26A10	3'	TGGCCCTGATGACATGTGTGTG	56036	TG	_____ G C_ TGGTT
	ATG		CAC	GT GTC GGCC		
			GTG	CA TAG CCGG		
			GT TGTA	G TC TT		
GAM1394	SLC26A10	3'	TGGCCCTGATGACATGTGTGTG	56036	TG	_____ G C_ TGGTT
	ATG		CAC	GT GTC GGCC		
			GTG	CA TAG CCGG		
			GT TGTA	G TC TT		
GAM1394	SLC26A6	3'	AGTCAGGCTGGCAGTGGCGCGG	56136	A_	TG T GT
	TA		TATTGC	CG G CCGGCCTG T		
			ATGGCG	GT C GGTCGGAC A		
			CG	GA_ TG		
GAM1394	SLC26A6	3'	AGTCAGGCTGGCAGTGGCGCGG	56136	A_	TG T GT
	TA		TATTGC	CG G CCGGCCTG T		
			ATGGCG	GT C GGTCGGAC A		
			CG	GA_ TG		
GAM1394	SLC26A6	3'	AGTCAGGCTGGCAGTGGCGCGG	56218	A_	TG T GT
	TA		TATTGC	CG G CCGGCCTG T		

			ATGGCG GT C GGTCGGAC A		
			CG GA_ TG		
GAM1394	SLC26A6	3'	AGTCAGGCTGGCAGTGGCGCGG 56218	A_ TG T	GT
	TA		TATTGC CG G CCGGCCTG T		
			ATGGCG GT C GGTCGGAC A		
			CG GA_ TG		
GAM1394	SLC26A6	3'	AGTCAGGCTGGCAGTGGCGCGG 43294	A_ TG T	GT
	TA		TATTGC CG G CCGGCCTG T		
			ATGGCG GT C GGTCGGAC A		
			CG GA_ TG		
GAM1394	SLC26A6	3'	AGTCAGGCTGGCAGTGGCGCGG 43294	A_ TG T	GT
	TA		TATTGC CG G CCGGCCTG T		
			ATGGCG GT C GGTCGGAC A		
			CG GA_ TG		
GAM1394	SLIT1	3'	GCTGGGCTGGGGTGCAG 11766	GTGG TG	
			TTGCAC TCCGGCC GT		
			GACGTG GGGTCGG CG		
			_____ GT		
GAM1394	SLIT1	3'	GCTGGGCTGGGGTGCAG 11766	GTGG TG	
			TTGCAC TCCGGCC GT		
			GACGTG GGGTCGG CG		
			_____ GT		
GAM1394	SLK	5'	GATCAGGCCGGGTGGGAGCGA 28225	ACGTGG	
			TTGC TCCGGCCTGGTT		
			AGCG GGGCCGGACTION		
			AGGGT_		
GAM1394	SLK	5'	GATCAGGCCGGGTGGGAGCGA 28225	ACGTGG	
			TTGC TCCGGCCTGGTT		
			AGCG GGGCCGGACTION		
			AGGGT_		
GAM1394	SMAP1	3'	TGGTCGGGCAGCACAAGTGTA 41655	___	TGGTT
	TG		TTGCAC GTG GTCCGGCC		
			AATGTG CAC CGGGCTGG		
			AA GA TT		
GAM1394	SMAP1	3'	TGGTCGGGCAGCACAAGTGTA 41655	___	TGGTT
	TG		TTGCAC GTG GTCCGGCC		
			AATGTG CAC CGGGCTGG		
			AA GA TT		
GAM1394	SMARCF1	3'	GACTGCTGAACTGTGTGTGGT 37436	TG TG C CT	
			AT CACG GT CGGC GGTT		

			TG GTGT CA GTCG TCAG		
			GT GT A _		
GAM1394	SMARCF1	3'	GACTGCTGAACTGTGTGTGGT 37436	TG	TG C CT
			AT CACG GT CGGC GGTT		
			TG GTGT CA GTCG TCAG		
			GT GT A _		
GAM1394	SMARCF1	3'	GGCTACGCTGCCACGTGT 37438	CC	C
			GCACGTGGT GGC TGGTT		
			TGTGCACCG TCG ATCGG		
			_ C		
GAM1394	SMARCF1	3'	GGCTACGCTGCCACGTGT 37438	CC	C
			GCACGTGGT GGC TGGTT		
			TGTGCACCG TCG ATCGG		
			_ C		
GAM1394	SMARCF1	3'	GACTGCTGAACTGTGTGTGGT 20040	TG	TG C CT
			AT CACG GT CGGC GGTT		
			TG GTGT CA GTCG TCAG		
			GT GT A _		
GAM1394	SMARCF1	3'	GACTGCTGAACTGTGTGTGGT 20040	TG	TG C CT
			AT CACG GT CGGC GGTT		
			TG GTGT CA GTCG TCAG		
			GT GT A _		
GAM1394	SMARCF1	3'	GGCTACGCTGCCACGTGT 20041	CC	C
			GCACGTGGT GGC TGGTT		
			TGTGCACCG TCG ATCGG		
			_ C		
GAM1394	SMARCF1	3'	GGCTACGCTGCCACGTGT 20041	CC	C
			GCACGTGGT GGC TGGTT		
			TGTGCACCG TCG ATCGG		
			_ C		
GAM1394	SMARCF1	3'	GACTGCTGAACTGTGTGTGGT 57486	TG	TG C CT
			AT CACG GT CGGC GGTT		
			TG GTGT CA GTCG TCAG		
			GT GT A _		
GAM1394	SMARCF1	3'	GACTGCTGAACTGTGTGTGGT 57486	TG	TG C CT
			AT CACG GT CGGC GGTT		
			TG GTGT CA GTCG TCAG		
			GT GT A _		
GAM1394	SMARCF1	3'	GGCTACGCTGCCACGTGT 57487	CC	C
			GCACGTGGT GGC TGGTT		

			TGTGCACCG TCG ATCGG	
			— C	
GAM1394	SMARCF1	3'	GGCTACGCTGCCACGTGT 57487	CC C
			GCACGTGGT GGC TGGTT	
			TGTGCACCG TCG ATCGG	
			— C	
GAM1394	SMOC2	5'	AGCCGGGCGCCGGGAGCGGTG 72369	ACG TC
			TATTGC TGG CGGCCTGGTT	
			GTGGCG GCC GCCGGGCCGA	
			AGG —	
GAM1394	SMOC2	5'	AGCCGGGCGCCGGGAGCGGTG 72369	ACG TC
			TATTGC TGG CGGCCTGGTT	
			GTGGCG GCC GCCGGGCCGA	
			AGG —	
GAM1394	SNPH	5'	AGCCGGGCGCGAGTGGTGCGA 28237	G G
			TTGCAC TG TCCGGCCTGGTT	
			AGCGTG GT AGGCCGGGCCGA	
			— G	
GAM1394	SNPH	5'	AGCCGGGCGCGAGTGGTGCGA 28237	G G
			TTGCAC TG TCCGGCCTGGTT	
			AGCGTG GT AGGCCGGGCCGA	
			— G	
GAM1394	SNX11	5'	GGCCGGCGTCCCAAGTGTAGTG 25270	G T__
			TATTGCAC TGG CCGGCC	
			GTGATGTG ACC GGCCGG	
			A CTGC	
GAM1394	SNX11	5'	GGCCGGCGTCCCAAGTGTAGTG 25270	G T__
			TATTGCAC TGG CCGGCC	
			GTGATGTG ACC GGCCGG	
			A CTGC	
GAM1394	SP2	5'	AATTGGGCTGATGATGTCAGTG 11883	C G C TG
			TATTG ACGT GTC GGCC GTT	
			GTGAC TGTA TAG TCGG TAA	
			— G — GT	
GAM1394	SP2	5'	AATTGGGCTGATGATGTCAGTG 11883	C G C TG
			TATTG ACGT GTC GGCC GTT	
			GTGAC TGTA TAG TCGG TAA	
			— G — GT	
GAM1394	STAM2	5'	GCCGGGCAGGTGCGGTG 19564	G G
			TATTGCAC TG TCCGGC	

			GTGGCGTG AC GGGCCG	
			G _	
GAM1394	STAM2	5'	GCCGGGCAGGTGCGGTG 19564	G G
			TATTGCAC TG TCCGGC	
			GTGGCGTG AC GGGCCG	
			G _	
GAM1394	STIM2	3'	ATCAGGGAGCATGTGCA 40470	G GGC GT
			TGCACGTG TCC CTG T	
			ACGTGTAC AGG GAC A	
			G _ _ _ TG	
GAM1394	STIM2	3'	ATCAGGGAGCATGTGCA 40470	G GGC GT
			TGCACGTG TCC CTG T	
			ACGTGTAC AGG GAC A	
			G _ _ _ TG	
GAM1394	STK22D	3'	GACCAGGCTGGGTTGGGGGT 49322	ACG GG
			GC T TCCGGCCTGGTT	
			TG G GGGTCGGACCAG	
			GGG TT	
GAM1394	STK22D	3'	GACCAGGCTGGGTTGGGGGT 49322	ACG GG
			GC T TCCGGCCTGGTT	
			TG G GGGTCGGACCAG	
			GGG TT	
GAM1394	STK38L	3'	GACTGTTTTGCTAGTGTGATA 69173	TG G CC CT
			TAT CAC TGGT GGC GGTT	
			ATA GTG ATCG TTG TCAG	
			GT _ TT _	
GAM1394	STK38L	3'	GACTGTTTTGCTAGTGTGATA 69173	TG G CC CT
			TAT CAC TGGT GGC GGTT	
			ATA GTG ATCG TTG TCAG	
			GT _ TT _	
GAM1394	STK39	3'	AATTGGAAGGGTTTTGTGCAAT 25072	T GT GG TGGTT
	G		TATTGCACG G CC CC	
			GTAACGTGT T GG GG	
			T TG AA TTAA	
GAM1394	STK39	3'	AATTGGAAGGGTTTTGTGCAAT 25072	T GT GG TGGTT
	G		TATTGCACG G CC CC	
			GTAACGTGT T GG GG	
			T TG AA TTAA	
GAM1394	SV2	3'	AGCTCCGCAGGACTGTGTGTGA 29303	TG TG G CT
			T CACG GTCC GC GGTT	

			A GTGT CAGG CG TCGA		
			GT GT A CC		
GAM1394	SV2	3'	AGCTCCGCAGGACTGTGTGTGA 29303	TG TG G CT	
			T CACG GTCC GC GGTT		
			A GTGT CAGG CG TCGA		
			GT GT A CC		
GAM1394	SYT12	5'	GGTCACAGCTGTGTGGGGTG 94736	G TG CC_	
			TATT CACG GT GGCC		
			GTGG GTGT CG CTGG		
			G GT ACA		
GAM1394	SYT12	5'	GGTCACAGCTGTGTGGGGTG 94736	G TG CC_	
			TATT CACG GT GGCC		
			GTGG GTGT CG CTGG		
			G GT ACA		
GAM1394	TACTILE	5'	ACTCAGGCGTGTGTGGTA 19466	TG TGGTC G _	
			TAT CACG CG CCTG GT		
			ATG GTGT GC GGAC CA		
			GT _ _ T		
GAM1394	TACTILE	5'	ACTCAGGCGTGTGTGGTA 19466	TG TGGTC G _	
			TAT CACG CG CCTG GT		
			ATG GTGT GC GGAC CA		
			GT _ _ T		
GAM1394	TAGAP	3'	CTGGATTTGTGCAATA 54030	T	
			TATTGCACG GGTCCGG		
			ATAACGTGT TTAGGTC		
			-		
GAM1394	TAGAP	3'	CTGGATTTGTGCAATA 54030	T	
			TATTGCACG GGTCCGG		
			ATAACGTGT TTAGGTC		
			-		
GAM1394	TESK2	5'	GACTGTGGGGCCATGGCAGTA 63182	A G CT	
			TATTGC CGTGGTCC GC GGTT		
			ATGACG GTACCGGG TG TCAG		
			- G _		
GAM1394	TESK2	5'	GACTGTGGGGCCATGGCAGTA 63182	A G CT	
			TATTGC CGTGGTCC GC GGTT		
			ATGACG GTACCGGG TG TCAG		
			- G _		
GAM1394	TIAF1	3'	CGTGTTATGTGCAATG 54328	TC	
			TATTGCACGTGG CG		



			GTAACGTGTATT GC		
			GT		
GAM1394	TIAF1	3'	CGTGTTATGTGCAATG 54328	TC	
			TATTGCACGTGG CG		
			GTAACGTGTATT GC		
			GT		
GAM1394	TIAM2	3'	CTGGGTTTTGTGCAGTA 24932	T GT	
			TATTGCACG G CCGG		
			ATGACGTGT T GGTC		
			T TG		
GAM1394	TIAM2	3'	CTGGGTTTTGTGCAGTA 24932	T GT	
			TATTGCACG G CCGG		
			ATGACGTGT T GGTC		
			T TG		
GAM1394	TIP47	3'	GGTACTGGGGCCTGTGTGGTA 19483	TG T G__	
			TAT CACG GGTCC GCC		
			ATG GTGT CCGGG TGG		
			GT _ GTCA		
GAM1394	TIP47	3'	GGTACTGGGGCCTGTGTGGTA 19483	TG T G__	
			TAT CACG GGTCC GCC		
			ATG GTGT CCGGG TGG		
			GT _ GTCA		
GAM1394	TP53INP1	3'	AACTAACCCATTAGTGCAGTA 52721	G CC CC	
			TATTGCAC TGGT GG TGGTT		
			ATGACGTG ATTA CC ATCAA		
			_ _ CA		
GAM1394	TP53INP1	3'	AACTAACCCATTAGTGCAGTA 52721	G CC CC	
			TATTGCAC TGGT GG TGGTT		
			ATGACGTG ATTA CC ATCAA		
			_ _ CA		
GAM1394	TP53INP1	3'	AACTAACCCATTAGTGCAGTA 72948	G CC CC	
			TATTGCAC TGGT GG TGGTT		
			ATGACGTG ATTA CC ATCAA		
			_ _ CA		
GAM1394	TP53INP1	3'	AACTAACCCATTAGTGCAGTA 72948	G CC CC	
			TATTGCAC TGGT GG TGGTT		
			ATGACGTG ATTA CC ATCAA		
			_ _ CA		
GAM1394	TPRA40	5'	GATTGGGTGCGTGACCTGTGTGG 33040	TG T _ TG	
			T CACG GGTC CGGCC GTT		

			G GTGT CCAG GCTGG TAG		
			GT _ T GT		
GAM1394	TPRA40	5'	GATTGGGTCGTGACCTGTGTGG 33040	TG T _ TG	
			T CACG GGTC CGGCC GTT		
			G GTGT CCAG GCTGG TAG		
			GT _ T GT		
GAM1394	TRIAD3	3'	GGCCAGGCCGCTGCGGTA 94505	C C	
			TATTGCA GTGGTC GGCC		
			ATGGCGT CGCCGG CCGG		
			_ A		
GAM1394	TRIAD3	3'	GGCCAGGCCGCTGCGGTA 94505	C C	
			TATTGCA GTGGTC GGCC		
			ATGGCGT CGCCGG CCGG		
			_ A		
GAM1394	TRIM38	3'	GCCGGGCATGGTGGTA 20987	TG A G	
			TAT C CGTG TCCGGC		
			ATG G GTAC GGGCCG		
			GT _ _		
GAM1394	TRIM38	3'	GCCGGGCATGGTGGTA 20987	TG A G	
			TAT C CGTG TCCGGC		
			ATG G GTAC GGGCCG		
			GT _ _		
GAM1394	TU3A	3'	AATTGTGTTGGTTATGTGAGTG 23183	G T C	
			TATT CACGTGG CCGGC TGGTT		
			GTGA GTGTATT GGTG GTTAA		
			_ _ T		
GAM1394	TU3A	3'	AATTGTGTTGGTTATGTGAGTG 23183	G T C	
			TATT CACGTGG CCGGC TGGTT		
			GTGA GTGTATT GGTG GTTAA		
			_ _ T		
GAM1394	TUBAL2	3'	GATCGGGCTGGGTCCAGCCCCA 38448	CACG _	
	A		TTG TGG TCCGGCCTGGTT		
			AAC ACC GGGTCGGGCTAG		
			CCCG T		
GAM1394	TUBAL2	3'	GATCGGGCTGGGTCCAGCCCCA 38448	CACG _	
	A		TTG TGG TCCGGCCTGGTT		
			AAC ACC GGGTCGGGCTAG		
			CCCG T		
GAM1394	UBCE7IP5	3'	GCTGGGCATGGTGGTG 30157	TG A G	
			TAT C CGTG TCCGGC		

			GTG G GTAC GGGTCG			
			GT _ _			
GAM1394	UBCE7IP5	3'	GCTGGGCATGGTGGTG	30157	TG A	G
			TAT C CGTG TCCGGC			
			GTG G GTAC GGGTCG			
			GT _ _			
GAM1394	ULK2	5'	GCCGGGCCGGGCCTCG	28002	T	
			CG GGTCCGGCCTGGT			
			GC CCGGGCCGGGCCG			
			T			
GAM1394	ULK2	5'	AGCGCGGGGCCGCGCGGTG	28001	A	G _
			TATTGC CGTGGTCC GC CT			
			GTGGCG GCGCCGGG CG GA			
			_ G C			
GAM1394	ULK2	5'	GCCGGGCCGGGCCTCG	28002	T	
			CG GGTCCGGCCTGGT			
			GC CCGGGCCGGGCCG			
			T			
GAM1394	ULK2	3'	GGCTAGGTTTATTTGGGCAGTA	28003	A	TGGTCC
			TATTGC CG GGCCTGGTT			
			ATGACG GT TTGGATCGG			
			G TTAT__			
GAM1394	ULK2	3'	GGCTAGGTTTATTTGGGCAGTA	28003	A	TGGTCC
			TATTGC CG GGCCTGGTT			
			ATGACG GT TTGGATCGG			
			G TTAT__			
GAM1394	ULK2	5'	AGCGCGGGGCCGCGCGGTG	28001	A	G _
			TATTGC CGTGGTCC GC CT			
			GTGGCG GCGCCGGG CG GA			
			_ G C			
GAM1394	UNC93B1	3'	GGCCGCGGACCCGGGCCGCGTG	48179	TG	__ _
	TGA		T CACGTGGTCCGG CC TGGTT			
			A GTGCGCCGGGCC GG GCCGG			
			GT CA C			
GAM1394	UNC93B1	3'	GGCCGCGGACCCGGGCCGCGTG	48179	TG	__ _
	TGA		T CACGTGGTCCGG CC TGGTT			
			A GTGCGCCGGGCC GG GCCGG			
			GT CA C			
GAM1394	USP25	3'	GACCATTATACTATGTGTA	25441	CCGGCC	
			TGCACGTGGT TGGTT			

		ATGTGTATCA	ACCAG	
		TATT__		
GAM1394	USP25	3' GACCATTATACTATGTGTA	25441	CCGGCC
		TGCACGTGGT	TGGTT	
		ATGTGTATCA	ACCAG	
		TATT__		
GAM1394	VILL	5' AGGCTGGGCCGTGTCCAGTA	68410	C
		TATTG ACGTGGTCCGGCCT		
		ATGAC TGTGCCGGGTCGGA		
		C		
GAM1394	VILL	5' AGGCTGGGCCGTGTCCAGTA	68410	C
		TATTG ACGTGGTCCGGCCT		
		ATGAC TGTGCCGGGTCGGA		
		C		
GAM1394	VRHO	3' AGCTAGGCCGGGCAGAC	56357	G_
		GT GTCCGGCCTGGTT		
		CA CGGGCCGGATCGA		
		GA		
GAM1394	VRHO	3' AGCTAGGCCGGGCAGAC	56357	G_
		GT GTCCGGCCTGGTT		
		CA CGGGCCGGATCGA		
		GA		
GAM1394	WIRE	3' CTGTTGCTATGTGTAG	78304	C_
		TTGCACGTGGT	CGG	
		GATGTGTATCG	GTC	
		TT		
GAM1394	WIRE	3' CTGTTGCTATGTGTAG	78304	C_
		TTGCACGTGGT	CGG	
		GATGTGTATCG	GTC	
		TT		
GAM1394	XPO5	3' AACTAGGCTACATCTGTGATG	91235	TG C GTCC
		TAT CA GTG	GGCCTGGTT	
		GTA GT TAC	TCGGATCAA	
		GT C A__		
GAM1394	XPO5	3' AACTAGGCTACATCTGTGATG	91235	TG C GTCC
		TAT CA GTG	GGCCTGGTT	
		GTA GT TAC	TCGGATCAA	
		GT C A__		
GAM1394	ZAK	3' CAAGTGGGGTATGTGTGGTG	56121	TG G G C
		TAT CACGTG	TCCG C TG	

			GTG GTGTAT GGGT G AC		
			GT G _ A		
GAM1394	ZAK	3'	AACCAGTGATTTTTTAACGTGCA 56115	GGTCCGGC_	
		GTG	TATTGCACGT CTGGTT		
			GTGACGTGCA GACCAA		
			ATTTT TAGT		
GAM1394	ZAK	3'	AACCAGTGATTTTTTAACGTGCA 56115	GGTCCGGC_	
		GTG	TATTGCACGT CTGGTT		
			GTGACGTGCA GACCAA		
			ATTTT TAGT		
GAM1394	ZAK	3'	CAAGTGGGGTATGTGTGGTG 56121	TG G G C	
			TAT CACGTG TCCG C TG		
			GTG GTGTAT GGGT G AC		
			GT G _ A		
GAM1394	ZFPL1	5'	AACTGGGCTGGTGAGAGCGTAG 59654	_ GGT_ TG	
		T	GC ACGT CCGGCC GTT		
			TG TGCG GGTCGG CAA		
			A AGAGT GT		
GAM1394	ZFPL1	5'	AACTGGGCTGGTGAGAGCGTAG 59654	_ GGT_ TG	
		T	GC ACGT CCGGCC GTT		
			TG TGCG GGTCGG CAA		
			A AGAGT GT		
GAM1394	ZNF197	3'	ACATGGGCTGGGTGCAGTG 22762	GTGGT _	
			TATTGCAC CCGGCCTG GT		
			GTGACGTG GGTCGGGT CA		
			A		
GAM1394	ZNF197	3'	ACATGGGCTGGGTGCAGTG 22762	GTGGT _	
			TATTGCAC CCGGCCTG GT		
			GTGACGTG GGTCGGGT CA		
			A		
GAM1394	ZNF297B	3'	TTCAGGGATCACGTCAATG 25790	C GGC TT	
			TATTG ACGTGGTCC CTGG		
			GTAAC TGCACTAGG GACT		
			TT		
GAM1394	ZNF297B	3'	TTCAGGGATCACGTCAATG 25790	C GGC TT	
			TATTG ACGTGGTCC CTGG		
			GTAAC TGCACTAGG GACT		
			TT		
GAM1394	ZNF300	5'	TCAGAGGCGGGATGTGTGCGGT 53478	GTG G GGTT	
		G	TATTGCAC GTCC GCCT		

			GTGGCGTG TAGG CGGA		
			TG_ G GACTG		
GAM1394	ZNF300	5'	TCAGAGGCGGGATGTGTGCGGT 53478	GTG	G GGTT
	G		TATTGCAC GTCC GCCT		
			GTGGCGTG TAGG CGGA		
			TG_ G GACTG		
GAM1394	ZNF339	3'	GCCGGGCATGGTGGTG 41120	TG A	G
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGCCG		
			GT _ _		
GAM1394	ZNF339	3'	GCCGGGCATGGTGGTG 41120	TG A	G
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGCCG		
			GT _ _		
GAM1394	LOC112687	3'	TAACAGGCTGGGTGCAATG 72866	GTGGT	GTT
			TATTGCAC CCGGCCTG		
			GTAACGTG GGTCGGAC		
			_____ AATG		
GAM1394	LOC112687	3'	TAACAGGCTGGGTGCAATG 72866	GTGGT	GTT
			TATTGCAC CCGGCCTG		
			GTAACGTG GGTCGGAC		
			_____ AATG		
GAM1394	LOC115110	3'	GGCTGGGCTGGACCTGC 71719	CGT	TG
			GCA GGTCCGGCC GTT		
			CGT CCAGGTCGG CGG		
			_____ GT		
GAM1394	LOC115110	3'	GGCTGGGCTGGACCTGC 71719	CGT	TG
			GCA GGTCCGGCC GTT		
			CGT CCAGGTCGG CGG		
			_____ GT		
GAM1394	LOC115207	3'	AACCTGATTGGACCGTGTCCAA 56596	C	CCT
	TG		TATTG ACGTGGTCCGG GGTT		
			GTAAC TGTGCCAGGTT CCAA		
			C AGT		
GAM1394	LOC115207	3'	AACCTGATTGGACCGTGTCCAA 56596	C	CCT
	TG		TATTG ACGTGGTCCGG GGTT		
			GTAAC TGTGCCAGGTT CCAA		
			C AGT		
GAM1394	LOC115219	5'	GACCAGGCTGGACTCGGGCTGT 73307	_ _	
	GCAG		GCAC GT GGTCCGGCCTGGTT		

		CGTG CG TCAGGTCGGACCAG		
		T GGC		
GAM1394	LOC115219 5'	GACCAGGCTGGA	CTCGGGCTGT 73307	— —
	GCAG	GCAC GT GGTCCGGCCTGGTT		
		CGTG CG TCAGGTCGGACCAG		
		T GGC		
GAM1394	LOC115811 5'	GCAGGGACCGCGGCGGTA	56615	A G_
		TATTGC CGTGGTCC GC		
		ATGGCG GCGCCAGG CG		
		— GA		
GAM1394	LOC115811 5'	GCAGGGACCGCGGCGGTA	56615	A G_
		TATTGC CGTGGTCC GC		
		ATGGCG GCGCCAGG CG		
		— GA		
GAM1394	LOC116173 5'	TAGGGGGCTGTGTTGGTG	56642	C TG GG
		TATTG ACG GTCC CCTG		
		GTGGT TGT CGGG GGAT		
		— GT —		
GAM1394	LOC116173 5'	TAGGGGGCTGTGTTGGTG	56642	C TG GG
		TATTG ACG GTCC CCTG		
		GTGGT TGT CGGG GGAT		
		— GT —		
GAM1394	LOC116349 3'	AACTAGGCAGGTGTGGTGGTG	73828	TG A TGGT G
		TAT C CG CC GCCTGGTT		
		GTG G GT GG CGGATCAA		
		GT_ GT_ A		
GAM1394	LOC116349 3'	AACTAGGCAGGTGTGGTGGTG	73828	TG A TGGT G
		TAT C CG CC GCCTGGTT		
		GTG G GT GG CGGATCAA		
		GT_ GT_ A		
GAM1394	LOC118812 5'	AGCCGGGCTGGGCCAATGCGG	73928	CG
		TTGCA TGGTCCGGCCTGGTT		
		GGCGT ACCGGGTCGGGCCGA		
		A_		
GAM1394	LOC118812 5'	AGCCGGGCTGGGCCAATGCGG	73928	CG
		TTGCA TGGTCCGGCCTGGTT		
		GGCGT ACCGGGTCGGGCCGA		
		A_		
GAM1394	LOC119548 5'	AACTGGGTTGGACCCAGC	73994	ACGT TG
		GC GGTCCGGCC GTT		

		CG	CCAGGTTGG	CAA		
		AC__	GT			
GAM1394	LOC119548 5'	AACTGGGTTGG	ACCCAGC	73994	ACGT	TG
		GC	GGTCCGGCC	GTT		
		CG	CCAGGTTGG	CAA		
		AC__	GT			
GAM1394	LOC120114 3'	GATTACGGCCGCCTGTGCAGTG	75527		T TC	_
		TATTGCACG	GG CGGCC	TGGTT		
		GTGACGTGT	CC GCCGG	ATTAG		
		_	__	C		
GAM1394	LOC120114 3'	GATTACGGCCGCCTGTGCAGTG	75527		T TC	_
		TATTGCACG	GG CGGCC	TGGTT		
		GTGACGTGT	CC GCCGG	ATTAG		
		_	__	C		
GAM1394	LOC121457 5'	GGCTGGGCTCTGGGCGGTG	74073		A T	
		TATTGC	CG GGTCCGGCC			
		GTGGCG	GT TCGGGTCGG			
		G	C			
GAM1394	LOC121457 5'	GGCTGGGCTCTGGGCGGTG	74073		A T	
		TATTGC	CG GGTCCGGCC			
		GTGGCG	GT TCGGGTCGG			
		G	C			
GAM1394	LOC122830 3'	GGCCAATCAGTGCAATG	74167		G CC	
		TATTGCAC	TGGT GGCC			
		GTAACGTG	ACTA CCGG			
		_	A_			
GAM1394	LOC122830 3'	GGCCAATCAGTGCAATG	74167		G CC	
		TATTGCAC	TGGT GGCC			
		GTAACGTG	ACTA CCGG			
		_	A_			
GAM1394	LOC122970 3'	GGTCAAGATTGGTGCAGTG	74184		G C_	
		TATTGCAC	TGGTC GGCC			
		GTGACGTG	GTTAG CTGG			
		_	AA			
GAM1394	LOC122970 3'	GGTCAAGATTGGTGCAGTG	74184		G C_	
		TATTGCAC	TGGTC GGCC			
		GTGACGTG	GTTAG CTGG			
		_	AA			
GAM1394	LOC123242 5'	GCAGGGCCACGTGAGGTA	75600		TG	G
		TAT	CACGTGGTCC	GC		



		ATG GTGCACCGGG CG			
		GA A			
GAM1394	LOC123242 5'	GCAGGGCCACGTGAGGTA 75600	TG	G	
		TAT CACGTGGTCC GC			
		ATG GTGCACCGGG CG			
		GA A			
GAM1394	LOC123872 5'	GGCTGGGCTGGGGCCGTAGC 74237	ACG	_	TG
		GC TGGTCC GGCC GTT			
		CG GCCGGG TCGG CGG			
		AT_ G GT			
GAM1394	LOC123872 5'	GGCTGGGCTGGGGCCGTAGC 74237	ACG	_	TG
		GC TGGTCC GGCC GTT			
		CG GCCGGG TCGG CGG			
		AT_ G GT			
GAM1394	LOC124220 3'	GCTGAGGCCATCTGTGTGGTG 59145	TG	_	_
		TAT CAC GTGGTC CGGC			
		GTG GTG TACCGG GTCG			
		GT TC A			
GAM1394	LOC124220 3'	GCTGAGGCCATCTGTGTGGTG 59145	TG	_	_
		TAT CAC GTGGTC CGGC			
		GTG GTG TACCGG GTCG			
		GT TC A			
GAM1394	LOC124935 5'	AACCAGGAGGCCTTCGTGTAGT 74369	T_	T	GG
	G	TATTGCACG GG CC CCTGGTT			
		GTGATGTGC CC GG GGACCAA			
		TT _ A_			
GAM1394	LOC124935 5'	AACCAGGAGGCCTTCGTGTAGT 74369	T_	T	GG
	G	TATTGCACG GG CC CCTGGTT			
		GTGATGTGC CC GG GGACCAA			
		TT _ A_			
GAM1394	LOC124944 5'	TGGTCTAAGCGACTGCGTCTGA 74376	C	TG	C____ TGGTT
	TG	TTG ACG GTC GGCC			
		AGT TGC CAG CTGG			
		C GT CGAAT TT			
GAM1394	LOC124944 5'	TGGTCTAAGCGACTGCGTCTGA 74376	C	TG	C____ TGGTT
	TG	TTG ACG GTC GGCC			
		AGT TGC CAG CTGG			
		C GT CGAAT TT			
GAM1394	LOC125268 3'	GGCCAGGCCCGAGCGTGCAG 76076	GGTCC		
		TTGCACGT GGCCTGGTT			

		GACGTGCG CCGGACCGG	
		AC__	
GAM1394	LOC125268 3'	GGCCAGGCCACGTCGATG 76076	GGTCC
		TTGCACGT GGCCTGGT	
		GACGTGCG CCGGACCGG	
		AC__	
GAM1394	LOC126167 5'	GGTCAGGGCTGTGCGATG 74460	GT _
		TATTGCAC GGTCC GGCC	
		GTAGCGTG TCGGG CTGG	
		_ A	
GAM1394	LOC126167 5'	GGTCAGGGCTGTGCGATG 74460	GT _
		TATTGCAC GGTCC GGCC	
		GTAGCGTG TCGGG CTGG	
		_ A	
GAM1394	LOC126272 3'	ATTGGGTAGGTGTGGAATA 76087	G TGGT G TG
		TATT CACG CC GCC GT	
		ATAA GTGT GG TGG TA	
		G _ A GT	
GAM1394	LOC126272 3'	ATTGGGTAGGTGTGGAATA 76087	G TGGT G TG
		TATT CACG CC GCC GT	
		ATAA GTGT GG TGG TA	
		G _ A GT	
GAM1394	LOC126282 3'	TTGAGGCCACGTGCAGTG 74480	_
		TATTGCACGTGGTC CGG	
		GTGACGTGCACCGG GTT	
		A	
GAM1394	LOC126282 3'	TTGAGGCCACGTGCAGTG 74480	_
		TATTGCACGTGGTC CGG	
		GTGACGTGCACCGG GTT	
		A	
GAM1394	LOC126755 3'	AACTAATAAACTCGTGTGCAAT 74566	TCCGGCC
	A	TATTGCACGTGG TGTT	
		ATAACGTGTGCT ATCAA	
		CAAATA_	
GAM1394	LOC126755 3'	AACTAATAAACTCGTGTGCAAT 74566	TCCGGCC
	A	TATTGCACGTGG TGTT	
		ATAACGTGTGCT ATCAA	
		CAAATA_	
GAM1394	LOC126917 3'	GGCCGGGCCAACCGGCCGTGGT 74590	_ C__
	GTAATG	GCAC GTGGTC GGCCTGGT	

		TGTG TGCCGG CCGGGCCGG		
		G CCAA		
GAM1394	LOC126917 3'	GGCCGGGCCAACCGGCCGTGGT 74590	_ C__	
		GTAATG GCAC GTGGTC GGCCTGGTT		
		TGTG TGCCGG CCGGGCCGG		
		G CCAA		
GAM1394	LOC126961 3'	TGGTCGGGTCCCCCTGCTGCGG 74631	C ____ GT	TGGTT
		TG TGCA GT G CCGGCC		
		GCGT CG C GGCTGG		
		_ TCCCC TG TT		
GAM1394	LOC126961 3'	TGGTCGGGTCCCCCTGCTGCGG 74631	C ____ GT	TGGTT
		TG TGCA GT G CCGGCC		
		GCGT CG C GGCTGG		
		_ TCCCC TG TT		
GAM1394	LOC127845 3'	ACTGGGCTGGGGCTGGT 74696	G _ TG	
		AC TGGTCC GGCC GT		
		TG GTCGGG TCGG CA		
		_ G GT		
GAM1394	LOC127845 3'	ACTGGGCTGGGGCTGGT 74696	G _ TG	
		AC TGGTCC GGCC GT		
		TG GTCGGG TCGG CA		
		_ G GT		
GAM1394	LOC128977 3'	GGCTAGGCTGGGTCTGTGC 74824	T GT	
		GCACG G CCGGCCTGGTT		
		CGTGT C GGTCGGATCGG		
		_ TG		
GAM1394	LOC128977 3'	GGTCAGGCTGGGCATGGTAGCA 74825	_ GTG	GT
		TGC AC GTCCGGCCTG T		
		ACG TG CGGGTCGGAC G		
		A GTA TG		
GAM1394	LOC128977 3'	GGTCAGGCTGGGCATGGTAGCA 74825	_ GTG	GT
		TGC AC GTCCGGCCTG T		
		ACG TG CGGGTCGGAC G		
		A GTA TG		
GAM1394	LOC128977 3'	GGCTAGGCTGGGTCTGTGC 74824	T GT	
		GCACG G CCGGCCTGGTT		
		CGTGT C GGTCGGATCGG		
		_ TG		
GAM1394	LOC129433 5'	AGCTGGGCTGGGCTTCGCAG 75725	ACGT	TG
		TTGC GGTCCGGCC GTT		

		GACG TCGGGTCGG CGA		
		CT__ GT		
GAM1394	LOC129433 5'	AGCTGGGCTGGGCTTCGCAG 75725	ACGT	TG
		TTGC GGTCCGGCC GTT		
		GACG TCGGGTCGG CGA		
		CT__ GT		
GAM1394	LOC130535 3'	GCATTGGCTGGGTGCAGTG 76152	GTGGT	TG_ T
		TATTGCAC CCGGCC GT		
		GTGACGTG GGTCGG CG		
		_____ TTA T		
GAM1394	LOC130535 3'	GCATTGGCTGGGTGCAGTG 76152	GTGGT	TG_ T
		TATTGCAC CCGGCC GT		
		GTGACGTG GGTCGG CG		
		_____ TTA T		
GAM1394	LOC130589 3'	GGCTCCAGGCCATGTCTAATG 57134	C	C__
		TATTG ACGTGGTC GGCC		
		GTAAT TGTACCGG TCGG		
		C ACC		
GAM1394	LOC130589 3'	GGCTCCAGGCCATGTCTAATG 57134	C	C__
		TATTG ACGTGGTC GGCC		
		GTAAT TGTACCGG TCGG		
		C ACC		
GAM1394	LOC131744 3'	CTAGGCCGGTGCGGTG 75869	CGTGGT	
		TATTGCA CCGGCCTGG		
		GTGGCGT GGCCGGATC		
		_____		
GAM1394	LOC131744 3'	CTAGGCCGGTGCGGTG 75869	CGTGGT	
		TATTGCA CCGGCCTGG		
		GTGGCGT GGCCGGATC		
		_____		
GAM1394	LOC133926 5'	GCCGGGCCGGAGCCGC 75132	_	
		GTGG TCCGGCCTGGT		
		CGCC AGGCCGGGCCG		
		G		
GAM1394	LOC133926 5'	GCCGGGCCGGAGCCGC 75132	_	
		GTGG TCCGGCCTGGT		
		CGCC AGGCCGGGCCG		
		G		
GAM1394	LOC134147 3'	CAGGCCGGGTGCGGTG 57159	GTGGT	
		TATTGCAC CCGGCCTG		

GTGGCGTG GGCCGGAC

GAM1394 LOC134147 3' GGTCTGACCAGGTGTAGTG 57165 G C  
TATTGCAC TGGTC GGCC  
||||||| ||||| ||||  
GTGATGTG ACCAG CTGG  
G T

GAM1394 LOC134147 3' CAGGCCGGGTGCGGTG 57159 GTGGT  
TATTGCAC CCGGCCTG  
||||||| |||||  
GTGGCGTG GGCCGGAC

GAM1394 LOC134147 3' GGTCTGACCAGGTGTAGTG 57165 G C  
TATTGCAC TGGTC GGCC  
||||||| ||||| ||||  
GTGATGTG ACCAG CTGG  
G T

GAM1394 LOC134285 5' GCCGAGGCCGCGTGCGG 76166 \_  
TTGCACGTGGTC CGGC  
||||||| |||||  
GGCGTGCGCCGG GCCG  
A

GAM1394 LOC134285 5' GCCGAGGCCGCGTGCGG 76166 \_  
TTGCACGTGGTC CGGC  
||||||| |||||  
GGCGTGCGCCGG GCCG  
A

GAM1394 LOC135818 3' ATTGGGCTGGGCACGATG 75229 \_ G TG  
CA CGTG TCCGGCC GT  
|| ||||| ||||| ||  
GT GCAC GGGTCGG TA  
A \_ GT

GAM1394 LOC135818 3' ATTGGGCTGGGCACGATG 75229 \_ G TG  
CA CGTG TCCGGCC GT  
|| ||||| ||||| ||  
GT GCAC GGGTCGG TA  
A \_ GT

GAM1394 LOC136120 5' GGCCGGGCCGGGCCGAGAGGC 76205 ACG\_  
GC TGGTCCGGCCTGGTT  
|| ||||| ||||| |||||  
CG GCCGGGCCGGGCCGG  
GAGA

GAM1394 LOC136120 5' GGCCGGGCCGGGCCGAGAGGC 76205 ACG\_  
GC TGGTCCGGCCTGGTT  
|| ||||| ||||| |||||  
CG GCCGGGCCGGGCCGG  
GAGA

GAM1394 LOC138241 5' GGCTGCGCCGCGTGGAGTG 75310 G C  
TATT CACGTGGT CGGCC  
||| ||||| |||||

	GTGA GTGCGCCG GTCGG	
	G C	
GAM1394 LOC138241 5'	GGCTGCGCCGCGTGGAGTG 75310	G C
	TATT CACGTGGT CGGCC	
	GTGA GTGCGCCG GTCGG	
	G C	
GAM1394 LOC138307 5'	GGCCAGGCTAACCCCTGCGGTG 75315	CGT CC
	TATTGCA GGT GGCCTGGTT	
	GTGGCGT CCA TCGGACCGG	
	CC_ A_	
GAM1394 LOC138307 5'	GGCCAGGCTAACCCCTGCGGTG 75315	CGT CC
	TATTGCA GGT GGCCTGGTT	
	GTGGCGT CCA TCGGACCGG	
	CC_ A_	
GAM1394 LOC138389 3'	GCCAGGCATGGTGGTAGTA 76228	ACGTGGT _
	TATTGC CCG GCCTGGT	
	ATGATG GGT CGGACCG	
	GT_____ A	
GAM1394 LOC138389 3'	GCCAGGCATGGTGGTAGTA 76228	ACGTGGT _
	TATTGC CCG GCCTGGT	
	ATGATG GGT CGGACCG	
	GT_____ A	
GAM1394 LOC138428 3'	GGCTTGAGGCCGGGTGCAGTG 75339	G _ _
	TATTGCAC TGGT CCG GCC	
	GTGACGTG GCCG GGT CGG	
	G GA T	
GAM1394 LOC138428 3'	GGCTTGAGGCCGGGTGCAGTG 75339	G _ _
	TATTGCAC TGGT CCG GCC	
	GTGACGTG GCCG GGT CGG	
	G GA T	
GAM1394 LOC138649 5'	GACCAGGCTGGATCGCG 75355	
	CGTGGTCCGGCCTGGTT	
	GCGCTAGGTCCGACCAG	
GAM1394 LOC138649 5'	GACCAGGCTGGATCGCG 75355	
	CGTGGTCCGGCCTGGTT	
	GCGCTAGGTCCGACCAG	
GAM1394 LOC139420 3'	AACCAGGTCGATAATGTTAATG 75836	C G C
	TATTG ACGT GTC GGCCTGGTT	

	GTAAT TGTA TAG CTGGACCAA	
	— A —	
GAM1394 LOC139420 3'	AACCAGGTCGATAATGTTAATG 75836	C G C
	TATTG ACGT GTC GGCCTGGTT	
	GTAAT TGTA TAG CTGGACCAA	
	— A —	
GAM1394 LOC139422 3'	AGCAAAGAGGGTTCGGGTGCGGT 75837	G GT GGCCTG
G	TATTGCAC TG CC GTT	
	GTGGCGTG GC GG CGA	
	G TG AGAAA_	
GAM1394 LOC139422 3'	AGCAAAGAGGGTTCGGGTGCGGT 75837	G GT GGCCTG
G	TATTGCAC TG CC GTT	
	GTGGCGTG GC GG CGA	
	G TG AGAAA_	
GAM1394 LOC142826 3'	GGCCAGGTACAGTATGTGTAA 76401	GTCCG
	TTGCACGTG GCCTGGTT	
	AATGTGTAT TGGACCGG	
	GACA_	
GAM1394 LOC142826 3'	GGCCAGGTACAGTATGTGTAA 76401	GTCCG
	TTGCACGTG GCCTGGTT	
	AATGTGTAT TGGACCGG	
	GACA_	
GAM1394 LOC143310 5'	AGTTAGGTTGGGTTATCTCAG 76525	CAC GT GG
	TTG GTG CCGGCCT TT	
	GAC TAT GGTTGGA GA	
	TC_ TG TT	
GAM1394 LOC143310 5'	AGTTAGGTTGGGTTATCTCAG 76525	CAC GT GG
	TTG GTG CCGGCCT TT	
	GAC TAT GGTTGGA GA	
	TC_ TG TT	
GAM1394 LOC143381 3'	GACCGGGTGA CTGTGGCAGTG 76549	A TG CG
	TATTGC CG GTC GCCTGGTT	
	GTGACG GT CAG TGGGCCAG	
	_ GT _	
GAM1394 LOC143381 3'	GACCGGGTGA CTGTGGCAGTG 76549	A TG CG
	TATTGC CG GTC GCCTGGTT	
	GTGACG GT CAG TGGGCCAG	
	_ GT _	
GAM1394 LOC143465 3'	GCTGGCCAGGTGTAGTG 82964	G T
	TATTGCAC TGG CCGGC	

		GTGATGTG ACC GGTCG		
		G _		
GAM1394	LOC143465 3'	GCTGGCCAGGTGTAGTG	82964	G T
		TATTGCAC TGG CCGGC		
		GTGATGTG ACC GGTCG		
		G _		
GAM1394	LOC144347 3'	GGCCAAGGCCATGTGTGA	76814	TG C_
		T CACGTGGTC GGCC		
		A GTGTACCGG CCGG		
		GT AA		
GAM1394	LOC144347 3'	GGCCAAGGCCATGTGTGA	76814	TG C_
		T CACGTGGTC GGCC		
		A GTGTACCGG CCGG		
		GT AA		
GAM1394	LOC144932 3'	GGCCAGGCCTGGCAGTG	76976	A T C
		TATTGC CG GGTC GGCC		
		GTGACG GT CCGG CCGG		
		_ _ A		
GAM1394	LOC144932 3'	GGCCAGGCCTGGCAGTG	76976	A T C
		TATTGC CG GGTC GGCC		
		GTGACG GT CCGG CCGG		
		_ _ A		
GAM1394	LOC145240 3'	AACTGGGTAAATGTGCA	77049	GGTCC TG
		TGCACGT GGCC GTT		
		ACGTGTA TTGG CAA		
		AA__ GT		
GAM1394	LOC145240 3'	AACTGGGTAAATGTGCA	77049	GGTCC TG
		TGCACGT GGCC GTT		
		ACGTGTA TTGG CAA		
		AA__ GT		
GAM1394	LOC145387 3'	AACTGCCAAGGCCAGGTGCAGT	83350	G C_ CT
	G	TATTGCAC TGGTC GGC GGTT		
		GTGACGTG ACCGG CCG TCAA		
		G AA _		
GAM1394	LOC145387 3'	AACTGCCAAGGCCAGGTGCAGT	83350	G C_ CT
	G	TATTGCAC TGGTC GGC GGTT		
		GTGACGTG ACCGG CCG TCAA		
		G AA _		
GAM1394	LOC145608 5'	GGCCCAAGGGATCAGTGTGGTG	83385	TG G _
		TAT CAC TGGTCC GGCC		



	GTG GTG ACTAGG CCGG		
	GT _ GAAC		
GAM1394 LOC145608 5'	GGCCCAAGGGATCAGTGTGGTG 83385	TG G	_____
	TAT CAC TGGTCC GGCC		
	GTG GTG ACTAGG CCGG		
	GT _ GAAC		
GAM1394 LOC145663 3'	ATGAGGCCGGGTGCAGTG 83412	GTGGT	G T
	TATTGCAC CCGGCCT GT		
	GTGACGTG GGCCGGA TA		
	_____ G T		
GAM1394 LOC145663 3'	ATGAGGCCGGGTGCAGTG 83412	GTGGT	G T
	TATTGCAC CCGGCCT GT		
	GTGACGTG GGCCGGA TA		
	_____ G T		
GAM1394 LOC145717 5'	GGCTGGGGCTACGTGCAG 66831		—
	TTGCACGTGGTCC GGCC		
	GACGTGCATCGGG TCGG		
	G		
GAM1394 LOC145717 5'	GGCTGGGGCTACGTGCAG 66831		—
	TTGCACGTGGTCC GGCC		
	GACGTGCATCGGG TCGG		
	G		
GAM1394 LOC145757 3'	GGAGGACATGTGTGGTG 77468	TG	G GG
	TAT CACGTG TCC CC		
	GTG GTGTAC AGG GG		
	GT _ A_		
GAM1394 LOC145757 3'	GGAGGACATGTGTGGTG 77468	TG	G GG
	TAT CACGTG TCC CC		
	GTG GTGTAC AGG GG		
	GT _ A_		
GAM1394 LOC145813 3'	GATCAGAATGGCCATGTTAATG 83508	C	T GC
	TATTG ACGTGG CCG CTGGTT		
	GTAAT TGTACC GGT GACTAG		
	_ _ AA		
GAM1394 LOC145813 3'	GATCAGAATGGCCATGTTAATG 83508	C	T GC
	TATTG ACGTGG CCG CTGGTT		
	GTAAT TGTACC GGT GACTAG		
	_ _ AA		
GAM1394 LOC145988 3'	AGTCAGGGACATATTTTGTGCA 77605	TG_____	GGC GT
ATA	TGCACG GTCC CTG T		

	ACGTGT	CAGG	GAC	A		
	TTTATA	___	TG			
GAM1394 LOC145988 3'	AGTCAGGGACATATTTTGTGCA	77605	TG___	GGC	GT	
	ATA	TGCACG	GTCC	CTG	T	
	ACGTGT	CAGG	GAC	A		
	TTTATA	___	TG			
GAM1394 LOC146059 3'	GCTGGGGCATGGTGGTG	77621	TG	A	G	
	TAT	C	CGTG	TCCGGC		
	GTG	G	GTAC	GGGTCG		
	GT	_	_			
GAM1394 LOC146059 3'	GCTGGGGCATGGTGGTG	77621	TG	A	G	
	TAT	C	CGTG	TCCGGC		
	GTG	G	GTAC	GGGTCG		
	GT	_	_			
GAM1394 LOC146136 5'	ATTGGGCTGCTGTGCAG	72940	TGGTC	TG		
	TTGCACG	CGGCC	GT			
	GACGTGT	GTCGG	TA			
	C___	GT				
GAM1394 LOC146136 5'	ATTGGGCTGCTGTGCAG	72940	TGGTC	TG		
	TTGCACG	CGGCC	GT			
	GACGTGT	GTCGG	TA			
	C___	GT				
GAM1394 LOC146272 5'	GCCAGCCAGGTGCAGTG	77788	G	CC		
	TATTGCAC	TGGT	GGC			
	GTGACGTG	ACCG	CCG			
	G	A_				
GAM1394 LOC146272 5'	GCCAGCCAGGTGCAGTG	77788	G	CC		
	TATTGCAC	TGGT	GGC			
	GTGACGTG	ACCG	CCG			
	G	A_				
GAM1394 LOC146315 5'	AACCTAGGCCAGTGTGTGGTG	60883	TG	TGGTCC	_	
	TAT	CACG	GGCCT	GGTT		
	GTG	GTGT	CCGGA	CCAA		
	GT	GA___	T			
GAM1394 LOC146315 5'	AACCTAGGCCAGTGTGTGGTG	60883	TG	TGGTCC	_	
	TAT	CACG	GGCCT	GGTT		
	GTG	GTGT	CCGGA	CCAA		
	GT	GA___	T			
GAM1394 LOC146445 3'	ACTGGGTTGACGTGCA	83675	GGTC	TG		
	TGCACGT	CGGCC	GT			

ACGTGCA GTTGG CA  
 \_\_\_\_\_ GT  
 GAM1394 LOC146445 3' ACTGGGTTGACGTGCA 83675 GGTC TG  
 TGCACGT CGGCC GT  
 ||||| ||| ||  
 ACGTGCA GTTGG CA  
 \_\_\_\_\_ GT  
 GAM1394 LOC146446 3' CCGGCCCATGGTGTGGTG 83686 TG \_ T  
 TAT CAC GTGG CCGG  
 ||| ||| ||| |||  
 GTG GTG TACC GGCC  
 GT G C  
 GAM1394 LOC146446 3' CCGGCCCATGGTGTGGTG 83686 TG \_ T  
 TAT CAC GTGG CCGG  
 ||| ||| ||| |||  
 GTG GTG TACC GGCC  
 GT G C  
 GAM1394 LOC146517 3' AATTGGGTTCTTGCTGCAGTG 77943 C TG TCC TG  
 TATTGCA G G GGCC GTT  
 ||||| | | ||| |||  
 GTGACGT C T TTGG TAA  
 C GT C\_\_ GT  
 GAM1394 LOC146517 3' AATTGGGTTCTTGCTGCAGTG 77943 C TG TCC TG  
 TATTGCA G G GGCC GTT  
 ||||| | | ||| |||  
 GTGACGT C T TTGG TAA  
 C GT C\_\_ GT  
 GAM1394 LOC146656 3' GCTGGGCATGGTGGTG 78073 TG A G  
 TAT C CGTG TCCGGC  
 ||| | ||| |||||  
 GTG G GTAC GGGTCG  
 GT \_ \_  
 GAM1394 LOC146656 3' GCTGGGCATGGTGGTG 78073 TG A G  
 TAT C CGTG TCCGGC  
 ||| | ||| |||||  
 GTG G GTAC GGGTCG  
 GT \_ \_  
 GAM1394 LOC146667 3' TCGGCCACGTGCGGTG 83709 T  
 TATTGCACGTGG CCGG  
 ||||| ||| |||  
 GTGGCGTGCACC GGCT  
 \_  
 GAM1394 LOC146667 3' TCGGCCACGTGCGGTG 83709 T  
 TATTGCACGTGG CCGG  
 ||||| ||| |||  
 GTGGCGTGCACC GGCT  
 \_  
 GAM1394 LOC146733 3' GATCAGGCTGGGCCATTATTGC 83765 C\_\_  
 AG TTGCA GTGGTCCGGCCTGGTT  
 |||| ||||| ||||| |||||

		GACGT TACCGGGTCGGACTAG		
		TAT		
GAM1394	LOC146733 3'	GATCAGGCTGGGCCATTATTGC 83765	C__	
	AG	TTGCA GTGGTCCGGCCTGGTT		
		GACGT TACCGGGTCGGACTAG		
		TAT		
GAM1394	LOC146754 3'	GGCCGAATTTGTGTGATG 78093	TG T C	
		TAT CACG GGT CGGCC		
		GTA GTGT TTA GCCGG		
		GT _ A		
GAM1394	LOC146754 3'	GGCCGAATTTGTGTGATG 78093	TG T C	
		TAT CACG GGT CGGCC		
		GTA GTGT TTA GCCGG		
		GT _ A		
GAM1394	LOC146895 3'	GCCGGGCATGGTGGTA 83823	TG A G	
		TAT C CGTG TCCGGC		
		ATG G GTAC GGGCCG		
		GT _ _		
GAM1394	LOC146895 3'	GCCGGGCATGGTGGTA 83823	TG A G	
		TAT C CGTG TCCGGC		
		ATG G GTAC GGGCCG		
		GT _ _		
GAM1394	LOC146953 5'	GCCGGGCTGGGGGTG 78213	GTGG	
		CAC TCCGGCCTGGT		
		GTG GGGTCGGGCCG		
		G__		
GAM1394	LOC146953 5'	GCCGGGCTGGGGGTG 78213	GTGG	
		CAC TCCGGCCTGGT		
		GTG GGGTCGGGCCG		
		G__		
GAM1394	LOC147515 5'	CGGGGGGTTGGTTGGGTGCAGT 84021	G T GGTT	
	A	TATTGCAC TGG CCGGCCT		
		ATGACGTG GTT GGTTGGG		
		G _ GGGCT		
GAM1394	LOC147515 5'	CGGGGGGTTGGTTGGGTGCAGT 84021	G T GGTT	
	A	TATTGCAC TGG CCGGCCT		
		ATGACGTG GTT GGTTGGG		
		G _ GGGCT		
GAM1394	LOC147660 3'	GCCGGGCATGGTGGTG 78394	TG A G	
		TAT C CGTG TCCGGC		

		GTG G GTAC GGGCCG		
		GT _ _		
GAM1394	LOC147660 3'	TTGGGCCAGGTGCAGTG	78401	G
		TATTGCAC TGGTCCGG		
		GTGACGTG ACCGGGTT		
		G		
GAM1394	LOC147660 3'	TTGGGCCAGGTGCAGTG	78401	G
		TATTGCAC TGGTCCGG		
		GTGACGTG ACCGGGTT		
		G		
GAM1394	LOC147660 3'	GCCGGGCATGGTGGTG	78394	TG A G
		TAT C CGTG TCCGGC		
		GTG G GTAC GGGCCG		
		GT _ _		
GAM1394	LOC147694 5'	TGGTCGTTTTGGTTCTGTGTGG	78458	TG T GT ____ TGGTT
	TG	T CACG G C CGGCC		
		G GTGT T G GCTGG		
		GT C TG TTTT TT		
GAM1394	LOC147694 5'	TGGTCGTTTTGGTTCTGTGTGG	78458	TG T GT ____ TGGTT
	TG	T CACG G C CGGCC		
		G GTGT T G GCTGG		
		GT C TG TTTT TT		
GAM1394	LOC148293 3'	ATCAGGCCAGGTGTGGTG	78777	TG G GGTCC
		TAT CAC T GGCCTGGT		
		GTG GTG A CCGGACTA		
		GT G ____		
GAM1394	LOC148293 3'	ATCAGGCCAGGTGTGGTG	78777	TG G GGTCC
		TAT CAC T GGCCTGGT		
		GTG GTG A CCGGACTA		
		GT G ____		
GAM1394	LOC148479 3'	CTGGACACCCACGTGCAG	78866	____
		TTGCACGTGG TCCGG		
		GACGTGCACC AGGTC		
		CAC		
GAM1394	LOC148479 3'	CTGGACACCCACGTGCAG	78866	____
		TTGCACGTGG TCCGG		
		GACGTGCACC AGGTC		
		CAC		
GAM1394	LOC148645 5'	GGCCAGGCTGGAGTGCGGCAGT	84182	A G
		ATTGC CGTG TCCGGCCTGGTT		

	TGACG GCGT AGGTCGGACCGG	
	_ G	
GAM1394 LOC148645 5'	GGCCAGGCTGGAGTGCGGCAGT 84182	A G
	ATTGC CGTG TCCGGCCTGGTT	
	TGACG GCGT AGGTCGGACCGG	
	_ G	
GAM1394 LOC148760 3'	AACCAGAACCACTGTGTAGTA 84201	_ CCGGC
	TATTGCAC GTGGT CTGGTT	
	ATGATGTG CACCA GACCAA	
	T A_	
GAM1394 LOC148760 3'	AACCAGAACCACTGTGTAGTA 84201	_ CCGGC
	TATTGCAC GTGGT CTGGTT	
	ATGATGTG CACCA GACCAA	
	T A_	
GAM1394 LOC148887 3'	GGTTAGCTCATGTGCAGT 84247	_ CC
	ATTGCACGTG GT GGCC	
	TGACGTGTAC CG TTGG	
	T A_	
GAM1394 LOC148887 3'	GGTTAGCTCATGTGCAGT 84247	_ CC
	ATTGCACGTG GT GGCC	
	TGACGTGTAC CG TTGG	
	T A_	
GAM1394 LOC149073 3'	TATCATTCTTGGCTGTGTGCGG 84332	TG C CC T
TG	TATTGCACG GTC GG TGGT	
	GTGGCGTGT CGG TC ACTA	
	GT T TT TA	
GAM1394 LOC149073 3'	TATCATTCTTGGCTGTGTGCGG 84332	TG C CC T
TG	TATTGCACG GTC GG TGGT	
	GTGGCGTGT CGG TC ACTA	
	GT T TT TA	
GAM1394 LOC149111 5'	GGCTTCTTGGCGTGTGTGGTG 79184	TG GT ____
	TAT CACGTG CC GGCC	
	GTG GTGTGC GG TCGG	
	GT ____ TTCT	
GAM1394 LOC149111 5'	GGCTTCTTGGCGTGTGTGGTG 79184	TG GT ____
	TAT CACGTG CC GGCC	
	GTG GTGTGC GG TCGG	
	GT ____ TTCT	
GAM1394 LOC149113 5'	GGTTGGGGCCAGGTGCGGTG 79169	G _
	TATTGCAC TGGTCC GGCC	

	GTGGCGTG ACCGGG TTGG		
	G G		
GAM1394 LOC149113 5'	GGTTGGGGCCAGGTGCGGTG 79169	G	_
	TATTGCAC TGGTCC GGCC		
	GTGGCGTG ACCGGG TTGG		
	G G		
GAM1394 LOC149157 5'	AGCCAGGCTCCCAGCGGCAATG 79200	A	_ TCC
	TATTGC CG TGG GGCCTGGTT		
	GTAACG GC ACC TCGGACCGA		
	_ G C_		
GAM1394 LOC149157 5'	AGCCAGGCTCCCAGCGGCAATG 79200	A	_ TCC
	TATTGC CG TGG GGCCTGGTT		
	GTAACG GC ACC TCGGACCGA		
	_ G C_		
GAM1394 LOC149271 5'	GATTATAGGAGCTGCGTGT 79241	TG	_ GGCC
	GCACG G TCC TGGTT		
	TGTGC C AGG ATTAG		
	GT G AT_		
GAM1394 LOC149271 5'	GATTATAGGAGCTGCGTGT 79241	TG	_ GGCC
	GCACG G TCC TGGTT		
	TGTGC C AGG ATTAG		
	GT G AT_		
GAM1394 LOC149297 5'	AGCCGGGCCGAGGAGTGTCTGGT 84391	_	GTGGTC
G	TATTG CAC CGGCCTGGTT		
	GTGGC GTG GCCGGGCCGA		
	T AGGA_		
GAM1394 LOC149297 5'	AGCCGGGCCGAGGAGTGTCTGGT 84391	_	GTGGTC
G	TATTG CAC CGGCCTGGTT		
	GTGGC GTG GCCGGGCCGA		
	T AGGA_		
GAM1394 LOC149297 3'	GACTGGCCTGACTGTGTGTGG 84395	TG	TG C T
	T CACG GTC GGCC GGTT		
	G GTGT CAG CCGG TCAG		
	GT GT T _		
GAM1394 LOC149297 3'	GACTGGCCTGACTGTGTGTGG 84395	TG	TG C T
	T CACG GTC GGCC GGTT		
	G GTGT CAG CCGG TCAG		
	GT GT T _		
GAM1394 LOC149320 3'	AGCTACTACTGCCACGTGGAGT 70692	G	CCGGCC
A	TATT CACGTGGT TGGTT		

		ATGA GTGCACCG	ATCGA		
		G	TCATC_		
GAM1394	LOC149320 3'	AGCTACTACTGCCACGTGGAGT	70692	G	CCGGCC
	A	TATT CACGTGGT	TGGTT		
		ATGA GTGCACCG	ATCGA		
		G	TCATC_		
GAM1394	LOC149351 5'	GGCTGGGCCCAGCGTGAGTA	79308	G	—
		TATT CACGT	GGTCCGGCC		
		ATGA GTGCG	CCGGGTCGG		
		—	AC		
GAM1394	LOC149351 5'	GGCTGGGCCCAGCGTGAGTA	79308	G	—
		TATT CACGT	GGTCCGGCC		
		ATGA GTGCG	CCGGGTCGG		
		—	AC		
GAM1394	LOC149351 3'	GTCATGCTCTGTGTAATA	79310	T	CC
		TATTGCACG	GGT GGC		
		ATAATGTGT	TCG CTG		
		C	TA		
GAM1394	LOC149351 3'	GTCATGCTCTGTGTAATA	79310	T	CC
		TATTGCACG	GGT GGC		
		ATAATGTGT	TCG CTG		
		C	TA		
GAM1394	LOC149506 3'	GCCAGGCTAGAGTGCAGTG	84469	GTGG	CG
		TATTGCAC	TC GCCTGGT		
		GTGACGTG	AG CGGACCG		
		—	AT		
GAM1394	LOC149506 3'	GCCAGGCTAGAGTGCAGTG	84469	GTGG	CG
		TATTGCAC	TC GCCTGGT		
		GTGACGTG	AG CGGACCG		
		—	AT		
GAM1394	LOC149603 3'	GCCGGGCTTGTGAGCGGTG	70641	A	GT_
		TATTGC	C GGTCCGGC		
		GTGGCG	G TCGGGCCG		
		A	TGT		
GAM1394	LOC149603 3'	GCCGGGCTTGTGAGCGGTG	70641	A	GT_
		TATTGC	C GGTCCGGC		
		GTGGCG	G TCGGGCCG		
		A	TGT		
GAM1394	LOC149685 3'	GGCTGGGCCGAGGGTGTGG	79481	TG	GTGG TG
		T CAC	TCCGGCC GTT		



		G GTG AGGCCGG CGG		
		GT GG__ GT		
GAM1394	LOC149685 3'	GGCTGGGCCGGAGGGTGTGG 79481	TG	GTGG TG
		T CAC TCCGGCC GTT		
		G GTG AGGCCGG CGG		
		GT GG__ GT		
GAM1394	LOC149692 3'	GGCTAAGATCATGTGCAGTA 84592		C_
		TATTGCACGTGGTC GGCC		
		ATGACGTGTACTAG TCGG		
		AA		
GAM1394	LOC149692 3'	GGCTAAGATCATGTGCAGTA 84592		C_
		TATTGCACGTGGTC GGCC		
		ATGACGTGTACTAG TCGG		
		AA		
GAM1394	LOC149705 3'	GGCTGGGCATGGTGGTG 84627	TG A	G
		TAT C CGTG TCCGGCC		
		GTG G GTAC GGGTCGG		
		GT _ _		
GAM1394	LOC149705 3'	GGCTGGGCATGGTGGTG 84627	TG A	G
		TAT C CGTG TCCGGCC		
		GTG G GTAC GGGTCGG		
		GT _ _		
GAM1394	LOC149995 5'	CGGGGGGTTGTTGGGTGCAGT 84843	G T	GGTT
	A	TATTGCAC TGG CCGGCCT		
		ATGACGTG GTT GGTTGGG		
		G _ GGGCT		
GAM1394	LOC149995 5'	CGGGGGGTTGTTGGGTGCAGT 84843	G T	GGTT
	A	TATTGCAC TGG CCGGCCT		
		ATGACGTG GTT GGTTGGG		
		G _ GGGCT		
GAM1394	LOC150150 5'	AACCGGGCTTGTTGTTGCAGT 84866	C TG T	_
	G	TATTGCA G G CCG GCCTGGTT		
		GTGACGT T T GGT CGGGCCAA		
		_GT_ T		
GAM1394	LOC150150 5'	AACCGGGCTTGTTGTTGCAGT 84866	C TG T	_
	G	TATTGCA G G CCG GCCTGGTT		
		GTGACGT T T GGT CGGGCCAA		
		_GT_ T		
GAM1394	LOC150170 5'	AATTAGGAGAAATATGTGCA 79587	GTCCGG	
		TGCACGTG CCTGGTT		

	ACGTGTAT GGATTAA	
	AAAGA_	
GAM1394 LOC150170 5'	AATTAGGAGAAATATGTGCA 79587	GTCCGG
	TGCACGTG CCTGGTT	
	ACGTGTAT GGATTAA	
	AAAGA_	
GAM1394 LOC150174 3'	ACCAGGTCCTCTGTGCA 79602	T TCC
	TGCACG GG GGCCTGGT	
	ACGTGT TC CTGGACCA	
	C _	
GAM1394 LOC150174 3'	ACCAGGTCCTCTGTGCA 79602	T TCC
	TGCACG GG GGCCTGGT	
	ACGTGT TC CTGGACCA	
	C _	
GAM1394 LOC150175 5'	AATTAGGAGAAATATGTGCA 79628	GTCCGG
	TGCACGTG CCTGGTT	
	ACGTGTAT GGATTAA	
	AAAGA_	
GAM1394 LOC150175 5'	AATTAGGAGAAATATGTGCA 79628	GTCCGG
	TGCACGTG CCTGGTT	
	ACGTGTAT GGATTAA	
	AAAGA_	
GAM1394 LOC150203 3'	CAGGCACCAGTGCAGTG 60518	G CCG
	TATTGCAC TGGT GCCTG	
	GTGACGTG ACCA CGGAC	
	- _	
GAM1394 LOC150203 3'	CAGGCACCAGTGCAGTG 60518	G CCG
	TATTGCAC TGGT GCCTG	
	GTGACGTG ACCA CGGAC	
	- _	
GAM1394 LOC150213 3'	ACCAGGTCCTCTGTGCA 74848	T TCC
	TGCACG GG GGCCTGGT	
	ACGTGT TC CTGGACCA	
	C _	
GAM1394 LOC150213 3'	ACCAGGTCCTCTGTGCA 74848	T TCC
	TGCACG GG GGCCTGGT	
	ACGTGT TC CTGGACCA	
	C _	
GAM1394 LOC150215 5'	AATTAGGAGAAATATGTGCA 79636	GTCCGG
	TGCACGTG CCTGGTT	

	ACGTGTAT	GGATTAA		
	AAAGA_			
GAM1394 LOC150215 5'	AATTAGGAGAAATATGTGCA	79636		GTCCGG
	TGCACGTG	CCTGGTT		
	ACGTGTAT	GGATTAA		
	AAAGA_			
GAM1394 LOC150218 5'	AATTAGGAGAAATATGTGCA	79715		GTCCGG
	TGCACGTG	CCTGGTT		
	ACGTGTAT	GGATTAA		
	AAAGA_			
GAM1394 LOC150218 5'	AATTAGGAGAAATATGTGCA	79715		GTCCGG
	TGCACGTG	CCTGGTT		
	ACGTGTAT	GGATTAA		
	AAAGA_			
GAM1394 LOC150225 3'	GGCTGGGCATGTGTTGTG	85005	T	G
	TAT GCACGTG	TCCGGCC		
	GTG TGTGTAC	GGGTCGG		
	T	_		
GAM1394 LOC150225 3'	GGCTGGGCATGTGTTGTG	85005	T	G
	TAT GCACGTG	TCCGGCC		
	GTG TGTGTAC	GGGTCGG		
	T	_		
GAM1394 LOC150236 5'	ACCAGGTCCTCTGTGCA	79679	T	TCC
	TGCACG GG	GGCCTGGT		
	ACGTGT TC	CTGGACCA		
	C	_		
GAM1394 LOC150236 5'	ACCAGGTCCTCTGTGCA	79679	T	TCC
	TGCACG GG	GGCCTGGT		
	ACGTGT TC	CTGGACCA		
	C	_		
GAM1394 LOC150295 3'	GCTGGCCATCTAGTGCAGTG	84962	_	T
	TATTGCAC	GTGG CCGGC		
	GTGACGTG	TACC GGTCG		
	ATC	_		
GAM1394 LOC150295 3'	GCTGGCCATCTAGTGCAGTG	84962	_	T
	TATTGCAC	GTGG CCGGC		
	GTGACGTG	TACC GGTCG		
	ATC	_		
GAM1394 LOC150587 3'	ATCAGACTCATGTGCAG	85058		GTCC C
	TTGCACGTG	GG CTGGT		

	GACGTGTAC TC GACTA	
	_____ A	
GAM1394 LOC150587 3'	ATCAGACTCATGTGCAG 85058	GTCC C
	TTGCACGTG GG CTGGT	
	GACGTGTAC TC GACTA	
	_____ A	
GAM1394 LOC150622 3'	AGCTGGGTTTCAAATGTGTA 79954	GGTCC TG
	TGCACGT GGCC GTT	
	ATGTGTA TTGG CGA	
	AACT_ GT	
GAM1394 LOC150622 3'	AGCTGGGTTTCAAATGTGTA 79954	GGTCC TG
	TGCACGT GGCC GTT	
	ATGTGTA TTGG CGA	
	AACT_ GT	
GAM1394 LOC150630 3'	AATTAGACAAGGGGCTGGGTGT 85097	TG G GGC__
	GGTG AT CAC TGGTCC CTGGTT	
	TG GTG GTCGGG GATTAA	
	GT G GAACA	
GAM1394 LOC150630 3'	AATTAGACAAGGGGCTGGGTGT 85097	TG G GGC__
	GGTG AT CAC TGGTCC CTGGTT	
	TG GTG GTCGGG GATTAA	
	GT G GAACA	
GAM1394 LOC150759 3'	AGCCAAGGCAGGCATGTGTGAT 80002	TG GT G _
	A TAT CACGTG CC GCCT GGTT	
	ATA GTGTAC GG CGGA CCGA	
	GT _ A A	
GAM1394 LOC150759 3'	AGCCAAGGCAGGCATGTGTGAT 80002	TG GT G _
	A TAT CACGTG CC GCCT GGTT	
	ATA GTGTAC GG CGGA CCGA	
	GT _ A A	
GAM1394 LOC150759 3'	GTTGGGCTGATGTTGT 80010	_ _
	GCA CGT GGTCCGGC	
	TGT GTA TCGGGTTG	
	T G	
GAM1394 LOC150759 3'	GTTGGGCTGATGTTGT 80010	_ _
	GCA CGT GGTCCGGC	
	TGT GTA TCGGGTTG	
	T G	
GAM1394 LOC150998 3'	GCTGGGTGTGGCGGTG 85186	_ TGG
	TATTGC ACG TCCGGC	

	GTGGCG TGT GGGTCG	
	G ____	
GAM1394 LOC150998 3'	GCTGGGTGTGGCGGTG 85186	_ TGG
	TATTGC ACG TCCGGC	
	GTGGCG TGT GGGTCG	
	G ____	
GAM1394 LOC151009 5'	TGCAGAGGAGCGCGTGCGATA 85198	G GGC GTT
	TATTGCACGTG TCC CTG	
	ATAGCGTGCGC AGG GAC	
	G A__ GTG	
GAM1394 LOC151009 5'	TGCAGAGGAGCGCGTGCGATA 85198	G GGC GTT
	TATTGCACGTG TCC CTG	
	ATAGCGTGCGC AGG GAC	
	G A__ GTG	
GAM1394 LOC151199 5'	GCTGGGTCTAAGTGTAGTG 80173	GT_ GT
	TATTGCAC G CCGGC	
	GTGATGTG C GGTCG	
	AAT TG	
GAM1394 LOC151199 5'	GCTGGGTCTAAGTGTAGTG 80173	GT_ GT
	TATTGCAC G CCGGC	
	GTGATGTG C GGTCG	
	AAT TG	
GAM1394 LOC151323 3'	AGCCAAGGCAGGCGTGTGTGGT 80214	TG GT G _
A	TAT CACGTG CC GCCT GGTT	
	ATG GTGTGC GG CGGA CCGA	
	GT _ A A	
GAM1394 LOC151323 3'	AGCCAAGGCAGGCGTGTGTGGT 80214	TG GT G _
A	TAT CACGTG CC GCCT GGTT	
	ATG GTGTGC GG CGGA CCGA	
	GT _ A A	
GAM1394 LOC151429 3'	AACCAAGTGTAGGCTGGGTGCAG 85342	G T G _
TG	TATTGCAC TGG CC GC CTGGTT	
	GTGACGTG GTC GG TG GACCAA	
	G _ A T	
GAM1394 LOC151429 3'	AACCAAGTGTAGGCTGGGTGCAG 85342	G T G _
TG	TATTGCAC TGG CC GC CTGGTT	
	GTGACGTG GTC GG TG GACCAA	
	G _ A T	
GAM1394 LOC151512 5'	GATCAGGTGATTGTGTTTGCAA 85431	_ TG CG
TG	TATTGC ACG GTC GCCTGGTT	

		GTAACG TGT TAG TGGACTAG		
		TT GT _		
GAM1394	LOC151512 5'	GATCAGGTGATTGTGTTTGCAA 85431	_	TG CG
	TG	TATTGC ACG GTC GCCTGGTT		
		GTAACG TGT TAG TGGACTAG		
		TT GT _		
GAM1394	LOC151516 3'	AGTTGGGCTGGGTCCTAGCTGC 80267	C _	GT GG
	AG	TTGCA GT G CCGGCCT TT		
		GACGT CG C GGTCGGG GA		
		_ ATC TG TT		
GAM1394	LOC151516 3'	AGTTGGGCTGGGTCCTAGCTGC 80267	C _	GT GG
	AG	TTGCA GT G CCGGCCT TT		
		GACGT CG C GGTCGGG GA		
		_ ATC TG TT		
GAM1394	LOC151778 3'	GGCCGCGGACCTGGGCTGCGTG 71451	TG TG _ _ _	
	TGA	T CACG GTCC GG CC TGGTT		
		A GTGC CGGG CC GG GCCGG		
		GT GT T A C		
GAM1394	LOC151778 3'	GGCCGCGGACCTGGGCTGCGTG 71451	TG TG _ _ _	
	TGA	T CACG GTCC GG CC TGGTT		
		A GTGC CGGG CC GG GCCGG		
		GT GT T A C		
GAM1394	LOC152078 5'	GGTTGGGCCCCGAACACGGCGGT 80455	A G C	GG
	A	TATTGC CGTG TC GGCCT TT		
		ATGGCG GCAC AG CCGGG GG		
		_ A C TT		
GAM1394	LOC152078 5'	GGTTGGGCCCCGAACACGGCGGT 80455	A G C	GG
	A	TATTGC CGTG TC GGCCT TT		
		ATGGCG GCAC AG CCGGG GG		
		_ A C TT		
GAM1394	LOC152195 5'	ATCAAGGCCACGTGTTGTG 85562	T	CGGCC
		TAT GCACGTGGTC TGGT		
		GTG TGTGCACCGG ACTA		
		T A _		
GAM1394	LOC152195 5'	ATCAAGGCCACGTGTTGTG 85562	T	CGGCC
		TAT GCACGTGGTC TGGT		
		GTG TGTGCACCGG ACTA		
		T A _		
GAM1394	LOC152200 3'	AGTTAGGTTGGGTCTATGCAG 85574	CGT GT	GG
		TTGCA G CCGGCCT TT		

	GACGT C GGTGGA GA		
	AT_TG TT		
GAM1394 LOC152200 3'	AGTTAGGTTGGGTCTATGCAG 85574	CGT GT	GG
	TTGCA G CCGGCCT TT		
	GACGT C GGTGGA GA		
	AT_TG TT		
GAM1394 LOC152286 5'	GGCTGGGCGGGTGCGGTG 85632	G G	
	TATTGCAC TG TCCGGCC		
	GTGGCGTG GC GGGTCGG		
	G _		
GAM1394 LOC152286 5'	GGCTGGGCGGGTGCGGTG 85632	G G	
	TATTGCAC TG TCCGGCC		
	GTGGCGTG GC GGGTCGG		
	G _		
GAM1394 LOC152445 3'	AGTTTGGGCCGGGTGCGGTG 85743	G	GC
	TATTGCAC TGGTCCG CT		
	GTGGCGTG GCCGGGT GA		
	G TT		
GAM1394 LOC152445 3'	AGTTTGGGCCGGGTGCGGTG 85743	G	GC
	TATTGCAC TGGTCCG CT		
	GTGGCGTG GCCGGGT GA		
	G TT		
GAM1394 LOC152447 3'	GGCGCCGCGCGGTGTGATG 80588	TG	T _
	TAT CACGTGG CCGGC CT		
	GTA GTGCGCC GGCCG GG		
	GT _ C		
GAM1394 LOC152447 3'	GGCGCCGCGCGGTGTGATG 80588	TG	T _
	TAT CACGTGG CCGGC CT		
	GTA GTGCGCC GGCCG GG		
	GT _ C		
GAM1394 LOC152453 5'	GCCAGGCTGGGGAAGGGTG 80599	GTGG_	
	CAC TCCGGCCTGGT		
	GTG GGGTCGGACCG		
	GGAAG		
GAM1394 LOC152453 5'	GCCAGGCTGGGGAAGGGTG 80599	GTGG_	
	CAC TCCGGCCTGGT		
	GTG GGGTCGGACCG		
	GGAAG		
GAM1394 LOC152633 5'	GGTCTTGATATGTGTAGTG 85816	G	___
	TATTGCACGTG TCCG GCC		

		GTGATGTGTAT AGGT TGG		
		— TCT		
GAM1394	LOC152633 5'	GGTTCTTGGATATGTGTAGTG 85816	G	—
		TATTGCACGTG TCCG GCC		
		GTGATGTGTAT AGGT TGG		
		— TCT		
GAM1394	LOC152793 3'	GCTATGGTCTGTGTGGTG 80665	TG	TGGTCC —
		TAT CACG GGCC TGGT		
		GTG GTGT CTGG ATCG		
		GT ——— T		
GAM1394	LOC152793 3'	GCTATGGTCTGTGTGGTG 80665	TG	TGGTCC —
		TAT CACG GGCC TGGT		
		GTG GTGT CTGG ATCG		
		GT ——— T		
GAM1394	LOC152804 3'	GCCGCCGGGTGCGGTG 85883	G	T
		TATTGCAC TGG CCGGC		
		GTGGCGTG GCC GGCCG		
		G —		
GAM1394	LOC152804 3'	GCCGCCGGGTGCGGTG 85883	G	T
		TATTGCAC TGG CCGGC		
		GTGGCGTG GCC GGCCG		
		G —		
GAM1394	LOC152915 3'	GGCCGCGGACCCGGGCCGCGTG 67024	TG	— —
	TGA	T CACGTGGTCCGG CC TGGTT		
		A GTGCGCCGGGCC GG GCCGG		
		GT CA C		
GAM1394	LOC152915 3'	GGCCGCGGACCCGGGCCGCGTG 67024	TG	— —
	TGA	T CACGTGGTCCGG CC TGGTT		
		A GTGCGCCGGGCC GG GCCGG		
		GT CA C		
GAM1394	LOC153205 5'	CCATGGGTTGTGTCAAGTG 85943	G	TC —
		CAC TGG CGGCCT GG		
		GTG ACT GTTGGG CC		
		— GT TA		
GAM1394	LOC153205 5'	CCATGGGTTGTGTCAAGTG 85943	G	TC —
		CAC TGG CGGCCT GG		
		GTG ACT GTTGGG CC		
		— GT TA		
GAM1394	LOC153514 3'	AACTATCTGCACATGTGTAGTA 80851	GTC	CC
		TATTGCACGTG CGG TGGTT		



	ATGATGTGTAC	GTC	ATCAA	
	AC_ T_			
GAM1394	LOC153514 3'	AACTATCTGCACATGTGTAGTA	80851	GTC CC
		TATTGCACGTG CGG TGGTT		
		ATGATGTGTAC GTC ATCAA		
		AC_ T_		
GAM1394	LOC153571 5'	GGCCAGGCCGGGTCCA	86050	_
		TGG TCCGGCCTGGTT		
		ACC GGGCCGGACCGG		
		T		
GAM1394	LOC153571 5'	GGCCAGGCCGGGTCCA	86050	_
		TGG TCCGGCCTGGTT		
		ACC GGGCCGGACCGG		
		T		
GAM1394	LOC153642 3'	GCTGGGCGCGGTGGTG	80909	TG A G
		TAT C CGTG TCCGGC		
		GTG G GCGC GGGTCG		
		GT _ _		
GAM1394	LOC153642 3'	GCTGGGCGCGGTGGTG	80909	TG A G
		TAT C CGTG TCCGGC		
		GTG G GCGC GGGTCG		
		GT _ _		
GAM1394	LOC153651 5'	TGGATACGTGCAGTG	80915	G
		TATTGCACGTG TCCG		
		GTGACGTGCAT AGGT		
		-		
GAM1394	LOC153651 5'	TGGATACGTGCAGTG	80915	G
		TATTGCACGTG TCCG		
		GTGACGTGCAT AGGT		
		-		
GAM1394	LOC153684 5'	CGGGCTGGTGCAGTG	86082	CGTGGT
		TATTGCA CCGGCCTG		
		GTGACGT GGTCTGGGC		
		-		
GAM1394	LOC153684 5'	CGGGCTGGTGCAGTG	86082	CGTGGT
		TATTGCA CCGGCCTG		
		GTGACGT GGTCTGGGC		
		-		
GAM1394	LOC154403 5'	GGTTGGGGCCAGGTGCGGTG	81074	G _
		TATTGCAC TGGTCC GGCC		

		GTGGCGTG ACCGGG TTGG			
		G G			
GAM1394	LOC154403 5'	GGTTGGGGCCAGGTGCGGTG	81074	G	_
		TATTGCAC TGGTCC GGCC			
		GTGGCGTG ACCGGG TTGG			
		G G			
GAM1394	LOC154421 3'	TGGCTGCAGTGGACAGCGTGTG	86216	TG G	_____ TGGTT
	GTG	CACGT GTCC GGCC			
		GTGCG CAGG TCGG			
		GT A TGACG TT			
GAM1394	LOC154421 3'	TGGCTGCAGTGGACAGCGTGTG	86216	TG G	_____ TGGTT
	GTG	CACGT GTCC GGCC			
		GTGCG CAGG TCGG			
		GT A TGACG TT			
GAM1394	LOC154807 5'	GGCTGGGTGCGGCCCG	86253	T TG	
		CG GGTCCGGCC GTT			
		GC CCGGGCTGG CGG			
		C GT			
GAM1394	LOC154807 5'	GGCTGGGTGCGGCCCG	86253	T TG	
		CG GGTCCGGCC GTT			
		GC CCGGGCTGG CGG			
		C GT			
GAM1394	LOC154822 3'	AGCCAGGCTGGAGTGCAATGTG	86257	_____ G	
	CAATG	TGCAC GTG TCCGGCCTGGTT			
		ACGTG CGT AGGTCGGACCGA			
		TAA G			
GAM1394	LOC154822 3'	AGCCAGGCTGGAGTGCAATGTG	86257	_____ G	
	CAATG	TGCAC GTG TCCGGCCTGGTT			
		ACGTG CGT AGGTCGGACCGA			
		TAA G			
GAM1394	LOC154881 3'	GGCCAGGCTGAAAAGTGCAAT	81171		GTGGTC
		ATTGCAC CGGCCTGGTT			
		TAACGTG GTCGGACCGG			
		AAAA_			
GAM1394	LOC154881 3'	GGCCAGGCTGAAAAGTGCAAT	81171		GTGGTC
		ATTGCAC CGGCCTGGTT			
		TAACGTG GTCGGACCGG			
		AAAA_			
GAM1394	LOC155038 3'	AGCTGCCTATTGCGTGTTATG	81254	T TG CC	CT
		TAT GCACG GT GGC GGTT			

		GTA TGTGC TA CCG TCGA		
		T GT T_ _		
GAM1394	LOC155038 3'	AGCTGCCTATTGCGTGTATG 81254	T	TG CC CT
		TAT GCACG GT GGC GGTT		
		GTA TGTGC TA CCG TCGA		
		T GT T_ _		
GAM1394	LOC155061 3'	TTGGGCCATCTGTGGTA 81272	TG	C
		TAT CA GTGGTCCGG		
		ATG GT TACCGGGTT		
		GT C		
GAM1394	LOC155061 3'	TTGGGCCATCTGTGGTA 81272	TG	C
		TAT CA GTGGTCCGG		
		ATG GT TACCGGGTT		
		GT C		
GAM1394	LOC155179 3'	GGCTGGGCTGGGCCGGG 81319	G	TG
		C TGGTCCGGCC GTT		
		G GCCGGGTCGG CGG		
		G GT		
GAM1394	LOC155179 3'	GGCTGGGCTGGGCCGGG 81319	G	TG
		C TGGTCCGGCC GTT		
		G GCCGGGTCGG CGG		
		G GT		
GAM1394	LOC155179 3'	GGCTGGGCTGGGCCGGGCGTGC 81320	—	TG
	GG	TTGCACGT GGTCCGGCC GTT		
		GGCGTGCG CCGGGTCGG CGG		
		GG GT		
GAM1394	LOC155179 3'	GGCTGGGCTGGGCCGGGCGTGC 81320	—	TG
	GG	TTGCACGT GGTCCGGCC GTT		
		GGCGTGCG CCGGGTCGG CGG		
		GG GT		
GAM1394	LOC155179 3'	GGCTGGGCTGGGCTGGGC 81321	ACGT	TG
		GC GGTCCGGCC GTT		
		CG TCGGGTCGG CGG		
		GG_ GT		
GAM1394	LOC155179 3'	GGCTGGGCTGGGCTGGGC 81321	ACGT	TG
		GC GGTCCGGCC GTT		
		CG TCGGGTCGG CGG		
		GG_ GT		
GAM1394	LOC155179 3'	GGCTGGGCTGGGCTGGGC 81323	ACGT	TG
		GC GGTCCGGCC GTT		

		CG	TCGGGTCGG	CGG		
		GG__	GT			
GAM1394	LOC155179 3'	GGCTGGGCTGGGCTGGGC	81323	ACGT	TG	
		GC	GGTCCGGCC	GTT		
		CG	TCGGGTCGG	CGG		
		GG__	GT			
GAM1394	LOC155179 3'	GGCTGGGCTGGGCTGGGC	81322	ACGT	TG	
		GC	GGTCCGGCC	GTT		
		CG	TCGGGTCGG	CGG		
		GG__	GT			
GAM1394	LOC155179 3'	GGCTGGGCTGGGCTGGGC	81322	ACGT	TG	
		GC	GGTCCGGCC	GTT		
		CG	TCGGGTCGG	CGG		
		GG__	GT			
GAM1394	LOC155340 3'	GGCCGCGGACCCGGGCCGCGTG	73379	TG	__	__
	TGA	T	CACGTGGTCCGG	CC	TGGTT	
		A	GTGCGCCGGGCC	GG	GCCGG	
		GT	CA	C		
GAM1394	LOC155340 3'	GGCCGCGGACCCGGGCCGCGTG	73379	TG	__	__
	TGA	T	CACGTGGTCCGG	CC	TGGTT	
		A	GTGCGCCGGGCC	GG	GCCGG	
		GT	CA	C		
GAM1394	LOC155376 3'	TCAGGCTGGGTGCAGTG	81339	GTGGT		
		TATTGCAC	CCGGCCTGG			
		GTGACGTG	GGTCGGA	CT		
		_____				
GAM1394	LOC155376 3'	TCAGGCTGGGTGCAGTG	81339	GTGGT		
		TATTGCAC	CCGGCCTGG			
		GTGACGTG	GGTCGGA	CT		
		_____				
GAM1394	LOC157273 3'	GGCCAGGTTGGACTTTCTG	86433	CGT		
		CA	GGTCCGGCCTGGTT			
		GT	TCAGGTTGGACCGG			
		CTT				
GAM1394	LOC157273 3'	GGCCAGGTTGGACTTTCTG	86433	CGT		
		CA	GGTCCGGCCTGGTT			
		GT	TCAGGTTGGACCGG			
		CTT				
GAM1394	LOC157317 3'	AGTGTGGTTTATGTGTAATA	81400	T	GC	
		TATTGCACGTGG	CCG	CT		

	ATAATGTGTATT GGT GA		
	T GT		
GAM1394 LOC157317 3'	AGTGTGGTTTATGTGTAATA 81400	T	GC
	TATTGCACGTGG CCG CT		
	ATAATGTGTATT GGT GA		
	T GT		
GAM1394 LOC157349 3'	GCTGTGTCACGTGCAG 81416	TC	
	TTGCACGTGG CGGC		
	GACGTGCACT GTCG		
	GT		
GAM1394 LOC157349 3'	GCTGTGTCACGTGCAG 81416	TC	
	TTGCACGTGG CGGC		
	GACGTGCACT GTCG		
	GT		
GAM1394 LOC157531 3'	ATTGGGCTGGGCTAGTGT 86471	G	TG
	GCAC TGGTCCGGCC GT		
	TGTG ATCGGGTCGG TA		
	— GT		
GAM1394 LOC157531 3'	ATTGGGCTGGGCTAGTGT 86471	G	TG
	GCAC TGGTCCGGCC GT		
	TGTG ATCGGGTCGG TA		
	— GT		
GAM1394 LOC157556 5'	GGCCTGGATCAGTGCAATG 86489	G	—
	TATTGCAC TGGTCC GGCC		
	GTAACGTG ACTAGG CCGG		
	— T		
GAM1394 LOC157556 5'	GGCCTGGATCAGTGCAATG 86489	G	—
	TATTGCAC TGGTCC GGCC		
	GTAACGTG ACTAGG CCGG		
	— T		
GAM1394 LOC157562 5'	GCCAGGCCAGGTGCAGTG 86477	G	C
	TATTGCAC TGGTC GGC		
	GTGACGTG ACCGG CCG		
	G A		
GAM1394 LOC157562 5'	GCCAGGCCAGGTGCAGTG 86477	G	C
	TATTGCAC TGGTC GGC		
	GTGACGTG ACCGG CCG		
	G A		
GAM1394 LOC157653 5'	GGCTGGGGGTATGTGTGG 81527	TG	G _
	T CACGTG TCC GGCC		

G GTGTAT GGG TCGG  
 GT G G  
 GAM1394 LOC157653 5' GGCTGGGGGTATGTGTGG 81527 TG G \_  
 T CACGTG TCC GGCC  
 | ||||| ||| ||||  
 G GTGTAT GGG TCGG  
 GT G G  
 GAM1394 LOC157657 3' GCTGGGCGCGGTGGTG 81520 TG A G  
 TAT C CGTG TCCGGC  
 ||| | ||| |||||  
 GTG G GCGC GGGTCG  
 GT \_ \_  
 GAM1394 LOC157657 3' GCTGGGCGCGGTGGTG 81520 TG A G  
 TAT C CGTG TCCGGC  
 ||| | ||| |||||  
 GTG G GCGC GGGTCG  
 GT \_ \_  
 GAM1394 LOC157663 3' GGCTGTGATTATGTTTGATA 81538 C \_  
 TATTG ACGTGGTC CGGCC  
 |||| ||||| ||||  
 ATAGT TGTATTAG GTCGG  
 T T  
 GAM1394 LOC157663 3' GGCTGTGATTATGTTTGATA 81538 C \_  
 TATTG ACGTGGTC CGGCC  
 |||| ||||| ||||  
 ATAGT TGTATTAG GTCGG  
 T T  
 GAM1394 LOC157807 5' GGCTGGGCGGCCGTGTGA 81614 TG \_ G  
 T CACG T GTCCGGCC  
 | |||| | |||||  
 A GTGC G CGGGTCGG  
 GT C G  
 GAM1394 LOC157807 5' GGCTGGGCGGCCGTGTGA 81614 TG \_ G  
 T CACG T GTCCGGCC  
 | |||| | |||||  
 A GTGC G CGGGTCGG  
 GT C G  
 GAM1394 LOC157860 5' GGCTGGTTTCTTGGGTGCAATG 86569 G T\_\_\_\_  
 TATTGCAC TGG CCGGCC  
 ||||| ||| |||||  
 GTAACGTG GTT GGTCGG  
 G CTTT  
 GAM1394 LOC157860 5' GGCTGGTTTCTTGGGTGCAATG 86569 G T\_\_\_\_  
 TATTGCAC TGG CCGGCC  
 ||||| ||| |||||  
 GTAACGTG GTT GGTCGG  
 G CTTT  
 GAM1394 LOC157931 3' AACTGGGCTGGAATTAGCAG 86653 ACGTGG TG  
 TTGC TCCGGCC GTT  
 ||| ||||| |||

	GACG	AGGTCGG	CAA		
	ATTA__	GT			
GAM1394	LOC157931	3'	AACTGGGCTGGAATTAGCAG	86653	ACGTGG TG
			TTGC TCCGGCC GTT		
			GACG AGGTCGG CAA		
			ATTA__ GT		
GAM1394	LOC158987	3'	ACCAGGCCAGGTGCGGTG	86958	G GGTCC
			TATTGCAC T GGCCTGGT		
			GTGGCGTG A CCGGACCA		
			G _____		
GAM1394	LOC158987	3'	ACCAGGCCAGGTGCGGTG	86958	G GGTCC
			TATTGCAC T GGCCTGGT		
			GTGGCGTG A CCGGACCA		
			G _____		
GAM1394	LOC159110	5'	GGCCGGCTTGGTGTGATA	82100	TG GT T
			TAT CAC GG CCGGCC		
			ATA GTG TC GGCCGG		
			GT GT _		
GAM1394	LOC159110	5'	GGCCGGCTTGGTGTGATA	82100	TG GT T
			TAT CAC GG CCGGCC		
			ATA GTG TC GGCCGG		
			GT GT _		
GAM1394	LOC159116	5'	GGCCGGCTTGGTGTGATA	82095	TG GT T
			TAT CAC GG CCGGCC		
			ATA GTG TC GGCCGG		
			GT GT _		
GAM1394	LOC159116	5'	GGCCGGCTTGGTGTGATA	82095	TG GT T
			TAT CAC GG CCGGCC		
			ATA GTG TC GGCCGG		
			GT GT _		
GAM1394	LOC159228	5'	TGGGCTACTGTAGTG	87055	C
			TATTGCA GTGGTCCG		
			GTGATGT CATCGGGT		
			—		
GAM1394	LOC159228	5'	TGGGCTACTGTAGTG	87055	C
			TATTGCA GTGGTCCG		
			GTGATGT CATCGGGT		
			—		
GAM1394	LOC162952	5'	GGCCAGGCCGGGGAGTATGAGT	82383	G CG GG
	G		TATT CA T TCCGGCCTGGTT		

		GTGA GT G GGGCCGGACCGG		
		_ AT AG		
GAM1394	LOC162952 5'	GGCCAGGCCGGGGAGTATGAGT 82383	G	CG GG
	G	TATT CA T TCCGGCCTGGTT		
		GTGA GT G GGGCCGGACCGG		
		_ AT AG		
GAM1394	LOC166341 3'	ACCATGCCATGTGGGGTG 82628	G	CCGGCC
		TATT CACGTGGT TGGT		
		GTGG GTGTACCG ACCA		
		G T_____		
GAM1394	LOC166341 3'	ACCATGCCATGTGGGGTG 82628	G	CCGGCC
		TATT CACGTGGT TGGT		
		GTGG GTGTACCG ACCA		
		G T_____		
GAM1394	LOC169436 5'	GCTGTTCATCACGTGGAATG 82741	G	C__
		TATT CACGTGGT CGGC		
		GTAA GTGCACTA GTCG		
		G CTT		
GAM1394	LOC169436 5'	GCTGTTCATCACGTGGAATG 82741	G	C__
		TATT CACGTGGT CGGC		
		GTAA GTGCACTA GTCG		
		G CTT		
GAM1394	LOC170394 5'	GGCCGGCTGCGTGCAG 82854	TG T	
		TTGCACG G CCGGCC		
		GACGTGC C GGCCGG		
		GT _		
GAM1394	LOC170394 5'	GGCCGGCTGCGTGCAG 82854	TG T	
		TTGCACG G CCGGCC		
		GACGTGC C GGCCGG		
		GT _		
GAM1394	LOC196074 5'	GGCTAGGCCGGAGCTGCTG 87582	C TG _	
		CA G G TCCGGCCTGGTT		
		GT C C AGGCCGGATCGG		
		_ GT G		
GAM1394	LOC196074 5'	GGCTAGGCCGGAGCTGCTG 87582	C TG _	
		CA G G TCCGGCCTGGTT		
		GT C C AGGCCGGATCGG		
		_ GT G		
GAM1394	LOC196264 3'	GGCTGGGCCTTCTTGTAAATG 87608	CGT_	
		TATTGCA GGTCCGGCC		



	GTAATGT CCGGGTCGG			
	TCTT			
GAM1394 LOC196264 3'	GGCTGGGCCTTCTTGTAAATG 87608	CGT_		
	TATTGCA GGTCCGGCC			
	GTAATGT CCGGGTCGG			
	TCTT			
GAM1394 LOC196411 3'	GGCTATAAATTATGTGAGTA 87676	G	CC_	
	TATT CACGTGGT GGCC			
	ATGA GTGTATTA TCGG			
	_ AATA			
GAM1394 LOC196411 3'	GGCTATAAATTATGTGAGTA 87676	G	CC_	
	TATT CACGTGGT GGCC			
	ATGA GTGTATTA TCGG			
	_ AATA			
GAM1394 LOC196510 3'	GGTTAGGCTGGGTTGAAGTTCG 87750	C	G_ GG	GG
A	TTG AC T TCCGGCCT TT			
	AGC TG G GGGTCGGA GG			
	T AA TT TT			
GAM1394 LOC196510 3'	GGTTAGGCTGGGTTGAAGTTCG 87750	C	G_ GG	GG
A	TTG AC T TCCGGCCT TT			
	AGC TG G GGGTCGGA GG			
	T AA TT TT			
GAM1394 LOC197201 3'	GTCTGGGGCCGGGTGCGGTG 87947	G	_	
	TATTGCAC TGGTCC GGC			
	GTGGCGTG GCCGGG CTG			
	G GT			
GAM1394 LOC197201 3'	GTCTGGGGCCGGGTGCGGTG 87947	G	_	
	TATTGCAC TGGTCC GGC			
	GTGGCGTG GCCGGG CTG			
	G GT			
GAM1394 LOC197358 3'	TTGGATCACTTGTAGTA 88055	C		
	TATTGCA GTGGTCCGG			
	ATGATGT CACTAGGTT			
	T			
GAM1394 LOC197358 3'	TTGGATCACTTGTAGTA 88055	C		
	TATTGCA GTGGTCCGG			
	ATGATGT CACTAGGTT			
	T			
GAM1394 LOC199692 3'	AGTCAGCGTTAACCATGTGCA 59238	CC _ GT		
	TGCACGTGGT GGC CTG T			

	ACGTGTACCA TTG GAC A		
	A_ C TG		
GAM1394 LOC199692 3'	AGTCAGCGTTAACCATGTGCA 59238	CC	_ GT
	TGCACGTGGT GGC CTG T		
	ACGTGTACCA TTG GAC A		
	A_ C TG		
GAM1394 LOC199733 5'	AGCCGGGCCGGAAGGTGTGCAG 89845	GG	
	TTGCACGT TCCGGCCTGGTT		
	GACGTGTG AGGCCGGGCCGA		
	GA		
GAM1394 LOC199733 5'	AGCCGGGCCGGAAGGTGTGCAG 89845	GG	
	TTGCACGT TCCGGCCTGGTT		
	GACGTGTG AGGCCGGGCCGA		
	GA		
GAM1394 LOC199796 5'	AGTTGGCCGAGACTATGTGCAG 74449	_	TGGTT
	TTGCACGTGGTC CGGCC		
	GACGTGTATCAG GCCGG		
	A TTGA		
GAM1394 LOC199796 5'	AGTTGGCCGAGACTATGTGCAG 74449	_	TGGTT
	TTGCACGTGGTC CGGCC		
	GACGTGTATCAG GCCGG		
	A TTGA		
GAM1394 LOC199858 5'	AACTCTCCGGCTATGTGTCATA 88414	T	T CCT
	TAT GCACGTGG CCGG GGTT		
	ATA TGTGTATC GGCC TCAA		
	C _ TC_		
GAM1394 LOC199858 5'	AACTCTCCGGCTATGTGTCATA 88414	T	T CCT
	TAT GCACGTGG CCGG GGTT		
	ATA TGTGTATC GGCC TCAA		
	C _ TC_		
GAM1394 LOC199870 5'	GGCCGGGCCGCGCGGGTCGGTG 88431	_ A _	
	TATTG C CGT GGTCCGGCC		
	GTGGC G GCG CCGGGCCGG		
	T G G		
GAM1394 LOC199870 5'	GGCCGGGCCGCGCGGGTCGGTG 88431	_ A _	
	TATTG C CGT GGTCCGGCC		
	GTGGC G GCG CCGGGCCGG		
	T G G		
GAM1394 LOC199958 3'	GGCCAGGCTGGGCAAC 89888	G	
	GT GTCCGGCCTGGTT		

		CA CGGGTCGGACCGG			
		A			
GAM1394	LOC199958 3'	GGCCAGGCTGGGCAAC	89888	G	
		GT GTCCGGCCTGGTT			
		CA CGGGTCGGACCGG			
		A			
GAM1394	LOC200014 3'	AGTCAGGCCGCGACTGTGCAG	88516	GT _	GT
		TTGCAC GGTC CGGCCTG T			
		GACGTG TCAG GCCGGAC A			
		_ C TG			
GAM1394	LOC200014 3'	AGTCAGGCCGCGACTGTGCAG	88516	GT _	GT
		TTGCAC GGTC CGGCCTG T			
		GACGTG TCAG GCCGGAC A			
		_ C TG			
GAM1394	LOC200081 3'	ATCAGGTTGTTTGTGGTA	88561	A TG TC	
		TGC CG G CGGCCTGGT			
		ATG GT T GTTGGACTA			
		_ GT T_			
GAM1394	LOC200081 3'	ATCAGGTTGTTTGTGGTA	88561	A TG TC	
		TGC CG G CGGCCTGGT			
		ATG GT T GTTGGACTA			
		_ GT T_			
GAM1394	LOC200220 3'	GGTTAGGCTGGGTTGAAGTTCG	88639	C G_ GG	GG
	A	TTG AC T TCCGGCCT TT			
		AGC TG G GGGTCGGA GG			
		T AA TT TT			
GAM1394	LOC200220 3'	GGTTAGGCTGGGTTGAAGTTCG	88639	C G_ GG	GG
	A	TTG AC T TCCGGCCT TT			
		AGC TG G GGGTCGGA GG			
		T AA TT TT			
GAM1394	LOC200301 5'	GGCTGGGCCGAGCGCGGC	88750	A G_	TG
		GC CGT G TCCGGCC GTT			
		CG GCG C AGGCCGG CGG			
		_ G G GT			
GAM1394	LOC200301 5'	GGCTGGGCCGAGCGCGGC	88750	A G_	TG
		GC CGT G TCCGGCC GTT			
		CG GCG C AGGCCGG CGG			
		_ G G GT			
GAM1394	LOC200310 3'	TCAGGCTCTGCAGTG	65743	CGTGGTCC	
		TATTGCA GGCCTGG			

		GTGACGT	TCGGA		
		C_____			
GAM1394	LOC200310 3'	TCAGGCTCTGCAGTG	65743	CGTGGTCC	
		TATTGCA	GGCCTGG		
		GTGACGT	TCGGA		
		C_____			
GAM1394	LOC200314 3'	CCGGGCTTTTTTGTAA	90005	CGT_	
		TATTGCA	GGTCCGG		
		GTAATGT	TCGGGCC		
		TTTT			
GAM1394	LOC200314 3'	CCGGGCTTTTTTGTAA	90005	CGT_	
		TATTGCA	GGTCCGG		
		GTAATGT	TCGGGCC		
		TTTT			
GAM1394	LOC200317 3'	ATCAGGCCGGGCACAGTG	88791	GTG	
		CAC	GTCCGGCCTGGT		
		GTG	CGGGCCGGA		
		ACA			
GAM1394	LOC200317 3'	ATCAGGCCGGGCACAGTG	88791	GTG	
		CAC	GTCCGGCCTGGT		
		GTG	CGGGCCGGA		
		ACA			
GAM1394	LOC200399 3'	AGCCAAGGCAGGCGTGTGTGGT	88805	TG	GT G _
	A	TAT	CACGTG CC GCCT GGTT		
		ATG	GTGTGC GG CGGA CCGA		
		GT	_ A A		
GAM1394	LOC200399 3'	AGCCAAGGCAGGCGTGTGTGGT	88805	TG	GT G _
	A	TAT	CACGTG CC GCCT GGTT		
		ATG	GTGTGC GG CGGA CCGA		
		GT	_ A A		
GAM1394	LOC200470 3'	GCCAAAGACCAGGTGTAGTG	90064	G	C_
		TATTGCAC	TGGTC GGC		
		GTGATGTG	ACCAG CCG		
		G	AAA		
GAM1394	LOC200470 3'	GCCAAAGACCAGGTGTAGTG	90064	G	C_
		TATTGCAC	TGGTC GGC		
		GTGATGTG	ACCAG CCG		
		G	AAA		
GAM1394	LOC200734 3'	GCTGAACAGTGTGTAGTA	88863	TG	C
		TATTGCACG	GT CGGC		

	ATGATGTGT CA GTCG		
	GA A		
GAM1394 LOC200734 3'	GCTGAACAGTGTGTAGTA 88863	TG C	
	TATTGCACG GT CGGC		
	ATGATGTGT CA GTCG		
	GA A		
GAM1394 LOC201191 3'	AGCTGGGCTGGGCATTTTCAGCA 89767	ACGTG_	TG
	TGC GTCCGGCC GTT		
	ACG CGGGTCGG CGA		
	ACTTTA GT		
GAM1394 LOC201191 3'	AGCTGGGCTGGGCATTTTCAGCA 89767	ACGTG_	TG
	TGC GTCCGGCC GTT		
	ACG CGGGTCGG CGA		
	ACTTTA GT		
GAM1394 LOC201294 3'	GATTAAATGGGTCATGTGAGGT 88208	TG	GT GCC
G	TAT CACGTG CCG TGGTT		
	GTG GTGTAC GGT ATTAG		
	GA TG AA_		
GAM1394 LOC201294 3'	GATTAAATGGGTCATGTGAGGT 88208	TG	GT GCC
G	TAT CACGTG CCG TGGTT		
	GTG GTGTAC GGT ATTAG		
	GA TG AA_		
GAM1394 LOC201564 3'	GCTGGGCATGGTGGTG 80438	TG A	G
	TAT C CGTG TCCGGC		
	GTG G GTAC GGGTCG		
	GT _ _		
GAM1394 LOC201564 3'	GCTGGGCATGGTGGTG 80438	TG A	G
	TAT C CGTG TCCGGC		
	GTG G GTAC GGGTCG		
	GT _ _		
GAM1394 LOC201689 3'	GCTGGGCATGGTGGTA 67146	TG A	G
	TAT C CGTG TCCGGC		
	ATG G GTAC GGGTCG		
	GT _ _		
GAM1394 LOC201689 3'	GCTGGGCATGGTGGTA 67146	TG A	G
	TAT C CGTG TCCGGC		
	ATG G GTAC GGGTCG		
	GT _ _		
GAM1394 LOC201868 5'	GGTTGGGGCCAGGTGCAGTG 89081	G	_
	TATTGCAC TGGTCC GGCC		

	GTGACGTG ACCGGG TTGG		
	G G		
GAM1394 LOC201868 5'	GGTTGGGGCCAGGTGCAGTG 89081	G	_
	TATTGCAC TGGTCC GGCC		
	GTGACGTG ACCGGG TTGG		
	G G		
GAM1394 LOC201895 3'	TTAGGCCAGTGCAGTG 89095	G	CG
	TATTGCAC TGGTC G		
	GTGACGTG ACCGG T		
	_ AT		
GAM1394 LOC201895 3'	TTAGGCCAGTGCAGTG 89095	G	CG
	TATTGCAC TGGTC G		
	GTGACGTG ACCGG T		
	_ AT		
GAM1394 LOC202134 5'	GTTGGGCTGTAGTTGTAGTG 90322	_ _	TG
	TATTGCA C G GTCCGGC		
	GTGATGT G T CGGGTTG		
	T A GT		
GAM1394 LOC202134 5'	GTTGGGCTGTAGTTGTAGTG 90322	_ _	TG
	TATTGCA C G GTCCGGC		
	GTGATGT G T CGGGTTG		
	T A GT		
GAM1394 LOC202451 3'	TGGCTACCTCGGGATTATGTGC 90355	_____	TGGTT
AA	GCACGTGGTCC GGCC		
	CGTGTATTAGG TCGG		
	GCTCCA TT		
GAM1394 LOC202451 3'	TGGCTACCTCGGGATTATGTGC 90355	_____	TGGTT
AA	GCACGTGGTCC GGCC		
	CGTGTATTAGG TCGG		
	GCTCCA TT		
GAM1394 LOC202908 5'	GATTAGAAGATTATGTGAAGTA 89236	G	CGGC
	TATT CACGTGGTC CTGGTT		
	ATGA GTGTATTAG GATTAG		
	A AA_		
GAM1394 LOC202908 5'	GATTAGAAGATTATGTGAAGTA 89236	G	CGGC
	TATT CACGTGGTC CTGGTT		
	ATGA GTGTATTAG GATTAG		
	A AA_		
GAM1394 LOC203054 3'	GCCAGGAGGCCGTGTAATG 89254	GT T	GG
	TATTGCAC GG CC CCTGGT		

		GTAATGTG CC GG GGACCG		
		— _ A_		
GAM1394	LOC203054 3'	GCCAGGAGGCCGTGTAATG 89254	GT T GG	
		TATTGCAC GG CC CCTGGT		
		GTAATGTG CC GG GGACCG		
		— _ A_		
GAM1394	LOC203286 3'	GCTGGGGCATGTGCAA 90500	G	
		TTGCACGTG TCCGGC		
		AACGTGTAC GGGTCG		
		G		
GAM1394	LOC203286 3'	GCTGGGGCATGTGCAA 90500	G	
		TTGCACGTG TCCGGC		
		AACGTGTAC GGGTCG		
		G		
GAM1394	LOC203411 5'	AACTAGGCCGGGTCTCCTGACA 90625	_ CGT GT	
		TG CA G CCGGCCTGGTT		
		AC GT C GGCCGGATCAA		
		A CCT TG		
GAM1394	LOC203411 5'	AACTAGGCCGGGTCTCCTGACA 90625	_ CGT GT	
		TG CA G CCGGCCTGGTT		
		AC GT C GGCCGGATCAA		
		A CCT TG		
GAM1394	LOC203636 3'	AGCCTGTGCTGGGTACCGTGC 89422	_ GT CT_	
		GGTG ATTGCACG TG CCGGC GGTT		
		TGGCGTGC AC GGTCG CCGA		
		C TG TGT		
GAM1394	LOC203636 3'	AGCCTGTGCTGGGTACCGTGC 89422	_ GT CT_	
		GGTG ATTGCACG TG CCGGC GGTT		
		TGGCGTGC AC GGTCG CCGA		
		C TG TGT		
GAM1394	LOC203636 3'	GCTGGGCTGGACGGTGTG 89427	G TG	
		CACGT GTCCGGCC GT		
		GTGTG CAGGTCGG CG		
		G GT		
GAM1394	LOC203636 3'	GCTGGGCTGGACGGTGTG 89428	G TG	
		CACGT GTCCGGCC GT		
		GTGTG CAGGTCGG CG		
		G GT		
GAM1394	LOC203636 3'	GCTGGGCTGGACGGTGTG 89428	G TG	
		CACGT GTCCGGCC GT		

			GTGTG CAGGTCGG CG			
			G GT			
GAM1394	LOC203636 3'	GCTGGGCTGGACGGTGTG	89427	G	TG	
		CACGT GTCCGGCC GT				
		GTGTG CAGGTCGG CG				
		G GT				
GAM1394	LOC203636 3'	GGCTGGGCTGGACGGTGTG	89431	G	TG	
		CACGT GTCCGGCC GTT				
		GTGTG CAGGTCGG CGG				
		G GT				
GAM1394	LOC203636 3'	GGCTGGGCTGGACGGTGTG	89430	G	TG	
		CACGT GTCCGGCC GTT				
		GTGTG CAGGTCGG CGG				
		G GT				
GAM1394	LOC203636 3'	GGCTGGGCTGGACGGTGTG	89431	G	TG	
		CACGT GTCCGGCC GTT				
		GTGTG CAGGTCGG CGG				
		G GT				
GAM1394	LOC203636 3'	GGCTGGGCTGGACGGTGTG	89430	G	TG	
		CACGT GTCCGGCC GTT				
		GTGTG CAGGTCGG CGG				
		G GT				
GAM1394	LOC203636 3'	GGCTGGCAGCCCGTGT	89429	T	__	
		GCACG GGT CCGGCC				
		TGTGC CCG GGTCGG				
		_ AC				
GAM1394	LOC203636 3'	GGCTGGCAGCCCGTGT	89429	T	__	
		GCACG GGT CCGGCC				
		TGTGC CCG GGTCGG				
		_ AC				
GAM1394	LOC206426 5'	GCTGGGTTGGGCGGTAA	89534	A	GGT	TG
		TTGC CGT CCGGCC GT				
		AATG GCG GGTTGG CG				
		_ _ GT				
GAM1394	LOC206426 5'	GCTGGGTTGGGCGGTAA	89534	A	GGT	TG
		TTGC CGT CCGGCC GT				
		AATG GCG GGTTGG CG				
		_ _ GT				
GAM1394	LOC219376 5'	AGCTGGGCCGGGCTGCTGTGC	93895	_ TG	TG	
		GCAC G GTCCGGCC GTT				



CGTG C CGGGCCGG CGA  
 T GT GT  
 GAM1394 LOC219376 5' AGCTGGGCCGGGCTGCTGTGC 93895 \_TG TG  
 GCAC G GTCCGGCC GTT  
 ||||| ||||| |||  
 CGTG C CGGGCCGG CGA  
 T GT GT  
 GAM1394 LOC219672 5' AGCCGGGTGTGGTGGTGTGGTG 91327 TG GTGGT \_  
 TAT CAC CCG GCCTGGTT  
 ||| ||| ||| |||||  
 GTG GTG GGT TGGGCCGA  
 GT GT\_\_ G  
 GAM1394 LOC219672 5' AGCCGGGTGTGGTGGTGTGGTG 91327 TG GTGGT \_  
 TAT CAC CCG GCCTGGTT  
 ||| ||| ||| |||||  
 GTG GTG GGT TGGGCCGA  
 GT GT\_\_ G  
 GAM1394 LOC219688 5' GGCTGGGCCCGGTGGTG 93053 TG A T  
 TAT C CG GGTCCGGCC  
 ||| ||| |||||  
 GTG G GC CCGGGTCCG  
 GT \_ \_  
 GAM1394 LOC219688 5' GGCTGGGCCCGGTGGTG 93053 TG A T  
 TAT C CG GGTCCGGCC  
 ||| ||| |||||  
 GTG G GC CCGGGTCCG  
 GT \_ \_  
 GAM1394 LOC220021 3' AACCAGGAAGACTCATGTGTGG 93389 TG \_ CGG  
 T CACGTG GTC CCTGGTT  
 | ||||| ||| |||||  
 G GTGTAC CAG GGACCAA  
 GT T AA\_  
 GAM1394 LOC220021 3' AACCAGGAAGACTCATGTGTGG 93389 TG \_ CGG  
 T CACGTG GTC CCTGGTT  
 | ||||| ||| |||||  
 G GTGTAC CAG GGACCAA  
 GT T AA\_  
 GAM1394 LOC220045 3' GCTGAAGCCATGTGTGGTA 93409 TG C\_  
 TAT CACGTGGT CGGC  
 ||| ||||| |||  
 ATG GTGTACCG GTCG  
 GT AA  
 GAM1394 LOC220045 3' GCTGAAGCCATGTGTGGTA 93409 TG C\_  
 TAT CACGTGGT CGGC  
 ||| ||||| |||  
 ATG GTGTACCG GTCG  
 GT AA  
 GAM1394 LOC220045 5' GGCCAGGCTGTCAACTGTGCA 93410 \_ GGTC  
 TGCAC GT CGGCCTGGTT  
 ||||| ||| |||||

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          ACGTG CA  GTCGGACCGG
            T ACT_
GAM1394 LOC220045 5' GGCCAGGCTGTCAACTGTGCA 93410  _ GGTC
          TGCAC GT  CGGCCTGGTT
          ||||| ||  |||||
          ACGTG CA  GTCGGACCGG
            T ACT_
GAM1394 LOC220114 5' CCCATGGTGACTGCGTGAGTG 91741  G  TG  CG  _  TT
          TATT CACG  GTC  GCC TGG
          ||||| |||  ||| |||
          GTGA GTGC  CAG  TGG ACC
            _  GT  _  T  CG
GAM1394 LOC220114 5' CCCATGGTGACTGCGTGAGTG 91741  G  TG  CG  _  TT
          TATT CACG  GTC  GCC TGG
          ||||| |||  ||| |||
          GTGA GTGC  CAG  TGG ACC
            _  GT  _  T  CG
GAM1394 LOC220514 3' CCATGCCGTGTGTAG 60444  TGGTC  C
          TTGCACG  CGGC TGG
          |||||  |||||
          GATGTGT  GCCG ACC
            _  T
GAM1394 LOC220514 3' CCATGCCGTGTGTAG 60444  TGGTC  C
          TTGCACG  CGGC TGG
          |||||  |||||
          GATGTGT  GCCG ACC
            _  T
GAM1394 LOC220522 3' GGCCAGGTCCGGATGGTGGT 60522  A TG  _
          GC CG  GTCCGG CCTGGTT
          || ||  ||||| |||||
          TG GT  TAGGCC GGACCGG
            _  GG  T
GAM1394 LOC220522 3' GGCCAGGTCCGGATGGTGGT 60522  A TG  _
          GC CG  GTCCGG CCTGGTT
          || ||  ||||| |||||
          TG GT  TAGGCC GGACCGG
            _  GG  T
GAM1394 LOC220565 3' ATTGGGCTGCTGTGCAG 90744  TGGTC  TG
          TTGCACG  CGGCC GT
          |||||  ||||| ||
          GACGTGT  GTCGG TA
            C_  GT
GAM1394 LOC220565 3' ATTGGGCTGCTGTGCAG 90744  TGGTC  TG
          TTGCACG  CGGCC GT
          |||||  ||||| ||
          GACGTGT  GTCGG TA
            C_  GT
GAM1394 LOC220587 3' GCCAGGCTGGGCCGGGC 90763  ACGT
          GC  GGTCCGGCCTGGT
          ||  |||||

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		CG CCGGGTCGGACCG			
		GG__			
GAM1394	LOC220587 3'	GCCAGGCTGGGCCGGGC	90763	ACGT	
		GC GGTCCGGCCTGGT			
		CG CCGGGTCGGACCG			
		GG__			
GAM1394	LOC221042 3'	GCTGGGCATGGTGGTG	93189	TG A G	
		TAT C CGTG TCCGGC			
		GTG G GTAC GGGTCG			
		GT _ _			
GAM1394	LOC221042 3'	GCTGGGCATGGTGGTG	93189	TG A G	
		TAT C CGTG TCCGGC			
		GTG G GTAC GGGTCG			
		GT _ _			
GAM1394	LOC221271 3'	AGGCCGGGTGCGGTG	91844	GTGGT	
		TATTGCAC CCGGCCT			
		GTGGCGTG GGCCGGA			
		_____			
GAM1394	LOC221271 3'	AGGCCGGGTGCGGTG	91844	GTGGT	
		TATTGCAC CCGGCCT			
		GTGGCGTG GGCCGGA			
		_____			
GAM1394	LOC221271 3'	TGGGCCGGGTGCAGTG	91881	G	
		TATTGCAC TGGTCCG			
		GTGACGTG GCCGGGT			
		G			
GAM1394	LOC221271 3'	TGGGCCGGGTGCAGTG	91881	G	
		TATTGCAC TGGTCCG			
		GTGACGTG GCCGGGT			
		G			
GAM1394	LOC221399 5'	GTCAGTCACATCACGTGTGA	93849	TG	CC C GT
		T CACGTGGT GGC TG T			
		A GTGCACTA CTG AC G			
		GT CA _ TG			
GAM1394	LOC221399 5'	GTCAGTCACATCACGTGTGA	93849	TG	CC C GT
		T CACGTGGT GGC TG T			
		A GTGCACTA CTG AC G			
		GT CA _ TG			
GAM1394	LOC221474 3'	GTTGGGCATGGTGGTG	92386	TG A G	
		TAT C CGTG TCCGGC			

		GTG G GTAC GGGTTG		
		GT _ _		
GAM1394	LOC221474 3'	GTTGGGCATGGTGGTG	92386	TG A G
		TAT C CGTG TCCGGC		
		GTG G GTAC GGGTTG		
		GT _ _		
GAM1394	LOC221474 3'	GGCTGGCCGGGTGCAGTA	92384	G T
		TATTGCAC TGG CCGGCC		
		ATGACGTG GCC GGTCGG		
		G _		
GAM1394	LOC221474 3'	GGCTGGCCGGGTGCAGTA	92384	G T
		TATTGCAC TGG CCGGCC		
		ATGACGTG GCC GGTCGG		
		G _		
GAM1394	LOC221504 5'	AATCGGGCCGGGACTCGCGGTG	92417	- - -
	T	GCAC GTG GTCC GGCCTGGTT		
		TGTG CGC CAGG CCGGGCTAA		
		G T G		
GAM1394	LOC221504 5'	AATCGGGCCGGGACTCGCGGTG	92417	- - -
	T	GCAC GTG GTCC GGCCTGGTT		
		TGTG CGC CAGG CCGGGCTAA		
		G T G		
GAM1394	LOC221876 5'	GGCTGGGCTGGGAGACCGTG	93922	TGG_ TG
		CACG TCCGGCC GTT		
		GTGC GGGTCGG CGG		
		CAGA GT		
GAM1394	LOC221876 5'	GGCTGGGCTGGGAGACCGTG	93922	TGG_ TG
		CACG TCCGGCC GTT		
		GTGC GGGTCGG CGG		
		CAGA GT		
GAM1394	LOC222060 5'	ATCAGGCCGGGCGCAGTG	94101	G _
		CAC TG GTCCGGCCTGGT		
		GTG AC CGGGCCGGA		
		_ G		
GAM1394	LOC222060 5'	ATCAGGCCGGGCGCAGTG	94101	G _
		CAC TG GTCCGGCCTGGT		
		GTG AC CGGGCCGGA		
		_ G		
GAM1394	LOC222962 5'	GGCCGGGCCGGCCGAGAGGC	92875	ACG_
		GC TGGTCCGGCCTGGTT		

	CG	GCCGGGCGGGCCGG			
	GAGA				
GAM1394 LOC222962 5'	GGCCGGGCGGGCCGAGAGGC	92875	ACG_		
	GC TGGTCCGGCCTGGTT				
	CG GCCGGGCGGGCCGG				
	GAGA				
GAM1394 LOC245727 5'	GGCTGGGGCTACGTGCAG	91128	_		
	TTGCACGTGGTCC GGCC				
	GACGTGCATCGGG TCGG				
	G				
GAM1394 LOC245727 5'	GGCTGGGGCTACGTGCAG	91128	_		
	TTGCACGTGGTCC GGCC				
	GACGTGCATCGGG TCGG				
	G				
GAM1394 LOC253001 5'	GCAGGGCCACGTGAGATA	96258	TG	G	
	TAT CACGTGGTCC GC				
	ATA GTGCACCGGG CG				
	GA A				
GAM1394 LOC253001 5'	GCAGGGCCACGTGAGATA	96258	TG	G	
	TAT CACGTGGTCC GC				
	ATA GTGCACCGGG CG				
	GA A				
GAM1394 LOC253148 3'	GCTGGAGGCCGTGTGCGG	96877	—		
	TTGCACGTGGT CCGGC				
	GGCGTGTGCCG GGTCG				
	GA				
GAM1394 LOC253148 3'	GCTGGAGGCCGTGTGCGG	96877	—		
	TTGCACGTGGT CCGGC				
	GGCGTGTGCCG GGTCG				
	GA				
GAM1394 LOC253532 3'	TCAGGCTGGGTGCAGTG	96031	GTGGT		
	TATTGCAC CCGGCCTGG				
	GTGACGTG GGTCGGA				
	—				
GAM1394 LOC253532 3'	TCAGGCTGGGTGCAGTG	96031	GTGGT		
	TATTGCAC CCGGCCTGG				
	GTGACGTG GGTCGGA				
	—				
GAM1394 LOC253816 3'	GCCAGGCAAGTGGCAGTG	94387	_	GTGGTCCG	
	TATTGC AC GCCTGGT				

		GTGACG TG	CGGACCG		
		G AA_____			
GAM1394	LOC253816 3'	GCCAGGCAAGTGGCAGTG	94387	_	GTGGTCCG
		TATTGC AC	GCCTGGT		
		GTGACG TG	CGGACCG		
		G AA_____			
GAM1394	LOC253868 5'	GCCGGGCTGGAGAGTG	95583		GTGG
		CAC TCCGGCCTGGT			
		GTG AGGTCGGGCCG			
		AG__			
GAM1394	LOC253868 5'	GCCGGGCTGGAGAGTG	95583		GTGG
		CAC TCCGGCCTGGT			
		GTG AGGTCGGGCCG			
		AG__			
GAM1394	LOC253962 5'	CCCAGTGACCATGTGTGG	96656	TG	CGGC TT
		T CACGTGGTC CTGG			
		G GTGTACCAG GACC			
		GT T__ CT			
GAM1394	LOC253962 5'	CCCAGTGACCATGTGTGG	96656	TG	CGGC TT
		T CACGTGGTC CTGG			
		G GTGTACCAG GACC			
		GT T__ CT			
GAM1394	LOC254057 3'	TCAGGGGCCTGTGCAGTG	97002	T	GGC
		TATTGCACG GGTCC CTGG			
		GTGACGTGT CCGGG GACT			
		— —			
GAM1394	LOC254057 3'	TCAGGGGCCTGTGCAGTG	97002	T	GGC
		TATTGCACG GGTCC CTGG			
		GTGACGTGT CCGGG GACT			
		— —			
GAM1394	LOC254120 3'	CCAGGCCTGGGCAGTG	97394	GTG	_
		CAC GTCC GGCCTGG			
		GTG CGGG CCGGACC			
		A__ T			
GAM1394	LOC254120 3'	CCAGGCCTGGGCAGTG	97394	GTG	_
		CAC GTCC GGCCTGG			
		GTG CGGG CCGGACC			
		A__ T			
GAM1394	LOC254251 3'	ATCATATATACGTGTAATA	95905		GTCCGGCC
		TATTGCACGTG TGGT			

	ATAATGTGCAT	ACTA	
	ATAT_____		
GAM1394 LOC254251 3'	ATCATATATACGTGTAATA	95905	GTCCGGCC
	TATTGCACGTG	TGGT	
	ATAATGTGCAT	ACTA	
	ATAT_____		
GAM1394 LOC254413 5'	GGCACTGTGGGCTGCGGCAGTA	97124	A TG _____
	TATTGC CG GTCCG	GCC	
	ATGACG GC CGGGT	CGG	
	_ GT GTCA		
GAM1394 LOC254413 5'	GGCACTGTGGGCTGCGGCAGTA	97124	A TG _____
	TATTGC CG GTCCG	GCC	
	ATGACG GC CGGGT	CGG	
	_ GT GTCA		
GAM1394 LOC254875 3'	TCAGGCTGGGTGCAGTG	96061	GTGGT
	TATTGCAC	CCGGCCTGG	
	GTGACGTG	GGTCGGACT	
	_____		
GAM1394 LOC254875 3'	TCAGGCTGGGTGCAGTG	96061	GTGGT
	TATTGCAC	CCGGCCTGG	
	GTGACGTG	GGTCGGACT	
	_____		
GAM1394 LOC254892 5'	GGCCGGGCCGGGCCGGGCGG	95528	ACGT
	TTGC	GGTCCGGCCTGGTT	
	GGCG	CCGGGCCGGGCCGG	
	GG_		
GAM1394 LOC254892 5'	GGCCGGGCCGGGCCGGGCGG	95528	ACGT
	TTGC	GGTCCGGCCTGGTT	
	GGCG	CCGGGCCGGGCCGG	
	GG_		
GAM1394 LOC255177 3'	GGCTAAGATCAAGTGTAGTA	96608	G C_
	TATTGCAC	TGGTC GGCC	
	ATGATGTG	ACTAG TCGG	
	A	AA	
GAM1394 LOC255177 3'	GGCTAAGATCAAGTGTAGTA	96608	G C_
	TATTGCAC	TGGTC GGCC	
	ATGATGTG	ACTAG TCGG	
	A	AA	
GAM1394 LOC255326 3'	GTCTGGCCGGGTGCAGTG	96379	G C
	TATTGCAC	TGGTC GGC	

	GTGACGTG GCCGG CTG		
	G T		
GAM1394 LOC255326 3'	GTCTGGCCGGGTGCAGTG 96379	G C	
	TATTGCAC TGGTC GGC		
	GTGACGTG GCCGG CTG		
	G T		
GAM1394 LOC255458 5'	GACCAGGCTGGAGTATAGTGGC 97148	_ _ G	
A	TGC AC GTG TCCGGCCTGGTT		
	ACG TG TAT AGGTCGGACCAG		
	G A G		
GAM1394 LOC255458 5'	GACCAGGCTGGAGTATAGTGGC 97148	_ _ G	
A	TGC AC GTG TCCGGCCTGGTT		
	ACG TG TAT AGGTCGGACCAG		
	G A G		
GAM1394 LOC255620 3'	GGCCTCGGACCCGGGCCGCGTG 97086	TG	_ _ T_
TGA	T CACGTGGTCCGG CC GGTT		
	A GTGCGCCGGGCC GG CCGG		
	GT CA CT		
GAM1394 LOC255620 3'	GGCCTCGGACCCGGGCCGCGTG 97086	TG	_ _ T_
TGA	T CACGTGGTCCGG CC GGTT		
	A GTGCGCCGGGCC GG CCGG		
	GT CA CT		
GAM1394 LOC255624 3'	ATTAGGCCAGGTGCGGTG 94520	G GGTCC	
	TATTGCAC T GGCCTGGT		
	GTGGCGTG A CCGGATTA		
	G _ _ _ _		
GAM1394 LOC255624 3'	ATTAGGCCAGGTGCGGTG 94520	G GGTCC	
	TATTGCAC T GGCCTGGT		
	GTGGCGTG A CCGGATTA		
	G _ _ _ _		
GAM1394 LOC255671 3'	GGCTCCAGACCAGGTGTGGTG 97261	TG G C_ _	
	TAT CAC TGGTC GGCC		
	GTG GTG ACCAG TCGG		
	GT G ACC		
GAM1394 LOC255671 3'	GGCTCCAGACCAGGTGTGGTG 97261	TG G C_ _	
	TAT CAC TGGTC GGCC		
	GTG GTG ACCAG TCGG		
	GT G ACC		
GAM1394 LOC255718 5'	GACCGGGCTGGATCGCGGATTG 97551	TG _ _ _	
TGG	CA CGTGGTCCGGCCTGGTT		



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GT GCGCTAGGTCGGGCCAG
GT TAG
GAM1394 LOC255718 5' GACCGGGCTGGATCGCGGATTG 97551 TG ____
TGG CA CGTGGTCCGGCCTGGTT
|| |||||
GT GCGCTAGGTCGGGCCAG
GT TAG
GAM1394 LOC255768 5' GGCTAGACCGGGCTGTGGCGAT 97507 A TG C
A TATTGC CG GTCCGG CTGGTT
||||| || |||||
ATAGCG GT CGGGCC GATCGG
_ GT A
GAM1394 LOC255768 5' GGCTAGACCGGGCTGTGGCGAT 97507 A TG C
A TATTGC CG GTCCGG CTGGTT
||||| || |||||
ATAGCG GT CGGGCC GATCGG
_ GT A
GAM1394 LOC255937 3' GCCGGGCATGGTGATG 95989 TG A G
TAT C CGTG TCCGGC
||| | |||
GTA G GTAC GGGCCG
GT _ _
GAM1394 LOC255937 3' GCCGGGCATGGTGATG 95989 TG A G
TAT C CGTG TCCGGC
||| | |||
GTA G GTAC GGGCCG
GT _ _
GAM1394 LOC256113 5' TGGTCATGAAGGCTGTGTGCAG 96772 TG C____ TGGTT
TG TTGCACG GTC GGCC
||||| ||| |||
GACGTGT CGG CTGG
GT AAGTA TT
GAM1394 LOC256113 5' TGGTCATGAAGGCTGTGTGCAG 96772 TG C____ TGGTT
TG TTGCACG GTC GGCC
||||| ||| |||
GACGTGT CGG CTGG
GT AAGTA TT
GAM1394 LOC256117 3' GACTGGGCTGGGTCCAGCTGGT 96357 TG ACG_ _ TG
GG T C TGG TCCGGCC GTT
| | ||| ||||| |||
G G ACC GGGTCGG CAG
GT GTCG T GT
GAM1394 LOC256117 3' GACTGGGCTGGGTCCAGCTGGT 96357 TG ACG_ _ TG
GG T C TGG TCCGGCC GTT
| | ||| ||||| |||
G G ACC GGGTCGG CAG
GT GTCG T GT
GAM1394 LOC256167 3' AGCTGGGTCATCTACGTGGTGG 97685 TG_ TCC TG
TG TAT C ACGTGG GGCC GTT
||| | ||||| ||| |||

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		GTG G TGCATC CTGG CGA		
		GT G TA_ GT		
GAM1394	LOC256167 3'	AGCTGGGTCATCTACGTGGTGG 97685	TG_	TCC TG
	TG	TAT C ACGTGG GGCC GTT		
		GTG G TGCATC CTGG CGA		
		GT G TA_ GT		
GAM1394	LOC256207 3'	GCTGGGCATGGTGGTG 95171	TG A	G
		TAT C CGTG TCCGGC		
		GTG G GTAC GGGTCG		
		GT _ _		
GAM1394	LOC256207 3'	GCTGGGCATGGTGGTG 95171	TG A	G
		TAT C CGTG TCCGGC		
		GTG G GTAC GGGTCG		
		GT _ _		
GAM1394	LOC256364 5'	GACCAGAGAGATCGTGTCTGAT 94798	C	CGGC
	G	TATTG ACGTGGTC CTGGTT		
		GTAGT TGTGCTAG GACCAG		
		C AGA_		
GAM1394	LOC256364 5'	GACCAGAGAGATCGTGTCTGAT 94798	C	CGGC
	G	TATTG ACGTGGTC CTGGTT		
		GTAGT TGTGCTAG GACCAG		
		C AGA_		
GAM1394	LOC256598 3'	GGCCGCGGACCCGGGCGCGTG 96353	TG	__ _
	TGA	T CACGTGGTCCGG CC TGGTT		
		A GTGCGCCGGGCC GG GCCGG		
		GT CA C		
GAM1394	LOC256598 3'	GGCCGCGGACCCGGGCGCGTG 96353	TG	__ _
	TGA	T CACGTGGTCCGG CC TGGTT		
		A GTGCGCCGGGCC GG GCCGG		
		GT CA C		
GAM1394	LOC256789 5'	GTAGGTCGGA CT CAGGT 97451	G _	GG
		AC TG GTCCGGCCT T		
		TG AC CAGGCTGGA G		
		G T TT		
GAM1394	LOC256789 5'	GTAGGTCGGA CT CAGGT 97451	G _	GG
		AC TG GTCCGGCCT T		
		TG AC CAGGCTGGA G		
		G T TT		
GAM1394	LOC256905 3'	ATCAGTCTTCCACGTGTAA 96863	TCC C	GT
		TTGCACGTGG GGC TG T		

	AATGTGCACC CTG AC A	
	TT_ _ TG	
GAM1394 LOC256905 3'	ATCAGTCTTCCACGTGTAA 96863	TCC C GT
	TTGCACGTGG GGC TG T	
	AATGTGCACC CTG AC A	
	TT_ _ TG	
GAM1394 LOC256946 3'	CTGGTTTATTGTGCAGTG 94547	_ T
	TATTGCACG TGG CCGG	
	GTGACGTGT ATT GGTC	
	T T	
GAM1394 LOC256946 3'	CTGGTTTATTGTGCAGTG 94547	_ T
	TATTGCACG TGG CCGG	
	GTGACGTGT ATT GGTC	
	T T	
GAM1394 LOC257054 5'	GGCTGGGTTTAGCTCCGTGTGG 95667	TG TG CC TG
	TG TAT CACG GT GGCC GTT	
	GTG GTGC CG TTGG CGG	
	GT CT AT GT	
GAM1394 LOC257054 5'	GGCTGGGTTTAGCTCCGTGTGG 95667	TG TG CC TG
	TG TAT CACG GT GGCC GTT	
	GTG GTGC CG TTGG CGG	
	GT CT AT GT	
GAM1394 LOC257095 5'	ACCAGGCTGGGTGCAATG 96935	GTGGT
	TATTGCAC CCGGCCTGGT	
	GTAACGTG GGTCGGACCA	
	_____	
GAM1394 LOC257095 5'	ACCAGGCTGGGTGCAATG 96935	GTGGT
	TATTGCAC CCGGCCTGGT	
	GTAACGTG GGTCGGACCA	
	_____	
GAM1394 LOC257095 5'	GGTCGGGTTGGGTCTGGGTG 96942	G GT GT
	CAC TG CCGGCCTG T	
	GTG GC GGTG GGC G	
	G TG TG	
GAM1394 LOC257095 5'	GGTCGGGTTGGGTCTGGGTG 96942	G GT GT
	CAC TG CCGGCCTG T	
	GTG GC GGTG GGC G	
	G TG TG	
GAM1394 LOC257095 5'	GGTCGGGTTGGGTCTGGGTG 96943	G GT GT
	CAC TG CCGGCCTG T	

		GTG GC GGTG GGC G			
		G TG TG			
GAM1394	LOC257095 5'	GTCGGGTCGGGTCGGGTCGG	96944	C G GT	GT
		TTG AC TG CCGGCCTG T			
		GGC TG GC GGCTGGGC G			
		_ G TG TG			
GAM1394	LOC257095 5'	GTCGGGTCGGGTCGGGTCGG	96944	C G GT	GT
		TTG AC TG CCGGCCTG T			
		GGC TG GC GGCTGGGC G			
		_ G TG TG			
GAM1394	LOC257095 5'	GGTCGGGTTGGGTCGGGTG	96943	G GT	GT
		CAC TG CCGGCCTG T			
		GTG GC GGTG GGC G			
		G TG TG			
GAM1394	LOC257277 5'	AGTTAGGTCGGAAGACCTGTGG	95261	TG C GG	GG
		T CA GT TCCGGCCT TT			
		G GT CA AGGCTGGA GA			
		GT C GA TT			
GAM1394	LOC257277 5'	AGTTAGGTCGGAAGACCTGTGG	95261	TG C GG	GG
		T CA GT TCCGGCCT TT			
		G GT CA AGGCTGGA GA			
		GT C GA TT			
GAM1394	LOC257358 5'	GCCAGGCTGGAATTTGGT	97101	A TGG	
		GC CG TCCGGCCTGGT			
		TG GT AGGTCGGACCG			
		_ TTA			
GAM1394	LOC257358 5'	GCCAGGCTGGAATTTGGT	97101	A TGG	
		GC CG TCCGGCCTGGT			
		TG GT AGGTCGGACCG			
		_ TTA			
GAM1394	LOC257395 3'	TGGTCGGGTCCCCCTGCTGCGG	95423	C ____ GT	TGGTT
	TG	TGCA GT G CCGGCC			
		GCGT CG C GGCTGG			
		_ TCCCC TG TT			
GAM1394	LOC257395 3'	TGGTCGGGTCCCCCTGCTGCGG	95423	C ____ GT	TGGTT
	TG	TGCA GT G CCGGCC			
		GCGT CG C GGCTGG			
		_ TCCCC TG TT			
GAM1394	LOC257396 5'	CCAGACACACGTGTAGTA	97135	_ C	
		TATTGCACGTG GTC GG			

	ATGATGTGCAC CAG CC		
	A A		
GAM1394 LOC257396 5'	CCAGACACACGTGTAGTA 97135	_ C	
	TATTGCACGTG GTC GG		
	ATGATGTGCAC CAG CC		
	A A		
GAM1394 LOC257408 5'	GGCCGGGTTGGACTGGGC 96072	ACGT	
	GC GGTCCGGCCTGGTT		
	CG TCAGGTTGGGCCGG		
	GG__		
GAM1394 LOC257408 5'	GACTGGGCTGGGGCGAGGAGT 96068	ACG_ G	TG
	GC TG TCCGGCC GTT		
	TG GC GGGTCGG CAG		
	AGGA G GT		
GAM1394 LOC257408 5'	GACTGGGCTGGGGCGAGGAGT 96068	ACG_ G	TG
	GC TG TCCGGCC GTT		
	TG GC GGGTCGG CAG		
	AGGA G GT		
GAM1394 LOC257408 5'	GGCCGGGTTGGACTGGG 96071	G	
	C TGGTCCGGCCTGGTT		
	G GTCAGGTTGGGCCGG		
	G		
GAM1394 LOC257408 5'	GGCCGGGTTGGACTGGG 96071	G	
	C TGGTCCGGCCTGGTT		
	G GTCAGGTTGGGCCGG		
	G		
GAM1394 LOC257408 5'	GGCCGGGTTGGACTGGGC 96072	ACGT	
	GC GGTCCGGCCTGGTT		
	CG TCAGGTTGGGCCGG		
	GG__		
GAM1394 LOC257408 5'	GGCTAGGCTGGGCCGGGT 96073	G	
	AC TGGTCCGGCCTGGTT		
	TG GCCGGGTCGGATCGG		
	G		
GAM1394 LOC257408 5'	GGCTAGGCTGGGCCGGGT 96073	G	
	AC TGGTCCGGCCTGGTT		
	TG GCCGGGTCGGATCGG		
	G		
GAM1394 LOC257459 5'	CAGCCTTACGTGCGG 89926	TCC C	
	TTGCACGTGG GGC TG		

GGCGTGCATT CCG AC

GAM1394 LOC257459 5' CAGCCTTACGTGCGG 89926 TCC C  
TTGCACGTGG GGC TG  
||||||| ||| ||  
GGCGTGCATT CCG AC

GAM1394 LOC257471 3' AATTAGGTAACTATGTACAAT 95683 C CC  
A TATTG ACGTGGT GGCCTGGTT  
||||| ||||| |||||  
ATAAC TGTATCA TTGGATTAA

A A\_  
GAM1394 LOC257471 3' AATTAGGTAACTATGTACAAT 95683 C CC  
A TATTG ACGTGGT GGCCTGGTT  
||||| ||||| |||||  
ATAAC TGTATCA TTGGATTAA

A A\_  
GAM1394 LOC51103 5' GGCCAGGCCGTGAGTGCG 62786 G \_  
CGTG TC CGGCCTGGTT  
||| || |||||  
GCGT AG GCCGGACCGG  
G T

GAM1394 LOC51103 5' GGCCAGGCCGTGAGTGCG 62786 G \_  
CGTG TC CGGCCTGGTT  
||| || |||||  
GCGT AG GCCGGACCGG  
G T

GAM1394 LOC51122 3' GCTAAGCTGGGTGCAGTG 65589 GTGGT C  
TATTGCAC CCGGC TGGT  
||||| |||| |||  
GTGACGTG GGTCG ATCG

A  
GAM1394 LOC51122 3' GCTAAGCTGGGTGCAGTG 65589 GTGGT C  
TATTGCAC CCGGC TGGT  
||||| |||| |||  
GTGACGTG GGTCG ATCG

A  
GAM1394 LOC51308 3' GGTCCAGGGCTGTGTGAGTG 33496 G TG \_ \_  
TATT CACG GTCC GG CC  
||| ||| ||| |||  
GTGA GTGT CGGG CC GG

\_ GT A T  
GAM1394 LOC51308 3' GGTCCAGGGCTGTGTGAGTG 33496 G TG \_ \_  
TATT CACG GTCC GG CC  
||| ||| ||| |||  
GTGA GTGT CGGG CC GG

\_ GT A T  
GAM1394 LOC51631 3' AGCTAGGCTAGATGTACAGTA 68080 C GTG CG  
TATTG AC GTC GCCTGGTT  
||||| || ||| |||||

	ATGAC TG TAG CGGATCGA	
	A ____ AT	
GAM1394 LOC51631 3'	AGCTAGGCTAGATGTACAGTA 68080	C GTG CG
	TATTG AC GTC GCCTGGTT	
	ATGAC TG TAG CGGATCGA	
	A ____ AT	
GAM1394 LOC51652 3'	ATCTTGGCTGGGTGCGGTG 32190	GTGGT T_
	TATTGCAC CCGGCC GGT	
	GTGGCGTG GGTCGG CTA	
	____ TT	
GAM1394 LOC51652 3'	ATCTTGGCTGGGTGCGGTG 32190	GTGGT T_
	TATTGCAC CCGGCC GGT	
	GTGGCGTG GGTCGG CTA	
	____ TT	
GAM1394 LOC51696 3'	GGTTGTGGAATTGTGTGTTG 32554	TG TG _ _
	AT CACG GT CCG GCC	
	TG GTGT TA GGT TGG	
	GT GT A GT	
GAM1394 LOC51696 3'	GGTTGTGGAATTGTGTGTTG 32554	TG TG _ _
	AT CACG GT CCG GCC	
	TG GTGT TA GGT TGG	
	GT GT A GT	
GAM1394 LOC51713 3'	AACCGGGCCGGGCACAGCGTG 32759	_ _
	CACG TG GTCCGGCCTGGTT	
	GTGC AC CGGGCCGGGCCAA	
	G A	
GAM1394 LOC51713 3'	AACCGGGCCGGGCACAGCGTG 32759	_ _
	CACG TG GTCCGGCCTGGTT	
	GTGC AC CGGGCCGGGCCAA	
	G A	
GAM1394 LOC56181 5'	TGGTTTTTTGGGGCTTGTGTGG 95544	TG T ____ TGGTT
TG	CACG GGTCC GGCC	
	GTGT TCGGG TTGG	
	GT _ GTTTT TT	
GAM1394 LOC56181 5'	TGGTTTTTTGGGGCTTGTGTGG 95544	TG T ____ TGGTT
TG	CACG GGTCC GGCC	
	GTGT TCGGG TTGG	
	GT _ GTTTT TT	
GAM1394 LOC57118 3'	ACTGGGCTGGGTGCAGTG 39865	GTGGT TG
	TATTGCAC CCGGCC GT	

		GTGACGTG	GGTCGG	CA		
		_____	GT			
GAM1394	LOC57118	3'	ACTGGGCTGGGTGCAGTG	39865	GTGGT	TG
			TATTGCAC	CCGGCC	GT	
			GTGACGTG	GGTCGG	CA	
			_____	GT		
GAM1394	LOC57151	5'	AGCCAGGTTGGAGCAGTGAGTG	39939	G	G G
			TATT CAC TG TCCGGCCTGGTT			
			GTGA	GTG AC AGGTTGGACCGA		
			—	—	G	
GAM1394	LOC57151	5'	AGCCAGGTTGGAGCAGTGAGTG	39939	G	G G
			TATT CAC TG TCCGGCCTGGTT			
			GTGA	GTG AC AGGTTGGACCGA		
			—	—	G	
GAM1394	LOC57805	3'	GGCTGGGGGCTGTGCTATGTGG	40990	G	TC
			GATG	ATT CACGTGG CGGCCT GGTT		—
			TAG	GTGTATC GTCGGG TCGG		
			G	GT	GG	
GAM1394	LOC57805	3'	GGCTGGGGGCTGTGCTATGTGG	40990	G	TC
			GATG	ATT CACGTGG CGGCCT GGTT		—
			TAG	GTGTATC GTCGGG TCGG		
			G	GT	GG	
GAM1394	LOC58512	3'	GCCAGGCCGGGCCGGGT	64657	G	
			AC TGGTCCGGCCTGGT			
			TG	GCCGGGCCGGACCG		
			G			
GAM1394	LOC58512	3'	GCCAGGCCGGGCCGGGT	64657	G	
			AC TGGTCCGGCCTGGT			
			TG	GCCGGGCCGGACCG		
			G			
GAM1394	LOC64167	5'	CTGGAGCCAGTGCAGTG	42278	G	—
			TATTGCAC TGG TCCGG			
			GTGACGTG	ACC AGGTC		
			—	G		
GAM1394	LOC64167	5'	CTGGAGCCAGTGCAGTG	42278	G	—
			TATTGCAC TGG TCCGG			
			GTGACGTG	ACC AGGTC		
			—	G		
GAM1394	LOC81501	3'	GCTGGGTCCCCTGGTGATG	47906	TG A T TCC	TG
			TAT C CG GG GGCC GT			



		GTA G GT CC CTGG CG		
		GT _ C _ _ GT		
GAM1394	LOC81501	3' GCTGGGTCCCCTGGTGATG	47906	TG A T TCC TG
		TAT C CG GG GGCC GT		
		GTA G GT CC CTGG CG		
		GT _ C _ _ GT		
GAM1394	LOC83468	3' AACCAAAAACTACTGTGTGCAA	48514	TG CCGGCC
		TTGCACG GT TGGTT		
		AACGTGT CA ACCAA		
		GT TCAAAA		
GAM1394	LOC83468	3' AACCAAAAACTACTGTGTGCAA	48514	TG CCGGCC
		TTGCACG GT TGGTT		
		AACGTGT CA ACCAA		
		GT TCAAAA		
GAM1394	LOC90050	5' AACCTGCCGGGCCACGTTGGTG	56378	C CT
		TATTG ACGTGGTCCGGC GGTT		
		GTGGT TGCACCGGGCCG CCAA		
		_ T _		
GAM1394	LOC90050	5' AACCTGCCGGGCCACGTTGGTG	56378	C CT
		TATTG ACGTGGTCCGGC GGTT		
		GTGGT TGCACCGGGCCG CCAA		
		_ T _		
GAM1394	LOC90092	3' GCTGGGCATGGTGGTG	61410	TG A G
		TAT C CGTG TCCGGC		
		GTG G GTAC GGGTCG		
		GT _ _		
GAM1394	LOC90092	3' GCTGGGCATGGTGGTG	61410	TG A G
		TAT C CGTG TCCGGC		
		GTG G GTAC GGGTCG		
		GT _ _		
GAM1394	LOC90141	5' AGCCAGGCTGGGAAAGCGGTGG	61624	TG A GG_
	TA	TAT C CGT TCCGGCCTGGTT		
		ATG G GCG GGGTCGGACCGA		
		GT _ AAA		
GAM1394	LOC90141	5' AGCCAGGCTGGGAAAGCGGTGG	61624	TG A GG_
	TA	TAT C CGT TCCGGCCTGGTT		
		ATG G GCG GGGTCGGACCGA		
		GT _ AAA		
GAM1394	LOC90183	3' TCCGGCGGCTGCGTGCGG	61734	TG T G T TT
		TTGCACG G CCG CC GG		

	GGCGTGC C GGC GG CC	
	GT _ _ _ TC	
GAM1394 LOC90183 3'	TCCGGCGGCTGCGTGCGG 61734	TG T G T TT
	TTGCACG G CCG CC GG	
	GGCGTGC C GGC GG CC	
	GT _ _ _ TC	
GAM1394 LOC90288 3'	GGCTGGGGTTGGTGCAGTA 62101	GTGG
	TATTGCAC TCCGGCC	
	ATGACGTG GGGTCGG	
	GTTG	
GAM1394 LOC90288 3'	GGCTGGGGTTGGTGCAGTA 62101	GTGG
	TATTGCAC TCCGGCC	
	ATGACGTG GGGTCGG	
	GTTG	
GAM1394 LOC90378 5'	CCGCGGCCGCGTGCAG 62522	_
	TTGCACGTGGTC CGG	
	GACGTGCGCCGG GCC	
	C	
GAM1394 LOC90378 5'	CCGCGGCCGCGTGCAG 62522	_
	TTGCACGTGGTC CGG	
	GACGTGCGCCGG GCC	
	C	
GAM1394 LOC90408 5'	AACCATTGGGCTGGGTGTGGT 62652	TG G CC
G	TAT CAC TGGTCCGG TGGTT	
	GTG GTG GTCGGGTT ACCAA	
	GT G T_	
GAM1394 LOC90408 5'	AACCATTGGGCTGGGTGTGGT 62652	TG G CC
G	TAT CAC TGGTCCGG TGGTT	
	GTG GTG GTCGGGTT ACCAA	
	GT G T_	
GAM1394 LOC90589 3'	GGTTTGGCCGGGTGCAGTG 59105	G CG
	TATTGCAC TGGTC GCC	
	GTGACGTG GCCGG TGG	
	G TT	
GAM1394 LOC90589 3'	GGTTTGGCCGGGTGCAGTG 59105	G CG
	TATTGCAC TGGTC GCC	
	GTGACGTG GCCGG TGG	
	G TT	
GAM1394 LOC90639 3'	CTGAAACCGTGTGTAA 63655	C_
	TTGCACGTGGT CGG	

AATGTGTGCCA GTC  
 AA  
 GAM1394 LOC90639 3' CTGAAACCGTGTGTAA 63655 C\_  
 TTGCACGTGGT CGG  
 ||||| |||  
 AATGTGTGCCA GTC  
 AA  
 GAM1394 LOC90639 5' GACCCCTGGGCCGTGTTTCAGTG 63657 C CCT  
 TATTG ACGTGGTCCGG GGT  
 |||| ||||| |||  
 GTGAC TGTGCCGGGTC CCAG  
 T C\_  
 GAM1394 LOC90639 5' GACCCCTGGGCCGTGTTTCAGTG 63657 C CCT  
 TATTG ACGTGGTCCGG GGT  
 |||| ||||| |||  
 GTGAC TGTGCCGGGTC CCAG  
 T C\_  
 GAM1394 LOC90639 5' GGTTGGCTGAGGCCTGCGTGTG 63661 TG \_ \_ TGGTT  
 GTG AT CACGT GGTC CGGCC  
 || |||| ||||  
 TG GTGCG CCGG GTCGG  
 GT T A TTGG  
 GAM1394 LOC90639 5' GGTTGGCTGAGGCCTGCGTGTG 63661 TG \_ \_ TGGTT  
 GTG AT CACGT GGTC CGGCC  
 || |||| ||||  
 TG GTGCG CCGG GTCGG  
 GT T A TTGG  
 GAM1394 LOC90750 3' ACCCAGGGCTGTGTAGTA 63911 C TG GGCCT  
 TATTG ACG GTCC GGT  
 |||| ||| ||| |||  
 ATGAT TGT CGGG CCA  
 \_ GT AC\_  
 GAM1394 LOC90750 3' ACCCAGGGCTGTGTAGTA 63911 C TG GGCCT  
 TATTG ACG GTCC GGT  
 |||| ||| ||| |||  
 ATGAT TGT CGGG CCA  
 \_ GT AC\_  
 GAM1394 LOC90768 5' ACCAGGCCGGGCCGGAGT 63950 G\_  
 AC TGGTCCGGCCTGGT  
 || ||||| |||||  
 TG GCCGGGCCGGACCA  
 AG  
 GAM1394 LOC90768 5' ACCAGGCCGGGCCGGAGT 63950 G\_  
 AC TGGTCCGGCCTGGT  
 || ||||| |||||  
 TG GCCGGGCCGGACCA  
 AG  
 GAM1394 LOC90785 5' GGCTGCAGGTCAGTGCAATG 64018 G GT\_  
 TATTGCAC TG C CGGCC  
 ||||| || | ||||

			GTAACGTG AC G GTCGG		
			_ TG AC		
GAM1394	LOC90785	5'	GGCTGCAGGTCAGTGCAATG 64018	G GT	__
			TATTGCAC TG C CGGCC		
			GTAACGTG AC G GTCGG		
			_ TG AC		
GAM1394	LOC90841	3'	ATTAGAACCCGTGTAGTA 64194	T	CCGGC
			TATTGCACG GGT CTGGT		
			ATGATGTGC CCA GATTA		
			_ A _		
GAM1394	LOC90841	3'	ATTAGAACCCGTGTAGTA 64194	T	CCGGC
			TATTGCACG GGT CTGGT		
			ATGATGTGC CCA GATTA		
			_ A _		
GAM1394	LOC90918	5'	GATTGGGCTGGGCATAGTG 64357	GTG	TG
			CAC GTCCGGCC GTT		
			GTG CGGGTCGG TAG		
			ATA GT		
GAM1394	LOC90918	5'	GATTGGGCTGGGCATAGTG 64357	GTG	TG
			CAC GTCCGGCC GTT		
			GTG CGGGTCGG TAG		
			ATA GT		
GAM1394	LOC90979	3'	GCTGGGCATGGTGGTG 64528	TG A	G
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGTCG		
			GT _ _		
GAM1394	LOC90979	3'	GCTGGGCATGGTGGTG 64528	TG A	G
			TAT C CGTG TCCGGC		
			GTG G GTAC GGGTCG		
			GT _ _		
GAM1394	LOC91050	3'	GGTCAGCCACGTGGATA 64748	G	CC
			TATT CACGTGGT GGCC		
			ATAG GTGCACCG CTGG		
			_ A _		
GAM1394	LOC91050	3'	GGTCAGCCACGTGGATA 64748	G	CC
			TATT CACGTGGT GGCC		
			ATAG GTGCACCG CTGG		
			_ A _		
GAM1394	LOC91056	3'	GGCCTGGGCTGGGTGCGGTG 94759	G	_
			TATTGCAC TGGTCC GGCC		

	GTGGCGTG GTCGGG CCGG	
	G T	
GAM1394 LOC91056 3'	GGCCTGGGCTGGGTGCGGTG 94759	G _
	TATTGCAC TGGTCC GGCC	
	GTGGCGTG GTCGGG CCGG	
	G T	
GAM1394 LOC91064 3'	AATTAGGCAGGCATGGTGGTG 64758	TG A GT G
	TAT C CGTG CC GCCTGGTT	
	GTG G GTAC GG CGGATTAA	
	GT _ _ A	
GAM1394 LOC91064 3'	AATTAGGCAGGCATGGTGGTG 64758	TG A GT G
	TAT C CGTG CC GCCTGGTT	
	GTG G GTAC GG CGGATTAA	
	GT _ _ A	
GAM1394 LOC91574 3'	ACTAGTTCAAGTGCAATG 66516	GTGGTCC GC
	TATTGCAC G CTGGT	
	GTAACGT C GATCA	
	AA _ _ TT	
GAM1394 LOC91574 3'	ACTAGTTCAAGTGCAATG 66516	GTGGTCC GC
	TATTGCAC G CTGGT	
	GTAACGT C GATCA	
	AA _ _ TT	
GAM1394 LOC91632 5'	GGCCAGGCCGGGCGGCGTTGT 66775	_ G
	GCA CGT GTCCGGCCTGGTT	
	TGT GCG CGGGCCGGACCGG	
	T G	
GAM1394 LOC91632 5'	GGCCAGGCCGGGCGGCGTTGT 66775	_ G
	GCA CGT GTCCGGCCTGGTT	
	TGT GCG CGGGCCGGACCGG	
	T G	
GAM1394 LOC91661 3'	GGCCAGGCTGGAATGCAATG 56403	CGTGG
	TATTGCA TCCGGCCTGGTT	
	GTAACGT AGGTCGGACCGG	
	A _	
GAM1394 LOC91661 3'	GGCCAGGCTGGAATGCAATG 56403	CGTGG
	TATTGCA TCCGGCCTGGTT	
	GTAACGT AGGTCGGACCGG	
	A _	
GAM1394 LOC91862 3'	GCCAGCGTTGGTGTGGTG 53466	TG CGTGGT _
	TAT CA CCGGC CTGGT	

			GTG GT	GGTTG GACCG		
			GT	_____ C		
GAM1394	LOC91862	3'	GCCAGCGTTGGTGTGGTG	53466	TG CGTGGT	_
			TAT CA	CCGGC CTGGT		
			GTG GT	GGTTG GACCG		
			GT	_____ C		
GAM1394	LOC92080	5'	AGCTAGGCTCTGTTTGTGATA	68039	TG C TG TCC	
			TAT CA G G	GGCCTGGTT		
			ATA GT T C	TCGGATCGA		
			GT T GT	_____		
GAM1394	LOC92080	5'	AGCTAGGCTCTGTTTGTGATA	68039	TG C TG TCC	
			TAT CA G G	GGCCTGGTT		
			ATA GT T C	TCGGATCGA		
			GT T GT	_____		
GAM1394	LOC92080	5'	ATCAAGACCATGTTAATG	68040	C	CGGCC
			TATTG ACGTGGTC	TGGT		
			GTAAT TGTACCAG	ACTA		
			_____ A	_____		
GAM1394	LOC92080	5'	ATCAAGACCATGTTAATG	68040	C	CGGCC
			TATTG ACGTGGTC	TGGT		
			GTAAT TGTACCAG	ACTA		
			_____ A	_____		
GAM1394	LOC92223	3'	GCTGGGCATGGTGGTG	68521	TG A	G
			TAT C CGTG	TCCGGC		
			GTG G GTAC	GGGTCG		
			GT	_ _		
GAM1394	LOC92223	3'	GCTGGGCATGGTGGTG	68521	TG A	G
			TAT C CGTG	TCCGGC		
			GTG G GTAC	GGGTCG		
			GT	_ _		
GAM1394	LOC92465	3'	AATTAGGTAGGCATGGTGATG	69401	TG A	GT G
			TAT C CGTG	CC GCCTGGTT		
			GTA G GTAC	GG TGGATTAA		
			GT	_ _ A		
GAM1394	LOC92465	3'	AATTAGGTAGGCATGGTGATG	69401	TG A	GT G
			TAT C CGTG	CC GCCTGGTT		
			GTA G GTAC	GG TGGATTAA		
			GT	_ _ A		
GAM1394	LOC92568	3'	GCTGGAGGCTGGGTGCAGTG	69774	G	_
			TATTGCAC	TGGT CCGGC		

		GTGACGTG GTCG GGTCG		
		G GA		
GAM1394	LOC92568	3' GCTGGAGGCTGGGTGCAGTG	69774	G _
		TATTGCAC TGGT CCGGC		
		GTGACGTG GTCG GGTCG		
		G GA		
GAM1394	LOC92659	3' GCTGGGCATGGTGGTG	70071	TG A G
		TAT C CGTG TCCGGC		
		GTG G GTAC GGGTCG		
		GT _ _		
GAM1394	LOC92659	3' GCTGGGCATGGTGGTG	70071	TG A G
		TAT C CGTG TCCGGC		
		GTG G GTAC GGGTCG		
		GT _ _		
GAM1394	LOC92736	3' GCTAGGCTGGGCGTGGTG	70429	GTG
		CAC GTCCGGCCTGGT		
		GTG CGGGTCGGATCG		
		GTG		
GAM1394	LOC92736	3' GCTAGGCTGGGCGTGGTG	70429	GTG
		CAC GTCCGGCCTGGT		
		GTG CGGGTCGGATCG		
		GTG		
GAM1394	LOC92771	3' GGCCCGGCTGAGTGTGGTG	53076	TG GT C
		TAT CAC GGTC GGCC		
		GTG GTG TCGG CCGG		
		GT AG C		
GAM1394	LOC92771	3' GGCCCGGCTGAGTGTGGTG	53076	TG GT C
		TAT CAC GGTC GGCC		
		GTG GTG TCGG CCGG		
		GT AG C		
GAM1394	LOC92973	5' ACTATGAGCTATTGCAGTG	71034	C TC GCC
		TATTGCA GTGG CG TGGT		
		GTGACGT TATC GT ATCA		
		_ GA _		
GAM1394	LOC92973	5' ACTATGAGCTATTGCAGTG	71034	C TC GCC
		TATTGCA GTGG CG TGGT		
		GTGACGT TATC GT ATCA		
		_ GA _		
GAM1394	LOC93349	3' TGGCTGGAGACCCCATGTGCAG	56471	_____ TGGTT
		TTGCACGTGG TCCGGCC		

			GACGTGTACC AGGTCGG		
			CCAG TT		
GAM1394	LOC93349	3'	TGGCTGGAGACCCCATGTGCAG 56471	_____	TGGTT
		T	TTGCACGTGG TCCGGCC		
			GACGTGTACC AGGTCGG		
			CCAG TT		
GAM1395	ASIC4	3'	TGTACATTTGTAAATATTTAGG 37922	_	GCCATCA
		G	CCC AAATATTTACAAA		
			GGG TTTATAAATGTTT		
			A ACATGT		
GAM1395	CCND1	3'	TGGAGGTGGGGTGTGTTGGGA 53893	A	AAG
			TCCCAAATATTT CA CCA		
			AGGGTTTGTGGG GT GGT		
			_ GGA		
GAM1395	CDKN2D	3'	TGGGGGTGTGAGTGTGTTGGGG 8399		AAG
			TCCCAAATATTTACA CCA		
			GGGGTTTGTGAGTGT GGT		
			GGG		
GAM1395	CDKN2D	3'	TGGGGGTGTGAGTGTGTTGGGG 54382		AAG
			TCCCAAATATTTACA CCA		
			GGGGTTTGTGAGTGT GGT		
			GGG		
GAM1395	CENTD1	3'	TGGTGGTTTACTATACATTTGG 57566		ATTTACA
		GG	TCCCAAAT AAGCCATCA		
			GGGGTTTA TTTGGTGGT		
			CATATCA		
GAM1395	CENTD1	3'	TGGTGGTTTACTATACATTTGG 30856		ATTTACA
		GG	TCCCAAAT AAGCCATCA		
			GGGGTTTA TTTGGTGGT		
			CATATCA		
GAM1395	DAAM2	3'	TGATGGAAATAAAGTGTGTTAGG 92294	_	ACAAAG
		G	CCC AAATATTT CCATCA		
			GGG TTTGTGAA GGTAGT		
			A ATAAA_		
GAM1395	EYA1	5'	GATGGCTCCGAGTTTGGGG 4954		ATTTACAA
			TCCCAAAT AGCCATC		
			GGGGTTTG TCGGTAG		
			AGCC_____		
GAM1395	LILRB4	3'	GCTGTAGCTTTGTAGGATATTT 22434	_	CATCA
		GGGG	CCCAAATATT TACAAAGC		



			GGGTTTATAG ATGTTTCG	
			G ATGTCGG	
GAM1395	MLLT2	3'	TGAGAGGATGTAGAGATTTGGG 19853 G TCCCAAAT TTTACA CC TCA              GGGGTTTA AGATGT GG AGT G A__ AG	A AAG A_
GAM1395	RAB5C	3'	GATGATGAGTATTTGGGG 59834 TCCCAAATATTTA CATC           GGGGTTTATGAGT GTAG A_____	CAAAGC
GAM1395	RXRB	3'	TGGTGGAGGTGGGTGTTTGGGA 41762 TCCCAAATATTTAC CCATCA           AGGGTTTGTGGGTG GGTGGT GA_____	AAAG
GAM1395	SLC12A4	3'	GGACCCTGGGATGTTTGGGG 17392 TCCCAAATATTT CC          GGGGTTTGTAGG GG GTCCCA	ACAAAG
GAM1395	SLC14A2	5'	TGATGGTTTTATAAGTGTGTGG 23142 CCAAATATTTA AAAGCCATCA             GGTTTGTGAAT TTTTGGTAGT A	C
GAM1395	SOX12	3'	TGGTGCTAGGGGTTTGGGA 22701 TCCCAAAT TTTA GCCA               AGGGTTTG GGAT TGGT G CG__	A CAAA
GAM1395	TPST2	3'	TGGTGGCTTTGTTTGCTGGGA 13177 TCCCA ACAAAGCCATCA           AGGGT TGTTCGGTGGT CGTT_____	AATATTT
GAM1395	ATP6V0A1	3'	GATGGTTTGCTGTTTGG 17730 CCAAATA AAGCCATC             GGTTTGT TTTGGTAG CG_____	TTTACA
GAM1395	C20orf162	3'	TGGTGAGGTTGAGGTTTGGGG 54605 TCCCAAAT AC GCCA              GGGGTTTG TG TGGT GAGT GAG	ATTT AAA
GAM1395	CSTL1	5'	TGGTGGCTTTGTAAGACAGTTG 56281 G CCAA TTTACAAAGCCATCA 	ATA_

GGTT GAATGTTTCGGTGGT  
GACA  
GAM1395 D21S2056E 3' TGGTGGTTTATATTCATGTTTG 13475 \_ TTACA\_  
TGA CC CAAATAT AAGCCATCA  
|| ||||| |||||  
GG GTTTGTA TTTGGTGGT  
T CTTATA  
GAM1395 DKFZP434C171 3' TGGTGGCCAAGTTATTTGGGG 31562 TTT AAA  
TCCCAAATA AC GCCATCA  
||||||| || |||||  
GGGGTTTAT TG CGGTGGT  
\_ AAC  
GAM1395 DNAM-1 3' TGGTAGGGTAGAAATTTGGGA 21641 A AAA  
TCCCAAAT TTTAC GCCA  
||||||| ||||| |||  
AGGGTTTA AGATG TGGT  
A GGA  
GAM1395 DNCI2 5' TGGTGGCTACAGTTGGTGTGG 60968 A TT AA\_  
GG TCCCAA TAT AC AGCCATCA  
||||||| ||| |||||  
GGGGTT GTG TG TCGGTGGT  
\_ GT ACA  
GAM1395 EAT2 3' GCATTGTGAGATTTGGGG 79278 A A  
TCCCAAAT TTTACAA GC  
||||||| ||||| |||  
GGGGTTTA GAGTGTT CG  
\_ A  
GAM1395 FLJ11021 3' TGATCACACTTGTAAGTTTGG 66444 A AGCC\_  
GA TCCCAAAT TTTACAA ATCA  
||||||| ||||| |||  
AGGGTTTG AAATGTT TAGT  
\_ CACAC  
GAM1395 FLJ12298 5' TGGTGGGGCCCGGTGTTTGGGA 49666 TACAAAG  
TCCCAAATATT CCATCA  
||||||| |||||  
AGGGTTTGTGG GGTGGT  
CCCGG\_  
GAM1395 FLJ12409 3' TGGTGCAATTAAGTGTGG 47055 CAAA  
CCAAATATTTA GCCA  
||||||| |||  
GGTTTGTGAAT TGGT  
TACG  
GAM1395 FLJ21272 5' TGATGGTTTTGTGTGCTGTTTG 46740 \_ TT\_  
GAGA C CCAAATA TACAAAGCCATCA  
| ||||| |||||  
G GGTGTTGT GTGTTTTGGTAGT  
A CGT  
GAM1395 FLJ22035 3' GTTTTGTGAGGGTTTGGGG 44540 A  
TCCCAAAT TTTACAAAGC  
||||||| |||||

		GGGGTTTG GAGTGTTTTG		
		G		
GAM1395	FLJ22329	3' TGGTGGGATCATGTGTTTGGGG 45075		TTACAAAG
		TCCCAAATAT CCATCA		
		GGGGTTTGTG GGTGGT		
		TACTAG__		
GAM1395	FLJ30567	3' TGGTGGTTGGAGAGTTTGGGG 58830	A	ACAA
		TCCCAAAT TTT AGCCATCA		
		GGGGTTTG AGA TTGGTGGT		
		_ GG__		
GAM1395	KCNS1	3' TGGTGCAGAGTAGGTATTTGG 9586	AAA__	TCA
		CCAAATATTTAC GCCA		
		GGTTTATGGATG TGGT		
		AGACG		
GAM1395	KIAA0146	3' GGTGGTGGTGATTTGGGG 81394	ATTTA	AA
		TCCCAAAT CA GCCATC		
		GGGGTTTA GT TGGTGG		
		_____ GG		
GAM1395	KIAA0193	5' TGGTCTGGTGGTATTTGGGA 28665	T	AAA
		TCCCAAATATT AC GCCA		
		AGGGTTTATGG TG TGGT		
		_ GTC		
GAM1395	KIAA0884	3' TGATTATTGTAAATATTTTGGGA 70207	C	AGCC
		TCC AAATATTTACAA ATCA		
		AGG TTTATAAATGTT TAGT		
		T AT__		
GAM1395	KIAA1376	3' TGGTGGTTTTATTTTGTGTTGA 63625	_	TTTAC
		GG CC CAAATA AAAGCCATCA		
		GG GTTTGT TTTTGGTGGT		
		A TTTTA		
GAM1395	LIN-28	3' TGATGGCAAAAAGGGTGTGTTGG 45151		ACAAA
		GG TCCCAAATATTT GCCATCA		
		GGGGTTTGTGGG CGGTAGT		
		AAAAA		
GAM1395	NPTXR	3' TGATTCCAGGTGGATATGTGGG 54190	A	AAAGCC
		G TCCCA ATATTTAC ATCA		
		GGGGT TATAGGTG TAGT		
		G GACCT_		
GAM1395	NPTXR	3' TGATTCCAGGTGGATATGTGGG 26654	A	AAAGCC
		G TCCCA ATATTTAC ATCA		

			GGGGT TATAGGTG TAGT		
			G GACCT_		
GAM1395	PRO0097	5'	ACCAGCTGTGGAATTTGGGG 26096	A	AA CATCA
			TCCCAAAT TTTACA GC		
			GGGGTTTA AGGTGT CG		
			_ _ ACCAA		
GAM1395	PXR2b	3'	GTTTTGTATGTGTTTGGGG 33339	T	
			TCCCAAATAT TACAAAGC		
			GGGGTTTGTG ATGTTTTG		
			T		
GAM1395	RNAH	3'	TTTGTGTATATTTGGGA 61961	T	
			TCCCAAATAT TACAAA		
			AGGGTTTATA GTGTTT		
			T		
GAM1395	SEMA5A	3'	TGGGCTCTGTAAGTTATTTGGG 14264	_	A ATCA
	G		TCCCAAATA TTTACA AGCC		
			GGGGTTTAT GAATGT TCGG		
			T C GT		
GAM1395	SLC31A2	3'	TGATGGCCGTGGGTGTCTGGGA 60130	A	AAA
			TCCCA ATATTTAC GCCATCA		
			AGGGT TGTGGGTG CGGTAGT		
			C C_		
GAM1395	TIX1	3'	TGGTGGCACATGGGTGTTGGGG 61751	A	CAAA
	G		TCCC AATATTTA GCCATCA		
			GGGG TTGTGGGT CGGTGGT		
			G ACA_		
GAM1395	UPB1	3'	TGGGGTATTGGAATGTTTGGG 32891	A	A A
	G		TCCCAAATATTT CAA GCC TCA		
			GGGGTTTGTAAGTT TGG GGT		
			G A _		
GAM1395	VDU1	3'	TGATGGCTTTGTTTGGTTTGG 30431	ATT	
	GG		TCCCAAAT ACAAAGCCATCA		
			GGGGTTTG TGTTCGGTAGT		
			GTTT		
GAM1395	ZFP106	3'	GGTGGAGGTGATTTGGGA 42476	TAT	AAAG
			TCCCAA TTAC CCATC		
			AGGGTTT AGTG GGTGG		
			_ GA_		
GAM1395	ZIM3	5'	TGATAGGAAGTGAGTGTTTGG 53540	_	AAAG _
	G		CCCAA TATTTAC CC ATCA		

	GGGTTT GTGAGTG GG TAGT		
	T AA__ A		
GAM1395 ZNF294 3'	GCTTTGTAAATGTTTGG 70828		
	CCAAATATTTACAAAGC		
	GGTTTGTAAATGTTTCG		
GAM1395 LOC113521 3'	TTTGAGATGTTTGGGA 73039	A	
	TCCCAAATATTT CAAA		
	AGGGTTTGTAGA GTTT		
GAM1395 LOC130644 3'	TTGTGTGTGTTTGGGG 75756	T	
	TCCCAAATAT TACAA		
	GGGGTTTGTG GTGTT		
	T		
GAM1395 LOC144501 3'	TGGTGGGAAGTATTTGG 83112	ACAAA	
	CCAAATATTT GCCA		
	GGTTTATGAA TGGT		
	GGG__		
GAM1395 LOC146229 3'	TGAGCCCTGTGGGTGTCTGGGG 77781	A	AA _
	TCCCA ATATTTACA GC CA		
	GGGGT TGTGGGTGT CG GT		
	C CC A		
GAM1395 LOC152359 3'	TGGTGGTTAGGAGAAGATTTGG 85706	A	ACAA
GG	TCCCAAAT TTT AGCCATCA		
	GGGGTTTA AAG TTGGTGGT		
	G AGGA		
GAM1395 LOC153339 5'	TGGTGGTTTTTTGTTTGGGG 86018	TTTAC	
	TCCCAAATA AAAGCCATCA		
	GGGGTTTGT TTTTGGTGGT		
	T__		
GAM1395 LOC154215 3'	AGATCTTTTTGTGGTATTTGGG 81051	T	CC A
G	TCCCAAATATT ACAAAG ATC		
	GGGGTTTATGG TGTTTT TAG		
	_ TC AG		
GAM1395 LOC161978 5'	TTTTGTGGATAATTTGGGA 82328	_	
	TCCCAAAT ATTTACAAAG		
	AGGGTTTA TAGGTGTTTT		
	A		
GAM1395 LOC219722 5'	TGGTGGCTCAGAGGTTTGGGA 93086	A	ACAA
	TCCCAAAT TTT AGCCATCA		

		AGGGTTTG AGA TCGGTGGT		
		G C__		
GAM1395	LOC219920 5'	TGATCCAAGGTGGGTGTTGGGG	93321	A AAAGCC
	A	TCCC AATATTTAC ATCA		
		AGGG TTGTGGGTG TAGT		
		G GAACC_		
GAM1395	LOC221760 5'	TGGTGGTTCCTGTGTGTTGGGG	93791	ATATT A_
		TCCCAA TACA AGCCATCA		
		GGGGTT GTGT TTGGTGGT		
		GT__ CC		
GAM1395	LOC222159 5'	TGGTGGCTTTGTAAAATAGAAG	94083	AAA _
	GG	CCC TATTT ACAAAGCCATCA		
		GGG ATAAA TGTTTCGGTGGT		
		AAG A		
GAM1395	LOC255520 3'	TGATGACTGGAGGTGTTTGGGG	95866	ACAA C
		TCCCAAATATTT AG CATCA		
		GGGGTTTGTGGA TC GTAGT		
		GG__ A		
GAM1396	LAMC2 3'	CCAGTCACACTGTGGCCAGTA	18710	TATG GA
		TACTG AT TGTGACTGG		
		ATGAC TG ACACTGACC		
		CGG_ TC		
GAM1396	LPIN2 3'	ACATCATCAGTACAGTA	27702	_
		TACTGTA TGATGATGT		
		ATGACAT ACTACTACA		
		G		
GAM1396	OTP 3'	CCAGTCACATCCGTGCAG	49494	AT
		CTGTATG GATGTGACTGG		
		GACGTGC CTACACTGACC		
		—		
GAM1396	P53AIP1 5'	CCAGTCACAGCAGCACAG	42081	ATGA A
		CTGT TG TGTGACTGG		
		GACA AC ACACTGACC		
		CG__ G		
GAM1396	VMD2 3'	ATCCAGTCACAGCCATACAG	14818	ATGA
		CTGTATG TGTGACTGGAT		
		GACATAC ACACTGACCTA		
		CG__		
GAM1396	LOC221755 3'	CCAGCCACGTTTATGCAG	92393	TG A
		CTGTATGA ATGTG CTGG		

GACGTATT TGCAC GACC  
 — C  
 GAM1397 PBX3 3' GCGAACTCATACAAACCA 20564 ATCC G  
 TGG GTATGAGTT GC  
 ||| ||||| ||  
 ACC CATACTCAA CG  
 AAA\_ G  
 GAM1397 DKFZp434P2235 3' AAGCCAACCATGCCCA 50038 ATCC A  
 TGG GTATG GTTGGCTT  
 ||| |||| |||||  
 ACC CGTAC CAACCGAA  
 — —  
 GAM1397 GAB3 3' AAGCCAAGACCCAGAGTCCA 54622 CCGTA A \_  
 TGGAT TG GT TGGCTT  
 |||| || || ||||  
 ACCTG AC CA ACCGAA  
 AG\_ C GA  
 GAM1397 KIAA0923 3' ATGAAGCTCCTGATAAAGATCC 25833 CG G TT  
 A TGGATC TAT AG GGCTTCAT  
 ||||| ||| || |||||  
 ACCTAG ATA TC TCGAAGTA  
 AA G C\_  
 GAM1397 PRPF8 3' AACCATACGAATTCA 61178 C A  
 TGGAT CGTATG GTT  
 |||| ||||| ||  
 ACTTA GCATAC CAA  
 A \_  
 GAM1397 SYNJ2 3' TGAAACCTCACGGATCC 61769 AT GTT C  
 GGATCCGT GA GG TTCA  
 ||||| || || ||||  
 CCTAGGCA CT CC AAGT  
 — — A  
 GAM1397 WIT-1 5' CGACCCCAACGGATCCA 31825 A A\_  
 TGGATCCGT TG GTTG  
 ||||| || ||||  
 ACCTAGGCA AC CAGC  
 \_ CC  
 GAM1397 LOC146782 3' AAGCCAACCATGCCCA 76289 ATCC A  
 TGG GTATG GTTGGCTT  
 ||| |||| |||||  
 ACC CGTAC CAACCGAA  
 — —  
 GAM1397 LOC219562 3' AAGCCAACCATGCCCA 90766 ATCC A  
 TGG GTATG GTTGGCTT  
 ||| |||| |||||  
 ACC CGTAC CAACCGAA  
 — —  
 GAM1397 LOC257181 3' AAGCCAACCATGCCCA 94588 ATCC A  
 TGG GTATG GTTGGCTT  
 ||| |||| |||||

ACC CGTAC CAACCGAA

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      _____
GAM1398 ADCY7  3' CTGTGTCGTGTGGCTTTAT 6638      GCTT
                  ATAAGGCTATA ACATAG
                  ||||| |||||
                  TATTTCCGGTGT TGTGTC
                        GC__
GAM1398 ARHC   5' CTGTGTGGGAGGAGTTTATGG 17708    G ATAG
                  TCATAAG CT CTTACATAG
                  ||||| || |||||
                  GGTATTT GA GGGTGTGTC
                        _ GGA_
GAM1398 ASPH   3' GTGATAGATCTTGTGAA 50620      _ A
                  TTCATAAGG CTAT GC
                  ||||| |||||
                  AAGTGTTCT GATA TG
                        A G
GAM1398 ASPH   3' GTGATAGATCTTGTGAA 50632      _ A
                  TTCATAAGG CTAT GC
                  ||||| |||||
                  AAGTGTTCT GATA TG
                        A G
GAM1398 ATP1B1 3' TGGTGCTGTGTCTTTATGAA 8043      C TTA
                  TTCATAAGG TATAGC CA
                  ||||| ||||| ||
                  AAGTATTC GTGTCT GT
                        T TG_
GAM1398 B4GALT1 3' CTGTGTGAACTGGCCTTTGG 7669    T AT C
                  TCA AAGGCT AG TTACATAG
                  || ||||| || |||||
                  GGT TTCCGG TC AGTGTGTC
                        _ _ A
GAM1398 BAZ1B  3' AGTTGTGGTCTTTTGAG 50538      T
                  TTCA AAGGCTATAGCT
                  ||| |||||
                  GAGT TTCTGGTGTGA
                        T
GAM1398 BDP1   5' TGGTGGTGTGGCTTTGTGG 37367      G TA
                  TCATAAGGCTATA CT CA
                  ||||| ||||| || ||
                  GGTGTTTCGGTGT GG GT
                        _ TG
GAM1398 BPGM   3' GTCATAGCCTTATGAG 8177          AG
                  TTCATAAGGCTAT C
                  ||||| ||||| |
                  GAGTATTCCGATA G
                        CT
GAM1398 BSN    3' CTGTGTGGGGATGTGCCTTGGA 12921  A T G_
      G
                  TTC TAAGGC ATA CTTACATAG
                  || ||||| || |||||
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			GAG GTTCCG TGT GGGTGTGTC		
			— — AG		
GAM1398	BTEB1	3'	TAAGTGTGGCCTTTATGAG 6851	—	C
			TTCATAA GGCTATAG TTA		
			GAGTATT CCGGTGTC AAT		
			T —		
GAM1398	CALU	3'	GCTATATCTTTGTGGA 6889		C
			TTCATAAGG TATAGC		
			AGGTGTTTC ATATCG		
			T		
GAM1398	CANX	3'	AGGCTGTGGCCTTCTGGA 87479		T
			TTCA AAGGCTATAGCTT		
			AGGT TTCCGGTGTCTGGA		
			C		
GAM1398	CASP3	3'	TGGGATTATGGTTTTGTGA 52198		—
			TCATAAGGCTATAG CTTA		
			AGTGTTTTGGTATT GGGT		
			A		
GAM1398	CASP3	3'	TGGGATTATGGTTTTGTGA 15104		—
			TCATAAGGCTATAG CTTA		
			AGTGTTTTGGTATT GGGT		
			A		
GAM1398	CDK2	3'	AGTTGCTTCACCATGGCCTTAT 8391	—	TTACATAG
	GAG		ATAAGGCTAT AGC		
			TATTCCGGTA TCG		
			CCACT TT GAT		
GAM1398	CENTD2	5'	CTGTGTGGGTCGGGGCTGTGTG 30869	A	ATA
	GA		TTCATA GGCT GCTTACATAG		
			AGGTGT TCGG TGGGTGTGTC		
			G GGC		
GAM1398	CGA	3'	TAGTGTTTATGGCTTTGTGAG 5597	CTT	AG
			TTCATAAGGCTATAG ACAT		
			GAGTGTTTCGGTATT TGTG		
			— ATT		
GAM1398	CLASP1	3'	TGTGCGTATGGTCTGTGTGG 65314	—	— TT
			TCATA AGGCTATA GC ACA		
			GGTGT TCTGGTAT CG TGT		
			G G —		
GAM1398	COX10	3'	TGTCTGTAGTTCTGTGAG 7127	AG	CTT
			TTCATA GCTATAG ACA		

			GAGTGT TGATGTC TGT		
			CT ____		
GAM1398	CXADR	3'	GTCTTAGTTTTGTGAA 7192	TA	
			TTCATAAGGCTA GC		
			AAGTGTTTTGAT TG		
			TC		
GAM1398	CYBB	3'	TTATGTGGAGCTCTATGGTTTT 76358 A	__	-
			GAGAG TAAGGCTAT AGCTT ACATAG		
			GTTTTGGTA TCGAG TGTATT		
			A TC G		
GAM1398	DNASE1L1	3'	TTATGTAAGCTAAAAAGCTGTG 22084 A A__		
			TGAA TCATA GGCT TAGCTTACATAG		
			AGTGT TCGA ATCGAATGTATT		
			G AAA		
GAM1398	DNMT2	3'	GTTATGCTTTATGGA 15331 T		
			TTCATAAGGC ATAGC		
			AGGTATTTTCG TATTG		
			-		
GAM1398	DSCR5	5'	TAAGGAGGTCGTGGTCTTGTGG 33153	TA	ACATAG
			A TTCATAAGGCTA GCTT		
			AGGTGTTCTGGT TGGA		
			GC GGAATT		
GAM1398	EXTL3	3'	CTGTGTTATCTGTGGTTTTTGG 7530 T	CTT	
			A TTCA AAGGCTATAG ACATAG		
			AGGT TTTTGGTGTC TGTGTC		
			TAT		
			-		
GAM1398	EYA2	3'	TTCTCCAAGTTGTGCTTTGTGG 17888	T	ACATAG
			TCATAAGGC ATAGCTT		
			GGTGTTTCG TGTTGAA		
			CCTCTTA		
			-		
GAM1398	FEZ1	3'	TGTCTATAGGTTTATGG 42583 G	CTT	
			TCATAAG CTATAG ACA		
			GGTATTT GATATC TGT		
			G ____		
GAM1398	FGF5	3'	TAATCTTGGCCTTGTGAG 15547	T	C
			TTCATAAGGCTA AG TTA		
			GAGTGTTCCGGT TC AAT		
			- T		
GAM1398	FGF7	3'	TCAGTAACTGTAGTCTTGTGAG 8887	C	ATAG
			TTCATAAGGCTATAG TTAC		

			GAGTGTTCCTGATGTC AATG		
			— ACTT		
GAM1398	GBAS	3'	TGTATATAGCTTGTGAG 7634	G	GCT
			TTCATAAG CTATA TACA		
			GAGTG TTC GATAT ATGT		
GAM1398	GGA1	3'	TGTCTCTTATGCCTTATGG 25347	T	CTT
			TCATAAGGC ATAG ACA		
			GGTATTCCG TATT TGT		
GAM1398	GLUL	3'	TATGTATGGTTTTGTGGA 9045		TAGCT
			TTCATAAGGCTA TACATA		
			AGGTGTTTTGGT ATGTAT		
GAM1398	GPR85	3'	CTGTAAATCTTTAGCCTTGTGA 38578	T C_	TAG
	A		TTCATAAGGCTA AG TTACA		
			AAGTGTTCCGAT TC AATGT		
			T TA C		
GAM1398	HCS	3'	TGTGGTCATAGTTTTGTGA 38484	AG T	
			TCATAAGGCTAT CT ACA		
			AGTGTTTTGATA GG TGT		
			CT _		
GAM1398	HDGF	3'	TGACTGTAGCTTTGGAA 15685	A	C
			TTC TAAGGCTATAG TTA		
			AAG GTTTCGATGTC AGT		
GAM1398	HIP12	3'	TGTCTGTGGCCTTCTGG 66233	T	CTT
			TCA AAGGCTATAG ACA		
			GGT TTCCGGTGTC TGT		
			C		
GAM1398	HOXB7	3'	TGTTCTGTAGCTTTCTGGA 15697	T	CTT
			TTCA AAGGCTATAG ACA		
			AGGT TTTCGATGTC TGT		
			C T_		
GAM1398	HRY	5'	GCTCAGTAGTTTTGTGAA 18638		
			TTCATAAGGCTAT AGC		
			AAGTGTTTTGATG TCG		
			AC		
GAM1398	HSPA6	5'	GATGAGGCTGTGGCCTATGG 76333	A	A AG
			TCATA GGCTATAGCTT CAT		

GGTAT CCGGTGTCGGA GTA  
\_ \_ GT  
GAM1398 HUNK 3' CTGTGCCCTGTGTGTTTTG 27450 \_ CTTA  
TGA CATAAGGC TATAG CATAG  
||||| ||| |||  
GTGTTTTG GTGTC GTGTC  
TGT CCC\_  
GAM1398 KCNA7 3' TTGTGTAGGATTCTGTGGTTTG 49064 A \_  
GTGG ATAGGCTATAG CTTACATAG  
|| ||||| |||||  
TG TTTGGTGTC GGATGTGTT  
G TTA  
GAM1398 KLRC1 3' TTATGTGAGTCAGCTT 23650 ATA  
AGGCT GCTTACATAG  
|||| |||||  
TTCGA TGAGTGTATT  
C\_  
GAM1398 KLRC1 3' TTATGTGAGTCAGCTT 9617 ATA  
AGGCT GCTTACATAG  
|||| |||||  
TTCGA TGAGTGTATT  
C\_  
GAM1398 KLRC2 3' TTATGTGAGTCAGCTT 94529 ATA  
AGGCT GCTTACATAG  
|||| |||||  
TTCGA TGAGTGTATT  
C\_  
GAM1398 LAPTM5 3' TGTGTAATTGCTTTGTG 22206 TATAGC  
CATAAGGC TTACATA  
||||| |||||  
GTGTTTCG AATGTGT  
TT\_  
GAM1398 LHX2 3' TTGTGTCACTGTACAGTTTTGT 16569 \_ CTT  
GGA TCATAAGGCT ATAG ACATAG  
||||| ||| |||||  
GGTGTTTTGA TGTC TGTGTT  
CA AC\_  
GAM1398 LIM2 3' GGACTGTGGGTTTGTGG 47668 G \_  
TCATAAG CTATAG CT  
||||| ||||| ||  
GGTGTTT GGTGTC GG  
G A  
GAM1398 M17S2 5' TGGAACTGTAGTCTTATGGA 49022 CTTA  
TTCATAAGGCTATAG CA  
||||||| ||  
AGGTATTCTGATGTC GT  
AAAG  
GAM1398 MBNL 3' GCTTATAGCCTTAGAA 40729 A \_  
TTC TAAGGCTATA GC  
||| ||||| ||

			AAG ATTCCGATAT CG		
			— T		
GAM1398	NEK6	3'	TGTGTAGTGAGCCTTTGAA 26935	T	ATA T
			TTCA AAGGCT GCT ACATA		
			AAGT TTCCGA TGA TGTGT		
			— G— —		
GAM1398	NRIP1	3'	TGTGGTTTAAGCTTTGTGAA 59956		AT T
			TTCATAAGGCT AGCT ACA		
			AAGTGTTTCGA TTGG TGT		
			AT —		
GAM1398	NRXN1	3'	TATGTGGGCAGGTTATGGA 57031	AG	ATA
			TTCATA GCT GCTTACATA		
			AGGTAT TGG CGGGTGTAT		
			— A—		
GAM1398	NRXN1	3'	TATGTGGGCAGGTTATGGA 16634	AG	ATA
			TTCATA GCT GCTTACATA		
			AGGTAT TGG CGGGTGTAT		
			— A—		
GAM1398	OGT	5'	TTATGTAGGTTGCCAGCTAATG 13206	AA	A—
	AA		TTCAT GGCT TAGCTTACATAG		
			AAGTA TCGA GTTGGATGTATT		
			A— CC		
GAM1398	PCMT1	3'	TGTGTAAGCTGTGTCCT 18227	C	
			AGG TATAGCTTACATA		
			TCC GTGTCGAATGTGT		
			T		
GAM1398	PCTP	3'	GCCTTATGCTTTGTGGA 41099	—	TA
			TTCATAAGGC TA GC		
			AGGTGTTTCG AT CG		
			T TC		
GAM1398	PCTP	3'	TGTGCATAGCCTTGTGAA 41102	A	TT
			TTCATAAGGCTAT GC ACA		
			AAGTGTTCCGATA CG TGT		
			— —		
GAM1398	PFN2	3'	GTTTGGGCCTTGTGGA 53828	AT	
			TTCATAAGGCT AGC		
			AGGTGTTCCGG TTG		
			GT		
GAM1398	PFN2	3'	GTTTGGGCCTTGTGGA 10529	AT	
			TTCATAAGGCT AGC		

			AGGTGTTCCGG TTG		
			GT		
GAM1398	PIG8	3'	AGCTGTTGTATTTTGTGAA 16867	___ T	
			TTCATAAG GC ATAGCT		
			AAGTGTTT TG TGTCGA		
			TA T		
GAM1398	PIGN	5'	GAGATGAGCTGTAGCCTTTGGA 24670	T	CATAG
			TTCA AAGGCTATAGCTTA		
			AGGT TTCCGATGTCGAGT		
			AGAGT		
GAM1398	PIP5K1B	3'	TACTGTAAACTATAGTTTTGTG 13061	C	TAG
	AG		TTCATAAGGCTATAG TTACA		
			GAGTGTTTTGATATC AATGT		
			A CATC		
GAM1398	PTGER3	3'	TTATGTCCTATTGTTTTGTGAA 6312	T	CTT
			TTCATAAGGC ATAG ACATAG		
			AAGTGTTTTG TATC TGTATT		
			T C__		
GAM1398	PTPN7	3'	GCTTGGCCTTATGGA 11071	T	
			TTCATAAGGCTA AGC		
			AGGTATTCCGGT TCG		
			—		
GAM1398	PTPN7	3'	GCTTGGCCTTATGGA 54553	T	
			TTCATAAGGCTA AGC		
			AGGTATTCCGGT TCG		
			—		
GAM1398	PTPN7	3'	GCTTGGCCTTATGGA 54564	T	
			TTCATAAGGCTA AGC		
			AGGTATTCCGGT TCG		
			—		
GAM1398	RANBP3	3'	TTATGTAAGATTGTCATATGAA 13260	A	TATAG
			TTCATA GGC CTTACATAG		
			AAGTAT CTG GAATGTATT		
			A TTA__		
GAM1398	RB1	3'	GCTGTGCTTTATGGA 90916	T	
			TTCATAAGGC ATAGC		
			AGGTATTTTCG TGTCG		
			—		
GAM1398	SERPINB13	3'	TTGGTATCTTGTAGTTTTGTG 24775	CT	ATAG
			CATAAGGCTATAG TAC		

			GTGTTTTGATGTT ATG		
			CT GTT		
GAM1398	SKI	3'	TGTAACCATGTAGTTTTGGAA 11706	A	GC_
			TTC TAAGGCTATA TTACA		
			AAG GTTTTGATGT AATGT		
			_ ACC		
GAM1398	SLC1A4	3'	TTATGTAAGGGACAGCTTTGGA 11720	A	ATAG
	G		TTC TAAGGCT CTTACATAG		
			GAG GTTTCGA GAATGTATT		
			_ CAGG		
GAM1398	SLC21A2	3'	CTGTGTACCCGGGCTGTGTGG 18858	A	ATAGCT
			TCATA GGCT TACATAG		
			GGTGT TCGG ATGTGTC		
			G GCCC_		
GAM1398	SOX12	3'	TGTCTGTGGTCTTGAG 22702	A	CTT
			TTC TAAGGCTATAG ACA		
			GAG GTTCTGGTGTC TGT		
			_ _		
GAM1398	SPF30	3'	TATGTAAGAAACCTTAGGA 19647	A	CTATAG
			TTC TAAGG CTTACATA		
			AGG ATTCC GAATGTAT		
			_ AAA_		
GAM1398	SPF30	3'	TTATGTACTCTTAGTTTTATG 19648	T	CT
			CATAAGGCTA AG TACATAG		
			GTATTTTGAT TC ATGTATT		
			_ TC		
GAM1398	SPP1	3'	AGTTTGTGGCTTCATGGA 5153	A	_
			TTCAT AGGCTATAG CT		
			AGGTA TTCGGTGTT GA		
			C T		
GAM1398	TAZ	3'	GCCCCATGGCTAAGCTTTATGG 31307	A	TACATAG
			TCATAAGGCT TAGCT		
			GGTATTTTCTGA ATCGG		
			_ TACCCCGT		
GAM1398	TCF20	3'	GTTATGGCCTTAAGAA 66959	A	
			TTC TAAGGCTATAGC		
			AAG ATTCCGGTATTG		
			A		
GAM1398	TEM6	3'	CTGCCAAGCTGTGATTTTGTGA 42744	C	ACATAG
	G		TTCATAAGG TATAGCTT		

			GAGTGT TTT GTGTCGAA	
			A CCGTC	
GAM1398	TK1	3'	GCTGTAGCTTATGAA 12305	G
			TTCATAAG CTATAGC	
			AAGTATTC GATGTCG	
			—	
GAM1398	TLL1	3'	CTGTGATGTCTTATGAA 24951	—
			TTCATAAGGC TATAG	
			AAGTATTCTG GTGTC	
			TA	
GAM1398	TLL2	3'	TTATGTAAGAATCATCGCCTTG 24966	T AG__
			TGGA TCATAAGGC AT CTTACATAG	
			GGTGTTCG TA GAATGTATT	
			C CTAA	
GAM1398	TNFSF5	3'	CTGGGTTCCCTATGGCCTTGT 3571	CTT A
			ATAAGGCTATAG AC TAG	
			TGTTCCGGTATC TG GTC	
			CT_ G	
GAM1398	WARS2	3'	AAGTTATAGTTTTGGGA 31728	A
			TTC TAAGGCTATAGCTT	
			AGG GTTTTGATATTGAA	
			—	
GAM1398	WEE1	3'	CTGTGGAGGTATTGCCTTGTGA 12652	T G A
			A TTCATAAGGC ATA CTT CATAG	
			AAGTGTTCG TAT GAG GTGTC	
			T G _	
GAM1398	ZHX1	3'	TAAGTATAGCTTTAT 23332	C
			ATAAGGCTATAG TTA	
			TATTTGATATC AAT	
			—	
GAM1398	ZNF132	3'	TTATGGAAGTGGTCTTTGTGAG 12827	_ ATA A
			TTCATAAGG CT GCTT CATAG	
			GAGTGTTC GG TGAA GTATT	
			T _ G	
GAM1398	ZNF136	3'	TGGCTCTGTGGCTTTGTGGG 59894	CTTA
			TTCATAAGGCTATAG CA	
			GGGTGTTTCGGTGTC GT	
			TCG_	
GAM1398	ABCC13	3'	AGTTGTGGCCTTTTGAG 56990	T
			TTCA AAGGCTATAGCT	



			GAGT TTCCGGTGTGGA		
			T		
GAM1398	AKAP7	3'	TGTGACAACATAGCTTATGAA 56840	G	AGC_
			TTCATAAG CTAT TTACA		
			AAGTATTC GATA AGTGT		
			_ CAAC		
GAM1398	AKAP7	3'	TGTGACAACATAGCTTATGAA 16727	G	AGC_
			TTCATAAG CTAT TTACA		
			AAGTATTC GATA AGTGT		
			_ CAAC		
GAM1398	AKAP7	3'	TGTGACAACATAGCTTATGAA 33052	G	AGC_
			TTCATAAG CTAT TTACA		
			AAGTATTC GATA AGTGT		
			_ CAAC		
GAM1398	ATP6M8-9	3'	CTGTGTAAGTTACTATGGTTTG 19274	G	___
			TGG ATAAG CTATAG CTTACATAG		
			TGTTT GGTATC GAATGTGTC		
			_ ATT		
GAM1398	C11orf23	3'	TGTTTACTGTACCTTGTGAG 37016	C	CTT
			TTCATAAGG TATAG ACA		
			GAGTGTTCC ATGTC TGT		
			_ ATT		
GAM1398	C1orf9	3'	TTATGTGATCTGTGTGTTGTGG 32639	G T	C
			TCATAA GC ATAG TTACATAG		
			GGTGTT TG TGTC AGTGTATT		
			G _ T		
GAM1398	C20orf36	3'	TTATGTGAGTTGCC 36801 TAT		
			GGC AGCTTACATAG		
			CCG TTGAGTGTATT		
			___		
GAM1398	C5orf3	3'	TTGTAGACTATTATAGCCATGT 37966	A	C___ TAG
			GAA CATA GGCTATAG TTACA		
			GTGT CCGATATT GATGT		
			A ATCA T		
GAM1398	C5orf7	3'	TATCCTGTGGCCTTTTGGA 63871	T	CT
			TTCA AAGGCTATAG TA		
			AGGT TTCCGGTGTC AT		
			T CT		
GAM1398	C6orf37	3'	AGTTATACCTTTGTGAA 67474	C	
			TTCATAAGG TATAGCT		

			AAGTGTTTC ATATTGA		
			C		
GAM1398	C6orf37	3'	TTGTGTGTACTATAGTCTTGTG 67483	CT	
			CATAAGGCTATAG TACATAG		
			GTGTTCTGATATC GTGTGTT		
			AT		
GAM1398	CAP350	3'	GTGATGTTGAGCTGTAGTCTTG 29046	_ AG	
	T		ATAAGGCTATAGCTTA CAT		
			TGTTCTGATGTCGAGT GTA		
			T GTGT		
GAM1398	CBX6	3'	TGTGTGTTGGCTTTGTGG 26634	TAGCT	
			TCATAAGGCTA TACATA		
			GGTGTTCGGT GTGTGT		
			T_____		
GAM1398	CCNB3	3'	TTATGTTGCTTGTTTTTATGAA 53371	CTAT TT	
			TTCATAAGG AGC ACATAG		
			AAGTATTTT TCG TGTATT		
			TGT_ T_		
GAM1398	CCNB3	3'	TTATGTTGCTTGTTTTTATGAA 53372	CTAT TT	
			TTCATAAGG AGC ACATAG		
			AAGTATTTT TCG TGTATT		
			TGT_ T_		
GAM1398	CCR1	3'	TAAGCCTTCTGGTTTTATGG 7108	TA__	
			TCATAAGGCTA GCTTA		
			GGTATTTTGGT CGAAT		
			CTTC		
GAM1398	CFDP1	5'	GCTGCGGTCTTGTGAG 20901	TA	
			TTCATAAGGC TAGC		
			GAGTGTTCTG GTCG		
			GC		
GAM1398	CLL-1	3'	CTATGGCTGAAGGCCTTATGAG 56365	A_ TTA	
			TTCATAAGGCT TAGC CATAG		
			GAGTATCCGG GTCG GTATC		
			AA ____		
GAM1398	CXorf2	3'	TTATGTAACCACCAGCCTGGTG 7819	A ATAGC	
	AA		TTCAT AGGCT TTACATAG		
			AAGTG TCCGA AATGTATT		
			G CCACC		
GAM1398	DDX33	3'	TGGAAGCTGTGGCCTGATGGA 39377	A A	
			TTCAT AGGCTATAGCTT CA		

		AGGTA TCCGGTGTGCGAA GT		
		G G		
GAM1398	DKFZp434C0328 3'	CTGCCATGCTGTATCTTTATGA 34133	C	TTACATAG
	A	TTCATAAGG TATAGC		
		AAGTATTTC ATGTCG		
		T TACCGTC		
GAM1398	DKFZp434C0923 3'	TTGTGTGAGGCTGGGGGTCTTG 34222	A_ _	
	TGG	TCATAAGGCT TAGC TTACATAG		
		GGTGTCTGG GTCG AGTGTGTT		
		GG G		
GAM1398	DKFZP434E2135 3'	CTATGTATAGTATGTATGTTTT 47953	_ _ _	
	GTGG	ATAAGGC TATA GCT TACATAG		
		TGTTTTG ATGT TGA ATGTATC		
		T A T		
GAM1398	DKFZP434H0820 3'	GGTCTGTGCCTTGTGG 63852	T _	
		TCATAAGGC ATAG CT		
		GGTGTCCG TGTC GG		
		_ T		
GAM1398	DKFZp547G183 3'	TTGTGTGGGTGGGTTGATGAG 38028	AAG ATA	
		TTCAT GCT GCTTACATAG		
		GAGTA TGG TGGGTGTGTT		
		GT_ G__		
GAM1398	DKFZP564I052 3'	TGTAATGTAGCTTTGGGAG 66723	A GC	
		TTC TAAGGCTATA TTACA		
		GAG GTTTCGATGT AATGT		
		G _		
GAM1398	DKFZp564K142 3'	ATGTGTGTCATGTGGTCTTCTG 49524	T GCT G	
	AA	TTCA AAGGCTATA TACATA		
		AAGT TTCTGGTGT GTGTGT		
		C ACT AT		
GAM1398	DKFZP572C163 5'	TTATGTGGGATTCAAACCTTTAT 61165	CTATAG_	
	GAA	TTCATAAGG CTTACATAG		
		AAGTATTTC GGGTGTATT		
		AAACTTA		
GAM1398	DKFZP586B0923 3'	TTATGTAAATTGCCTTGT 93120	TATAGC	
		ATAAGGC TTACATAG		
		TGTTCCG AATGTATT		
		TTA__		
GAM1398	DKFZp762P2111 3'	TGAGCTAGGTCTTGTGAG 86366	A	
		TTCATAAGGCT TAGCTTA		

GAGTGTTCCTGG ATCGAGT

GAM1398 EDR1 3' TGTCCTATAGCTTTAT 15387 CTT  
ATAAGGCTATAG ACA  
||||||| |||  
TATTTGATATC TGT

C\_\_  
GAM1398 EE1E1 3' TTATGTGAGCTAGTAAATGTGG 15002 AG\_ AT  
G TTCATA GCT AGCTTACATAG  
||||| ||| |||||  
GGGTGT TGA TCGAGTGTATT

AAA \_  
GAM1398 EIF4ENIF1 3' CTGTGTGAAGCTGTTTGGTGGG 39051 AAGGCT \_  
TTCAT ATAGCT TACATAG  
||||| ||||| |||||  
AGGTG TGTCGA GTGTGTC  
GTT\_\_ A

GAM1398 ELF4 3' TGTGCAGCAGCTTTGTGAG 7439 ATA \_  
TTCATAAGGCT GCT TACA  
||||||| ||| |||  
GAGTGTTCGA CGA GTGT  
\_\_ C

GAM1398 FBXO21 3' CTGTGTAAGTTGGTATTTGG 53237 TAAG TA  
TCA GCTA GCTTACATAG  
||| ||| |||||  
GGT TGGT TGAATGTGTC  
TTA\_ \_

GAM1398 FLJ10246 3' CTATGTAGGTTGTGGTCTGAGG 35943 ATA  
A TC AGGCTATAGCTTACATAG  
|| |||||  
AG TCTGGTGTGGATGTATC  
GAG

GAM1398 FLJ10450 3' TGTTCTATAGCCTGTGAA 36122 A CTT  
TTCATA GGCTATAG ACA  
||||| ||||| |||  
AAGTGT CCGATATC TGT  
\_ T\_\_

GAM1398 FLJ10483 3' CTATGTAGGAAATGCCTTGTGA 36169 TATAG  
TCATAAGGC CTTACATAG  
||||||| |||||  
AGTGTTCG GGATGTATC  
TAAA\_

GAM1398 FLJ10498 3' CTGTGAGGTCAGTGGCCTTA 36193 A \_\_\_\_ TAG  
TGGA ATAAGGCT TAG CTTACA  
||||||| ||| |||||  
TATTCGG GTC GAGTGT  
A ACTG C

GAM1398 FLJ10525 3' CTATGTAAGTAATCCAATGGTT 36223 A\_\_\_\_  
TTAGAA AAGGCTAT GCTTACATAG  
||||||| |||||

		TTTTGGTA	TGAATGTATC		
		ACCTAA			
GAM1398	FLJ10620	3'	TTGTGTGAGTGGCCCTTCTGA	36360	T CTATA
	A		TTCA AAGG GCTTACATAG		
			AAGT TTCC TGAGTGTGTT		
			C CCGG_		
GAM1398	FLJ10851	3'	CTGTGTAGGTCTCGCTGTGG	36765	AA TATA
			TCAT GGC GCTTACATAG		
			GGTG TCG TGGATGTGTC		
			_ CTC_		
GAM1398	FLJ11220	3'	TGATGTGAAGTTATAGTTTTAT	37169	_ AG
			ATAAGGCTATAGCT TACAT		
			TATTTTGATATTGA GTGTA		
			A GTT		
GAM1398	FLJ11273	3'	CTGTATTAGTTATAGTTTTGTG	37198	_ TAG
	AA		TTCATAAGGCTATAGCT TACA		
			AAGTGTTTTGATATTGA ATGT		
			TT C		
GAM1398	FLJ11712	3'	GGCTATGGCCTTTTGGA	44694	T
			TTCA AAGGCTATAGCT		
			AGGT TTCCGGTATCGG		
			T		
GAM1398	FLJ12229	5'	TGTTGGTTGGCCTTGTGG	45922	TA T
			TCATAAGGCTA GCT ACA		
			GGTGTTCCGGT TGG TGT		
			_ T		
GAM1398	FLJ12552	3'	TATGTAAGGCCCTGTGAG	43092	A TATAG
			TTCATA GGC CTTACATA		
			GAGTGT CCG GAATGTAT		
			C _		
GAM1398	FLJ12604	3'	GCTTGCAGCTTTGTGAA	64438	AT_
			TTCATAAGGCT AGC		
			AAGTGTTTCGA TCG		
			CGT		
GAM1398	FLJ12747	3'	TTGTAGTCTTCTATGGTTTTGT	49731	C_ TAG
			ATAAGGCTATAG TTACA		
			TGTTTTGGTATC GATGT		
			TTCT T		
GAM1398	FLJ12888	5'	GGGCTGTGGTCTGTGG	46321	A
			TCATA GGCTATAGCTT		

GGTGT CTGGTGTCTGGG

GAM1398 FLJ12903 3' TGTGTTTAGTTTTGTGA 42781 TAGCTT  
TCATAAGGCTA ACATA  
||||||| ||||  
AGTGTTTTGAT TGTGT  
T\_\_\_\_\_

GAM1398 FLJ20055 3' TGAGGCTATGGTTTTGT 34444 A  
ATAAGGCTATAGCTT CA  
||||||| ||  
TGTTTTGGTATCGGA GT

GAM1398 FLJ20281 3' TGCCAGTTGTACTTTATGGA 90986 C TA  
TTCATAAGG TATAGCT CA  
||||||| ||||| ||  
AGGTATTTT ATGTTGA GT  
CC

GAM1398 FLJ20729 3' TTATGTAACCTTACCCTTGTGAG 35652 C T C  
TTCATAAGG TA AG TTACATAG  
||||||| || || |||||  
GAGTGTTCC AT TC AATGTATT  
C \_ \_

GAM1398 FLJ21047 3' GATCTTCAGTTGTATTTTTGTG 44691 C TACATAG  
AA  
TTCATAAGG TATAGCT  
||||||| |||||  
AAGTGTTTT ATGTTGA  
T CTTCTAGT

GAM1398 FLJ21290 5' TGTGCTTATAGCTTTTGGG 46745 T CT  
TTCA AAGGCTATAG TACA  
||| ||||| |||  
AGGT TTTCGATATT GTGT  
CT

GAM1398 FLJ21596 3' TTATGTGAGTTTTGGCTTGTTG 45706 TA T  
AG  
TTCA AGGCTA AGCTTACATAG  
||| ||||| |||||  
GAGT TTCGGT TTGAGTGTATT  
TG T

GAM1398 FLJ21742 3' CTGTGTGAATTCAGGCCTTGTG 49846 ATAGC  
GA  
TTCATAAGGCT TTACATAG  
||||||| |||||  
AGGTGTTCCGG AGTGTGTC  
ACTTA

GAM1398 FLJ22087 3' GTATTGTATCTGTAGTTTTGT 41957 CT TAG  
ATAAGGCTATAG TACA  
||||||| |||  
TGTTTTGATGTC ATGT  
T\_ TATGT

GAM1398 FLJ22405 3' GCTGTGTGGGGTTCCCTGGGG 42520 A \_\_\_\_\_  
CCTTGTGGA GGCT TAG CTTACATAG C  
||| ||| ||||| |

CCGG GTC GGGTGTGTC G  
G CCTTTG

GAM1398 FLJ23027 3' AGCTGTACTTTTGTGG 49929 C  
TCATAAGG TATAGCT  
||||| |||||  
GGTGTTTT ATGTCGA  
C

GAM1398 FLJ23071 3' TTATGTAGGTTGCCAGCTAATG 47267 AA A\_  
AA TTCAT GGCT TAGCTTACATAG  
|||| ||| |||||  
AAGTA TCGA GTTGGATGTATT  
A\_ CC

GAM1398 FLJ23119 3' TGTGTTTATAGCTTTGT 45037 CT  
ATAAGGCTATAG TACA  
||||||| |||  
TGTTTCGATATT GTGT  
T\_

GAM1398 FLJ23168 3' TATTAAATGTTGTAGCTCTGTG 46824 AG TTACATAG  
AA TTCATA GCTATAGC  
||||| |||||  
AAGTGT CGATGTTG  
CT TAAATTATT

GAM1398 GDF10 3' TTGTGTATGTTATGTGTTTTTA 17114 \_\_ T  
TGGA TCATAAGG C TATAGC TACATAG  
||||| | ||||| |||||  
GGTATTTT G GTATTG ATGTGTT  
T T T

GAM1398 GMFB 3' GGTTTAGTCTTGTGAA 14669 T  
TTCATAAGGCTA AGCT  
||||||| |||  
AAGTGTTCTGAT TTGG

GAM1398 GW112 3' CTGTAAAGTGCTGAGTTTTATG 21188 A \_\_ TAG  
GA TCATAAGGCT TAGC TTACA  
||||||| ||| |||||  
GGTATTTTGA GTCG AATGT  
\_ TGA C

GAM1398 HDAC9-PENDING 3' TGTGTAGGTTGCAATTGAA 28176 TAAG TAT  
TTCA GC AGCTTACATA  
||| || |||||  
AAGT CG TTGGATGTGT  
TAA\_ \_\_

GAM1398 HELO1 3' TTGGTTCTCTATTAGTCTTGTG 41499 \_ CTT ATAG  
G TCATAAGGCTA TAG AC  
||||||| ||| |||  
GGTGTTCTGAT ATC TG  
T TCT GTT

GAM1398 HMT-1 3' GCAGTGGGCTTGGCTTTGTGAG 38898 T ATAG  
TTCATAAGGCTA AGCTTAC  
||||||| |||||

		GAGTGTTCGGT TCGGGTG	
		— ACGT	
GAM1398 HSPC039	3'	CTATGTAAATGGTTTTATGGA 32241	— AGC
		TTCATAAGG CTAT TTACATAG	
		AGGTATTTT GGTA AATGTATC	
		T —	
GAM1398 HSPC129	3'	CTATGTAAGTTTCATTTAGAA 33070	A GCTAT
		TTC TAAG AGCTTACATAG	
		AAG ATTT TTGAATGTATC	
		— ACT—	
GAM1398 HSPC177	3'	GTTGTGTCTTGTGAA 33089	T
		TTCATAAGGC ATAGC	
		AAGTGTCTG TGTG	
		—	
GAM1398 HSPC228	3'	TAAGTTTATAAGTTTTGTGG 33228	AT—
		TCATAAGGCT AGCTTA	
		GGTGTTTGA TTGAAT	
		ATAT	
GAM1398 HSXIAPAF1	3'	GTGGTGGTCTTGTGAA 34031	A
		TTCATAAGGCTAT GC	
		AAGTGTCTGGTG TG	
		G	
GAM1398 KCNH8	3'	TTGTCCCATGTGGCTTTTGTGA 58261	— GCTT TAG
A		TTCATAAG GCTATA ACA	
		AAGTGTTCGGTGT TGT	
		T ACCC T	
GAM1398 KIAA0026	3'	TTGTGTAGCCACGGTTTTCTGG 24411	T ATA T
A		TTCA AAGGCT GCT ACATAG	
		AGGT TTTTGG CGA TGTGTT	
		C CAC —	
GAM1398 KIAA0187	3'	AGTGATGTAAGCTGTGGTTATG 28568	AG AG
TGGA		TTCATA GCTATAGCTTACAT	
		AGGTGT TGGTGTCGAATGTA	
		AT GTGAA	
GAM1398 KIAA0212	3'	CTATGTAGTCAGTGGTTTGTGG 27937	G A_ T
		TCATAAG CTAT GCT ACATAG	
		GGTGTTCGGTG TGA TGTATC	
		— AC —	
GAM1398 KIAA0410	3'	TTAGTTTCTTGTGGTTTTGTGA 28782	CTT ATAG
		TCATAAGGCTATAG AC	



AGTGTTTTGGTGTT TG  
 CTT ATT  
 GAM1398 KIAA0471 3' ATGTGTGAATGAAGCCTTGTGA 29385 A GC G  
 A TTCATAAGGCT TA TTACATA  
 ||||| || |||||  
 AAGTGTTCCGA GT AGTGTGT  
 A A\_ AT  
 GAM1398 KIAA0522 3' TGTGTGAGCTCTCTGTGAG 71972 AG CTAT  
 TTCATA G AGCTTACATA  
 |||| | |||||  
 GAGTGT C TCGAGTGTGT  
 CT \_\_\_\_  
 GAM1398 KIAA0547 3' GCATACCTTGTGAA 28910 C A  
 TTCATAAGG TAT GC  
 ||||| ||| ||  
 AAGTGTTCC ATA CG  
 - -  
 GAM1398 KIAA0721 3' AGCTATGTCTTGTGAA 41336 T  
 TTCATAAGGC ATAGCT  
 ||||| |||||  
 AAGTGTTCTG TATCGA  
 -  
 GAM1398 KIAA0721 3' AGCTATGTCTTGTGAA 95963 T  
 TTCATAAGGC ATAGCT  
 ||||| |||||  
 AAGTGTTCTG TATCGA  
 -  
 GAM1398 KIAA0788 3' TGTCCCCTGTAGCCTCGTGAG 71340 TA CTT  
 TTCA AGGCTATAG ACA  
 ||| ||||| |||  
 GAGT TCCGATGTC TGT  
 GC CCC  
 GAM1398 KIAA0820 3' CTGTGTAGGTGAAACTTTAAGA 69024 A CTATA  
 A TTC TAAGG GCTTACATAG  
 ||| ||| |||||  
 AAG ATTC TGGATGTGTC  
 A AAAG\_  
 GAM1398 KIAA0984 3' TGTGTGGGCTTTTTTTGAA 65533 T CTAT  
 TTCA AAGG AGCTTACATA  
 ||| ||| |||||  
 AAGT TTTT TCGGGTGTGT  
 T \_\_\_\_  
 GAM1398 KIAA1046 3' CTATGTTCTGTTTTGTAGCCTT 29994 A \_ TT\_  
 AAGAA TAAGGCTATA GC ACATAG  
 ||||| || |||||  
 ATTCCGATGT TG TGTATC  
 A TT TCT  
 GAM1398 KIAA1198 3' CTGTTACACCTGTGGGTTTGTG 63307 G CTT\_ TAG  
 AA TTCATAAG CTATAG ACA  
 ||||| ||||| |||

			AAGTGTTT GGTGTC	TGT		
			G CACAT C			
GAM1398	KIAA1265	3'	TTGTGTGAGCTTCAGTTTAATG	70796	A	AT
	AA		TTCAT AGGCT AGCTTACATAG			
			AAGTA TTTGA TCGAGTGTGTT			
			A CT			
GAM1398	KIAA1423	3'	TTATGTGGACTGCGTTTTGTG	61729	TA	CT
			CATAAGGC TAG TACATAG			
			GTGTTTTG GTC GTGTATT			
			C_ AG			
GAM1398	KIAA1546	3'	GAATTATGGCTTTTTGAA	67907	T	C
			TTCA AAGGCTATAG TT			
			AAGT TTTCCGGTATT AG			
			T A			
GAM1398	KIAA1576	3'	AATGTCTTTGTGGCTTTAGAG	65903	A	CTT AG
			TTC TAAGGCTATAG ACAT			
			GAG ATTTCGGTGTT TGTA			
			_ TC_ AT			
GAM1398	KIAA1715	3'	TGTGCTGTAGCCATATGGA	68132	A	TT
			TTCATA GGCTATAGC ACA			
			AGGTAT CCGATGTCG TGT			
			A _			
GAM1398	KIAA1724	5'	TGTGTGTACACAGCCTTGT	67047	ATA	T
			ATAAGGCT GC TACA			
			TGTTCCGA TG GTGT			
			CAC T			
GAM1398	KIAA1727	3'	TAAGTTTGTGGATTTGTGGA	64063	G	_
			TTCATAAG CTATAG CTTA			
			AGGTGTTT GGTGTT GAAT			
			A T			
GAM1398	KIAA1735	3'	TGTGAAGGTAGTTTTGTG	87632	AGC	
			CATAAGGCTAT TTACA			
			GTGTTTTGATG AGTGT			
			GA_			
GAM1398	KIAA1775	3'	AGAATGGAGCTGTAGCCTCATG	52371	A	A AG
	GA		TTCAT AGGCTATAGCTT CAT			
			AGGTA TCCGATGTCGAG GTA			
			C _ AGAG			
GAM1398	KIAA1826	3'	CTATGTTTTATAGTTTTAGAA	67216	A	CTT
			TTC TAAGGCTATAG ACATAG			

AAG ATTTTGATATT TGTATC  
 \_ T\_  
 GAM1398 KIAA1841 3' AGTTAGGTTTTATGAA 80044 A  
 TTCATAAGGCT TAGCT  
 ||||| ||||  
 AAGTATTTTGG ATTGA

\_  
 GAM1398 KIAA1843 3' TATGATGGTAGTCTTAGGA 62192 A AGCTTA  
 TTC TAAGGCTAT CATA  
 || ||||| ||||  
 AGG ATTCTGATG GTAT  
 \_ GTA\_  
 GAM1398 LSM4 3' GGTGTTTTTTGGTTTTGTGAA 24638 TAGCTT AG  
 TTCATAAGGCTA ACAT  
 ||||| ||||  
 AAGTGTTTTGGT TGTG  
 TTTT\_ GT  
 GAM1398 MAP4K3 3' TTATGTAGATAATGTACTTTTA 13244 C GC\_  
 TGAG TCATAAGG TATA TTACATAG  
 ||||| |||| |||||  
 AGTATTTT ATGT GATGTATT  
 C AATA  
 GAM1398 MGC12518 3' TAATTCTGTAGCTTTGT 64082 C\_  
 ATAAGGCTATAG TTA  
 ||||| ||||  
 TGTTTCGATGTC AAT  
 TT  
 GAM1398 MGC13090 3' CTTTTTTAGGCTGTGGTTTGGT 51139 A CATAG  
 GAA TTCAT AGGCTATAGCTTA  
 |||| |||||  
 AAGTG TTTGGTGTCGGAT  
 G TTTTCA  
 GAM1398 MGC14793 3' AGCTCTATGCTTTATGAA 51936 \_ T  
 TTCATAAGGC TA AGCT  
 ||||| || ||||  
 AAGTATTTTCG AT TCGA  
 T C  
 GAM1398 MGC16025 3' TTGTGTAGGTTATCCAGATGAG 51927 AA CT  
 TTCAT GG ATAGCTTACATAG  
 |||| || |||||  
 GAGTA CC TATTGGATGTGTT  
 GA \_  
 GAM1398 MGC17330 3' TGTGGGGCCTTGTGAG 53534 TATAG  
 TTCATAAGGC CTTACA  
 ||||| ||||  
 GAGTGTTCG GGGTGT  
 \_  
 GAM1398 MGC17337 3' GTTATAGTCTTCTGAA 54690 T  
 TTCA AAGGCTATAGC  
 |||| |||||

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AAGT TTCTGATATTG
C
GAM1398 MGC3113 3' TTGTGTGGGGACTTCCATGTGA 43855 A CTATAG
G      TTCATA GG   CTTACATAG
      ||||| ||   |||||
      GAGTGT CC   GGGTGTGTT
      A TTCAG_
GAM1398 MGC4677 5' TTGTGTGCTACTGTATCTTGTG 53512 C CT_
AA      TTCATAAGG TATAG TACATAG
      ||||| ||||| |||||
      AAGTGTTC ATGTC GTGTGTT
      _ ATC
GAM1398 MLZE 3' TGTGAGTGTCTTATGG 48630 CTATA
      TCATAAGG GCTTACA
      ||||| |||||
      GGTATTCC TGAGTGT
      TG_
GAM1398 MRP63 3' TTGTGTGAAAATGAGCCTTTGG 43812 T ATAGC
A      TTCA AAGGCT TTACATAG
      ||| ||||| |||||
      AGGT TTCCGA AGTGTGTT
      _ GTAAA
GAM1398 MRPL36 3' GGTGTATCTTATGGA 50648 C
      TTCATAAGG TATAGCT
      ||||| |||||
      AGGTATTCT ATGTTGG
      _
GAM1398 MUF1 3' TGGGTTTATAGTCTTTGG 95491 T _
      TCA AAGGCTATAG CTTA
      ||| ||||| |||||
      GGT TTCTGATATT GGGT
      _ T
GAM1398 NEDD5 3' CTGTGTCACACTCTGTGTTTTG 15312 T CTT_
TGAG      CATAAGGC ATAG ACATAG
      ||||| ||||| |||||
      GTGTTTTG TGTC TGTGTC
      _ TCACAC
GAM1398 NRF 5' TGTTGATAAAGTCTTGTGG 34084 A GCTT
      TCATAAGGCT TA ACA
      ||||| || |||
      GGTGTTCTGA AT TGT
      A AGT_
GAM1398 NSBP1 3' TGTGTAAGTTATATGTC 47774 _
      GGC TATAGCTTACATA
      ||| ||||| |||||
      CTG ATATTGAATGTGT
      T
GAM1398 PC326 3' AGGTTATGGTTTTTGG 37413 T
      TTCA AAGGCTATAGCTT
      ||| ||||| |||||

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AGGT TTTTGGTATTGGA

GAM1398 PDK2 3' CTGTGTATATAGTTAGTTTTAT 10504 TAGCT\_  
ATAAGGCTA TACATAG  
||||||| |||||  
TATTTTGAT ATGTGTC  
TGATAT

GAM1398 PDZ-GEF1 3' TTGTGTCCTGTCTGAGCCTTAT 26499 \_\_\_\_ CT TAG  
GGA CATAAGGCT ATAG TACA  
||||||| ||| |||  
GTATTCCGA TGTC GTGT  
GTC CT T

GAM1398 PGR1 3' TTATGTAACCTGTCTGGTGAG 52758 A TAT C  
TTCAT AGGC AG TTACATAG  
||||| ||| || |||||  
GAGTG TCTG TC AATGTATT  
G \_\_\_\_ C

GAM1398 PLCL1 3' TGTGTGGATGCCTGTGGA 20638 A TATAG T  
TTCATA GGC CT ACATA  
||||| ||| || |||||  
AGGTGT CCG GG TGTGT  
\_ TA\_\_ \_

GAM1398 POLYDOM 3' CTGTGTGAGAAATGCCTTTGAA 44426 T TATAG  
TTCA AAGGC CTTACATAG  
||| ||||| |||||  
AAGT TTCCG GAGTGTGTC  
\_ TAAA\_

GAM1398 PRO0529 5' CTGTCTCCCCTGTGGCTTTGTT 25992 \_ CTTAC  
GA TCA TAAGGCTATAG ATAG  
||| ||||| ||||| |||  
AGT GTTTCGGTGTC TGTC  
T CCCTC

GAM1398 PRO2325 5' TTATGTATATATGGCTGTGTGA 37589 A GCT  
A TTCATA GGCTATA TACATAG  
||||| ||||| |||||  
AAGTGT TCGGTAT ATGTATT  
G AT\_

GAM1398 PTBP2 3' CTATGTGGAAAGCATTGTGGA 41036 G ATAG T  
TTCATAA GCT CT ACATAG  
||||| ||| || |||||  
AGGTGTT CGA GG TGTATC  
A AA\_\_ \_

GAM1398 PTD012 3' GGATGTTAGCTATGTCTTGTGA 25893 T T AG  
G TTCATAAGGC ATAGCT ACAT  
||||||| ||||| |||  
GAGTGTTCTG TATCGA TGTA  
\_ T GGT

GAM1398 PTP4A1 3' GGTTATAGTTCTGTGG 12940 AG  
TCATA GCTATAGCT  
||||| |||||

			GGTGT TGATATTGG		
			CT		
GAM1398	PTPNS1	3'	GGTTGGGTCTTGTGAA 55002	A	
			TTCATAAGGCT TAGCT		
			AAGTGTCTGG GTTGG		
			—		
GAM1398	RAB1B	3'	TGAGTCTGTGGCTTTG 48289	—	
			TAAGGCTATAG CTTA		
			GTTTCGGTGTC GAGT		
			T		
GAM1398	RAI17	3'	CTGTTGGTTATAGCATTTGTGA 91281	—	T TAG
	G		TTCATAAG GCTATAGCT ACA		
			GAGTGTTT CGATATTGG TGT		
			A T C		
GAM1398	RASSF2	3'	GTTTTAGCCTTGTGAA 28444	T	
			TTCATAAGGCTA AGC		
			AAGTGTCCGAT TTG		
			T		
GAM1398	RBM5	3'	TTATGTGGGTTGCCTGGTGAA 19333	A	TAT
			TTCAT AGGC AGCTTACATAG		
			AAGTG TCCG TTGGGTGTATT		
			G —		
GAM1398	RGS17	3'	TGTGCAATATGGTCTTAAGAA 24843	A	GCT
			TTC TAAGGCTATA TACA		
			AAG ATTCTGGTAT GTGT		
			A AAC		
GAM1398	RODH-4	5'	CTGTGTGTAAGCCTGTGTGAG 13532	—	ATAGCT
			TTCATA AGGCT TACATAG		
			GAGTGT TCCGA GTGTGTC		
			G AT—		
GAM1398	SBB103	5'	GGGTTGGAGCCTTGTGAA 19360	A	
			TTCATAAGGCT TAGCTT		
			AAGTGTCCGA GTTGGG		
			G		
GAM1398	SEC15B	3'	TGTTCTTGTGGCCATGTGAG 66690	A	CTT
			TTCATA GGCTATAG ACA		
			GAGTGT CCGGTGTT TGT		
			A CCT		
GAM1398	SLC6A13	3'	CTGTGTGCCTGGCCTTGGGGA 33516	A	TA TT
			TTC TAAGGCTA GC ACATAG		

			AGG GTTCCGGT CG TGTGTC		
			G C_ _		
GAM1398	SNRK	3'	TGTATTATAGCCTTAT 34773	CT	
			ATAAGGCTATAG TACA		
			TATTCCGATATT ATGT		
GAM1398	Spir-1	3'	TTGTGTGTGTGTGGCTTTGGAA 64705	A	G T
			TTC TAAGGCTATA C TACATAG		
			AAG GTTTCGGTGT G GTGTGTT		
GAM1398	STRIN	3'	TGTGTTTTAAAGTTTTGTGAA 32771	A	CT
			TTCATAAGGCT TAG TACA		
			AAGTGTTTTGA ATT GTGT		
			A TT		
GAM1398	TA-LRRP	3'	TAACCTGAAGTTTTGTGAA 31072	A	C
			TTCATAAGGCT TAG TTA		
			AAGTGTTTTGA GTC AAT		
			A C		
GAM1398	THEA	3'	CTGGAAGGTTGTGGGTTTATGG 66281	G	A_ TAG
			TCATAAG CTATAGCTT CA		
			GGTATTT GGTGTTGGA GT		
			G AG C		
GAM1398	TIP47	3'	CTGTGTGGTAAGCCTTGTTGAA 19480	_	ATA T
			TTCA TAAGGCT GCT ACATAG		
			AAGT GTTCCGA TGG TGTGTC		
			T A_ _		
GAM1398	TNFRSF21	3'	TTGTGTGGGTGGGGTTTGTGG 27083	G	ATA
			TCATAAG CT GCTTACATAG		
			GGTGTTT GG TGGGTGTGTT		
			_ GG_		
GAM1398	TOPBP1	3'	TGAAGCTGTAGCTTAGTGGA 22840	A	A
			TTCAT AGGCTATAGCTT CA		
			AGGTG TTCGATGTCGAA GT		
			A _		
GAM1398	USP22	3'	TTGTGTTTGATGTGTTCTTGTTG 68033	GC	GCTT
	AA		TTCATAAG TATA ACATAG		
			AAGTGTTT GTGT TGTGTT		
			TT AGTT		
GAM1398	ZDHC8	3'	GCTTTATGCTCTTGTGG 63906	_ _	T
			TCATAAG GC TA AGC		

			GGTGTTC CG AT TCG		
			T T T		
GAM1398	ZFP106	3'	GCTGGCATTTAGTGGCTTTGTG 42473	A____	TACATAG
	AA		CATAAGGCTAT GCT		
			GTGTTTCGGTG CGG		
			ATTTA TC GA		
GAM1398	ZFP91	3'	TGTTGCTATATTTTGTGG 53821	C	TT
			TCATAAGG TATAGC ACA		
			GGTGTTTT ATATCG TGT		
			_ T_		
GAM1398	ZNF238	3'	TGTGAAAATGGCCTTGGAG 20970	A	AGC
			TTC TAAGGCTAT TTACA		
			GAG GTTCCGGTA AGTGT		
			_ AA_		
GAM1398	ZNF287	5'	TGTTGCCTGTGGCCTTA 40299		CTT
			TAAGGCTATAG ACA		
			ATTCCGGTGTC TGT		
			CGT		
GAM1398	ZNF396	3'	TTATGTAGGTATCCTAATGAG 75671	A	CTATA
			TTCAT AGG GCTTACATAG		
			GAGTA TCC TGGATGTATT		
			A TA____		
GAM1398	LOC115286	3'	TTGTGTAAGGGTAGGCTTTGTT 73375	_ _	AG
	GA		TCA TAAGGC TAT CTTACATAG		
			AGT GTTTCG ATG GAATGTGTT		
			T G G_		
GAM1398	LOC115297	3'	CTGTGTGAGTCCATCACTGTGA 72886	A	GCTATA
	A		TTCATA G GCTTACATAG		
			AAGTGT C TGAGTGTGTC		
			_ ACTACC		
GAM1398	LOC116068	3'	CAAAAAGCTGATAGTTTTATGA 73725	_	ACATAG
	A		TTCATAAGGCTAT AGCTT		
			AAGTATTTTGATA TCGAA		
			G AAAC		
GAM1398	LOC120856	3'	TGTGGCAGTTAGCTTTGTGAA 74032	TA_	T
			TTCATAAGGCTA GCT ACA		
			AAGTGTTCGAT CGG TGT		
			TGA _		
GAM1398	LOC124470	3'	GCGTTTGGCTTTGTGGA 75638	TA_	
			TTCATAAGGCTA GC		



	AGGTGTTTCGGT CG		
	TTG		
GAM1398 LOC129892 5'	TGTTTTATAGTTTATGA 74906	CTT	
	TCATAAGGCTATAG ACA		
	AGTATTTTGATATT TGT		
	T__		
GAM1398 LOC132321 3'	TGAATGTTGTAGCTTGTGAG 75060	G	TTA
	TTCATAAG CTATAGC CA		
	GAGTGTTT C GATGTTG GT		
	__ TAA		
GAM1398 LOC142893 5'	TGTAGTTGTACTTTGTGGA 82880	C	T
	TTCATAAGG TATAGCT ACA		
	AGGTGTTTC ATGTTGA TGT		
	__ __		
GAM1398 LOC143717 3'	CTATGTGCGAGAGCCTGTGAG 76601	A	ATA TT
	TTCATA GGCT GC ACATAG		
	GAGTGT CCGA CG TGTATC		
	__ GAG __		
GAM1398 LOC144603 3'	GCTGTGTGGGGTTTCCCTGGGG 60368	A	_____
	CCTTGTGGA GGCT TAG CTTACATAG C		
	CCGG GTC GGGTGTGTC G		
	G CCTTTG		
GAM1398 LOC144715 3'	TATGTAATGTCTTATGA 76930	TATAGC	
	TCATAAGGC TTACATA		
	AGTATTCTG AATGTAT		
	T_____		
GAM1398 LOC145790 3'	TATGATTGTGCTTTGTGAA 77488	T	CTTA
	TTCATAAGGC ATAG CATA		
	AAGTGTTCG TGTT GTAT		
	__ A__		
GAM1398 LOC148753 3'	GAATGTGGCAGTGGCTTTGTGA 84217	A	T AG
	G TTCATAAGGCTAT GCT ACAT		
	GAGTGTTCGGTG CGG TGTA		
	A _ AGA		
GAM1398 LOC148753 3'	TTGTGTGGATGCAGTCCTGTGA 84220	A	A GC
	G TTCATA GGCT TA TTACATAG		
	GAGTGT CTGA GT GGTGTGTT		
	C C A_		
GAM1398 LOC149773 5'	CGGGAGAGTTATGGCATTATG 79475	_	ACATAG
	AA TTCATAAG GCTATAGCTT		

		AAGTATTT CGGTATTGAG		
		A AGGGC		
GAM1398	LOC150218 5'	CTATGTAGCGGTGTTTTGATGG 79718	_	TATA T
	A	TTCAT AAGGC GCT ACATAG		
		AGGTA TTTTG CGA TGTATC		
		G TGG_ _		
GAM1398	LOC150481 3'	TTGTGAAGTCATGGCTTTGTGG 79901		AG A
	A	TTCATAAGGCTAT CTT CATAG		
		AGGTGTTTCGGTA GAA GTGTT		
		CT _		
GAM1398	LOC150960 3'	AAGCTGTGCTTTGTGG 80053	T	
		TCATAAGGC ATAGCTT		
		GGTGTTTCG TGTCGAA		
		_		
GAM1398	LOC151619 3'	GCAGCGGGCTTGGCTTTGTGAG 68749	T	ACATAG
		TTCATAAGGCTA AGCTT		
		GAGTGTTTCGGT TCGGG		
		_ CGACGT		
GAM1398	LOC152633 5'	TGTGTGGGCCCTCGTGG 85829	TA	CTATA
		TCA AGG GCTTACATA		
		GGT TCC CGGGTGTGT		
		GC _		
GAM1398	LOC152804 3'	CTGTGTAGGAATGCTCTTGAG 85882	TAA	TATAG
		TTCA GGC CTTACATAG		
		GAGT TCG GGATGTGTC		
		TC_ TAA_		
GAM1398	LOC153651 3'	TGTCTGTGGTCTTTTGAG 80916	T	CTT
		TTCA AAGGCTATAG ACA		
		GAGT TTCTGGTGTC TGT		
		T _		
GAM1398	LOC153688 3'	TTATGTGAAAGGGCTTTGGAA 86127	A	ATAGC
		TTC TAAGGCT TTACATAG		
		AAG GTTTCGG AGTGTATT		
		_ GAA_		
GAM1398	LOC154043 3'	TTATGTAGGGACCTTATG 81031		CTATAG
		CATAAGG CTTACATAG		
		GTATTCC GGATGTATT		
		AG_		
GAM1398	LOC157531 5'	TGTGTGCAGTCTTGTG 86474	ATA	T
		CATAAGGCT GC TACA		

	GTGTTCTGA CG GTGT	
	___ T	
GAM1398 LOC157860 3'	TGTGAAATGCTTTATGAG 86571	TATAGC
	TTCATAAGGC TTACA	
	GAGTATTTTCG AGTGT	
	TAA___	
GAM1398 LOC157867 5'	TTATGTTATTTTATAGTTTGTAG 86562	A CTT_
	GAG TTC TAAGGCTATAG ACATAG	
	GAG ATTTTGATATT TGTATT	
	G TTAT	
GAM1398 LOC158014 5'	CTATAGCTCTATAGCTTTGTGA 81647	CTTAC
	TCATAAGGCTATAG ATAG	
	AGTGTTTCGATATC TATC	
	TCGA_	
GAM1398 LOC158116 3'	TCAGTAACTGTAGTCTTGTGAG 60323	C ATAG
	TTCATAAGGCTATAG TTAC	
	GAGTGTTCGTATGTC AATG	
	_ ACTT	
GAM1398 LOC158191 3'	CGTGAAGTCATGGCTTTGTGGA 81773	AG A AG
	TTCATAAGGCTAT CTT CAT	
	AGGTGTTTCGGTA GAA GTG	
	CT _ CT	
GAM1398 LOC161877 5'	AGCTGTGACTTTGTGG 82325	C
	TCATAAGG TATAGCT	
	GGTGTTTC GTGTCGA	
	A	
GAM1398 LOC164971 5'	TGTAAGTATATTTTGTGAA 82461	C G
	TTCATAAGG TATA CTTACA	
	AAGTGTTTT ATAT GAATGT	
	- -	
GAM1398 LOC167606 5'	GCTGTAGCTTTCTGAA 87273	T
	TTCA AAGGCTATAGC	
	AAGT TTTTCGATGTGC	
	C	
GAM1398 LOC199692 3'	CTGTGTGAATACAGGCTGTATG 59240	A ATAGC
	GA TTCATA GGCT TTACATAG	
	AGGTAT TCGG AGTGTGTC	
	G ACATA	
GAM1398 LOC199704 3'	TTATGTGAGTTGTTTCGTTGTGG 88333	GGCT
	A TTCATAA ATAGCTTACATAG	

	AGGTGTT	TGTTGAGTGTATT		
	GCT_			
GAM1398	LOC199858	3' TTGTGTAAGTTAATACTTAATG 88427	A	CTA
	AA	TTCAT AGG TAGCTTACATAG		
		AAGTA TTC ATTGAATGTGTT		
		A ATA		
GAM1398	LOC199907	3' CTATGTAGGCTGTGACTTG 88464	GC	
		TAAG TATAGCTTACATAG		
		GTTC GTGTCGGATGTATC		
		A_		
GAM1398	LOC200107	5' TTGTGTGGGCTTGGGCGTGTGA 88579	AG	AT
	A	TTCATA GCT AGCTTACATAG		
		AAGTGT CGG TCGGGTGTGTT		
		G_ GT		
GAM1398	LOC200132	3' TAGCAATGCTGTAGTCTTAAGG 88584	A	TTACATAG
	A	TTC TAAGGCTATAGC		
		AGG ATTCTGATGTCG		
		A TAACGATT		
GAM1398	LOC200609	5' TGAGTATTATAGCTTTGT 90104	—	
		ATAAGGCTATA GCTTA		
		TGTTTCGATAT TGAGT		
		TA		
GAM1398	LOC200772	3' CTGTGTGGGCTGACCTATG 90135	A	CTA
		CATA GG TAGCTTACATAG		
		GTAT CC GTCGGGTGTGTC		
		_ A_		
GAM1398	LOC200985	3' TGTGAAAATAGCTTTTGTGAG 88963	_	AGC
		TTCATAAG GCTAT TTACA		
		GAGTGTTT CGATA AGTGT		
		T AA_		
GAM1398	LOC219347	5' CAAATAACTGTAGCCTTATGGA 92980	C	CATAG
		TTCATAAGGCTATAG TTA		
		AGGTATTCCGATGTC AAT		
		_ AACT		
GAM1398	LOC219376	3' GAAGTAGCATGGCCTTGTGAA 93898	A	T ATAG
		TTCATAAGGCTAT GCT AC		
		AAGTGTTCCGGTA CGA TG		
		_ _ AAGG		
GAM1398	LOC220143	5' GGGCAGTGGCTTTATGGA 93590	A	
		TTCATAAGGCTAT GCTT		

	AGGTATTTCCGGTG CGGG	
	A	
GAM1398 LOC220534 3'	TTGTGTGTGCTCTGGGCTTATG 90725	G T T
AA	TTCATAAG CTA AGC TACATAG	
	AAGTATTC GGT TCG GTGTGTT	
	G C T	
GAM1398 LOC220565 5'	AAGCAGTGGCCTTGTGAG 90741	A
	TTCATAAGGCTAT GCTT	
	GAGTGTTCCGGTG CGAA	
	A	
GAM1398 LOC221060 3'	TTGTGTGAGTTAGCTATGATGA 93219	AA_ TA
A	TTCAT GGCTA GCTTACATAG	
	AAGTA TCGAT TGAGTGTGTT	
	GTA _	
GAM1398 LOC221663 3'	TGTATGTCTATGGTTTTAT 93827	_ T
	ATAAGGCTATAG C TACA	
	TATTTTGGTATC G ATGT	
	T T	
GAM1398 LOC221830 3'	TGCCAGTTGTGTTTTATGAA 92512	T TA
	TTCATAAGGC ATAGCT CA	
	AAGTATTTTG TGTTGA GT	
	_ CC	
GAM1398 LOC253351 5'	TGGTGTTTCAGCTGTGGCTTGAT 96296	A T_ AG
GAG	TTCAT AGGCTATAGCT ACAT	
	GAGTA TTCGGTGTCTGA TGTG	
	G CT GTC	
GAM1398 LOC255042 3'	CTATGGGGTGTGGTCTGTGAA 95313	A G TA
	TTCATA GGCTATA CT CATAG	
	AAGTGT CTGGTGT GG GTATC	
	_ G _	
GAM1398 LOC255728 3'	GGGTGATGGCTTTGTGAA 96781	A
	TTCATAAGGCTAT GCTT	
	AAGTGTTTCGGTA TGGG	
	G	
GAM1398 LOC256435 3'	TAAGATTGTGGCTTTGTG 95435	_
	CATAAGGCTATAG CTTA	
	GTGTTTCGGTGTT GAAT	
	A	
GAM1398 LOC256905 3'	CTGTTAGTTTTCTGGTTTTGTG 96866	T__ T TAG
G	TCATAAGGCTA AGCT ACA	

	GGTGTTTTGGT TTGA TGT		
	CTT T C		
GAM1398 LOC257358 3'	GGCTATGGCTCTTGTGAG 97104	—	
	TTCATAAG GCTATAGCT		
	GAGTG TTC CGGTATCGG		
	T		
GAM1398 LOC51018 3'	CTATGTATCTGTAGTTTTTGG 32125	T	CT
	TCA AAGGCTATAG TACATAG		
	GGT TTTTGATGTC ATGTATC		
	— T_		
GAM1398 LOC51308 3'	CTGTGTGAGTGTGTCTTTCTGG 33495	T_	TATA
	TCA AAGGC GCTTACATAG		
	GGT TTCTG TGAGTGTGTC		
	CT TG_		
GAM1398 LOC54466 3'	CTATGTGGGTTAGGGTGTTG 38654	G A	
	TAA GCT TAGCTTACATAG		
	GTT TGG ATTGGGTGTATC		
	G G		
GAM1398 LOC57795 3'	TTAAAATGTTGTTGTTTTGTGA 69325	T	TTACATAG
A	TTCATAAGGC ATAGC		
	AAGTGTTTTG TGTTG		
	T TAAAATT		
GAM1398 LOC57826 3'	TTATTAGCTTTGTGGCTTTGTG 41019	—	TACATAG
AA	TTCATAAGGCTAT AGCT		
	AAGTGTTTCGGTG TCGA		
	TT TTATT		
GAM1398 LOC63923 3'	GAGCCCTGGGTTTTGTGG 67121	ATA_	
	TCATAAGGCT GCTT		
	GGTGTTTTGG CGAG		
	GTCC		
GAM1398 LOC84549 3'	GCTGTGGCTTTGAGAA 50701	A	
	TTC TAAGGCTATAGC		
	AAG GTTTCGGTGTCG		
	A		
GAM1398 LOC90777 3'	TGTCTCCTATAGCTTGTGG 63969	G	CTT
	TCATAAG CTATAG ACA		
	GGTG TTC GATATC TGT		
	— CTC		
GAM1398 LOC91149 3'	TGTGAATGTGGCTTTAT 65087	GC	
	ATAAGGCTATA TTACA		

		TATTTCGGTGT AGTGT			
		A_			
GAM1398	LOC91149	3'	TTATGTGAGCTTCAGTGTGAG 65088	AAG	AT
			TTCAT GCT AGCTTACATAG		
			GAGTG TGA TCGAGTGTATT		
			___ CT		
GAM1398	LOC91445	3'	TTATGACTGCATAGTTTATGGA 60553	G	A TTA
			TTCATAAG CTAT GC CATAG		
			AGGTATTT GATA CG GTATT		
			_ _ TCA		
GAM1398	LOC91974	5'	GGCTGTAGCTTTAGGA 67756	A	
			TTC TAAGGCTATAGCT		
			AGG ATTTTCGATGTCGG		
			-		
GAM1398	LOC92140	3'	TGTGTATGGCTTATGAA 68285	G	GCT
			TTCATAAG CTATA TACA		
			AAGTATTC GGTAT GTGT		
			- -		
GAM1398	LOC92391	3'	AGTTGTGCCTTTGTGGA 69154	_	T
			TTCATAA GGC ATAGCT		
			AGGTGTT CCG TGTTGA		
			T _		
GAM1398	LOC92606	3'	TTATGTGGCTGTTGGTTTTTTTG 69994	T	_ T
AG			TTCA AAGGCTA TAGCT ACATAG		
			GAGT TTTTGGT GTCGG TGTATT		
			T T _		
GAM1398	LOC93017	5'	CTATGGTAGCTATAGTCTTAT 71154		TA
			ATAAGGCTATAGCT CATAG		
			TATTCTGATATCGA GTATC		
			TG		
GAM1398	LOC93132	5'	TTATGTACATTATATGTCTTTG 71508	_ _	CT
TGGA			TCATAAGG C TATAG TACATAG		
			GGTGTTC G ATATT ATGTATT		
			T T AC		
GAM1398	LOC96810	3'	CTATTTACTCTGTGACTTTATG 70563	C	CT C
AG			TTCATAAGG TATAG TA ATAG		
			GAGTATTTTC GTGTC AT TATC		
			A TC T		
GAM1399	A1BG	3'	TCAGCCTCCCAAAGTGCTGGGA 55434	A	C
T			ATC CAGCACTTTGGGAGGC GA		

			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	A1BG	3'	TCAGCCTCCCAAAGTGTGGGA 55435	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTTGTGAAACCCTCCG CT		
			G A		
GAM1399	ADAMTS4	3'	TCGGCCTCCCAAAGTGCTGGGA 17521	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	ADRA1A	3'	TCAGCCTCCCAAAGTGCTGGGA 52790	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	AIM1	3'	TCGGCCTCCCAAATGCTGGGA 91830	A	C
	T		ATC CAGCA TTTGGGAGGCCGA		
			TAG GTCGT AAACCCTCCGGCT		
			G A		
GAM1399	ALDH1B1	3'	TCAGCCTCCCAAAGTGCTGGGA 5498	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	APAF1	3'	TCAGCCTCCCAAAGTGTGGGA 6739	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTTGTGAAACCCTCCG CT		
			G A		
GAM1399	APAF1	3'	TCAGCCTCCCAAAGTGTGGGA 25048	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTTGTGAAACCCTCCG CT		
			G A		
GAM1399	APM1	3'	TCGACCTCCCAAAGTGCTGGGA 16604	A	C
	T		ATC CAGCACTTTGGGAGG CGA		
			TAG GTCGTGAAACCCTCC GCT		
			G A		
GAM1399	APM1	3'	TCGGCCTCCCAAAGTGCTGGGA 16605	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	APPL	3'	TCGGCCTCCCAAAGTGCTGGGA 23932	A	
	T		ATC CAGCACTTTGGGAGGCCGA		



			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	AQP6	3'	TCGGCCTCCCAAAGTGCTGGGA 7963	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	AQP6	3'	TCGGCCTCCCAAAGTGCTGGGA 53943	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	ARCN1	3'	TCAGCCTCCCAAAGTGTTGGGA 7987	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTTGTGAAACCCTCCG CT		
			G            A		
GAM1399	ARSF	5'	TCGGCCTCCCAAAGTGCTGGGA 64604	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	ATP1B2	3'	TCGGCCTCCCAAAGTGTTGGGA 8056	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTTGTGAAACCCTCCGGCT		
			G		
GAM1399	ATP8B2	3'	CCTCCCAAAGTGCTGAGAT 65220	A	
			ATC CAGCACTTTGGGAGG		
			TAG GTCGTGAAACCCTCC		
			A		
GAM1399	AXL	3'	TCAGCCTCCCAAAGTGCTGAGA 41604	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			A            A		
GAM1399	AXL	3'	TCAGCCTCCCAAAGTGCTGAGA 8107	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			A            A		
GAM1399	BAZ2B	5'	TCGGCCTCCCAAAGTGCTGGGA 25624	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	CAMLG	3'	TCGGCCTCCCAAAGTGCTGGGA 8246	A	
	T		ATC CAGCACTTTGGGAGGCCGA		

			TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	CASP2	3'	TCAGCCTCCCAAAGTGTTGGGA 6904	A	C
	T		ATC CAGCACTTTGGGAGGC GA 		
			TAG GTTGTGAAACCCTCCG CT G            A		
GAM1399	CASP2	3'	TCAGCCTCCCAAAGTGTTGGGA 52146	A	C
	T		ATC CAGCACTTTGGGAGGC GA 		
			TAG GTTGTGAAACCCTCCG CT G            A		
GAM1399	CASP2	3'	TCAGCCTCCCAAAGTGTTGGGA 52160	A	C
	T		ATC CAGCACTTTGGGAGGC GA 		
			TAG GTTGTGAAACCCTCCG CT G            A		
GAM1399	CASP2	3'	TCAGCCTCCCAAAGTGTTGGGA 52175	A	C
	T		ATC CAGCACTTTGGGAGGC GA 		
			TAG GTTGTGAAACCCTCCG CT G            A		
GAM1399	CASP8	3'	TCGGCCTCCCAAAGTGCTGGGA 52928	A	
	T		ATC CAGCACTTTGGGAGGCCGA 		
			TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	CASP8	3'	TCGGCCTCCCAAAGTGCTGGGA 52939	A	
	T		ATC CAGCACTTTGGGAGGCCGA 		
			TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	CASP8	3'	TCGGCCTCCCAAAGTGCTGGGA 52954	A	
	T		ATC CAGCACTTTGGGAGGCCGA 		
			TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	CASP8	3'	TCGGCCTCCCAAAGTGCTGGGA 6922	A	
	T		ATC CAGCACTTTGGGAGGCCGA 		
			TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	CDC25B	3'	GCCCCTACTGCTGTGA 41564	CTT A	
			TCACAGCA TGGG GGC 		
			AGTGTCGT ATCC CCG C__ _		
GAM1399	CDC25B	3'	GCCCCTACTGCTGTGA 41568	CTT A	
			TCACAGCA TGGG GGC 		

			AGTGTCTGT ATCC CCG		
			C__ _		
GAM1399	CHRNA4	3'	TCGGCCTCCCAAAGTGCTGGGA 5636	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	CLECSF11	5'	TCAGCCTCCCAAAGTGCTGAGA 55277	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			A A		
GAM1399	CNGA1	5'	TCAGCCTCCCAAAGTGCTG 59512		C
			CAGCACTTTGGGAGGC GA		
			GTCGTGAAACCCTCCG CT		
			A		
GAM1399	COX15	3'	GCCTCCTGGGACTGTGA 54316	CA TT	
			TCACAG CT GGGAGGC		
			AGTGTC GG TCCTCCG		
			AG _		
GAM1399	CR1	3'	TCGGCCTCCCAAAGTGCTGCGA 5137	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			C		
GAM1399	CYP1A2	3'	TCAGCCTCCCAAAGTGCTGGGA 5707	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	CYP1A2	3'	TCAGCCTCCCAAAGTGCTGGGA 69127	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	CYP4F3	3'	TCGGCCTCCCAAAGTGCTGGGA 6127	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	CYP8B1	3'	TCGGCCTCCCAAAGTTCTGGGA 15275	A C	
	T		ATC CAG ACTTTGGGAGGCCGA		
			TAG GTC TGAAACCCTCCGGCT		
			G T		
GAM1399	DFFB	3'	TCAGCCTCCCAAAGTGCTGGGA 87394	A	C
	TG		TATC CAGCACTTTGGGAGGC GA		

			GTAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	DHFR	3'	TCAGCCTCCCAAAGTGCTGGGA 5816	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	DISC1	3'	CGCCTTCCATGCTGTG 37873	CTT	C
			CACAGCA TGGGAGGC G		
			GTGTCGT ACCTTCCG C		
			— A		
GAM1399	DNASE1L1	5'	TCAGCCTCCCAAAGTGCTGGGA 22081	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	DSC3	3'	TCGGCCTCCCAAAGTGCTGGGA 8682	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	DSC3	3'	TCGGCCTCCCAAAGTGCTGGGA 44347	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	EHD2	3'	TCGGCCTCCCAAAGTGATGGGA 27501	A G	
	T		ATC CA CACTTTGGGAGGCCGA		
			TAG GT GTGAAACCCTCCGGCT		
			G A		
GAM1399	F2RL2	3'	TCAGCCTCCCAAAGTGCTGGAT 14625	A	C
			ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			— A		
GAM1399	F2RL3	3'	TCAGCCTCCCAAAGTAGCTGGGA 14193	A	— T C
	TA		TATC CAGC ACTT GGGAGGC GA		
			ATAG GTCG TGAA CCCTCCG CT		
			G A — A		
GAM1399	FCAR	3'	TCGGCCTCCCAAAGTGCTGGGA 55805	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	FCGR2A	3'	TCGGCCTCCCAAAGTGCTGGGA 79266	A	
	TG		TATC CAGCACTTTGGGAGGCCGA		

			GTAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	FZD4	3'	TCAGCCTCCCAAAGTGCTGGGA 24151	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	GHR	3'	TCGGCCTCCCAAAGTGCTGGGA 3890	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	GLTSCR1	5'	TCAGCCTCCCAAAGTGCTGAGA 31676	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			A A		
GAM1399	GPR81	3'	TCGGCCTCCCAAAGTGCTTGGGA 50767	AC	
	T		ATC AGCACTTTGGGAGGCCGA		
			TAG TCGTGAAACCCTCCGGCT		
			GT		
GAM1399	HCS	3'	TCGGCCTCCCAAAGTGCTGGGA 38481	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	HLCS	5'	TCGGCCTCCCAAAGTGCTGGGA 4679	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	HTR1E	5'	TCGGCCTCCCAAAGTGCTGGA 6017	A	
			TC CAGCACTTTGGGAGGCCGA		
			AG GTCGTGAAACCCTCCGGCT		
			—		
GAM1399	HYAL4	5'	TCAGCCTCCCAAATGTTGGGT 24375	A	C C
	A		TATC CAGCA TTTGGGAGGC GA		
			ATGG GTTGT AAACCCTCCG CT		
			— A A		
GAM1399	IL11	3'	TCGGCCTCCCAAAGTGCTGGGA 5339	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	IL1RAP	3'	GGTTAACAAAGAACTGTGATA 9313	CA	GGA
			TATCACAG CTTTG GGCC		

ATAGTGTC GAAAC TTGG

AA AA\_

GAM1399	INMT	3'	TCGGCCTCCCAAAGTGCTGGGA 22280	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	KMO	3'	TCAGCCTCCCAAAGTACAGGGA 13457	ACAGC	C
	T		ATC ACTTTGGGAGGC GA		
			TAG TGAAACCCTCCG CT		
			GGACA A		
GAM1399	LTB4R	5'	TCAGCCTCCCAAAGTGCTGGGA 5653	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	LYZ	3'	TCGGCCTCCCAAAGTGCTGGGA 4110	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	MAK	3'	TCGGCCTCCCAAAGTGC 19768		
			GCACTTTGGGAGGCCGA		
			CGTGAAACCCTCCGGCT		
GAM1399	MATN3	3'	TCAGCCTCCCAAAGTGCTGGGA 9938	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	MDM2	3'	TCGGCCTCCCAAAGTGCTGGGA 9974	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	MDM2	3'	TCGGCCTCCCAAAGTGCTGGGA 22512	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	MDM2	3'	TCGGCCTCCCAAAGTGCTGGGA 22516	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	MDM2	3'	TCGGCCTCCCAAAGTGCTGGGA 22520	A	
	T		ATC CAGCACTTTGGGAGGCCGA		

Cell Line	Gene	Position	Sequence	Reference	Variant	Allele	Frequency
GAM1399	MDM2	22524	3' TCGGCCTCCCAAAGTGCTGGGA ATC CAGCACTTTGGGAGGCCGA 	A			
GAM1399	MEFV	4152	3' TCAGCCTCCCAAAGTGCAAGGA ATC GCACTTTGGGAGGC GA 	ACA			
GAM1399	MEFV	4153	3' TCAGCCTCCCAAAGTGCTGGGA ATC CAGCACTTTGGGAGGC GA 	A			
GAM1399	MHC2TA	4189	3' TCAGCCTCCCAAAGTGCTGGGA ATC CAGCACTTTGGGAGGC GA 	A			
GAM1399	MHC2TA	4190	3' TCAGCCTCCCAAAGTGCTGGGA ATC CAGCACTTTGGGAGGC GA 	A			
GAM1399	MLANA	18589	3' TCAGCCTCCCAAAGTGCTGGA TC CAGCACTTTGGGAGGC GA 	A			
GAM1399	MTR	4219	3' TCAGCCTCCCAAATGCTGGGA ATC CAGCA TTTGGGAGGC GA 	A	C		
GAM1399	NDRG3	49306	3' TCAGCCTCCCAAAGTGCTGGGA ATC CAGCACTTTGGGAGGC GA 	A			
GAM1399	NONO	82024	3' TCGGCCTCCCAAATGCTGGGA ATC CAGCA TTTGGGAGGCCGA 	A	C		
GAM1399	NQO1	6167	3' TCAGCCTCCCAAAGTGCTGGGA ATC CAGCACTTTGGGAGGC GA 	A			

Accession	Gene	Strand	Sequence	Position	Start	End	Score
GAM1399	NT5C2	5'	TCGGCCTCCCAAAGTTCTGGGA	24242	A	C	
	T		ATC CAG ACTTTGGGAGGCCGA				
			TAG GTC TGAAACCCTCCGGCT				
			G T				
GAM1399	PAICS	3'	TCAGCCTCCCAAAGTGCTAGGG	21262	AC	C	
	T		ATC AGCACTTTGGGAGGC GA				
			TGG TCGTGAAACCCTCCG CT				
			GA A				
GAM1399	PCDHA9	3'	TCAGCCTCCCAAATGCTGGGA	25769	A	C	C
	T		ATC CAGCA TTTGGGAGGC GA				
			TAG GTCGT AAACCCTCCG CT				
			G A A				
GAM1399	PCDHA9	3'	TCGGCCTCCCAAAGTGCTGGGA	25772	A		
	T		ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT				
			G				
GAM1399	PCDHB11	3'	TCAGCCTCCCAAAGTGCTGGGA	38422	A	C	
	T		ATC CAGCACTTTGGGAGGC GA				
			TAG GTCGTGAAACCCTCCG CT				
			G A				
GAM1399	PCDHB11	3'	TCCCAAAGTGCTGTGAT	38425			
			ATCACAGCACTTTGGGA				
			TAGTGTCGTGAAACCCT				
GAM1399	PCDHB16	3'	TCAGCCTCCCAAATTCTGGGA	40556	A	CAC	C
	T		ATC CAG TTTGGGAGGC GA				
			TAG GTC AAACCCTCCG CT				
			G TTA A				
GAM1399	PER2	3'	TCGGCCTCCCAAAGTGCTGGGA	43047	A		
	T		ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT				
			G				
GAM1399	PIK3C2B	3'	CCAAAGGAGAGCGCTGTGATA	10562	A	_____	
			TATCACAGC CTTTGG				
			ATAGTGTGCG GAAACC				
			CGAGAG				
GAM1399	PPEF2	3'	TCAGCCTCCCAAAGTGCTGGGA	20676	A	C	
	T		ATC CAGCACTTTGGGAGGC GA				



			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	PRIM2A	3'	TCAGCCTCCCAAGTAGTTAGGA 6276	AC _ T C	
			TC AGC ACTT GGGAGGC GA		
			AG TTG TGAA CCCTCCG CT		
			GA A _ A		
GAM1399	PRKR	3'	TCGGCCTCCCAAAGTGCTGGGA 10888	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	PTGES	3'	TCGGCCTCCCAAAGTGCTGGGA 16865	A	
	TG		TATC CAGCACTTTGGGAGGCCGA		
			GTAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	PTGIS	3'	TCGGCCTCCCAAAGTGCTGGGA 6346	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	PTPN18	3'	TCAGCCTCCCAAAGTGCTGAGA 26870	A C	
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			A A		
GAM1399	RAB36	3'	TCGGCCTCCCAAAGTGCTGGGA 16977	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	RAB36	3'	TCGGCCTCCCAAAGTGCTGGGA 16978	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	RABL2A	3'	TCGGCCTCCCAAAGTGCTGGGA 25506	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	RABL2B	3'	TCGGCCTCCCAAAGTGCTGGGA 23007	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	RAD52	3'	CCAGCCATGCTGTGATA 56194	CTT GA	
			TATCACAGCA TGG GG		

			ATAGTGTCTG ACC CC	
			___ GA	
GAM1399	RAD52	3'	CCAGCCATGCTGTGATA 56202	CTT GA
			TATCACAGCA TGG GG	
			ATAGTGTCTG ACC CC	
			___ GA	
GAM1399	RAD52	3'	CCAGCCATGCTGTGATA 56211	CTT GA
			TATCACAGCA TGG GG	
			ATAGTGTCTG ACC CC	
			___ GA	
GAM1399	RBBP9	3'	TCAGCCTCCCAAGTAGTGTGA 70142	GC T C
			TCACA ACTT GGGAGGC GA	
			AGTGT TGAA CCCTCCG CT	
			GA _ A	
GAM1399	RGS9	5'	TCGGCCTCCCAAAGTGCTGGGA 13840	A
	T		ATC CAGCACTTTGGGAGGCCGA	
			TAG GTCGTGAAACCCTCCGGCT	
			G	
GAM1399	RHD	3'	TCGGCCTCCCAAAGTGCTGGA 32319	A
			TC CAGCACTTTGGGAGGCCGA	
			AG GTCGTGAAACCCTCCGGCT	
			—	
GAM1399	RHD	3'	TCGGCCTCCCAAAGTGCTGGGA 32320	A
	T		ATC CAGCACTTTGGGAGGCCGA	
			TAG GTCGTGAAACCCTCCGGCT	
			G	
GAM1399	RHD	3'	TCGGCCTCCCAAAGTGCTGGA 32628	A
			TC CAGCACTTTGGGAGGCCGA	
			AG GTCGTGAAACCCTCCGGCT	
			—	
GAM1399	RHD	3'	TCGGCCTCCCAAAGTGCTGGGA 32629	A
	T		ATC CAGCACTTTGGGAGGCCGA	
			TAG GTCGTGAAACCCTCCGGCT	
			G	
GAM1399	RPH3AL	3'	TCGGCCTCCCAAAGTGCTGGGA 22758	A
	T		ATC CAGCACTTTGGGAGGCCGA	
			TAG GTCGTGAAACCCTCCGGCT	
			G	
GAM1399	RPP30	3'	TCGGCCTCCCAAAGTGCTGGGA 21173	A
	T		ATC CAGCACTTTGGGAGGCCGA	

			TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	SCNN1G	3'	TCAGCCTCCCAAAGTGCAGGGA 6436	ACA	C
	T		ATC GCACTTTGGGAGGC GA		
			TAG CGTGAAACCCTCCG CT		
			GGA A		
GAM1399	SEDL	3'	TCAGCCTCCCAAAGTGCTAGGA 27361	AC	C
	T		ATC AGCACTTTGGGAGGC GA		
			TAG TCGTGAAACCCTCCG CT		
			GA A		
GAM1399	SEDL	3'	TCAGCCTCCCAAAGTGCTGGGA 27362	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	SEPN1	3'	TCAGCCTCCCAAAGTGCTGGGA 66380	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	SERPINB9	3'	TCAGCCTCCCAAAGTGCTAGGA 14765	AC	C
	T		ATC AGCACTTTGGGAGGC GA		
			TAG TCGTGAAACCCTCCG CT		
			GA A		
GAM1399	SERPINB9	3'	TCGGCCTCCCAAAGTGCTGGGA 14769	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	SIL	5'	TCGGCCTCCCAAATGCTGGGA 11699	A	C
	T		ATC CAGCA TTTGGGAGGCCGA		
			TAG GTCGT AAACCCTCCGGCT		
			G A		
GAM1399	SLC24A1	3'	TCGGCCTCCCAAAGTGCTGGGA 16380	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	SPN	3'	TCAGCCTCCCAAAGTGCTGAGA 11927	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			A A		
GAM1399	TAPBP	3'	TCAGCCTCCCAAAGTGCTGGGA 12135	A	C
	T		ATC CAGCACTTTGGGAGGC GA		

			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	TAPBP	3'	TCGGCCTCCCAAAGTGCTGGGA 12138	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	TBXA2R	3'	TCAGCCTCCCAAAGTGCTGGGA 6504	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	TERF1	3'	TCGGCCTCCCAAAGTGCTGAGA 33981	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			A		
GAM1399	TERF2	3'	TCGGCCTCCCAAAGTGCTGGGA 18950	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	TIM3	3'	TCGGCCTCCCAAAGCACTGGGA 51349	A	CA
	T		ATC CAG CTTTGGGAGGCCGA		
			TAG GTC GAAACCCTCCGGCT		
			G AC		
GAM1399	TNFRSF11A	3'	TCGGCCTCCCAAAGTACTGGGA 13856	A	C
	T		ATC CAG ACTTTGGGAGGCCGA		
			TAG GTC TGAAACCCTCCGGCT		
			G A		
GAM1399	TP53BP2	5'	TCGGCCTCCCAAAGTGCTGGAT 18303	A	
			ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			—		
GAM1399	TPMT	3'	TCGGCCTCCCAAAGTGCTGGGA 4547	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	TRAF5	3'	TCGGCCTCCCAAAGTGCTGAGA 16090	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			A		
GAM1399	TRPV1	3'	TCGGCCTCCCAAAGTGCTGGGA 54817	A	
	T		ATC CAGCACTTTGGGAGGCCGA		

			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	TRPV1	3'	TCGGCCTCCCAAAGTGCTGGGA 54849	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	TRPV1	3'	TCGGCCTCCCAAAGTGCTGGGA 54882	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	TRPV1	3'	TCGGCCTCCCAAAGTGCTGGGA 38099	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	UGDH	3'	TCGGCCTCCCAAAGTGCTGGGA 12547	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	VENTX2	3'	TCGGCCTCCCAAAGTGCTGGGA 27121	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	VHL	3'	TCAGCCTCCCAAATGGTGGGA 5086	A G C		C
	T		ATC CA CA TTTGGGAGGC GA			
			TAG GT GT AAACCCTCCG CT			
			G G A A			
GAM1399	VHL	3'	TCAGCCTCCCAAAGTGGTGGGA 5087	A G		C
	T		ATC CA CACTTTGGGAGGC GA			
			TAG GT GTGAAACCCTCCG CT			
			G G A			
GAM1399	VIPR2	3'	TCGGCCTCCCAAAGTGCTGGGA 12617	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	WHSC1	5'	TCAGCCTCCCAAAGTGCTGGGA 23667	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	WHSC1	5'	TCAGCCTCCCAAAGTGCTGGGA 29917	A		C
	T		ATC CAGCACTTTGGGAGGC GA			

			TAG GTCGTGAAACCCCTCCG CT			
			G A			
GAM1399	WHSC1	5'	TCAGCCTCCCAAAGTGCTGGGA 55835	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCCTCCG CT			
			G A			
GAM1399	WHSC1	5'	TCAGCCTCCCAAAGTGCTGGGA 55852	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCCTCCG CT			
			G A			
GAM1399	XKRY	3'	CCAGAAGCACTGTGATA 60016	CA	G	
			TATCACAG CTTT GG			
			ATAGTGTC GAAG CC			
			AC A			
GAM1399	XKRY	3'	CCAGAAGCACTGTGATA 16255	CA	G	
			TATCACAG CTTT GG			
			ATAGTGTC GAAG CC			
			AC A			
GAM1399	XRCC2	3'	TCGGCCTCCCAAAGTGCTAGGA 18331	AC		
	T		ATC AGCACTTTGGGAGGCCGA			
			TAG TCGTGAAACCCTCCGGCT			
			GA			
GAM1399	YES1	3'	TCGGCCTCCCAAAGTGCTGGGA 18358	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	ZNF133	5'	TCAGCCTCCCAAATGCTGGGA 12841	A	C	C
	T		ATC CAGCA TTTGGGAGGC GA			
			TAG GTCGT AAACCCTCCG CT			
			G A A			
GAM1399	ZNF138	5'	GCCTCTGTGGCGCTGTGAT 81187	A	TTG	
			ATCACAGC CT GGAGGC			
			TAGTGTCG GG TCTCCG			
			C TG_			
GAM1399	ZNF264	3'	TCGGCCCCCCAAAGTGCTGGGG 12766	A		A
	T		ATC CAGCACTTTGGG GGCCGA			
			TGG GTCGTGAAACCC CCGGCT			
			G C			
GAM1399	ZNF74	5'	TCGGCCTCCCAAAGTGCTGGGA 12805	A		
	T		ATC CAGCACTTTGGGAGGCCGA			

			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	APOL2	3'	TCGGCCTCCCAAAGTGCTGGGA 48055	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	ARHGAP11A	3'	TCAGCCTCCCAAAGTGCTGGGA 28801	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	ARHGAP5	5'	TCAGCCTCCCAAAGTGCTGCGA 77079	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			C A		
GAM1399	ARPP-19	3'	TCGGCCTCCCAAAGTGCTGGGA 21805	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	ASE-1	3'	TCCCAAAGTGCTAGGATA 23955	AC	
			TATC AGCACTTTGGGA		
			ATAG TCGTGAAACCCT		
			GA		
GAM1399	BAG5	3'	TCGGCCCCCCAAAGTGCTGGGA 16854	A	A
	T		ATC CAGCACTTTGGG GGCCGA		
			TAG GTCGTGAAACCC CCGGCT		
			G C		
GAM1399	BNIP-S	3'	TCGGCCTCCCAAAGTGCCGAGA 56269	ACA	
	T		ATC GCACTTTGGGAGGCCGA		
			TAG CGTGAAACCCTCCGGCT		
			AGC		
GAM1399	C13orf1	3'	TCAGCCTCCCAAAGTGCTGGA 39976	A	C
			TC CAGCACTTTGGGAGGC GA		
			AG GTCGTGAAACCCTCCG CT		
			— A		
GAM1399	C20orf142	3'	TCGGCCTCCCAAAGTGCTGGGA 74788	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	C22orf19	3'	TCGGCCTCCCAAAGTGCTAGGA 13436	AC	
	T		ATC AGCACTTTGGGAGGCCGA		

				TAG TCGTGAAACCCTCCGGCT		
				GA		
GAM1399	C6orf33	3'	TCAGCCTCCCAAAGTGTTGGGA	55888	A	C
	T		ATC CAGCACTTTGGGAGGC	GA		
			TAG GTTGTGAAACCCTCCG	CT		
			G	A		
GAM1399	C6orf5	3'	TCGGCCTCCCAAAGTGCTGGGA	31365	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	C9orf9	3'	TCGGCCTCCCAAAGTGCTGGGA	38530	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	C9orf9	3'	TCGGCCTCCCAAAGTGCTGGGA	38531	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	CEACAM8	3'	TCAGCCTCCCAAAGTTCTGGGA	8425	A C	C
	T		ATC CAG ACTTTGGGAGGC	GA		
			TAG GTC TGAAACCCTCCG	CT		
			G T	A		
GAM1399	CECR1	3'	TCGGCCTCCCAAAGCACTGGGA	33821	A CA	
	T		ATC CAG CTTTGGGAGGCCGA			
			TAG GTC GAAACCCTCCGGCT			
			G AC			
GAM1399	CENPH	3'	TCAGCCTCCCAAGTAGCTGTGA	43278	_ T	C
			TCACAGC ACTT GGGAGGC	GA		
			AGTGTGCG TGAA CCCTCCG	CT		
			A _	A		
GAM1399	CHRA1	3'	TCAGCCTCCCAAAGTGC	33878	C	
			GCACTTTGGGAGGC	GA		
			CGTGAAACCCTCCG	CT		
			A			
GAM1399	DKFZp434A2417	3'	TCGGCCTCCCAAAGTGCTGGGA	66110	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	DKFZP434J037	3'	TCGGCCTCCCAAAGTGCTGGGA	48221	A	
	T		ATC CAGCACTTTGGGAGGCCGA			



		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1399	DKFZp547H025 3'	TCAGCCTCCCAAAGTGCTGGGA	39365	A	C
	T	ATC CAGCACTTTGGGAGGC GA			
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1399	DKFZP564K0322 3'	TCGGCCTCCCAAATGCTGGGA	49364	A	C
	T	ATC CAGCA TTTGGGAGGCCGA			
		TAG GTCGT AAACCCTCCGGCT			
		G A			
GAM1399	DKFZP564O0523 3'	CGCCTCCCAAAGGGATG	49512	GCA	C
		CA CTTTGGGAGGC G			
		GT GAAACCCTCCG C			
		AGG A			
GAM1399	DKFZP566I1024 3'	TCGACCTCCCAAAGTGCTGGGA	70109	A	C
	T	ATC CAGCACTTTGGGAGG CGA			
		TAG GTCGTGAAACCCTCC GCT			
		G A			
GAM1399	DKFZp761N1114 3'	TCAGCCTCCCAAAGTAGCTGTGA	79026	_	T C
		TCACAGC ACTT GGGAGGC GA			
		AGTGTCG TGAA CCCTCCG CT			
		A _ A			
GAM1399	DKFZp761N1114 3'	TCGGCCTCCCAAAGTGCTGGGA	79028	A	
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1399	DRIM 3'	TCGGCCTCCCAAAGTGCTGGGA	27183	A	
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1399	EVI5 3'	TCAGCCTCCCAAAGTGCTGGGA	19011	A	C
	T	ATC CAGCACTTTGGGAGGC GA			
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1399	EVI5 3'	TCAGCCTCCCAAAGTGTGGGGA	19012	ACA	C
	T	ATC GCACTTTGGGAGGC GA			
		TAG TGTGAAACCCTCCG CT			
		GGG A			
GAM1399	FBP17 3'	TCAGCCTCCCAAAGTGCTGAGA	72805	A	C
	T	ATC CAGCACTTTGGGAGGC GA			

				TAG GTCGTGAAACCCTCCG CT		
				A A		
GAM1399	FBP17	3'	TCAGCCTCCCAAATAGCTGTGA 72807	AC	C	
	T		ATCACAGC TTTGGGAGGC GA			
			TAGTGTGCG AAACCCTCCG CT			
			AT A			
GAM1399	FKBP9	3'	TCGGCCTCCCAAAGTGTTGGGA 94070	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTTGTGAAACCCTCCGGCT			
			G			
GAM1399	FLJ00060	5'	TCGGCCTCCCAAAGTGCTGGGA 61105	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	FLJ10298	3'	TCGGCCTCCCAAAGTGCTGGGA 35994	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	FLJ10346	5'	TCGGCCTCCCAAAGTGCTGGGA 36049	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	FLJ10535	3'	TCAGCCTCCCAAAGTGCTGGGA 36250	A	C	
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	FLJ10560	3'	TCGGCCTCCCAAAGTGCTGGGA 36285	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	FLJ10607	3'	TCAGCCTCCCAAAGTGCTTGGA 77128	AC	C	
	TG		TATC AGCACTTTGGGAGGC GA			
			GTAG TCGTGAAACCCTCCG CT			
			GT A			
GAM1399	FLJ10687	3'	TCAGCCTCCCAAAGTGCTGAGA 36412	A	C	
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			A A			
GAM1399	FLJ10713	3'	TCAGCCTCCCAAATGCTGGGA 36473	A	C	C
			TC CAGCA TTTGGGAGGC GA			

		AG GTCGT AAACCCCTCCG CT		
		G A A		
GAM1399	FLJ10846	3' TCGGCCTCCCAAAGTGCTGGA 36743	A	
		TC CAGCACTTTGGGAGGCCGA		
		AG GTCGTGAAACCCTCCGGCT		
		—		
GAM1399	FLJ10956	3' TCAGCCTCCCAAAGTGCTGGGA 36919	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT		
		G A		
GAM1399	FLJ11186	3' TCAGCCTCCCAAAGTGTTGGGA 37147	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTTGTGAAACCCTCCG CT		
		G A		
GAM1399	FLJ12610	3' CCTCCCAAAGTGCTGGGAT 45511	A	
		ATC CAGCACTTTGGGAGG		
		TAG GTCGTGAAACCCTCC		
		G		
GAM1399	FLJ12747	3' TCGGCCTCCCAAAGTGCTGGGA 49727	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1399	FLJ12975	3' TCGGCCTCCCAAAGTGCTGGGA 69593	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1399	FLJ13072	5' TCAGCCTCCCAAAGTGCTGGGA 89827	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT		
		G A		
GAM1399	FLJ13197	3' TCAGCCTCCCAAAGTGCTGGGA 44863	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT		
		G A		
GAM1399	FLJ13993	3' GCCCCACACTGTGATG 60460	CACTT _ A	
		TATCACAG TG GG GGC		
		GTAGTGTC AC CC CCG		
		_____ A _		
GAM1399	FLJ14351	3' TCAGCCTCCCAAAGTGCTAGGA 45331	AC	C
	T	ATC AGCACTTTGGGAGGC GA		

			TAG TCGTGAAACCCTCCG CT		
			GA A		
GAM1399	FLJ14442	3'	TCGGCCTCCCAAAGTGCTGAGA 51377	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			A		
GAM1399	FLJ14950	3'	TCGGCCTCCCAAAGTGCTGGGA 51730	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	FLJ14957	3'	TCAGCCTCCCAAAGTGCTGAGA 51760	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			A A		
GAM1399	FLJ20097	3'	TCGGCCTCCCAAAGTGCTGGGA 34565	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	FLJ20136	3'	TCAGCCTCCCAAAGTGCTGGGA 34617	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	FLJ20342	3'	TCAGCCTCCCAAAGTGCTGGGA 34995	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	FLJ20344	3'	TCAGCCTCCCAAAGTGCTGGGA 35017	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	FLJ20699	3'	CCCAAAGTGCTGTGATG 35562		
			TATCACAGCACTTTGGG		
			GTAGTGTCGTGAAACCC		
GAM1399	FLJ20700	3'	TCAGCCTCCCAAAGTGCTGGGA 35586	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	FLJ20897	5'	TCGGCCTCCCAAAGTGTTGGGA 50470	A	
	T		ATC CAGCACTTTGGGAGGCCGA		

			TAG GTTGTGAAACCCTCCGGCT G			
GAM1399	FLJ21302	3'	TCGGCCTCCCAAAGTGCTGGGA 43223	A		
	T		ATC CAGCACTTTGGGAGGCCGA 			
			TAG GTCGTGAAACCCTCCGGCT G			
GAM1399	FLJ21777	3'	TCGACCTCCCAAAGCGTTAGGA 49866	AC A	C	
	T		ATC AGC CTTTGGGAGG CGA 			
			TAG TTG GAAACCCTCC GCT GA C A			
GAM1399	FLJ22002	3'	TCGGCCTCCCAAAGTGCTAGGA 45780	AC		
	T		ATC AGCACTTTGGGAGGCCGA 			
			TAG TCGTGAAACCCTCCGGCT GA			
GAM1399	FLJ22316	5'	TCGGCCTCCCAAAGTGCTGGGA 46924	A		
	T		ATC CAGCACTTTGGGAGGCCGA 			
			TAG GTCGTGAAACCCTCCGGCT G			
GAM1399	FLJ22800	3'	TCAGCCTCCTAAAGTGCTGCGA 45607	A	C	
	T		ATC CAGCACTTTGGGAGGC GA 			
			TAG GTCGTGAAATCCTCCG CT C A			
GAM1399	FLJ22969	3'	TCGGCCTCCCAAAGTGCTGGGA 68665	A		
	T		ATC CAGCACTTTGGGAGGCCGA 			
			TAG GTCGTGAAACCCTCCGGCT G			
GAM1399	FLJ23392	3'	TCAGCCTCCCAAAGTGCTGGGA 45546	A	C	
	T		ATC CAGCACTTTGGGAGGC GA 			
			TAG GTCGTGAAACCCTCCG CT G A			
GAM1399	FLJ23563	3'	TCGGCCTCCCAAAGTTCTGGGA 67602	A C		
	T		ATC CAG ACTTTGGGAGGCCGA 			
			TAG GTC TGAAACCCTCCGGCT G T			
GAM1399	FLJ30532	3'	TCAGCCTCCCAAAGTGTGGGA 58552	A	C	
	T		ATC CAGCACTTTGGGAGGC GA 			
			TAG GTTGTGAAACCCTCCG CT G A			
GAM1399	FLJ31153	3'	GCCTCCCAAAGCGCTGGGAT 58124	A A		
			ATC CAGC CTTTGGGAGGC 			

				TAG GTCG GAAACCCTCCG		
				G C		
GAM1399	FLJ32334	3'	TCGACCTCCCAAAGTGCTGGGA	57986	A	C
	T		ATC CAGCACTTTGGGAGG CGA			
			TAG GTCGTGAAACCCTCC GCT			
			G A			
GAM1399	FLJ32865	3'	TCAGCCTCCCAAAGTGCTGGGA	58183	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	FLJ32894	3'	TCAGCCTCCCAAAGTGCTGGGA	58341	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	GNG4	3'	TCGGCCTCCCAAAGCGCTGGGA	15626	A A	
	T		ATC CAGC CTTTGGGAGGCCGA			
			TAG GTCG GAAACCCTCCGGCT			
			G C			
GAM1399	GOLGA3	3'	TCAGCCTCCCAAAGTGCTGGA	19721	A	C
			TC CAGCACTTTGGGAGGC GA			
			AG GTCGTGAAACCCTCCG CT			
			— A			
GAM1399	GREB1	3'	TCGGCCTCCCAAAGTGCTGGGA	27889	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	GTF2E1	3'	TCGGCCTCCCAAAGTGCTGT	18620		
			ACAGCACTTTGGGAGGCCGA			
			TGTCGTGAAACCCTCCGGCT			
GAM1399	HARS2	3'	TCGGCCTCCCAAAGTGCTGGGA	55039	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	HSMPP8	3'	TCGGCCTCCCAAAGTGCTTGA	93485	AC	
	T		ATC AGCACTTTGGGAGGCCGA			
			TAG TCGTGAAACCCTCCGGCT			
			GT			
GAM1399	HSNOV1	3'	CGACCTCCCAAAGTGCTGGGAT	34007	A	C
			ATC CAGCACTTTGGGAGG CG			

			TAG GTCGTGAAACCCTCC GC		
			G A		
GAM1399	HT002	3'	CGGCCTCCACAGCTGTGA 25937	ACTT _	
			TCACAGC TG GGAGGCCG		
			AGTGTCG AC CCTCCGGC		
			_____ A		
GAM1399	HT002	3'	CGGCCTCCCAAATCGCT 25938	AC	
			AGC TTTGGGAGGCCG		
			TCG AAACCCTCCGGC		
			CT		
GAM1399	KIAA0087	3'	TCGGCCTCCCAAATGCTGGGA 28706	A C	
	T		ATC CAGCA TTTGGGAGGCCGA		
			TAG GTCGT AAACCCTCCGGCT		
			G A		
GAM1399	KIAA0210	5'	TCAGCCTCCCAAAGTGCTGGGA 28486	A C	
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	KIAA0391	3'	TCAGCCTCCCAAAGTGCTGGGA 27922	A C	
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	KIAA0459	3'	TCAGCCTCCCAAAGTGCTAGGA 61006	AC C	
	T		ATC AGCACTTTGGGAGGC GA		
			TAG TCGTGAAACCCTCCG CT		
			GA A		
GAM1399	KIAA0469	3'	TCAGCCTCCCAAAGTGCTAGGA 29352	AC C	
	T		ATC AGCACTTTGGGAGGC GA		
			TAG TCGTGAAACCCTCCG CT		
			GA A		
GAM1399	KIAA0469	3'	TCAGCCTCCCAAAGTGCTGGGA 29353	A C	
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	KIAA0472	5'	GCCTCCCAAAGTGCTGGGAT 71865	A	
			ATC CAGCACTTTGGGAGGC		
			TAG GTCGTGAAACCCTCCG		
			G		
GAM1399	KIAA0513	3'	TCAGCCTCCCAAAGTGCTGGGA 28374	A C	
	T		ATC CAGCACTTTGGGAGGC GA		

			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	KIAA0513	5'	TCGGCCTCCCAAAGTGTTGGGA 28377	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTTGTGAAACCCTCCGGCT		
			G		
GAM1399	KIAA0555	3'	TCAGCCTCCCAAAGTGCTAGGA 28887	AC	C
	T		ATC AGCACTTTGGGAGGC GA		
			TAG TCGTGAAACCCTCCG CT		
			GA A		
GAM1399	KIAA0557	3'	TCGGCCTCCCAAAGTGCTGGGA 78010	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	KIAA0563	5'	TCGGCCTCCCAAAGTTCTGGGA 29194	A C	
	T		ATC CAG ACTTTGGGAGGCCGA		
			TAG GTC TGAAACCCTCCGGCT		
			G T		
GAM1399	KIAA0594	3'	TCAGCCTCCCAAGTAAGTGGGA 64903	A CAC	C
			TC CAG TTTGGGAGGC GA		
			AG GTC GAACCCTCCG CT		
			G AAT A		
GAM1399	KIAA0594	3'	TCGGCCTCCCAAAGTGCTGGGA 64905	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	KIAA0599	3'	TCGGCCTCCCAAAGTGCTGGGA 77193	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	KIAA0682	3'	TCGGCCTCCCAAAGTGTTGGGGA 29373	ACA	
	T		ATC GCACTTTGGGAGGCCGA		
			TAG TGTGAAACCCTCCGGCT		
			GGG		
GAM1399	KIAA0798	3'	TCAGCCTCCCAAAGTGCTGGGA 27729	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	KIAA0831	5'	TCCCAAAGTGCTGCGAT 29982	A	
			ATC CAGCACTTTGGGA		



Accession	Gene	Position	Sequence	Start	End	Strand	Quality	Flags
GAM1399	KIAA0841	3'	TCGGCCTCCCAAAGTGCTGGGA	71403		A		
	T		ATC CAGCACTTTGGGAGGCCGA					
			TAG GTCGTGAAACCCTCCGGCT					
			G					
GAM1399	KIAA0861	3'	TCGGCCTCCCAAAGTGCTGGGA	88935		A		
	T		ATC CAGCACTTTGGGAGGCCGA					
			TAG GTCGTGAAACCCTCCGGCT					
			G					
GAM1399	KIAA0931	3'	TCCCAAAGTGCTGTGAT	67425				
			ATCACAGCACTTTGGGA					
			TAGTGTCGTGAAACCCT					
GAM1399	KIAA1054	3'	TCAGCCTCCCAAATGCTGGGA	68451		A	C	C
	T		ATC CAGCA TTTGGGAGGC GA					
			TAG GTCGT AAACCCTCCG CT					
			G A A					
GAM1399	KIAA1143	3'	TCGGCCTCCCAAAGTGCTGGGA	68690		A		
	T		ATC CAGCACTTTGGGAGGCCGA					
			TAG GTCGTGAAACCCTCCGGCT					
			G					
GAM1399	KIAA1155	3'	TCAGCCTCCCAAAGTGCTGGGA	62242		A		C
	T		ATC CAGCACTTTGGGAGGC GA					
			TAG GTCGTGAAACCCTCCG CT					
			G A					
GAM1399	KIAA1185	3'	TCAGCCTCCCAAAGTGCTGGGA	62608		A		C
	T		ATC CAGCACTTTGGGAGGC GA					
			TAG GTCGTGAAACCCTCCG CT					
			G A					
GAM1399	KIAA1193	3'	TCGGCCTCCCAAAGTGCTGGGA	67651		A		
	T		ATC CAGCACTTTGGGAGGCCGA					
			TAG GTCGTGAAACCCTCCGGCT					
			G					
GAM1399	KIAA1198	3'	TCGGCCTCCCAAAGTGCTGGGA	63338		A		
	T		ATC CAGCACTTTGGGAGGCCGA					
			TAG GTCGTGAAACCCTCCGGCT					
			G					
GAM1399	KIAA1198	3'	TCGGCCTCCCAAAGTGCTGGGA	63339		A		
	T		ATC CAGCACTTTGGGAGGCCGA					

				TAG GTCGTGAAACCCTCCGGCT			
				G			
GAM1399	KIAA1210	3'	TCAGCCTCCCAAAGCTGGGAT	96335	A	AC	C
			ATC CAGC TTTGGGAGGC GA				
			TAG GTCG AAACCCTCCG CT				
			G A_ A				
GAM1399	KIAA1257	3'	TCAGCCTCCCAAAGTGCTGGGA	62759	A		C
	T		ATC CAGCACTTTGGGAGGC GA				
			TAG GTCGTGAAACCCTCCG CT				
			G A				
GAM1399	KIAA1280	5'	TCAGCCTCCCAAAGTTC TGAGA	69732	A	C	C
	TG		TATC CAG ACTTTGGGAGGC GA				
			GTAG GTC TGAAACCCTCCG CT				
			A T A				
GAM1399	KIAA1320	5'	TCGGCCTCCCAAAGTGCTGGGA	69312	A		
	T		ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT				
			G				
GAM1399	KIAA1328	5'	TCGGCCTCCCAAAGTGCTGGGA	61656	A		
	T		ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT				
			G				
GAM1399	KIAA1571	3'	TCAGCCTCCCAAAGTGCTGGGA	60962	A		C
	T		ATC CAGCACTTTGGGAGGC GA				
			TAG GTCGTGAAACCCTCCG CT				
			G A				
GAM1399	KIAA1615	3'	TCAGCCTCCCAAAGTGCTGGGA	68731	A		C
	T		ATC CAGCACTTTGGGAGGC GA				
			TAG GTCGTGAAACCCTCCG CT				
			G A				
GAM1399	KIAA1615	3'	TCGGCCTCCCAAAGTGCTGGGA	68736	A		
	T		ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT				
			G				
GAM1399	KIAA1655	3'	TCAGCCTCCCAAAGTGCTGGGA	66626	A		C
	T		ATC CAGCACTTTGGGAGGC GA				
			TAG GTCGTGAAACCCTCCG CT				
			G A				
GAM1399	KIAA1671	3'	TCAGCCTCCCAAAGTGCTCGGA	65693	AC		C
	T		ATC AGCACTTTGGGAGGC GA				

				TAG TCGTGAAACCCTCCG CT		
				GC A		
GAM1399	KIAA1671	3'	TCAGCCTCCCAAAGTGCTGGGA 65694	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	KIAA1727	3'	TCAGCCTCCCAAAGTGCTGGGA 64066	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	KIAA1737	3'	TCAGCCTCCCAAAGTGCTG 67364			C
			CAGCACTTTGGGAGGC GA			
			GTCGTGAAACCCTCCG CT			
			A			
GAM1399	KIAA1755	3'	TCAGCCTCCCAAAGTGCTGGGA 61355	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	KIAA1789	5'	TCACAAAGCCTGTGATA 67104	CA		G
			TATCACAG CTTTG GA			
			ATAGTGTC GAAAC CT			
			C_ A			
GAM1399	KIAA1877	3'	TCGGCCTCCCAAAGTGATGGGA 66178	A		G
	T		ATC CA CACTTTGGGAGGCCGA			
			TAG GT GTGAAACCCTCCGGCT			
			G A			
GAM1399	KIAA1924	3'	TCAGCCTCCCAAAGTGCTGGGA 73688	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	LAMP3	3'	TCAGCCTCCCAAAGTGCTGGGA 59495	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	LY75	3'	TCGGCCTCCCAAAGTGCTGGGA 9844	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	MARCKS	3'	TCAACCAAGCTGTGATA 9872	ACT		GA
			TATCACAGC TTGG GG			

ATAGTGTCTG AACCTCT

\_\_\_ AA

GAM1399	MCLC	3'	TCGGCCTCCCAAAGTGCTGGGA	30694	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	MEF-2	3'	TCGGCCTCCCAAATCCTGGGA	64397	A	CAC
	T		ATC CAG TTTGGGAGGCCGA			
			TAG GTC AAACCCTCCGGCT			
			G CTA			
GAM1399	MGC10200	3'	TCAGCCTCCCAAAGTGCTGGGA	58994	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	MGC10911	5'	TCGGCCTCCCAAAGTGCCGGGA	50212	ACA	
	TG		TATC GCACTTTGGGAGGCCGA			
			GTAG CGTGAAACCCTCCGGCT			
			GGC			
GAM1399	MGC10955	5'	CCTCCCACTGCCATGGTA	51045	CA	CTT
			TATCA GCA TGGGAGG			
			ATGGT CGT ACCCTCC			
			AC C__			
GAM1399	MGC12518	3'	TCAGCCTCCCAAAGTGCTGGGA	64085	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	MGC1842	3'	TCGGCCTCCCAAAGTG	65660		
			CACTTTGGGAGGCCGA			
			GTGAAACCCTCCGGCT			
GAM1399	MGC21738	3'	TCAGCCTCCCAAAGTGCTGGGA	58918	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	MGC2477	5'	TCGGCCTCCCAAAGTGCTGGGA	44070	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	MGC2603	3'	TCAGCCTCCCAAAGTGCTGAGA	43862	A	C
	T		ATC CAGCACTTTGGGAGGC GA			

				TAG GTCGTGAAACCCTCCG CT		
				A A		
GAM1399	MGC26914	3'	GCCTCCCAAACCATGAGA	58666	A GCAC	
			TC CA TTTGGGAGGC			
			AG GT AAACCCTCCG			
			A ACC_			
GAM1399	MGC4415	3'	GCCTCCGGTGCTGT	48951	TTG	
			ACAGCACT GGAGGC			
			TGTCGTGG CCTCCG			
GAM1399	MLZE	5'	TCAGCCTCCCAAAGTGCTGGGA	48627	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	moblak	3'	TCAGCCTCCCAAAGTGCTGGGA	55512	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	moblak	3'	TCGGCCTCCCAAAGTGCTGGA	55515	A	
			TC CAGCACTTTGGGAGGCCGA			
			AG GTCGTGAAACCCTCCGGCT			
GAM1399	MRPS27	3'	TCAGCCTCCCAAAGTGCTGGGA	30644	A	C
	TG		TATC CAGCACTTTGGGAGGC GA			
			GTAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	MtFMT	3'	TCAGCCTCCCAAAGTGCTATGA	57659	C	C
	T		ATCA AGCACTTTGGGAGGC GA			
			TAGT TCGTGAAACCCTCCG CT			
			A A			
GAM1399	MYO5C	3'	TCAGCCTCCCAAAGTGCTAGGA	38111	AC	C
	T		ATC AGCACTTTGGGAGGC GA			
			TAG TCGTGAAACCCTCCG CT			
			GA A			
GAM1399	NINJ2	3'	TCGGCCTCCCAAAGTGCTGGGA	33289	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	Nup43	3'	TCAGCCTCCCAAATGCTGGGA	45008	A C	C
	T		ATC CAGCA TTTGGGAGGC GA			

			TAG GTCGT AAACCCTCCG CT G    A    A		
GAM1399	Nup43	3'	TCGGCCTCCAAAGTGCTGTGAT 45010 ATCACAGCACTTTGG AGGCCGA       TAGTGTGCTGAAACC TCCGGCT	G	
GAM1399	NXN	3'	TCGGCCTCCCAAAGTGCTGGGA 42426 ATC CAGCACTTTGGGAGGCCGA           TAG GTCGTGAAACCCTCCGGCT G	A	
GAM1399	OR51E2	3'	TCAGCCTCCCAAAGTGTTGGGA 47799 ATC CAGCACTTTGGGAGGC GA           TAG GTTGTGAAACCCTCCG CT G            A	A	C
GAM1399	OSBPL2	3'	CCTCCCAAAGTGCTGGGAT 29208 ATC CAGCACTTTGGGAGG           TAG GTCGTGAAACCCTCC G	A	
GAM1399	OSBPL2	3'	CCTCCCAAAGTGCTGGGAT 57859 ATC CAGCACTTTGGGAGG           TAG GTCGTGAAACCCTCC G	A	
GAM1399	PEL1	5'	TCGACCTCCCAAAGTGCTGGGA 40290 ATC CAGCACTTTGGGAGG CGA           TAG GTCGTGAAACCCTCC GCT G            A	A	C
GAM1399	PP2447	5'	TCAGCCTCCCAAAGTGCTGGGA 47321 TATC CAGCACTTTGGGAGGC GA           GTAG GTCGTGAAACCCTCCG CT G            A	A	C
GAM1399	PPIL3	5'	TCGGCCTCCCAAAGTGTTAGGA 55661 ATC AGCACTTTGGGAGGCCGA           TAG TTGTGAAACCCTCCGGCT GA	AC	
GAM1399	PRO0245	5'	GCCTCCCAAAGTGCTGAGAT 26129 ATC CAGCACTTTGGGAGGC           TAG GTCGTGAAACCCTCCG A	A	
GAM1399	PRO0365	5'	CCTTCCAAAATGCTGCGAT 26156 ATC CAGCA TTTGGGAGG 	A	C

			TAG GTCGT AAACCTTCC		
			C A		
GAM1399	PRO0365	5'	TCGGCCTCCCAAAGTGCTGGGA 26172	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	PRO0899	5'	TCGGCCTCCCAAAGTGCTGGGG 37697	A	
			TC CAGCACTTTGGGAGGCCGA		
			GG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	PRO2955	3'	TCGGCCTCCCAAAGTGCTGGGA 37649	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	PSPH	3'	TCAGCCTCCCAAAGTGCTGGGA 15917	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	PSTPIP2	3'	TCGGCCTCCCAAAGTGCTGGGA 44400	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	RAB21	3'	TCGGCCTCCCAAAGTGCTGGGA 30392	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	RAI	5'	CGGCCTCCCAAAGTTCTGGGAT 21876	A C	
			ATC CAG ACTTTGGGAGGCCG		
			TAG GTC TGAAACCCTCCGGC		
			G T		
GAM1399	RAP140	3'	TCAGCCTCCCAAAGTGCTGGGA 30847	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	RNO2	5'	TCAGCCTCCCAAAGTGCTGGGA 52777	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	SCAMP-4	3'	TCCCAAAGTGCTGGGATA 54401	A	
			TATC CAGCACTTTGGGA		

			ATAG GTCGTGAAACCCT		
			G		
GAM1399	SCYA22	3'	TCAGCCTCCCAAAGTGCTGGGA 90956	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	SCYA22	3'	TCAGCCTCCCAAAGTGCTGGGA 90957	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	SERF1B	3'	TCGGCCTCCCAAAGTGCTGGGA 43426	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	SFRS10	3'	GGTGCTTCAAAGTACATGATA 15978	CAGC	AG
			TATCA ACTTTGGG GCC		
			ATAGT TGAACTT TGG		
			ACA_ CG		
GAM1399	SLC12A8	3'	TCAGCCTCCCAAAGTACTGGGA 44904	A C	C
	T		ATC CAG ACTTTGGGAGGC GA		
			TAG GTC TGAAACCCTCCG CT		
			G A A		
GAM1399	SLC19A3	3'	TCGGCCTCCCAAAGAGCTGAGA 47497	A A	
			TC CAGC CTTTGGGAGGCCGA		
			AG GTCG GAAACCCTCCGGCT		
			A A		
GAM1399	SMCR7	3'	CGGCCTCCCAGTGTGC 57507	T	
			GCAC TTGGGAGGCCG		
			CGTG GACCCTCCGGC		
			T		
GAM1399	SNAPC1	3'	TCAGCCTCCCAAAGTACTGGGA 11845	A C	C
	T		ATC CAG ACTTTGGGAGGC GA		
			TAG GTC TGAAACCCTCCG CT		
			G A A		
GAM1399	SQV7L	5'	TCCCAAAGTGCTGTGAT 70580		
			ATCACAGCACTTTGGGA		
			TAGTGTCGTGAAACCCT		
GAM1399	SRP54	3'	TCAATTAAAGTGCTGT 11962	GA	
			ACAGCACTTTGG GG		



TGTCGTGAAATT CT

AA

GAM1399	SUN1	3'	TCGGCCTCCCAAAGTGCTGTTG	47163	_
	G		TCA CAGCACTTTGGGAGGCCGA		
			GGT GTCGTGAAACCCTCCGGCT		
			T		
GAM1399	SYT13	3'	TCGGCCTCCCAAAGTACTGGGA	93460	A C
	T		ATC CAG ACTTTGGGAGGCCGA		
			TAG GTC TGAAACCCTCCGGCT		
			G A		
GAM1399	SYTL4	5'	TCAGCCTCCCAAAGTGCTGGGA	54945	A C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	TADA3L	3'	TCGGCCTCCCAAAGTGCCGGGA	56000	ACA
	T		ATC GCACTTTGGGAGGCCGA		
			TAG CGTGAAACCCTCCGGCT		
			GGC		
GAM1399	TCL6	5'	TCGGCCTCCCAAAGTGCTGGGA	27008	A
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	TCL6	3'	TCGGCCTCCCAAAGTGCTGGGA	27009	A
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	TCL6	5'	TCGGCCTCCCAAAGTGCTGGGA	24992	A
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	TCL6	3'	TCGGCCTCCCAAAGTGCTGGGA	24993	A
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	TCL6	5'	TCGGCCTCCCAAAGTGCTGGGA	40090	A
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	TCL6	5'	TCGGCCTCCCAAAGTGCTGGGA	40116	A
	T		ATC CAGCACTTTGGGAGGCCGA		

			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	TRIM16	3'	TCGGCCTCCCAAAGTGCTGGGA 21345	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	TRIM5	3'	TCGGCCTCCCAAAGTGCTGGGA 52305	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	TRIM5	3'	TCGGCCTCCCAAAGTGCTGGGA 52369	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	TUCAN	3'	TCAGCCTCCCAAAGTGCTGGGA 30283	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G            A		
GAM1399	TUSP	3'	TCGGCCTCCCAAAGTGCTGGGA 39643	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	TXNL2	3'	TCAGCCTCCCAAAGTGCTGGA 21553	A	C
			TC CAGCACTTTGGGAGGC GA		
			AG GTCGTGAAACCCTCCG CT		
			—            A		
GAM1399	VDU1	3'	TCGGCCTCCCAAAGTGCTGGGA 30430	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	YAP	5'	CCTCCCAAAGTGCTGGA 36785	A	
			TC CAGCACTTTGGGAGG		
			AG GTCGTGAAACCCTCC		
			—		
GAM1399	ZNF338	3'	TCAGCCTCCCAAAGTGCTGGGA 42016	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G            A		
GAM1399	LOC112687	3'	TCAGCCTCCCAAAGTGCTGGGA 72867	A	C
	T		ATC CAGCACTTTGGGAGGC GA		

		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1399	LOC112817 3'	TCGGCCTCCCAAAGTGCTGGGA 56518	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC115098 5'	TCAGCCTCCCAAAGCACGGGGA 56595	ACAGCA	C
	T	ATC    CTTTGGGAGGC GA 		
		TAG    GAAACCCTCCG CT GGGCAC        A		
GAM1399	LOC126272 3'	TCGGCCTCCCAAAGTGCTGGGA 76091	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC128077 3'	TCAGCCTCCCAAAGTGCTGGGA 74722	A	C
	T	ATC CAGCACTTTGGGAGGC GA 		
		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1399	LOC128989 3'	TCGGCCTCCCAAAGTGCTGGGA 74819	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC130813 3'	TCAGCCTCCCAAAGTGCTGGGA 75778	A	C
	T	ATC CAGCACTTTGGGAGGC GA 		
		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1399	LOC132625 3'	TCGGCCTCCCAAAGTGCTGGGA 75916	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC135154 3'	TCAGCCTCCCAAAGTGCTGGGA 75222	A	C
	T	ATC CAGCACTTTGGGAGGC GA 		
		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1399	LOC144305 3'	TCGGCCTCCCAAAGTGTTGGGA 83037	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTTGTGAAACCCTCCGGCT G		
GAM1399	LOC144317 5'	TCGGCCTCCCAAAGTGCTGGGA 76801	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		

		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC144524 5'	TCGGCCTCCCAAAGTGCTGGGA 83139	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC145009 3'	TCGGCCTCCCAAAGTGCTGGGA 60352	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC145622 3'	TCAGCCTCCCAAAGTGCTGGGA 77313	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1399	LOC146050 3'	TCGGCCTCCCAAAGTGCTGGGA 77652	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC146455 3'	TCAGCCTCCCAAATGCTGGGA 77909	A	C
	T	ATC CAGCA TTTGGGAGGC GA		
		TAG GTCGT AAACCCTCCG CT G    A        A		
GAM1399	LOC146599 5'	TCAGCCTCCCAAAGTGCTAGGA 78028	AC	C
	T	ATC AGCACTTTGGGAGGC GA		
		TAG TCGTGAAACCCTCCG CT GA            A		
GAM1399	LOC146603 5'	TCGGCCTCCCAAAGTGTTGGGA 78021	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTTGTGAAACCCTCCGGCT G		
GAM1399	LOC146784 5'	TCGGCCTCCCAAAGTGCTGGGA 78127	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC146909 3'	TCGGCCTCCCAAAGTGCTGGGA 78187	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC147071 5'	TCGGCCTCCCAAAGTTCTGGGA 73008	A	C
	T	ATC CAG ACTTTGGGAGGCCGA		

		TAG GTC TGAAACCCTCCGGCT G T		
GAM1399	LOC147080 5'	TCGGCCTCCCAAAGTGCTGGGA 83939	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC147160 5'	TCAGCCTCCCAAAGTGCTGGGA 83972	A	C
	T	ATC CAGCACTTTGGGAGGC GA 		
		TAG GTCGTGAAACCCTCCG CT G A		
GAM1399	LOC147166 3'	TCGGCCTCCCAAAGTGCTGGGA 78292	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC147990 3'	TCAGCCTCCCAAAGTGCTGGGA 84101	A	C
	T	ATC CAGCACTTTGGGAGGC GA 		
		TAG GTCGTGAAACCCTCCG CT G A		
GAM1399	LOC148137 3'	TCGGCCTCCCAAAGTGCTGGGA 58442	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC148887 5'	TCGGCCTCCCAAAGTGCTGGGA 84249	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC148918 5'	TCAGCCTCCCAAATGCTTCGA 79084	AC	C C
	T	ATC AGCA TTTGGGAGGC GA 		
		TAG TCGT AAACCCTCCG CT CT A A		
GAM1399	LOC149421 3'	TCAGCCTCCCAAAGTGCTGGGA 79363	A	C
	T	ATC CAGCACTTTGGGAGGC GA 		
		TAG GTCGTGAAACCCTCCG CT G A		
GAM1399	LOC149478 3'	TCGGCCTCCCAAAGTGCTGGGA 79384	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC149577 3'	TCGGCCTCCCAAATGCTGGGA 84523	A	C
	T	ATC CAGCA TTTGGGAGGCCGA 		

		TAG GTCGT AAACCCTCCGGCT G A		
GAM1399	LOC149692 3'	TCGGCCTCCCAAAGTGCTG 84595 CAGCACTTTGGGAGGCCGA       GTCGTGAAACCCTCCGGCT		
GAM1399	LOC149703 5'	TCAGCCTCCCAAAGTGCTGGGA 84659 T ATC CAGCACTTTGGGAGGC GA           TAG GTCGTGAAACCCTCCG CT G A	A	C
GAM1399	LOC150212 5'	TCAGCCTCCCAAAGTGCTGGA 79707 TC CAGCACTTTGGGAGGC GA          AG GTCGTGAAACCCTCCG CT — A	A	C
GAM1399	LOC150225 3'	TCAGCCTCCCAAAGTGCTGGGA 85012 T ATC CAGCACTTTGGGAGGC GA           TAG GTCGTGAAACCCTCCG CT G A	A	C
GAM1399	LOC150282 5'	TCAGCCCCCAAAGTGCTGGGA 79732 T ATC CAGCACTTTGGG GGC GA                  TAG GTCGTGAAACCC CCG CT G C A	A	A C
GAM1399	LOC150290 3'	TCAGCCTCCCAAAGTGTTGATG 79778 A TCA CAGCACTTTGGGAGGC GA           AGT GTTGTGAAACCCTCCG CT A A	—	C
GAM1399	LOC150407 3'	TCAGCCTCCCAAAGTACTGGGA 79831 T ATC CAG ACTTTGGGAGGC GA                  TAG GTC TGAAACCCTCCG CT G A A	A C	C
GAM1399	LOC150407 3'	TCAGCCTCCCAAAGTGCTGGGA 79832 T ATC CAGCACTTTGGGAGGC GA           TAG GTCGTGAAACCCTCCG CT G A	A	C
GAM1399	LOC150587 3'	TCGGCCTCCCAAAGTGCATGA 85067 TCA GCACTTTGGGAGGCCGA           AGT CGTGAAACCCTCCGGCT A_	CA	
GAM1399	LOC150630 5'	TCAGCCTCCCAAAGTGCTGGGA 85113 T ATC CAGCACTTTGGGAGGC GA 	A	C

		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1399	LOC150960 3'	TCAGCCTCCCAAGTAGCTGGGA 80071 TC CAGC ACTT GGGAGGC GA                     AG GTCG TGAA CCCTCCG CT G   A   _   A	A	_ T C
GAM1399	LOC150960 3'	TCGGCCTCCCAAAGTGCTGT 80074 ACAGCACTTTGGGAGGCCGA       TGTCGTGAAACCCTCCGGCT		
GAM1399	LOC151201 3'	TCGGCCTCCCAAAGTAGTGGA 85294 T            ATC GC ACTTTGGGAGGCCGA              TAG TG TGAAACCCTCCGGCT GG_ A	ACA	_
GAM1399	LOC151475 5'	TCGGCCTCCCAAAGTGCTGGGA 85422 T            ATC CAGCACTTTGGGAGGCCGA           TAG GTCGTGAAACCCTCCGGCT G	A	
GAM1399	LOC151484 3'	GCCTCCACCTGTGA 80264 TCACAG TGGGAGGC             AGTGTC ACCCTCCG C____	CACTT	
GAM1399	LOC151826 3'	TCGGCCTCCCAAAGTGCTGGGA 80369 T            ATC CAGCACTTTGGGAGGCCGA           TAG GTCGTGAAACCCTCCGGCT G	A	
GAM1399	LOC151979 5'	TCGGCCTCCCAAAGTGCTGGGA 80427 T            ATC CAGCACTTTGGGAGGCCGA           TAG GTCGTGAAACCCTCCGGCT G	A	
GAM1399	LOC152348 3'	TCAGCCTCCCAAAGTGCTGGGA 85699 T            ATC CAGCACTTTGGGAGGC GA                  TAG GTCGTGAAACCCTCCG CT G            A	A	C
GAM1399	LOC152445 3'	TCAGCCTCCCAAATGTTGAGA 85762 T            ATC CAGCA TTTGGGAGGC GA                    TAG GTTGT AAACCCTCCG CT A   A   A	A	C C
GAM1399	LOC152445 3'	TCGGCCTCCCAAAGTGCTGGGA 85764 T            ATC CAGCACTTTGGGAGGCCGA 	A	

		TAG GTCGTGAAACCCTCCGGCT G			
GAM1399	LOC153077 3'	TCGGCCTCCCAAAGTGCTGGGT 85919 ATC CAGCACTTTGGGAGGCCGA           TGG GTCGTGAAACCCTCCGGCT	A		
GAM1399	LOC153883 5'	TCAGCCTCCCAAATGCTTGA 80987 T ATC AGCA TTTGGGAGGC GA           TAG TCGT AAACCCTCCG CT GT A A	AC	C	C
GAM1399	LOC154007 3'	TCAGCCTCCCAAATGCTGGGA 81022 TC CAGCA TTTGGGAGGC GA          AG GTCGT AAACCCTCCG CT G A A	A	C	C
GAM1399	LOC154141 5'	TCGGCCTCCCAAAGTGCTGGGA 86175 T ATC CAGCACTTTGGGAGGCCGA           TAG GTCGTGAAACCCTCCGGCT G	A		
GAM1399	LOC154282 5'	TCAGCCTCCCAAAGTGCTGGGA 86209 T ATC CAGCACTTTGGGAGGC GA           TAG GTCGTGAAACCCTCCG CT G A	A		C
GAM1399	LOC154726 5'	TCAGCCTCCCAAAGTGCTGGGA 81108 T ATC CAGCACTTTGGGAGGC GA           TAG GTCGTGAAACCCTCCG CT G A	A		C
GAM1399	LOC154877 3'	TCAGCCTCCCAAAGTCCTGGGA 86310 T ATC CAG ACTTTGGGAGGC GA           TAG GTC TGAAACCCTCCG CT G C A	A	C	C
GAM1399	LOC154877 3'	TCGGCCTCCCAAAGTGCTGGAT 86315 ATC CAGCACTTTGGGAGGCCGA           TAG GTCGTGAAACCCTCCGGCT	A		
GAM1399	LOC154877 5'	TCGGCCTCCCAAAGTTCTGGGA 86316 T ATC CAG ACTTTGGGAGGCCGA           TAG GTC TGAAACCCTCCGGCT G T	A	C	
GAM1399	LOC154930 3'	TCCCAAAGTGCTGGAATA 81182 TAT CAGCACTTTGGGA 	CA		



		ATA GTCGTGAAACCCT		
		AG		
GAM1399	LOC157247 5'	TCGGCCTCCCAAAGTGCTGGGA	81379	A
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1399	LOC157506 3'	TCGGCCTCCCAAAGTGCTGGGA	81447	A
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1399	LOC157507 5'	TCAGCCTCCCAAAGTGCTGGGA	81461	A C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT		
		G A		
GAM1399	LOC157681 5'	TCGGCCTCCCAAAGTGCTGGGA	81546	A
		TC CAGCACTTTGGGAGGCCGA		
		AG GTCGTGAAACCCTCCGGCT		
		G		
GAM1399	LOC158014 5'	CGCCTCCCAAAGGGCT	81646	A C
		AGC CTTTGGGAGGC G		
		TCG GAAACCCTCCG C		
		G A		
GAM1399	LOC158476 3'	TCGGCCTCCCAAAGTGCTGGGA	86856	A
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1399	LOC158549 5'	TCGGCCTCCCAAAGTGTTGGGA	86868	A
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTTGTGAAACCCTCCGGCT		
		G		
GAM1399	LOC158709 3'	TCAGCCTCCCAAAGTGCTGGGA	81985	A C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT		
		G A		
GAM1399	LOC163590 5'	TCAGCCTCCCAAAGTGCTGGGA	58864	A C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT		
		G A		
GAM1399	LOC169611 3'	TCAGCCTCCCAAAGTGTTGGGA	82777	A C
	T	ATC CAGCACTTTGGGAGGC GA		

		TAG GTTGTGAAACCCTCCG CT G            A		
GAM1399	LOC170082 5'	TCGGCCTCCCAAAGTGCTGGGA 82566	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC170409 5'	TCGGCCTCCCAAAGTGCTGGGA 82869	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC196047 5'	TCGGCCTCCCAAAGTGCTGCGA 89612	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT C		
GAM1399	LOC196264 3'	TCGGCCTCCCAAAGTGTTGGGA 87615	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTTGTGAAACCCTCCGGCT G		
GAM1399	LOC196411 3'	TCAGCCTCCCAAAGTGCTG 87687		C
		CAGCACTTTGGGAGGC GA 		
		GTCGTGAAACCCTCCG CT A		
GAM1399	LOC196529 3'	TCAGCCTCCCAAAGTGCTGGGA 87781	A	C
	TG	TATC CAGCACTTTGGGAGGC GA 		
		GTAG GTCGTGAAACCCTCCG CT G            A		
GAM1399	LOC197358 3'	TCAGCCTCCCAAAGTGCTGGGA 88049	A	C
	T	ATC CAGCACTTTGGGAGGC GA 		
		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1399	LOC199699 3'	TCGGCCTCCCAAAGTGCTGGGA 88315	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC199775 5'	TCGGCCTCCCAAAGTGCTGGGA 88360	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC199786 3'	TCAGCCTCCCAAAGTGCTGGGA 88393	A	C
	T	ATC CAGCACTTTGGGAGGC GA 		

		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1399	LOC199906 3'	TCAGCCTCCCAAAGTTCTGGGA 88488	A	C
	T	ATC CAG ACTTTGGGAGGC GA 		C
		TAG GTC TGAAACCCTCCG CT G T        A		
GAM1399	LOC200014 3'	TCAGCCTCCCAAAGTGCTGGGA 88539	A	C
	T	ATC CAGCACTTTGGGAGGC GA 		
		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1399	LOC200301 5'	TCAGCCTCCCAAAGTGCTGGGA 88752	A	C
	T	ATC CAGCACTTTGGGAGGC GA 		
		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1399	LOC200310 3'	TCGGCCTCCCAAAGTGCTAGGA 65745	AC	
	T	ATC AGCACTTTGGGAGGCCGA 		
		TAG TCGTGAAACCCTCCGGCT GA		
GAM1399	LOC200316 5'	TCGGCCTCCCAAAGTGCTGGGA 88777	A	
	T	ATC CAGCACTTTGGGAGGCCGA 		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC200845 5'	TCAGCCTCCCAAAGTGCTGGGA 88907	A	C
	T	ATC CAGCACTTTGGGAGGC GA 		
		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1399	LOC201173 5'	TCGGCCTCCCAAAGTTCTGGGA 87337	A	C
	T	ATC CAG ACTTTGGGAGGCCGA 		
		TAG GTC TGAAACCCTCCGGCT G T		
GAM1399	LOC201220 5'	TCGGCCTCCCAAAGTTCTGGGA 87358	A	C
	T	ATC CAG ACTTTGGGAGGCCGA 		
		TAG GTC TGAAACCCTCCGGCT G T		
GAM1399	LOC201294 3'	TCGACCTCCCAAAGTGCTGGGA 88225	A	C
	T	ATC CAGCACTTTGGGAGG CGA 		
		TAG GTCGTGAAACCCTCC GCT G            A		
GAM1399	LOC201411 3'	TCAGCCTCCCAAAGTGCTGGGA 62962	A	C
	T	ATC CAGCACTTTGGGAGGC GA 		

			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1399	LOC201626 3'	TCGGCCTCCCAAAGTGTTGGGA 88999	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTTGTGAAACCCTCCGGCT			
		G			
GAM1399	LOC201627 3'	TCGGCCTCCCAAAGTGCTGGGA 89026	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1399	LOC203339 3'	TCAGCCTCCCAAAGTGCTGGGA 90550	A		C
	T	ATC CAGCACTTTGGGAGGC GA			
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1399	LOC219445 5'	TCGGCCTCCCAAAGAGC 91579	A		_
		GC CTTT GGGAGGCCGA			
		CG GAAA CCCTCCGGCT			
		A A			
GAM1399	LOC219673 3'	TCAGCCTCCCAAAGCACTG 93042	CA		C
		CAG CTTTGGGAGGC GA			
		GTC GAAACCCTCCG CT			
		AC A			
GAM1399	LOC219673 5'	TCAGCCTCCCAAAGTGCTAGGA 93043	AC		C
	T	ATC AGCACTTTGGGAGGC GA			
		TAG TCGTGAAACCCTCCG CT			
		GA A			
GAM1399	LOC219673 5'	TCAGCCTCCCAGAGTGCTGT 93044			C
		ACAGCACTTTGGGAGGC GA			
		TGTCGTGAGACCCTCCG CT			
		A			
GAM1399	LOC219735 3'	TCGGCCTCCCAAAGTGTTGGGA 93117	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTTGTGAAACCCTCCGGCT			
		G			
GAM1399	LOC219894 3'	TCGGCCTCCCAAAGTGCTGGGA 93289	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1399	LOC220074 3'	TCAGCCTCCCAAAGTGCTAGGA 59281	AC		C
	T	ATC AGCACTTTGGGAGGC GA			

		TAG TCGTGAAACCCTCCG CT GA A		
GAM1399	LOC220074 3'	TCAGCCTCCCCAGTAGCTGTGA 59282	_	TT C
	T	ATCACAGC ACT GGGAGGC GA                   TAGTGTCTG TGA CCCTCCG CT A C_ A		
GAM1399	LOC221271 3'	TCAGCCTCCCAAAGTGTTGAGA 91876	A	C
	T	ATC CAGCACTTTGGGAGGC GA                   TAG GTTGTGAAACCCTCCG CT A A		
GAM1399	LOC253842 5'	TCGGCCTCCCAAAGTGCTGGGA 97392	A	
	T	ATC CAGCACTTTGGGAGGCCGA                   TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC253981 3'	TCGGCCTCCCAAAGTTCTGGGA 95834	A C	
	T	ATC CAG ACTTTGGGAGGCCGA                      TAG GTC TGAAACCCTCCGGCT G T		
GAM1399	LOC254016 3'	CGGCCTCTCGCTGTGCT 96922	TT	
		AGCAC TGGGAGGCCG               TCGTG GCTCTCCGGC TC		
GAM1399	LOC254100 3'	TCAGCCTCCCAAAGTGCTGGGA 96417	A	C
	T	ATC CAGCACTTTGGGAGGC GA                   TAG GTCGTGAAACCCTCCG CT G A		
GAM1399	LOC256221 3'	TCGGCCTCCCAAAGTGCTGGGA 95214	A	
	T	ATC CAGCACTTTGGGAGGCCGA                   TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC256267 5'	TCGGCCTCCCAAAGTGCTGT 96810		
		ACAGCACTTTGGGAGGCCGA                TGTCTGAAACCCTCCGGCT		
GAM1399	LOC256306 3'	TCGGCCTCCCAAAGTGTTGGGA 96699	A	
	T	ATC CAGCACTTTGGGAGGCCGA                   TAG GTTGTGAAACCCTCCGGCT G		
GAM1399	LOC257486 3'	TCAGCCTCCCAAAGCTGGGAT 69250	A AC	C
		ATC CAGC TTTGGGAGGC GA 		

			TAG GTCG AAACCCTCCG CT G A_ A		
GAM1399	LOC51026	3'	CGCCTTCTGTCTGT 32170 C TTT C ACAG AC GGGAGGC G                 TGTC TG TCTTCCG C _ _ _ A		
GAM1399	LOC51193	5'	TCGGCCTCCCAAAGTGCTGGGA 32912 A T ATC CAGCACTTTGGGAGGCCGA           TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC51219	5'	TCGGCCTCCCAAAGTGCTGGGA 33129 A T ATC CAGCACTTTGGGAGGCCGA           TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC51696	3'	TCGGCCTCCCAAAGTGCTGGGA 32560 A T ATC CAGCACTTTGGGAGGCCGA           TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC56181	5'	TCGGCCTCCCAAAGTGCTGGGA 95543 A T ATC CAGCACTTTGGGAGGCCGA           TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC57107	3'	TCGGCCTCCCAAAGTGCTGGGA 39845 A T ATC CAGCACTTTGGGAGGCCGA           TAG GTCGTGAAACCCTCCGGCT G		
GAM1399	LOC89231	3'	TCAGCCTCCCAAAGTGCTGGGA 92736 A C T ATC CAGCACTTTGGGAGGC GA              TAG GTCGTGAAACCCTCCG CT G A		
GAM1399	LOC89919	3'	TCGGCCTCCCAAAGTGCTG 60731 CAGCACTTTGGGAGGCCGA       GTCGTGAAACCCTCCGGCT		
GAM1399	LOC89932	3'	TCAGCCTCCCAAAGTGCTGGGA 60817 A C T ATC CAGCACTTTGGGAGGC GA              TAG GTCGTGAAACCCTCCG CT G A		
GAM1399	LOC89932	3'	TCGGCCTCCCAAATGCTGGGA 60821 A C T ATC CAGCA TTTGGGAGGCCGA 		

			TAG GTCGT AAACCCTCCGGCT		
			G A		
GAM1399	LOC90288	3'	TCAGCCTCCCAAAGTACCCTG	62105	C__ C
			CAG ACTTTGGGAGGC GA		
			GTC TGAAACCCTCCG CT		
			CCA A		
GAM1399	LOC90288	3'	TCGGCCTCCCAAAGTGCTGGGA	62108	A
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	LOC90485	3'	TCGGCCTCCCAAAGTGCTGGGA	63029	A
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	LOC90591	3'	TCAGCCTCCCAAAGTGCTGTG	63441	C
			CACAGCACTTTGGGAGGC GA		
			GTGTCGTGAAACCCTCCG CT		
			A		
GAM1399	LOC90826	5'	CCAGCAAGTGCTGTTATA	64089	C _
			TAT ACAGCACTT TGG		
			ATA TGTCGTGAA ACC		
			T CG		
GAM1399	LOC90918	3'	TCGGCCTCCCAAAGTGCCGGGA	64362	ACA
	T		ATC GCACTTTGGGAGGCCGA		
			TAG CGTGAAACCCTCCGGCT		
			GGC		
GAM1399	LOC91115	3'	TCGGCCTCCCAAAGTGCTGGGA	64955	A
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	LOC91250	5'	TCGGCCTCCCAAAGTGCTGGGA	65329	A
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	LOC91308	3'	TCGGCCTCCCAAAGTGCTGGGA	65566	A
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1399	LOC91373	3'	TCGGCCTCCCAAAGTGCTGGGA	65846	A
	T		ATC CAGCACTTTGGGAGGCCGA		

			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	LOC91893	3'	TCGGCCTCCCAAAGTGCTGGGA	67464	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	LOC92303	3'	TCGGCCTCCCAAAGTGCTGGGA	68829	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	LOC92466	5'	TCGGCCTCCCAAAGTGCTGT	69435		
			ACAGCACTTTGGGAGGCCGA			
			TGTCGTGAAACCCTCCGGCT			
GAM1399	LOC92661	5'	TCAGCCTCCCAAAGTGCTGGGA	70086	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	LOC92689	3'	TCAGCCTCCCAAAGTGCTGGGA	70230	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1399	LOC92697	5'	TCAGCCTCCCAAAGTTCTGGGA	70280	A C	C
	T		ATC CAG ACTTTGGGAGGC GA			
			TAG GTC TGAACCCTCCG CT			
			G T A			
GAM1399	LOC92841	3'	TCGGCCTCCCAAAGTGCTGGGA	70725	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	LOC93129	3'	TCGGCCTCCCAAAGTGCTGGGA	71470	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1399	LOC93268	5'	GCCTCCCGGATGGCCAGATA	71882	ACA AC	
			TATC GC TTTGGGAGGC			
			ATAG CG AGGCCCTCCG			
			AC_ GT			
GAM1399	LOC93408	5'	TCGGCCTCCCAAAGTGCTGGGA	56484	A	
	T		ATC CAGCACTTTGGGAGGCCGA			



		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1399	LOC93496	3'	TCGACCTCCCAAAGTGCTGGGA 72439	A	C
	T		ATC CAGCACTTTGGGAGG CGA		
		TAG GTCGTGAAACCCTCC GCT			
		G A			
GAM1400	A1BG	3'	TCAGCCTCCCAAAGTGCTGGGA 55434	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400	A1BG	3'	TCAGCCTCCCAAAGTGTTGGGA 55435	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
		TAG GTTGTGAAACCCTCCG CT			
		G A			
GAM1400	ADAMTS4	3'	TCGGCCTCCCAAAGTGCTGGGA 17521	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400	ADRA1A	3'	TCAGCCTCCCAAAGTGCTGGGA 52790	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400	AIM1	3'	TCGGCCTCCCAAATGCTGGGA 91830	A	C
	T		ATC CAGCA TTTGGGAGGCCGA		
		TAG GTCGT AAACCCTCCGGCT			
		G A			
GAM1400	ALDH1B1	3'	TCAGCCTCCCAAAGTGCTGGGA 5498	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400	APAF1	3'	TCAGCCTCCCAAAGTGTTGGGA 6739	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
		TAG GTTGTGAAACCCTCCG CT			
		G A			
GAM1400	APAF1	3'	TCAGCCTCCCAAAGTGTTGGGA 25048	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
		TAG GTTGTGAAACCCTCCG CT			
		G A			
GAM1400	APM1	3'	TCGACCTCCCAAAGTGCTGGGA 16604	A	C
	T		ATC CAGCACTTTGGGAGG CGA		

			TAG GTCGTGAAACCCTCC GCT		
			G            A		
GAM1400	APM1	3'	TCGGCCTCCCAAAGTGCTGGGA 16605	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	APPL	3'	TCGGCCTCCCAAAGTGCTGGGA 23932	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	AQP6	3'	TCGGCCTCCCAAAGTGCTGGGA 53943	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	AQP6	3'	TCGGCCTCCCAAAGTGCTGGGA 7963	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	ARCN1	3'	TCAGCCTCCCAAAGTGTTGGGA 7987	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTTGTGAAACCCTCCG CT		
			G            A		
GAM1400	ARSF	5'	TCGGCCTCCCAAAGTGCTGGGA 64604	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	ATP1B2	3'	TCGGCCTCCCAAAGTGTTGGGA 8056	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTTGTGAAACCCTCCGGCT		
			G		
GAM1400	ATP8B2	3'	CCTCCCAAAGTGCTGAGAT 65220	A	
			ATC CAGCACTTTGGGAGG		
			TAG GTCGTGAAACCCTCC		
			A		
GAM1400	AXL	3'	TCAGCCTCCCAAAGTGCTGAGA 8107	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			A            A		
GAM1400	AXL	3'	TCAGCCTCCCAAAGTGCTGAGA 41604	A	C
	T		ATC CAGCACTTTGGGAGGC GA		

			TAG GTCGTGAAACCCTCCG CT		
			A A		
GAM1400	BAZ2B	5'	TCGGCCTCCCAAAGTGCTGGGA 25624	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	CAMLG	3'	TCGGCCTCCCAAAGTGCTGGGA 8246	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	CASP2	3'	TCAGCCTCCCAAAGTGTTGGGA 6904	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTTGTGAAACCCTCCG CT		
			G A		
GAM1400	CASP2	3'	TCAGCCTCCCAAAGTGTTGGGA 52146	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTTGTGAAACCCTCCG CT		
			G A		
GAM1400	CASP2	3'	TCAGCCTCCCAAAGTGTTGGGA 52160	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTTGTGAAACCCTCCG CT		
			G A		
GAM1400	CASP2	3'	TCAGCCTCCCAAAGTGTTGGGA 52175	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTTGTGAAACCCTCCG CT		
			G A		
GAM1400	CASP8	3'	TCGGCCTCCCAAAGTGCTGGGA 52928	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	CASP8	3'	TCGGCCTCCCAAAGTGCTGGGA 52939	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	CASP8	3'	TCGGCCTCCCAAAGTGCTGGGA 52954	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	CASP8	3'	TCGGCCTCCCAAAGTGCTGGGA 6922	A	
	T		ATC CAGCACTTTGGGAGGCCGA		

			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	CDC25B	3'	GCCCCTACTGCTGTGA 41564	CTT	A	
			TCACAGCA TGGG GGC			
			AGTGTCGT ATCC CCG			
			C__ _			
GAM1400	CDC25B	3'	GCCCCTACTGCTGTGA 41568	CTT	A	
			TCACAGCA TGGG GGC			
			AGTGTCGT ATCC CCG			
			C__ _			
GAM1400	CHRNA4	3'	TCGGCCTCCCAAAGTGCTGGGA 5636	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	CLECSF11	5'	TCAGCCTCCCAAAGTGCTGAGA 55277	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			A A			
GAM1400	CNGA1	5'	TCAGCCTCCCAAAGTGCTG 59512			C
			CAGCACTTTGGGAGGC GA			
			GTCGTGAAACCCTCCG CT			
			A			
GAM1400	COX15	3'	GCCTCCTGGGACTGTGA 54316	CA	TT	
			TCACAG CT GGGAGGC			
			AGTGTC GG TCCTCCG			
			AG _			
GAM1400	CR1	3'	TCGGCCTCCCAAAGTGCTGCGA 5137	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			C			
GAM1400	CYP1A2	3'	TCAGCCTCCCAAAGTGCTGGGA 5707	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	CYP1A2	3'	TCAGCCTCCCAAAGTGCTGGGA 69127	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	CYP4F3	3'	TCGGCCTCCCAAAGTGCTGGGA 6127	A		
	T		ATC CAGCACTTTGGGAGGCCGA			

				TAG GTCGTGAAACCCTCCGGCT		
				G		
GAM1400	CYP8B1	3'	TCGGCCTCCCAAAGTTCTGGGA	15275	A	C
	T		ATC CAG ACTTTGGGAGGCCGA			
			TAG GTC TGAAACCCTCCGGCT			
			G T			
GAM1400	DFFB	3'	TCAGCCTCCCAAAGTGCTGGGA	87394	A	C
	TG		TATC CAGCACTTTGGGAGGC GA			
			GTAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	DHFR	3'	TCAGCCTCCCAAAGTGCTGGGA	5816	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	DISC1	3'	CGCCTTCCATGCTGTG	37873	CTT	C
			CACAGCA TGGGAGGC G			
			GTGTCGT ACCTTCCG C			
			— A			
GAM1400	DNASE1L1	5'	TCAGCCTCCCAAAGTGCTGGGA	22081	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	DSC3	3'	TCGGCCTCCCAAAGTGCTGGGA	44347	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	DSC3	3'	TCGGCCTCCCAAAGTGCTGGGA	8682	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	EHD2	3'	TCGGCCTCCCAAAGTGATGGGA	27501	A	G
	T		ATC CA CACTTTGGGAGGCCGA			
			TAG GT GTGAAACCCTCCGGCT			
			G A			
GAM1400	F2RL2	3'	TCAGCCTCCCAAAGTGCTGGAT	14625	A	C
			ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			— A			
GAM1400	F2RL3	3'	TCAGCCTCCCAAAGTAGCTGGGA	14193	A	— T C
	TA		TATC CAGC ACTT GGGAGGC GA			

			ATAG GTCG TGAA CCCTCCG CT		
			G A _ A		
GAM1400 FCAR	3'	TCGGCCTCCCAAAGTGCTGGGA 55805	A		
T		ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400 FCGR2A	3'	TCGGCCTCCCAAAGTGCTGGGA 79266	A		
TG		TATC CAGCACTTTGGGAGGCCGA			
		GTAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400 FZD4	3'	TCAGCCTCCCAAAGTGCTGGGA 24151	A		C
T		ATC CAGCACTTTGGGAGGC GA			
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400 GHR	3'	TCGGCCTCCCAAAGTGCTGGGA 3890	A		
T		ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400 GLTSCR1	5'	TCAGCCTCCCAAAGTGCTGAGA 31676	A		C
T		ATC CAGCACTTTGGGAGGC GA			
		TAG GTCGTGAAACCCTCCG CT			
		A A			
GAM1400 GPR81	3'	TCGGCCTCCCAAAGTGCTTGA 50767	AC		
T		ATC AGCACTTTGGGAGGCCGA			
		TAG TCGTGAAACCCTCCGGCT			
		GT			
GAM1400 HCS	3'	TCGGCCTCCCAAAGTGCTGGGA 38481	A		
T		ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400 HLCS	5'	TCGGCCTCCCAAAGTGCTGGGA 4679	A		
T		ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400 HTR1E	5'	TCGGCCTCCCAAAGTGCTGGA 6017	A		
		TC CAGCACTTTGGGAGGCCGA			
		AG GTCGTGAAACCCTCCGGCT			
		—			
GAM1400 HYAL4	5'	TCAGCCTCCCAAATGTTGGGT 24375	A C C		
A		TATC CAGCA TTTGGGAGGC GA			

			ATGG GTTGT AAACCCTCCG CT		
			— A A		
GAM1400 IL11	3'	TCGGCCTCCCAAAGTGCTGGGA 5339	A		
T		ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400 IL1RAP	3'	GGTTAACAAAGAACTGTGATA 9313	CA GGA		
		TATCACAG CTTTG GGCC			
		ATAGTGTC GAAAC TTGG			
		AA AA_			
GAM1400 INMT	3'	TCGGCCTCCCAAAGTGCTGGGA 22280	A		
T		ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400 KMO	3'	TCAGCCTCCCAAAGTACAGGGA 13457	ACAGC C		
T		ATC ACTTTGGGAGGC GA			
		TAG TGAAACCCTCCG CT			
		GGACA A			
GAM1400 LTB4R	5'	TCAGCCTCCCAAAGTGCTGGGA 5653	A C		
T		ATC CAGCACTTTGGGAGGC GA			
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400 LYZ	3'	TCGGCCTCCCAAAGTGCTGGGA 4110	A		
T		ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400 MAK	3'	TCGGCCTCCCAAAGTGC 19768			
		GCACTTTGGGAGGCCGA			
		CGTGAAACCCTCCGGCT			
GAM1400 MATN3	3'	TCAGCCTCCCAAAGTGCTGGGA 9938	A C		
T		ATC CAGCACTTTGGGAGGC GA			
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400 MDM2	3'	TCGGCCTCCCAAAGTGCTGGGA 9974	A		
T		ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400 MDM2	3'	TCGGCCTCCCAAAGTGCTGGGA 22512	A		
T		ATC CAGCACTTTGGGAGGCCGA			

Cell Line	Gene	Strand	Sequence	Position	Start	End	RefSeq	GenBank
GAM1400	MDM2	3'	TCGGCCTCCCAAAGTGCTGGGA	22516	A			
	T		ATC CAGCACTTTGGGAGGCCGA					
			TAG GTCGTGAAACCCTCCGGCT					
			G					
GAM1400	MDM2	3'	TCGGCCTCCCAAAGTGCTGGGA	22520	A			
	T		ATC CAGCACTTTGGGAGGCCGA					
			TAG GTCGTGAAACCCTCCGGCT					
			G					
GAM1400	MDM2	3'	TCGGCCTCCCAAAGTGCTGGGA	22524	A			
	T		ATC CAGCACTTTGGGAGGCCGA					
			TAG GTCGTGAAACCCTCCGGCT					
			G					
GAM1400	MEFV	3'	TCAGCCTCCCAAAGTGCGAGGGA	4152	ACA			
	T		ATC GCACTTTGGGAGGC GA					
			TAG CGTGAAACCCTCCG CT					
			GGA A					
GAM1400	MEFV	3'	TCAGCCTCCCAAAGTGCTGGGA	4153	A			
	T		ATC CAGCACTTTGGGAGGC GA					
			TAG GTCGTGAAACCCTCCG CT					
			G A					
GAM1400	MHC2TA	3'	TCAGCCTCCCAAAGTGCTGGGA	4189	A			
	T		ATC CAGCACTTTGGGAGGC GA					
			TAG GTCGTGAAACCCTCCG CT					
			G A					
GAM1400	MHC2TA	3'	TCAGCCTCCCAAAGTGCTGGGA	4190	A			
	T		ATC CAGCACTTTGGGAGGC GA					
			TAG GTCGTGAAACCCTCCG CT					
			G A					
GAM1400	MLANA	3'	TCAGCCTCCCAAAGTGCTGGA	18589	A			
			TC CAGCACTTTGGGAGGC GA					
			AG GTCGTGAAACCCTCCG CT					
			- A					
GAM1400	MTR	3'	TCAGCCTCCCAAATGCTGGGA	4219	A	C		
	T		ATC CAGCA TTTGGGAGGC GA					
			TAG GTCGT AAACCCTCCG CT					
			G A A					
GAM1400	NDRG3	3'	TCAGCCTCCCAAAGTGCTGGGA	49306	A			
	T		ATC CAGCACTTTGGGAGGC GA					



				TAG GTCGTGAAACCCTCCG CT G            A		
GAM1400	NONO	3'	TCGGCCTCCCAAATGCTGGGA 82024	A   C		
	T		ATC CAGCA TTTGGGAGGCCGA			
			TAG GTCGT AAACCCTCCGGCT			
			G            A			
GAM1400	NQO1	3'	TCAGCCTCCCAAAGTGCTGGGA 6167	A            C		
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G            A			
GAM1400	NT5C2	5'	TCGGCCTCCCAAAGTTCTGGGA 24242	A   C		
	T		ATC CAG ACTTTGGGAGGCCGA			
			TAG GTC TGAAACCCTCCGGCT			
			G   T			
GAM1400	PAICS	3'	TCAGCCTCCCAAAGTGCTAGGG 21262	AC            C		
	T		ATC AGCACTTTGGGAGGC GA			
			TGG TCGTGAAACCCTCCG CT			
			GA            A			
GAM1400	PCDHA9	3'	TCAGCCTCCCAAATGCTGGGA 25769	A   C            C		
	T		ATC CAGCA TTTGGGAGGC GA			
			TAG GTCGT AAACCCTCCG CT			
			G   A            A			
GAM1400	PCDHA9	3'	TCGGCCTCCCAAAGTGCTGGGA 25772	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	PCDHB11	3'	TCAGCCTCCCAAAGTGCTGGGA 38422	A            C		
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G            A			
GAM1400	PCDHB11	3'	TCCCAAAGTGCTGTGAT    38425			
			ATCACAGCACTTTGGGA			
			TAGTGTCTGTAACCCT			
GAM1400	PCDHB16	3'	TCAGCCTCCCAAATTCTGGGA 40556	A   CAC            C		
	T		ATC CAG   TTTGGGAGGC GA			
			TAG GTC   AAACCCTCCG CT			
			G   TTA            A			
GAM1400	PER2	3'	TCGGCCTCCCAAAGTGCTGGGA 43047	A		
	T		ATC CAGCACTTTGGGAGGCCGA			

				TAG GTCGTGAAACCCTCCGGCT		
				G		
GAM1400	PIK3C2B	3'	CCAAAGGAGAGCGCTGTGATA 10562	A_____		
			TATCACAGC CTTTGG			
			ATAGTGTCG GAAACC			
			CGAGAG			
GAM1400	PPEF2	3'	TCAGCCTCCCAAAGTGCTGGGA 20676	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	PRIM2A	3'	TCAGCCTCCCAAAGTAGTTAGGA 6276	AC _ T C		
			TC AGC ACTT GGGAGGC GA			
			AG TTG TGAA CCCTCCG CT			
			GA A _ A			
GAM1400	PRKR	3'	TCGGCCTCCCAAAGTGCTGGGA 10888	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	PTGES	3'	TCGGCCTCCCAAAGTGCTGGGA 16865	A		
	TG		TATC CAGCACTTTGGGAGGCCGA			
			GTAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	PTGIS	3'	TCGGCCTCCCAAAGTGCTGGGA 6346	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	PTPN18	3'	TCAGCCTCCCAAAGTGCTGAGA 26870	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			A A			
GAM1400	RAB36	3'	TCGGCCTCCCAAAGTGCTGGGA 16977	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	RAB36	3'	TCGGCCTCCCAAAGTGCTGGGA 16978	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	RABL2A	3'	TCGGCCTCCCAAAGTGCTGGGA 25506	A		
	T		ATC CAGCACTTTGGGAGGCCGA			

			TAG GTCGTGAAACCCTCCGGCT G	
GAM1400	RABL2B	3'	TCGGCCTCCCAAAGTGCTGGGA 23007	A
	T		ATC CAGCACTTTGGGAGGCCGA	
			TAG GTCGTGAAACCCTCCGGCT	
			G	
GAM1400	RAD52	3'	CCAGCCATGCTGTGATA 56194	CTT GA
			TATCACAGCA TGG GG	
			ATAGTGTCTGT ACC CC	
			— GA	
GAM1400	RAD52	3'	CCAGCCATGCTGTGATA 56202	CTT GA
			TATCACAGCA TGG GG	
			ATAGTGTCTGT ACC CC	
			— GA	
GAM1400	RAD52	3'	CCAGCCATGCTGTGATA 56211	CTT GA
			TATCACAGCA TGG GG	
			ATAGTGTCTGT ACC CC	
			— GA	
GAM1400	RBBP9	3'	TCAGCCTCCCAAAGTAGTGTGA 70142	GC T C
			TCACA ACTT GGGAGGC GA	
			AGTGT TGAA CCCTCCG CT	
			GA _ A	
GAM1400	RGS9	5'	TCGGCCTCCCAAAGTGCTGGGA 13840	A
	T		ATC CAGCACTTTGGGAGGCCGA	
			TAG GTCGTGAAACCCTCCGGCT	
			G	
GAM1400	RHD	3'	TCGGCCTCCCAAAGTGCTGGA 32319	A
			TC CAGCACTTTGGGAGGCCGA	
			AG GTCGTGAAACCCTCCGGCT	
			—	
GAM1400	RHD	3'	TCGGCCTCCCAAAGTGCTGGGA 32320	A
	T		ATC CAGCACTTTGGGAGGCCGA	
			TAG GTCGTGAAACCCTCCGGCT	
			G	
GAM1400	RHD	3'	TCGGCCTCCCAAAGTGCTGGA 32628	A
			TC CAGCACTTTGGGAGGCCGA	
			AG GTCGTGAAACCCTCCGGCT	
			—	
GAM1400	RHD	3'	TCGGCCTCCCAAAGTGCTGGGA 32629	A
	T		ATC CAGCACTTTGGGAGGCCGA	

			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	RPH3AL	3'	TCGGCCTCCCAAAGTGCTGGGA 22758	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	RPP30	3'	TCGGCCTCCCAAAGTGCTGGGA 21173	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	SCNN1G	3'	TCAGCCTCCCAAAGTGCGAGGGA 6436	ACA	C
	T		ATC GCACTTTGGGAGGC GA		
			TAG CGTGAAACCCTCCG CT		
			GGA A		
GAM1400	SEDL	3'	TCAGCCTCCCAAAGTGCTAGGA 27361	AC	C
	T		ATC AGCACTTTGGGAGGC GA		
			TAG TCGTGAAACCCTCCG CT		
			GA A		
GAM1400	SEDL	3'	TCAGCCTCCCAAAGTGCTGGGA 27362	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1400	SEPN1	3'	TCAGCCTCCCAAAGTGCTGGGA 66380	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1400	SERPINB9	3'	TCAGCCTCCCAAAGTGCTAGGA 14765	AC	C
	T		ATC AGCACTTTGGGAGGC GA		
			TAG TCGTGAAACCCTCCG CT		
			GA A		
GAM1400	SERPINB9	3'	TCGGCCTCCCAAAGTGCTGGGA 14769	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	SIL	5'	TCGGCCTCCCAAATGCTGGGA 11699	A	C
	T		ATC CAGCA TTTGGGAGGCCGA		
			TAG GTCGT AAACCCTCCGGCT		
			G A		
GAM1400	SLC24A1	3'	TCGGCCTCCCAAAGTGCTGGGA 16380	A	
	T		ATC CAGCACTTTGGGAGGCCGA		

				TAG GTCGTGAAACCCTCCGGCT		
				G		
GAM1400	SPN	3'	TCAGCCTCCCAAAGTGCTGAGA 11927	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			A A			
GAM1400	TAPBP	3'	TCAGCCTCCCAAAGTGCTGGGA 12135	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	TAPBP	3'	TCGGCCTCCCAAAGTGCTGGGA 12138	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	TBXA2R	3'	TCAGCCTCCCAAAGTGCTGGGA 6504	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	TERF1	3'	TCGGCCTCCCAAAGTGCTGAGA 33981	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			A			
GAM1400	TERF2	3'	TCGGCCTCCCAAAGTGCTGGGA 18950	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	TIM3	3'	TCGGCCTCCCAAAGCACTGGGA 51349	A CA		
	T		ATC CAG CTTTGGGAGGCCGA			
			TAG GTC GAAACCCTCCGGCT			
			G AC			
GAM1400	TNFRSF11A	3'	TCGGCCTCCCAAAGTACTGGGA 13856	A C		
	T		ATC CAG ACTTTGGGAGGCCGA			
			TAG GTC TGAAACCCTCCGGCT			
			G A			
GAM1400	TP53BP2	5'	TCGGCCTCCCAAAGTGCTGGAT 18303	A		
			ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			—			
GAM1400	TPMT	3'	TCGGCCTCCCAAAGTGCTGGGA 4547	A		
	T		ATC CAGCACTTTGGGAGGCCGA			

Accession	Gene	Strand	Sequence	Position	Orientation	Reference
GAM1400	TRAF5	3'	TCGGCCTCCCAAAGTGCTGAGA	16090	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			A			
GAM1400	TRPV1	3'	TCGGCCTCCCAAAGTGCTGGGA	54817	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	TRPV1	3'	TCGGCCTCCCAAAGTGCTGGGA	54849	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	TRPV1	3'	TCGGCCTCCCAAAGTGCTGGGA	54882	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	TRPV1	3'	TCGGCCTCCCAAAGTGCTGGGA	38099	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	UGDH	3'	TCGGCCTCCCAAAGTGCTGGGA	12547	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	VENTX2	3'	TCGGCCTCCCAAAGTGCTGGGA	27121	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	VHL	3'	TCAGCCTCCCAAATGGTGGGA	5086	A G C	C
	T		ATC CA CA TTTGGGAGGC GA			
			TAG GT GT AAACCCTCCG CT			
			G G A A			
GAM1400	VHL	3'	TCAGCCTCCCAAATGGTGGGA	5087	A G	C
	T		ATC CA CACTTTGGGAGGC GA			
			TAG GT GTGAAACCCTCCG CT			
			G G A			
GAM1400	VIPR2	3'	TCGGCCTCCCAAAGTGCTGGGA	12617	A	
	T		ATC CAGCACTTTGGGAGGCCGA			

		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400	WHSC1	5'	TCAGCCTCCCAAAGTGCTGGGA 23667	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400	WHSC1	5'	TCAGCCTCCCAAAGTGCTGGGA 29917	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400	WHSC1	5'	TCAGCCTCCCAAAGTGCTGGGA 55835	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400	WHSC1	5'	TCAGCCTCCCAAAGTGCTGGGA 55852	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400	XKRY	3'	CCAGAAGCACTGTGATA 16255	CA	G
		TATCACAG CTTT GG			
		ATAGTGTC GAAG CC			
		AC A			
GAM1400	XKRY	3'	CCAGAAGCACTGTGATA 60016	CA	G
		TATCACAG CTTT GG			
		ATAGTGTC GAAG CC			
		AC A			
GAM1400	XRCC2	3'	TCGGCCTCCCAAAGTGCTAGGA 18331	AC	
	T		ATC AGCACTTTGGGAGGCCGA		
		TAG TCGTGAAACCCTCCGGCT			
		GA			
GAM1400	YES1	3'	TCGGCCTCCCAAAGTGCTGGGA 18358	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400	ZNF133	5'	TCAGCCTCCCAAATGCTGGGA 12841	A	C C
	T		ATC CAGCA TTTGGGAGGC GA		
		TAG GTCGT AAACCCTCCG CT			
		G A A			
GAM1400	ZNF138	5'	GCCTCTGTGGCGCTGTGAT 81187	A	TTG
		ATCACAGC CT GGAGGC			

		TAGTGTCTG GG TCTCCG			
		C TG_			
GAM1400	ZNF264	3'	TCGGCCCCC	AAAGTGCTGGGG	12766 A A
	T		ATC CAGCACTTTGGG	GGCCGA	
			TGG GTCGTGAAACCC	CCGGCT	
			G	C	
GAM1400	ZNF74	5'	TCGGCCTCCCA	AAAGTGCTGGGA	12805 A
	T		ATC CAGCACTTTGGG	GAGGCCGA	
			TAG GTCGTGAAACCCT	CCGGCT	
			G		
GAM1400	APOL2	3'	TCGGCCTCCCA	AAAGTGCTGGGA	48055 A
	T		ATC CAGCACTTTGGG	GAGGCCGA	
			TAG GTCGTGAAACCCT	CCGGCT	
			G		
GAM1400	ARHGAP11A	3'	TCAGCCTCCCA	AAAGTGCTGGGA	28801 A C
	T		ATC CAGCACTTTGGG	GAGGC GA	
			TAG GTCGTGAAACCCT	CCG CT	
			G	A	
GAM1400	ARHGAP5	5'	TCAGCCTCCCA	AAAGTGCTGCGA	77079 A C
	T		ATC CAGCACTTTGGG	GAGGC GA	
			TAG GTCGTGAAACCCT	CCG CT	
			C	A	
GAM1400	ARPP-19	3'	TCGGCCTCCCA	AAAGTGCTGGGA	21805 A
	T		ATC CAGCACTTTGGG	GAGGCCGA	
			TAG GTCGTGAAACCCT	CCGGCT	
			G		
GAM1400	ASE-1	3'	TCCCAAAGTGCT	AGGATA	23955 AC
			TATC AGCACTTTGGGA		
			ATAG TCGTGAAACCCT		
			GA		
GAM1400	BAG5	3'	TCGGCCCCC	AAAGTGCTGGGA	16854 A A
	T		ATC CAGCACTTTGGG	GGCCGA	
			TAG GTCGTGAAACCC	CCGGCT	
			G	C	
GAM1400	BNIP-S	3'	TCGGCCTCCCA	AAAGTGCCGAGA	56269 ACA
	T		ATC GCACTTTGGG	GAGGCCGA	
			TAG CGTGAAACCCT	CCGGCT	
			AGC		
GAM1400	C13orf1	3'	TCAGCCTCCCA	AAAGTGCTGGA	39976 A C
			TC CAGCACTTTGGG	GAGGC GA	



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AG GTCGTGAAACCCTCCG CT
      _      A
GAM1400 C20orf142 3' TCGGCCTCCCAAAGTGCTGGGA 74788  A
      T      ATC CAGCACTTTGGGAGGCCGA
              ||| |||||
              TAG GTCGTGAAACCCTCCGGCT
              G
GAM1400 C22orf19 3' TCGGCCTCCCAAAGTGCTAGGA 13436  AC
      T      ATC AGCACTTTGGGAGGCCGA
              ||| |||||
              TAG TCGTGAAACCCTCCGGCT
              GA
GAM1400 C6orf33 3' TCAGCCTCCCAAAGTGTTGGGA 55888  A      C
      T      ATC CAGCACTTTGGGAGGC GA
              ||| |||||
              TAG GTTGTGAAACCCTCCG CT
              G      A
GAM1400 C6orf5 3' TCGGCCTCCCAAAGTGCTGGGA 31365  A
      T      ATC CAGCACTTTGGGAGGCCGA
              ||| |||||
              TAG GTCGTGAAACCCTCCGGCT
              G
GAM1400 C9orf9 3' TCGGCCTCCCAAAGTGCTGGGA 38530  A
      T      ATC CAGCACTTTGGGAGGCCGA
              ||| |||||
              TAG GTCGTGAAACCCTCCGGCT
              G
GAM1400 C9orf9 3' TCGGCCTCCCAAAGTGCTGGGA 38531  A
      T      ATC CAGCACTTTGGGAGGCCGA
              ||| |||||
              TAG GTCGTGAAACCCTCCGGCT
              G
GAM1400 CEACAM8 3' TCAGCCTCCCAAAGTTCTGGGA 8425  A C      C
      T      ATC CAG ACTTTGGGAGGC GA
              ||| ||| |||||
              TAG GTC TGAAACCCTCCG CT
              G T      A
GAM1400 CECR1 3' TCGGCCTCCCAAAGCACTGGGA 33821  A CA
      T      ATC CAG CTTTGGGAGGCCGA
              ||| ||| |||||
              TAG GTC GAAACCCTCCGGCT
              G AC
GAM1400 CENPH 3' TCAGCCTCCCAAAGTAGCTGTGA 43278  _ T      C
              TCACAGC ACTT GGGAGGC GA
              ||||| ||| |||||
              AGTGTCTG TGAA CCCTCCG CT
              A _      A
GAM1400 CHRAC1 3' TCAGCCTCCCAAAGTGC 33878  C
              GCACTTTGGGAGGC GA
              ||||| |||

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		CGTGAAACCCTCCG CT			
		A			
GAM1400	DKFZp434A2417 3'	TCGGCCTCCCAAAGTGCTGGGA 66110	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400	DKFZP434J037 3'	TCGGCCTCCCAAAGTGCTGGGA 48221	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400	DKFZp547H025 3'	TCAGCCTCCCAAAGTGCTGGGA 39365	A		C
	T	ATC CAGCACTTTGGGAGGC GA			
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400	DKFZP564K0322 3'	TCGGCCTCCCAAAATGCTGGGA 49364	A		C
	T	ATC CAGCA TTTGGGAGGCCGA			
		TAG GTCGT AAACCCTCCGGCT			
		G A			
GAM1400	DKFZP564O0523 3'	CGCCTCCCAAAGGGATG 49512	GCA		C
		CA CTTTGGGAGGC G			
		GT GAAACCCTCCG C			
		AGG A			
GAM1400	DKFZP566I1024 3'	TCGACCTCCCAAAGTGCTGGGA 70109	A		C
	T	ATC CAGCACTTTGGGAGG CGA			
		TAG GTCGTGAAACCCTCC GCT			
		G A			
GAM1400	DKFZp761N1114 3'	TCAGCCTCCCAAGTAGCTGTGA 79026	_	T	C
		TCACAGC ACTT GGGAGGC GA			
		AGTGTGCG TGAA CCCTCCG CT			
		A _ A			
GAM1400	DKFZp761N1114 3'	TCGGCCTCCCAAAGTGCTGGGA 79028	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400	DRIM 3'	TCGGCCTCCCAAAGTGCTGGGA 27183	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400	EVI5 3'	TCAGCCTCCCAAAGTGCTGGGA 19011	A		C
	T	ATC CAGCACTTTGGGAGGC GA			

			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1400	EVI5	3'	TCAGCCTCCCAAAGTG TGGGGA 19012	ACA	C
	T		ATC GCACTTTGGGAGGC GA		
			TAG TGTGAAACCCTCCG CT		
			GGG A		
GAM1400	FBP17	3'	TCAGCCTCCCAAAGTGCTGAGA 72805	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			A A		
GAM1400	FBP17	3'	TCAGCCTCCCAAATAGCTGTGA 72807	AC	C
	T		ATCACAGC TTTGGGAGGC GA		
			TAGTGTCTG AAACCCTCCG CT		
			AT A		
GAM1400	FKBP9	3'	TCGGCCTCCCAAAGTGTTGGGA 94070	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTTGTGAAACCCTCCGGCT		
			G		
GAM1400	FLJ00060	5'	TCGGCCTCCCAAAGTGCTGGGA 61105	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	FLJ10298	3'	TCGGCCTCCCAAAGTGCTGGGA 35994	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	FLJ10346	5'	TCGGCCTCCCAAAGTGCTGGGA 36049	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	FLJ10535	3'	TCAGCCTCCCAAAGTGCTGGGA 36250	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1400	FLJ10560	3'	TCGGCCTCCCAAAGTGCTGGGA 36285	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	FLJ10607	3'	TCAGCCTCCCAAAGTGCTTGA 77128	AC	C
	TG		TATC AGCACTTTGGGAGGC GA		

				GTAG TCGTGAAACCCTCCG CT		
				GT A		
GAM1400	FLJ10687	3'	TCAGCCTCCCAAAGTGCTGAGA 36412	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			A A			
GAM1400	FLJ10713	3'	TCAGCCTCCCAAATGCTGGGA 36473	A	C	C
			TC CAGCA TTTGGGAGGC GA			
			AG GTCGT AAACCCTCCG CT			
			G A A			
GAM1400	FLJ10846	3'	TCGGCCTCCCAAAGTGCTGGA 36743	A		
			TC CAGCACTTTGGGAGGCCGA			
			AG GTCGTGAAACCCTCCGGCT			
			—			
GAM1400	FLJ10956	3'	TCAGCCTCCCAAAGTGCTGGGA 36919	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	FLJ11186	3'	TCAGCCTCCCAAAGTGTTGGGA 37147	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTTGTGAAACCCTCCG CT			
			G A			
GAM1400	FLJ12610	3'	CCTCCCAAAGTGCTGGGAT 45511	A		
			ATC CAGCACTTTGGGAGG			
			TAG GTCGTGAAACCCTCC			
			G			
GAM1400	FLJ12747	3'	TCGGCCTCCCAAAGTGCTGGGA 49727	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	FLJ12975	3'	TCGGCCTCCCAAAGTGCTGGGA 69593	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	FLJ13072	5'	TCAGCCTCCCAAAGTGCTGGGA 89827	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	FLJ13197	3'	TCAGCCTCCCAAAGTGCTGGGA 44863	A		C
	T		ATC CAGCACTTTGGGAGGC GA			

				TAG GTCGTGAAACCCTCCG CT		
				G A		
GAM1400	FLJ13993	3'	GCCCCACACTGTGATG	60460	CACTT _ A	
			TATCACAG TG GG GGC			
			GTAGTGTC AC CC CCG			
			_____ A _			
GAM1400	FLJ14351	3'	TCAGCCTCCCAAAGTGCTAGGA	45331	AC	C
	T		ATC AGCACTTTGGGAGGC GA			
			TAG TCGTGAAACCCTCCG CT			
			GA A			
GAM1400	FLJ14442	3'	TCGGCCTCCCAAAGTGCTGAGA	51377	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			A			
GAM1400	FLJ14950	3'	TCGGCCTCCCAAAGTGCTGGGA	51730	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	FLJ14957	3'	TCAGCCTCCCAAAGTGCTGAGA	51760	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			A A			
GAM1400	FLJ20097	3'	TCGGCCTCCCAAAGTGCTGGGA	34565	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	FLJ20136	3'	TCAGCCTCCCAAAGTGCTGGGA	34617	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	FLJ20342	3'	TCAGCCTCCCAAAGTGCTGGGA	34995	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	FLJ20344	3'	TCAGCCTCCCAAAGTGCTGGGA	35017	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	FLJ20699	3'	CCCAAAGTGCTGTGATG	35562		
			TATCACAGCACTTTGGG			

GTAGTGTCGTGAAACCC

GAM1400	FLJ20700	3'	TCAGCCTCCCAAAGTGCTGGGA	35586	A	C
		T	ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	FLJ20897	5'	TCGGCCTCCCAAAGTGTTGGGA	50470	A	
		T	ATC CAGCACTTTGGGAGGCCGA			
			TAG GTTGTGAAACCCTCCGGCT			
			G			
GAM1400	FLJ21302	3'	TCGGCCTCCCAAAGTGCTGGGA	43223	A	
		T	ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	FLJ21777	3'	TCGACCTCCCAAAGCGTTAGGA	49866	AC A	C
		T	ATC AGC CTTTGGGAGG CGA			
			TAG TTG GAAACCCTCC GCT			
			GA C A			
GAM1400	FLJ22002	3'	TCGGCCTCCCAAAGTGCTAGGA	45780	AC	
		T	ATC AGCACTTTGGGAGGCCGA			
			TAG TCGTGAAACCCTCCGGCT			
			GA			
GAM1400	FLJ22316	5'	TCGGCCTCCCAAAGTGCTGGGA	46924	A	
		T	ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	FLJ22800	3'	TCAGCCTCCTAAAGTGCTGCGA	45607	A	C
		T	ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAATCCTCCG CT			
			C A			
GAM1400	FLJ22969	3'	TCGGCCTCCCAAAGTGCTGGGA	68665	A	
		T	ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	FLJ23392	3'	TCAGCCTCCCAAAGTGCTGGGA	45546	A	C
		T	ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	FLJ23563	3'	TCGGCCTCCCAAAGTTCTGGGA	67602	A C	
		T	ATC CAG ACTTTGGGAGGCCGA			

				TAG GTC TGAAACCCTCCGGCT		
				G T		
GAM1400	FLJ30532	3'	TCAGCCTCCCAAAGTGTTGGGA	58552	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTTGTGAAACCCTCCG CT			
			G A			
GAM1400	FLJ31153	3'	GCCTCCCAAAGCGCTGGGAT	58124	A A	
			ATC CAGC CTTTGGGAGGC			
			TAG GTCG GAAACCCTCCG			
			G C			
GAM1400	FLJ32334	3'	TCGACCTCCCAAAGTGCTGGGA	57986	A	C
	T		ATC CAGCACTTTGGGAGG CGA			
			TAG GTCGTGAAACCCTCC GCT			
			G A			
GAM1400	FLJ32865	3'	TCAGCCTCCCAAAGTGCTGGGA	58183	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	FLJ32894	3'	TCAGCCTCCCAAAGTGCTGGGA	58341	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	GNG4	3'	TCGGCCTCCCAAAGCGCTGGGA	15626	A A	
	T		ATC CAGC CTTTGGGAGGCCGA			
			TAG GTCG GAAACCCTCCGGCT			
			G C			
GAM1400	GOLGA3	3'	TCAGCCTCCCAAAGTGCTGGA	19721	A	C
			TC CAGCACTTTGGGAGGC GA			
			AG GTCGTGAAACCCTCCG CT			
			- A			
GAM1400	GREB1	3'	TCGGCCTCCCAAAGTGCTGGGA	27889	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	GTF2E1	3'	TCGGCCTCCCAAAGTGCTGT	18620		
			ACAGCACTTTGGGAGGCCGA			
			TGTCGTGAAACCCTCCGGCT			
GAM1400	HARS2	3'	TCGGCCTCCCAAAGTGCTGGGA	55039	A	
	T		ATC CAGCACTTTGGGAGGCCGA			

			TAG GTCGTGAAACCCTCCGGCT G		
GAM1400	HSMPP8	3'	TCGGCCTCCCAAAGTGCTTGGGA 93485	AC	
	T		ATC AGCACTTTGGGAGGCCGA		
			TAG TCGTGAAACCCTCCGGCT		
			GT		
GAM1400	HSNOV1	3'	CGACCTCCCAAAGTGCTGGGAT 34007	A	C
			ATC CAGCACTTTGGGAGG CG		
			TAG GTCGTGAAACCCTCC GC		
			G A		
GAM1400	HT002	3'	CGGCCTCCACAGCTGTGA 25937	ACTT	_
			TCACAGC TG GGAGGCCG		
			AGTGTCTG AC CCTCCGGC		
			_____ A		
GAM1400	HT002	3'	CGGCCTCCCAAATCGCT 25938	AC	
			AGC TTTGGGAGGCCG		
			TCG AAACCCTCCGGC		
			CT		
GAM1400	KIAA0087	3'	TCGGCCTCCCAAATGCTGGGA 28706	A	C
	T		ATC CAGCA TTTGGGAGGCCGA		
			TAG GTCGT AAACCCTCCGGCT		
			G A		
GAM1400	KIAA0210	5'	TCAGCCTCCCAAAGTGCTGGGA 28486	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1400	KIAA0391	3'	TCAGCCTCCCAAAGTGCTGGGA 27922	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1400	KIAA0459	3'	TCAGCCTCCCAAAGTGCTAGGA 61006	AC	C
	T		ATC AGCACTTTGGGAGGC GA		
			TAG TCGTGAAACCCTCCG CT		
			GA A		
GAM1400	KIAA0469	3'	TCAGCCTCCCAAAGTGCTAGGA 29352	AC	C
	T		ATC AGCACTTTGGGAGGC GA		
			TAG TCGTGAAACCCTCCG CT		
			GA A		
GAM1400	KIAA0469	3'	TCAGCCTCCCAAAGTGCTGGGA 29353	A	C
	T		ATC CAGCACTTTGGGAGGC GA		



				TAG GTCGTGAAACCCTCCG CT			
				G	A		
GAM1400	KIAA0472	5'	GCCTCCCAAAGTGCTGGGAT	71865	A		
				ATC CAGCACTTTGGGAGGC			
				TAG GTCGTGAAACCCTCCG			
				G			
GAM1400	KIAA0513	3'	TCAGCCTCCCAAAGTGCTGGGA	28374	A	C	
		T	ATC CAGCACTTTGGGAGGC GA				
			TAG GTCGTGAAACCCTCCG CT				
			G	A			
GAM1400	KIAA0513	5'	TCGGCCTCCCAAAGTGTTGGGA	28377	A		
		T	ATC CAGCACTTTGGGAGGCCGA				
			TAG GTTGTGAAACCCTCCGGCT				
			G				
GAM1400	KIAA0555	3'	TCAGCCTCCCAAAGTGCTAGGA	28887	AC	C	
		T	ATC AGCACTTTGGGAGGC GA				
			TAG TCGTGAAACCCTCCG CT				
			GA	A			
GAM1400	KIAA0557	3'	TCGGCCTCCCAAAGTGCTGGGA	78010	A		
		T	ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT				
			G				
GAM1400	KIAA0563	5'	TCGGCCTCCCAAAGTTCTGGGA	29194	A	C	
		T	ATC CAG ACTTTGGGAGGCCGA				
			TAG GTC TGAAACCCTCCGGCT				
			G	T			
GAM1400	KIAA0594	3'	TCAGCCTCCCAAGTAACTGGGA	64903	A	CAC	C
			TC CAG TTTGGGAGGC GA				
			AG GTC GAACCCTCCG CT				
			G	AAT	A		
GAM1400	KIAA0594	3'	TCGGCCTCCCAAAGTGCTGGGA	64905	A		
		T	ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT				
			G				
GAM1400	KIAA0599	3'	TCGGCCTCCCAAAGTGCTGGGA	77193	A		
		T	ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT				
			G				
GAM1400	KIAA0682	3'	TCGGCCTCCCAAAGTGTTGGGGA	29373	ACA		
		T	ATC GCACTTTGGGAGGCCGA				

				TAG TGTGAAACCCTCCGGCT		
				GGG		
GAM1400	KIAA0798	3'	TCAGCCTCCCAAAGTGCTGGGA	27729	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	KIAA0831	5'	TCCCAAAGTGCTGCGAT	29982	A	
			ATC CAGCACTTTGGGA			
			TAG GTCGTGAAACCCT			
			C			
GAM1400	KIAA0841	3'	TCGGCCTCCCAAAGTGCTGGGA	71403	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	KIAA0861	3'	TCGGCCTCCCAAAGTGCTGGGA	88935	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	KIAA0931	3'	TCCCAAAGTGCTGTGAT	67425		
			ATCACAGCACTTTGGGA			
			TAGTGTGTCGTGAAACCCT			
GAM1400	KIAA1054	3'	TCAGCCTCCCAAATGCTGGGA	68451	A	C C
	T		ATC CAGCA TTTGGGAGGC GA			
			TAG GTCGT AAACCCTCCG CT			
			G A A			
GAM1400	KIAA1143	3'	TCGGCCTCCCAAAGTGCTGGGA	68690	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	KIAA1155	3'	TCAGCCTCCCAAAGTGCTGGGA	62242	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	KIAA1185	3'	TCAGCCTCCCAAAGTGCTGGGA	62608	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	KIAA1193	3'	TCGGCCTCCCAAAGTGCTGGGA	67651	A	
	T		ATC CAGCACTTTGGGAGGCCGA			

				TAG GTCGTGAAACCCTCCGGCT				
				G				
GAM1400	KIAA1198	3'	TCGGCCTCCCAAAGTGCTGGGA	63338	A			
	T		ATC CAGCACTTTGGGAGGCCGA					
			TAG GTCGTGAAACCCTCCGGCT					
			G					
GAM1400	KIAA1198	3'	TCGGCCTCCCAAAGTGCTGGGA	63339	A			
	T		ATC CAGCACTTTGGGAGGCCGA					
			TAG GTCGTGAAACCCTCCGGCT					
			G					
GAM1400	KIAA1210	3'	TCAGCCTCCCAAAGCTGGGAT	96335	A	AC	C	
			ATC CAGC TTTGGGAGGC GA					
			TAG GTCG AAACCCTCCG CT					
			G A_ A					
GAM1400	KIAA1257	3'	TCAGCCTCCCAAAGTGCTGGGA	62759	A		C	
	T		ATC CAGCACTTTGGGAGGC GA					
			TAG GTCGTGAAACCCTCCG CT					
			G A					
GAM1400	KIAA1280	5'	TCAGCCTCCCAAAGTTCGAGA	69732	A	C	C	
	TG		TATC CAG ACTTTGGGAGGC GA					
			GTAG GTC TGAAACCCTCCG CT					
			A T A					
GAM1400	KIAA1320	5'	TCGGCCTCCCAAAGTGCTGGGA	69312	A			
	T		ATC CAGCACTTTGGGAGGCCGA					
			TAG GTCGTGAAACCCTCCGGCT					
			G					
GAM1400	KIAA1328	5'	TCGGCCTCCCAAAGTGCTGGGA	61656	A			
	T		ATC CAGCACTTTGGGAGGCCGA					
			TAG GTCGTGAAACCCTCCGGCT					
			G					
GAM1400	KIAA1571	3'	TCAGCCTCCCAAAGTGCTGGGA	60962	A		C	
	T		ATC CAGCACTTTGGGAGGC GA					
			TAG GTCGTGAAACCCTCCG CT					
			G A					
GAM1400	KIAA1615	3'	TCAGCCTCCCAAAGTGCTGGGA	68731	A		C	
	T		ATC CAGCACTTTGGGAGGC GA					
			TAG GTCGTGAAACCCTCCG CT					
			G A					
GAM1400	KIAA1615	3'	TCGGCCTCCCAAAGTGCTGGGA	68736	A			
	T		ATC CAGCACTTTGGGAGGCCGA					

Accession	Gene	Strand	Sequence	Start	End	RefSeq	GenBank
GAM1400	KIAA1655	3'	TCAGCCTCCCAAAGTGCTGGGA	66626		A	C
	T		ATC CAGCACTTTGGGAGGC GA				
			TAG GTCGTGAAACCCTCCG CT				
			G A				
GAM1400	KIAA1671	3'	TCAGCCTCCCAAAGTGCTCGGA	65693		AC	C
	T		ATC AGCACTTTGGGAGGC GA				
			TAG TCGTGAAACCCTCCG CT				
			GC A				
GAM1400	KIAA1671	3'	TCAGCCTCCCAAAGTGCTGGGA	65694		A	C
	T		ATC CAGCACTTTGGGAGGC GA				
			TAG GTCGTGAAACCCTCCG CT				
			G A				
GAM1400	KIAA1727	3'	TCAGCCTCCCAAAGTGCTGGGA	64066		A	C
	T		ATC CAGCACTTTGGGAGGC GA				
			TAG GTCGTGAAACCCTCCG CT				
			G A				
GAM1400	KIAA1737	3'	TCAGCCTCCCAAAGTGCTG	67364			C
			CAGCACTTTGGGAGGC GA				
			GTCGTGAAACCCTCCG CT				
			A				
GAM1400	KIAA1755	3'	TCAGCCTCCCAAAGTGCTGGGA	61355		A	C
	T		ATC CAGCACTTTGGGAGGC GA				
			TAG GTCGTGAAACCCTCCG CT				
			G A				
GAM1400	KIAA1789	5'	TCACAAAGCCTGTGATA	67104		CA	G
			TATCACAG CTTTG GA				
			ATAGTGTC GAAAC CT				
			C_ A				
GAM1400	KIAA1877	3'	TCGGCCTCCCAAAGTGATGGGA	66178		A G	
	T		ATC CA CACTTTGGGAGGCCGA				
			TAG GT GTGAAACCCTCCGGCT				
			G A				
GAM1400	KIAA1924	3'	TCAGCCTCCCAAAGTGCTGGGA	73688		A	C
	T		ATC CAGCACTTTGGGAGGC GA				
			TAG GTCGTGAAACCCTCCG CT				
			G A				
GAM1400	LAMP3	3'	TCAGCCTCCCAAAGTGCTGGGA	59495		A	C
	T		ATC CAGCACTTTGGGAGGC GA				

			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1400	LY75	3'	TCGGCCTCCCAAAGTGCTGGGA 9844	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	MARCKS	3'	TCAACCAAGCTGTGATA 9872	ACT GA	
			TATCACAGC TTGG GG		
			ATAGTGTCTG AACC CT		
			AA		
GAM1400	MCLC	3'	TCGGCCTCCCAAAGTGCTGGGA 30694	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	MEF-2	3'	TCGGCCTCCCAAATCCTGGGA 64397	A CAC	
	T		ATC CAG TTTGGGAGGCCGA		
			TAG GTC AAACCCTCCGGCT		
			G CTA		
GAM1400	MGC10200	3'	TCAGCCTCCCAAAGTGCTGGGA 58994	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1400	MGC10911	5'	TCGGCCTCCCAAAGTGCCGGGA 50212	ACA	
	TG		TATC GCACTTTGGGAGGCCGA		
			GTAG CGTGAAACCCTCCGGCT		
			GGC		
GAM1400	MGC10955	5'	CCTCCCACTGCCATGGTA 51045	CA CTT	
			TATCA GCA TGGGAGG		
			ATGGT CGT ACCCTCC		
			AC C__		
GAM1400	MGC12518	3'	TCAGCCTCCCAAAGTGCTGGGA 64085	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1400	MGC1842	3'	TCGGCCTCCCAAAGTG 65660		
			CACTTTGGGAGGCCGA		
			GTGAAACCCTCCGGCT		
GAM1400	MGC21738	3'	TCAGCCTCCCAAAGTGCTGGGA 58918	A	C
	T		ATC CAGCACTTTGGGAGGC GA		

				TAG GTCGTGAAACCCTCCG CT		
				G A		
GAM1400	MGC2477	5'	TCGGCCTCCCAAAGTGCTGGGA 44070	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	MGC2603	3'	TCAGCCTCCCAAAGTGCTGAGA 43862	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			A A			
GAM1400	MGC26914	3'	GCCTCCCAAACCATGAGA 58666	A		
			TC CA TTTGGGAGGC			
			AG GT AAACCCTCCG			
			A ACC_			
GAM1400	MGC4415	3'	GCCTCCGGTGCTGT 48951	TTG		
			ACAGCACT GGAGGC			
			TGTCGTGG CCTCCG			
GAM1400	MLZE	5'	TCAGCCTCCCAAAGTGCTGGGA 48627	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	moblak	3'	TCAGCCTCCCAAAGTGCTGGGA 55512	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	moblak	3'	TCGGCCTCCCAAAGTGCTGGA 55515	A		
			TC CAGCACTTTGGGAGGCCGA			
			AG GTCGTGAAACCCTCCGGCT			
GAM1400	MRPS27	3'	TCAGCCTCCCAAAGTGCTGGGA 30644	A		C
	TG		TATC CAGCACTTTGGGAGGC GA			
			GTAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	MtFMT	3'	TCAGCCTCCCAAAGTGCTATGA 57659	C		C
	T		ATCA AGCACTTTGGGAGGC GA			
			TAGT TCGTGAAACCCTCCG CT			
			A A			
GAM1400	MYO5C	3'	TCAGCCTCCCAAAGTGCTAGGA 38111	AC		C
	T		ATC AGCACTTTGGGAGGC GA			

		TAG TCGTGAAACCCTCCG CT			
		GA A			
GAM1400	NINJ2 T	3'	TCGGCCTCCCAAAGTGCTGGGA 33289	A	
		ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400	Nup43 T	3'	TCAGCCTCCCAAATGCTGGGA 45008	A	C C
		ATC CAGCA TTTGGGAGGC GA			
		TAG GTCGT AAACCCTCCG CT			
		G A A			
GAM1400	Nup43	3'	TCGGCCTCCCAAAGTGCTGTGAT 45010		G
		ATCACAGCACTTTGG AGGCCGA			
		TAGTGTGCTGAAACC TCCGGCT			
		—			
GAM1400	NXN T	3'	TCGGCCTCCCAAAGTGCTGGGA 42426	A	
		ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400	OR51E2 T	3'	TCAGCCTCCCAAAGTGTTGGGA 47799	A	C
		ATC CAGCACTTTGGGAGGC GA			
		TAG GTTGTGAAACCCTCCG CT			
		G A			
GAM1400	OSBPL2	3'	CCTCCCAAAGTGCTGGGAT 57859	A	
		ATC CAGCACTTTGGGAGG			
		TAG GTCGTGAAACCCTCC			
		G			
GAM1400	OSBPL2	3'	CCTCCCAAAGTGCTGGGAT 29208	A	
		ATC CAGCACTTTGGGAGG			
		TAG GTCGTGAAACCCTCC			
		G			
GAM1400	PELI1 T	5'	TCGACCTCCCAAAGTGCTGGGA 40290	A	C
		ATC CAGCACTTTGGGAGG CGA			
		TAG GTCGTGAAACCCTCC GCT			
		G A			
GAM1400	PP2447 TG	5'	TCAGCCTCCCAAAGTGCTGGGA 47321	A	C
		TATC CAGCACTTTGGGAGGC GA			
		GTAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400	PPIL3 T	5'	TCGGCCTCCCAAAGTGTTAGGA 55661	AC	
		ATC AGCACTTTGGGAGGCCGA			

				TAG TTGTGAAACCCCTCCGGCT			
				GA			
GAM1400	PRO0245	5'	GCCTCCCAAAGTGCTGAGAT	26129	A		
			ATC CAGCACTTTGGGAGGC				
			TAG GTCGTGAAACCCTCCG				
			A				
GAM1400	PRO0365	5'	CCTTCCAAAATGCTGCGAT	26156	A	C	
			ATC CAGCA TTTGGGAGG				
			TAG GTCGT AAACCTTCC				
			C A				
GAM1400	PRO0365	5'	TCGGCCTCCCAAAGTGCTGGGA	26172	A		
	T		ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT				
			G				
GAM1400	PRO0899	5'	TCGGCCTCCCAAAGTGCTGGGG	37697	A		
			TC CAGCACTTTGGGAGGCCGA				
			GG GTCGTGAAACCCTCCGGCT				
			G				
GAM1400	PRO2955	3'	TCGGCCTCCCAAAGTGCTGGGA	37649	A		
	T		ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT				
			G				
GAM1400	PSPH	3'	TCAGCCTCCCAAAGTGCTGGGA	15917	A		C
	T		ATC CAGCACTTTGGGAGGC GA				
			TAG GTCGTGAAACCCTCCG CT				
			G A				
GAM1400	PSTPIP2	3'	TCGGCCTCCCAAAGTGCTGGGA	44400	A		
	T		ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT				
			G				
GAM1400	RAB21	3'	TCGGCCTCCCAAAGTGCTGGGA	30392	A		
	T		ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT				
			G				
GAM1400	RAI	5'	CGGCCTCCCAAAGTTCTGGGAT	21876	A	C	
			ATC CAG ACTTTGGGAGGCCG				
			TAG GTC TGAAACCCTCCGGC				
			G T				
GAM1400	RAP140	3'	TCAGCCTCCCAAAGTGCTGGGA	30847	A		C
	T		ATC CAGCACTTTGGGAGGC GA				



				TAG GTCGTGAAACCCTCCG CT		
				G A		
GAM1400	RNO2	5'	TCAGCCTCCCAAAGTGCTGGGA 52777	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	SCAMP-4	3'	TCCCAAAGTGCTGGGATA 54401	A		
			TATC CAGCACTTTGGGA			
			ATAG GTCGTGAAACCCT			
			G			
GAM1400	SCYA22	3'	TCAGCCTCCCAAAGTGCTGGGA 90956	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	SCYA22	3'	TCAGCCTCCCAAAGTGCTGGGA 90957	A		C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	SERF1B	3'	TCGGCCTCCCAAAGTGCTGGGA 43426	A		
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	SFRS10	3'	GGTGCTTCAAAGTACATGATA 15978	CAGC		AG
			TATCA ACTTTGGG GCC			
			ATAGT TGAACTT TGG			
			ACA_ CG			
GAM1400	SLC12A8	3'	TCAGCCTCCCAAAGTACTGGGA 44904	A C		C
	T		ATC CAG ACTTTGGGAGGC GA			
			TAG GTC TGAAACCCTCCG CT			
			G A A			
GAM1400	SLC19A3	3'	TCGGCCTCCCAAAGAGCTGAGA 47497	A A		
			TC CAGC CTTTGGGAGGCCGA			
			AG GTCG GAAACCCTCCGGCT			
			A A			
GAM1400	SMCR7	3'	CGGCCTCCCAGTGTGC 57507	T		
			GCAC TTGGGAGGCCG			
			CGTG GACCCTCCGGC			
			T			
GAM1400	SNAPC1	3'	TCAGCCTCCCAAAGTACTGGGA 11845	A C		C
	T		ATC CAG ACTTTGGGAGGC GA			

			TAG GTC TGAAACCCTCCG CT		
			G A A		
GAM1400	SQV7L	5'	TCCCAAAGTGCTGTGAT 70580		
			ATCACAGCACTTTGGGA		
			TAGTGTCGTGAAACCCT		
GAM1400	SRP54	3'	TCAATTAAAGTGCTGT 11962	GA	
			ACAGCACTTTGG GG		
			TGTCGTGAAATT CT		
			AA		
GAM1400	SUN1	3'	TCGGCCTCCCAAAGTGCTGTTG 47163	_	
	G		TCA CAGCACTTTGGGAGGCCGA		
			GGT GTCGTGAAACCCTCCGGCT		
			T		
GAM1400	SYT13	3'	TCGGCCTCCCAAAGTACTGGGA 93460	A C	
	T		ATC CAG ACTTTGGGAGGCCGA		
			TAG GTC TGAAACCCTCCGGCT		
			G A		
GAM1400	SYTL4	5'	TCAGCCTCCCAAAGTGCTGGGA 54945	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1400	TADA3L	3'	TCGGCCTCCCAAAGTGCCGGGA 56000	ACA	
	T		ATC GCACTTTGGGAGGCCGA		
			TAG CGTGAAACCCTCCGGCT		
			GGC		
GAM1400	TCL6	5'	TCGGCCTCCCAAAGTGCTGGGA 27008	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	TCL6	3'	TCGGCCTCCCAAAGTGCTGGGA 27009	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	TCL6	5'	TCGGCCTCCCAAAGTGCTGGGA 24992	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	TCL6	3'	TCGGCCTCCCAAAGTGCTGGGA 24993	A	
	T		ATC CAGCACTTTGGGAGGCCGA		

			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	TCL6	5'	TCGGCCTCCCAAAGTGCTGGGA 40090	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	TCL6	5'	TCGGCCTCCCAAAGTGCTGGGA 40116	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	TRIM16	3'	TCGGCCTCCCAAAGTGCTGGGA 21345	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	TRIM5	3'	TCGGCCTCCCAAAGTGCTGGGA 52305	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	TRIM5	3'	TCGGCCTCCCAAAGTGCTGGGA 52369	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	TUCAN	3'	TCAGCCTCCCAAAGTGCTGGGA 30283	A	C
	T		ATC CAGCACTTTGGGAGGC GA		
			TAG GTCGTGAAACCCTCCG CT		
			G            A		
GAM1400	TUSP	3'	TCGGCCTCCCAAAGTGCTGGGA 39643	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	TXNL2	3'	TCAGCCTCCCAAAGTGCTGGA 21553	A	C
			TC CAGCACTTTGGGAGGC GA		
			AG GTCGTGAAACCCTCCG CT		
			—            A		
GAM1400	VDU1	3'	TCGGCCTCCCAAAGTGCTGGGA 30430	A	
	T		ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	YAP	5'	CCTCCCAAAGTGCTGGA 36785	A	
			TC CAGCACTTTGGGAGG		

AG GTCGTGAAACCCTCC

GAM1400	ZNF338	3'	TCAGCCTCCCAAAGTGCTGGGA	42016	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	LOC112687	3'	TCAGCCTCCCAAAGTGCTGGGA	72867	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	LOC112817	3'	TCGGCCTCCCAAAGTGCTGGGA	56518	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	LOC115098	5'	TCAGCCTCCCAAAGCACGGGGA	56595	ACAGCA	C
	T		ATC CTTTGGGAGGC GA			
			TAG GAAACCCTCCG CT			
			GGGCAC A			
GAM1400	LOC126272	3'	TCGGCCTCCCAAAGTGCTGGGA	76091	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	LOC128077	3'	TCAGCCTCCCAAAGTGCTGGGA	74722	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	LOC128989	3'	TCGGCCTCCCAAAGTGCTGGGA	74819	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	LOC130813	3'	TCAGCCTCCCAAAGTGCTGGGA	75778	A	C
	T		ATC CAGCACTTTGGGAGGC GA			
			TAG GTCGTGAAACCCTCCG CT			
			G A			
GAM1400	LOC132625	3'	TCGGCCTCCCAAAGTGCTGGGA	75916	A	
	T		ATC CAGCACTTTGGGAGGCCGA			
			TAG GTCGTGAAACCCTCCGGCT			
			G			
GAM1400	LOC135154	3'	TCAGCCTCCCAAAGTGCTGGGA	75222	A	C
	T		ATC CAGCACTTTGGGAGGC GA			

		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1400	LOC144305 3'	TCGGCCTCCCAAAGTGTTGGGA 83037	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTTGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC144317 5'	TCGGCCTCCCAAAGTGCTGGGA 76801	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC144524 5'	TCGGCCTCCCAAAGTGCTGGGA 83139	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC145009 3'	TCGGCCTCCCAAAGTGCTGGGA 60352	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC145622 3'	TCAGCCTCCCAAAGTGCTGGGA 77313	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT		
		G            A		
GAM1400	LOC146050 3'	TCGGCCTCCCAAAGTGCTGGGA 77652	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC146455 3'	TCAGCCTCCCAAAATGCTGGGA 77909	A	C    C
	T	ATC CAGCA TTTGGGAGGC GA		
		TAG GTCGT AAACCCTCCG CT		
		G    A        A		
GAM1400	LOC146599 5'	TCAGCCTCCCAAAGTGCTAGGA 78028	AC	C
	T	ATC AGCACTTTGGGAGGC GA		
		TAG TCGTGAAACCCTCCG CT		
		GA            A		
GAM1400	LOC146603 5'	TCGGCCTCCCAAAGTGTTGGGA 78021	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTTGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC146784 5'	TCGGCCTCCCAAAGTGCTGGGA 78127	A	
	T	ATC CAGCACTTTGGGAGGCCGA		

		TAG GTCGTGAAACCCTCCGGCT G			
GAM1400	LOC146909 3'	TCGGCCTCCCAAAGTGCTGGGA 78187	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT G			
GAM1400	LOC147071 5'	TCGGCCTCCCAAAGTTCTGGGA 73008	A	C	
	T	ATC CAG ACTTTGGGAGGCCGA			
		TAG GTC TGAAACCCTCCGGCT G T			
GAM1400	LOC147080 5'	TCGGCCTCCCAAAGTGCTGGGA 83939	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT G			
GAM1400	LOC147160 5'	TCAGCCTCCCAAAGTGCTGGGA 83972	A		C
	T	ATC CAGCACTTTGGGAGGC GA			
		TAG GTCGTGAAACCCTCCG CT G A			
GAM1400	LOC147166 3'	TCGGCCTCCCAAAGTGCTGGGA 78292	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT G			
GAM1400	LOC147990 3'	TCAGCCTCCCAAAGTGCTGGGA 84101	A		C
	T	ATC CAGCACTTTGGGAGGC GA			
		TAG GTCGTGAAACCCTCCG CT G A			
GAM1400	LOC148137 3'	TCGGCCTCCCAAAGTGCTGGGA 58442	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT G			
GAM1400	LOC148887 5'	TCGGCCTCCCAAAGTGCTGGGA 84249	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT G			
GAM1400	LOC148918 5'	TCAGCCTCCCAAATGCTTCGA 79084	AC	C	C
	T	ATC AGCA TTTGGGAGGC GA			
		TAG TCGT AAACCCTCCG CT CT A A			
GAM1400	LOC149421 3'	TCAGCCTCCCAAAGTGCTGGGA 79363	A		C
	T	ATC CAGCACTTTGGGAGGC GA			

		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1400	LOC149478 3'	TCGGCCTCCCAAAGTGCTGGGA 79384	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC149577 3'	TCGGCCTCCCAAAATGCTGGGA 84523	A	C
	T	ATC CAGCA TTTGGGAGGCCGA		
		TAG GTCGT AAACCCTCCGGCT		
		G    A		
GAM1400	LOC149692 3'	TCGGCCTCCCAAAGTGCTG 84595		
		CAGCACTTTGGGAGGCCGA		
		GTCGTGAAACCCTCCGGCT		
GAM1400	LOC149703 5'	TCAGCCTCCCAAAGTGCTGGGA 84659	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT		
		G            A		
GAM1400	LOC150212 5'	TCAGCCTCCCAAAGTGCTGGA 79707	A	C
		TC CAGCACTTTGGGAGGC GA		
		AG GTCGTGAAACCCTCCG CT		
		—            A		
GAM1400	LOC150225 3'	TCAGCCTCCCAAAGTGCTGGGA 85012	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT		
		G            A		
GAM1400	LOC150282 5'	TCAGCCCCCAAAGTGCTGGGA 79732	A	A C
	T	ATC CAGCACTTTGGG GGC GA		
		TAG GTCGTGAAACCC CCG CT		
		G            C    A		
GAM1400	LOC150290 3'	TCAGCCTCCCAAAGTGTTGATG 79778	—	C
	A	TCA CAGCACTTTGGGAGGC GA		
		AGT GTTGTGAAACCCTCCG CT		
		A            A		
GAM1400	LOC150407 3'	TCAGCCTCCCAAAGTACTGGGA 79831	A C	C
	T	ATC CAG ACTTTGGGAGGC GA		
		TAG GTC TGAAACCCTCCG CT		
		G    A            A		
GAM1400	LOC150407 3'	TCAGCCTCCCAAAGTGCTGGGA 79832	A	C
	T	ATC CAGCACTTTGGGAGGC GA		

		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1400	LOC150587 3'	TCGGCCTCCCAAAGTGCA	85067	CA
		TCA GCACTTTGGGAGGCCGA		
		AGT CGTGAAACCCTCCGGCT		
		A_		
GAM1400	LOC150630 5'	TCAGCCTCCCAAAGTGCTGGGA	85113	A            C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT		
		G            A		
GAM1400	LOC150960 3'	TCAGCCTCCCAAAGTAGCTGGGA	80071	A _ T    C
		TC CAGC ACTT GGGAGGC GA		
		AG GTCG TGAA CCCTCCG CT		
		G A _ A		
GAM1400	LOC150960 3'	TCGGCCTCCCAAAGTGCTGT	80074	
		ACAGCACTTTGGGAGGCCGA		
		TGTCGTGAAACCCTCCGGCT		
GAM1400	LOC151201 3'	TCGGCCTCCCAAAGTAGTGGGA	85294	ACA _
	T	ATC GC ACTTTGGGAGGCCGA		
		TAG TG TGAAACCCTCCGGCT		
		GG_ A		
GAM1400	LOC151475 5'	TCGGCCTCCCAAAGTGCTGGGA	85422	A
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC151484 3'	GCCTCCACCTGTGA	80264	CACTT
		TCACAG TGGGAGGC		
		AGTGTC ACCCTCCG		
		C_		
GAM1400	LOC151826 3'	TCGGCCTCCCAAAGTGCTGGGA	80369	A
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC151979 5'	TCGGCCTCCCAAAGTGCTGGGA	80427	A
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC152348 3'	TCAGCCTCCCAAAGTGCTGGGA	85699	A            C
	T	ATC CAGCACTTTGGGAGGC GA		



		TAG GTCGTGAAACCCTCCG CT G            A			
GAM1400	LOC152445 3'	TCAGCCTCCCAAATGTTGAGA 85762	A	C	C
	T	ATC CAGCA TTTGGGAGGC GA 			
		TAG GTTGT AAACCCTCCG CT A    A    A			
GAM1400	LOC152445 3'	TCGGCCTCCCAAAGTGCTGGGA 85764	A		
	T	ATC CAGCACTTTGGGAGGCCGA 			
		TAG GTCGTGAAACCCTCCGGCT G			
GAM1400	LOC153077 3'	TCGGCCTCCCAAAGTGCTGGGT 85919	A		
		ATC CAGCACTTTGGGAGGCCGA 			
		TGG GTCGTGAAACCCTCCGGCT			
		—			
GAM1400	LOC153883 5'	TCAGCCTCCCAAATGCTTGA 80987	AC	C	C
	T	ATC AGCA TTTGGGAGGC GA 			
		TAG TCGT AAACCCTCCG CT GT    A    A			
GAM1400	LOC154007 3'	TCAGCCTCCCAAATGCTGGGA 81022	A	C	C
		TC CAGCA TTTGGGAGGC GA 			
		AG GTCGT AAACCCTCCG CT G    A    A			
GAM1400	LOC154141 5'	TCGGCCTCCCAAAGTGCTGGGA 86175	A		
	T	ATC CAGCACTTTGGGAGGCCGA 			
		TAG GTCGTGAAACCCTCCGGCT G			
GAM1400	LOC154282 5'	TCAGCCTCCCAAAGTGCTGGGA 86209	A		C
	T	ATC CAGCACTTTGGGAGGC GA 			
		TAG GTCGTGAAACCCTCCG CT G            A			
GAM1400	LOC154726 5'	TCAGCCTCCCAAAGTGCTGGGA 81108	A		C
	T	ATC CAGCACTTTGGGAGGC GA 			
		TAG GTCGTGAAACCCTCCG CT G            A			
GAM1400	LOC154877 3'	TCAGCCTCCCAAAGTCCTGGGA 86310	A	C	C
	T	ATC CAG ACTTTGGGAGGC GA 			
		TAG GTC TGAAACCCTCCG CT G    C    A			
GAM1400	LOC154877 3'	TCGGCCTCCCAAAGTGCTGGAT 86315	A		
		ATC CAGCACTTTGGGAGGCCGA 			

TAG GTCGTGAAACCCTCCGGCT

GAM1400 LOC154877 5' TCGGCCTCCCAAAGTTCTGGGA 86316 A C  
T ATC CAG ACTTTGGGAGGCCGA

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TAG GTC TGAAACCCTCCGGCT

G T

GAM1400 LOC154930 3' TCCCAAAGTGCTGGAATA 81182 CA  
TAT CAGCACTTTGGGA

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ATA GTCGTGAAACCCT

AG

GAM1400 LOC157247 5' TCGGCCTCCCAAAGTGCTGGGA 81379 A  
T ATC CAGCACTTTGGGAGGCCGA

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TAG GTCGTGAAACCCTCCGGCT

G

GAM1400 LOC157506 3' TCGGCCTCCCAAAGTGCTGGGA 81447 A  
T ATC CAGCACTTTGGGAGGCCGA

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TAG GTCGTGAAACCCTCCGGCT

G

GAM1400 LOC157507 5' TCAGCCTCCCAAAGTGCTGGGA 81461 A C  
T ATC CAGCACTTTGGGAGGC GA

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TAG GTCGTGAAACCCTCCG CT

G A

GAM1400 LOC157681 5' TCGGCCTCCCAAAGTGCTGGGA 81546 A  
TC CAGCACTTTGGGAGGCCGA

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AG GTCGTGAAACCCTCCGGCT

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GAM1400 LOC158014 5' CGCCTCCCAAAGGGCT 81646 A C  
AGC CTTTGGGAGGC G

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TCG GAAACCCTCCG C

G A

GAM1400 LOC158476 3' TCGGCCTCCCAAAGTGCTGGGA 86856 A  
T ATC CAGCACTTTGGGAGGCCGA

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TAG GTCGTGAAACCCTCCGGCT

G

GAM1400 LOC158549 5' TCGGCCTCCCAAAGTGTTGGGA 86868 A  
T ATC CAGCACTTTGGGAGGCCGA

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TAG GTTGTGAAACCCTCCGGCT

G

GAM1400 LOC158709 3' TCAGCCTCCCAAAGTGCTGGGA 81985 A C  
T ATC CAGCACTTTGGGAGGC GA

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			TAG GTCGTGAAACCCTCCG CT		
			G A		
GAM1400	LOC163590 5'	TCAGCCTCCCAAAGTGCTGGGA 58864	A		C
	T	ATC CAGCACTTTGGGAGGC GA			
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400	LOC169611 3'	TCAGCCTCCCAAAGTGTTGGGA 82777	A		C
	T	ATC CAGCACTTTGGGAGGC GA			
		TAG GTTGTGAAACCCTCCG CT			
		G A			
GAM1400	LOC170082 5'	TCGGCCTCCCAAAGTGCTGGGA 82566	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400	LOC170409 5'	TCGGCCTCCCAAAGTGCTGGGA 82869	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		G			
GAM1400	LOC196047 5'	TCGGCCTCCCAAAGTGCTGCGA 89612	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTCGTGAAACCCTCCGGCT			
		C			
GAM1400	LOC196264 3'	TCGGCCTCCCAAAGTGTTGGGA 87615	A		
	T	ATC CAGCACTTTGGGAGGCCGA			
		TAG GTTGTGAAACCCTCCGGCT			
		G			
GAM1400	LOC196411 3'	TCAGCCTCCCAAAGTGCTG 87687			C
		CAGCACTTTGGGAGGC GA			
		GTCGTGAAACCCTCCG CT			
		A			
GAM1400	LOC196529 3'	TCAGCCTCCCAAAGTGCTGGGA 87781	A		C
	TG	TATC CAGCACTTTGGGAGGC GA			
		GTAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400	LOC197358 3'	TCAGCCTCCCAAAGTGCTGGGA 88049	A		C
	T	ATC CAGCACTTTGGGAGGC GA			
		TAG GTCGTGAAACCCTCCG CT			
		G A			
GAM1400	LOC199699 3'	TCGGCCTCCCAAAGTGCTGGGA 88315	A		
	T	ATC CAGCACTTTGGGAGGCCGA			

		TAG GTCGTGAAACCCTCCGGCT G		
GAM1400	LOC199775 5'	TCGGCCTCCCAAAGTGCTGGGA 88360	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1400	LOC199786 3'	TCAGCCTCCCAAAGTGCTGGGA 88393	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1400	LOC199906 3'	TCAGCCTCCCAAAGTTCTGGGA 88488	A C	C
	T	ATC CAG ACTTTGGGAGGC GA		
		TAG GTC TGAAACCCTCCG CT G T            A		
GAM1400	LOC200014 3'	TCAGCCTCCCAAAGTGCTGGGA 88539	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1400	LOC200301 5'	TCAGCCTCCCAAAGTGCTGGGA 88752	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1400	LOC200310 3'	TCGGCCTCCCAAAGTGCTAGGA 65745	AC	
	T	ATC AGCACTTTGGGAGGCCGA		
		TAG TCGTGAAACCCTCCGGCT GA		
GAM1400	LOC200316 5'	TCGGCCTCCCAAAGTGCTGGGA 88777	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT G		
GAM1400	LOC200845 5'	TCAGCCTCCCAAAGTGCTGGGA 88907	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT G            A		
GAM1400	LOC201173 5'	TCGGCCTCCCAAAGTTCTGGGA 87337	A C	
	T	ATC CAG ACTTTGGGAGGCCGA		
		TAG GTC TGAAACCCTCCGGCT G T		
GAM1400	LOC201220 5'	TCGGCCTCCCAAAGTTCTGGGA 87358	A C	
	T	ATC CAG ACTTTGGGAGGCCGA		

		TAG GTC TGAAACCCTCCGGCT G T		
GAM1400	LOC201294 3'	TCGACCTCCCAAAGTGCTGGGA 88225	A	C
	T	ATC CAGCACTTTGGGAGG CGA		
		TAG GTCGTGAAACCCTCC GCT		
		G A		
GAM1400	LOC201411 3'	TCAGCCTCCCAAAGTGCTGGGA 62962	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT		
		G A		
GAM1400	LOC201626 3'	TCGGCCTCCCAAAGTGTTGGGA 88999	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTTGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC201627 3'	TCGGCCTCCCAAAGTGCTGGGA 89026	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC203339 3'	TCAGCCTCCCAAAGTGCTGGGA 90550	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT		
		G A		
GAM1400	LOC219445 5'	TCGGCCTCCCAAAAGAGC 91579	A	_
		GC CTTT GGGAGGCCGA		
		CG GAAA CCCTCCGGCT		
		A A		
GAM1400	LOC219673 3'	TCAGCCTCCCAAAGCACTG 93042	CA	C
		CAG CTTTGGGAGGC GA		
		GTC GAAACCCTCCG CT		
		AC A		
GAM1400	LOC219673 5'	TCAGCCTCCCAAAGTGCTAGGA 93043	AC	C
	T	ATC AGCACTTTGGGAGGC GA		
		TAG TCGTGAAACCCTCCG CT		
		GA A		
GAM1400	LOC219673 5'	TCAGCCTCCCAGAGTGCTGT 93044		C
		ACAGCACTTTGGGAGGC GA		
		TGTCGTGAGACCCTCCG CT		
		A		
GAM1400	LOC219735 3'	TCGGCCTCCCAAAGTGTTGGGA 93117	A	
	T	ATC CAGCACTTTGGGAGGCCGA		

		TAG GTTGTGAAACCCTCCGGCT G		
GAM1400	LOC219894 3'	TCGGCCTCCCAAAGTGCTGGGA 93289	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC220074 3'	TCAGCCTCCCAAAGTGCTAGGA 59281	AC	C
	T	ATC AGCACTTTGGGAGGC GA		
		TAG TCGTGAAACCCTCCG CT		
		GA A		
GAM1400	LOC220074 3'	TCAGCCTCCCCAGTAGCTGTGA 59282	_ TT	C
	T	ATCACAGC ACT GGGAGGC GA		
		TAGTGTCTG TGA CCCTCCG CT		
		A C_ A		
GAM1400	LOC221271 3'	TCAGCCTCCCAAAGTGTTGAGA 91876	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTTGTGAAACCCTCCG CT		
		A A		
GAM1400	LOC253842 5'	TCGGCCTCCCAAAGTGCTGGGA 97392	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC253981 3'	TCGGCCTCCCAAAGTTCTGGGA 95834	A C	
	T	ATC CAG ACTTTGGGAGGCCGA		
		TAG GTC TGAAACCCTCCGGCT		
		G T		
GAM1400	LOC254016 3'	CGGCCTCTCGCTGTGCT 96922	TT	
		AGCAC TGGGAGGCCG		
		TCGTG GCTCTCCGGC		
		TC		
GAM1400	LOC254100 3'	TCAGCCTCCCAAAGTGCTGGGA 96417	A	C
	T	ATC CAGCACTTTGGGAGGC GA		
		TAG GTCGTGAAACCCTCCG CT		
		G A		
GAM1400	LOC256221 3'	TCGGCCTCCCAAAGTGCTGGGA 95214	A	
	T	ATC CAGCACTTTGGGAGGCCGA		
		TAG GTCGTGAAACCCTCCGGCT		
		G		
GAM1400	LOC256267 5'	TCGGCCTCCCAAAGTGCTGT 96810		
		ACAGCACTTTGGGAGGCCGA		

TGTCGTGAAACCCTCCGGCT

GAM1400 LOC256306 3' TCGGCCTCCCAAAGTGTTGGGA 96699 A  
T ATC CAGCACTTTGGGAGGCCGA

||| ||||||||||||||

TAG GTTGTGAAACCCTCCGGCT  
G

GAM1400 LOC257486 3' TCAGCCTCCCAAAGCTGGGAT 69250 A AC C  
ATC CAGC TTTGGGAGGC GA

||| ||| |||||||| ||

TAG GTCG AAACCCTCCG CT  
G A\_ A

GAM1400 LOC51026 3' CGCCTTCTGTCTGT 32170 C TTT C  
ACAG AC GGGAGGC G

|||| || |||||| |

TGTC TG TCTTCCG C  
\_ \_ \_ A

GAM1400 LOC51193 5' TCGGCCTCCCAAAGTGCTGGGA 32912 A  
T ATC CAGCACTTTGGGAGGCCGA

||| ||||||||||||||

TAG GTCGTGAAACCCTCCGGCT  
G

GAM1400 LOC51219 5' TCGGCCTCCCAAAGTGCTGGGA 33129 A  
T ATC CAGCACTTTGGGAGGCCGA

||| ||||||||||||||

TAG GTCGTGAAACCCTCCGGCT  
G

GAM1400 LOC51696 3' TCGGCCTCCCAAAGTGCTGGGA 32560 A  
T ATC CAGCACTTTGGGAGGCCGA

||| ||||||||||||||

TAG GTCGTGAAACCCTCCGGCT  
G

GAM1400 LOC56181 5' TCGGCCTCCCAAAGTGCTGGGA 95543 A  
T ATC CAGCACTTTGGGAGGCCGA

||| ||||||||||||||

TAG GTCGTGAAACCCTCCGGCT  
G

GAM1400 LOC57107 3' TCGGCCTCCCAAAGTGCTGGGA 39845 A  
T ATC CAGCACTTTGGGAGGCCGA

||| ||||||||||||||

TAG GTCGTGAAACCCTCCGGCT  
G

GAM1400 LOC89231 3' TCAGCCTCCCAAAGTGCTGGGA 92736 A C  
T ATC CAGCACTTTGGGAGGC GA

||| |||||||||||| ||

TAG GTCGTGAAACCCTCCG CT  
G A

GAM1400 LOC89919 3' TCGGCCTCCCAAAGTGCTG 60731  
CAGCACTTTGGGAGGCCGA

||||||||||||||

GTCGTGAAACCCTCCGGCT

```
GAM1400 LOC89932 3' TCAGCCTCCCAAAGTGCTGGGA 60817  A      C
      T      ATC CAGCACTTTGGGAGGC GA
      ||| ||||| ||
      TAG GTCGTGAAACCCTCCG CT
      G      A

GAM1400 LOC89932 3' TCGGCCTCCCAAATGCTGGGA 60821  A      C
      T      ATC CAGCA TTTGGGAGGCCGA
      ||| ||||| |||||
      TAG GTCGT AAACCCTCCGGCT
      G      A

GAM1400 LOC90288 3' TCAGCCTCCCAAAGTACCCTG 62105  C__      C
      CAG ACTTTGGGAGGC GA
      ||| ||||| ||
      GTC TGAAACCCTCCG CT
      CCA      A

GAM1400 LOC90288 3' TCGGCCTCCCAAAGTGCTGGGA 62108  A
      T      ATC CAGCACTTTGGGAGGCCGA
      ||| ||||| |||||
      TAG GTCGTGAAACCCTCCGGCT
      G

GAM1400 LOC90485 3' TCGGCCTCCCAAAGTGCTGGGA 63029  A
      T      ATC CAGCACTTTGGGAGGCCGA
      ||| ||||| |||||
      TAG GTCGTGAAACCCTCCGGCT
      G

GAM1400 LOC90591 3' TCAGCCTCCCAAAGTGCTGTG 63441      C
      CACAGCACTTTGGGAGGC GA
      ||||| ||||| ||
      GTGTCGTGAAACCCTCCG CT
      A

GAM1400 LOC90826 5' CCAGCAAGTGCTGTTATA 64089  C      _
      TAT ACAGCACTT TGG
      ||| ||||| ||
      ATA TGTCTGTA ACC
      T      CG

GAM1400 LOC90918 3' TCGGCCTCCCAAAGTGCCGGGA 64362  ACA
      T      ATC GCACTTTGGGAGGCCGA
      ||| ||||| |||||
      TAG CGTGAAACCCTCCGGCT
      GGC

GAM1400 LOC91115 3' TCGGCCTCCCAAAGTGCTGGGA 64955  A
      T      ATC CAGCACTTTGGGAGGCCGA
      ||| ||||| |||||
      TAG GTCGTGAAACCCTCCGGCT
      G

GAM1400 LOC91250 5' TCGGCCTCCCAAAGTGCTGGGA 65329  A
      T      ATC CAGCACTTTGGGAGGCCGA
      ||| ||||| |||||
```



				TAG GTCGTGAAACCCTCCGGCT G			
GAM1400	LOC91308	3'	TCGGCCTCCCAAAGTGCTGGGA	65566	A		
	T		ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT G				
GAM1400	LOC91373	3'	TCGGCCTCCCAAAGTGCTGGGA	65846	A		
	T		ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT G				
GAM1400	LOC91893	3'	TCGGCCTCCCAAAGTGCTGGGA	67464	A		
	T		ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT G				
GAM1400	LOC92303	3'	TCGGCCTCCCAAAGTGCTGGGA	68829	A		
	T		ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT G				
GAM1400	LOC92466	5'	TCGGCCTCCCAAAGTGCTGT	69435			
			ACAGCACTTTGGGAGGCCGA				
			TGTCGTGAAACCCTCCGGCT				
GAM1400	LOC92661	5'	TCAGCCTCCCAAAGTGCTGGGA	70086	A		C
	T		ATC CAGCACTTTGGGAGGC GA				
			TAG GTCGTGAAACCCTCCG CT				
			G            A				
GAM1400	LOC92689	3'	TCAGCCTCCCAAAGTGCTGGGA	70230	A		C
	T		ATC CAGCACTTTGGGAGGC GA				
			TAG GTCGTGAAACCCTCCG CT				
			G            A				
GAM1400	LOC92697	5'	TCAGCCTCCCAAAGTTCTGGGA	70280	A	C	C
	T		ATC CAG ACTTTGGGAGGC GA				
			TAG GTC TGAAACCCTCCG CT				
			G T         A				
GAM1400	LOC92841	3'	TCGGCCTCCCAAAGTGCTGGGA	70725	A		
	T		ATC CAGCACTTTGGGAGGCCGA				
			TAG GTCGTGAAACCCTCCGGCT G				
GAM1400	LOC93129	3'	TCGGCCTCCCAAAGTGCTGGGA	71470	A		
	T		ATC CAGCACTTTGGGAGGCCGA				

			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	LOC93268	5'	GCCTCCCGGATGGCCAGATA 71882	ACA AC	
			TATC GC TTTGGGAGGC		
			ATAG CG AGGCCCTCCG		
			AC_ GT		
GAM1400	LOC93408	5'	TCGGCCTCCCAAAGTGCTGGGA 56484	A	
		T	ATC CAGCACTTTGGGAGGCCGA		
			TAG GTCGTGAAACCCTCCGGCT		
			G		
GAM1400	LOC93496	3'	TCGACCTCCCAAAGTGCTGGGA 72439	A	C
		T	ATC CAGCACTTTGGGAGG CGA		
			TAG GTCGTGAAACCCTCC GCT		
			G A		
GAM1401	A1BG	3'	CTCAAGCGATCCTCGCCTCA 55417	T	GATA
			TGAGGCAG AGGAT CTTGAG		
			ACTCCGTC TCCTA GAACTC		
			C GC__		
GAM1401	A1BG	3'	CTCAAGCGATCCTCGCCTCA 55417	T	GATA
			TGAGGCAG AGGAT CTTGAG		
			ACTCCGTC TCCTA GAACTC		
			C GC__		
GAM1401	A1BG	3'	CTCAAGTGATCCTCCCGCCTCA 55418	AGT	GA
			TGAGGC AGGAT TACTTGAG		
			ACTCCG TCCTA GTGAACTC		
			CCC _		
GAM1401	A1BG	3'	CTCAAGTGATCCTCCCGCCTCA 55418	AGT	GA
			TGAGGC AGGAT TACTTGAG		
			ACTCCG TCCTA GTGAACTC		
			CCC _		
GAM1401	AIM1	3'	CTCAGGTGATCCTCCACCTCA 91823	CAGT	GA
			TGAGG AGGAT TACTTGAG		
			ACTCC TCCTA GTGGA CTG		
			ACCC _		
GAM1401	AIM1	3'	CTCAGGTGATCCTCCACCTCA 91823	CAGT	GA
			TGAGG AGGAT TACTTGAG		
			ACTCC TCCTA GTGGA CTG		
			ACCC _		
GAM1401	APAF1	3'	CTCAAGTAATCCTCGCCTCA 6729	T	GA
			TGAGGCAG AGGAT TACTTGAG		

			ACTCCGTC TCCTA ATGAACTC		
			C _		
GAM1401	APAF1	3'	CTCAAGTAATCCTCCTGCCTCA 6729	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTA ATGAACTC		
			C _		
GAM1401	APAF1	3'	CTCAAGTAATCCTCCTGCCTCA 25038	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTA ATGAACTC		
			C _		
GAM1401	APAF1	3'	CTCAAGTAATCCTCCTGCCTCA 25038	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTA ATGAACTC		
			C _		
GAM1401	FABP2	3'	CTCAAGCAATCCTCCTGCCTCA 3744	T	GATA
			TGAGGCAG AGGAT CTTGAG		
			ACTCCGTC TCCTA GAACTC		
			C AC_		
GAM1401	FABP2	3'	CTCAAGCAATCCTCCTGCCTCA 3744	T	GATA
			TGAGGCAG AGGAT CTTGAG		
			ACTCCGTC TCCTA GAACTC		
			C AC_		
GAM1401	GLS	5'	TGTCATCTCACCGCCCCA 29790 A A AG		
			TG GGC GT GATGATA		
			AC CCG CA CTACTGT		
			C C CT		
GAM1401	GLS	5'	TGTCATCTCACCGCCCCA 29790 A A AG		
			TG GGC GT GATGATA		
			AC CCG CA CTACTGT		
			C C CT		
GAM1401	ICAM1	3'	CTCAAGTGATCCTCCACCTCA 71576	CAGT	GA
			TGAGG AGGAT TACTTGAG		
			ACTCC TCCTA GTGAACTC		
			ACCC _		
GAM1401	ICAM1	3'	CTCAAGTGATCCTCCACCTCA 71576	CAGT	GA
			TGAGG AGGAT TACTTGAG		
			ACTCC TCCTA GTGAACTC		
			ACCC _		
GAM1401	LZTS1	3'	CTCAAGCAATCCTCCTGCCTCA 40689	T	GATA
			TGAGGCAG AGGAT CTTGAG		

			ACTCCGTC TCCTA GAACTC		
			C AC__		
GAM1401 LZTS1	3'	CTCAAGCAATCCTCCTGCCTCA 40689	T	GATA	
		TGAGGCAG AGGAT CTTGAG			
		ACTCCGTC TCCTA GAACTC			
		C AC__			
GAM1401 MADD	3'	CAAGCCGGCAGCTACTGCCCA 55331	A	GA ATA_	
		TG GGCAGTAG TG CTTG			
		AC CCGTCATC AC GAAC			
		_ G_ GGCC			
GAM1401 MADD	3'	CAAGCCGGCAGCTACTGCCCA 55331	A	GA ATA_	
		TG GGCAGTAG TG CTTG			
		AC CCGTCATC AC GAAC			
		_ G_ GGCC			
GAM1401 MADD	3'	CAAGCCGGCAGCTACTGCCCA 55338	A	GA ATA_	
		TG GGCAGTAG TG CTTG			
		AC CCGTCATC AC GAAC			
		_ G_ GGCC			
GAM1401 MADD	3'	CAAGCCGGCAGCTACTGCCCA 55338	A	GA ATA_	
		TG GGCAGTAG TG CTTG			
		AC CCGTCATC AC GAAC			
		_ G_ GGCC			
GAM1401 MADD	3'	CAAGCCGGCAGCTACTGCCCA 55343	A	GA ATA_	
		TG GGCAGTAG TG CTTG			
		AC CCGTCATC AC GAAC			
		_ G_ GGCC			
GAM1401 MADD	3'	CAAGCCGGCAGCTACTGCCCA 55343	A	GA ATA_	
		TG GGCAGTAG TG CTTG			
		AC CCGTCATC AC GAAC			
		_ G_ GGCC			
GAM1401 MADD	3'	CAAGCCGGCAGCTACTGCCCA 55348	A	GA ATA_	
		TG GGCAGTAG TG CTTG			
		AC CCGTCATC AC GAAC			
		_ G_ GGCC			
GAM1401 MADD	3'	CAAGCCGGCAGCTACTGCCCA 55348	A	GA ATA_	
		TG GGCAGTAG TG CTTG			
		AC CCGTCATC AC GAAC			
		_ G_ GGCC			
GAM1401 MADD	3'	CAAGCCGGCAGCTACTGCCCA 55354	A	GA ATA_	
		TG GGCAGTAG TG CTTG			

			AC CCGTCATC AC GAAC		
			— G_ GGCC		
GAM1401	MADD	3'	CAAGCCGGCAGCTACTGCCCA 55354	A	GA ATA_
			TG GGCAGTAG TG CTTG		
			AC CCGTCATC AC GAAC		
			— G_ GGCC		
GAM1401	MADD	3'	CAAGCCGGCAGCTACTGCCCA 13463	A	GA ATA_
			TG GGCAGTAG TG CTTG		
			AC CCGTCATC AC GAAC		
			— G_ GGCC		
GAM1401	MADD	3'	CAAGCCGGCAGCTACTGCCCA 13463	A	GA ATA_
			TG GGCAGTAG TG CTTG		
			AC CCGTCATC AC GAAC		
			— G_ GGCC		
GAM1401	MHC2TA	3'	CTCAAGTGATTCTCCTGCCTCA 4173	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCTTA GTGAACTC		
			C —		
GAM1401	MHC2TA	3'	CTCAAGTGATTCTCCTGCCTCA 4173	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCTTA GTGAACTC		
			C —		
GAM1401	PIGR	3'	CTCAAGTGATCTGCCGCCTCA 72599	A	ATGA
			TGAGGC GTAGG TACTTGAG		
			ACTCCG CGTCT GTGAACTC		
			C A_		
GAM1401	PIGR	3'	CTCAAGTGATCTGCCGCCTCA 72599	A	ATGA
			TGAGGC GTAGG TACTTGAG		
			ACTCCG CGTCT GTGAACTC		
			C A_		
GAM1401	PRIM2A	3'	CTCAAGTGATCCTCCTACCTCA 6272	C T	GA
			TGAGG AG AGGAT TACTTGAG		
			ACTCC TC TCCTA GTGAACTC		
			A C —		
GAM1401	PRIM2A	3'	CTCAAGTGATCCTCCTACCTCA 6272	C T	GA
			TGAGG AG AGGAT TACTTGAG		
			ACTCC TC TCCTA GTGAACTC		
			A C —		
GAM1401	PTPN18	3'	CTCAAGCAATCCTCCTGCCTCA 26864	T	GATA
			TGAGGCAG AGGAT CTTGAG		

			ACTCCGTC TCCTA GAACTC		
			C AC__		
GAM1401	PTPN18	3'	CTCAAGCAATCCTCCTGCCTCA 26864	T	GATA
			TGAGGCAG AGGAT CTTGAG		
			ACTCCGTC TCCTA GAACTC		
			C AC__		
GAM1401	PVR	3'	CAAGTCATCCTCCCACCTCA 21472	CAGT	TA
			TGAGG AGGATGA CTTG		
			ACTCC TCCTACT GAAC		
			ACCC _		
GAM1401	PVR	3'	CAAGTCATCCTCCCACCTCA 21472	CAGT	TA
			TGAGG AGGATGA CTTG		
			ACTCC TCCTACT GAAC		
			ACCC _		
GAM1401	RBM8A	3'	CTCAAGCCATCCTTCTGCCTCA 17543	T	ATA
			TGAGGCAG AGGATG CTTGAG		
			ACTCCGTC TCCTAC GAACTC		
			T C__		
GAM1401	RBM8A	3'	CTCAAGCCATCCTTCTGCCTCA 17543	T	ATA
			TGAGGCAG AGGATG CTTGAG		
			ACTCCGTC TCCTAC GAACTC		
			T C__		
GAM1401	TNFRSF9	3'	CTCAAGTGATCCTCCTGCCTCA 7788	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTA GTGAACTC		
			C _		
GAM1401	TNFRSF9	3'	CTCAAGTGATCCTCCTGCCTCA 7788	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTA GTGAACTC		
			C _		
GAM1401	UMPS	3'	CTCAAGCGATCCTCCTGCCTCA 4551	T	GATA
			TGAGGCAG AGGAT CTTGAG		
			ACTCCGTC TCCTA GAACTC		
			C GC__		
GAM1401	UMPS	3'	CTCAAGCGATCCTCCTGCCTCA 4551	T	GATA
			TGAGGCAG AGGAT CTTGAG		
			ACTCCGTC TCCTA GAACTC		
			C GC__		
GAM1401	C20orf150	3'	CTCAAACTGGCCACTGCCTCA 65396	A	ATGATAC
			TGAGGCAGT GG TTGAG		

		ACTCCGTCA CC	AACTC	
		_ GGTCAA_		
GAM1401	C20orf150 3'	CTCAAAACTGGCCACTGCCTCA	65396	A ATGATAC
		TGAGGCAGT GG	TTGAG	
		ACTCCGTCA CC	AACTC	
		_ GGTCAA_		
GAM1401	C20orf188 3'	CAAGCCTGCCCCTCTGCCTCA	31578	T ATGATA
		TGAGGCAG AGG	CTTG	
		ACTCCGTC TCC	GAAC	
		_ CCGTCC		
GAM1401	C20orf188 3'	CAAGCCTGCCCCTCTGCCTCA	31578	T ATGATA
		TGAGGCAG AGG	CTTG	
		ACTCCGTC TCC	GAAC	
		_ CCGTCC		
GAM1401	COLEC12 3'	CTCAAGCAACCCTCCTGCCTCA	47864	T ATGATA
		TGAGGCAG AGG	CTTGAG	
		ACTCCGTC TCC	GAACTC	
		C CAAC__		
GAM1401	COLEC12 3'	CTCAAGCAACCCTCCTGCCTCA	47864	T ATGATA
		TGAGGCAG AGG	CTTGAG	
		ACTCCGTC TCC	GAACTC	
		C CAAC__		
GAM1401	DKFZP547N043 3'	CTCAAGTACCACCTGTATTATC	49317	GC _ A A
	TCA	TGAG AGT AGG TG TACTTGAG		
		ACTC TTA TCC AC ATGAACTC		
		TA TG _ C		
GAM1401	DKFZP547N043 3'	CTCAAGTACCACCTGTATTATC	49317	GC _ A A
	TCA	TGAG AGT AGG TG TACTTGAG		
		ACTC TTA TCC AC ATGAACTC		
		TA TG _ C		
GAM1401	EVI5 3'	CTCAAGTGGTCCTCCTGCCTCA	18997	T GA
		TGAGGCAG AGGAT TACTTGAG		
		ACTCCGTC TCCTG GTGAACTC		
		C _		
GAM1401	EVI5 3'	CTCAAGTGGTCCTCCTGCCTCA	18997	T GA
		TGAGGCAG AGGAT TACTTGAG		
		ACTCCGTC TCCTG GTGAACTC		
		C _		
GAM1401	FLB6421 3'	CTCAAGTGATCCTCCTACCTCA	39224	C T GA
		TGAGG AG AGGAT TACTTGAG		

	ACTCC TC TCCTA GTGAACTC		
	A C _		
GAM1401 FLB6421	3' CTCAAGTGATCCTCCTACCTCA 39224	C T	GA
	TGAGG AG AGGAT TACTTGAG		
	ACTCC TC TCCTA GTGAACTC		
	A C _		
GAM1401 FLJ10297	3' CTCAAGTGATCCTCCTGCCTCA 35980	T	GA
	TGAGGCAG AGGAT TACTTGAG		
	ACTCCGTC TCCTA GTGAACTC		
	C _		
GAM1401 FLJ10297	3' CTCAAGTGATCCTCCTGCCTCA 35980	T	GA
	TGAGGCAG AGGAT TACTTGAG		
	ACTCCGTC TCCTA GTGAACTC		
	C _		
GAM1401 FLJ10607	3' CTCAAGTGATCCTCCCACCTCA 77111	CAGT	GA
	TGAGG AGGAT TACTTGAG		
	ACTCC TCCTA GTGAACTC		
	ACCC _		
GAM1401 FLJ10607	3' CTCAAGTGATCCTCCCACCTCA 77111	CAGT	GA
	TGAGG AGGAT TACTTGAG		
	ACTCC TCCTA GTGAACTC		
	ACCC _		
GAM1401 FLJ10687	3' CTCAAGGATCCTCCTGCCTCA 36409	T	GATA
	TGAGGCAG AGGAT CTTGAG		
	ACTCCGTC TCCTA GAACTC		
	C G _		
GAM1401 FLJ10687	3' CTCAAGGATCCTCCTGCCTCA 36409	T	GATA
	TGAGGCAG AGGAT CTTGAG		
	ACTCCGTC TCCTA GAACTC		
	C G _		
GAM1401 FLJ10847	3' CTCAAGTGATCCTCCCACCTCA 36748	CAGT	GA
	TGAGG AGGAT TACTTGAG		
	ACTCC TCCTA GTGAACTC		
	ACCC _		
GAM1401 FLJ10847	3' CTCAAGTGATCCTCCCACCTCA 36748	CAGT	GA
	TGAGG AGGAT TACTTGAG		
	ACTCC TCCTA GTGAACTC		
	ACCC _		
GAM1401 FLJ12442	5' CTCGAGCCCATCCTACGGCCTC 43265	A	ATA
A	TGAGGC GTAGGATG CTTGAG		



		ACTCCG CATCCTAC GAGCTC		
		G CC_		
GAM1401	FLJ12442	5' CTCGAGCCCATCCTACGGCCTC 43265	A	ATA
	A	TGAGGC GTAGGATG CTTGAG		
		ACTCCG CATCCTAC GAGCTC		
		G CC_		
GAM1401	FLJ13072	5' CTCAAGCAATTCTCCTGCCTCA 89809	T	GATA
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCTTA GAACTC		
		C AC_		
GAM1401	FLJ13072	5' CTCAAGCAATTCTCCTGCCTCA 89809	T	GATA
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCTTA GAACTC		
		C AC_		
GAM1401	FLJ13072	5' CTCAGGTAATCCTCCCACCTCA 89810	CAGT	GA
		TGAGG AGGAT TACTTGAG		
		ACTCC TCCTA ATGGA CTG		
		ACCC _		
GAM1401	FLJ13072	5' CTCAGGTAATCCTCCCACCTCA 89810	CAGT	GA
		TGAGG AGGAT TACTTGAG		
		ACTCC TCCTA ATGGA CTG		
		ACCC _		
GAM1401	FLJ13984	5' GTCATCCTCCTGCCTCA 45453	T	
		TGAGGCAG AGGATGAT		
		ACTCCGTC TCCTACTG		
		C		
GAM1401	FLJ13984	5' GTCATCCTCCTGCCTCA 45453	T	
		TGAGGCAG AGGATGAT		
		ACTCCGTC TCCTACTG		
		C		
GAM1401	FLJ14351	3' CTCAAGCAATCCTCCTGCCTCA 45323	T	GATA
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCCTA GAACTC		
		C AC_		
GAM1401	FLJ14351	3' CTCAAGCAATCCTCCTGCCTCA 45323	T	GATA
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCCTA GAACTC		
		C AC_		
GAM1401	FLJ14803	3' CTCAAGCAATTCTCCTGCCTCA 51616	T	GATA
		TGAGGCAG AGGAT CTTGAG		

		ACTCCGTC TCTTA	GA	ACTC	
		C	AC	__	
GAM1401	FLJ14803	3'	CTCAAGCAATTCTCCTGCCTCA	51616	T GATA
			TGAGGCAG AGGAT	CTTGAG	
			ACTCCGTC TCTTA	GA	ACTC
			C	AC	__
GAM1401	FLJ20671	3'	CTCAAGCAATTCTCCTGCCTCA	35522	T GATA
			TGAGGCAG AGGAT	CTTGAG	
			ACTCCGTC TCTTA	GA	ACTC
			C	AC	__
GAM1401	FLJ20671	3'	CTCAAGCAATTCTCCTGCCTCA	35522	T GATA
			TGAGGCAG AGGAT	CTTGAG	
			ACTCCGTC TCTTA	GA	ACTC
			C	AC	__
GAM1401	FLJ22316	5'	CTCAAGTAATCCTACCGCCTCA	46919	A GA
			TGAGGC GTAGGAT	TACTTGAG	
			ACTCCG CATCCTA	ATGA	ACTC
			C	__	
GAM1401	FLJ22316	5'	CTCAAGTAATCCTACCGCCTCA	46919	A GA
			TGAGGC GTAGGAT	TACTTGAG	
			ACTCCG CATCCTA	ATGA	ACTC
			C	__	
GAM1401	FLJ23416	3'	CTCAAGCAATCCTGCTGCCTCA	49949	GATA
			TGAGGCAGTAGGAT	CTTGAG	
			ACTCCGTCGTCCTA	GA	ACTC
			AC	__	
GAM1401	FLJ23416	3'	CTCAAGCAATCCTGCTGCCTCA	49949	GATA
			TGAGGCAGTAGGAT	CTTGAG	
			ACTCCGTCGTCCTA	GA	ACTC
			AC	__	
GAM1401	KIAA0212	3'	CTCAAGTGATCCTTCTGCCTCA	27938	T GA
			TGAGGCAG AGGAT	TACTTGAG	
			ACTCCGTC TCCTA	GTGA	ACTC
			T	__	
GAM1401	KIAA0212	3'	CTCAAGTGATCCTTCTGCCTCA	27938	T GA
			TGAGGCAG AGGAT	TACTTGAG	
			ACTCCGTC TCCTA	GTGA	ACTC
			T	__	
GAM1401	KIAA0377	3'	CAAGTGCCCCTTCTGCCTCA	27794	T ATGA
			TGAGGCAG AGG	TACTTG	

		ACTCCGTC TCC GTGAAC		
		T CC__		
GAM1401	KIAA0377	3' CAAGTGCCCCTTCTGCCTCA 27794	T	ATGA
		TGAGGCAG AGG TACTTG		
		ACTCCGTC TCC GTGAAC		
		T CC__		
GAM1401	KIAA0446	5' CTCAGGTGATCCTCCCACCTCA 68865	CAGT	GA
		TGAGG AGGAT TACTTGAG		
		ACTCC TCCTA GTGGACTC		
		ACCC _		
GAM1401	KIAA0446	5' CTCAGGTGATCCTCCCACCTCA 68865	CAGT	GA
		TGAGG AGGAT TACTTGAG		
		ACTCC TCCTA GTGGACTC		
		ACCC _		
GAM1401	KIAA0557	3' CTCAAGTGTTCTCCTGCCTCA 77995	T	TG
		TGAGGCAG AGGA ATACTTGAG		
		ACTCCGTC TCCT TGTGAACTC		
		C _		
GAM1401	KIAA0557	3' CTCAAGTGTTCTCCTGCCTCA 77995	T	TG
		TGAGGCAG AGGA ATACTTGAG		
		ACTCCGTC TCCT TGTGAACTC		
		C _		
GAM1401	KIAA0802	3' ATTCCCCCACTGCCTCA 62564	A	AT
		TGAGGCAGT GG GAT		
		ACTCCGTCA CC TTA		
		C CC		
GAM1401	KIAA0802	3' ATTCCCCCACTGCCTCA 62564	A	AT
		TGAGGCAGT GG GAT		
		ACTCCGTCA CC TTA		
		C CC		
GAM1401	KIAA0828	3' CTCAAGCAATCCTCCTGCCTCA 81195	T	GATA
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCCTA GAACTC		
		C AC__		
GAM1401	KIAA0828	3' CTCAAGCAATCCTCCTGCCTCA 81195	T	GATA
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCCTA GAACTC		
		C AC__		
GAM1401	KIAA1026	3' CTCAAACAATTCTCCTGCCTCA 71191	T	GATAC
		TGAGGCAG AGGAT TTGAG		

		ACTCCGTC TCTTA AACTC	
		C ACA__	
GAM1401 KIAA1026	3'	CTCAAACAATTCTCCTGCCTCA 71191	T GATAC
		TGAGGCAG AGGAT TTGAG	
		ACTCCGTC TCTTA AACTC	
		C ACA__	
GAM1401 KIAA1037	3'	CTCAAAACCCCTTCTGCCTCA 30435	T ATGATAC
		TGAGGCAG AGG TTGAG	
		ACTCCGTC TCC AACTC	
		T CCAA__	
GAM1401 KIAA1037	3'	CTCAAAACCCCTTCTGCCTCA 30435	T ATGATAC
		TGAGGCAG AGG TTGAG	
		ACTCCGTC TCC AACTC	
		T CCAA__	
GAM1401 KIAA1271	3'	TCAGACCCTCCTGCCTCA 69552	T A__
		TGAGGCAG AGG TGA	
		ACTCCGTC TCC ACT	
		C CAG	
GAM1401 KIAA1271	3'	TCAGACCCTCCTGCCTCA 69552	T A__
		TGAGGCAG AGG TGA	
		ACTCCGTC TCC ACT	
		C CAG	
GAM1401 KIAA1280	5'	CTCAAGTGACCCTCCTGCCTCA 69714	T ATGA
		TGAGGCAG AGG TACTTGAG	
		ACTCCGTC TCC GTGAACTC	
		C CA__	
GAM1401 KIAA1280	5'	CTCAAGTGACCCTCCTGCCTCA 69714	T ATGA
		TGAGGCAG AGG TACTTGAG	
		ACTCCGTC TCC GTGAACTC	
		C CA__	
GAM1401 KIAA1396	3'	CTCAAGTGACCCTCCACCTCA 62988	CAGT ATGA
		TGAGG AGG TACTTGAG	
		ACTCC TCC GTGAACTC	
		ACCC CA__	
GAM1401 KIAA1396	3'	CTCAAGTGACCCTCCACCTCA 62988	CAGT ATGA
		TGAGG AGG TACTTGAG	
		ACTCC TCC GTGAACTC	
		ACCC CA__	
GAM1401 KIAA1649	3'	CTCAAGTGATCCTCCACCTCA 50257	CAGT GA
		TGAGG AGGAT TACTTGAG	

	ACTCC TCCTA GTGAACTC	
	ACCC _	
GAM1401 KIAA1649 3'	CTCAAGTGATCCTCCCACCTCA 50257	CAGT GA
	TGAGG AGGAT TACTTGAG	
	ACTCC TCCTA GTGAACTC	
	ACCC _	
GAM1401 KIAA1671 3'	CTCAAGTGATTCTACTGCCTCA 65672	GA
	TGAGGCAGTAGGAT TACTTGAG	
	ACTCCGTCATCTTA GTGAACTC	
	—	
GAM1401 KIAA1671 3'	CTCAAGTGATTCTACTGCCTCA 65672	GA
	TGAGGCAGTAGGAT TACTTGAG	
	ACTCCGTCATCTTA GTGAACTC	
	—	
GAM1401 KIAA1671 3'	CTCAAGTGATTCTCCCACCTCA 65673	CAGTA T _
	TGAGG GGA GAT ACTTGAG	
	ACTCC CCT TTA TGA ACTC	
	AC_ C G	
GAM1401 KIAA1671 3'	CTCAAGTGATTCTCCCACCTCA 65673	CAGTA T _
	TGAGG GGA GAT ACTTGAG	
	ACTCC CCT TTA TGA ACTC	
	AC_ C G	
GAM1401 KIAA1727 3'	CTCAAGTGATCCTCCCACCTCA 64056	CAGT GA
	TGAGG AGGAT TACTTGAG	
	ACTCC TCCTA GTGAACTC	
	ACCC _	
GAM1401 KIAA1727 3'	CTCAAGTGATCCTCCCACCTCA 64056	CAGT GA
	TGAGG AGGAT TACTTGAG	
	ACTCC TCCTA GTGAACTC	
	ACCC _	
GAM1401 KIAA1751 3'	CTCAAGCAATCCTCCTGCCTCA 71692	T GATA
	TGAGGCAG AGGAT CTTGAG	
	ACTCCGTC TCCTA GAACTC	
	C AC_	
GAM1401 KIAA1751 3'	CTCAAGCAATCCTCCTGCCTCA 71692	T GATA
	TGAGGCAG AGGAT CTTGAG	
	ACTCCGTC TCCTA GAACTC	
	C AC_	
GAM1401 KIAA1821 3'	CTCAAGTGATCCTCCCACCTCA 71782	CAGT GA
	TGAGG AGGAT TACTTGAG	

	ACTCC TCCTA GTGAACTC ACCC _	
GAM1401 KIAA1821	3' CTCAAGTGATCCTCCCACCTCA 71782 TGAGG AGGAT TACTTGAG                   ACTCC TCCTA GTGAACTC ACCC _	CAGT GA
GAM1401 KIAA1924	3' CTCCAGCCATCCTCCTGCCTCA 73670 TGAGGCAG AGGATG CT GAG                      ACTCCGTC TCCTAC GA CTC C C_ C	T ATA T
GAM1401 KIAA1924	3' CTCCAGCCATCCTCCTGCCTCA 73670 TGAGGCAG AGGATG CT GAG                      ACTCCGTC TCCTAC GA CTC C C_ C	T ATA T
GAM1401 LNIR	3' CTCAAGCAATCCTCCTGCCTCA 48130 TGAGGCAG AGGAT CTTGAG                     ACTCCGTC TCCTA GAACTC C AC_	T GATA
GAM1401 LNIR	3' CTCAAGCAATCCTCCTGCCTCA 48130 TGAGGCAG AGGAT CTTGAG                     ACTCCGTC TCCTA GAACTC C AC_	T GATA
GAM1401 MGC10200	3' CTCAAGTGATCCTCCCACCTCA 58984 TGAGG AGGAT TACTTGAG                   ACTCC TCCTA GTGAACTC ACCC _	CAGT GA
GAM1401 MGC10200	3' CTCAAGTGATCCTCCCACCTCA 58984 TGAGG AGGAT TACTTGAG                   ACTCC TCCTA GTGAACTC ACCC _	CAGT GA
GAM1401 MGC12466	3' CTCAAGCTATCCTCCTGCCTCA 79032 TGAGGCAG AGGATG CTTGAG                     ACTCCGTC TCCTAT GAACTC C C_	T ATA
GAM1401 MGC12466	3' CTCAAGCTATCCTCCTGCCTCA 79032 TGAGGCAG AGGATG CTTGAG                     ACTCCGTC TCCTAT GAACTC C C_	T ATA
GAM1401 MGC2477	5' CAAGCGATCCTCCTGCCTCA 44058 TGAGGCAG AGGAT CTTG 	T GATA

			ACTCCGTC TCCTA GAAC		
			C GC__		
GAM1401	MGC2477	5'	CAAGCGATCCTCCTGCCTCA 44058	T	GATA
			TGAGGCAG AGGAT CTTG		
			ACTCCGTC TCCTA GAAC		
			C GC__		
GAM1401	MGC2488	3'	CTCAAGTGATCCTCCTGCCTCA 43868	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTA GTGAACTC		
			C _		
GAM1401	MGC2488	3'	CTCAAGTGATCCTCCTGCCTCA 43868	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTA GTGAACTC		
			C _		
GAM1401	MGC3113	3'	CTCAAGCAATTCATCTGCCTCA 43845	TA	GATA
			TGAGGCAG GGAT CTTGAG		
			ACTCCGTC CTTA GAACTC		
			TA AC__		
GAM1401	MGC3113	3'	CTCAAGCAATTCATCTGCCTCA 43845	TA	GATA
			TGAGGCAG GGAT CTTGAG		
			ACTCCGTC CTTA GAACTC		
			TA AC__		
GAM1401	MRPL35	3'	CTCAAGTGGTCCTCCTGCCTCA 33542	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTG GTGAACTC		
			C _		
GAM1401	MRPL35	3'	CTCAAGTGGTCCTCCTGCCTCA 33542	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTG GTGAACTC		
			C _		
GAM1401	OSBPL2	3'	CTCAAGTAGTCTGCCTGCCTCA 29213	TA	GA
			TGAGGCAG GGAT TACTTGAG		
			ACTCCGTC TCTG ATGAACTC		
			CG _		
GAM1401	OSBPL2	3'	CTCAAGTAGTCTGCCTGCCTCA 29213	TA	GA
			TGAGGCAG GGAT TACTTGAG		
			ACTCCGTC TCTG ATGAACTC		
			CG _		
GAM1401	OSBPL2	3'	CTCAAGTAGTCTGCCTGCCTCA 57864	TA	GA
			TGAGGCAG GGAT TACTTGAG		

		ACTCCGTC TCTG ATGAACTC CG _	
GAM1401 OSBPL2	3'	CTCAAGTAGTCTGCCTGCCTCA 57864 TGAGGCAG GGAT TACTTGAG 	TA GA
		ACTCCGTC TCTG ATGAACTC CG _	
GAM1401 POFUT1	3'	CTCAAGCGATCCTTCTGCCTCA 70468 TGAGGCAG AGGAT CTTGAG 	T GATA
		ACTCCGTC TCCTA GAACTC T GC_	
GAM1401 POFUT1	3'	CTCAAGCGATCCTTCTGCCTCA 70468 TGAGGCAG AGGAT CTTGAG 	T GATA
		ACTCCGTC TCCTA GAACTC T GC_	
GAM1401 PPIL2	3'	CTCAAGCAATCCTCCTGCCTCA 26764 TGAGGCAG AGGAT CTTGAG 	T GATA
		ACTCCGTC TCCTA GAACTC C AC_	
GAM1401 PPIL2	3'	CTCAAGCAATCCTCCTGCCTCA 26764 TGAGGCAG AGGAT CTTGAG 	T GATA
		ACTCCGTC TCCTA GAACTC C AC_	
GAM1401 PRO1048	3'	CTCAAGCGATCCTCCTGCCTCA 37515 TGAGGCAG AGGAT CTTGAG 	T GATA
		ACTCCGTC TCCTA GAACTC C GC_	
GAM1401 PRO1048	3'	CTCAAGCGATCCTCCTGCCTCA 37515 TGAGGCAG AGGAT CTTGAG 	T GATA
		ACTCCGTC TCCTA GAACTC C GC_	
GAM1401 SAMHD1	3'	CTCAAGCGACCCTCCTGCCTCA 61311 TGAGGCAG AGG CTTGAG 	T ATGATA
		ACTCCGTC TCC GAACTC C CAGC_	
GAM1401 SAMHD1	3'	CTCAAGCGACCCTCCTGCCTCA 61311 TGAGGCAG AGG CTTGAG 	T ATGATA
		ACTCCGTC TCC GAACTC C CAGC_	
GAM1401 SARM	3'	CTCAAGTGATCCTCCTGCCTCA 30602 TGAGGCAG AGGAT TACTTGAG 	T GA



			ACTCCGTC TCCTA GTGAACTC		
			C _		
GAM1401	SARM	3'	CTCAAGTGATCCTCCTGCCTCA 30602	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTA GTGAACTC		
			C _		
GAM1401	SARM	3'	CTCAAGTGGTCCTCCTGCCTCA 30603	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTG GTGAACTC		
			C _		
GAM1401	SARM	3'	CTCAAGTGGTCCTCCTGCCTCA 30603	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTG GTGAACTC		
			C _		
GAM1401	SCYA16	3'	CAAGCAATCCACCTGCCTCA 15955	TA	GATA
			TGAGGCAG GGAT CTTG		
			ACTCCGTC CCTA GAAC		
			CA AC_		
GAM1401	SCYA16	3'	CAAGCAATCCACCTGCCTCA 15955	TA	GATA
			TGAGGCAG GGAT CTTG		
			ACTCCGTC CCTA GAAC		
			CA AC_		
GAM1401	SCYA16	3'	CTCAAGTGATCCTCCCACCCC 15957	CA A T _	
			GG GT GGA GAT ACTTGAG		
			CC CA CCT CTA TGA ACTC		
			C_ C C G		
GAM1401	SCYA16	3'	CTCAAGTGATCCTCCCACCCC 15957	CA A T _	
			GG GT GGA GAT ACTTGAG		
			CC CA CCT CTA TGA ACTC		
			C_ C C G		
GAM1401	SDC3	5'	CTCAAGCAGTTCCCCTGCCTCA 27750	TA	GATA
			TGAGGCAG GGAT CTTGAG		
			ACTCCGTC CTTG GAACTC		
			CC AC_		
GAM1401	SDC3	5'	CTCAAGCAGTTCCCCTGCCTCA 27750	TA	GATA
			TGAGGCAG GGAT CTTGAG		
			ACTCCGTC CTTG GAACTC		
			CC AC_		
GAM1401	SNAPC1	3'	CTCAAGCTATCCTCCTGCCTCA 11841	T	ATA
			TGAGGCAG AGGATG CTTGAG		

			ACTCCGTC TCCTAT GAACTC		
			C C__		
GAM1401	SNAPC1	3'	CTCAAGCTATCCTCCTGCCTCA 11841	T	ATA
			TGAGGCAG AGGATG CTTGAG		
			ACTCCGTC TCCTAT GAACTC		
			C C__		
GAM1401	SYTL4	5'	CTCAAGAGATCCTCCTGCCTCA 54941	T	GATA
			TGAGGCAG AGGAT CTTGAG		
			ACTCCGTC TCCTA GAACTC		
			C GA__		
GAM1401	SYTL4	5'	CTCAAGAGATCCTCCTGCCTCA 54941	T	GATA
			TGAGGCAG AGGAT CTTGAG		
			ACTCCGTC TCCTA GAACTC		
			C GA__		
GAM1401	TIEG2	3'	TCTCCCACTGCCTCA 13182	A T	
			TGAGGCAGT GGA GA		
			ACTCCGTCA CCT CT		
			C _		
GAM1401	TIEG2	3'	TCTCCCACTGCCTCA 13182	A T	
			TGAGGCAGT GGA GA		
			ACTCCGTCA CCT CT		
			C _		
GAM1401	TPRSS5	3'	CTCACTGCACACCACTGCCTCA 47783	A A	ATACT
			TGAGGCAGT GG TG TGAG		
			ACTCCGTCA CC AC ACTC		
			_ _ ACGTC		
GAM1401	TPRSS5	3'	CTCACTGCACACCACTGCCTCA 47783	A A	ATACT
			TGAGGCAGT GG TG TGAG		
			ACTCCGTCA CC AC ACTC		
			_ _ ACGTC		
GAM1401	USP3	5'	CTCAAGTGATTCTTCTGCCTCA 89676	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCTTA GTGAACTC		
			T _		
GAM1401	USP3	5'	CTCAAGTGATTCTTCTGCCTCA 89676	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCTTA GTGAACTC		
			T _		
GAM1401	WIRE	3'	TCACCCCACTGCTTCA 78308	A A	
			TGAGGCAGT GG TGA		

		ACTTCGTCA CC ACT		
		C C		
GAM1401 WIRE	3'	TCACCCCACTGCTTCA 78308	A A	
		TGAGGCAGT GG TGA		
		ACTTCGTCA CC ACT		
		C C		
GAM1401 YAP	5'	CTCAAGTAATCTTCCTGCCTCA 36787	T GA	
		TGAGGCAG AGGAT TACTTGAG		
		ACTCCGTC TTCTA ATGAACTC		
		C _		
GAM1401 YAP	5'	CTCAAGTAATCTTCCTGCCTCA 36787	T GA	
		TGAGGCAG AGGAT TACTTGAG		
		ACTCCGTC TTCTA ATGAACTC		
		C _		
GAM1401 ZNF177	5'	CTCAAGTGATCCTCCTGCCTCA 12899	T GA	
		TGAGGCAG AGGAT TACTTGAG		
		ACTCCGTC TCCTA GTGAACTC		
		C _		
GAM1401 ZNF177	5'	CTCAAGTGATCCTCCTGCCTCA 12899	T GA	
		TGAGGCAG AGGAT TACTTGAG		
		ACTCCGTC TCCTA GTGAACTC		
		C _		
GAM1401 LOC113026	3'	CTCAAGTGATCCTCCTGCCCA 55901	A T GA	
		TG GGCAG AGGAT TACTTGAG		
		AC CCGTC TCCTA GTGAACTC		
		C C _		
GAM1401 LOC113026	3'	CTCAAGTGATCCTCCTGCCCA 55901	A T GA	
		TG GGCAG AGGAT TACTTGAG		
		AC CCGTC TCCTA GTGAACTC		
		C C _		
GAM1401 LOC115098	5'	CTCAAGCAATCCTCCTGCCTCA 56593	T GATA	
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCCTA GAACTC		
		C AC__		
GAM1401 LOC115098	5'	CTCAAGCAATCCTCCTGCCTCA 56593	T GATA	
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCCTA GAACTC		
		C AC__		
GAM1401 LOC115196	3'	CTCAAGTAATCCTCCACCCC 73264	CA A T _	
		GG GT GGA GAT ACTTGAG		

	CC CA CCT CTA TGA ACTC		
	C_ C C A		
GAM1401 LOC115196 3'	CTCAAGTAATCCTCCACCCC 73264	CA A T _	
	GG GT GGA GAT ACTTGAG		
	CC CA CCT CTA TGA ACTC		
	C_ C C A		
GAM1401 LOC130639 5'	CTCAAGTGATCCTCCACCTCA 74969	CAGT GA	
	TGAGG AGGAT TACTTGAG		
	ACTCC TCCTA GTGAACTC		
	ACCC _		
GAM1401 LOC130639 5'	CTCAAGTGATCCTCCACCTCA 74969	CAGT GA	
	TGAGG AGGAT TACTTGAG		
	ACTCC TCCTA GTGAACTC		
	ACCC _		
GAM1401 LOC131965 3'	CTCAAGCAGTCTTCCTGCCTCA 75030	T GATA	
	TGAGGCAG AGGAT CTTGAG		
	ACTCCGTC TTCTG GAACTC		
	C AC_		
GAM1401 LOC131965 3'	CTCAAGCAGTCTTCCTGCCTCA 75030	T GATA	
	TGAGGCAG AGGAT CTTGAG		
	ACTCCGTC TTCTG GAACTC		
	C AC_		
GAM1401 LOC134266 3'	CAAGCAATCCTGCCTCA 75163	GTA GATA	
	TGAGGCA GGAT CTTG		
	ACTCCGT CCTA GAAC		
	_ AC_		
GAM1401 LOC134266 3'	CAAGCAATCCTGCCTCA 75163	GTA GATA	
	TGAGGCA GGAT CTTG		
	ACTCCGT CCTA GAAC		
	_ AC_		
GAM1401 LOC134266 3'	CTCAAGTGATCCTCCACCTCA 75165	CAGT GA	
	TGAGG AGGAT TACTTGAG		
	ACTCC TCCTA GTGAACTC		
	ACCC _		
GAM1401 LOC134266 3'	CTCAAGTGATCCTCCACCTCA 75165	CAGT GA	
	TGAGG AGGAT TACTTGAG		
	ACTCC TCCTA GTGAACTC		
	ACCC _		
GAM1401 LOC135397 5'	CTCAAACATCACATCCCCTCA 75934	CAGTA _ AC	
	TGAGG GGA TGAT TTGAG		

	ACTCC CCT ACTA AACTC	
	_____ AC CA	
GAM1401 LOC135397 5'	CTCAAACATCACATCCCCTCA 75934	CAGTA ____ AC
	TGAGG GGA TGAT TTGAG	
	ACTCC CCT ACTA AACTC	
	_____ AC CA	
GAM1401 LOC144776 5'	CTCAAGTGATTCTCCTGCCTCA 76958	T GA
	TGAGGCAG AGGAT TACTTGAG	
	ACTCCGTC TCTTA GTGAACTC	
	C ____	
GAM1401 LOC144776 5'	CTCAAGTGATTCTCCTGCCTCA 76958	T GA
	TGAGGCAG AGGAT TACTTGAG	
	ACTCCGTC TCTTA GTGAACTC	
	C ____	
GAM1401 LOC144920 3'	CTCAAGTATATAGACACTACTT 83191	C AGGATG
CA	TGAGG AGT ATACTTGAG	
	ACTTC TCA TATGAACTC	
	A CAGATA	
GAM1401 LOC144920 3'	CTCAAGTATATAGACACTACTT 83191	C AGGATG
CA	TGAGG AGT ATACTTGAG	
	ACTTC TCA TATGAACTC	
	A CAGATA	
GAM1401 LOC146599 5'	CTCAAGTGATCCTCCTGCCTCA 78024	T GA
	TGAGGCAG AGGAT TACTTGAG	
	ACTCCGTC TCCTA GTGAACTC	
	C ____	
GAM1401 LOC146599 5'	CTCAAGTGATCCTCCTGCCTCA 78024	T GA
	TGAGGCAG AGGAT TACTTGAG	
	ACTCCGTC TCCTA GTGAACTC	
	C ____	
GAM1401 LOC147935 3'	CTCAAGTGATCCTCCTGCCTCA 84081	T GA
	TGAGGCAG AGGAT TACTTGAG	
	ACTCCGTC TCCTA GTGAACTC	
	C ____	
GAM1401 LOC147935 3'	CTCAAGTGATCCTCCTGCCTCA 84081	T GA
	TGAGGCAG AGGAT TACTTGAG	
	ACTCCGTC TCCTA GTGAACTC	
	C ____	
GAM1401 LOC148443 3'	CTCAAGTGACCCTCCCACCTCA 78855	CAGT ATGA
	TGAGG AGG TACTTGAG	

	ACTCC TCC GTGAACTC ACCC CA__		
GAM1401 LOC148443 3'	CTCAAGTGACCCTCCACCTCA 78855 TGAGG AGG TACTTGAG                 ACTCC TCC GTGAACTC ACCC CA__	CAGT ATGA	
GAM1401 LOC150587 3'	CTCAAGCAATCCTCGCCTCA 85060 TGAGGCAG AGGAT CTTGAG                     ACTCCGTC TCCTA GAACTC C AC__	T GATA	
GAM1401 LOC150587 3'	CTCAAGCAATCCTCGCCTCA 85060 TGAGGCAG AGGAT CTTGAG                     ACTCCGTC TCCTA GAACTC C AC__	T GATA	
GAM1401 LOC154822 3'	CTCAAGCAATTCTTCTGCCTCA 86260 TGAGGCAG AGGAT CTTGAG                     ACTCCGTC TCTTA GAACTC T AC__	T GATA	
GAM1401 LOC154822 3'	CTCAAGCAATTCTTCTGCCTCA 86260 TGAGGCAG AGGAT CTTGAG                     ACTCCGTC TCTTA GAACTC T AC__	T GATA	
GAM1401 LOC159765 5'	CTCAACCGTCATCCTCCCACCC 82196 CA TG GG AGGATGAT TTGAG                   AC CC TCCTACTG AACTC C ACCC CC	A CAGT AC	
GAM1401 LOC159765 5'	CTCAACCGTCATCCTCCCACCC 82196 CA TG GG AGGATGAT TTGAG                   AC CC TCCTACTG AACTC C ACCC CC	A CAGT AC	
GAM1401 LOC162461 5'	CTCAAGTGATCCTCCTACCTCA 82359 TGAGG AG AGGAT TACTTGAG                      ACTCC TC TCCTA GTGAACTC A C _	C T GA	
GAM1401 LOC162461 5'	CTCAAGTGATCCTCCTACCTCA 82359 TGAGG AG AGGAT TACTTGAG                      ACTCC TC TCCTA GTGAACTC A C _	C T GA	
GAM1401 LOC199699 3'	CTCAAGCAGTTCTCCTGCCTCA 88304 TGAGGCAG AGGAT CTTGAG 	T GATA	

	ACTCCGTC TCTTG	GAACTC		
	C	AC__		
GAM1401 LOC199699 3'	CTCAAGCAGTTCTCCTGCCTCA	88304	T	GATA
	TGAGGCAG AGGAT	CTTGAG		
	ACTCCGTC TCTTG	GAACTC		
	C	AC__		
GAM1401 LOC200268 3'	CTCAAGTGATCCTCCACCTCA	88683	CAGT	GA
	TGAGG	AGGAT TACTTGAG		
	ACTCC	TCCTA GTGAACTC		
	ACCC	__		
GAM1401 LOC200268 3'	CTCAAGTGATCCTCCACCTCA	88683	CAGT	GA
	TGAGG	AGGAT TACTTGAG		
	ACTCC	TCCTA GTGAACTC		
	ACCC	__		
GAM1401 LOC201304 3'	CTCAAACACTTCATGCTGCTGC	88231	A	G TAC__
	CCCA	TG GGCAGTAG ATGA		TTGAG
	AC CCGTCGTC	TACT AACTC		
	C	G TCACA		
GAM1401 LOC201304 3'	CTCAAACACTTCATGCTGCTGC	88231	A	G TAC__
	CCCA	TG GGCAGTAG ATGA		TTGAG
	AC CCGTCGTC	TACT AACTC		
	C	G TCACA		
GAM1401 LOC202908 5'	CTCAAGCAATTCTCCTGCCTCA	89232	T	GATA
	TGAGGCAG AGGAT	CTTGAG		
	ACTCCGTC TCTTA	GAACTC		
	C	AC__		
GAM1401 LOC202908 5'	CTCAAGCAATTCTCCTGCCTCA	89232	T	GATA
	TGAGGCAG AGGAT	CTTGAG		
	ACTCCGTC TCTTA	GAACTC		
	C	AC__		
GAM1401 LOC219529 5'	CAGGTGATCCTCCTGCCTCA	92968	T	GA
	TGAGGCAG AGGAT	TACTTG		
	ACTCCGTC TCCTA	GTGGAC		
	C	__		
GAM1401 LOC219529 5'	CAGGTGATCCTCCTGCCTCA	92968	T	GA
	TGAGGCAG AGGAT	TACTTG		
	ACTCCGTC TCCTA	GTGGAC		
	C	__		
GAM1401 LOC219673 5'	CTCAAGTAATCCACCTGCCTCA	93027	TA	GA
	TGAGGCAG	GGAT TACTTGAG		

	ACTCCGTC CCTA ATGAACTC CA _		
GAM1401 LOC219673 5'	CTCAAGTAATCCACCTGCCTCA 93027 TGAGGCAG GGAT TACTTGAG                     ACTCCGTC CCTA ATGAACTC CA _	TA	GA
GAM1401 LOC219673 5'	CTCAAGTGATCCTCCCGCCTCA 93028 TGAGGC AGGAT TACTTGAG                    ACTCCG TCCTA GTGAACTC CCC _	AGT	GA
GAM1401 LOC219673 5'	CTCAAGTGATCCTCCCGCCTCA 93028 TGAGGC AGGAT TACTTGAG                    ACTCCG TCCTA GTGAACTC CCC _	AGT	GA
GAM1401 LOC221540 3'	CTCAGGCAATCCTCCTGCCTCA 93837 TGAGGCAG AGGAT CTTGAG                    ACTCCGTC TCCTA GGA CTC C AC_	T	GATA
GAM1401 LOC221540 3'	CTCAGGCAATCCTCCTGCCTCA 93837 TGAGGCAG AGGAT CTTGAG                    ACTCCGTC TCCTA GGA CTC C AC_	T	GATA
GAM1401 LOC221760 5'	CTCAAGGGATCCTCCTGCCTCA 93785 TGAGGCAG AGGAT CTTGAG                    ACTCCGTC TCCTA GAA CTC C GG_	T	GATA
GAM1401 LOC221760 5'	CTCAAGGGATCCTCCTGCCTCA 93785 TGAGGCAG AGGAT CTTGAG                    ACTCCGTC TCCTA GAA CTC C GG_	T	GATA
GAM1401 LOC253783 5'	CAAGTCATCCTCCACCTCA 95267 TGAGG AGGATGA CTTG                   ACTCC TCCTACT GAAC ACCC _	CAGT	TA
GAM1401 LOC253783 5'	CAAGTCATCCTCCACCTCA 95267 TGAGG AGGATGA CTTG                   ACTCC TCCTACT GAAC ACCC _	CAGT	TA
GAM1401 LOC257545 3'	CTCAGGCAATCCTCCTGCCTCA 97805 TGAGGCAG AGGAT CTTGAG 	T	GATA



		ACTCCGTC TCCTA GGA		
		C AC__		
GAM1401	LOC257545 3'	CTCAGGCAATCCTCCTGCCTCA 97805	T	GATA
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCCTA GGA		
		C AC__		
GAM1401	LOC257598 3'	CTCAGGCAATCCTCCTGCCTCA 97920	T	GATA
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCCTA GGA		
		C AC__		
GAM1401	LOC257598 3'	CTCAGGCAATCCTCCTGCCTCA 97920	T	GATA
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCCTA GGA		
		C AC__		
GAM1401	LOC91963 3'	CTCAAGTAATCTTCCCGCCTCA 67693	AGTA T _	
		TGAGGC GGA GAT ACTTGAG		
		ACTCCG CCT CTA TGA		
		C__ T A		
GAM1401	LOC91963 3'	CTCAAGTAATCTTCCCGCCTCA 67693	AGTA T _	
		TGAGGC GGA GAT ACTTGAG		
		ACTCCG CCT CTA TGA		
		C__ T A		
GAM1402	A1BG 3'	CTCAAGCGATCCTCCTGCCTCA 55417	T	GATA
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCCTA GAA		
		C GC__		
GAM1402	A1BG 3'	CTCAAGTGATCCTCCCGCCTCA 55418	AGT	GA
		TGAGGC AGGAT TACTTGAG		
		ACTCCG TCCTA GTGA		
		CCC _		
GAM1402	AIM1 3'	CTCAGGTGATCCTCCACCTCA 91823	CAGT	GA
		TGAGG AGGAT TACTTGAG		
		ACTCC TCCTA GTGGA		
		ACCC _		
GAM1402	APAF1 3'	CTCAAGTAATCCTCCTGCCTCA 6729	T	GA
		TGAGGCAG AGGAT TACTTGAG		
		ACTCCGTC TCCTA ATGA		
		C _		
GAM1402	APAF1 3'	CTCAAGTAATCCTCCTGCCTCA 25038	T	GA
		TGAGGCAG AGGAT TACTTGAG		

			ACTCCGTC TCCTA ATGAACTC		
			C _		
GAM1402	FABP2	3'	CTCAAGCAATCCTCCTGCCTCA 3744	T	GATA
			TGAGGCAG AGGAT CTTGAG		
			ACTCCGTC TCCTA GAACTC		
			C AC_		
GAM1402	GLS	5'	TGTCATCTCACCGCCCCA 29790 A A AG		
			TG GGC GT GATGATA		
			AC CCG CA CTACTGT		
			C C CT		
GAM1402	ICAM1	3'	CTCAAGTGATCCTCCCACCTCA 71576	CAGT	GA
			TGAGG AGGAT TACTTGAG		
			ACTCC TCCTA GTGAACTC		
			ACCC _		
GAM1402	LZTS1	3'	CTCAAGCAATCCTCCTGCCTCA 40689	T	GATA
			TGAGGCAG AGGAT CTTGAG		
			ACTCCGTC TCCTA GAACTC		
			C AC_		
GAM1402	MADD	3'	CAAGCCGGCAGCTACTGCCCA 55331	A	GA ATA_
			TG GGCAGTAG TG CTTG		
			AC CCGTCATC AC GAAC		
			_ G_ GGCC		
GAM1402	MADD	3'	CAAGCCGGCAGCTACTGCCCA 55338	A	GA ATA_
			TG GGCAGTAG TG CTTG		
			AC CCGTCATC AC GAAC		
			_ G_ GGCC		
GAM1402	MADD	3'	CAAGCCGGCAGCTACTGCCCA 55343	A	GA ATA_
			TG GGCAGTAG TG CTTG		
			AC CCGTCATC AC GAAC		
			_ G_ GGCC		
GAM1402	MADD	3'	CAAGCCGGCAGCTACTGCCCA 55348	A	GA ATA_
			TG GGCAGTAG TG CTTG		
			AC CCGTCATC AC GAAC		
			_ G_ GGCC		
GAM1402	MADD	3'	CAAGCCGGCAGCTACTGCCCA 55354	A	GA ATA_
			TG GGCAGTAG TG CTTG		
			AC CCGTCATC AC GAAC		
			_ G_ GGCC		
GAM1402	MADD	3'	CAAGCCGGCAGCTACTGCCCA 13463	A	GA ATA_
			TG GGCAGTAG TG CTTG		

			AC CCGTCATC AC GAAC		
			— G_ GGCC		
GAM1402	MHC2TA	3'	CTCAAGTGATTCTCCTGCCTCA 4173	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCTTA GTGAACTC		
			C —		
GAM1402	PIGR	3'	CTCAAGTGATCTGCCGCCTCA 72599	A	ATGA
			TGAGGC GTAGG TACTTGAG		
			ACTCCG CGTCT GTGAACTC		
			C A__		
GAM1402	PRIM2A	3'	CTCAAGTGATCCTCCTACCTCA 6272	C T	GA
			TGAGG AG AGGAT TACTTGAG		
			ACTCC TC TCCTA GTGAACTC		
			A C —		
GAM1402	PTPN18	3'	CTCAAGCAATCCTCCTGCCTCA 26864	T	GATA
			TGAGGCAG AGGAT CTTGAG		
			ACTCCGTC TCCTA GAACTC		
			C AC__		
GAM1402	PVR	3'	CAAGTCATCCTCCCACCTCA 21472	CAGT	TA
			TGAGG AGGATGA CTTG		
			ACTCC TCCTACT GAAC		
			ACCC —		
GAM1402	RBM8A	3'	CTCAAGCCATCCTTCTGCCTCA 17543	T	ATA
			TGAGGCAG AGGATG CTTGAG		
			ACTCCGTC TCCTAC GAACTC		
			T C__		
GAM1402	TNFRSF9	3'	CTCAAGTGATCCTCCTGCCTCA 7788	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTA GTGAACTC		
			C —		
GAM1402	UMPS	3'	CTCAAGCGATCCTCCTGCCTCA 4551	T	GATA
			TGAGGCAG AGGAT CTTGAG		
			ACTCCGTC TCCTA GAACTC		
			C GC__		
GAM1402	C20orf150	3'	CTCAAACTGGCCACTGCCTCA 65396	A	ATGATAC
			TGAGGCAGT GG TTGAG		
			ACTCCGTCA CC AACTC		
			_ GGTCAA_		
GAM1402	C20orf188	3'	CAAGCCTGCCCCTCTGCCTCA 31578	T	ATGATA
			TGAGGCAG AGG CTTG		

		ACTCCGTC TCC	GAAC		
		_ CCGTCC			
GAM1402	COLEC12	3'	CTCAAGCAACCCTCCTGCCTCA 47864	T	ATGATA
			TGAGGCAG AGG CTTGAG		
			ACTCCGTC TCC GAACTC		
			C CAAC_		
GAM1402	DKFZP547N043	3'	CTCAAGTACCACCTGTATTATC 49317	GC	_ A A
			TCA TGAG AGT AGG TG TACTTGAG		
			ACTC TTA TCC AC ATGAACTC		
			TA TG _ C		
GAM1402	EVI5	3'	CTCAAGTGGTCCTCCTGCCTCA 18997	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTG GTGAACTC		
			C _		
GAM1402	FLB6421	3'	CTCAAGTGATCCTCCTACCTCA 39224	C T	GA
			TGAGG AG AGGAT TACTTGAG		
			ACTCC TC TCCTA GTGAACTC		
			A C _		
GAM1402	FLJ10297	3'	CTCAAGTGATCCTCCTGCCTCA 35980	T	GA
			TGAGGCAG AGGAT TACTTGAG		
			ACTCCGTC TCCTA GTGAACTC		
			C _		
GAM1402	FLJ10607	3'	CTCAAGTGATCCTCCCACCTCA 77111	CAGT	GA
			TGAGG AGGAT TACTTGAG		
			ACTCC TCCTA GTGAACTC		
			ACCC _		
GAM1402	FLJ10687	3'	CTCAAGGATCCTCCTGCCTCA 36409	T	GATA
			TGAGGCAG AGGAT CTTGAG		
			ACTCCGTC TCCTA GAACTC		
			C G_		
GAM1402	FLJ10847	3'	CTCAAGTGATCCTCCCACCTCA 36748	CAGT	GA
			TGAGG AGGAT TACTTGAG		
			ACTCC TCCTA GTGAACTC		
			ACCC _		
GAM1402	FLJ12442	5'	CTCGAGCCCATCCTACGGCCTC 43265	A	ATA
			A TGAGGC GTAGGATG CTTGAG		
			ACTCCG CATCCTAC GAGCTC		
			G CC_		
GAM1402	FLJ13072	5'	CTCAAGCAATTCTCCTGCCTCA 89809	T	GATA
			TGAGGCAG AGGAT CTTGAG		

		ACTCCGTC TCTTA GAACTC		
		C AC__		
GAM1402	FLJ13072	5' CTCAGGTAATCCTCCCACCTCA 89810	CAGT	GA
		TGAGG AGGAT TACTTGAG		
		ACTCC TCCTA ATGGA		
		CTC AC__		
GAM1402	FLJ13984	5' GTCATCCTCCTGCCTCA 45453	T	
		TGAGGCAG AGGATGAT		
		ACTCCGTC TCCTACTG		
		C		
GAM1402	FLJ14351	3' CTCAAGCAATCCTCCTGCCTCA 45323	T	GATA
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCCTA GAACTC		
		C AC__		
GAM1402	FLJ14803	3' CTCAAGCAATTCTCCTGCCTCA 51616	T	GATA
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCTTA GAACTC		
		C AC__		
GAM1402	FLJ20671	3' CTCAAGCAATTCTCCTGCCTCA 35522	T	GATA
		TGAGGCAG AGGAT CTTGAG		
		ACTCCGTC TCTTA GAACTC		
		C AC__		
GAM1402	FLJ22316	5' CTCAAGTAATCCTACCGCCTCA 46919	A	GA
		TGAGGC GTAGGAT TACTTGAG		
		ACTCCG CATCCTA ATGA		
		C		
GAM1402	FLJ23416	3' CTCAAGCAATCCTGCTGCCTCA 49949		GATA
		TGAGGCAGTAGGAT CTTGAG		
		ACTCCGTCGTCCTA GAACTC		
		AC__		
GAM1402	KIAA0212	3' CTCAAGTGATCCTTCTGCCTCA 27938	T	GA
		TGAGGCAG AGGAT TACTTGAG		
		ACTCCGTC TCCTA GTGA		
		T		
GAM1402	KIAA0377	3' CAAGTGCCCCTTCTGCCTCA 27794	T	ATGA
		TGAGGCAG AGG TACTTG		
		ACTCCGTC TCC GTGA		
		T CC__		
GAM1402	KIAA0446	5' CTCAGGTGATCCTCCCACCTCA 68865	CAGT	GA
		TGAGG AGGAT TACTTGAG		

	ACTCC TCCTA GTGGA		
	CTCC		
GAM1402 KIAA0557	3' CTCAAGTGTTCCTCCTGCCTCA 77995	T	TG
	TGAGGCAG AGGA ATACTTGAG		
	ACTCCGTC TCCT TGTGAACTC		
	C		
GAM1402 KIAA0802	3' ATTCCCCCACTGCCTCA 62564	A	AT
	TGAGGCAGT GG GAT		
	ACTCCGTCA CC TTA		
	C CC		
GAM1402 KIAA0828	3' CTCAAGCAATCCTCCTGCCTCA 81195	T	GATA
	TGAGGCAG AGGAT CTTGAG		
	ACTCCGTC TCCTA GAACTC		
	C AC		
GAM1402 KIAA1026	3' CTCAAACAATTCTCCTGCCTCA 71191	T	GATAC
	TGAGGCAG AGGAT TTGAG		
	ACTCCGTC TCTTA AACTC		
	C ACA		
GAM1402 KIAA1037	3' CTCAAAACCCCTTCTGCCTCA 30435	T	ATGATAC
	TGAGGCAG AGG TTGAG		
	ACTCCGTC TCC AACTC		
	T CCAA		
GAM1402 KIAA1271	3' TCAGACCCTCCTGCCTCA 69552	T	A
	TGAGGCAG AGG TGA		
	ACTCCGTC TCC ACT		
	C CAG		
GAM1402 KIAA1280	5' CTCAAGTGACCCTCCTGCCTCA 69714	T	ATGA
	TGAGGCAG AGG TACTTGAG		
	ACTCCGTC TCC GTGAACTC		
	C CA		
GAM1402 KIAA1396	3' CTCAAGTGACCCTCCACCTCA 62988	CAGT	ATGA
	TGAGG AGG TACTTGAG		
	ACTCC TCC GTGAACTC		
	CTCC CA		
GAM1402 KIAA1649	3' CTCAAGTGATCCTCCACCTCA 50257	CAGT	GA
	TGAGG AGGAT TACTTGAG		
	ACTCC TCCTA GTGAACTC		
	CTCC		
GAM1402 KIAA1671	3' CTCAAGTGATTCTACTGCCTCA 65672		GA
	TGAGGCAGTAGGAT TACTTGAG		

ACTCCGTCATCTTA GTGAACTC

GAM1402 KIAA1671 3' CTCAAGTGATTCTCCACCTCA 65673 CAGTA T \_  
TGAGG GGA GAT ACTTGAG  
||||| ||| ||| |||||  
ACTCC CCT TTA TGA ACTC  
AC\_\_ C G

GAM1402 KIAA1727 3' CTCAAGTGATCCTCCACCTCA 64056 CAGT GA  
TGAGG AGGAT TACTTGAG  
||||| ||||| |||||  
ACTCC TCCTA GTGAACTC  
ACCC \_

GAM1402 KIAA1751 3' CTCAAGCAATCCTCCTGCCTCA 71692 T GATA  
TGAGGCAG AGGAT CTTGAG  
||||||| ||||| |||||  
ACTCCGTC TCCTA GAACTC  
C AC\_\_

GAM1402 KIAA1821 3' CTCAAGTGATCCTCCACCTCA 71782 CAGT GA  
TGAGG AGGAT TACTTGAG  
||||| ||||| |||||  
ACTCC TCCTA GTGAACTC  
ACCC \_

GAM1402 KIAA1924 3' CTCCAGCCATCCTCCTGCCTCA 73670 T ATA T  
TGAGGCAG AGGATG CT GAG  
||||||| ||||| || |||  
ACTCCGTC TCCTAC GA CTC  
C C\_\_ C

GAM1402 LNIR 3' CTCAAGCAATCCTCCTGCCTCA 48130 T GATA  
TGAGGCAG AGGAT CTTGAG  
||||||| ||||| |||||  
ACTCCGTC TCCTA GAACTC  
C AC\_\_

GAM1402 MGC10200 3' CTCAAGTGATCCTCCACCTCA 58984 CAGT GA  
TGAGG AGGAT TACTTGAG  
||||| ||||| |||||  
ACTCC TCCTA GTGAACTC  
ACCC \_

GAM1402 MGC12466 3' CTCAAGCTATCCTCCTGCCTCA 79032 T ATA  
TGAGGCAG AGGATG CTTGAG  
||||||| ||||| |||||  
ACTCCGTC TCCTAT GAACTC  
C C\_\_

GAM1402 MGC2477 5' CAAGCGATCCTCCTGCCTCA 44058 T GATA  
TGAGGCAG AGGAT CTTG  
||||||| ||||| |||||  
ACTCCGTC TCCTA GAAC  
C GC\_\_

GAM1402 MGC2488 3' CTCAAGTGATCCTCCTGCCTCA 43868 T GA  
TGAGGCAG AGGAT TACTTGAG  
||||||| ||||| |||||

		ACTCCGTC TCCTA GTGAACTC	
		C _	
GAM1402	MGC3113	3' CTCAAGCAATTCATCTGCCTCA 43845	TA GATA
		TGAGGCAG GGAT CTTGAG	
		ACTCCGTC CTTA GAACTC	
		TA AC_	
GAM1402	MRPL35	3' CTCAAGTGGTCCTCCTGCCTCA 33542	T GA
		TGAGGCAG AGGAT TACTTGAG	
		ACTCCGTC TCCTG GTGAACTC	
		C _	
GAM1402	OSBPL2	3' CTCAAGTAGTCTGCCTGCCTCA 29213	TA GA
		TGAGGCAG GGAT TACTTGAG	
		ACTCCGTC TCTG ATGAACTC	
		CG _	
GAM1402	OSBPL2	3' CTCAAGTAGTCTGCCTGCCTCA 57864	TA GA
		TGAGGCAG GGAT TACTTGAG	
		ACTCCGTC TCTG ATGAACTC	
		CG _	
GAM1402	POFUT1	3' CTCAAGCGATCCTTCTGCCTCA 70468	T GATA
		TGAGGCAG AGGAT CTTGAG	
		ACTCCGTC TCCTA GAACTC	
		T GC_	
GAM1402	PPIL2	3' CTCAAGCAATCCTCCTGCCTCA 26764	T GATA
		TGAGGCAG AGGAT CTTGAG	
		ACTCCGTC TCCTA GAACTC	
		C AC_	
GAM1402	PRO1048	3' CTCAAGCGATCCTCCTGCCTCA 37515	T GATA
		TGAGGCAG AGGAT CTTGAG	
		ACTCCGTC TCCTA GAACTC	
		C GC_	
GAM1402	SAMHD1	3' CTCAAGCGACCCTCCTGCCTCA 61311	T ATGATA
		TGAGGCAG AGG CTTGAG	
		ACTCCGTC TCC GAACTC	
		C CAGC_	
GAM1402	SARM	3' CTCAAGTGATCCTCCTGCCTCA 30602	T GA
		TGAGGCAG AGGAT TACTTGAG	
		ACTCCGTC TCCTA GTGAACTC	
		C _	
GAM1402	SARM	3' CTCAAGTGGTCCTCCTGCCTCA 30603	T GA
		TGAGGCAG AGGAT TACTTGAG	



ACTCCGTC TCCTG GTGAACTC  
 C \_  
 GAM1402 SCYA16 3' CAAGCAATCCACCTGCCTCA 15955 TA GATA  
 TGAGGCAG GGAT CTTG  
 ||||| ||| |||  
 ACTCCGTC CCTA GAAC  
 CA AC\_  
 GAM1402 SCYA16 3' CTCAAGTGATCCTCCCACCCC 15957 CA A T \_  
 GG GT GGA GAT ACTTGAG  
 || ||| ||| |||||  
 CC CA CCT CTA TGA ACTC  
 C\_ C C G  
 GAM1402 SDC3 5' CTCAAGCAGTTCCCCTGCCTCA 27750 TA GATA  
 TGAGGCAG GGAT CTTGAG  
 ||||| ||| |||||  
 ACTCCGTC CTTG GAACTC  
 CC AC\_  
 GAM1402 SNAPC1 3' CTCAAGCTATCCTCCTGCCTCA 11841 T ATA  
 TGAGGCAG AGGATG CTTGAG  
 ||||| ||||| |||||  
 ACTCCGTC TCCTAT GAACTC  
 C C\_  
 GAM1402 SYTL4 5' CTCAAGAGATCCTCCTGCCTCA 54941 T GATA  
 TGAGGCAG AGGAT CTTGAG  
 ||||| ||||| |||||  
 ACTCCGTC TCCTA GAACTC  
 C GA\_  
 GAM1402 TIEG2 3' TCTCCCACTGCCTCA 13182 A T  
 TGAGGCAGT GGA GA  
 ||||| ||| ||  
 ACTCCGTCA CCT CT  
 C \_  
 GAM1402 TMPRSS5 3' CTCACCTGCACACCACTGCCTCA 47783 A A ATACT  
 TGAGGCAGT GG TG TGAG  
 ||||| ||| |||  
 ACTCCGTCA CC AC ACTC  
 \_ \_ ACGTC  
 GAM1402 USP3 5' CTCAAGTGATTCTTCTGCCTCA 89676 T GA  
 TGAGGCAG AGGAT TACTTGAG  
 ||||| ||||| |||||  
 ACTCCGTC TCTTA GTGAACTC  
 T \_  
 GAM1402 WIRE 3' TCACCCCACTGCTTCA 78308 A A  
 TGAGGCAGT GG TGA  
 ||||| || |||  
 ACTTCGTCA CC ACT  
 C C  
 GAM1402 YAP 5' CTCAAGTAATCTTCCTGCCTCA 36787 T GA  
 TGAGGCAG AGGAT TACTTGAG  
 ||||| ||||| |||||

	ACTCCGTC TTCTA ATGAACTC		
	C _		
GAM1402 ZNF177	5' CTCAAGTGATCCTCCTGCCTCA 12899	T	GA
	TGAGGCAG AGGAT TACTTGAG		
	ACTCCGTC TCCTA GTGAACTC		
	C _		
GAM1402 LOC113026	3' CTCAAGTGATCCTCCTGCCCA 55901	A	T GA
	TG GGCAG AGGAT TACTTGAG		
	AC CCGTC TCCTA GTGAACTC		
	C C _		
GAM1402 LOC115098	5' CTCAAGCAATCCTCCTGCCTCA 56593	T	GATA
	TGAGGCAG AGGAT CTTGAG		
	ACTCCGTC TCCTA GAACTC		
	C AC_		
GAM1402 LOC115196	3' CTCAAGTAATCCTCCCACCCC 73264	CA	A T _
	GG GT GGA GAT ACTTGAG		
	CC CA CCT CTA TGA ACTC		
	C_ C C A		
GAM1402 LOC130639	5' CTCAAGTGATCCTCCCACCTCA 74969	CAGT	GA
	TGAGG AGGAT TACTTGAG		
	ACTCC TCCTA GTGAACTC		
	ACCC _		
GAM1402 LOC131965	3' CTCAAGCAGTCTTCCTGCCTCA 75030	T	GATA
	TGAGGCAG AGGAT CTTGAG		
	ACTCCGTC TTCTG GAACTC		
	C AC_		
GAM1402 LOC134266	3' CAAGCAATCCTGCCTCA 75163	GTA	GATA
	TGAGGCA GGAT CTTG		
	ACTCCGT CCTA GAAC		
	_ AC_		
GAM1402 LOC134266	3' CTCAAGTGATCCTCCCACCTCA 75165	CAGT	GA
	TGAGG AGGAT TACTTGAG		
	ACTCC TCCTA GTGAACTC		
	ACCC _		
GAM1402 LOC135397	5' CTCAAACATCACATCCCCTCA 75934	CAGTA	_ AC
	TGAGG GGA TGAT TTGAG		
	ACTCC CCT ACTA AACTC		
	_ AC CA		
GAM1402 LOC144776	5' CTCAAGTGATTCTCCTGCCTCA 76958	T	GA
	TGAGGCAG AGGAT TACTTGAG		

	ACTCCGTC TCTTA GTGAACTC	
	C _	
GAM1402 LOC144920 3'	CTCAAGTATATAGACACTACTT 83191	C AGGATG
CA	TGAGG AGT ATACTTGAG	
	ACTTC TCA TATGAACTC	
	A CAGATA	
GAM1402 LOC146599 5'	CTCAAGTGATCCTCCTGCCTCA 78024	T GA
	TGAGGCAG AGGAT TACTTGAG	
	ACTCCGTC TCCTA GTGAACTC	
	C _	
GAM1402 LOC147935 3'	CTCAAGTGATCCTCCTGCCTCA 84081	T GA
	TGAGGCAG AGGAT TACTTGAG	
	ACTCCGTC TCCTA GTGAACTC	
	C _	
GAM1402 LOC148443 3'	CTCAAGTGACCCTCCACCTCA 78855	CAGT ATGA
	TGAGG AGG TACTTGAG	
	ACTCC TCC GTGAACTC	
	ACCC CA_	
GAM1402 LOC150587 3'	CTCAAGCAATCCTCCTGCCTCA 85060	T GATA
	TGAGGCAG AGGAT CTTGAG	
	ACTCCGTC TCCTA GAACTC	
	C AC_	
GAM1402 LOC154822 3'	CTCAAGCAATTCTTCTGCCTCA 86260	T GATA
	TGAGGCAG AGGAT CTTGAG	
	ACTCCGTC TCTTA GAACTC	
	T AC_	
GAM1402 LOC159765 5'	CTCAACCGTCATCCTCCCACCC 82196	A CAGT AC
CA	TG GG AGGATGAT TTGAG	
	AC CC TCCTACTG AACTC	
	C ACCC CC	
GAM1402 LOC162461 5'	CTCAAGTGATCCTCCTACCTCA 82359	C T GA
	TGAGG AG AGGAT TACTTGAG	
	ACTCC TC TCCTA GTGAACTC	
	A C _	
GAM1402 LOC199699 3'	CTCAAGCAGTTCTCCTGCCTCA 88304	T GATA
	TGAGGCAG AGGAT CTTGAG	
	ACTCCGTC TCTTG GAACTC	
	C AC_	
GAM1402 LOC200268 3'	CTCAAGTGATCCTCCCACCTCA 88683	CAGT GA
	TGAGG AGGAT TACTTGAG	

	ACTCC TCCTA GTGAACTC		
	ACCC _		
GAM1402 LOC201304 3'	CTCAAACACTTCATGCTGCTGC 88231	A	G TAC_
	CCCA TG GGCAGTAG ATGA TTGAG		
	AC CCGTCGTC TACT AACTC		
	C G TCACA		
GAM1402 LOC202908 5'	CTCAAGCAATTCTCCTGCCTCA 89232	T	GATA
	TGAGGCAG AGGAT CTTGAG		
	ACTCCGTC TCTTA GAACTC		
	C AC_		
GAM1402 LOC219529 5'	CAGGTGATCCTCCTGCCTCA 92968	T	GA
	TGAGGCAG AGGAT TACTTG		
	ACTCCGTC TCCTA GTGGAC		
	C _		
GAM1402 LOC219673 5'	CTCAAGTAATCCACCTGCCTCA 93027	TA	GA
	TGAGGCAG GGAT TACTTGAG		
	ACTCCGTC CCTA ATGAACTC		
	CA _		
GAM1402 LOC219673 5'	CTCAAGTGATCCTCCCGCCTCA 93028	AGT	GA
	TGAGGC AGGAT TACTTGAG		
	ACTCCG TCCTA GTGAACTC		
	CCC _		
GAM1402 LOC221540 3'	CTCAGGCAATCCTCCTGCCTCA 93837	T	GATA
	TGAGGCAG AGGAT CTTGAG		
	ACTCCGTC TCCTA GGA CTC		
	C AC_		
GAM1402 LOC221760 5'	CTCAAGGGATCCTCCTGCCTCA 93785	T	GATA
	TGAGGCAG AGGAT CTTGAG		
	ACTCCGTC TCCTA GAACTC		
	C GG_		
GAM1402 LOC253783 5'	CAAGTCATCCTCCACCTCA 95267	CAGT	TA
	TGAGG AGGATGA CTTG		
	ACTCC TCCTACT GAAC		
	ACCC _		
GAM1402 LOC257545 3'	CTCAGGCAATCCTCCTGCCTCA 97805	T	GATA
	TGAGGCAG AGGAT CTTGAG		
	ACTCCGTC TCCTA GGA CTC		
	C AC_		
GAM1402 LOC257598 3'	CTCAGGCAATCCTCCTGCCTCA 97920	T	GATA
	TGAGGCAG AGGAT CTTGAG		

			ACTCCGTC TCCTA GGA	CTC	
			C AC		
GAM1402	LOC91963	3'	CTCAAGTAATCTTCCCGCCTCA	67693	AGTA T _
			TGAGGC GGA GAT ACTTGAG		
			ACTCCG CCT CTA TGA	ACTC	
			C T A		
GAM1403	APC	3'	TTGCCACTTAACCATTCATGC	3483	GTACT A A
			GCA GTGGTTAA TG CAA		
			CGT TACCAATT AC GTT		
			ACCT C C		
GAM1403	APG5L	3'	TGTCATTTAATAACATAC	16764	C G
			GTA TGT GTTAAATGACA		
			CAT ACA TAATTTACTGT		
			_ A		
GAM1403	CA14	3'	TGTCATTCCAGGAAGAACTGCA	24004	A G TTA
			TGCAGT CT TGG AATGACA		
			ACGTCA GA ACC TTA	CTGT	
			A AGG		
GAM1403	FDX1	3'	TTGTCACTTCTTGAAAGTATGCA	60344	G GTGGTTA
			TGCA TACT AATGACAA		
			ACGT ATGA TTA	CTGT	
			_ AAGTTC		
GAM1403	FGFR2	5'	GCCATTCAAGTGACTGCA	43481	_ _
			TGCAGT ACT GTGGT		
			ACGTCA TGA TACCG		
			G ACT		
GAM1403	FGFR2	5'	GCCATTCAAGTGACTGCA	43491	_ _
			TGCAGT ACT GTGGT		
			ACGTCA TGA TACCG		
			G ACT		
GAM1403	FGFR2	5'	GCCATTCAAGTGACTGCA	43501	_ _
			TGCAGT ACT GTGGT		
			ACGTCA TGA TACCG		
			G ACT		
GAM1403	FGFR2	5'	GCCATTCAAGTGACTGCA	43358	_ _
			TGCAGT ACT GTGGT		
			ACGTCA TGA TACCG		
			G ACT		
GAM1403	FGFR2	5'	GCCATTCAAGTGACTGCA	43364	_ _
			TGCAGT ACT GTGGT		

		ACGTCA TGA TACCG			
		G ACT			
GAM1403	FGFR2	5' GCCATTCAAGTGA	43370	—	—
		TGCAGT ACT GTGGT			
		ACGTCA TGA TACCG			
		G ACT			
GAM1403	FGFR2	5' GCCATTCAAGTGA	43378	—	—
		TGCAGT ACT GTGGT			
		ACGTCA TGA TACCG			
		G ACT			
GAM1403	FGFR2	5' GCCATTCAAGTGA	43384	—	—
		TGCAGT ACT GTGGT			
		ACGTCA TGA TACCG			
		G ACT			
GAM1403	FGFR2	5' GCCATTCAAGTGA	43388	—	—
		TGCAGT ACT GTGGT			
		ACGTCA TGA TACCG			
		G ACT			
GAM1403	FGFR2	5' GCCATTCAAGTGA	43391	—	—
		TGCAGT ACT GTGGT			
		ACGTCA TGA TACCG			
		G ACT			
GAM1403	FGFR2	5' GCCATTCAAGTGA	3762	—	—
		TGCAGT ACT GTGGT			
		ACGTCA TGA TACCG			
		G ACT			
GAM1403	KHK	3' TGCCATTTAATTAGCTGCA	4036	ACTG	A
		TGCAGT TGGTTAAATG CA			
		ACGTCG ATTAATTTAC GT			
		— C			
GAM1403	KHK	3' TGCCATTTAATTAGCTGCA	21406	ACTG	A
		TGCAGT TGGTTAAATG CA			
		ACGTCG ATTAATTTAC GT			
		— C			
GAM1403	MBL2	3' TGTCACCTTAATTGCTAC	4119	CT TG	A
		GTA G GTTAA TGACA			
		CAT C TAATT ACTGT			
		— GT C			
GAM1403	MPL	3' TGTCACCCAGGCTGCAGTGC	18159	TG AAA_	
		GTA CTG GTT TGACA			

			CGTGAC CGG ACTGT		
			GT ACCC		
GAM1403 PAICS	3'	TAACCACAGT	ACTACA	21259	C _
			TG AGT ACTGTGGTTA		
			AC TCA TGACACCAAT		
			A G		
GAM1403 PKHD1	3'	TGTCATTTAA	AATTCATGCA	56918	GTACT GG
			TGCA GT TTAAATGACA		
			ACGT TA AATTTACTGT		
			ACT__ A_		
GAM1403 PRKCN	3'	TGTCATCTGC	AGTGCTGCA	19450	TG TTAA
			TGCAGTACTG G ATGACA		
			ACGTCGTGAC C TACTGT		
			GT ____		
GAM1403 RUNX1	5'	TCATAAACA	ACCACAGAACCAC	8268	CA A AA__
A			TG GT CTGTGGTT ATGA		
			AC CA GACACCAA TACT		
			AC A CAAA		
GAM1403 TFDP1	3'	TCATTTAA	AAGACATGTACTG	23050	_ GG
			CAGTAC TGT TTAAATGA		
			GTCATG ACA AATTTACT		
			T GA		
GAM1403 AKT3	3'	TGCCATTTA	ACCCCTTGGTACT	18437	T__ A
G			CAGTACTG GGTAAATG CA		
			GTCATGGT CCAATTTAC GT		
			TCC C		
GAM1403 DNAL4	3'	TGCCATCCCC	AGTACTGC	19219	T TTAA A
			GCAGTACTG GG ATG CA		
			CGTCATGAC CC TAC GT		
			_ C__ C		
GAM1403 FLJ10718	3'	TCACCCTCC	ACAGTACTCCA	36497	C TTAAA
			TG AGTACTGTGG TGA		
			AC TCATGACACC ACT		
			C TCCC_		
GAM1403 KIAA0205	3'	TGTCACCC	CAGGCTGTAGTGC	29591	TG AAA_
			GTACTG GTT TGACA		
			CGTGAT CGG ACTGT		
			GT ACCC		
GAM1403 KIAA1052	5'	TGTCACTC	CAGGCTGCAGTGC	30254	TG AAA_
			GTACTG GTT TGACA		

CGTGAC CGG ACTGT  
 GT ACTC  
 GAM1403 KIAA1881 3' TGCCAGGAGCCACAGCAGC 95346 AGTA AAA A  
 GC CTGTGGTT TG CA  
 || ||||| ||  
 CG GACACCGA AC GT  
 AC\_\_ GG\_ C  
 GAM1403 KIAA1950 3' TCATACCACTGTACTGCA 92598 T TAA  
 TGCAGTAC GTGGT ATGA  
 ||||| ||| ||  
 ACGTCATG CACCA TACT  
 T \_\_\_\_  
 GAM1403 MADHIP 5' GTCATTTAACCCTACT 16622 CTGT  
 AGTA GGTTAAATGAC  
 ||| |||||  
 TCAT CCAATTTACTG  
 C\_\_\_\_  
 GAM1403 MGC16279 5' TCATCTCCACGGTACCACA 62876 CA TTAA  
 TG GTACTGTGG ATGA  
 || ||||| ||  
 AC CATGGCACC TACT  
 AC CTC\_  
 GAM1403 MGC16279 5' TCATCTCCACGGTACCACA 51890 CA TTAA  
 TG GTACTGTGG ATGA  
 || ||||| ||  
 AC CATGGCACC TACT  
 AC CTC\_  
 GAM1403 MGC5395 5' TAGCCGCAGCACCGCA 43933 A A  
 TGC GT CTGTGGTTA  
 ||| || |||||  
 ACG CA GACGCCGAT  
 C C  
 GAM1403 PAPOLG 3' TGCCATCTACAGTATTACA 43174 C TTAA A  
 TG AGTACTGTGG ATG CA  
 || ||||| |||  
 AC TTATGACATC TAC GT  
 A \_\_\_\_ C  
 GAM1403 PRO0902 5' TTGCCATTCTACTCTCCAGCAC 53900 A T\_\_ TA A  
 TGCA TGCAGT CTG GGT AATG CAA  
 ||||| ||| ||| |||  
 ACGTCA GAC TCA TTAC GTT  
 C CTC TC C  
 GAM1403 RBM11 3' TTGTCATTTTATTAGTAC 58585 TGGTT  
 GTACTG AAATGACAA  
 ||||| |||||  
 CATGAT TTTACTGTT  
 TAT\_\_  
 GAM1403 TNFRSF13B 3' TCACCTAACCACACGTGC 24923 \_ AA  
 GTAC TGTGGTTA TGA  
 ||| ||||| ||



		CGTG ACACCAAT ACT		
		C CC		
GAM1403	YKT6	3' TCATTACATCAGAACTGCA	21608	A _ GTTA
		TGCAGT CTG TG AATGA		
		ACGTCA GAC AC T TACT		
		A T AC__		
GAM1403	LOC115297	3' GTCATTTGGAAGTAGTAC	72888	GG
		GTACTGT TTAAATGAC		
		CATGATG GGTTTACTG		
		AA		
GAM1403	LOC133686	3' TTGTCACCCAGGCTGGACTGCA	75129	A GT AAA_
		TGCAGT CT GGTT TGACAA		
		ACGTCA GG TCGG ACTGTT		
		_ _ ACCC		
GAM1403	LOC143162	3' TCATATTCACAGTACT	76497	TTAA
		AGTACTGTGG ATGA		
		TCATGACACT TACT		
		TA__		
GAM1403	LOC148195	5' TGTCACCTAGGCTGCAGTGC	84139	TG AAA_
		GTACTG GTT TGACA		
		CGTGAC CGG ACTGT		
		GT ATCC		
GAM1403	LOC148195	5' TTGTCATCTTGATCACACTAC	84140	C _
		GTA TGTGGTTAA ATGACAA		
		CAT ACACTAGTT TACTGTT		
		C C		
GAM1403	LOC150142	5' TCACTTAATTACATCTGCA	79580	TAC A
		TGCAG TGTGGTTAA TGA		
		ACGTC ACATTAATT ACT		
		T__ C		
GAM1403	LOC157450	5' TCATCTCCACGGTACCACA	70975	CA TTAA
		TG GTACTGTGG ATGA		
		AC CATGGCACC TACT		
		AC CTC_		
GAM1403	LOC196483	5' TCATCTCTCACGGTACCACA	60393	CA TTAA
		TG GTACTGTGG ATGA		
		AC CATGGCACT TACT		
		AC CTC_		
GAM1403	LOC196738	3' TCATATTCACAGTACT	87505	TTAA
		AGTACTGTGG ATGA		

TCATGACACT TACT  
 TA\_\_  
 GAM1403 LOC255974 5' GTCAACCACAGCGCTGCA 97478 TA TAAA  
 TGCAG CTGTGGT TGAC  
 |||| ||||| |||  
 ACGTC GACACCA ACTG  
 GC \_\_\_\_  
 GAM1403 LOC90529 3' TGTCATTTAACCTTCACAC 63166 ACTGT  
 GT GGTAAATGACA  
 || |||||  
 CA CCAATTTACTGT  
 CACTT  
 GAM1404 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
 GTA GGAT GGGTTGTTT  
 ||| ||| |||||  
 CGT CCTA CCCAACAAA  
 C CGTG\_  
 GAM1404 LCT 3' AACCGTAAAAATCCTT 9697 G  
 AAGGATTTTTTA GGTT  
 ||||| |||  
 TTCCTAAAAAT CCAA  
 G  
 GAM1404 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
 GTAAGGATTTTTAGGGTTGTTT  
 |||||  
 CATTCTAAAAATCCCAACAAA  
  
 GAM1404 FBXO30 3' AACTAAAAAAATCCTGAC 49573 A AG  
 GT AGGATTTTT GGTT  
 || ||||| |||  
 CA TCCTAAAAA TCAA  
 G AA  
 GAM1404 KIAA0494 3' AACAACCCTTACTTAC 28736 GATTTTT  
 GTAAG AGGGTTGTT  
 |||| |||||  
 CATTCTCCCAACAA  
 AT\_\_\_\_  
 GAM1404 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
 TAAG TTTT GGGTTGTTT  
 ||| ||| |||||  
 GTTC AAAA CCAACAAA  
 \_\_\_\_ C  
 GAM1404 SMT3H2 3' AACAACATAAAAAATCCTTGC 22670 GG  
 GTAAGGATTTTTA GTTGTT  
 ||||| |||||  
 CGTTCCTAAAAAT CAACAA  
 A\_  
 GAM1404 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_  
 GTAAGGATTTTT GGGTT  
 ||||| |||||

CGTTCCTAAAAA TCCAA  
 GTA  
 GAM1404 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
 GGAT TT GGGTTGTTT  
 |||| || |||||  
 CCTG AA CCCAACAAA  
 T\_ C  
 GAM1404 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
 C GTA GGATTTTT TTGTTT  
 ||| ||||| |||||  
 CGT CCTAAAAA AACAAA  
 C GATAA  
 GAM1404 LOC148089 3' GGCCCTAAAAATTCCTAC 78637 A  
 GTA GGATTTTTTAGGGTT  
 ||| |||||  
 CAT CTTAAAAATCCCGG  
 C  
 GAM1404 LOC154547 3' AACACATAAAAAATCCTTGC 76050 GG  
 GTAAGGATTTTTA GTTGTT  
 ||||| |||||  
 CGTTCCTAAAAAT CAACAA  
 A\_  
 GAM1404 LOC158104 3' ACAGCCAAAAATCCTTA 60313 AG  
 TAAGGATTTTT GTTGT  
 ||||| |||||  
 ATTCCTAAAAA CCGACA  
 —  
 GAM1404 LOC205880 5' AAACAACCATCATCCTGAC 90709 A TTTTAG  
 GT AGGAT GGTGTTT  
 || |||| |||||  
 CA TCCTA CCAACAAA  
 G CTA\_\_\_  
 GAM1404 LOC221561 3' AACACATAAAAAATCCTTGC 92130 GG  
 GTAAGGATTTTTA GTTGTT  
 ||||| |||||  
 CGTTCCTAAAAAT CAACAA  
 A\_  
 GAM1404 LOC257591 3' AACACATAAAAAATCCTTGC 97840 GG  
 GTAAGGATTTTTA GTTGTT  
 ||||| |||||  
 CGTTCCTAAAAAT CAACAA  
 A\_  
 GAM1404 LOC51145 3' AGCTAAAATCCTTAC 32393 TAG  
 GTAAGGATTTT GTT  
 ||||| |||||  
 CATTCCTAAAA TCGA  
 —  
 GAM1405 AMPD3 3' CACTATTCCATTAGACCCC 4895 A GGT  
 GG GTT TGAATAGTG  
 || ||| |||||

		CC CAG ACCTTATCAC	
		C ATT	
GAM1405 APAF1	3'	CACTATTCTGCTCCCTCT 6726	AGTT T
		AGAGG GGT GGAATAGTG	
		TCTCC TCG CCTTATCAC	
		C__ T	
GAM1405 APAF1	3'	CACTATTCTGCTCCCTCT 25035	AGTT T
		AGAGG GGT GGAATAGTG	
		TCTCC TCG CCTTATCAC	
		C__ T	
GAM1405 ATF5	3'	CACCAAACCAACCAACTCCTCT 23805	T AATA
		AGAGGAGTTGG TGG GTG	
		TCTCCTCAACC ACC CAC	
		C AAAC	
GAM1405 CKTSF1B1	3'	CTAAACCAACCAACTCCTCT 25365	_ AA
		AGAGGAGTTGGTT GG TAG	
		TCTCCTCAACCAA CC ATC	
		A AA	
GAM1405 ECEL1	3'	CACCTGCCTTCCAGCCCCTC 16701	A TT AATA
		GAGG GTTGG GG GTG	
		CTCC CGACC CC CAC	
		C TT GTC_	
GAM1405 EZH1	3'	CCAGTGCTCCAGCTCCTC 8814	_____
		GAGGAGTTGG TTGG	
		CTCCTCGACC GACC	
		TCGT	
GAM1405 GPC4	5'	CCAACTCCAACCTCCTT 7552	_____
		GAGGAGTTGG TTGG	
		TTCCTCAACC AACC	
		TC	
GAM1405 KCNAB2	3'	CACTATTCCAGAAGGCTCC 13301	GG
		GGAGTT TTGGAATAGTG	
		CCTCGG GACCTTATCAC	
		AA	
GAM1405 NRG1	3'	CACCATTCGTCATCACTCCTCT 15688	T TG_ A
		AGAGGAGT GGT GAAT GTG	
		TCTCCTCA CTA CTTA CAC	
		_ CTG C	
GAM1405 PPP1R3D	3'	CACCACCCTCCAAGTCCTCT 20701	G TT AATA
		AGAGGA TTGG GG GTG	

TCTCCT AACC CC CAC  
 G TC AC\_\_  
 GAM1405 RHAG 3' ACCATTCTGCTCTCC 4376 TT T A  
 GGAG GGT GGAAT GT  
 |||| ||||| ||  
 CCTC TCG CCTTA CA  
 \_\_ T C  
 GAM1405 SHMT1 3' CTGAGATAACCAACTCCCT 14790 A GAA  
 AG GGAGTTGGTTG TAG  
 || ||||| ||  
 TC CCTCAACCAAT GTC  
 \_ AGA  
 GAM1405 SORCS2 3' CACCATCCCGCAGGCTTCTC 40414 TG T ATA  
 GAGGAGT GT GGA GTG  
 ||||| || ||  
 CTCTTCG CG CCT CAC  
 GA C AC\_  
 GAM1405 SRGAP1 3' CACTACTCCACGAACTCCTC 72260 G T A  
 GAGGAGTT GT GGA TAGTG  
 ||||| || || |||||  
 CTCCTCAA CA CCT ATCAC  
 G \_ C  
 GAM1405 STIM1 3' CACCACTCCCCAACTTC 60145 TT ATA  
 GGAGTTGG GGA GTG  
 ||||| || ||  
 CTTCAACC CCT CAC  
 \_ CAC  
 GAM1405 ACP33 3' CACTACCCCACTGTTTGCTCT 33557 G TT T AA  
 AGAG AG GGT GG TAGTG  
 |||| || || || |||||  
 TCTC TT TCA CC ATCAC  
 G TG \_ CC  
 GAM1405 ARHGAP9 5' CACTACCCAGGACCAACTCCT 50677 \_ AA  
 AGGAGTTGGT TGG TAGTG  
 ||||| || |||||  
 TCCTCAACCA ACC ATCAC  
 GG C\_  
 GAM1405 C9orf7 3' CACTACCCAGCCCTACTCCTCT 34165 T\_ AA  
 AGAGGAGT GGTTGG TAGTG  
 ||||| ||||| |||||  
 TCTCCTCA CCGACC ATCAC  
 TC C\_  
 GAM1405 FLJ10619 3' CACTATGAGGCAACTCCTT 36349 G GGA  
 GAGGAGTTG TT ATAGTG  
 ||||| || |||||  
 TTCCTCAAC GG TATCAC  
 \_ AG\_  
 GAM1405 FLJ12910 5' CACCCCCATTCTCAGCTCCTC 44703 \_T\_ AATA  
 GAGGAGTTG G TGG GTG  
 ||||| | || |||

CTCCTCGAC C ACC CAC  
 T TT CC\_\_  
 GAM1405 FLJ20689 3' CACCACCAGAACCAACTCCTCT 35536 \_\_ AATA  
 AGAGGAGTTGGT TGG GTG  
 ||||| ||| |||  
 TCTCCTCAACCA ACC CAC  
 AG AC\_\_  
 GAM1405 FLJ20689 3' CACCACCAGAACCAACTCCTCT 35743 \_\_ AATA  
 AGAGGAGTTGGT TGG GTG  
 ||||| ||| |||  
 TCTCCTCAACCA ACC CAC  
 AG AC\_\_  
 GAM1405 KIAA0237 3' ACTATTCCACCTCTCT 28519 TT T  
 GGAG GGT GGAATAGT  
 ||| ||| |||||  
 TCTC CCA CCTTATCA  
 T\_ \_  
 GAM1405 KIAA0450 3' CACCACCCTGATCCGACTCCTC 27618 \_TG AATA  
 T AGAGGAGTTGG T G GTG  
 ||||| | | |||  
 TCTCCTCAGCC A C CAC  
 T GT CCAC  
 GAM1405 KIAA0513 3' CACTATTCCCCAGTCTCC 28341 \_ TT  
 GGAG TTGG GGAATAGTG  
 ||| ||| |||||  
 CCTC GACC CCTTATCAC  
 T \_  
 GAM1405 KIAA1538 3' CACCTCCCCCAACTCTTC 71534 TT ATA  
 GAGGAGTTGG GGA GTG  
 ||||| ||| |||  
 CTTCTCAACC CCT CAC  
 C\_ C\_\_  
 GAM1405 LIECG3 3' CACTACCCCAACCCCACTCCT 87408 T T AA  
 AGGAGT GG TGG TAGTG  
 |||| | ||| |||||  
 TCCTCA CC ACC ATCAC  
 C C CC  
 GAM1405 MGC9753 5' CACCATCCCTGTCCACGTCCTC 53046 GT TT\_ A A  
 T AGAGGA TGG GG AT GTG  
 |||| | ||| |||  
 TCTCCT ACC CC TA CAC  
 GC TGT C C  
 GAM1405 NAV1 3' CACTGCCAACAACCTCCTC 39950 G AA  
 GAGGAGTTG TTGG TAGTG  
 ||||| ||| |||||  
 CTCCTCAAC AACC GTCAC  
 \_ \_  
 GAM1405 PRO0611 3' CACCATCTCTTCAACCTCTCT 26008 GA TT ATA  
 AGAG GTTGG GGA GTG  
 ||| |||| | |||

TCTC CAACT TCT CAC  
 TC TC AC\_  
 GAM1405 PSMD12 3' CACTGCACCCAACTCCTCT 10997 T GAA  
 AGAGGAGTTGG TG TAGTG  
 ||||| || ||||  
 TCTCCTCAACC AC GTCAC  
 C \_\_\_\_  
 GAM1405 PSTPIP2 3' CACTATTCTTCTAACCCTT 44383 A TT  
 GAGG GTTGG GGAATAGTG  
 ||| |||| |||||  
 TTCC CAATC TCTTATCAC  
 \_ T\_  
 GAM1405 SLC31A2 3' CACTATACTTCCAAGTCCCT 60128 A \_ TT A  
 AG GG AGTTGG GG ATAGTG  
 || || |||| || ||||  
 TC CC TCAACC TC TATCAC  
 \_ G T\_ A  
 GAM1405 SMUG1 3' CACTACTCCTGTTTGCCCTC 26692 A TG TT A  
 GAGG GT G GGA TAGTG  
 ||| || | || ||||  
 CTCC CG T CCT ATCAC  
 \_ TT GT C  
 GAM1405 TM4SF11 3' CACCGTTTCAACCAACCTCTC 32036 GA TA  
 GAG GTTGGTTGGAA GTG  
 ||| ||||| |||  
 CTC CAACCAACTTT CAC  
 TC GC  
 GAM1405 LOC129676 5' CACCATCCAGGGTCCAGCTCCT 75731 \_\_\_\_ ATA  
 C GAGGAGTTGG TTGGA GTG  
 ||||| |||| |||  
 CTCCTCGACC GACCT CAC  
 TGG AC\_  
 GAM1405 LOC150577 3' CACTATCCCAAACTCCTCT 85073 GG A  
 AGAGGAGTT TTGG ATAGTG  
 ||||| ||| |||||  
 TCTCCTCAA AACC TATCAC  
 \_ C  
 GAM1405 LOC151176 3' CACCACTCCCCTGGTCTCCATC 85259 \_ \_ TG TT ATA  
 T AGA GGAG T G GGA GTG  
 ||| |||| | || |||  
 TCTCCTC G C CCT CAC  
 A T G T C\_ CAC  
 GAM1405 LOC152579 3' CACCACTCCAAATACTCCTC 80623 TGG ATA  
 GAGGAGT TTGGA GTG  
 ||||| |||| |||  
 CTCCTCA AACCT CAC  
 TA\_ CAC  
 GAM1405 LOC200081 3' CACCACCCCACTTGGCTCCTTT 88562 TG T AATA  
 AGAGGAGT G TGG GTG  
 ||||| | || |||

		TTTCCTCG T ACC CAC		
		GT C CCAC		
GAM1405	LOC203084 3'	CACTGGTACCAACTCACCT	87489	AG TGGAA
		AG GAGTTGGT TAGTG		
		TC CTCAACCA GTCAC		
		CA TG__		
GAM1405	LOC207043 3'	CCAGCTCGAACTCCTC	89511	__
		GAGGAGTT GGTTGG		
		CTCCTCAA TCGACC		
		GC		
GAM1405	LOC221943 5'	CACTACCTGGGCCGACTCCTC	93988	__ AA
		GAGGAGTTGGTT GG TAGTG		
		CTCCTCAGCCGG CC ATCAC		
		GT __		
GAM1405	LOC51145 3'	ACTATTAGGACTCCTCT	32392	GGTTGG
		AGAGGAGTT AATAGT		
		TCTCCTCAG TTATCA		
		GA__		
GAM1406	ADAM29 5'	GGGACTTCAAATCACTGTGAT	87447	C CC
	T	AATCACAGT ATTTT GAGTCCC		
		TTAGTGTCA TAAAA TTCAGGG		
		C C_		
GAM1406	CAPZA1 3'	ACTCAAGTGTAAGTGTGAT	72623	__ TCC
		ATCACAGT CATTT GAGT		
		TAGTGTCA GTGAA CTCA		
		AT __		
GAM1406	COG6 3'	GATTAAAAATGACTGT	72879	CCG
		ACAGTCATTTT AGTC		
		TGTCAGTAAAA TTAG		
		A__		
GAM1406	CYP7A1 3'	GGATATTTCAAATGATTATGAT	5762	C TCCGA
	T	AATCA AGTCATTT GTCC		
		TTAGT TTAGTAAA TAGG		
		A CTTA		
GAM1406	HCN4 5'	GGGACTCGGAGCGGACTAGGA	18492	AC ATT
	T	ATC AGTC TTCCGAGTCCC		
		TAG TCAG GAGGCTCAGGG		
		GA GGC		
GAM1406	IRTA1 3'	GACTTCACTAAAATGACCAGGA	48419	ACA CC__
	T	ATC GTCATTTT GAGTC		



			TAG	CAGTAAAA	TTCAG			
			GAC	TCAC				
GAM1406	KCNJ5	5'	GGACTCGGAAGCTCCGAT	6094	AC	CATT		
			ATC AGT TTCCGAGTCC					
			TAG TCG AAGGCTCAGG					
			CC _____					
GAM1406	MNT	3'	GGACTCGGCCACTGTG	39714	CATTTT			
			CACAGT CCGAGTCC					
			GTGTCA GGCTCAGG					
			CC_____					
GAM1406	NIPSNAP1	3'	GGA ACTCGGAAGGTAGA	13291	_	_		
			TC ATTTTCCGAGT CC					
			AG TGGAAGGCTCA GG					
			A        A					
GAM1406	NPY1R	3'	ATTTGAAAATGACTAAGATT	6176	AC	C		
			AATC AGTCATTTTC GAGT					
			TTAG TCAGTAAAAG TTTA					
			AA           _					
GAM1406	PRKCSH	3'	GGGACTAGTGAATGACTTGA	10817	C	TCCG		
			TCA AGTCATTT AGTCCC					
			AGT TCAGTAAG TCAGGG					
			_        TGA_					
GAM1406	RNGTT	3'	TTGAAAAACGACTGTGG	13734	A	C		
			TCACAGTC TTTT CGA					
			GGTGT CAG AAAA GTT					
			C     A					
GAM1406	CECR7	3'	CTTGAAAAATGACTGGA	79622	A	C		
			TC CAGTCATTTT CGAG					
			AG GTCAGTAAAA GTTC					
			_        A					
GAM1406	DIO2	3'	GGTTTGGAATAACT	5833	C	T		
			AGT ATTTTCCGAG CC					
			TCA TAAAAGGTTT GG					
			A           _					
GAM1406	DIO2	3'	GGTTTGGAATAACT	25685	C	T		
			AGT ATTTTCCGAG CC					
			TCA TAAAAGGTTT GG					
			A           _					
GAM1406	DKFZP564A1164	3'	GA CT CAGAAAGACTTGG	70977	C	AT	C	
			TCA AGTC TTTC GAGTC					

		GGT TCAG AAAG CTCAG		
		— — A		
GAM1406	FLJ10936	3' GCTGGA <sup>AAAT</sup> GCTATGATT 36910	C T	G
		AATCA AG CATT <sup>TTCC</sup> AGT		
		TTAGT TC GTAAAAGG TCG		
		A — —		
GAM1406	FLJ12799	3' CTAAAAAAGTAACTGTGATT 42559	C	CCG
		AATCACAGT ATTTT AG		
		TTAGTGTCA TGAAA TC		
		A AAA		
GAM1406	gm117	3' ACTCAACTGGTGACTTGTGATT 78844	—	TTCC
		AATCACA GTCATT GAGT		
		TTAGTGT CAGTGG CTCA		
		T TCAA		
GAM1406	JM11	5' GACTCGTGGCTGTGA 53259	TTTTC	
		TCACAGTCA CGAGTC		
		AGTGTCGGT GCTCAG		
		—		
GAM1406	KIAA0534	5' GGGACTCGGACGGGCGCCGGGA 71432	ACA__	ATTT
		TT AATC GTC TCCGAGTCCC		
		TTAG CGG AGGCTCAGGG		
		GGCCG GC__		
GAM1406	KIAA0601	3' TCTGGAAATGACTATGATT 62514	C	C
		AATCA AGTCATTTTC GA		
		TTAGT TCAGTAAAGG CT		
		A T		
GAM1406	LRP1B	5' GGGATTA <sup>AAATA</sup> AATTGTGATT 37671	C	CCG
		AATCACAGT ATTTT AGTCCC		
		TTAGTGTTA TAAAA TTAGGG		
		A —		
GAM1406	MAGEB1	5' GGTTGCAAAAGGACTGTGAT 9885	A C	GT
		ATCACAGTC TTTT CGA CC		
		TAGTGTCAAG AAAA GTT GG		
		G C —		
GAM1406	MGC15705	5' GGCTCA <sup>AAAT</sup> GGCTG 51283	CC	
		CAGTCATTTT GAGTC		
		GTCGGTAAAA CTCGG		
		A_		
GAM1406	MRPL33	3' GGATTGAA <sup>AAAT</sup> GACTTTGATT 16886	C	CG
		AATCA AGTCATTTTC AGTCC		

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          TTAGT TCAGTAAAAG TTAGG
            T      _
GAM1406 NSBP1  3' GACTCTGACGATGATT  47772      T C
          AGTCATT TC GAGTC
          ||||| || ||||
          TTAGTAG AG CTCAG
            C T
GAM1406 NUCKS  3' GACTCGGAGCCAGTGAT  42698      _
          GTCATT TTCCGAGTC
          ||||| |||||
          TAGTGA GAGGCTCAG
            CC
GAM1406 LOC144776 3' GGAAAACAACACTGTGAT  76961      CA
          ATCACAGT TTTTCC
          ||||| |||||
          TAGTGTCA AAAAGG
            AC
GAM1406 LOC151248 5' GGTTACTAAAATGACAGTGATT 80192      A      CCG T
          AATCAC GTCATTTT AG CC
          ||||| ||||| || ||
          TTAGTG CAGTAAAA TT GG
            A      TCA _
GAM1406 LOC152457 3' GGACTCCTCTCCCAGACTGTGA 80608      ATTTTCC_
          TCACAGTC      GAGTCC
          |||||      |||||
          AGTGTCAG      CTCAGG
          ACCCTCTC
GAM1406 LOC153139 3' GGAATTGAAACACTGTGATT  85925      CAT  CGAG
          AATCACAGT TTTC  TCC
          ||||| |||| |||
          TTAGTGTCA AAAG  AGG
            C_  TTA_
GAM1406 LOC205115 5' ACTCGGGAGCCTGTGA  89495      TCAT
          TCACAG  TTTCCGAGT
          ||||| |||||
          AGTGTC  GAGGGCTCA
            C_
GAM1406 LOC253187 5' ACTCGGAGACATGATT  97110      _
          AGTCAT TTTCCGAGT
          ||||| |||||
          TTAGTA AGAGGCTCA
            C
GAM1406 LOC93070 3' GCTGGAAAATGCTATGATT  71295      C T      G
          AATCA AG CATTTTCC AGT
          |||| || ||||| |||
          TTAGT TC GTAAAAGG TCG
            A _      _
GAM1407 CLASP1  3' TTGGCAAGAACAGTCTGAAGA 65316      A _  CTCA
          TC TCA ACT  GTTCTTGCCAA
          || ||| ||| |||||

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			AG AGT TGA CAAGAACGGTT			
			A C ____			
GAM1407 COL5A3	3'	AACTCAGAGCTGATGA	31692	A C		
		TCATCA CTCT AGTT				
		AGTAGT GAGA TCAA				
		C C				
GAM1407 FGFR4	5'	GGTCCCTGAGAGCTGTGA	43352	T A	TTCTT	
		TCA CA CTCTCAG	GCC			
		AGT GT GAGAGTC	TGG			
		_ C CC__				
GAM1407 FGFR4	5'	GGTCCCTGAGAGCTGTGA	8892	T A	TTCTT	
		TCA CA CTCTCAG	GCC			
		AGT GT GAGAGTC	TGG			
		_ C CC__				
GAM1407 H3F3B	3'	TAAGGTACTAGAGTTGAT	18024	C _		
		ATCAACTCT AGT TCTTG				
		TAGTTGAGA TCA GGAAT				
		_ T				
GAM1407 MAP3K4	3'	GCGCGACTGAGAACCGTGA	19800	CAAC	CT	
		TCAT TCTCAGTT TGC				
		AGTG AGAGTCAG GCG				
		CCA_ C_				
GAM1407 MAP3K4	3'	GCGCGACTGAGAACCGTGA	22048	CAAC	CT	
		TCAT TCTCAGTT TGC				
		AGTG AGAGTCAG GCG				
		CCA_ C_				
GAM1407 MGAT5	5'	GCAAATTTAAGAGTTGA	10024	C TTC		
		TCAACTCT AG TTGC				
		AGTTGAGA TT AACG				
		A TA_				
GAM1407 ONECUT1	3'	TGGCAAGACAAATGATGA	62135	ACTCTCAGT		
		TCATCA TCTTGCCA				
		AGTAGT AGAACGGT				
		AAAC_____				
GAM1407 SHANK2	3'	GCAAGACTAAAGAGCTGAT	24585	A C_ T		
		ATCA CTCT AGT CTTGC				
		TAGT GAGA TCA GAACG				
		C AA _				
GAM1407 TUFT1	3'	TGGCAAGGCCTGGTGAGAGCCA	39268	CAA	__ TT	
	GTGA	TCAT CTCTCA G CTTGCCA				

AGTG GAGAGT C GAACGGT  
 ACC GGT CG  
 GAM1407 ARHF 3' TGGCCTCCTTTGAGAACTGATG 38750 AC TTCTT  
 G TCATCA TCTCAG GCCA  
 ||||| ||||| ||||  
 GGTAGT AGAGTT CGGT  
 CA TCCTC  
 GAM1407 CEBPG 3' AGCACTGAAGAGTTGAT 8405 \_ T  
 ATCAACTCT CAGT CT  
 ||||| ||||| ||  
 TAGTTGAGA GTCA GA  
 A C  
 GAM1407 DKFZP564K1964 3' AGGAACTACAAAGTTGATGA 31421 CTC\_  
 TCATCAACT AGTTCTT  
 ||||| |||||  
 AGTAGTTGA TCAAGGA  
 AACA  
 GAM1407 DKFZp762K222 5' GGCAAGGGGAAGATTGACGA 71119 A C CAG  
 TC TCAA TCT TTCTTGCC  
 || ||||| |||||  
 AG AGTT AGA GGGAACGG  
 C \_ AG\_  
 GAM1407 EIF5 3' TTGGACACACAAGAGTTGAT 8763 CA TCT \_  
 ATCAACTCT GT TG CCAA  
 ||||| || |||||  
 TAGTTGAGA CA AC GGTT  
 A\_ C\_\_ A  
 GAM1407 FLJ10193 3' GAGCTCTTAAAAGTTGATGA 35885 CTC\_\_\_\_  
 TCATCAACT AGTTC  
 ||||| |||||  
 AGTAGTTGA TCGAG  
 AAATTC  
 GAM1407 FLJ10979 3' TTGGCAGGAATAAAATTGATGA 36937 CTCTCA  
 TCATCAA GTTCTTGCCAA  
 ||||| |||||  
 AGTAGTT TAAGGACGGTT  
 AAAA\_  
 GAM1407 FLJ14906 3' TTGGCAAGAAGTGAAATTGAGA 51694 A CTC G  
 TC TCAA TCA TTCTTGCCAA  
 || ||||| |||||  
 AG AGTT AGT AAGAACGGTT  
 \_ AA\_ G  
 GAM1407 FLJ20152 3' AAGGACTAAAGAGCTGA 38644 A C\_  
 TCA CTCT AGTTCTT  
 || ||||| |||||  
 AGT GAGA TCAGGAA  
 C AA  
 GAM1407 FLJ20309 3' AGAGCTGAGTGCTGATGA 34919 ACT  
 TCATCA CTCAGTTCT  
 ||||| |||||

			AGTAGT GAGTCGAGA		
			CGT		
GAM1407	Grcc9	3'	CAGCTGCTGAAAGCTGGTGA 50970	A C	TC
			TCATCA CT TCAGT TTG		
			AGTGGT GA AGTCG GAC		
			C A TC		
GAM1407	KIAA0349	3'	TGGTTCTGAGGACTGATGA 92310	AC	TTCTT
			TCATCA TCTCAG GCCA		
			AGTAGT GGAGTC TGGT		
			CA T____		
GAM1407	KIAA0352	3'	CGAGTGGCTGAGAGCAGAT 29155	AA	_
			ATC CTCTCAGTT CTTG		
			TAG GAGAGTCGG GAGC		
			AC T		
GAM1407	KIAA0668	3'	TGGTGCCTGGGAGCTGATGA 66527	A	TTCT
			TCATCA CTCTCAG TGCCA		
			AGTAGT GAGGGTC GTGGT		
			C C____		
GAM1407	KIAA1634	3'	TGGCTTGGAAGTTGATGA 63394	CT	TTCTT
			TCATCAACT CAG GCCA		
			AGTAGTTGA GTT CGGT		
			AG _____		
GAM1407	KIAA1753	3'	GGCAAGAGCTGGATGA 64884	AACTCT	
			TCATC CAGTTCTTGCC		
			AGTAG GTCGAGAACGG		
			_____		
GAM1407	KIAA1775	3'	AGGGCTGAGAATTGACGA 52375	A C	
			TC TCAA TCTCAGTTCT		
			AG AGTT AGAGTCGGGA		
			C A		
GAM1407	KIAA1948	3'	CAAGACAACCAAAAGTTGGTGA 82400	CTCA	_
			TCATCAACT GT TCTTG		
			AGTGGTTGA CA AGAAC		
			AAAC AC		
GAM1407	MGC2376	3'	TTGGCAAGAGATGTGAGATGA 43706	A T G	
			TCA CTC CA TTCTTGCCAA		
			AGT GAG GT GAGAACGGTT		
			A T A		
GAM1407	PHRET1	3'	TTGGCAAGTATGCAGAGCCGTG 41066	CAA	_ GTT
	A		TCAT CTCT CA CTTGCCAA		

			AGTG GAGA GT GAACGGTT		
			CC_ C AT_		
GAM1407	RAI16	5'	AGAGCCTGAGAGCTATGA 42752	CAA	_
			TCAT CTCTCAG TTCT		
			AGTA GAGAGTC GAGA		
			TC_ C		
GAM1407	SNPH	3'	TGGCAAGAGCTGATGAG 28248		_
			CTC TCAGTTCTTGCCA		
			GAG AGTCGAGAACGGT		
			T		
GAM1407	SRP54	5'	GCTGGTGGGAGTTGACGA 11960	A	GTT T
			TC TCAACTCTCA CT GC		
			AG AGTTGAGGGT GG CG		
			C _ T		
GAM1407	LOC138255	5'	GGCGACTGGGAACCGATGA 75306	AAC	CTT
			TCATC TCTCAGTT GCC		
			AGTAG AGGGTCAG CGG		
			CCA _		
GAM1407	LOC145919	5'	GCAAGAATTACTGATG 77571	ACTCTC	
			CATCA AGTTCTTGC		
			GTAGT TTAAGAACG		
			CA_		
GAM1407	LOC151154	3'	GCACCTGAGTGTTGATGA 85235	T	TTCT
			TCATCAAC CTCAG TGC		
			AGTAGTTG GAGTC ACG		
			T C_		
GAM1407	LOC158295	5'	GCAAATAAGAGTTGATG 86735	C	CT
			CATCAACTCT AGTT TGC		
			GTAGTTGAGA TCAA ACG		
			A _		
GAM1407	LOC158450	3'	CAACAGCTGCTCAAAGTTGATG 81930	CT_	C
	A		TCATCAACT CAGTT TTG		
			AGTAGTTGA GTCGA AAC		
			AACTC C		
GAM1407	LOC158504	3'	CAACAGCTGCTCAAAGTTGATG 81938	CT_	C
	A		TCATCAACT CAGTT TTG		
			AGTAGTTGA GTCGA AAC		
			AACTC C		
GAM1407	LOC162333	5'	TGATGGAACAAGAGTTGATGA 87141	CA	TGC
			TCATCAACTCT GTTCT CA		

AGTAGTTGAGA CAAGG GT  
 A\_ TA\_  
 GAM1407 LOC196694 5' GCAAGAAGTTGTTGA 89582 T CTCAGT  
 TCA CAACT TCTTGC  
 ||| |||| |||||  
 AGT GTTGA AGAACG  
 T \_\_\_\_\_  
 GAM1407 LOC199907 3' AGTTCCTGAGATACTGATGA 88461 AC\_ TT\_  
 TCATCA TCTCAG CT  
 ||||| ||||| ||  
 AGTAGT AGAGTC GA  
 CAT CTT  
 GAM1407 LOC222233 5' GGCTTGAGAATTGAT 94257 C TTCTT  
 ATCAA TCTCAG GCC  
 ||||| ||||| |||  
 TAGTT AGAGTT CGG  
 A \_\_\_\_\_  
 GAM1407 LOC254479 3' AGCTGAGAGTTGATGA 97084  
 TCATCAACTCTCAGTT  
 |||||  
 AGTAGTTGAGAGTCGA  
 \_\_\_\_\_  
 GAM1407 LOC256310 5' GCAAAGAGCCAGAGCTGATG 96347 A CA \_  
 CATCA CTCT GTTCTT GC  
 ||||| ||||| ||||| ||  
 GTAGT GAGA CGAGAA CG  
 C C\_ A  
 GAM1407 LOC56267 3' CAAATGCTAAGAGTTGTTGA 39009 T C TC  
 TCA CAACTCT AGT TTG  
 ||| ||||| ||| |||  
 AGT GTTGAGA TCG AAC  
 T A TA  
 GAM1407 LOC90288 3' TGGCAAGTCTAAGAGGACTGA 62111 TCAA C TT  
 TCA CTCT AG CTTGCCA  
 ||| ||||| |||||  
 AGT GAGA TC GAACGGT  
 CAG\_ A T\_  
 GAM1408 ADH4 3' ACAAACCTGCACATCCTGCAC 5407 AAAA TTCA  
 GTGCAG GT AGGTTTGT  
 ||||| || |||||  
 CACGTC CA TCCAAACA  
 CTA\_ CG\_  
 GAM1408 CHRNA5 3' ATTTTAAAACCTTTTCTGCAT 59753 C  
 GTGCAGAAAAGTTT AAGGT  
 |||||  
 TACGTCTTTTCAAA TTTTA  
 A  
 GAM1408 GOCAP1 3' TTGAAACTTTTCTGCAC 42704  
 GTGCAGAAAAGTTTCAA  
 |||||



CACGTCTTTTCAAAGTT

GAM1408 ZNF3 3' GCCCAAAAGCTTTTCCACAC 34757 CA CAA  
GTG GAAAAGTTT GGT  
||| ||||| |||  
CAC CTTTTCGAA CCG  
AC AAC

GAM1408 COVA1 3' ACAAACCTGCACATCCTGCAC 73258 AAAA TTCA  
GTGCAG GT AGGTTTGT  
||||| || |||||  
CACGTC CA TCCAAACA  
CTA\_ CG\_

GAM1408 KIAA0172 5' ATGTTGAAACTTCTCCTCAC 64967 CA A G  
GTG GA AAGTTTCAA GT  
||| || ||||| |||  
CAC CT TTCAAAGTT TA  
TC C G

GAM1408 MGC12538 5' ACAAACCCGCATGTTCTGCAC 51240 AA\_ TTCAA  
GTGCAGAA GT GGTTTGT  
||||| || |||||  
CACGTCTT CG CCAAACA  
GTA C\_

GAM1408 LOC145678 3' AGCCCTGAAACTTTCTACAC 83418 C A A  
GTG AGAAA GTTTCA GGTT  
||| |||| ||||| |||  
CAC TCTTT CAAAGT CCGA  
A \_ C

GAM1408 LOC146512 3' ACAAACCTGCACATCCTGCAC 77939 AAAA TTCA  
GTGCAG GT AGGTTTGT  
||||| || |||||  
CACGTC CA TCCAAACA  
CTA\_ CG\_

GAM1408 LOC149157 3' ACAAACCTGCATATCCTGCAC 79199 AAAAGTTTCA  
GTGCAG AGGTTTGT  
||||| |||||  
CACGTC TCCAAACA  
CTATACG\_

GAM1408 LOC149401 3' ACAAACCTGCACATTCTGCAC 79331 AA TTCA  
GTGCAGAA GT AGGTTTGT  
||||| || |||||  
CACGTCTT CA TCCAAACA  
A\_ CG\_

GAM1408 LOC149876 3' ACAAACCTCATTGCTGCCCCC 79526 CAGAAA TTCA  
AC GTG AGT AGGTTTGT  
||| ||| |||||  
CAC TCG TCCAAACA  
CCCCCG TTAC

GAM1408 LOC152794 3' ACAAACCTGCATGTTCTGCAC 80668 AAGTTTCA  
GTGCAGAA AGGTTTGT  
||||| |||||

			CACGTCTT	TCCAAACA		
			GTACG__			
GAM1408	LOC90917	3'	TTGAGACTTCTCTGCAC	64343	A	
			GTGCAGA AAGTTTCAA			
			CACGTCT TTCAGAGTT			
			C			
GAM1409	MAP3K12	3'	AAGGCAATAGAAAAGC	20861	A G	
			GCTT TTC TGTTGCCTT			
			CGAA AAG ATAACGGAA			
			- -			
GAM1409	SLC25A12	3'	CAGTAAGGCAAAGGCCAAGCT	13521	ATTC G_	
			AGCTT GT TTGCCTTACTG			
			TCGAA CG AACGGAATGAC			
			C__ GA			
GAM1409	DIS3	3'	AGTAAGGCTTAATAAGT	30226	CGTGTT	
			GCTTATT GCCTTACT			
			TGAATAA CGGAATGA			
			TT__			
GAM1409	KIAA0182	3'	CAGTAAGGCAACACGAATAAAC	72024	C	
	TA		TAG TTATTCGTGTTGCCTTACTG			
			ATC AATAAGCACACGGAATGAC			
			A			
GAM1409	PRO0529	3'	CAGAATCCAACCGAATAAGC	25988	T CC A	
			GCTTATTCG GTTG TT CTG			
			CGAATAAGC CAAC AA GAC			
			- CT -			
GAM1410	ARHGEF6	3'	CAAACCTGAAGCCAGGC	68197	ACCA	
			GCCTGG CAAGTTTG			
			CGGACC GTTCAAAC			
			GAA_			
GAM1410	CNTN2	3'	GTCACAACCCAGGTGA	17411	ACCACAA _	
			TCGCCTGG GTT TGAC			
			AGTGGACC CAA ACTG			
			_____ C			
GAM1410	CORO2A	3'	AAACTGTGGTCCAGAGA	53398	GC A	
			TC CTGGACCACA GTTT			
			AG GACCTGGTGT CAAA			
			A_ _			
GAM1410	CORO2A	3'	AAACTGTGGTCCAGAGA	12642	GC A	
			TC CTGGACCACA GTTT			

AG GACCTGGTGT CAAA  
 A\_ \_  
 GAM1410 GRLF1 3' AGGTCAGAAAAGTGGCCCAGG 78551 A AAG  
 CCTGG CCAC TTTGACCT  
 ||||| |||| |||||  
 GGACC GGTG A GACTGGA  
 C AA\_  
 GAM1410 LAPTM5 3' AGGCTTGTGGTCAAGC 22199 CTG  
 GC GACCACAAGTTT  
 || |||||  
 CG CTGGTGTTCGGA  
 AA\_  
 GAM1410 POU2AF1 3' AGATTTACAGTCCAGGC 20647 CAC  
 GCCTGGAC AAGTTT  
 ||||| |||||  
 CGGACCTG TTTAGA  
 ACA  
 GAM1410 PTGS1 3' GTCTCCTGTCTTATGGTCCAG 6355 C TTT\_\_  
 CTGGACCA AAG GAC  
 ||||| ||| |||  
 GACCTGGT TTC CTG  
 A TGCCT  
 GAM1410 PTGS1 3' GTCTCCTGTCTTATGGTCCAG 54574 C TTT\_\_  
 CTGGACCA AAG GAC  
 ||||| ||| |||  
 GACCTGGT TTC CTG  
 A TGCCT  
 GAM1410 TRIM34 5' AGGTCAAGTTGAGCCCAG 55224 ACCA G  
 CTGG CAA TTTGACCT  
 |||| ||| |||||  
 GACC GTT GAACTGGA  
 CGA\_ \_  
 GAM1410 TRIM9 5' AGGCCAGGCAAGTCCAGGC 30749 CACAA A  
 GCCTGGAC GTTTG CCT  
 ||||| ||||| |||  
 CGGACCTG CGGAC GGA  
 AA\_ C  
 GAM1410 ABLIM 5' GATATGTAACCCAGGCGG 22030 ACC A  
 TCGCCTGG ACA GTT  
 ||||| ||| |||  
 GGCGGACC TGT TAG  
 CAA A  
 GAM1410 AMOT 3' AGGCATCTTCATGGTCCAGGGA 55716 G C\_ TT A  
 TC CCTGGACCA AAG TG CCT  
 || ||||| ||| |||  
 AG GGACCTGGT TTC AC GGA  
 \_ AC T\_ \_  
 GAM1410 DKFZp434D177 5' TTAGACCCAGGCGA 50056 ACCACAA  
 TCGCCTGG GTTTGA  
 ||||| |||||

AGCGGACC CAGATT

GAM1410 DKFZp434D177 5' TTAGACCCAGGCGA 79443 ACCACAA  
TCGCCTGG GTTTGA  
||||||| |||||  
AGCGGACC CAGATT

GAM1410 FLJ23420 3' CAAGTGGGTCCAGGC 46845 A AG  
GCCTGGACC CA TTTG  
||||||| || |||||  
CGGACCTGG GT GAAC

GAM1410 HSA249128 5' GGCGCGGTCCAGGCGG 34152 ACAA  
TCGCCTGGACC GTT  
||||||| |||||  
GGCGGACCTGG CGG  
CG\_\_

GAM1410 MGC15668 5' AGACCCGGTGGTCCAGACG 51277 C AA\_  
CG CTGGACCAC GTTT  
|| ||||| |||||  
GC GACCTGGTG CAGA  
A GCC

GAM1410 MGC22014 3' AGGTCCCGAGTGTAAACCAGGT 64486 ACC AGTTT  
GA TCGCCTGG ACA GACCT  
||||||| || |||||  
AGTGGACC TGT CTGGA  
CAA GAGCC

GAM1410 SDCCAG10 5' AGAGTTGTGGTCCAAAGA 19641 GCC G  
TC TGGACCACAA TTT  
|| ||||| |||||  
AG ACCTGGTGTT AGA  
AA\_ G

GAM1410 LOC115442 3' AGGTCAGGGATGGTCCAG 72676 CAAG  
CTGGACCA TTTGACCT  
||||||| |||||  
GACCTGGT GGACTGGA  
AG\_\_

GAM1410 LOC129011 5' AGACCTGCGGTCCAGGC 74862 A A  
GCCTGGACC CA GTTT  
||||||| || |||||  
CGGACCTGG GT CAGA  
C C

GAM1410 LOC130536 5' GCAAAGTCCAGGCG 75746 CACAAG A  
CGCCTGGAC TTTG C  
||||||| |||||  
GCGGACCTG AAAC G  
C

GAM1410 LOC149108 3' AGACTTCACTGTGGTCCA 84357  
TGGACCACA AGTTT  
||||||| |||||

ACCTGGTGT TCAGA  
 CACT  
 GAM1410 LOC221688 5' AGACTCGGGCCAGACGA 93674 C A ACA  
 TCG CTGG CC AGTTT  
 ||| ||| || ||||  
 AGC GACC GG TCAGA  
 A C GC\_  
 GAM1410 LOC256228 5' AGACTTGTGGTCAAAGC 96233 CTG  
 GC GACCACAAGTTT  
 || |||||  
 CG CTGGTGTTTCAGA  
 AAA  
 GAM1410 LOC257441 5' TTAGACCCAGGCGA 95566 ACCACAA  
 TCGCCTGG GTTTGA  
 ||||| ||||  
 AGCGGACC CAGATT  
  
 GAM1410 LOC91960 3' AGGTGCCTCTCGTGGTCCAAGC 67657 C A TTTG  
 GC TGGACCAC AG ACCT  
 || ||||| || |||  
 CG ACCTGGTG TC TGGA  
 A C TCCG  
 GAM1410 LOC92840 3' GTCCCTCGGGTCCAGGC 56435 ACA TTT  
 GCCTGGACC AG GAC  
 ||||| || |||  
 CGGACCTGG TC CTG  
 GC\_ C\_  
 GAM1411 ABCA3 3' GGTGAATTTCTCCAGGC 6564 CCAC TG  
 GCCTGGA AAGTT ACC  
 ||||| |||| |||  
 CGGACCT TTAA TGG  
 C\_ GT  
 GAM1411 ADCY3 3' AGGTCTCCATGTGGTCCGAGTG 14455 C AGTTT  
 A TCGC TGGACCACA GACCT  
 ||| ||||| ||||  
 AGTG GCCTGGTGT CTGGA  
 A ACCT\_  
 GAM1411 APAF1 5' GGGTCAGGCTGCGTTGGGTGG 6734 TG ACCACA  
 TCGCC G AGTTTGACCT  
 |||| | |||||  
 GGTGG T TCGGACTGGG  
 GT GCG\_  
 GAM1411 APAF1 5' GGGTCAGGCTGCGTTGGGTGG 25043 TG ACCACA  
 TCGCC G AGTTTGACCT  
 |||| | |||||  
 GGTGG T TCGGACTGGG  
 GT GCG\_  
 GAM1411 ATP1A2 3' GGTCAGGAGTTCGAGGCGA 5529 G CCACAAG  
 TCGCCT GA TTTGACC  
 ||||| || |||||

			AGCGGA CT	GGA	CTGG	
			G TGA_____			
GAM1411	AVPR1A	5'	AGGTCGAGAGCCAGGTT	CAGGT	5534	ACAAG
	G		CGCCTGGACC	TTTGACCT		
			GTGGACTTGG	GAGCTGGA		
			ACCGA			
GAM1411	CACNG6	3'	AGGTCAGGGGGTCTTGGGTGG	49100		_ ACAAGT
			TCGCCTG GACC	TTGACCT		
			GGTGGGT CTGG	GA	CTGGA	
			T GG_____			
GAM1411	CREBL1	3'	GGGTTAAGCACTTATTTGAGGT	15210		G CCACAA
	GG		TCGCCT GA	GTTTGACCT		
			GGTGGA TT	CGAATTGGG		
			G TATTCA			
GAM1411	CSRP1	3'	TTTGGGTCTAGGTGA	14539		A
			TCGCCTGGACC CAAG			
			AGTGGATCTGG GTTT			
			_____			
GAM1411	CXCL16	5'	AGGTCGGCGGACGGGCCAGGCG	41915		A ACAA_ T
	G		TCGCCTGG CC	GTT GACCT		
			GGCGGACC GG	CGG CTGGA		
			_ GCAGG _			
GAM1411	EGLN2	5'	AGGTCAAGACAGATGGTCCGGG	34096		CAAG_
	C		GCCTGGACCA	TTTGACCT		
			CGGGCCTGGT	GA	AACTGGA	
			AGACA			
GAM1411	ESRRB	5'	AGGTTAGGCTCACTGTCTAGGC	67317		CACA
			GCCTGGAC	AGTTTGACCT		
			CGGATCTG	TCGGATTGGA		
			TCAC			
GAM1411	FLI1	5'	AGGTCAGGCTGTAACCGGGT	76608		ACC A
			GCCTGG ACA	GTTTGACCT		
			TGGGCC	TGT CGGACTGGA		
			AA_ _			
GAM1411	FLT4	3'	GGTTAGGCCTCCGGATGA	8922		C CCACAA
			TCG CTGGA	GTTTGACC		
			AGT GGCCT	CGGATTGG		
			A C_____			
GAM1411	HD	3'	GGTCAAGTTAGCCGCGTGA	9190		C ACC AAGT
			TCGC TGG AC	TTGACC		

			AGTG GCC TG AACTGG	
			C GAT ____	
GAM1411 HSPG2	3'	GGGTCAGGAACAGTGGCTGGGT 18644	TG A AAG_	
GG		TCGCC G CCAC TTTGACCT		
		GGTGG C GGTG GGA CTGGG		
		GT_ ACAA		
GAM1411 IHPK1	3'	GGTTGGGGTGCTCAGGTGA 95762	AC AAG TG	
		TCGCCTGG CAC TT ACC		
		AGTGGA CT GTG GG TGG		
		C_ ____ GT		
GAM1411 KCNA7	3'	GGGTTGAGTTGGA CTGTGCGA 49057	C A CAAG TG	
		TCGC TGG CCA TT ACCT		
		AGCG GTC GGT GA TGGG		
		T A T_ ____ GT		
GAM1411 KRTHA5	3'	GGGTCAGGTTTTCTCTTAGGT 9648	CCAC TT	
G		CGCCTGGA AAG TGACCT		
		GTGGATCT TTT ACTGGG		
		TCCT GG		
GAM1411 LARGE	3'	AGGTCAAGCATCTTCGGCCGA 16433	C CCACAA	
		TCG CTGGA GTTTGACCT		
		AGC GGCTT CGAACTGGA		
		C CTA_ ____		
GAM1411 LARGE	3'	AGGTCAAGCATCTTCGGCCGA 56107	C CCACAA	
		TCG CTGGA GTTTGACCT		
		AGC GGCTT CGAACTGGA		
		C CTA_ ____		
GAM1411 MAP4	3'	AGGTTGGGAGGGGGTTGGGGTG 48057	G ACAAG TG	
G		TCGCCT GACC TT ACCT		
		GGTGGG TTGG GG TGA		
		G GGGA_ GT		
GAM1411 MAP4	3'	AGGTTGGGAGGGGGTTGGGGTG 9905	G ACAAG TG	
G		TCGCCT GACC TT ACCT		
		GGTGGG TTGG GG TGA		
		G GGGA_ GT		
GAM1411 MOG	5'	GGTTGGATCTCCAGGAGG 10106	G CCACAA TG	
		TC CCTGGA GTT ACC		
		GG GGACCT TAG TGG		
		A C_ ____ GT		
GAM1411 MSH4	5'	GGGTCAGGGAAGGTTTGGGAGG 59324	G TG ACAAG	
		TC CC GACC TTTGACCT		

		GG GG TTGG GGA	
		A GT AAG__	
GAM1411 MSN	3'	AGGTTAGATTTTGTATTCAGGG 60250	G CC _
G		C CCTGGA ACAAG TTTGACCT	
		G GGA	
		G A_ T	
GAM1411 NR2E3	3'	GGGTCAGACCCGGTGTGGGT 32972	TG C AA_
GA		TCGCC GAC AC GTTGACCT	
		AGTGG TTG TG CAGACTGGG	
		GT _ GCC	
GAM1411 PAX6	5'	AGGTCAGGCTTCGCTAATGGGC 7832	GACCAC
		GCCTG AAGTTTGACCT	
		CGGGT TTCGGA	
		AATCGC	
GAM1411 PAX6	5'	AGGTCAGGCTTCGCTAATGGGC 4267	GACCAC
		GCCTG AAGTTTGACCT	
		CGGGT TTCGGA	
		AATCGC	
GAM1411 PKP1	3'	GGGTTAGGGAGGTTGGGGCGG 4317	G ACAAG
		TCGCCT GACC TTTGACCT	
		GGCGGG TTGG GGATTGGG	
		G AG__	
GAM1411 PSAP	3'	GGGTTCTGTGGGTTTGGGTGG 69357	TG A AGTTT
		TCGCC GACC CA GACCT	
		GGTGG TTGG GT TTGGG	
		GT _ GTC__	
GAM1411 PXR1	3'	GGGTTGAATTGTTGATTTGGC 4353	T C CA TG
		GCC GGA CA AGTT ACCT	
		CGG TTT GT TTAA TGGG	
		_ A TG GT	
GAM1411 PYGB	3'	GGTCGGATCCTCTAGGC 11177	CCACAA
		GCCTGGA GTTTGACC	
		CGGATCT TAGGCTGG	
		CC__	
GAM1411 RAB6A	3'	AGGTTGGGTCTTTCAGGC 11191	CCACA _ TG
		GCCTGGA AG TT ACCT	
		CGGACTT TC GG TGGA	
		_____ T GT	
GAM1411 RP2	3'	AGGTTGAACTTGTGAGAAGGC 22613	GGAC TG
		GCCT CACAAGTT ACCT	



			CGGA GTGTTCAA TGGA		
			AGA_ GT		
GAM1411 RUNX3	3'	AGGTTAGGCAGTCCTTCTGGTG 15110	T___ CACAA		
A		CGCC GGAC GTTTGACCT			
		GTGG CCTG CGGATTGGA			
		TCTT A___			
GAM1411 SYNGR1	3'	GGGTCAGTCAGGGTTCGGGGG 16322	G ACAAGT		
		C CCTGGACC TTGACCT			
		G GGGCTTGG GACTGGG			
		G GACT__			
GAM1411 TCF2	3'	GTCGTTGGTTTAGGC 21384	CAAGTT		
		GCCTGGACCA TGAC			
		CGGATTTGGT GCTG			
		T___			
GAM1411 TNFAIP1	3'	AGGTCAGAGGGTCTGGGC 40915	TG ACAAG		
		GCC GACC TTTGACCT			
		CGG CTGG AACTGGA			
		GT G___			
GAM1411 TRAF1	3'	GGGTCAGAAACAGGACCGGGTG 18974	A ACAAG		
G		TCGCCTGG CC TTTGACCT			
		GGTGGGCC GG AACTGGG			
		A ACAA_			
GAM1411 ARHU	3'	GGGTCGGGCTTGCGGTGGGTGA 41075	GG A		
		TCGCCT ACC CAAGTTTGACCT			
		AGTGGG TGG GTTCGGGCTGGG			
		_ C			
GAM1411 BRD2	5'	GGGTTATGCTGGACCGGGCGG 17538	A CAA T		
		TCGCCTGG CCA GT TGACCT			
		GGCGGGCC GGT CG ATTGGG			
		A _ T			
GAM1411 BRD7	3'	AGGTTGGAAGTTGTATTAGGT 25165	ACC TG		
		GCCTGG ACAAGTT ACCT			
		TGGATT TGTTCAG TGGA			
		A_ GT			
GAM1411 C1orf17	3'	GGGTTGAAGGAAGTTTGGGTTG 68217	_ TG CACAAG TG		
A		TCG CC GAC TT ACCT			
		AGT GG TTG AA TGGG			
		T GT AAGG_ GT			
GAM1411 CDT1	3'	GGTTGGGTAGTGTGGGTGG 77676	G C AAGT TG		
		TCGCCTG AC AC T ACC			

GGTGGGT TG TG G TGG  
G A \_\_\_\_ GT  
GAM1411 CENTB5 3' AGGTCAGGCTAAGGCCAGTCGG 95482 C A ACA  
TCG CTGG CC AGTTTGACCT  
||| ||| || |||||  
GGC GACC GG TCGGACTGGA  
T \_ AA\_  
GAM1411 CHODL 5' GGGTCGGGCAGCTGGGCTCGGG 46312 GA A A\_  
CGG CGCCTG CC CA GTTTGACCT  
||||| || || |||||  
GCGGGC GG GT CGGGCTGGG  
TC \_ CGA  
GAM1411 CHST3 3' AGGTTGATTCTTGGCCTGGGTG 14966 TG A CAAGT TG  
G TCGCC G CCA T ACCT  
||||| | || | |||  
GGTGG C GGT A TGGA  
GT C TCTT\_ GT  
GAM1411 CYYR1 3' GGGTCAGATAATGTGTCAGGTG 53674 AC A\_  
G TCGCCTGG CACA GTTTGACCT  
||||| ||| |||||  
GGTGGACT GTGT TAGACTGGG  
\_ AA  
GAM1411 DKFZP564B1023 5' GGGTCAGGGCTTGTCTGGGCGG 48542 GACC \_  
TCGCCTG ACAAGTT TGACCT  
||||| ||||| |||||  
GGCGGGC TGTTCGG ACTGGG  
\_ G  
GAM1411 DSCR1L1 3' AGGTTGGGTTTGGGGAGGGGGG 19494 G GGA A GT TG  
TC CCT CC CAA T ACCT  
|| ||| || ||| | |||  
GG GGG GG GTT G TGGA  
G AG\_ \_ TG GT  
GAM1411 FIGN 5' GGTCAGACGCGTTCAGTGG 95641 C CACAA  
TCGC TGGAC GTTTGACC  
|||| |||| |||||  
GGTG ACTTG CAGACTGG  
\_ CG\_  
GAM1411 FLJ10979 5' GGGTCGGCAGGGGGCCGGGTGG 36936 A ACAA T  
TCGCCTGG CC GTT GACCT  
||||| || || |||||  
GGTGGGCC GG CGG CTGGG  
\_ GGGA \_  
GAM1411 FLJ12076 3' AGGTTGGGCTCAGGCTGGGTG 47232 TG A ACA TG  
CGCC G CC AGTT ACCT  
|||| | || ||| |||  
GTGG C GG TCGG TGGA  
GT \_ AC\_ GT  
GAM1411 FLJ12443 3' GGGTCAGGTTCCCTGCCGGGCG 45730 ACCACA TT  
G TCGCCTGG AG TGACCT  
||||| || |||||

GGCGGGCC TT ACTGGG  
GTCCC\_ GG  
GAM1411 FLJ12610 3' GGTAAACTACCAGTGG 45515 C ACCACA  
TCGC TGG AGTTTGACC  
||||| ||| |||||  
GGTG ACC TCAAATTGG  
C A\_\_\_\_  
GAM1411 FLJ12960 3' TTTCAACTTGAGGTTTGGGCGG 44957 TG A T CCT  
TCGCC GACC CAAGTT GA  
||||| ||| ||||| ||  
GGCGG TTGG GTTCAA CT  
GT A \_ TTA  
GAM1411 FLJ13189 3' GGTCAGATAATCTTGGTGG 45987 T CCACAA  
TCGCC GGA GTTTGACC  
||||| ||| |||||  
GGTGG TCT TAGACTGG  
T AA\_\_\_\_  
GAM1411 FLJ13441 3' GGGAAGTTGTGGTCTGCGTGG 43667 C G GA  
TCGC TGGACCACAA TTT CC  
||||| ||||| ||| ||  
GGTG GTCTGGTGTT AAG GG  
C G \_  
GAM1411 FLJ13441 3' GGGAAGTTGTGGTCTGCGTGG 43668 C G GA  
TCGC TGGACCACAA TTT CC  
||||| ||||| ||| ||  
GGTG GTCTGGTGTT AAG GG  
C G \_  
GAM1411 FLJ14442 3' AGGTCAGGTAAAGTTCTAGGC 51361 CCACAA TT  
GCCTGGA G TGACCT  
||||| | |||||  
CGGATCT T ACTGGA  
TGAAA\_ GG  
GAM1411 FLJ14494 3' AGGTTGAATTTGGTCTACAGGC 90867 \_ CA TG  
GCCTG GACCA AGTT ACCT  
||||| ||||| ||| |||  
CGGAC CTGGT TTAA TGGA  
AT \_ GT  
GAM1411 FLJ20232 3' GGTTGAATTTCTTGGTGG 38672 T CCACA TG  
TCGCC GGA AGTT ACC  
||||| ||| ||| |||  
GGTGG TCT TTAA TGG  
T \_ GT  
GAM1411 FLJ20758 5' GGGTCGGCGGGCGGGTTTGTGT 35644 C GG ACAA\_ T  
GA TCGC T ACC GTT GACCT  
||||| | ||| |||||  
AGTG G TGG CGG CTGGG  
T TT GCGGG \_  
GAM1411 FLJ23153 3' AGGTAAAGTATTATTAGGT 44925 CCACAAG  
GCCTGGA TTTGACCT  
||||| |||||

			TGGATTT	GAATTGGA		
			ATTAT__			
GAM1411	GBL	3'	AGGTCGGGGGCTCAGTCTGGGA	42334	G TG CACA	__
	GG		TC CC GAC AGTT TGACCT			
			GG GG CTG TCGG GCTGGA			
			A GT AC__ GG			
GAM1411	GK001	3'	GGTTGGGTTTTCTGGTGG	39499	T CCAC GT TG	
			TCGCC GGA AA T ACC			
			GGTGG TCT TT G TGG			
			_ ____ TG GT			
GAM1411	GRID1	3'	GGGTTAGTTGCATGGACCAGGT	68500	A CAAGT	
	GA		TCGCCTGG CCA TTGACCT			
			AGTGGACC GGT GATTGGG			
			A ACGTT			
GAM1411	HSPC219	5'	GGTTGAATGCGTCGGGTGG	33223	ACCACAA TG	
			TCGCCTGG GTT ACC			
			GGTGGGCT TAA TGG			
			GCG____ GT			
GAM1411	KIAA0194	3'	GGGTCAGGGTGGAGGTCCTGGG	65987	_ A_ AG	
	TGG		CGCCT GGACC CA TTTGACCT			
			GTGGG CCTGG GT GGA CTGGG			
			T AG G_			
GAM1411	KIAA0460	3'	GGGTCGGATTTTGT TTTT TAGT	78890	C CC _	
	GA		TCGC TGGA ACAAG TTTGACCT			
			AGTG ATTT TGTTT AGGCTGGG			
			_ TT T			
GAM1411	KIAA0537	3'	GGGTTAAGTTTTCCTTCCAGTG	29256	C CCAC GT	
	A		TCGC TGGA AA TTGACCT			
			AGTG ACCT TT AATTGGG			
			_ TCCT TG			
GAM1411	KIAA0552	5'	GGGTTGGGCTTTATCAGGTGG	28319	ACCAC TG	
			TCGCCTGG AAGTT ACCT			
			GGTGGACT TTCGG TGGG			
			AT__ GT			
GAM1411	KIAA0690	3'	TCCTGCCTGTGGTCTGGGTGA	30796	TG A TT	
			TCGCC GACCACA GT GA			
			AGTGG CTGGTGT CG CT			
			GT C TC			
GAM1411	KIAA0720	3'	GGGTTGGGGCGAGAGTCGGGGT	62327	G CACAA _ TG	
	GG		TCGCCT GAC GT T ACCT			

GGTGGG CTG CG G TGGG  
G AGAG\_ G GT  
GAM1411 KIAA1045 3' GGGTCAGCTCTGGTCTGGGC 71056 TG CA T  
GCC GACCA AGTT GACCT  
||| |||| ||| ||||  
CGG CTGGT TCGA CTGGG  
GT C\_ \_  
GAM1411 KIAA1538 3' GGGTCAGGCTGCTTTGTGTGA 71552 C GG CCACA  
TCGC T A AGTTTGACCT  
|||| | |||||  
AGTG G T TCGGACTGGG  
T TT CG\_\_  
GAM1411 KIAA1822 3' GGGTTGGAAGAGGTCTGGGTGG 67572 TG ACAAG TG  
TCGCC GACC TT ACCT  
|||| ||| || |||  
GGTGG CTGG AG TGGG  
GT AGA\_\_ GT  
GAM1411 KIAA1878 3' GGTTAGGTGTTTTAGGT 91715 C AAGT  
GCCTGGA CAC TTGACC  
||||| ||| |||||  
TGGATTT GTG GATTGG  
T \_\_\_\_  
GAM1411 KIAA1957 3' GGGTCAGGCTTGGCTCTGGGAG 75720 G TG CCA  
A TC CC GA CAAGTTTGACCT  
|| || || |||||  
AG GG CT GTTCGGA CTGGG  
A GT CG\_  
GAM1411 KPTN 5' AGGTTGGGTAGTGCGGGTTGGG 73409 G A\_ AG\_ TG  
GCGG CGCCT GACC CA TT ACCT  
|||| ||| || || |||  
GCGGG TTGG GT GG TGGA  
G GC GAT GT  
GAM1411 MAP2K6 3' AGGTTGAATTAATTCCTGGGC 10867 \_ CCACA TG  
GCCT GGA AGTT ACCT  
|||| ||| ||| |||  
CGGG CCT TTAA TGGA  
T TAA\_\_ GT  
GAM1411 MAP2K6 3' AGGTTGAATTAATTCCTGGGC 49241 \_ CCACA TG  
GCCT GGA AGTT ACCT  
|||| ||| ||| |||  
CGGG CCT TTAA TGGA  
T TAA\_\_ GT  
GAM1411 MGC13064 5' GGGTTAGGAGGTCTGGGCGA 50354 TG ACAAG  
TCGCC GACC TTTGACCT  
|||| ||| |||||  
AGCGG CTGG GGATTGGG  
GT A\_\_\_\_  
GAM1411 MGC16025 3' GGGTCGAGCTGTGACCGTTCAG 51924 \_ A  
GTGA GCCTGGAC CACA GTTTGACCT  
||||| ||| |||||

		TGGA	CTTG	GTGT	CGAGCTGGG		
		CCA	_				
GAM1411	MGC16153	5'	AGGTCAGGCCCGGGTCCAGGGG	51296	G	ACAA	
	A		TC CCTGGACC GTTTGACCT				
			AG GGACCTGG CGGACTGGA				
			G GCC_				
GAM1411	MGC20533	5'	GGTCGGGCCTTGAGGTGG	72060	GGACCA	_	
			TCGCCT CAAG TTTGACC				
			GGTGGA GTTC GGGCTGG				
			_____ C				
GAM1411	MGC4655	3'	GGGTTAAGCTTGGCTCCTGGCG	52804	T	CCA	
	G		TCGCC GGA CAAGTTTGACCT				
			GGCGG CCT GTTCGAATTGGG				
			T CG_				
GAM1411	MGC7036	5'	AGGTCGGCGGGGGTCTGGGTGG	58968	TG	ACAA	T
			TCGCC GACC GTT GACCT				
			GGTGG CTGG CGG CTGGA				
			GT GGG_ _				
GAM1411	NFAT5	5'	GGGTTGGCGGCTGTCCGGGCGA	56947	CACAA	T	TG
			TCGCCTGGAC G T ACCT				
			AGCGGGCCTG C G TGGG				
			TCGG_ _ GT				
GAM1411	NRF	3'	GGGTTGGA	34083	A_ _	TG	
	GGT		CCTGGACCAC AGTT ACCT				
			GGATTG				
			GTGG GT				
GAM1411	OAZIN	3'	GGTAAAGCTTGTCTGGTC	31875	_		
			GACC ACAAGTTTGACC				
			CTGG TGTTCAATTGG				
			TC				
GAM1411	RAB6C	3'	AGGTTGGGTCTTTCAGGC	49566	CCACA	_	TG
			GCCTGGA AG TT ACCT				
			CGGACTT TC GG TGGA				
			_____ T GT				
GAM1411	SERP1	3'	AGGTTGGATTATGCATGTTTAG	27058	CA_ _	TG	
	GT		GCCTGGAC CA AGTT ACCT				
			TGGATTG GT TTAG TGGA				
			TAC A GT				
GAM1411	SETMAR	3'	AGGTTAAAAGGAGTCTAGGTG	73658	CACAAG		
			CGCCTGGAC TTTGACCT				

			GTGGATCTG	AAATTGGA		
			AGGA__			
GAM1411	SMARCA4	3'	GGTCAGACTCGCCGGGGG	11795	G	ACCACA
			C CCTGG			AGTTTGACC
			G GGGCC			TCAGACTGG
			G			GC__
GAM1411	UPLC1	3'	GGGTTGGGCTTGGGGAATAGGC	34727		GA A TG
			GCCTG CC CAAGTT			ACCT
			CGGAT GG GTTCGG			TGGG
			AA _			GT
GAM1411	USP20	3'	AGGTTGGATTCTGCCAGTGG	21923		C AC C TG
			TCGC TGG CA AAGTT			ACCT
			GGTG ACC GT TTTAG			TGGA
			_ _ C			GT
GAM1411	ZDHC9	5'	GGGTCTCCGTGGTTCAGGC	61682		AAGTTT
			GCCTGGACCAC			GACCT
			CGGACTTGGTG			CTGGG
			CCT__			
GAM1411	LOC114971	3'	GGGTCAAGCTTGTAGGTGTTGG	73152		TGG _
			CC ACC ACAAGTTTGACCT			
			GG TGG TGTCGAACTGGG			
			TTG A			
GAM1411	LOC118738	3'	GGTTAAGCTGAGCAGGTGG	75492		GACCACA
			TCGCCTG			AGTTTGACC
			GGTGGAC			TCGAATTGG
			GAG__			
GAM1411	LOC122664	5'	GGGTCAGACCACCATCCGGGT	74146		CCACAA
			GCCTGGA			GTTTGACCT
			TGGGCCT			CAGACTGGG
			ACCAC_			
GAM1411	LOC123242	5'	AGGTCAGGCTTGTCCTGGGC	75591		TG ACC
			GCC G ACAAGTTTGACCT			
			CGG C TGTCGGA			CTGGA
			GT C_			
GAM1411	LOC138654	5'	GGGTCAGGCTGACCCAGCTGG	75950		C ACCACA
			TCG CTGG			AGTTTGACCT
			GGT GACC			TCGGA
			C			CAG__
GAM1411	LOC143666	3'	GGTTAGGCCTCCGGATGA	82974		C CCACAA
			TCG CTGGA			GTTTGACC

AGT GGCCT CGGATTGG  
 A C\_\_\_\_  
 GAM1411 LOC143872 3' GGGTTGAATTTGGCTTATGGGT 76650 GACCA TG  
 GCCTG CAAGTT ACCT  
 |||| |||| ||||  
 TGGGT GTTTAA TGGG  
 ATTCG GT  
 GAM1411 LOC145676 5' AGGTTGAGTTTGTGGAAGTCC 77332 \_\_\_\_ GT TG  
 GGA CCACAA T ACCT  
 || |||| | ||||  
 CCT GGTGTT A TGGA  
 GAA TG GT  
 GAM1411 LOC145790 5' GGGTCAGATATCTGTTCATGTG 77487 C CACAA  
 G TCGC TGGAC GTTTGACCT  
 |||| |||| ||||  
 GGTG ACTTG TAGACTGGG  
 T TCTA\_  
 GAM1411 LOC146988 5' GGTCAGCAGGTCAGGTGA 83895 G ACAA T  
 TCGCCTG ACC GTT GACC  
 |||| || ||||  
 AGTGGAC TGG CGA CTGG  
 \_ A \_  
 GAM1411 LOC147118 3' GGTGGTTAGGTCTGGTGA 83953 T ACAAGT TG  
 TCGCC GGACC T ACC  
 |||| |||| | ||||  
 AGTGG TCTGG G TGG  
 \_ ATT\_\_ GT  
 GAM1411 LOC147229 5' AGGTCAGGTGAGCTGTCTAGGA 78318 G CACAA TT  
 GA TC CCTGGAC G TGACCT  
 || |||| | ||||  
 AG GGATCTG T ACTGGA  
 A TCGAG GG  
 GAM1411 LOC147515 5' GCTTGTGGTCCGGGTGG 84024  
 TCGCCTGGACCACAAGT  
 |||||  
 GGTGGGCCTGGTGTTG  
 GAM1411 LOC147622 5' TTAAATTTGTGGTTCAGCGA 84056 C  
 TCGC TGGACCACAAGTTTGA  
 |||||  
 AGCG ACTTGGTGTTTAAATT  
 \_  
 GAM1411 LOC148181 3' GGTGGGCCTCCCGGCGA 78702 T CCACAA TG  
 TCGCC GGA GTT ACC  
 |||| || ||||  
 AGCGG CCT CGG TGG  
 C C\_\_\_\_ GT  
 GAM1411 LOC149313 5' GGGTTGGAAGAAGTCAAGGTGA 87054 G CACAAG TG  
 TCGCCT GAC TT ACCT  
 |||| || ||||



AGTGGA CTG AG TGGG  
 A AAGA\_\_ GT  
 GAM1411 LOC150245 5' AGGTTAGAAGCTAGTTCTGGTG 84932 T CACAAG  
 G TCGCC GGAC TTTGACCT  
 ||||| |||| |||||  
 GGTGG CTTG AGATTGGA  
 T ATCGA\_  
 GAM1411 LOC151475 3' GGGTTGAGTTTGGATTCCCTGGT 85415 T CCA GT TG  
 GG TCGCC GGA CAA T ACCT  
 ||||| ||| ||| |||||  
 GGTGG CCT GTT A TGGG  
 T TAG TG GT  
 GAM1411 LOC157567 5' GGGTTAGGGCTGTGGTCCGGGG 81483 G AG  
 A TC CCTGGACCACA TTTGACCT  
 || ||||| |||||  
 AG GGGCCTGGTGT GGATTGGG  
 \_ CG  
 GAM1411 LOC164507 5' AGGTTGGCAGTGGTTGGGTGG 82537 TG A AA T TG  
 TCGCC G CCAC G T ACCT  
 ||||| |||| || |||||  
 GGTGG T GGTG C G TGGA  
 GT \_ A \_ GT  
 GAM1411 LOC196955 5' AGGTCAGGCTTGTCTCTGGGC 77363 TG ACC  
 GCC G ACAAGTTTGACCT  
 ||| | |||||  
 CGG C TGTCGGACTGGA  
 GT C\_  
 GAM1411 LOC200860 3' GGGTCAGGGCTCAGCCAGGTGG 90168 ACCACA \_  
 TCGCCTGG AGTT TGACCT  
 ||||| |||||  
 GGTGGACC TCGG ACTGGG  
 GAC\_\_ G  
 GAM1411 LOC201685 3' GGTTAGACTTTTGGGC 90248 TG CCACA  
 GCC GA AGTTTGACC  
 ||| || |||||  
 CGG TT TCAGATTGG  
 GT \_\_\_\_  
 GAM1411 LOC202915 3' GGGTCAGACTCCCTGGTTCAGG 90395 G CA\_  
 AGA TC CCTGGACCA AGTTTGACCT  
 || ||||| |||||  
 AG GGA CT TGGT TCAGACTGGG  
 A CCC  
 GAM1411 LOC203411 5' GGGTTGAACTTCGGAACTAGGC 90628 A\_ AC TG  
 GCCTGG CC AAGTT ACCT  
 ||||| || ||||| |||||  
 CGGATC GG TTCAA TGGG  
 AA C\_ GT  
 GAM1411 LOC221490 5' GGTCAGACTGCCAGTTGA 93667 C ACCACA  
 TCG CTGG AGTTTGACC  
 ||| ||||| |||||

AGT GACC TCAGACTGG  
 T CG\_\_\_\_  
 GAM1411 LOC221849 5' GGGTCGGGCTTCGAGGTCAGCT 92490 TG\_\_ AC\_  
 GG CC GACC AAGTTTGACCT  
 || ||| |||||  
 GG CTGG TTCGGGCTGGG  
 TCGA AGC  
 GAM1411 LOC222183 3' AGGTAAAAAGGGGTTTCAGGT 94164 ACAAG  
 GCCTGGACC TTTGACCT  
 ||||| |||||  
 TGGACTTGG AAATTGGA  
 GGA\_\_\_\_  
 GAM1411 LOC253258 3' GGTTAGGCCTCCGGATGA 96475 C CCACAA  
 TCG CTGGA GTTTGACC  
 ||| ||| |||||  
 AGT GGCCT CGGATTGG  
 A C\_\_\_\_  
 GAM1411 LOC253955 5' GGTGGGGGGTTCGGGTGA 94430 GA ACAAG TG  
 TCGCCTG CC TT ACC  
 ||||| || |||  
 AGTGGGC GG GG TGG  
 TG \_\_\_\_ GT  
 GAM1411 LOC254120 3' AGGTCGGGGAAGGGGGCCGGGT 97393 A ACAAG  
 GG TCGCCTGG CC TTTGACCT  
 ||||| || |||||  
 GGTGGGCC GG GGGCTGGA  
 G GGAAG  
 GAM1411 LOC255056 5' GGTGACGATCCAGGT 97629 CCACAA  
 GCCTGGA GTTTGACC  
 ||||| |||||  
 TGGACCT CAGACTGG  
 AG\_\_\_\_  
 GAM1411 LOC256980 3' AGGTAAAGATGGAGATGGTCT 95215 TG \_\_\_\_ AG  
 GGGCGG C GACCA CA TTTGACCT  
 | ||| || |||||  
 G CTGGT GT AAATTGGA  
 GT AGAG AG  
 GAM1411 LOC257160 5' GGGTTGAAGGAGTCCGAGTGG 94850 C CACAAG TG  
 TCGC TGGAC TT ACCT  
 ||| ||| || |||  
 GGTG GCCTG AA TGGG  
 A AGG\_\_\_\_ GT  
 GAM1411 LOC257408 5' GGGTTGGAAGTGGGCTGGGGCGA 96074 \_TG A A A TG  
 TCGC C G CC CA GTT ACCT  
 ||| | ||| ||| |||  
 AGCG G C GG GT CAG TGGG  
 G GT \_ \_ \_ GT  
 GAM1411 LOC257476 3' GGTGGGGTGCTCAGGTGA 61257 AC AAG TG  
 TCGCCTGG CAC TT ACC  
 ||||| || |||

			AGTGGACT GTG GG TGG		
			C_ _ _ GT		
GAM1411	LOC55565	5'	GGGTCAGGTGAACAGCCAGGCG 34038		ACCACAA TT
	G		TCGCCTGG G TGACCT		
			GGCGGACC T ACTGGG		
			GACAAG_ GG		
GAM1411	LOC89941	5'	GGGTCGGGGAGCGGCTCCGGGC 57061		_ ACAAG
	GG		TCGCCTGGA CC TTTGACCT		
			GGCGGGCCT GG GGGCTGGG		
			C CGAG_		
GAM1411	LOC91300	5'	GGA	CTTGTGTTTGGGTGG 57069	TG C
			TCGCC GAC ACAAGTTT		
			GGTGG TTG TG	TTTCAGG	
			GT _		
GAM1411	LOC91300	5'	GGA	CTTGTGTTTGGGTGG 94596	TG C
			TCGCC GAC ACAAGTTT		
			GGTGG TTG TG	TTTCAGG	
			GT _		
GAM1411	LOC92710	3'	GGGTTGGGCCCTGTTTAGGT 70358		CACAA TG
			GCCTGGAC GTT ACCT		
			TGGATTTG CGG TGGG		
			TCC_ _ GT		
GAM1412	ADH1B	3'	CTTAGACATAAAGTAAAT 72644	C	CAC
			ATTT ACTTT TGTCTGAG		
			TAAA TGAAA ACAGATTC		
			A T_ _		
GAM1412	AHR	3'	ATCTCAGATGT	TAAAATAAATG 7875	CAC C T
			CATTT TTT AC GTCTGAGAT		
			GTAAA AAA TG TAGACTCTA		
			TA_ T _		
GAM1412	FDFT1	3'	TAGGAAAGTGAAATG 15518		A
			CATTTCACTTTC CTG		
			GTAAAGTGAAAG GAT		
			_		
GAM1412	JTB	3'	ATCTCAGACAGTGAAAGTGAAA 21959		
	TG		CATTTCACTTTCACTGTCTGAGAT		
			GTAAAGTGAAAGTGACAGACTCTA		
GAM1412	KLF4	3'	TCCCAGACAGTGGATATG 14891	CT	A
			CA TTCACTGTCTG GA		

			GT AGGTGACAGAC CT		
			AT C		
GAM1412	PHYH	3'	ACAGTAAAAGTGAAAT 20608	C	
			ATTTCACTTT ACTGT		
			TAAAGTGAAA TGACA		
			A		
GAM1412	PKD2	3'	TCCAGGTTGAAAAGTGAAA 60096	CTG A	
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T _ _		
GAM1412	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1412	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA CTG	
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C _ CG _		
GAM1412	CG012	5'	CTCACTCTGAAAAGTGAA 83218	CT CT	
			TTCACTTTCA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1412	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G T _	
			CTTTCACT TC GAGAT		
			GAAAGTGA AG TTCTA		
			G TC		
GAM1412	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT 45802	ACTTTCACT	
	G		CATTTC GTCTGAGAT		
			GTAAAG CAGACTCTA		
			AAACATTT _		
GAM1412	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281	CTT	
			CATTTC TCACTGTCTGAGAT		
			GTAAAGT AGTGACAGACTCTA		
			C _		
GAM1412	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C TC	
			TTCA TTTCACTG TGAG		
			AAGT AAAGTGAC GTTT		
			A CT		
GAM1412	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A _	
			TTTC CTG TCTGAGAT		

		AAAG GAC AGACTCTA		
		— G		
GAM1412 NIR3	3'	GCAGTGAAAAGTGCAAT 66242	T	
		ATT CACTTTTCACTGT		
		TAA GTGAAAAGTGACG		
		C		
GAM1412 PORIMIN	3'	ATCTCAGAGGGCCAAAAGTGAA 53598	CA	G
		TTCAC TTT CT TCTGAGAT		
		AAGTGAAA GG AGACTCTA		
		CC G		
GAM1412 PP35	3'	ATCTCAGACTGAAA 22814	CT	
		TTTCA GTCTGAGAT		
		AAAGT CAGACTCTA		
		—		
GAM1412 PRD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148	TCAC	C_
		CATTTCACTT TGT TGAG		
		GTAAAGTGAA ACG ACTC		
		TA_ TT		
GAM1412 SEP15	3'	TCCTACAGTAAGAGTGAAA 14934	C	CT
		TTTCACTTT ACTGT GA		
		AAAGTGAGA TGACA CT		
		A TC		
GAM1412 SFXN2	3'	CTCAGGGGAAAAAAGTGAAA 73941	CACTG	
		TTTCACTTT TCTGAG		
		AAAGTGAAA GGA CTC		
		AAAGG		
GAM1412 LOC149703	3'	ATCTCAGACAGCCGTTTGAAA 84647	ACTTTCA	
		TTTC CTGTCTGAGAT		
		AAAG GACAGACTCTA		
		GTTTGCC		
GAM1412 LOC154007	3'	ATCTCAAACCCTTTAGTGAAA 81015	TTCAC T	C
		TTTCACT GT TGAGAT		
		AAAGTGA CA ACTCTA		
		TTTCC_ A		
GAM1412 LOC155004	3'	TCATTTAAGTGAAAAGGAAA 81226	A	GTC_
		TTTC CTTTCACT TGA		
		AAAG GAAAGTGA ACT		
		_ ATTT		
GAM1412 LOC222134	5'	ACAGTGAAGTGAAATG 94136	T	
		CATTTCACTT CACTGT		

GTAAAGTGAA GTGACA

GAM1413 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
GTA GGAT GGGTTGTTT  
||| ||| |||||  
CGT CCTA CCCAACAAA  
C CGTG\_

GAM1413 LCT 3' AACCGTAAAAATCCTT 9697 G  
AAGGATTTTTA GGTT  
||||||| |||  
TTCCTAAAAAT CCAA  
G

GAM1413 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
GTAAGGATTTT TAGGGTTGTTT  
|||||||  
CATTCCTAAAAATCCCAACAAA

GAM1413 FBXO30 3' AACTAAAAAATCCTGAC 49573 A AG  
GT AGGATTTT GGTT  
|| ||||| |||  
CA TCCTAAAAA TCAA  
G AA

GAM1413 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTT  
GTAAG AGGGTTGTT  
|||| |||||  
CATTC TCCCAACAA  
AT\_\_\_\_\_

GAM1413 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
TAAG TTTT GGGTTGTTT  
||| ||| |||||  
GTTT AAAA CCCAACAAA  
C

GAM1413 SMT3H2 3' AACCAACATAAAAAATCCTTGC 22670 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1413 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
GTAAGGATTTT GGGTT  
||||||| |||  
CGTTCCTAAAAA TCCAA  
GTA

GAM1413 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
GGAT TT GGGTTGTTT  
||| || |||||  
CCTG AA CCCAACAAA  
T\_ C

GAM1413 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
C GTA GGATTTT TTGTTT  
||| ||||| |||

		CGT CCTAAAAA AACAAA		
		C GATAA		
GAM1413	LOC148089 3'	GGCCCTAAAAATTCCTAC	78637	A
		GTA GGATTTTTAGGGTT		
		CAT CTTAAAAATCCCGG		
		C		
GAM1413	LOC154547 3'	AACAACATAAAAAATCCTTGC	76050	GG
		GTAAGGATTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1413	LOC158104 3'	ACAGCCAAAAATCCTTA	60313	AG
		TAAGGATTTTT GTTGT		
		ATTCCTAAAAA CCGACA		
		—		
GAM1413	LOC205880 5'	AAACAACCATCATCCTGAC	90709	A TTTAG
		GT AGGAT GGTGTTT		
		CA TCCTA CCAACAAA		
		G CTA_		
GAM1413	LOC221561 3'	AACAACATAAAAAATCCTTGC	92130	GG
		GTAAGGATTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1413	LOC257591 3'	AACAACATAAAAAATCCTTGC	97840	GG
		GTAAGGATTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1413	LOC51145 3'	AGCTAAAATCCTTAC	32393	TAG
		GTAAGGATTTT GTT		
		CATTCCTAAAA TCGA		
		—		
GAM1414	ARCN1 3'	TTCCACCA GTCTGTCC	7991	GACA
		GGACAGAT GTGGAG		
		CCTGTCTG CACCTT		
		AC_		
GAM1414	CBS 5'	ACTGTCAGCACCATCTGTCC	3568	_____
		GGACAGA TGACAGT		
		CCTGTCT ACTGTCA		
		ACCACG		
GAM1414	CSF3 3'	GCTCCACTGTCACCCTCC	5665	CAGA
		GGA TGACAGTGGAGC		

CCT ACTGTCACCTCG  
 CCC\_  
 GAM1414 FOXI1 3' CTCCACTGCCTTCTGTCC 24108 TGA  
 GGACAGA CAGTGGAG  
 ||||| |||||  
 CCTGTCT GTCACCTC  
 TCC  
 GAM1414 M6PR 3' TGCTGCTGCACCTGTCC 9864 A A GG  
 GGACAG TG CAGT AGCA  
 ||||| || ||| |||  
 CCTGTC AC GTCG TCGT  
 C \_ \_  
 GAM1414 NEU3 3' TGCCTGGAGTCGTCTGTCC 21853 AG A  
 GGACAGATGAC TGG GCA  
 ||||| ||| |||  
 CCTGTCTGCTG GTC CGT  
 AG \_  
 GAM1414 C4S-2 3' CTCCACTGCCTCTATCC 37820 C TGA  
 GGA AGA CAGTGGAG  
 ||| ||| |||||  
 CCT TCT GTCACCTC  
 A CC\_  
 GAM1414 DKFZP434L1435 5' ATGTGCTCTCTCTATCC 92167 C T CAGT  
 GGA AGA GA GGAGCACAT  
 ||| ||| || |||||  
 CCT TCT CT TCTCGTGTA  
 A \_ C\_  
 GAM1414 DKFZP434L1435 5' ATGTGCTCTCTCTATCC 97742 C T CAGT  
 GGA AGA GA GGAGCACAT  
 ||| ||| || |||||  
 CCT TCT CT TCTCGTGTA  
 A \_ C\_  
 GAM1414 DKFZP434L1435 5' ATGTGCTCTCTCTATCC 97858 C T CAGT  
 GGA AGA GA GGAGCACAT  
 ||| ||| || |||||  
 CCT TCT CT TCTCGTGTA  
 A \_ C\_  
 GAM1414 DKFZP564B167 3' TTCTACCATTGTCC 31216 ACA  
 GGACAGATG GTGGAG  
 ||||| |||||  
 CCTGTTTAC CATCTT  
 \_  
 GAM1414 FAM8A1 3' TCCACTGTCTCCCATCC 32725 CA\_ T  
 GGA GA GACAGTGGA  
 ||| || |||||  
 CCT CT CTGTCACCT  
 ACC \_  
 GAM1414 FLJ12816 3' TCCCTGCCATCTGTCC 41935 A T  
 GGACAGATG CAG GGA  
 ||||| ||| |||



CCTGTCTAC GTC CCT  
 C \_  
 GAM1414 KIAA1492 3' TGCACAATCTATCATCTGTCC 64510 C \_ GA  
 GGACAGATGA AG TG GCA  
 ||||| || || ||  
 CCTGTCTACT TC AC CGT  
 A TA A\_  
 GAM1414 KIAA1904 3' CTCCACTGCCACCTCC 73483 CA A A  
 GGA G TG CAGTGGAG  
 || | || |||||  
 CCT C AC GTCACCTC  
 \_ C C  
 GAM1414 p25 3' AATGGCACACTGCCACTGTCC 22843 A A GA A  
 GGACAG TG CAGTG GC CATT  
 |||| | |||| | ||||  
 CCTGTC AC GTCAC CG GTAA  
 \_ C A\_ \_  
 GAM1414 RNF9 3' TGCTCTGTCATCTCC 53415 CA GTG  
 GGA GATGACA GAGCA  
 || ||||| ||||  
 CCT CTACTGT CTCGT  
 \_ \_  
 GAM1414 SCYB10 3' TTCCACTGCCATCCTCC 7800 CA A  
 GGA GATG CAGTGGAG  
 || ||| |||||  
 CCT CTAC GTCACCTT  
 C\_ C  
 GAM1414 TTTY2 5' GGTGGTGCACCTGTCT 87006 A GA A  
 GGACAG TGACAGTG GC CATT  
 |||| ||||| || ||||  
 TCTGTC ACTGTCAC TG GTGG  
 C G\_ \_  
 GAM1414 VR22 5' TGCCCCACTGTCATCTGCC 25171 A A  
 GG CAGATGACAGTGG GCA  
 || ||||| ||||| ||||  
 CC GTCTACTGTCACC CGT  
 \_ C  
 GAM1414 ZER6 3' GTGCTCTTCATCTGTC 63381 CAGT  
 GACAGATGA GGAGCAC  
 ||||| |||||  
 CTGTCTACT TCTCGTG  
 \_ \_  
 GAM1414 ZNF317 3' CTCCTGTCTCATCTGCC 72014 A T  
 GG CAGATGACAG GGAG  
 || ||||| ||||  
 CC GTCTACTGTC CTTC  
 \_ \_  
 GAM1414 LOC150005 3' AATGTGCTTGCTCCTCTACCC 84813 AC T CA TG A  
 GG AGA GA G G GCACATT  
 || ||| || | |||||

		CC TCT CT C T CGTGTA		
		CA C _ GT _		
GAM1414	LOC157860 3'	AATGTGCTCTACTCCACCCACT 86563	CAGATGAC	
	CC	GGA AGTGGAGCACATT		
		CCT TCATCTCGTGTA		
		CACCCACC		
GAM1414	LOC159148 5'	GGTGGTGCACCTGTCT 87015	A GA A	
		GGACAG TGACAGTG GC CATT		
		TCTGTC ACTGTCAC TG GTGG		
		C G _		
GAM1414	LOC199704 3'	CCACTGTCATCTACC 88327 AC		
		GG AGATGACAGTGG		
		CC TCTACTGTCACC		
		A _		
GAM1414	LOC221421 3'	GTCCCACTGTCCCCTGTCC 92281	AT AG	
		GGACAG GACAGTGG C		
		CCTGTC CTGTCACC G		
		CC CT		
GAM1414	LOC221773 3'	GCTCCACTGCCATGTACC 91048	_ GA A	
		GG ACA TG CAGTGGAGC		
		CC TGT AC GTCACCTCG		
		A _ C		
GAM1414	LOC51161 3'	CTCCACCGTCACTGTCC 32509	A A	
		GGACAG TGAC GTGGAG		
		CCTGTC ACTG CACCTC		
		_ C		
GAM1414	LOC90630 5'	GCCTCCCTGTTCATCCGTCC 63632	A T _	
		GGAC GATGACAG GGAG C		
		CCTG CTA CTGTC CCTC G		
		C _ C		
GAM1415	ARNT2 3'	AAACAACCCGTGCATCCCTGC 29450	A TTTA	
		GTA GGAT GGGTTGTTT		
		CGT CCTA CCAACAAA		
		C CGTG _		
GAM1415	LCT 3'	AACCGTAAAAATCCTT 9697	G	
		AAGGATTTTTA GGTT		
		TTCCTAAAAAT CCAA		
		G		
GAM1415	RPL15 3'	AAACAACCCTAAAAATCCTTAC 11382		
		GTAAGGATTTT TAGGGTTGTTT		

CATTCCTAAAAATCCCAACAAA

GAM1415 FBXO30 3' AACTAAAAAATCCTGAC 49573 A AG  
GT AGGATTTTT GTT  
|| ||||| |||  
CA TCCTAAAAA TCAA  
G AA

GAM1415 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTT  
GTAAG AGGGTTGTT  
|||| |||||  
CATTC TCCCAACAA  
AT\_\_\_\_

GAM1415 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
TAAG TTTT GGGTTGTT  
||| ||| |||||  
GTTC AAAA CCAACAAA  
\_\_\_ C

GAM1415 SMT3H2 3' AACAACATAAAAATCCTTGC 22670 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1415 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
GTAAGGATTTTT GGGTT  
||||||| |||||  
CGTTCCTAAAAA TCCAA  
GTA

GAM1415 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
GGAT TT GGGTTGTT  
||| || |||||  
CCTG AA CCAACAAA  
T\_ C

GAM1415 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
C GTA GGATTTTT TTGTTT  
|| ||||| |||||  
CGT CCTAAAAA AACAAA  
C GATAA

GAM1415 LOC148089 3' GGCCCTAAAAATCCTAC 78637 A  
GTA GGATTTTTAGGGTT  
|| |||||  
CAT CTAAAAATCCCGG  
C

GAM1415 LOC154547 3' AACACATAAAAATCCTTGC 76050 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1415 LOC158104 3' ACAGCCAAAAATCCTTA 60313 AG  
TAAGGATTTTT GGTGT  
||||||| |||||

ATTCCTAAAAA CCGACA

GAM1415 LOC205880 5' AAACAACCATCATCCTGAC 90709 A TTTTAG  
GT AGGAT GGTGTGTT  
|| |||| |||||  
CA TCCTA CCAACAAA  
G CTA\_\_

GAM1415 LOC221561 3' AACAAACATAAAAAATCCTTGC 92130 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA

A\_  
GAM1415 LOC257591 3' AACAAACATAAAAAATCCTTGC 97840 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA

A\_  
GAM1415 LOC51145 3' AGCTAAAATCCTTAC 32393 TAG  
GTAAGGATTTT GTT  
||||||| |||  
CATTCCTAAAA TCGA

GAM1416 THBD 3' ACTGGTAGACCAAATAAAA 4491 C A\_  
TTTTA TTTTGGTC CGGT  
|||| ||||| |||  
AAAAT AAAACCAG GTCA  
\_ ATG

GAM1416 XPNPEP1 3' GCCAAGAATAAAATTG 39848 C  
CAATTTTA TTTTGGT  
||||| |||||  
GTTAAAAT AGAACCG  
A

GAM1416 FLJ21615 3' GCACTTGGCCAAAAACAAAATT 49836 AC C  
G CAATTTT TTTTGGTCA GGTGC  
||||| ||||| |||||  
GTTAAAA AAAACCGGT TCACG  
CA \_

GAM1416 KIAA1363 3' GCACCACGGAGAGAAAGTAGAA 69263 GG AC\_  
TTTTACTTTT TC GGTGC  
||||||| || |||||  
AAGATGAAAG AG CCACG  
AG GCA

GAM1416 KIAA1550 3' CACCACCATAAAGTGAAATCA 66551 A \_ CAC  
C ATTTTACTTT TGGT GGTG  
| ||||| ||| |||  
A TAAAGTGAAA ACCA CCAC  
C T \_

GAM1416 KSR 3' GCACCGTGACTTCTGCTAAAAT 64043 CTTTT  
ATTTTA GGTACCGGTGC  
||||| |||||

	TAAAAT TCAGTGCCACG		
	CGTCT		
GAM1416 STK17B	3' TGACAAAAAGTAAAATTG 14874	G	
	CAATTTTACTTTT GTCA		
	GTTAAAATGAAAA CAGT		
	A		
GAM1416 LOC145844	3' GCACCACTGGCTAAGTAAA 77538	TT	C_
	TTTACT TGGTCA GGTGC		
	AAATGA ATCGGT CCACG		
	CA		
GAM1416 LOC157793	3' GCACCTCTGAAAAGTAAAAT 81612	TGG	C_
	ATTTTACTTT TCA GGTGC		
	TAAAATGAAA AGT CCACG		
	CT		
GAM1416 LOC90918	5' CACCATGACCAAATGGGATT 64352	CT	C
	AATTTTA TTTGGTCA GGTG		
	TTAGGGT AAACCAGT CCAC		
	A		
GAM1417 DKFZp434A1010	3' CCCACATGCCCCACTAAACCA 71342	A	AT CTA
TC	GAT GTTTAGTG GTA GGGG		
	CTA CAAATCAC CGT CCCC		
	C CC ACA		
GAM1417 KIAA1189	3' CCCTACCTACCAAACCTATC 72041	A	ATGTAC
	GATAGTTT GTG TAGGG		
	CTATCAAA CAT ATCCC		
	C CC_		
GAM1418 KIAA1908	5' AGCACACAGCCCTGA 73392	A	CGTTT
	TTAGGGCT GT GTGCT		
	AGTCCCGA CA CACGA		
GAM1418 LOC124739	5' AGCACAGTGGCAGCCCTGA 74324	A	GTT
	TTAGGGCT GTC TGTGCT		
	AGTCCCGA CGG ACACGA		
	TG_		
GAM1418 LOC145988	5' CACACACAACCCAGCCCTAA 77607	A_	C T
	TTAGGGCT GT GT TGTG		
	AATCCCGA CA CA ACAC		
	CC A C		
GAM1418 LOC219654	3' AGTCCAACGACTAACCCTGA 91298	C	T TG
	TTAGGG TAGTCGTT G CT		

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AGTCCC ATCAGCAA C GA
A _ CT
GAM1419 EEF1A2 3' AGTGCCCGTTTTACCAATAAAC 61417 C
TG CAGTT ATTGGTAAAACGGGCACT
||||| |||||||||
GTCAA TAACCATTTTGCCCGTGA
A
GAM1419 ESRRG 3' TGCTATACCAATGGAC 66395 AAACG
GTTTCATTGGTA GGCA
||||||| |||
CAGGTAACCAT TCGT
A____
GAM1419 GJA1 3' TTTGTTTTACCAAGAAACTG 3909 CA
CAGTT TTGGTAAAACGGG
||||| |||||||||
GTCAA AACCATTTTGTTT
AG
GAM1419 MDM4 5' GTTTTACCAACAGACTG 9980 CA
CAGTT TTGGTAAAAC
||||| |||||||
GTCAG AACCATTTTG
AC
GAM1419 PKD2 3' GATCCCAGCAATGAACTG 33197 GTAAAAC CA_
CAGTTCATTG GGG C
||||||| ||| |
GTCAAGTAAC CCC G
GA____ TAG
GAM1419 ZFP103 5' AGTGCCCGCCCCGGGGAA 19021 A TAAAA
TTC TTGG CGGGCACT
||| ||| |||||||
AAG GGCC GCCCGTGA
G CC____
GAM1419 FLJ22029 3' TGCTAGCCAATGAAC 46333 AAAACG
GTTTCATTGGT GGCA
||||||| |||
CAAGTAACCG TCGT
A____
GAM1419 FLJ25059 3' CCGTGTACTTACCAATAAACT 58682 C A____
AGTT ATTGGTAA ACGG
||||| |||
TCAA TAACCATT TGCC
A CATG
GAM1419 KIAA0528 3' TGCCCGTTGTAAATGAAC 72382 GGTA
GTTTCATT AACGGGCA
||||| |||||||
CAAGTAA TTGCCCGT
ATG____
GAM1419 KIAA0964 5' GTGCCCGCTCCTGAGCTG 29766 TT TAAAA
CAGTTCA GG CGGGCAC
||||| || |||||||

```

GTCGAGT CC GCCCGTG  
 \_\_\_ TC\_\_\_  
 GAM1419 KIAA1297 3' AGTGCTCGGCCACCAACGTACT 72168 TCA AAAA  
 G CAGT TTGGT CGGGCACT  
 ||| ||| |||||  
 GTCA AACCA GCTCGTGA  
 TGC CCG\_

GAM1419 MACF1 3' GCTCTACCAATGAACTG 23890 AAAC  
 CAGTTCATTGGTA GGGC  
 ||||| |||  
 GTCAAGTAACCAT CTCG

GAM1419 NET-5 3' AGTGCCCGCCCGTGGA 21922 T TAAAA  
 TTCAT GG CGGGCACT  
 ||| || |||||  
 AGGTG CC GCCCGTGA  
 C C\_\_\_

GAM1419 NYD-SP16 3' TGCCCAAATGCAAATGAACT 49220 G AAAC  
 AGTTCATT GTA GGGCA  
 ||||| || |||  
 TCAAGTAA CGT CCCGT  
 A AAAA

GAM1419 RFX4 3' AGTGCCCATTTTCCTAATGAAC 50661 T C  
 GTTCATTGG AAAA GGGCACT  
 ||||| ||| |||||  
 CAAGTAATC TTTT CCCGTGA  
 C A

GAM1419 SIAT8D 3' GCATCCACCAATGAACTG 19029 AAAACGG  
 CAGTTCATTGGT GC  
 ||||| ||  
 GTCAAGTAACCA CG  
 CCTA\_\_\_

GAM1419 TRIM5 3' TGTTACCAATGAAT 52308 AAAAC  
 GTTCATTGGT GGGCA  
 ||||| |||  
 TAAGTAACCA CTTGT

GAM1419 USP10 3' AGTGCCCGCTTCGTAGGAC 63944 AT TAAAA  
 GTTC TGG CGGGCACT  
 ||| || |||||  
 CAGG GCT GCCCGTGA  
 AT TC\_\_\_

GAM1419 LOC144871 5' GTCTATTTCTTACCAATAAACT 83201 C \_\_\_ CG  
 AGTT ATTGGTAA AA GGC  
 ||| ||||| || |||  
 TCAA TAACCATT TT CTG  
 A CT AT

GAM1419 LOC147976 3' AGTGGTATTATCAATAAACTG 78586 C A GGG  
 CAGTT ATTGGTAA AC CACT  
 |||| ||||| || |||

			GTCAA TAACTATT TG GTGA		
			A A _		
GAM1419	LOC154834	5'	CCCGCTTTACCGGGTGGC	86263	CA A
			GTT TTGGTAAA CGGG		
			CGG GGCCATTT GCCC		
			TG C		
GAM1419	LOC221362	5'	TCGTCTCACCAATGAAC	93762	AAA
			GTTTCATTGGT ACGG		
			CAAGTAACCA TGCT		
			CTC		
GAM1419	LOC222223	3'	GCCCACCAATGCACTG	94216	T AAAAC
			CAGT CATTGGT GGGC		
			GTCA GTAACCA CCGG		
			C _		
GAM1419	LOC90246	3'	TGCCCATCAGCTAATGAAT	61911	AAAAC
			GTTTCATTGGT GGGCA		
			TAAGTAATCG CCGT		
			ACTA_		
GAM1419	LOC92876	5'	TGCAGCTTTTACCAACAAAT	70805	CA CGG
			GTT TTGGTAAAA GCA		
			TAA AACCATTTT CGT		
			AC CGA		
GAM1420	ADRBK2	3'	TGAGGAATGAATGTGTCAA	17686	GA TGG C
			TTG AC ATTCATTCC CA		
			AAC TG TAAGTAAGG GT		
			TG _ A		
GAM1420	CD8A	3'	TGGAAAATGAATCCCTCTA	8335	ACT CC
			TGGA GGATTCATT CCA		
			ATCT CCTAAGTAA GGT		
			C_ AA		
GAM1420	CTLA4	3'	GGAATGGCACAGCCCAA	17810	AA GAT
			TTGG CTG TCATTCCC		
			AACC GAC GGTAAGGG		
			C_ AC_		
GAM1420	CUL5	3'	TTGGGGAATGAACAGCAGCAA	12978	GAA GA
			TTG CTG TTCATTCCCCAA		
			AAC GAC AAGTAAGGGGT		
			GAC _		
GAM1420	DDT	5'	GGGACCCTGCCCAGTTCCAG	7219	ATTCAT
			TTGGAACTGG TCCC		



			GACCTTGACC	AGGG		
			CGTCCC			
GAM1420	EML1	3'	TGGGGAATGTATCTCA	59730	_	T
			TG GAT CATTCCCCA			
			AC CTA GTAAGGGGT			
			T T			
GAM1420	GRLF1	3'	GGAGAACAAACCCAGGGTTCAG	78557	A_	A CA C
			TTGGA CTGG TT TTC CC			
			GACTT GACC AA AAG GG			
			GG C AC A			
GAM1420	HNRPF	3'	TGGAGAACTTTAGTTTCAA	17122		TTCA C
			TTGGA ACTGGA TTC CCA			
			AACTTTGATTT AAG GGT			
			C_ A			
GAM1420	MAP1A	5'	GGGATTATCCAGTTCC	9900		TCAT
			GGA ACTGGAT TCCC			
			CCTTGACCTA AGGG			
			TT_			
GAM1420	MLLT7	5'	GGGGAGGTCCAACTCCA	19867	AC	TCA
			TGGA TGGAT TTCCCC			
			ACCT ACCTG GAGGGG			
			CA _			
GAM1420	NTSR1	3'	GGGGAGTCCAGCCCCAG	10298	AA	TCAT
			TTGG CTGGAT TCCCC			
			GACC GACCTG AGGGG			
			CC _			
GAM1420	PCDHB5	5'	TGGGGAATCCAAACTCTAA	31613	AC_	TCAT
			TTGGA TGGAT TCCCCA			
			AATCT ACCTA AGGGGT			
			CAA _			
GAM1420	SH3GL3	5'	GAAGAAGCAGTTCCA	11632	GA	A
			TGGA ACTG TTC TTC			
			ACCTTGAC AAG AAG			
			G_ _			
GAM1420	TCF3	3'	GGGATCCCATCCAGTTCCA	70733		TCAT
			TGGA ACTGGAT TCCC			
			ACCTTGACCTA AGGG			
			CCCT			
GAM1420	A4GALT	3'	TGGGGGAGACCCAGCCCCAA	33842	AA	AT A
			TTGG CTGG TC TTCCCCA			

			AACC GACC AG AGGGGGT		
			CC C_ _		
GAM1420	C15orf15	3'	TTGGAGAATACTCAGTTCCAA 32835	ATTC	C
			TTGGAACTGG ATTCCAA		
			AACCTTGACT TAAG GGTT		
			CA_ A		
GAM1420	CPLX1	3'	TTGGGGGACGCCAGCCCC 21838	AA	ATTCA
			GG CTGG TTCCCCAA		
			CC GACC AGGGGGT		
			CC CGC_		
GAM1420	DDR2	5'	TGATACTCCAGTTCCAA 20525	T_	
			TTGGAACTGGA TCA		
			AACCTTGACCT AGT		
			CAT		
GAM1420	FLJ10120	3'	GGGAGTCCAGCCCCAA 35834	AA	TCAT
			TTGG CTGGAT TCCC		
			AACC GACCTG AGGG		
			CC _		
GAM1420	FLJ10520	3'	TGGGGAATATGACATCC 36216	_ _	
			GGAT TCAT TCCCCA		
			CCTA AGTA AGGGGT		
			C TA		
GAM1420	FLJ14641	3'	GGAAAGACCAGTTCC 51487	AT	A
			GGAAGTGG TC TTCC		
			CCTTGACC AG AAGG		
			_ A		
GAM1420	FLJ14810	3'	TGGGGACCCACGCTCCAA 51633	AC_	ATTCAT
			TTGGA TGG TCCCCA		
			AACCT ACC AGGGGT		
			CGC C_		
GAM1420	GAL3ST-4	5'	TGGGGAATGACCCCCGA 44943	AACT	AT
			TTGG GG TCATTCCCCA		
			AGCC CC AGTAAGGGGT		
			_ CC		
GAM1420	GLP	3'	TGAGGAATGAAAGGCTCC 37849	A GGA	C
			GGA CT TTCATTCC CA		
			CCT GG AAGTAAGG GT		
			C A_ A		
GAM1420	HSJ1	3'	GAATCGCTGCACAGTTCCAA 22130		
			TTGGAACTG GATTC		

AACCTTGAC CTAAG  
 ACGTCG  
 GAM1420 KIAA0447 3' GGTGGGTCCAGTGCCAA 71674 A  
 TTGG ACTGGATTCATT  
 ||| |||||  
 AACC TGACCTGGGTGG  
 G  
 GAM1420 KIAA0515 3' AATCAGTTCAGTTCCAA 63800 C  
 TTGGA ACTGGATT ATT  
 ||||| |||  
 AACCTTGA CTTGA TAA  
 C  
 GAM1420 KIAA0644 3' TGGGGAACACCAGTGTTCAG 29066 \_ ATTCA  
 TTGGA ACTGG TTCCCCA  
 ||| ||| |||||  
 GACCT TGACC AAGGGGT  
 TG AC\_  
 GAM1420 KIAA0844 3' TGGGGAACGTTGTTCAG 30207 TG TCA  
 TTGGAAC GAT TTCCCCA  
 ||||| || |||||  
 GACCTTG TTG AAGGGGT  
 \_ C\_  
 GAM1420 KIAA1061 3' GGAATGAACTCTTCAA 71178 CT GA  
 TTGGAA G TTCATTCC  
 ||||| | |||||  
 AACTTT C AAGTAAGG  
 \_ TC  
 GAM1420 KIAA1538 3' GAATGTACCAAGTTCCAA 71546 \_ ATT  
 TTGGA ACT GG CATTG  
 ||||| || |||||  
 AACCTTGA CC GTAAG  
 A AT\_  
 GAM1420 KIAA1671 3' TTGAGGAATCAGCAGTTCCAA 65700 GATTG C  
 TTGGA ACTG ATTCC CAA  
 ||||| ||| |||  
 AACCTTGAC TAAGG GTT  
 GAC\_ A  
 GAM1420 KIAA1754 3' GGGAATGAACCAGCTC 63239 A A  
 GA CTGG TTCATTCCC  
 || ||| |||||  
 CT GACC AAGTAAGGG  
 C \_  
 GAM1420 KIAA1765 3' GGGAATCTGTCCAGCCCC 70611 AA TC  
 GG CTGGAT ATTCCC  
 || |||| |||||  
 CC GACCTG TAAGGG  
 CC TC  
 GAM1420 KIAA1913 3' GGAGTACAAATTCAGTCCCAA 73886 A C\_  
 TTGG ACTGGATT ATTCC  
 ||| ||||| |||||

		AACC TGA	CTTAA	TGAGG		
		C	ACA			
GAM1420	KRTAP4-13	3'	GGAAAACTTCAGTTCCAA	52597	TTCA	
			TTGGA	ACTGGA	TTCC	
			AACCTTGA	CTT	AAGG	
			CAA_			
GAM1420	KRTAP4-4	3'	GGAAAACTTCAGTTCCAA	50719	TTCA	
			TTGGA	ACTGGA	TTCC	
			AACCTTGA	CTT	AAGG	
			CAA_			
GAM1420	LAT1-3TM	3'	TTGGGGAACGCTTCAGCCCAA	48317	AA	TTCA
			TTGG	CTGGA	TTCCCAA	
			AACC	GACTT	AAGGGGTT	
			C_	CGC_		
GAM1420	MACF1	3'	TGAGGAATGAATTCCA	23895	_	C
			TGGA	TTCATTCC	CA	
			ACCT	AAGTAAGG	GT	
			T	A		
GAM1420	MAP3K3	3'	TTGGGGAAACAGCATCTCCAA	10002	AC	GATTCA
			TTGGA	TG	TTCCCAA	
			AACCT	AC	AAGGGGTT	
			CT	GACA__		
GAM1420	N4BP3	3'	TGGGGGATCACCAGCCCAA	66272	AA	ATTC
			TTGG	CTGG	ATTCCCA	
			AACC	GACC	TAGGGGGT	
			CC	AC__		
GAM1420	PRO0659	3'	TGAGATCCAGTTTCAA	26219	_	
			TTGGA	ACTGGAT	TCA	
			AACTTTGACCTA	AGT		
			G			
GAM1420	R32184_3	3'	GGGCCGTGGTCCAGTCCCA	53069	A	T TC
			TGG	ACTGGAT	CAT CCC	
			ACC	TGACCTG	GTG GGG	
			C	_	CC	
GAM1420	RAB1B	3'	TGGGGAATGTGGGTTCCA	48291	GGATT	
			TGGA	ACT	CATTCCCA	
			ACCTTG	G	GTAAGGGGT	
			GT__			
GAM1420	SELM	3'	TTGGGGAGGTTCTCCCAACCCC	54437	AACT_	TTCA
	A		TGG	GGA	TTCCCAA	

		ACC CCT GAGGGGTT	
		CCAAC CTTG	
GAM1420	SLC22A4	5' TTGGGGAGCGCCCCAGCTACAA 11762	GAA ATTCA
		TTG CTGG TTCCCCAA	
		AAC GACC GAGGGGTT	
		ATC CCGC_	
GAM1420	TCEB3L	3' TTGGGGAACGAAACTTCCAA 33143	ACT A A
		TTGGA GG TTC TTCCCCAA	
		AACCT TC AAG AAGGGGTT	
		___ A C	
GAM1420	YAP	5' GGAATTACAGTTCCAA 36789	GATTC
		TTGGAACTG ATTCC	
		AACCTTGAC TAAGG	
		AT___	
GAM1420	ZNF31	5' GGGAGTTCAGTTTCAA 64985	TTC
		TTGGAACTGGA ATTCCC	
		AACTTTGACCT TGAGGG	
		___	
GAM1420	LOC116236	3' GGAATGCGAAGTTCCAA 73814	GGATT
		TTGGAACT CATTCC	
		AACCTTGA GTAAGG	
		AGC___	
GAM1420	LOC143308	5' TTGGGGAAAAACAGCCCCA 82941	AA GATTCA
		TGG CTG TTCCCCAA	
		ACC GAC AAGGGGTT	
		CC AAA___	
GAM1420	LOC145082	5' GGTATGATCCAATTTCAA 83246	C T TC
		TTGGAA TGGAT CAT CC	
		AACTTT ACCTA GTA GG	
		A _ TT	
GAM1420	LOC145678	3' GAATGGAATCAAGTTCCAA 83421	G _
		TTGGAACT GATTC ATTC	
		AACCTTGA CTAAG TAAG	
		A G	
GAM1420	LOC145900	3' TGAGGAATGAAAGGTTCC 77566	GGA C
		GGA ACT TTCATTCC CA	
		CCTTGG AAGTAAGG GT	
		A__ A	
GAM1420	LOC147219	5' GGAATATTCAGTTCCAA 83991	TC
		TTGGAACTGGAT ATTCC	

AACCTTGACTTA TAAGG

GAM1420 LOC148936 5' GGGGAGTGCAAGCCCCAA 84300 AACT A \_  
TTGG GG TT CATTCCCC  
|||| ||| |||||  
AACC CC AA GTGAGGGG  
\_\_\_\_ G C

GAM1420 LOC148938 5' GGGGAGTGCAAGCCCCAA 84281 AACT A \_  
TTGG GG TT CATTCCCC  
|||| ||| |||||  
AACC CC AA GTGAGGGG  
\_\_\_\_ G C

GAM1420 LOC149483 3' TGAGTACAGAAAACCAGTTCCA 79388 \_\_\_\_\_  
A TTGGA ACTGG ATTCA  
||||||| |||||  
AACCTTGACC TGAGT  
AAAAGACA

GAM1420 LOC149559 5' TGAGGAATGAGCGACAGTTC 79444 GA\_ C  
GAACTG TTCATTCC CA  
||||| ||||| ||  
CTTGAC GAGTAAGG GT  
AGC A

GAM1420 LOC149842 3' ATGAATCCAGGTTCCAA 84721 \_  
TTGGAAC TGGATTCAT  
||||| |||||  
AACCTTG ACCTAAGTA  
G

GAM1420 LOC150421 3' GGAATGAATCCCCGA 85038 AACT  
TTGG GGATTCA TTCC  
||| |||||  
AGCC CCTAAGTAAGG

GAM1420 LOC150606 3' GAATGAATTTCCAA 85088 ACTG  
TTGGA GATTCATTC  
||||| |||||  
AACCT TTAAGTAAG

GAM1420 LOC151171 5' GGGGGCTGCCCAGTTCCAG 80145 ATT TT  
TTGGA ACTGG CA CCCC  
||||||| || |||  
GACCTTGACC GT GGGG  
C\_ CG

GAM1420 LOC153914 5' GAAGAAACCCAGTTCCAA 80989 A CA  
TTGGA ACTGG TT TTC  
||||||| || |||  
AACCTTGACC AA AAG  
C AG

GAM1420 LOC155081 3' GGAGTGTTTCCAGTTCCA 81294 TT  
TGGA ACTGGA CATTCC  
||||||| |||||

	ACCTTGACCT GTGAGG	
	TT	
GAM1420 LOC167937 5'	TGGGGAATATTCTTAATCCAA 87274	ACT TTC
	TTGGA GGA ATTCCCCA	
	AACCT TCT TAAGGGGT	
	AAT TA_	
GAM1420 LOC200298 5'	GAGGAGTCCAGTTCC 89973	A
	GGAAGTGGATTTC TTC	
	CCTTGACCTGAG GAG	
	—	
GAM1420 LOC200300 3'	GAATGAATCCACCCCAA 89968	AAC
	TTGG TGGATTCATTC	
	AACC ACCTAAGTAAG	
	CC_	
GAM1420 LOC200304 3'	GAATGAATCCACCCCAA 89986	AAC
	TTGG TGGATTCATTC	
	AACC ACCTAAGTAAG	
	CC_	
GAM1420 LOC200305 3'	GAATGAATCCATCCCAA 89980	AAC
	TTGG TGGATTCATTC	
	AACC ACCTAAGTAAG	
	CT_	
GAM1420 LOC200982 3'	GGGAAGCCCAGTTCCA 90223	ATTCA
	TGGAAGTGG TTCCC	
	ACCTTGACC AAGGG	
	CG_	
GAM1420 LOC201685 5'	GGAGACTCCAGTTCCAA 90245	T AT
	TTGGAAGTGGG TC TCC	
	AACCTTGACCT AG AGG	
	C _	
GAM1420 LOC202020 3'	TGAGGAAAGACATTTCAGTTCCA 89139	_ A C
A	TTGGAAGTGGAT TC TTCC CA	
	AACCTTGACTTA AG AAGG GT	
	C A A	
GAM1420 LOC202802 3'	GGAGTGTTTCCAGTTCCA 89208	TT
	TGGAAGTGGG CATTCC	
	ACCTTGACCT GTGAGG	
	TT	
GAM1420 LOC219529 3'	TGGGTGACCCAGTTCC 92977	AT TTC
	GGAAGTGG TCA CCCA	

		CCTTGACC AGT GGGT		
		C_ ____		
GAM1420	LOC219743 3'	TGGGGAGCCCACTCCAA	93128	AC ATTCA
		TTGGA TGG TTCCCCA		
		AACCT ACC GAGGGGT		
		C_ C____		
GAM1420	LOC220534 3'	TGAGGAATGAAAGGCTCC	90723	A GGA C
		GGA CT TTCATTCC CA		
		CCT GG AAGTAAGG GT		
		C A__ A		
GAM1420	LOC220538 3'	TGAGGAATGAAAGGCTCC	90735	A GGA C
		GGA CT TTCATTCC CA		
		CCT GG AAGTAAGG GT		
		C A__ A		
GAM1420	LOC220565 5'	TTGGGGAACGCTTCAGCCCAA	90758	AA TTCA
		TTGG CTGGA TTCCCCAA		
		AACC GACTT AAGGGGTT		
		C_ CGC_		
GAM1420	LOC220595 3'	TTGGGGAACATTTTCAATTCCA	91143	C TTCA
		TGGAA TGGA TTCCCCAA		
		ACCTT ACTT AAGGGGTT		
		A TTAC		
GAM1420	LOC221060 3'	TGGCAAATCCAGTCTCAA	93218	GA CATTCC
		TTG ACTGGATT CCA		
		AAC TGACCTAA GGT		
		TC AC____		
GAM1420	LOC222228 3'	GGAGCGTTTCCAGTTCCA	94299	TTCA
		TGGAAGTGA TTCC		
		ACCTTGACCT GAGG		
		TTGC		
GAM1420	LOC222233 3'	GGAGCGTTTCCAGTTCCA	94256	TTCA
		TGGAAGTGA TTCC		
		ACCTTGACCT GAGG		
		TTGC		
GAM1420	LOC253805 3'	GGCGAAATCCAATTCC	96433	C CAT C
		GGAA TGGATT TC CC		
		CCTT ACCTAA AG GG		
		A ____ C		
GAM1420	LOC254936 3'	TGAGGAATGAAAGGTTCC	94973	GGA C
		GGAAGT TTCATTCC CA		



			CCTTGG	AAGTAAGG	GT		
			A__	A			
GAM1420	LOC255527	5'	TGAGGCCTCATCCAGTTCCA	96857		TCATT	C
			TGGA	ACTGGAT	CC CA		
			ACCTTGACCTA	GG GT			
			CTCC_	A			
GAM1420	LOC255654	5'	TGAGGACCTCCCAGGTTCCAA	96890		_	ATTCAT C
			TTGGAAC	TGG	TCC CA		
			AACCTTG	ACC	AGG GT		
			G	CTCC_	A		
GAM1420	LOC255855	3'	GGAAAATCCAGCTTCCAA	96227		_	CA
			TTGGAA	CTGGATT	TTCC		
			AACCTT	GACCTAA	AAGG		
			C				
GAM1420	LOC257286	3'	TGAGGAATGAAAGGCTCC	94557		A	GGA C
			GGA	CT	TTCATTCC CA		
			CCT	GG	AAGTAAGG GT		
			C	A_	A		
GAM1420	LOC90750	3'	GGGAATGAGTTGCTCTAA	63923		ACTG	
			TTGGA	GATT	CATTCCC		
			AATCT	TTGAGTAAGGG			
			CG_				
GAM1421	FLJ22672	3'	AACCAGGCCGAGAGGCCAC	46066			
			GTGGTC	CGGCCTGGTT			
			CACCGG	GCCGGACCAA			
			AGA				
GAM1421	RBT1	3'	AACCAGGCCGGACCACGTGCAA	25348			
	TA		TATTGCACGTGGTCCGGCCTGGTT				
			ATAACGTGCACCAGGCCGGACCAA				
GAM1422	ABCC8	3'	AACTGTAAATCACTTGTA	4457		ACT_	
			TTTACAAGTGG	CAGTT			
			AAATGTTCACT	GTCAA			
			AAAT				
GAM1422	ACADS	3'	GTGGGGCTGGGCCAT	3411		A	
			GTGG	CTCAGTTCCAT			
			TACC	GGGTCGGGGTG			
GAM1422	ACLY	3'	GATGGGGTCTTCCTCATTGTAG	65060		GT_	CTCA TT
			TTACAA	GGA	G CCATC		

			GATGTT CCT T GGTA		
			ACT TC__GG		
GAM1422	AGT	3'	GCTGGGTTTATTTTAGA 3457	C	
			TTTA AAGTGGACTCAGT		
			AGAT TTTATTTGGGTCG		
			—		
GAM1422	AP1B1	3'	ATGGGGCTGGGTAAGC 6666	GG	
			GT ACTCAGTTCCAT		
			CG TGGGTCGGGGTA		
			AA		
GAM1422	AP1G1	3'	ACCTTGCGAGTTTATTTGTAAA 6670		A TCCATC
			TTTACAAGTGGACTC GT		
			AAATGTTTATTTGAG CG		
			— TTCCAG		
GAM1422	APBA1	3'	CTGAGTTTATCTGTGG 69916	AG	
			TTACA TGGACTCAG		
			GGTGT ATTTGAGTC		
			CT		
GAM1422	BCS1L	5'	GATGGGCAGATTTTCATTTGGG 15078	TA	C_ A T
	GA		TT CAAGTGGA TC GT CCATC		
			AG GTTACTT AG CG GGTA		
			GG TT A _		
GAM1422	CACNA1C	3'	GGTCTTTCGACTCTGCTTGTAG 5563		TG C _ TT_ ATC
	A		TTTACAAG GA TC AG CC		
			AGATGTTT CT AG TT GG		
			GT C C TCT		
GAM1422	CARD15	3'	GATGTTTCGTCTCAGTTTGTTTG 42214		TG C TTC__
	TGAG		TTACAAG GACT AG CATC		
			AGTGTTT TTGA TC GTAG		
			GT C TGCTT		
GAM1422	CCNT2	3'	TGGAGCTGCTTGTAAG 54269		TGGACT
			TTTACAAG CAGTTCCA		
			GAATGTTT GTCGAGGT		
			—		
GAM1422	CD3Z	3'	GAGTTGTTGAGTCTGTTTGTGTA 5593	_TG	__ CATC
	AA		TACAA G GACTCAG TTC		
			ATGTT T CTGAGTT GAG		
			TGT GTT C		
GAM1422	CYP2B6	3'	GATGGGGTTTCACTGTGTAG 5730	_	CTCA TT
			TTACA AGTGGA G CCATC		

			GATGT TCACTT T GGTAG		
			G ____ GG		
GAM1422 DAAM1	3'	GATGGA	ACTGGAGTTGTTG 30377	GTG _	
		CAA	GA	CTC	AGTTCCATC
		GTT	TTGAG TCAAGGTAG		
		G__	G		
GAM1422 DMRT1	3'	ATGGCG	GTTCACTTG 41697	CAGTT	
		CAAGTGGACT	CCAT		
		GTTCACTTGG	GGTA		
		C__			
GAM1422 DMXL1	3'	GATGGG	ACTAAGTGTTTATGGG 18577	AA TC__	
		C	GTGGAC	AGTTCCATC	
		G	TATTTG TCAGGGTAG		
		GG	TGAA		
GAM1422 FGB	3'	GATGTTTAA	AGTCCACTTTTA 17637	C CAGTTC	
AA		TTTA	AAGTGGACT CATC		
		AAAT	TTCACCTGA GTAG		
		T	AAATTT		
GAM1422 FGB	3'	GATGTTTAA	AGTCCACTTTTA 17637	C CAGTTC	
AA		TTTA	AAGTGGACT CATC		
		AAAT	TTCACCTGA GTAG		
		T	AAATTT		
GAM1422 GRLF1	3'	AACCAAGT	CCACTGGGGA 78549	TA A CA	
		TT	CA GTGGACT GTT		
		AG	GT CACCTGA CAA		
		GG _	AC		
GAM1422 GSBS	3'	CTGAGAC	CACTTGTA 91093	A	
		TTTACA	AGTGG CTCAG		
		AAATGTT	CACC GAGTC		
		A			
GAM1422 GSBS	3'	GTTCCC	CTGAGACCACTTGTA 91096	A TTCCATC	
A		TTTACA	AGTGG CTCAG		
		AAATGTT	CACC GAGTC		
		A	CCCTTG		
GAM1422 HIRA	3'	GATTGAG	CCATTTGTGAG 12436	A	
		TTTACA	AGTGG CTCAGTT		
		GAGTGTT	TACC GAGTTAG		
		-			
GAM1422 HIRA	3'	GGTGGG	CGATTTCTTTTGTAAG 12441	T C A T	
		TTTACA	AG GGA TC GT CCATC		

GAATGTTT CTT AG CG GGTGG  
T T \_ \_  
GAM1422 HIVEP2 3' GGTGGGAAGAGCATTTGTAG 22120 GA AG  
TTACAAGTG CTC TTCCATC  
||||||| ||| |||||||  
GATGTTTAC GAG AGGGTGG  
\_ A \_  
GAM1422 HLCS 3' GATGGAGCTTTCAGCTTTGAA 4666 C G CTC  
TTTA AAGT GA AGTTCCATC  
||||| ||| |||||||  
AAGT TTCG CT TCGAGGTAG  
\_ A T \_  
GAM1422 KIAA0857 3' CTGGTTTGCTTGTAGA 66674 TG T  
TTTACAAG GAC CAG  
||||||| ||| |||  
AGATGTTC TTG GTC  
GT \_  
GAM1422 KLHL3 3' GGTGGCCACGGCTGCTTGTGAA 87461 TG A CAGTT  
TTTACAAG G CT CCATC  
||||||| | || |||||  
AAGTGTTC C GG GGTGG  
GT \_ CACC \_  
GAM1422 KLK3 3' GATGGGGTGTCTGTGTTATTTG 7920 G T \_  
TGG TACAAGTG AC CAG TTCCATC  
||||||| || ||| |||||||  
GTGTTTAT TG GTC GGGGTAG  
\_ T TGT  
GAM1422 MAX 3' ATGGGGTTCCATTTTGTGAA 59037 C CTCA TT  
TTTA AAGTGGA G CCAT  
||||| ||||||| | |||||  
AAGT TTTACCT T GGTA  
T \_ \_ GG  
GAM1422 NFIB 5' GGA CTGGGTTTGTGTGAA 18793 A TG  
TTTACA G GACTCAGTTC  
||||| | |||||||||  
AAGTGT T TTGGGTCAGG  
\_ GT  
GAM1422 NLGN3 3' GATGGAGCTGGAGGGTC 38599 \_  
GACT CAGTTCCATC  
||||| |||||||||  
CTGG GTCGAGGTAG  
GAG  
GAM1422 OPA3 3' GGTGGGGTGCGCTTGTA 47112 G AGTT  
TTACAAGTG ACTC CC  
||||||| |||| ||  
AATGTTTCGC TGGG GG  
G GT \_  
GAM1422 P23 3' GATGGAGCTGGACTGTGTAGA 21717 \_ GGAC  
TTTACA AGT TCAGTTCCATC  
||||||| ||| |||||||||

AGATGT TCA GGTCTGAGGTAG  
 G \_\_\_\_  
 GAM1422 PAFAH1B1 5' GGTGGAATGAATCTTACTTGT 4729 \_ C G  
 ACAAGTG GA TCA TTCCATC  
 ||||| || || |||||  
 TGTTTCAT CT AGT AAGGTGG  
 T A \_  
 GAM1422 PAFAH1B1 5' GGTTACTAGTTGGATTCATTTG 4730 CT \_\_\_\_ T\_ ATC  
 TGAA CAAGTGGA CA GT CC  
 ||||| || || ||  
 GTTTACTT GT CA GG  
 AG TGAT TT C  
 GAM1422 PGK1 3' ATGAAATTCATTTGTAG 4302 CTC A C  
 TTACAAGTGGA GTT CAT  
 ||||| || || ||  
 GATGTTTACCT TAA GTA  
 \_\_\_\_ A  
 GAM1422 PIK3CD 3' ATGGGGCTAGGACTGTGG 17240 A GGA TC  
 TTACA GT C AGTTCCAT  
 |||| || | |||||  
 GGTGT CA G TCGGGGTA  
 \_ \_\_\_\_ GA  
 GAM1422 PLCG1 3' GATGGATCCTTCCATCTTGTGG 10619 \_ CTCAGT  
 TTACAAG TGGA TCCATC  
 ||||| || || |||||  
 GGTGTTT ACCT AGGTAG  
 T TCCT\_\_  
 GAM1422 PLEK 3' GGTGGGAAGTTTTCATTTG 10634 CTCAG  
 CAAGTGGA TTCCATC  
 ||||| || || |||||  
 GTTTACTT AGGGTGG  
 TTGA\_  
 GAM1422 PRX 3' GGTGGAGCTGACCGGCTTTGGG 40537 TA \_ \_ AC  
 GA TT CAA GT GG TCAGTTCCATC  
 || ||| || || |||||  
 AG GTT CG CC AGTCGAGGTGG  
 GG T G \_  
 GAM1422 PYGO2 3' GGTGGAGCTGACAACCTTTG 63988 T AC\_  
 CAAG GG TCAGTTCCATC  
 ||| || |||||  
 GTTT CC AGTCGAGGTGG  
 \_ AAC  
 GAM1422 RAD51L1 3' GATGGGGGTGTGATTTGTGAA 56062 GGACT G  
 TTTACAAGT CA TTCCATC  
 ||||| || |||||  
 AAGTGTTA GT GGGGTAG  
 GT\_\_ G  
 GAM1422 RENT1 3' GATGGGGGTGATTGCTTCTG 11289 C TG AC\_ G  
 G TTA AAG G TCA TTCCATC  
 ||| || | || |||||

			GGT TTC C AGT GGGGTAG		
			C GT GTT _		
GAM1422	RPS6KA5	3'	GATTTGAGCTGCTTGTAAG 16467	TG A	T
			TTTACAAG G CTCAG TC		
			GAATGTTC C GAGTT AG		
			GT _ T		
GAM1422	RU2	3'	AATTGCCACTTGTAAG 33019	ACT	
			TTTACAAGTGG CAGTT		
			AAATGTTCACC GTTAA		
			_____		
GAM1422	SCG3	3'	ATTGAGTTTACTTATAAA 25096	C	
			TTTA AAGTGGACTCAGT		
			AAAT TTCATTTGAGTTA		
			A		
GAM1422	SF3B3	3'	GGTGGGACTGGGTAGGGTA 24858	AAGTGG	
			TAC ACTCAGTTCCATC		
			ATG TGGGTCAGGGTGG		
			GGA_____		
GAM1422	SIRT6	3'	TGGGGCTTTTTGTAGA 33297	TGGACTC	
			TTTACAAG AGTTCCA		
			AGATGTTT TCGGGGT		
			T_____		
GAM1422	SLC26A4	3'	TAAATTCTGGGTTTCAATTTGTGA 4788	TTCCATC	
			TTACAAGTGGACTCAG		
			AGTGTTTACTTGGGTC		
			TTAAATG		
GAM1422	TAP2	3'	GGTGGGATCATGAGTTTGCTTT 38113	_TG	__
	G		CAA G GACTCA GTTCCATC		
			GTT C TTGAGT TAGGGTGG		
			T GT AC		
GAM1422	TCF2	5'	GATTTGGGTTTTGCTTGTGAA 21378	TG _	T
			TTTACAAG GA CTCAG TC		
			AAGTGTTC TT GGGTT AG		
			GT T T		
GAM1422	TCF2	5'	GATTTGGGTTTTGCTTGTGAA 4857	TG _	T
			TTTACAAG GA CTCAG TC		
			AAGTGTTC TT GGGTT AG		
			GT T T		
GAM1422	TRH	3'	GGTGGGACTGAAGCGTTGTG 23057	_ GGAC	
			TACAA GT TCAGTTCCATC		

			GTGTT CG AGTCAGGGTGG		
			G A__		
GAM1422	UPF3B	3'	GGTGGAGCAGAGTCGCTTTGAA 43453	C	G A
			TTTA AAGTG ACTC GTTCCATC		
			AAGT TTCGC TGAG CGAGGTGG		
			_ _ A		
GAM1422	UPF3B	3'	GGTGGAGCAGAGTCGCTTTGAA 54661	C	G A
			TTTA AAGTG ACTC GTTCCATC		
			AAGT TTCGC TGAG CGAGGTGG		
			_ _ A		
GAM1422	ZNF265	3'	AGCTGTGTTTATTTGTGAA 18395	T	
			TTTACAAGTGGAC CAGTT		
			AAGTGTTTATTTG GTCGA		
			T		
GAM1422	AGTRL2	5'	GATGGGGCTTCCTACCATTTGT 17692	ACTC_	
			ACAAGTGG AGTTCATC		
			TGTTTACC TCGGGGTAG		
			ATCCT		
GAM1422	AKAP5	5'	GATGGAACATACATTTTGA 16775	C	GA CTCA
			TTTA AAGTG GTTCCATC		
			AGAT TTTAC CAAGGTAG		
			T ATA__		
GAM1422	AND-1	3'	ATGAAACTTTCTCATTTGTAAA 23016	_ CTC	C
			TTTACAAGTG GA AGTT CAT		
			AAATGTTTAC CT TCAA GTA		
			T T__ A		
GAM1422	ARPP-19	3'	TTGAGTTTTGTTTGTA 21808	TG _	
			TTTACAAG GA CTCAG		
			AAATGTTT TT GAGTT		
			GT T		
GAM1422	C12orf8	3'	GGCTGTGAGTCCCTTGTGGA 22363	T	GTT
			TTTACAAG GGA CTCA CC		
			AGGTGTTT CCTGAGT GG		
			_ GTC		
GAM1422	C20orf82	5'	GAAGTGAGTCTGCTTGCGG 84713	TA TG	G
			T CAAG GACTCA TTC		
			G GTTC CTGAGT AAG		
			GC GT G		
GAM1422	C9orf12	3'	GGTGGGATTGCCTCTTG 42793	T ACT	
			CAAG GG CAGTTCATC		

GTTC CC GTTAGGGTGG  
 T \_\_\_\_  
 GAM1422 CARD14 3' TGTGTTTACTTGTA 44108 T  
 TTTACAAGTGGAC CA  
 ||||| ||  
 AAATGTTCAATTTG GT  
 T  
 GAM1422 CBX6 3' GATGGGGCTGGGTAGTTG 26617 GTGG  
 CAA ACTCAGTTCCATC  
 || |||||  
 GTT TGGGTCGGGGTAG  
 GA\_\_  
 GAM1422 CDCA7 3' GGTGGAATCTAAGTGTTTGTA 49204 TGG C \_  
 TACAAG ACT AG TTCCATC  
 |||| || |||||  
 ATGTTT TGA TC AAGGTGG  
 G\_\_ A T  
 GAM1422 CHR3SYT 5' GATGGAAGTGAATCCATCTG 95781 AG C\_  
 CA TGGA TCAGTTCCATC  
 || |||||  
 GT ACCT AGTCAAGGTAG  
 CT TA  
 GAM1422 CHST3 3' TTGGTGGGTTTGCTTGTA 14985 TG GTT TC  
 TTTACAAG GACTCA CCA  
 ||||| |||||  
 AAGTGTTT TTGGGT GGT  
 GT \_\_\_\_ TG  
 GAM1422 CLPTM1 3' GGCCAGGGTTTGTGTTGTA 7103 TG AGTT  
 TTTACAAG GACTC CC  
 ||||| |||||  
 AGGTGTTT TTGGG GG  
 GT ACC\_  
 GAM1422 CMG1 5' GGTGGAGTTGGGTTAAC 47021 G GT  
 GT GACTCA TCCATC  
 || ||||| |||||  
 CA TTGGGT AGGTGG  
 A TG  
 GAM1422 CSAGE 5' GGTGGAGCTGCACCCCTTGTAG 86862 T ACT  
 A TTTACAAG GG CAGTTCCATC  
 ||||| || |||||  
 AGATGTTT CC GTCGAGGTGG  
 \_ CAC  
 GAM1422 CUL4A 3' AGCTGAGTTCCTTGTA 13150 T  
 TTTACAAG GGAAGTCAAGT  
 ||||| |||||  
 AAGTGTTT CTTGAGTCGA  
 \_  
 GAM1422 DCLRE1B 3' GGTGGGAAAGAGTTTGTGTTTGTG 43096 C TG AG  
 G TTA AAG GACTC TTCCATC  
 || || ||||| |||||



GGT TTT TTGAG AGGGTGG  
T GT AA  
GAM1422 DCTN4 3' GATGGGACATAGTCCTTGTAAG 67788 GT CA  
TTTACAA GGACT GTTCCATC  
||||| |||| |||||  
GAATGTT CCTGA CAGGGTAG  
\_\_ TA  
GAM1422 DKFZP566J091 3' ATGGGAACATGCTTGTAAG 48118 GACTCAG  
TTTACAAGTG TTCCAT  
||||||| ||||  
AAATGTTTCGT AGGGTA  
ACA\_\_  
GAM1422 DKFZP566N034 3' AACTGGGTCCATTTTGTAG 80138 C  
TTTA AAGTGGACTCAGTT  
||| |||||  
GAGT TTTACCTGGGTCAA  
T  
GAM1422 DKFZp761B0514 3' GATGGAGATGCCGTTTGTGG 50156 ACTCAG  
TTACAAGTGG TTCCATC  
||||||| ||||  
GGTGTTTGCC GAGGTAG  
GTA\_\_  
GAM1422 E2IG4 3' GATGGAGACATGTCATTTGTAA 90910 G TCAG  
A  
TTTACAAGTG AC TTCCATC  
||||||| || |||||  
AAATGTTTAC TG GAGGTAG  
\_ TACA  
GAM1422 EDR2 3' GATGGGGCTTTATGCTTGTAAG 60493 GACTC  
TTTACAAGTG AGTTCCATC  
||||||| |||||  
AAATGTTTCGT TCGGGGTAG  
ATT\_\_  
GAM1422 EML4 3' GGTGGAGTTGCTGTAAAGTCTTG 38811 TGG\_ T\_ GT  
TAAG  
TTACAAG AC CA TCCATC  
||||| || || |||||  
AATGTTT TG GT AGGTGG  
TGAA TC TG  
GAM1422 FAM3B 3' GATGAGTATTTGGGTTTGTG 54209 A TG TTC\_\_  
TAAA  
TACA G GACTCAG CATC  
||| | ||||| |||  
ATGT T TTGGGTT GTAG  
\_ GT TTATGA  
GAM1422 FBP17 3' GAATTCGTTGAGTTTGCTTTTA 72792 C TG \_\_\_\_ CATC  
GA  
TA AAG GACTCA GTTC  
|| ||| ||||| |||  
AT TTC TTGAGT TAAG  
T GT TGCT C  
GAM1422 FBP17 3' GATGGGGCTGTCTTTACTTGTG 72793 CT  
GA  
TTTACAAGTGGA CAGTTCCATC  
||||||| |||||

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AGGTGTTTCATTT GTCGGGGTAG
CT
GAM1422 FGF19 3' AATGGAGTTTGTGTGAAA 17584 TG A
TTTACAAG GACTC GTT
||||||| ||||| |||
AAATGTTT TTGAG TAA
GT G
GAM1422 FHR5 3' GGTGGGGCTGCCTCTGGTGAG 47902 A T ACT
TTTAC AG GG CAGTTCCATC
||||| ||| |||||
GAGTG TC CC GTCGGGGTGG
G T ____
GAM1422 FLJ00024 3' TGAGCCACTTGTAAG 63771 A
TTTACAAGTGG CTCA
||||||| |||||
GAATGTTCCACC GAGT
-
GAM1422 FLJ10193 3' GATGGGACGTTTTATTTGTG 35886 CTCA
TACAAGTGA GTTCCATC
||||||| |||||
GTGTTTATTT CAGGGTAG
TG____
GAM1422 FLJ10468 3' CTGAAGTCTGCTTGTGGA 36146 TG _
TTTACAAG GACT CAG
||||||| |||||
AGGTGTTT CTGA GTC
GT A
GAM1422 FLJ10511 3' GATGGAGTTGCTTTGTTTAT 36205 TC ____
GTGGAC AGT TCCATC
||||| ||| |||||
TATTTG TCG AGGTAG
TT TTG
GAM1422 FLJ10702 3' ACTGGTTCATTTGTAAA 36435 T
TTTACAAGTGGAC CAGT
||||||| |||||
AAATGTTTACTTG GTCA
-
GAM1422 FLJ10761 3' AAGTGATTCATTTGTAAA 36578 C G
TTTACAAGTGA TCA TT
||||||| ||||| |||
AAATGTTTACTT AGT AA
_ G
GAM1422 FLJ10781 3' TTAA AATTGAGTTTCTTGTA 36639 T CCATC
TTTACAAG GGA CTGAG CCATC
||||||| |||||
AAATGTTTCTTGAGTTAA
_ AATTC
GAM1422 FLJ11939 3' GGTGGGGTTGGGTTCCA ACTCT 45176 _ _ _ TT
G CA AGT GGA CTCAG CCATC
|| ||| ||| ||||| |||||

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		GT TCA CCT GGGTT GGTGG	
		C A T GG	
GAM1422	FLJ12660	3' GATGTTACAAGTCCATTTTG 47143	_ CA TC
		CAAG TGGACT GT CATC	
		GTTT ACCTGA CA GTAG	
		T A_ TT	
GAM1422	FLJ12668	3' GGTCTTTCCTGAATCTGTTTGT 46521	TG C TT____ ATC
	AGA	ACAAG GA TCAG CC	
		TGTTT CT AGTC GG	
		GT A CTTTCT C	
GAM1422	FLJ13441	5' GGTGGAACCTAAAATGCTGTGA 43670	A GACTC
	G	TTTACA GTG AGTTCCATC	
		GAGTGT CGT TCAAGGTGG	
		_ AAAAT	
GAM1422	FLJ13868	3' GGTGGAGCTGGGGAGGGTGGG 42731	AAGTGGA
		TTTAC CTCAGTTCCATC	
		GGGTG GGGTCGAGGTGG	
		GGAG__	
GAM1422	FLJ13910	3' GGAGAGCTGGGGTTTGTGTTGTG 42928	TG _ CATC
	AG	TTTACAAG GACTC AGTTC	
		GAGTGTTT TTGGG TCGAG	
		GT G AGG	
GAM1422	FLJ13993	3' GATGGAGCAGCCTCATTATGTG 60459	_ ACTCA
	G	TTACA AGTGG GTTCCATC	
		GGTGT TTA CT CGAGGTAG	
		A CCGA_	
GAM1422	FLJ14124	3' GGTGGAGCTGGGCTGCTTAGTG 45889	_ TG A
	G	TTAC AAG G CTCAGTTCCATC	
		GGTG TTC C GGGTCGAGGTGG	
		A GT_	
GAM1422	FLJ14326	5' GGTGGGGCTTGCTGCTTG 49817	TG ACTC
		CAAG G AGTTCCATC	
		GTTC C TCGGGGTGG	
		GT GT__	
GAM1422	FLJ14457	3' GGTGGGGCCATTTGTA 51387	A AGTT
		TACAAGTGG CTC CC	
		ATGTTTACC GGG GG	
		_ GT__	
GAM1422	FLJ20330	3' GGTGGAATTGAGTATCA 38621	_
		TGG ACTCAGTTCCATC	

				ACT TGAGTTAAGGTGG			
		A					
GAM1422	FLJ20331	5'	GGTGGGCTGCAGCTTCT	34954	T A _		
			AG GG CT CAGTTCCATC				
			TC TC GA GTCGGGGTGG				
			T _ C				
GAM1422	FLJ20436	3'	GGAGCTGTCTTTGTGAG	35170	GT TC		
			TTTACAA GGAC AGTTCC				
			GAGTGTT TCTG TCGAGG				
			_ _				
GAM1422	FLJ22055	3'	GGTGGGGTTCTGAGACACTTG	45499	GA _		
			CAAGTG CTCAG TTCCATC				
			G TTCAC GAGTC GGGGTGG				
			A_ TT				
GAM1422	FLJ22419	5'	GGGTGGAGGGGTCTGCTTGTAG	45206	TG AG		
			TTACAAG GACTC TTCCATC				
			GATGTTC CTGGG GAGGTGG				
			GT _ GG				
GAM1422	FLJ22659	5'	CATCTACTAGTCCATTTGTGAG	46260	C TCCATC		
			TTTACAAGTGGACT AGT				
			GAGTGTTTACCTGA TCA				
			_ TCTACC				
GAM1422	FLJ22693	3'	TCACTTTTGGGTTCCTAGTGG	42763	A TTCCATC		
	A		TTTAC AGTGGACTCAG				
			AGGTG TCACTTGGGTT				
			A T TCACTG				
GAM1422	FLJ23584	5'	GGTGGAGTTGAGGATGTTG	44742	G GA GT		
			CAA TG CTCA TCCATC				
			GTT GT GAGT AGGTGG				
			_ AG TG				
GAM1422	GABARAP	3'	GGTGGAGTTGGCATCTTGTA	23459	_ GAC GT		
			TTACAAG TG TCA TCCATC				
			AATGTTC AC GGT AGGTGG				
			T _ TG				
GAM1422	HBOA	3'	GATTTGAGTTCACCTGTGG	22965	A T		
			TTACA GTGGACTCAG TC				
			GGTGT CACTTGAGTT AG				
			C T				
GAM1422	HMP19	3'	CTGAGTCACCTGTAAA	87471	A G		
			TTTACA GTG ACTCAG				

AAATGT CAC TGAGTC  
 C \_  
 GAM1422 HSPC039 3' GGTGGAGCAGCACATTGTGGA 32242 G GA CA  
 TTTACAA TG CT GTTCCATC  
 ||||| || || |||||  
 AGGTGTT AC GA CGAGGTGG  
 \_ AC \_  
 GAM1422 KIAA0143 3' GATGGACTTTTAATTTGTAAG 64786 GGACTC T  
 TTTACAAGT AGT CCATC  
 ||||| || |||||  
 GAATGTTA TCA GG TAG  
 ATTT \_ \_  
 GAM1422 KIAA0298 3' TGAGTTCTGCTTGTGAA 76583 TG \_  
 TTTACAAG GA CTCA  
 ||||| || |||||  
 AAGTGTC CT GAGT  
 GT T  
 GAM1422 KIAA0431 3' GGTGGAGTCCATGTGTGAA 30895 A AGTT  
 TTTACA GTGGACTC CC  
 ||||| ||||| ||  
 AAGTGT TACCTGAG GG  
 G GT\_  
 GAM1422 KIAA0669 3' GGTGGAGCTGAGCTAGTGTA 28789 AG A  
 TACA TGG CTCAGTTCCATC  
 ||| || |||||  
 ATGT ATC GAGTCGAGGTGG  
 G\_ \_  
 GAM1422 KIAA0737 3' GGTGGGGTTGAAGAACTTGT 29145 GGAC TT  
 ACAAGT TCAG CCATC  
 ||||| ||| |||||  
 TGTTC A GTT GGTGG  
 AAGA GG  
 GAM1422 KIAA0775 5' GATGGGGCTGAGGAGTCTG 28281 AG GGA  
 CA T CTCAGTTCCATC  
 || | |||||  
 GT G GAGTCGGGGTAG  
 CT AG\_  
 GAM1422 KIAA0892 3' ATGGAGCTGGGAGCT 71008 GGA  
 AGT CTCAGTTCCAT  
 || |||||  
 TCG GGGTCGAGGTA  
 A\_  
 GAM1422 KIAA0945 3' GTGTGGCCCACTTGTGG 30215 ACTCA TC  
 TTACAAGTGG GT CAT  
 ||||| || |||  
 GGTGTTCAACC CG GTG  
 \_ GT  
 GAM1422 KIAA1143 3' GGTGGAATTCTGCTTG 68686 TG CTCA  
 CAAG GA GTTCCATC  
 ||| || |||||

		GTTC CT TAAGGTGG		
		GT ____		
GAM1422 KIAA1157	3'	GGTGGAGATCATTTGTAAG 72250	A	AGTT
		TTTACAAGTGG CTC CC		
		GAATGTTTACT GAG GG		
		A GT__		
GAM1422 KIAA1165	3'	AGTCTTCCAGCTTGTAAG 67404	_____	
		TTTACAAGT GGA CT		
		AAATGTTTCG TCTGA		
		ACCT		
GAM1422 KIAA1170	3'	GATGGTATGTCCACTTGTGG 69853	TCAGTT	
		TTACAAGTGGAC CCATC		
		GGTGTTACCTG GGTAG		
		TAT__		
GAM1422 KIAA1254	3'	TGAGTTTCTTGTAAG 70026	T	
		TTTACAAG GGA CTCA		
		GAATGTTTC TTTGAGT		
		—		
GAM1422 KIAA1274	3'	GGTGGGGCTGGCAGGATGGTGG 91368	AAGTGGAC	
A		TTTAC TCAGTTCCATC		
		AGGTG GGTCGGGGTGG		
		G TAGGAC_		
GAM1422 KIAA1416	3'	ATGGGACTAGGCTGGTG 86457	AG A TC	
		CA TGG C AGTTCCAT		
		GT GTC G TCAGGGTA		
		G_ _ GA		
GAM1422 KIAA1437	3'	GAGCCTGGGGCCGCTTGTGAG 60586	A _	
		TTTACAAGTGG CTCAG TTC		
		GAGTGTTGCGCC GGGTC GAG		
		G C		
GAM1422 KIAA1467	3'	GGTGCTGGTTTCTTGTAAG 71615	T T T	
		TTTACAAG GGAC CAGT CC		
		AAGTGTTTC TTTG GTCG GG		
		_ _ T		
GAM1422 KIAA1546	3'	GATGTACAGTTCACCTTCTGAA 67908	C CA TC	
		TTTA AAGTGGACT GT CATC		
		AAGT TTCACCTTGA CA GTAG		
		C _ T_		
GAM1422 KIAA1644	3'	CTATAGCTGGGACCACTTGTGA 85027	A CCATC	
A		TTTACAAGTGG CTCAGTT		

AAGTGTTCACC GGGTCGA  
 A TATCG  
 GAM1422 KIAA1679 3' GGTGGAGTCTGTGGTTGTGAG 70156 \_\_\_TG AGTT  
 TTTACAA G GACTC CC  
 ||||| | |||| ||  
 GAGTGTT T CTGAG GG  
 GG GT GT\_\_  
 GAM1422 KIAA1729 3' GATGGAGCTTAATTGTGTGAG 89128 AGTGGA CTC  
 TTTACA AGTTCCATC  
 ||||| |||||  
 GAGTGT TCGAGGTAG  
 GTTAAT\_\_  
 GAM1422 KIAA1755 3' ATGGAACTGACTTGTGAG 61339 TGGAC \_  
 TTTACAAG TCAGTT CCAT  
 ||||| ||||| |||||  
 GAGTGTT C AGTCAA GGTA  
 \_\_\_\_\_ A  
 GAM1422 KIAA1908 3' TGGGTTTCATTGTGGA 73406 G  
 TTTACAA TGGACTCA  
 ||||| |||||  
 AGGTGTT ACTTGGGT  
 -  
 GAM1422 KIAA1957 3' GTGGGACACACCTGTGAG 75721 A GACTCA  
 TTTACA GTG GTTCCAT  
 ||||| ||||| |||||  
 GAGTGT CAC CAGGGTG  
 C A\_\_\_\_  
 GAM1422 KOC1 3' GATTTTTTGTGATTTTGTGTA 91075 TG \_ TTCCATC  
 AG  
 TTTACAAG GA CTCAG  
 ||||| ||||| |||||  
 GAATGTTT TT GAGTT  
 GT T TTTTAG  
 GAM1422 L3MBTL 3' GGTGGCTGATCACTTGTGG 69531 AC \_  
 TTACAAGTGG TCAGTT CC  
 ||||| ||||| |||||  
 GGTGTTCACT AGTCGG GG  
 \_\_\_\_\_ T  
 GAM1422 LANO 3' GATGGTATGTGCCATTTGTAAA 36622 ACT GTT  
 TTTACAAGTGG CA CCATC  
 ||||| ||||| |||||  
 AAATGTTTACC GT GGTAG  
 GT\_ AT\_  
 GAM1422 LIG-1 3' GATGAACTGAGCTGGGACT 63896 \_\_\_ A C  
 AGT GG CTCAGTT CATC  
 ||| ||||| |||||  
 TCA TC GAGTCAA GTAG  
 GGG \_ A  
 GAM1422 LUC7A 3' GATGGAAGTAAGCCGAGTAAG 33136 AAG A C  
 TTTAC TGG CT AGTTCCATC  
 ||||| ||||| |||||

		GAATG GCC GA TCAAGGTAG		
		A__ _ A		
GAM1422	MDS025	5' GAACTGTGGGTCTGTCTGTGAA 41539	AG	__
		TTTACA TGGACT CAGTTC		
		AAGTGT GTCTGG GTCAAG		
		CT GT		
GAM1422	MGC13168	3' GGTGGAGTTACTTTTGTGAA 51213	TG_	AGTT
		TTTACAAG GACTC CC		
		AAGTGTTT TTGAG GG		
		TCA GT__		
GAM1422	MGC15548	5' GGCTGTGAGCTCCATTTGTAAA 51255	_	GTT
		TTTACAAGTGGA CTCA CC		
		AAATGTTTACCT GAGT GG		
		C GTC		
GAM1422	MGC4737	5' GGTGGAGCTGCTGCGTTCTGTG 48851	AGT	T__
	AA	TTACA GGAC CAGTTCCATC		
		AGTGT CTTG GTCGAGGTGG		
		__ CGTC		
GAM1422	MISS	3' CTGAGTCTGTTTGTAAA 58030	TG	
		TTTACAAG GACTCAG		
		AAATGTTT CTGAGTC		
		GT		
GAM1422	MRPL45	3' TGAGCCTACTTGTGAG 50376	A	
		TTTACAAGTG CTCA		
		GAGTGTTTCATC GAGT		
		C		
GAM1422	MSP	3' GATGGGGCTGGGTACACT 49417	G	
		AGTG ACTCAGTTCCATC		
		TCAC TGGGTCGGGGTAG		
		A		
GAM1422	MSTP028	3' GGTGGGGACGTGTGCTTGTGG 49223	G	TCAG
		TTACAAGTG AC TTCCATC		
		GGTGTTTCGT TG GGGGTGG		
		G CA__		
GAM1422	MYT1	3' GGTGGAGTCCTGTTGCTGTGAG 15779	A ____	AGTT
		TTTACA GT GGA CTC CC		
		GAGTGT CG CCTGAG GG		
		_ TTGT GT__		
GAM1422	NMT1	3' GGTGTGCAGGGTTTGGCTTGTG 40788	G _	A TC
	G	TTACAAGT GA CTC GT CATC		



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GGTGTTTCG TT GGG CG GTGG
G T A T_
GAM1422 NOPAR 5' GGTGGGTTTGGGTCCATTGGTG 53809 A TT
AA TTTAC AGTGGACTCAG CCATC
||||| |||||
AAGTG TTACCTGGGTT GGTGG
G TG
GAM1422 OSBPL5 3' GGTGGGGCCACTGGTGG 72690 A A AGTT
TTAC AGTGG CTC CC
||||| ||| ||
GGTG TCACC GGG GG
G _ GT_
GAM1422 PELI2 3' AGTTGAGTTAGTTTGTGAA 41179 TG GT
TTTACAAG GACTCA T
||||| ||||| |
AAGTGTTT TTGAGT A
GA TG
GAM1422 PEX11A 3' GGTGGGACAGACATTTGTA 13889 GA CA
TACAAGTG CT GTTCCATC
||||| || |||||
ATGTTTAC GA CAGGGTGG
A_ _
GAM1422 PIP5K2B 3' GATGTGAAGATCGCTTGTGAA 13073 A CAGT _
TTTACAAGTGG CT TC CATC
||||| || |||||
AAGTGTTTCGCT GA AG GTAG
A _ _ T
GAM1422 PPFIA4 3' GATGGAACCGAGGGCTTCAT 70324 _ A
GTGGA CTC GTTCCATC
||||| ||| |||||
TACTT GAG CAAGGTAG
CGG C
GAM1422 PRO0159 5' ATTCAGGCTGGGTTTATTTTGA 26110 C CCATC
A TTTA AAGTGGACTCAGTT
||||| |||||
AAGT TTTATTTGGGTCGG
_ ACTTAA
GAM1422 QKI 3' GATGGGAGTGTCTGCTTGTA 65442 ACT G
TACAAGTGG CA TTCCATC
||||| || |||||
ATGTTTCGCT GT AGGGTAG
_ G
GAM1422 RACGAP1 3' GAACTTTGGGTTTCATTTG 25196 _
CAAGTGGACTCA GTTC
||||| |||
GTTTACTTGGGT CAAG
TT
GAM1422 REM 3' GTGGGTGTCTTTTGTAAA 25811 T TCAGT
TTTACAAG GGAC TCCAT
||||| ||| |||||

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AAATGTTT TCTG GGGTG  
 T T\_\_\_\_  
 GAM1422 RPIA 3' GACTTGAGTCTGCTGGTAAA 57966 A TG T  
 TTTAC AG GACTCAG TC  
 ||||| || ||||| ||  
 AAATG TC CTGAGTT AG  
 G GT C  
 GAM1422 SARCOSIN 3' GATGGGGAAAAGTCTCTTGTA 20234 T CAG  
 G TTTACAAG GGACT TTCCATC  
 ||||| ||||| |||||  
 GAATGTTT TCTGA GGGGTAG  
 \_ AAA  
 GAM1422 SCYD1 3' GATGGGGGCCCTGCCTCCTTTGT 90931 T CT \_  
 GAG TTACAAG GGA CA GTTCCATC  
 ||||| ||||| |||||  
 AGTGTTT CCT GT CGGGGTAG  
 \_ CC CC  
 GAM1422 SDS3 3' GGTGAGAAGTCCATTTTGAG 69232 C CAGTT  
 TTTA AAGTGGACT CC  
 ||||| ||||| ||  
 GAGT TTTACCTGA GG  
 \_ AGAGT  
 GAM1422 SGKL 3' GATGGGACTGAACTTCTATTT 25143 C\_\_\_\_  
 GTG ACAAGTGGA TCAGTTCCATC  
 ||||| ||||| |||||  
 TGTTTATCT AGTCAGGGTAG  
 TCAA  
 GAM1422 SHAPY 5' GATGGAGTAATTTTGCTGTGGA 57110 A TG CTCAG  
 TTTACA G GA TTCCATC  
 ||||| ||||| |||||  
 AGGTGT C TT GAGGTAG  
 \_GT TAAT\_  
 GAM1422 SLAC2-B 3' ATGGAAC TAAGGTGTAC 30510 G C\_  
 GTG ACT AGTTCCAT  
 ||||| ||||| |||||  
 CAT TGG TCAAGGTA  
 G AA  
 GAM1422 SLC26A10 5' GTGGGACTCTGACTGTGGA 56034 AG CTCA  
 TTTACA TGGA GTTCCAT  
 ||||| ||||| |||||  
 AGGTGT GTCT CAGGGTG  
 CA \_\_\_\_  
 GAM1422 SUN1 3' GATGGACAGAGTTTGCTTGTGA 47157 TG A T  
 A TTTACAAG GACTC GT CCATC  
 ||||| ||||| |||||  
 AAGTGTTT TTGAG CA GGTAG  
 GT A \_  
 GAM1422 SYNE-2 3' GAATTCTGGTTTGTGTTGTAAA 30799 TG C\_  
 TTTACAAG GACT AGTTC  
 ||||| ||||| |||||

		AAATGTTT TTGG TTAAG	
		GT TC	
GAM1422	SYT13	3' GTGGAGCACTGTATGTGGA 93457	A TG ACTCA
		TTTACA G G GTTCCAT	
		AGGTGT T C CGAGGTG	
		A GT A____	
GAM1422	TACTILE	5' GGTGGCTGGAGTTTGCTTG 19475	TG AGTT
		CAAG GACTC CCATC	
		G TTC TTGAG GGTGG	
		GT GTC_	
GAM1422	TGIF2	3' ACTCTGCTTGGGTTTGTTGTA 41446	G GG TTCCATC
	AG	TTTACAA T ACTCAG	
		GAATGTT G TGGGT	
		G TT CGTCTCAG	
GAM1422	TNKS2	3' AACTGTTCACTTGTA 47449	TC
		TTTACAAGTGGAC AGTT	
		AAATGTTCACTTG TCAA	
		—	
GAM1422	TRIM2	3' GGCAGTGATTGGTCTGTTTG 30944	TG T ____ ATC
	GA	TACAAG GAC CAGTT CC	
		GTGTTT CTG GTTAG GG	
		GT _ TGAC	
GAM1422	TU12B1-TY	3' GATGGGGTTGACTTCATGTG 33383	A C TT
		CA GTGGA TCAG CCATC	
		GT TACTT AGTT GGTAG	
		G C GG	
GAM1422	TUBGCP3	3' GGTGGGGGGGATTGTTTTTTGT 20895	T __ AG
	AAA	TTACAAG GGAC TC TTCCATC	
		AATGTTT TTTG AG GGGGTGG	
		_ TT GG	
GAM1422	UBE3B	5' GGTGGGGCTGGGGACTTTG 76926	TGGA
		CAAG CTCAGTTCCATC	
		GTTT GGGTCGGGGTGG	
		CAG_	
GAM1422	YAP	5' ATGGAAGATCTGTTTG 36784	TG C AG
		CAAG GA TC TTCCAT	
		GTTT CT AG AAGGTA	
		GT _ _	
GAM1422	YAP	5' ATGGAAGATCTGTTTG 57461	TG C AG
		CAAG GA TC TTCCAT	

		GTTT CT AG AAGGTA		
		GT _ _		
GAM1422	YAP	5' ATGGAAGATCTGTTTG	57464	TG C AG
		CAAG GA TC TTCCAT		
		GTTT CT AG AAGGTA		
		GT _ _		
GAM1422	ZNF387	3' AATTGGGTCTTTTGTA	27993	T
		TTTACAAG GGA		
		AAATGTTT TCTGGGTAA		
		-		
GAM1422	LOC116441	3' TTGGTGT	57091	-
		TTTACAAGTGGAC TCAG		
		AAATGTTTATTTG GGT		
		T		
GAM1422	LOC122704	3' GGTGGGGTGC	74142	G AGTT
		TTACAAGTG ACTC CC		
		AATGTTTCGC TGGG GG		
		G GT_		
GAM1422	LOC123722	5' GGTGTA	74231	G C
		TTACAA TGGACTCAGTT CATC		
		GGTGTT GTCTGAGTCAA GTGG		
		- T		
GAM1422	LOC127703	3' GATGTTGGCTTTACTTGTAG	74677	CT TTC
		TTACAAGTGGA CAG CATC		
		GATGTTTCATTT GTT GTAG		
		CG _		
GAM1422	LOC128344	3' GATGGGATTTGGGCTTGCT	74736	TG A _
		AG G CTCAG TTCCATC		
		TC T GGGTT AGGGTAG		
		GT C T		
GAM1422	LOC130940	3' GATAAACTGAGTCCTGTGTAG	57138	AGT CC
	A	TTTACA GGA		
		AGATGT CCTGAGTCAA TAG		
		GT_ AA		
GAM1422	LOC134553	3' GATGGGACACATATTTGTA	75198	GACTCA
		TACAAGTG GTTCCATC		
		ATGTTTAT CAGGGTAG		
		ACA_		
GAM1422	LOC144262	5' GATGGGGCTGGGAGGGGCTGTG	76750	A GGA_
	AG	TTTACA GT CTCAGTTCCATC		

GAGTGT CG GGGTCGGGGTAG  
 \_ GGGA  
 GAM1422 LOC145447 3' GGTGGGACTGAGCTCT 77205 \_  
 GGA CTCAGTTCCATC  
 ||| |||||  
 TCT GAGTCAGGGTGG  
 C  
 GAM1422 LOC145609 5' GATGGAACTGAGTTAAGC 83377 G\_  
 GT GACTCAGTTCCATC  
 || |||||  
 CG TTGAGTCAAGGTAG  
 AA  
 GAM1422 LOC145609 5' GATGGAACTGAGTTAAGC 83377 G\_  
 GT GACTCAGTTCCATC  
 || |||||  
 CG TTGAGTCAAGGTAG  
 AA  
 GAM1422 LOC145748 3' GGTCCCTCGGGCTGCTTGTGAG 83470 TG A \_ TT  
 TTTACAAG G CTC AG CC  
 ||||| | || ||  
 GAGTGTT C GGG TC GG  
 GT \_ C CT  
 GAM1422 LOC146108 3' CTGAGTCATTTGTAA 77664 G  
 TTTACAAGTG ACTCAG  
 ||||| |||||  
 AAATGTTTAC TGAGTC  
 \_  
 GAM1422 LOC146443 5' GGTGGAGTTTTTTGTAGA 77885 T AGTT  
 TTTACAAG G GACTC CC  
 ||||| ||||| ||  
 AGATGTTT TTTGAG GG  
 \_ GT\_  
 GAM1422 LOC149464 5' GGTGGGGCTGGGTCTCCAGCTG 84432 A \_\_\_\_  
 GT AC AGT G GACTCAGTTCCATC  
 || ||| |||||  
 TG TCG TCTGGGTCGGGGTGG  
 G ACC  
 GAM1422 LOC149506 3' GGTCTTGGGGTTCATTTGTG 84476 AGTT\_  
 TACAAGTG GACTC CC  
 ||||| ||||| ||  
 GTGTTTACTTGGG GG  
 GTTCT  
 GAM1422 LOC151126 5' GATGGAATTATTTACTTTTAAA 80127 C CTC  
 TTTA AAGTGGA AGTTCCATC  
 ||| ||||| |||||  
 AAAT TTCATTT TTAAGGTAG  
 T A\_  
 GAM1422 LOC151959 5' GGTGGAGTGGCCAACGCTTGTA 85524 GAC\_ G  
 AA TTTACAAGTG TCA TTCCATC  
 ||||| ||| |||||

	AAATGTTTCGC	GGT GAGGTGG	
	AACC	_	
GAM1422 LOC152715 5'	GGTGGGATTTTCGATTTGCTGAA	80648	_ G CTC
	TTTA CAAGT GA AGTTCCATC		
	AAGT GTTTA CT TTAGGGTGG		
	C G		
GAM1422 LOC153196 5'	GGTGGCATGTCTGCTTGTG	85972	TG TCAGTT
	TACAAG GAC CCATC		
	GTGTTC CTG GGTGG		
	GT TAC		
GAM1422 LOC158235 3'	GGTGGGAGGATCACTTGTGG	86702	AC AG
	TTACAAGTGG TC TTCCATC		
	GGTGTTCACT AG AGGGTGG		
	_ G		
GAM1422 LOC158281 3'	GATGGAGCTGGACTGTGTAGA	81852	_ GGAC
	TTTACA AGT TCAGTTCCATC		
	AGATGT TCA GGTCGAGGTAG		
	G		
GAM1422 LOC158656 5'	GATGGAACAGTACAT	73036	G CA
	GTG ACT GTTCCATC		
	TAC TGA CAAGGTAG		
	A		
GAM1422 LOC160292 3'	GATGGGGCTGGGTCTTGGGGCT	87062	
	AGT GGA CT CAGTTCCATC		
	TCG TCTGGGTCGGGGTAG		
	GGGT		
GAM1422 LOC164507 5'	GGTGGGGGGGATCTGTTTG	82538	TG C AG
	CAAG GA TC TTCCATC		
	GTTT CT AG GGGGTGG		
	GT _ G		
GAM1422 LOC165254 5'	GTGGGGCGCCAGTTGTGG	87192	G ACTCA
	TTACAA TGG GTTCCAT		
	GGTGTT ACC CGGGGTG		
	G G		
GAM1422 LOC165904 3'	GATGGGGGCTCCCAGCTGCTTG	82608	TG A C _
TGGA	TACAAG G CT AGTTCC ATC		
	GTGTTC C GA TCGGGG TAG		
	GT _ CCC G		
GAM1422 LOC200609 3'	GAAATGGGTACTTGTGGA	90098	G G
	TTTACAAGTG ACTCA TTC		

	AGGTGTTTCAT TGGGT AAG		
	— A		
GAM1422 LOC200830 3'	GGTGGAGCAAAAGTTCGTTTG 90148	CA_	
	CAAGTGGACT GTTCCATC		
	GTTTGCTTGA CGAGGTGG		
	AAA		
GAM1422 LOC201294 3'	GGTGGGGCTGGGTCACT 88217 G		
	AGTG ACTCAGTTCCATC		
	TCAC TGGGTCGGGGTGG		
	—		
GAM1422 LOC201910 3'	GATGGAAAAGTTTATTTGTAAA 89101	CAG	
	TTTACAAGTGGACT TTCCATC		
	AAATGTTTATTTGA AAGGTAG		
	A_		
GAM1422 LOC202134 5'	GATGGAGTCCCTTCGCTGGTAG 90321	A	CTCAG
	TTAC AGTGGA TTCCATC		
	GATG TCGCTT GAGGTAG		
	G CCCT_		
GAM1422 LOC202454 5'	CGTGTGGCTGGTCTACTTGTGG 90350	T	TC C
	TTACAAGTGGAC CAGT CAT		
	GGTGTTTCATCTG GTCG GTG		
	— GT CT		
GAM1422 LOC202460 5'	TGGAACACTTGTGAA 89191	GA	CTCAG
	TTTACAAGTG TTCCA		
	AAGTGTTTCAC AAGGT		
	A_____		
GAM1422 LOC202934 5'	GAAGTGAGTTTCTTGTAGA 90411	T	G
	TTTACAAG GGA		
	AGATGTTC TTTGAGT AAG		
	— G		
GAM1422 LOC219673 5'	AACTGGGTCTCTTGTA	T	
	TTTACAAG GGA		
	AAATGTTC TCTGGGTCAA		
	—		
GAM1422 LOC220883 3'	GATTTGAGTTCACCTGTGG 91261	A	T
	TTACA GTGGACTCAG TC		
	GGTGT CACTTGAGTT AG		
	C T		
GAM1422 LOC221042 3'	GGTCAGAGTCCACCTGTAGA 93190	A	AGTT
	TTTACA GTGGACTC CC		

AGATGT CACCTGAG GG  
 C ACT\_  
 GAM1422 LOC221543 5' ATGGGGCCGCCATTTTGAA 93735 C ACTCA  
 TTTA AAGTGG GTTCCAT  
 |||| |||| ||||  
 AAGT TTTACC CGGGGTA  
 \_ GC\_  
 GAM1422 LOC221576 3' TGAAATCCATTTGTAAA 93706 C\_  
 TTTACAAGTGGA TCA  
 ||||| ||  
 AAATGTTTACCT AGT  
 AA  
 GAM1422 LOC255158 3' TGAGTTCACCTTAAA 96173 C  
 TTTA AAGTGGACTCA  
 ||| |||||  
 AAAT TTCACCTTGAGT  
 \_  
 GAM1422 LOC255452 3' GGTGGGTTTCGCTTG 97542 \_ GTT  
 CAAGTGGA CTCA CC  
 ||||| ||| ||  
 GTTCGCTT GGGT GG  
 T \_  
 GAM1422 LOC255855 5' ATTTGTTTGAGTTCGTTGTAGA 96225 G TTCCATC  
 TTTACAA TGGACTCAG  
 ||||| |||||  
 AGATGTT GCTTGAGTT  
 \_ TGTTTAA  
 GAM1422 LOC256021 3' GGTGGGACCCTTGTGG 96516 T A GTT  
 TTACAAG GG CTCA CC  
 ||||| || ||| ||  
 GGTGTTT CC GGGT GG  
 \_ A \_  
 GAM1422 LOC256286 3' GGTGGAGCCGCTGTGG 95202 A A AGTT  
 TTACA GTGG CTC CC  
 |||| ||| ||| ||  
 GGTGT CGCC GAG GG  
 \_ \_ GT\_  
 GAM1422 LOC257358 5' GGTGGGGCTTGATGCATGTGG 97105 A GAC \_  
 TTACA GTG TCA GTTCCATC  
 |||| ||| ||| |||||  
 GGTGT CGT AGT CGGGGTGG  
 A \_ T  
 GAM1422 LOC257407 5' ATGGCTGTCCGCTTTGAG 96984 C TCAGTT  
 TTTA AAGTGGAC CCAT  
 ||| ||||| |||  
 GAGT TTCGCCTG GGTA  
 \_ TC\_  
 GAM1422 LOC257451 3' GGTGGAGCTGACAACCTTTG 95558 T AC\_  
 CAAG GG TCAGTTCCATC  
 ||| || |||||



	GTTT CC AGTCGAGGTGG		
	_ AAC		
GAM1422 LOC257515 3'	TGAAATCCATTTGTAAA 97786	C_	
	TTTACAAGTGA TCA		
	AAATGTTTACCT AGT		
	AA		
GAM1422 LOC257572 3'	TGAAATCCATTTGTAAA 97915	C_	
	TTTACAAGTGA TCA		
	AAATGTTTACCT AGT		
	AA		
GAM1422 LOC257596 5'	ATGGGGCCGCCATTTTGAA 97928	C	ACTCA
	TTTA AAGTGG GTTCCAT		
	AAGT TTTACC CGGGGTA		
	_ GC__		
GAM1422 LOC51604 3'	GATGGAGTTTACTGTTTGTGGA 31945		TG ACTC GT
	TTTACAAG G A TCCATC		
	AGGTGTTT C T AGGTAG		
	GT AT__ TG		
GAM1422 LOC55885 3'	GATGGAGCTTTGATTTCTGAG 37817	C	G CTC
	TTTA AAGT GA AGTTCCATC		
	GAGT TTTA TT TCGAGGTAG		
	C G _		
GAM1422 LOC58525 3'	GTGGGGTTGGGGGGTGGG 78652	AAGTGGA	TT
	TTTAC CTCAG CCAT		
	GGGTG GGGTT GGTG		
	GG____ GG		
GAM1422 LOC91421 3'	GGTGAATATTGGTGTTTGT 65992	TG _ _	
	G GAC TCA GTTCCATC		
	T TTG GGT TAAGGTGG		
	GT T TA		
GAM1422 LOC92573 5'	GATGGGACTATAGTGCTTTG 69806	_ GG C_	
	CAA GT ACT AGTTCCATC		
	GTT CG TGA TCAGGGTAG		
	T _ TA		
GAM1422 LOC92876 5'	TTGAGTTCATTGTAGA 70807	G	
	TTTACAA TGGACTCAG		
	AGATGTT ACTTGAGTT		
	-		
GAM1422 LOC92997 3'	ATGGCTGTCCGCTTTGAG 71086	C	TCAGTT
	TTTA AAGTGGAC CCAT		

			GAGT TTCGCCTG GGTA		
			TC_____		
GAM1423	FSTL3	3'	ACTGTGACCTTAGCCCAG 19606	AA A	T
			CTG GT AAGGTCAC AGT		
			GAC CG TTCCAGTG TCA		
			C_ A _		
GAM1423	GSS	3'	AATACTGGTACCTTCCCCCAG 3930	AAGTA	C
			CTG AAGGT ACTAGTATT		
			GAC TTCCA TGGTCATAA		
			CCCC_ _		
GAM1423	ZNF137	3'	ACAGTACCTTTATCTCAGT 12856	AG	C A
			ACTGA TAAAGGT ACT GT		
			TGACT ATTTCCA TGA CA		
			CT _ _		
GAM1423	C11orf21	3'	TGGTGACCCCCACTGCAG 26247	A AAA	
			CTG AGT GGTCACATA		
			GAC TCA CCAGTGGT		
			G CCC		
GAM1423	COVA1	3'	ATACTATGTTTACTTCA 73259	G CACT	
			TGAAGTAAA GT AGTAT		
			ACTTCATTT TA TCATA		
			G _____		
GAM1423	E2F5	3'	ATACTTTCTTTACTTCA 8707	TCACT	
			TGAAGTAAAGG AGTAT		
			ACTTCATTTCT TCATA		
			T_____		
GAM1423	FLJ10006	3'	ATACTAGTCATACTTC 80093	AAGGTC	
			GAAGTA ACTAGTAT		
			CTTCAT TGATCATA		
			AC_____		
GAM1423	FLJ23403	3'	ACCAGTGA CTTCAG 41952	A TAA	A
			CTGA G AGGTCAGT GT		
			GACT C TTCAGTGA CA		
			_____ C		
GAM1423	GPS2	3'	CTCCTGACCCTCACTTCAGT 87158	AAA	CT
			ACTGAAGT GGTCA AG		
			TGACTTCA CCAGT TC		
			CTC CC		
GAM1423	NTT5	3'	AATACTAGTGATGTCTACCAGT 25878	AA AAG	
			ACTG GTA GTCAGTAGTATT		

		TGAC CAT TAGTGATCATAA	
		___ CTG	
GAM1423	STK17A	3' ATACTAGTAACATATCAGT 16475	AGTAAAG C
		ACTGA GT ACTAGTAT	
		TGACT CA TGATCATA	
		ATA___ A	
GAM1423	LOC139274	5' AATACTAGTGGAAGTCCA 75829	A AAAGG
		TG AGT TCACTAGTATT	
		AC TCA GGTGATCATAA	
		C AA___	
GAM1423	LOC158527	5' AGTGACCTTTGCTTCAGT 81944	
		ACTGAAGTAAAGGTCAGT	
		TGACTTCGTTTCCAGTGA	
GAM1423	LOC51064	3' TGGCAACCTTTACTTC 31921	CA
		GAAGTAAAGGT CTA	
		CTTCATTTCCA GGT	
		AC	
GAM1423	LOC92405	3' AATACTAATGCTAATACTTCA 69191	AA T C
		TGAAGTA GG CA TAGTATT	
		ACTTCAT TC GT ATCATAA	
		AA _ A	
GAM1424	CYP39A1	3' CAAAAACACACTGCTTCA 33444	AC
		TGAAGTAGT GTTTTGT	
		ACTTCGTCA CAAAAAC	
		CA	
GAM1424	CYP39A1	3' CAAAAACACACTGCTTCA 33444	AC
		TGAAGTAGT GTTTTGT	
		ACTTCGTCA CAAAAAC	
		CA	
GAM1424	FREB	3' ATAATGCACAGGGCAGTAC 51226	_ _
		GTAC GTTTT TGCATTAT	
		CATG CGGGA ACGTAATA	
		A C	
GAM1424	FREB	3' ATAATGCACAGGGCAGTAC 51226	_ _
		GTAC GTTTT TGCATTAT	
		CATG CGGGA ACGTAATA	
		A C	
GAM1424	TSLP	3' ATAATGCAGGGGAAGTACTACT 52309	GT_
		AGTAGTAC TTTTGCATTAT	

		TCATCATG GGGACGTAATA	
		AAG	
GAM1424 TSLP	3'	ATAATGCAGGGGAAGTACTACT 52309	GT_
		AGTAGTAC TTTTGCATTAT	
		TCATCATG GGGACGTAATA	
		AAG	
GAM1424 TSLP	3'	ATAATGCAGGGGAAGTACTACT 56720	GT_
		AGTAGTAC TTTTGCATTAT	
		TCATCATG GGGACGTAATA	
		AAG	
GAM1424 TSLP	3'	ATAATGCAGGGGAAGTACTACT 56720	GT_
		AGTAGTAC TTTTGCATTAT	
		TCATCATG GGGACGTAATA	
		AAG	
GAM1424 CTSO	3'	ATAATGCAATGTAACATAGTAC 7189	G C T_
	TTCA	TGAAGTA TA GTT TTGCATTAT	
		ACTTCAT AT CAA AACGTAATA	
		G A TGT	
GAM1424 CTSO	3'	ATAATGCAATGTAACATAGTAC 7189	G C T_
	TTCA	TGAAGTA TA GTT TTGCATTAT	
		ACTTCAT AT CAA AACGTAATA	
		G A TGT	
GAM1424 LOC221656	3'	TAATGCAAACCTATTTCA 92231	TACGTT
		TGAAGTAG TTTGCATTA	
		ACTTTATC AAACGTAAT	
		C_____	
GAM1424 LOC221656	3'	TAATGCAAACCTATTTCA 92231	TACGTT
		TGAAGTAG TTTGCATTA	
		ACTTTATC AAACGTAAT	
		C_____	
GAM1425 ABCB9	3'	TAGGGAGCGTGGAG 39037	GAAG A
		CTCCAT GC TCTCTG	
		GAGGTG CG AGGGAT	
		_____ -	
GAM1425 ABCC3	3'	AGTGGAGTTCGTGGGG 39140	GGCAT TG
		CTCCATGAA CTC TT	
		GGGGTGCTT GAG GA	
		_____ GT	
GAM1425 ABCC3	3'	AGTGGAGTTCGTGGGG 39152	GGCAT TG
		CTCCATGAA CTC TT	

GGGGTGCTT GAG GA  
\_\_\_\_ GT  
GAM1425 ADRA2A 5' GGACGGGGGTGCCTTCATGCGG 5454 C  
CT CATGAAGGCATCTCTGTTT  
|| |||||  
GG GTACTTCCGTGGGGGCAGG  
C  
GAM1425 AKAP1 3' AAGCAGGGGCGCTATGTGAGT 57705 \_ GAA AT  
ACTC CAT GGC CTCTGTTT  
|||| ||| |||||  
TGAG GTA TCG GGGACGAA  
T \_\_\_\_ CG  
GAM1425 ALDH3B1 3' GGACAGGGGTGGACCTGAGT 91530 CATGA \_  
ACTC AGG CATCTCTGTTT  
|||| ||| |||||  
TGAG TCC GTGGGGACAGG  
\_\_\_\_ AG  
GAM1425 ALDOC 3' GAGCAGAGATGCCTTCACCTGG 17701 \_  
CCA TGAAGGCATCTCTGTTT  
||| |||||  
GGT ACTTCCGTAGAGACGAG  
CC  
GAM1425 AMELX 3' TACTTCAGATGCTTTCAGGAGT 6693 A CTGTTT  
ACTCC TGAAGGCATCT  
|||| |||||  
TGAGG ACTTTCGTAGA  
\_\_\_\_ CTTCATA  
GAM1425 ANKRD3 3' GGATAGGGATAGTGTGTTTGGGG 40199 T G \_  
T ACTCCA GAA GC ATCTCTGTTT  
|||| ||| |||||  
TGGGGT TTT TG TAGGGATAGG  
\_\_\_\_ G A  
GAM1425 ANXA6 3' GGGCAGGGGTGGGGGGAG 14449 ATGAAGG  
CTCC CATCTCTGTTT  
|||| |||||  
GAGG GTGGGGACGGG  
GGG\_\_\_\_  
GAM1425 APPBP2 3' AAGTAGGGATGTTTAGGA 21065 ATGA  
TCC AGGCATCTCTGTTT  
||| |||||  
AGG TTTGTAGGGATGAA  
A\_\_\_\_  
GAM1425 AQP6 5' AGATGGGGGTGGAGTGGAG 53908 GAAGG  
CTCCAT CATCTCTGTTT  
|||| |||||  
GAGGTG GTGGGGGTAGA  
AG\_\_\_\_  
GAM1425 AQP6 5' GAGTGGAGGACACAGGGAGT 53926 A AAGGCA TG  
ACTCC TG TCTC TTT  
|||| ||| |||

			TGAGG AC	GGAG GAG		
			G ACA__	GT		
GAM1425	ARSB	3'	GGTGGGGGTGGCTGGGT	3500	CATGA G	TG
			ACTC AG CATCTC TT			
			TGGG TC GTGGGG GG			
			__ G GT			
GAM1425	ATP1B1	3'	GGGTGGGGGTTTGTTCATGGGG	8041	AG C	TG
			CTCCATGA G ATCTC TTT			
			GGGGTACT T TGGGG GGG			
			GT_ GT			
GAM1425	ATRX	5'	AGATGGGCTTCATGGG	56246	G_	
			TCCATGAAG CATCT			
			GGGTACTTC GTAGA			
			GG			
GAM1425	B4GALT5	3'	GCGGGGGGCGGGGGT	16504	ATGAAG A	
			ACTCC GC TCTCTGT			
			TGGGG CG GGGGGCG			
			G__ _			
GAM1425	B4GALT5	3'	GGGTGGGGATTGAGGGTGGAG	16510	GAAGGC	TG
			CTCCAT ATCTC TTT			
			GAGGTG TAGGG GGG			
			GGAGT_ GT			
GAM1425	BACE	3'	GACAGAAGCTTGTGGGGT	23980	GA	ATC
			ACTCCAT AGGC TCTGTT			
			TGGGGTG TTCG AGACAG			
			_ A_			
GAM1425	BACE	3'	GACAGAAGCTTGTGGGGT	57290	GA	ATC
			ACTCCAT AGGC TCTGTT			
			TGGGGTG TTCG AGACAG			
			_ A_			
GAM1425	BAPX1	3'	GGGTGGGGGTGCCCCGATTCGGG	6812	A _	TG
			CC TGAA GGCATCTC TTT			
			GG GCTT CCGTGGGG GGG			
			_ AGC GT			
GAM1425	BASP1	3'	AAATAGTATTTTTGTGGGG	75964	TG	CATCT
			CTCCA AAGG CTGTTT			
			GGGGT TTTT GATAAA			
			GT AT__			
GAM1425	BAT2	3'	GGGCGGGGAGGGGTTGTGGGG	16158	TG	AGGCA
			CTCCA A TCTCTGTTT			

		GGGGT T AGGGGCGGG		
		GT GGGG_		
GAM1425 BAT2	3'	GGGCGGGGAGGGGTTGTGGGG 54776	TG AGGCA	
		CTCCA A TCTCTGTTT		
		GGGGT T AGGGGCGGG		
		GT GGGG_		
GAM1425 BAZ2A	3'	GGGTGGGGTGCCAGGTGAGGT 25607	TC GAA TG	
		AC CAT GGCATCTC TTT		
		TG GTG CCGTGGGG GGG		
		GA GA_ GT		
GAM1425 BCRP2	3'	AAATAGAGCTAGTCATGGA 62402	AGGCAT	
		TCCATGA CTCTGTTT		
		AGGTACT GAGATAAA		
		GATC_		
GAM1425 BMPR1B	3'	AGGCGGAGAAACCGTTGGG 6832	TGAA CA	
		TCCA GG TCTCTGTTT		
		GGGT CC AGAGGCGGA		
		TG_ AA		
GAM1425 C1orf1	3'	AAGCAGAGATTCCAGTGAGT 6856	C GAA C	
		ACTC AT GG ATCTCTGTTT		
		TGAG TG CC TAGAGACGAA		
		_ A_ T		
GAM1425 C5R1	3'	AACAGAAAGTCCATGGAGT 8197	AA ATC	
		ACTCCATG GGC TCTGTT		
		TGAGGTAC CTG AGACAA		
		_ A_		
GAM1425 C5R1	3'	AACAGAAAGTCCATGGAGT 8197	AA ATC	
		ACTCCATG GGC TCTGTT		
		TGAGGTAC CTG AGACAA		
		_ A_		
GAM1425 CA11	5'	GAACGGAGAGGAGGTGTGGG 6872	AAGGCA	
		TCCATG TCTCTGTTT		
		GGGTGT AGAGGCAAG		
		GGAGG_		
GAM1425 CACNA1S	3'	GGGTGGGGAAGTTGCTGGGGT 3567	TGAA A TG	
		ACTCCA GGC TCTC TTT		
		TGGGGT TTG AGGG GGG		
		CG_ A GT		
GAM1425 CACNG3	5'	AGCGGGGGTGTCGGGAG 21539	ATGAA	
		CTCC GGCATCTCTGTT		

			GAGG CTGTGGGGGCGA		
			G_____		
GAM1425 CALM3	3'	GGGCAGGGGTGCCAAGAGAG 17744	CATGAA		
		CTC GGCATCTCTGTTT			
		GAG CCGTGGGGACGGG			
		AGAA_____			
GAM1425 CARD4	3'	TTGGATGCTTTCCTGTTTCATGG 20334	_____ CTGTTT		
GGT		CCATGAA GGCATCT			
		GGTACTT TCGTAGG			
		GTCCTT TTT			
GAM1425 CASQ2	3'	AAATAGAGCAATACTTTTTGTG 6934	___ GCAT_		
GA		TCCAT GAAG CTCTGTTT			
		AGGTG TTTC GAGATAAA			
		TT ATAAC			
GAM1425 CCKBR	3'	GAGTAGAGGGGCCGTGGGG 5587	GAA AT		
		CTCCAT GGC CTCTGTTT			
		GGGGTG CCG GAGATGAG			
		___ GG			
GAM1425 CCNA1	5'	GAGCGGGGCCCGCTTTGGGGT 14035	TGA AT_		
		ACTCCA AGGC CTCTGTTT			
		TGGGGT TTCG GGGGCGAG			
		___ CCC			
GAM1425 CD1A	5'	GAATAGAGATATCGTGGGGT 71182	AGGC		
		ACTCCATGA ATCTCTGTTT			
		TGGGGTGCT TAGAGATAAG			
		A_____			
GAM1425 CD1D	5'	AAATAGAGATGAGTTGGAG 79460	TGAAGG		
		CTCCA CATCTCTGTTT			
		GAGGT GTAGAGATAAA			
		TGA_____			
GAM1425 CDH19	3'	AACAGAGATGTGGGGAG 40952	ATGAAG		
		CTCC GCATCTCTGTT			
		GAGG TGTAGAGACAA			
		GG_____			
GAM1425 CDH23	3'	AGACAGGGAAGCCTTGTTGGGTG 42097	_ G A		
T		AC TCCAT AAGGC TCTCTGTTT			
		TG GGGTG TTCCG AGGGACAGA			
		T _ A			
GAM1425 CDKN2A	5'	GAGTGGGGGTGGGGTGGGG 54224	GAAGG TG		
		CTCCAT CATCTC TTT			



			GGGGTG GTGGGG GAG		
			GG___ GT		
GAM1425	CDKN2A	5'	GGGTGGGGGTGAAGGTGGGG 54227	GAAGG	TG
			CTCCAT CATCTC TTT		
			GGGGTG GTGGGG GGG		
			GAA___ GT		
GAM1425	CHI3L1	3'	AGGTAGGGATGGGGCTGTGGGG 7045	GAAGG	TT
			CTCCAT CATCTCTG T		
			GGGGTG GTAGGGAT A		
			TCGGG GG		
GAM1425	CLIC3	5'	GACGGGGAGAGCGTGGG 16242	AAGGCA	
			TCCATG TCTCTGTT		
			GGGTGC AGGGGCAG		
			GAG___		
GAM1425	COL11A1	3'	AAATACCGATGCCTTTGTGGGG 8493	TG	TC
			CTCCA AAGGCATC TGTTT		
			GGGGT TTCCGTAG ATAAA		
			GT CC		
GAM1425	COL11A1	3'	AAATACCGATGCCTTTGTGGGG 54652	TG	TC
			CTCCA AAGGCATC TGTTT		
			GGGGT TTCCGTAG ATAAA		
			GT CC		
GAM1425	COL19A1	3'	AAACAGAAGAATAATTCATGGA 8505	GGCA	_
			TCCATGAA TCT CTGTTT		
			AGGTACTT AGA GACAAA		
			AATA A		
GAM1425	COL1A2	3'	AGACAGAGATGAACTGAG 3611	CATGAAGG	
			CTC CATCTCTGTTT		
			GAG GTAGAGACAGA		
			TCAA___		
GAM1425	COL4A4	5'	GGTGGGGCGTTTGGGGGT 3627	A G AT T	
			ACTCC TGAA GC C CT		
			TGGGG GTTT CG G GG		
			_ G GG T		
GAM1425	COL9A3	3'	GAGCGGGGGTGTGGCAGGCGGG 8491	CA_ AAG	
	T		ACTC TG GCATCTCTGTTT		
			TGGG AC TGTGGGGGCGAG		
			CGG GG_		
GAM1425	CRB1	5'	GGACAGAGATGGCACCTGGGGG 23866	ATGAAG	_
	T		ACTCC GC ATCTCTGTTT		

		TGGGG	CG TAGAGACAGG		
		GTCCA_	G		
GAM1425	CRHR2	3'	GACAGGGATGAGTGGGG	8542	GAAGG
			CTCCAT CATCTCTGTT		
			GGGGTG GTAGGGACAG		
			A_____		
GAM1425	CRY2	5'	AGCGGGGGTGGCTGGAG	72203	TGAA G
			CTCCA G CATCTCTGTT		
			GAGGT C GTGGGGGCGA		
			_____G		
GAM1425	CSNK2A1	3'	AGCAGAGGTGGGGGAGT	8554	ATGAAGG
			ACTCC CATCTCTGTT		
			TGAGG GTGGAGACGA		
			GG_____		
GAM1425	CYP4F3	3'	AGGCGGAGGTTGCGGTGGG	6106	GAAG _
			TCCAT GCA TCTCTGTTT		
			GGGTG CGT GGAGGCGGA		
			G__ T		
GAM1425	DDAH2	5'	GAGTGGGGGTGGCCGCTGGAG	25663	TGAA _ TG
			CTCCA GGC ATCTC TTT		
			GAGGT CCG TGGGG GAG		
			CG__ G GT		
GAM1425	DGKB	3'	AGGTGTAATTTTTCATGGA	92531	_____
			TCCATGAAG GCATCT		
			AGGTACTTT TGTGGA		
			TTAA		
GAM1425	DHCR24	3'	GGGTGGAGATGGGTGTGGCAGT	28632	_ AAGG TG
			ACTCCATG CATCTC TTT		
			TGA GGTGT GTAGAG GGG		
			C GG__ GT		
GAM1425	DNM2	3'	GGCAGGGGGCGCTGGGGT	17057	TGAAG A_
			ACTCCA GC TCTCTGTT		
			TGGGGT CG GGGGACGG		
			_____CG		
GAM1425	DPP4	3'	AAATAGGAATTGTTTTATGGA	8655	TC_
	G		CTCCATGAAGGCA TCTGTTT		
			GAGGTATTTTGT GGATAAA		
			TAA		
GAM1425	DPYSL2	3'	GAGCAGCCAGTTCATGGGGT	7298	_ AT
			ACTCCATGAA GGC CTC		

			TGGGGTACTT CCG GAG		
			GA AC		
GAM1425 DSP	3'	AGGTGTCTTTATGAAGT	15338	C	
		ACT CATGAAGGCATCT			
		TGA GTATTTCTGTGGA			
		A			
GAM1425 DVL1	3'	GGGCTTGCCTTCGTGGGG	59337	T_	
		CTCCATGAAGGCA CTC			
		GGGGTGCTTCCGT GGG			
		TC			
GAM1425 DVL3	3'	AAGCGGAGGTTGCAGTGAGT	15364	CATGAAG _	
		ACTC GCA TCTCTGTTT			
		TGAG CGT GGAGGCGAA			
		TGA___ T			
GAM1425 EDN3	3'	GAATATTTGCTTTCATGAGT	3674	C	TCTC
		ACTC ATGAAGGCA TGTTT			
		TGAG TACTTTCGT ATAAG			
		_ TT__			
GAM1425 EFNA4	3'	AGACGGACTCTTCATGAGGT	17834	TC	CATC
		AC CATGAAGG TCTGTTT			
		TG GTACTTCT AGGCAGA			
		GA C__			
GAM1425 EGFL4	3'	GGCAGAGGCCCTGGGGT	61815	TGAA	AT
		ACTCCA GGC CTCTGTT			
		TGGGGT CCG GAGACGG			
		C__ _			
GAM1425 EGFL5	3'	GAACAGAGGAAACATGGG	86620	AAGGCA	
		TCCATG TCTCTGTTT			
		GGGTAC GGAGACAAG			
		AAA__			
GAM1425 EGLN1	5'	AAATAGAGGCTGTATGGTGT	41892	T	AA AT
		AC CCATG GGC CTCTGTTT			
		TG GGTAT TCG GAGATAAA			
		T G_ _			
GAM1425 EGLN2	3'	GGACAGGGGGCAGCCGTGGAG	34101	AAG	A
		CTCCATG GC TCTCTGTTT			
		GAGGTGC CG GGGGACAGG			
		CGA _			
GAM1425 EGLN2	3'	GGACAGGGGGCAGCCGTGGAG	53854	AAG	A
		CTCCATG GC TCTCTGTTT			

		GAGGTGC CG GGGGACAGG	
		CGA _	
GAM1425 EGLN2	3'	GGACAGGGGGCAGCCGTGGAG 54930	AAG A
		CTCCATG GC TCTCTGTTT	
		GAGGTGC CG GGGGACAGG	
		CGA _	
GAM1425 EN2	5'	GAGCGGGGCGGCTCGTGGTGT 7463	T AG AT
		AC CCATGA GC CTCTGTTT	
		TG GGTGCT CG GGGGCGAG	
		T _ GC	
GAM1425 ENC1	3'	AGTAGAGAAACCGTGGAG 13278	GAA CA TT
		CTCCAT GG TCTCTG T	
		GAGGTG CC AGAGAT A	
		_ AA GG	
GAM1425 EPHB3	3'	AGGCAGGGGCAGGCTGAGGAGT 15454	ATGAA A_
		ACTCC GGC TCTCTGTTT	
		TGAGG TCG GGGGACGGA	
		AG_ GAC	
GAM1425 EXTL3	5'	AAACAGAGATCGTTTTGTGGA 7524	G _
		TCCAT AAGGC ATCTCTGTTT	
		AGGTG TTTTG TAGAGACAAA	
		_ C	
GAM1425 FBP2	3'	AAACAGAGATGGTAGCTATGAG 13842	CATGAAGG
T		ACTC CATCTCTGTTT	
		TGAG GTAGAGACAAA	
		TATCGATG	
GAM1425 FBP2	3'	AAACAGAGATGGTAGCTATGAG 13842	CATGAAGG
T		ACTC CATCTCTGTTT	
		TGAG GTAGAGACAAA	
		TATCGATG	
GAM1425 FBXL11	3'	GGACAGAGGAACCTGGGGAGT 24574	ATGA CA
		ACTCC AGG TCTCTGTTT	
		TGAGG TCC GGAGACAGG	
		GG_ AA	
GAM1425 FDX1	3'	AAATAGGAATATTTTCATGGA 60342	C CT
		TCCATGAAGG AT CTGTTT	
		AGGTACTTTT TA GATAAA	
		A AG	
GAM1425 FEZ1	5'	GGATGGGGGTGTCCGGCTGAG 42576	CATGAA
		CTC GGCATCTCTGTTT	

		GAG CTGTGGGGGTAGG	
		TCGGC_	
GAM1425 FEZ1	5'	GGATGGGGGTGTCCGGCTGAG 17530	CATGAA
		CTC GGCATCTCTGTTT	
		GAG CTGTGGGGGTAGG	
		TCGGC_	
GAM1425 FGF2	3'	AAACAAAATTTCTTCATGGA 8863	C CTC
		TCCATGAAGG AT TGT TT	
		AGGTACTTCT TA ACAA	
		T AA_	
GAM1425 FLNB	3'	AGGCAGAGATTGTGCCCATGGG 62172	AA ____
G		CTCCATG GGCA TCTCTGTTT	
		GGGGTAC CCGT AGAGACGGA	
		__ GTT	
GAM1425 FPGS	3'	GGACAGAGGGTGGCTGGAGT 17088	TGAA G _
		ACTCCA G CATC TCTGTTT	
		TGAGGT C GTGG AGACAGG	
		__ G G	
GAM1425 FRAP1	3'	AAACAGAAATACTGTCATGGAG 17094	A C C
		CTCCATGA GG AT TCTGTTT	
		GAGGTACT TC TA AGACAAA	
		G A A	
GAM1425 FUT9	3'	AGGTGAAATTATTCATGGAGT 67844	GG____
		ACTCCATGAA CATCT	
		TGAGGTACTT GTGGA	
		ATTAAA	
GAM1425 GAA	3'	GGTGGAGGTGTGGGGT 3844	ATGAAG TG
		ACTCC GCATCTC TT	
		TGGGG TGTGGAG GG	
		__ GT	
GAM1425 GJB1	3'	GCAGAGGGCAGGGGT 59971	ATGAAG A
		ACTCC GC TCTCTGT	
		TGGGG CG GGAGACG	
		A____ _	
GAM1425 GLUL	3'	AGATGGGGACAGGGCTGGAGT 9039	TGAAG A____
		ACTCCA GC TCTCTGTTT	
		TGAGGT CG AGGGGTAGA	
		__ GGAC	
GAM1425 GNA11	3'	GGGCAGGGGTGCCTGCCCCAG 76104	CCATGA
		CT AGGCATCTCTGTTT	

			GA	TCCGTGGGGACGGG		
			CCCCG_			
GAM1425	GNAO1	3'	GGATAGCCTTTGTAGGGGT	90968	_TG	_
			ACTCC A AAGGC ATCT			
			I			
			TGGGG T TTCCG TAGG			
			A GT A			
GAM1425	GNAQ	5'	GAGCAGGGGTGCCGGCGGG	9062	A AA	
			CC TG GGCATCTCTGTTT			
			GG GC CCGTGGGGACGAG			
			_ GG			
GAM1425	GOSR2	3'	GGACATCTTTTCGTGGTGT	53963	T	C C
			AC CCATGAAGG AT TCT			
			TG GGTGCTTTT TA AGG			
			T C C			
GAM1425	GPR81	3'	GGACAGAATGTGCATGGAGT	50764	AAG	C
			ACTCCATG GCAT TCTGTTT			
			TGAGGTAC TGTA AGACAGG			
			G__ _			
GAM1425	GPRK7	3'	GAACAGAGAATGGAACCTTTGTG	57628	T TG	G__ _
	GTGT		CCA AAG CAT CTCTGTTT			
			GGT TTC GTA GAGACAAG			
			T GT AAG A			
GAM1425	GRF2	3'	GAGTGGAGGCCTCCTGGGGT	17995	T A	AT TG
			ACTCCA GA GGC CTC TTT			
			TGGGGT CT CCG GAG GAG			
			C _ _ GT			
GAM1425	GRLF1	3'	GGGTGGAGGGAAAGCATGGTGG	78561	_	AAGGCA TG
	T		ACT CCATG TCTC TTT			
			TGG GGTAC GGAG GGG			
			T GAAAG_ GT			
GAM1425	GUCY1A3	5'	AGGCGGAGGACACCTGTGGGG	63487	GA	CA_
			CTCCAT AGG TCTCTGTTT			
			GGGGTG TCC GGAGGCGGA			
			_ ACA			
GAM1425	GUCY1B2	3'	AGATGGGGACTCCATGGAG	14683	A	GCA
			CTCCATG AG TCTCTGTTT			
			GAGGTAC TC AGGGGTAGA			
			C _			
GAM1425	HCFC1	5'	AGATGGCGGCCTCCATGGAGT	70987	A	ATCT
			ACTCCATG AGGC CTGTTT			

TGAGGTAC TCCG GGTAGA  
 C GC\_\_  
 GAM1425 HD 3' AAACAGAGCCATTCCCTTGA 9178 T\_\_ \_ ATC  
 TCCA GAA GGC TCTGTTT  
 |||| ||| ||| |||||  
 AGGT CTT CCG AGACAAA  
 TCC A \_\_\_\_  
 GAM1425 HDAC4 5' GGC GGGGGCGCGGGGGT 20114 ATGAAG AT  
 ACTCC GC CTCTGTT  
 |||| | |||||  
 TGGGG CG GGGGCGG  
 G\_\_\_\_ CG  
 GAM1425 HDGF 5' GAGTGGGGACCGGGCGGGGGGT 15681 A AA\_ CA TG  
 ACTCC TG GG TCTC TTT  
 |||| | | ||| |||  
 TGGGG GC CC AGGG GAG  
 G GGG \_ GT  
 GAM1425 HELLS 3' AGTAGGCTTTTCATGGGG 36034 \_ AT\_  
 CTCCATGAAG GC CT  
 ||||| || ||  
 GGGGTACTTT CG GA  
 T GAT  
 GAM1425 HLF 3' AGATGGGGGTGTATTGGA 9214 TGAAG  
 TCCA GCATCTCTGTTT  
 ||| |||||  
 AGGT TGTGGGGGTAGA  
 TA\_\_\_\_  
 GAM1425 HOXB13 3' AAGTGGGGGTGTCCTGGGGAG 21012 ATGA \_ TG  
 CTCC AGG CATCTC TTT  
 ||| ||| |||| |||  
 GAGG TCC GTGGGG GAA  
 GG\_ T GT  
 GAM1425 HSD17B3 3' GATGGAGGGGGCTGGGGT 3974 TGAAG A\_  
 ACTCCA GC TCTCTGTT  
 |||| | |||||  
 TGGGGT CG GGAGGTAG  
 \_\_\_\_ GG  
 GAM1425 ID3 3' GGGTGGGGGCAGCGTGGGG 79047 AAG AT TG  
 CTCCATG GC CTC TTT  
 |||| | ||| |||  
 GGGGTGC CG GGG GGG  
 GA\_ \_ GT  
 GAM1425 IDH1 5' AGCGGAGGCACTGGGAGT 61431 ATGAAG AT  
 ACTCC GC CTCTGTT  
 |||| | |||||  
 TGAGG CG GAGGCGA  
 GTCA\_\_ \_\_  
 GAM1425 IGHMBP2 3' GAGCGGAGGGGCCTATGGGG 9304 GA AT  
 CTCCAT AGGC CTCTGTTT  
 |||| ||| |||||

GGGGTA TCCG GAGGCGAG  
— GG  
GAM1425 IGHMBP2 3' GGCAGGGAGCAGGGAGT 9305 ATGAAG A  
ACTCC GC TCTCTGTT  
|||| | |||||  
TGAGG CG AGGGACGG  
GA— —  
GAM1425 IL13RA1 3' AAACAGAGATGAGGTGG 7772 GAAGG  
CCAT CATCTCTGTTT  
||| |||||  
GGTG GTAGAGACAAA  
GA—  
GAM1425 IL17E 5' GAGCAGAGATGCTGCTGAGGGT 42964 \_ TGAA  
ACTC CA GGCATCTCTGTTT  
||| | |||||  
TGGG GT TCGTAGAGACGAG  
A CG—  
GAM1425 IL20RA 3' AGATGGATTCTGGGGT 27045 T GG  
ACTCCA GAA CATCT  
|||| | |||  
TGGGGT CTT GTAGA  
— AG  
GAM1425 IMPG1 3' AGACAGGCATATTCATGGG 7795 GGCATC  
TCCATGAA TCTGTTT  
|||| | |||||  
GGGTACTT GGACAGA  
ATAC—  
GAM1425 JUN 5' GAGTGGAGGTGCGCGGAGT 9479 ATGAAG TG  
ACTCC GCATCTC TTT  
|||| | ||||| |  
TGAGG CGTGGAG GAG  
CG— GT  
GAM1425 JUP 3' AGATGGGGAGGAGATATGGAGT 9485 AAGGCA  
ACTCCATG TCTCTGTTT  
|||| | |||||  
TGAGGTAT AGGGGTAGA  
AGAGG—  
GAM1425 KIAA0857 3' AGTCATGCTTTTGGGGGT 66672 A CT  
ACTCC TGAAGGCAT CT  
|||| ||||| ||  
TGGGG GTTTTCGTA GA  
— CT  
GAM1425 KIF3B 3' AGGCGGAGGTTGCAGTGAGT 16607 CATGAAG \_  
ACTC GCA TCTCTGTTT  
||| | |||||  
TGAG CGT GGAGGCGGA  
TGA— T  
GAM1425 KLK3 3' GGATGGGGTGTCTGTGTTATTT 7921 TG \_\_\_\_\_ TGTTT  
GTGGGGT A AGGCATCTC  
| |||||



T TCTGTGGGG  
 GT TATTGTG TAGG T  
 GAM1425 KRTHA5 5' GGGCAGAGATATAAATCTGGGG 9647 T AGGC\_  
 T ACTCCA GA ATCTCTGTTT  
 ||||| || |||||  
 TGGGGT CT TAGAGACGGG  
 \_ AAATA  
 GAM1425 LAMA4 3' GGTGGAAGCTTTCATCGAGT 9670 C A \_  
 ACTC ATGAAGGC TCT CT  
 ||| ||||| || ||  
 TGAG TACTTTCG AGG GG  
 C A T  
 GAM1425 LEP 3' GAGTGGTCTTTCCTATCATGGA 4050 \_ CATCT TG  
 GT ACTCCATGA AGG C TTT  
 ||||| || | |||  
 TGAGGTACT TCC G GAG  
 A TTTCT GT  
 GAM1425 LETM1 3' GACAGAGGTGTCTGCCAT 24620 A\_  
 ATG AGGCATCTCTGTT  
 ||| |||||  
 TAC TCTGTGGAGACAG  
 CG  
 GAM1425 LIF 3' AGACATAGTGTGTGGGGT 9725 GAAG T C  
 ACTCCAT GCA CT TGTTT  
 ||||| || || |||||  
 TGGGGT TGT GA ACAGA  
 \_ \_ T  
 GAM1425 LIG3 5' AAACAGATCTGCTTCATGGA 9752 G TC  
 TCCATGAAG CA TCTGTTT  
 ||||| || |||||  
 AGGTACTTC GT AGACAAA  
 \_ CT  
 GAM1425 LIG3 5' AAACAGATCTGCTTCATGGA 25664 G TC  
 TCCATGAAG CA TCTGTTT  
 ||||| || |||||  
 AGGTACTTC GT AGACAAA  
 \_ CT  
 GAM1425 LOH11CR2A 3' GACAGAGACTGCAGGGGT 27540 ATGAAG \_  
 ACTCC GCA TCTCTGTT  
 |||| || |||||  
 TGGGG CGT AGAGACAG  
 A\_ C  
 GAM1425 LPL 3' GGGTGGAGAGGTTTCTGGGGT 4089 T GGCA TG  
 ACTCCA GAA TCTC TTT  
 ||||| || ||| |||  
 TGGGGT CTT AGAG GGG  
 C GG\_ GT  
 GAM1425 LZTR1 5' GAGCAGCATGTTTGTCTTTGGG 22240 A TCT\_  
 GGT CTCC TGAAGGCA CTGTTT  
 ||| ||||| |||||

			GGGG GTTTCTGT	GACGAG	
			— TTGTAC		
GAM1425	MADH7	3'	AAGCGGGGATGTCCCTGGGAG	19741	ATGAA
			CTCC GGCATCTCTGTTT		
			GAGG CTGTAGGGGCGAA		
			GTCC_		
GAM1425	MAP3K10	3'	GACAGGGGCATCATGGGG	67971	AG ATC
			CTCCATGA GC TCTGTT		
			GGGGTACT CG GGACAG		
			A_ —		
GAM1425	MAPK3	3'	GGGCAGAGGTGGAGGGTGGGG	73385	GAAGG
			CTCCAT CATCTCTGTTT		
			GGGGTG GTGGAGACGGG		
			GGAG_		
GAM1425	MEN1	5'	GATGGGGATTGTGGGG	93372	TG AGGCA
			CTCCA A TCTCTGTT		
			GGGGT T AGGGGTAG		
			GT —		
GAM1425	MGA	3'	AAGTAGGGATGCTTTTA	62802	
			TGAAGGCATCTCTGTTT		
			ATTTTCGTAGGGATGAA		
GAM1425	MLC1	3'	AGATACCTTCATGGTGT	57584	T C
			AC CCATGAAGG ATCT		
			TG GGTACTTCC TAGA		
			T A		
GAM1425	MLC1	3'	AGATACCTTCATGGTGT	57585	T C
			AC CCATGAAGG ATCT		
			TG GGTACTTCC TAGA		
			T A		
GAM1425	MLC1	3'	AGATACCTTCATGGTGT	30773	T C
			AC CCATGAAGG ATCT		
			TG GGTACTTCC TAGA		
			T A		
GAM1425	MLC1	3'	AGATACCTTCATGGTGT	30774	T C
			AC CCATGAAGG ATCT		
			TG GGTACTTCC TAGA		
			T A		
GAM1425	MMP19	3'	AGGCGGAGGTGGGGGTGGGG	10080	GAAGG
			CTCCAT CATCTCTGTTT		

		GGGGTG GTGGAGGCGGA		
		GGG__		
GAM1425	MMP19	3' AGGCGGAGGTGGGGGTGGGG	42967	GAAGG
		CTCCAT CATCTCTGTTT		
		GGGGTG GTGGAGGCGGA		
		GGG__		
GAM1425	MN1	3' GAGCAGAGATGAGTGGTGG	10092	GAAGG
		CCAT CATCTCTGTTT		
		GGTG GTAGAGACGAG		
		GTGA_		
GAM1425	MPP2	3' GGTGGGCATTTCATGGGGT	59827	G A T
		ACTCCATGAA GC TC CT		
		TGGGGTACTT CG GG GG		
		A _ T		
GAM1425	MPZ	3' GGCGGGGGATCGGGGGT	4998	A AGGCA
		ACTCC TGA TCTCTGTT		
		TGGGG GCT GGGGGCGG		
		_ A _ _		
GAM1425	MTR	3' AAACAAGCAGGTGTTTATATGG	4207	A _ _
	AGT	ACTCCATG AGGCATCT CT GTTT		
		TGAGGTAT TTTGTGGA GA CAAA		
		A C A		
GAM1425	NDN	3' ACACCCTCGTGGAGT	10191	A CATCTC
		ACTCCATGA GG TGT		
		TGAGGTGCT CC ACA		
		C _ _ _		
GAM1425	NDN	3' ACACCCTCGTGGAGT	10191	A CATCTC
		ACTCCATGA GG TGT		
		TGAGGTGCT CC ACA		
		C _ _ _		
GAM1425	NDRG1	3' GGGTGGGGGTGGAATTGGGGT	59570	TGAAGG TG
		ACTCCA CATCTC TTT		
		TGGGGT GTGGGG GGG		
		TAAG_ GT		
GAM1425	NEU3	3' AAGTAGAGATGCCTTTTGT	21843	T
		CA GAAGGCATCTCTGTTT		
		GT TTTCCGTAGAGATGAA		
		T		
GAM1425	NFE2L1	3' AGGCAGGGGTGGTGGTGGAGT	12168	GAAGG
		ACTCCAT CATCTCTGTTT		

			TGAGGTG GTGGGGACGGA	
			GTG__	
GAM1425 NKTR	3'	GGACAACATTCCTTCATGGAG	18200	C CTC
		CTCCATGAAGG AT TGTTT		
		GAGGTA CTTC TA ACAGG		
		T CA_		
GAM1425 NR2E3	3'	AGATGGTTCCATGGAGT	32968	A G
		ACTCCATG AG CATCT		
		TGAGGTAC TT GTAGA		
		C G		
GAM1425 NR4A1	3'	GAGGGGGATGCCTTCATGGGG	9238	G T
		CTCCATGAAGGCATCTCT TT		
		GGGGTACTTCCGTAGGGG AG		
		G		
GAM1425 NUMB	3'	GACAGGGAGCAGGGGGT	13623	ATGAAG A
		ACTCC GC TCTCTGTT		
		TGGGG CG AGGGACAG		
		GA_____		
GAM1425 OXTR	3'	GGGTGGCTTCAGTGGGGT	6213	_ G
		ACTCCA TGAAG CATCT		
		TGGGGT ACTTC GTGGG		
		G G		
GAM1425 PABPN1	3'	GTAGGGGAAGGCCAGGGAGT	16183	A AA A_ GTTT
		ACTCC TG GGC TCTCT		
		TGAGG AC CCG AGGGG		
		G _ GA ATGA		
GAM1425 PAIP2	3'	AGCTATGCCTGTATGGAGT	33220	A CT
		ACTCCATG AGGCAT CT		
		TGAGGTAT TCCGTA GA		
		G TC		
GAM1425 PBX2	3'	AGACAGAGAAGGGCCAATGGGG	10441	GAA A_
T		ACTCCAT GGC TCTCTGTTT		
		TGGGGTA CCG AGAGACAGA		
		A_ GGA		
GAM1425 PCDH1	3'	GGACGGGGGTGGGAGTGGAG	50563	GAAGG
		CTCCAT CATCTCTGTTT		
		GAGGTG GTGGGGGCAGG		
		AGG__		
GAM1425 PDE5A	5'	GGCGGGGAAGCTGGGGT	53080	TGAAG A
		ACTCCA GC TCTCTGTT		

			TGGGGT CG AGGGGCGG		
			_____ A		
GAM1425	PFKFB4	3'	CAGGTCTTCATGGGG 15867	ATCT	
			CTCCATGAAGGC CTG		
			GGGGTACTTCTG GAC		
GAM1425	PIGA	3'	AAATAACCTTGCTTTTGGGGGG 10550	AT	TCTC
	T		ACTCC GAAGGCA TGTTT		
			TGGGG TTTTCGT ATAAA		
			GG TCCA		
GAM1425	PIGA	3'	AAATAACCTTGCTTTTGGGGGG 40001	AT	TCTC
	T		ACTCC GAAGGCA TGTTT		
			TGGGG TTTTCGT ATAAA		
			GG TCCA		
GAM1425	PIGA	3'	AAATAACCTTGCTTTTGGGGGG 40010	AT	TCTC
	T		ACTCC GAAGGCA TGTTT		
			TGGGG TTTTCGT ATAAA		
			GG TCCA		
GAM1425	PIK3R3	3'	GAATAGCATTCTTTTGTGGGG 61057	TG	CATCT
			CTCCA AAGG CTGTTT		
			GGGGT TTTT GATAAG		
			GT CTTAC		
GAM1425	PLA2G2D	3'	AGTAGGGATACCCATGGGG 24785	AA C	TT
			CTCCATG GG ATCTCTG T		
			GGGGTAC CC TAGGGAT A		
			_____ A GG		
GAM1425	PLXNA2	3'	AGCAGAGATGCTGAGAG 47207	CATGAA	
			CTC GGCATCTCTGTT		
			GAG TCGTAGAGACGA		
			AG_____		
GAM1425	PPP2R4	3'	GGGCAGAGGCTGGGTCAGGAGT 60561	A AGG _	
			ACTCC TGA CA TCTCTGTTT		
			TGAGG ACT GT GGAGACGGG		
			_ GG_ C		
GAM1425	PPP4C	3'	AGACGGAGGCTGGGCGTGGGG 10764	AA_ AT	
			CTCCATG GGC CTCTGTTT		
			GGGGTGC TCG GAGGCAGA		
			GGG _		
GAM1425	PSG1	3'	AAGTAGAGATGCCCATAGAG 22601	C AA	
			CTC ATG GGCATCTCTGTTT		

		GAG TAC CCGTAGAGATGAA		
		A _		
GAM1425 PSMC1	3'	AAACATCCTGTGTCTTTTGGAG 10966	T	CTC_
	T	ACTCCA GAAGGCAT TGT TT		
		TGAGGT TTTCTGTG ACAA		
		_ TCCT		
GAM1425 PTK7	3'	AGGTAGGGGTGGGCCCTGGAG 11015	TGAA _	TT
		CTCCA GGC ATCTCTG T		
		GAGGT CCG TGGGGAT A		
		C_ GG GG		
GAM1425 PTPRA	5'	AAACAAAGGTATTTATGGA 11086	GGC	C
		TCCATGAA ATCT TGT TT		
		AGGTATTT TGGA ACAA		
		A_ A		
GAM1425 PTPRA	5'	AAACAAAGGTATTTATGGA 55077	GGC	C
		TCCATGAA ATCT TGT TT		
		AGGTATTT TGGA ACAA		
		A_ A		
GAM1425 PTPRA	5'	AAACAAAGGTATTTATGGA 55085	GGC	C
		TCCATGAA ATCT TGT TT		
		AGGTATTT TGGA ACAA		
		A_ A		
GAM1425 PVR	3'	AACAGAGAAGTGTGGGG 21468	GAAG	A
		CTCCAT GC TCTCTGTT		
		GGGGTG TG AGAGACAA		
		_ A		
GAM1425 PXN	3'	GGACAGAGGGCCGTGAGGGGT 11163	ATGAA	A
		ACTCC GGC TCTCTGTT		
		TGGGG CCG GGAGACAGG		
		AGTG_ _		
GAM1425 RAB4A	3'	AGTAGATCTTTATGGGG 15920	GC	_
		CTCCATGAAG ATCT CT		
		GGGGTATTTT TAGA GA		
		_ T		
GAM1425 RAB5B	3'	AGTAGAGGTGAGAATGGGG 11188	GAAGG	TT
		CTCCAT CATCTCTG T		
		GGGGTA GTGGAGAT A		
		AGA_ GG		
GAM1425 RABIF	3'	GGGCATGGTCCTCATGGAGT 11208	A C	TC
		ACTCCATGA GG ATC TGT TT		

				TGAGGTACT CC TGG ACGGG		
				— — T—		
GAM1425	RAD54B	3'	AAGCAAGGTCTTTGTGGGG	56230	TG	ATCTC
			CTCCA AAGGC TGTTT			
			GGGGT TTCTG ACGAA			
			GT GA—			
GAM1425	RALBP1	3'	AGACAGGGGCTGCCTGTGGAG	22292	GA	—
			CTCCAT AGGCA TCTCTGTTT			
			GAGGTG TCCGT GGGGACAGA			
			— C			
GAM1425	RANBP3	3'	GGGCCCTGCCTTTGTGGGG	13259	TG	T—
			CTCCA AAGGCA CTC			
			GGGGT TTCCGT GGG			
			GT CCC			
GAM1425	RANBP3	3'	GGGCCCTGCCTTTGTGGGG	23635	TG	T—
			CTCCA AAGGCA CTC			
			GGGGT TTCCGT GGG			
			GT CCC			
GAM1425	RARB	5'	GGCAGAGTTTGATGGAGT	6373	G	GCAT
			ACTCCAT AAG CTCTGTT			
			TGAGGTA TTT GAGACGG			
			G —			
GAM1425	RASD1	3'	AGCGGGGGGGCGTG	32219	AAGGCA	
			TCCATG TCTCTGTT			
			GGGTGC GGGGGCGA			
			GG—			
GAM1425	RASGRP2	3'	AGCAGGGAGCCTGGGGGT	19508	ATGA	A
			ACTCC AGGC TCTCTGTT			
			TGGGG TCCG AGGGACGA			
			G— —			
GAM1425	RASGRP2	3'	GGATGGGGGTGGGATATGAGGG	19511	—	AAGG
			ACTC CATG CATCTCTGTTT			
			TGGG GTAT GTGGGGGTAGG			
			A AGG—			
GAM1425	RBBP5	3'	AGGCAGAGGTTGCAGTGAGT	17329	CATGAAG	—
			ACTC GCA TCTCTGTTT			
			TGAG CGT GGAGACGGA			
			TGA— T			
GAM1425	RECQL5	3'	GACAGAGCTAGTGGGGT	14930	GA	GCAT
			ACTCCAT AG CTCTGTT			

TGGGGTG TC GAGACAG  
 A\_ \_\_\_\_  
 GAM1425 RERE 3' GGGCGGGTGTCTGGGGT 23967 T G AT\_  
 ACTCCA GAA GC CTC  
 ||||| ||| || |||  
 TGGGGT CTT TG GGG  
 \_ G GGC  
 GAM1425 RFXANK 5' GGACAGAGGAGGCTCGTGGGG 13562 AG A\_  
 CTCCATGA GC TCTCTGTTT  
 ||||| || |||||  
 GGGGTGCT CG GGAGACAGG  
 \_ GA  
 GAM1425 RFXANK 5' GGACAGAGGAGGCTCGTGGGG 56240 AG A\_  
 CTCCATGA GC TCTCTGTTT  
 ||||| || |||||  
 GGGGTGCT CG GGAGACAGG  
 \_ GA  
 GAM1425 RGS1 3' GAACAGCTTGGCCTTTTGTGGG 11326 \_ TG \_ ATCT  
 TGT AC TCCA AA GGC CTGTTT  
 || ||| || ||| |||||  
 TG GGGT TT CCG GACAAG  
 T GT T GTTC  
 GAM1425 RREB1 3' AAGCGTCTATACTTCATGGGGT 11395 GCATCTC  
 ACTCCATGAAG TGTTT  
 ||||| |||||  
 TGGGGTACTTC GCGAA  
 ATATCT\_  
 GAM1425 SCA7 5' GGGCGGGGGTGCTCAATGAG 4404 C GAA  
 CTC AT GGCATCTCTGTTT  
 ||| || |||||  
 GAG TA TCGTGGGGGCGGG  
 \_ AC\_  
 GAM1425 SCGB3A2 3' GAGCGGAGGTGGATGGGG 53964 GAAGG  
 CTCCAT CATCTCTGTTT  
 ||||| |||||  
 GGGGTA GTGGAGGCGAG  
 G\_  
 GAM1425 SCN1A 3' AAGTGGAGGTGCTTTGTTG 88850 TG TG  
 CA AAGGCATCTC TTT  
 || ||||| |||  
 GT TTTCGTGGAG GAA  
 TG GT  
 GAM1425 SCRT1 3' AGACGGGGGTGAGGTGAGGT 48546 TC GAAGG  
 AC CAT CATCTCTGTTT  
 || ||| |||||  
 TG GTG GTGGGGGCAGA  
 GA GA\_  
 GAM1425 SF1 3' AAGCGGGGATGTTCCATTGA 16144 C AA  
 TC ATG GGCATCTCTGTTT  
 || ||| |||||



			AG TAC TTGTAGGGGCGAA		
			T C_		
GAM1425	SGCA	3'	GGGTGGGGTGAGAGTGTGTGGA 3429	AAGG__	TGTTT
	GT		ACTCCATG CATCTC		
			TGAGGTGT GTGGGG		
			GTGAGA TGGG		
GAM1425	SIRT1	3'	AAATAGATTGTTTTTCATGGA 24263	_ TC	
			TCCATGAAGG CA TCTGTTT		
			AGGTACTTTT GT AGATAAA		
			T T_		
GAM1425	SLC8A2	3'	GGTGGGGATGGGTGGGG 66335	GAAGG	TG
			CTCCAT CATCTC TT		
			GGGGTG GTAGGG GG		
			G__ GT		
GAM1425	SMARCB1	3'	GGGTGGGGGTGGAGTGGGG 65584	GAAGG	TG
			CTCCAT CATCTC TTT		
			GGGGTG GTGGGG GGG		
			AG__ GT		
GAM1425	SMG1	3'	AACAGAGAAAAGTGGGGT 30647	TGAA	GCA
			ACTCCA G TCTCTGTT		
			TGGGGT C AGAGACAA		
			__ AAA		
GAM1425	SORBS1	3'	GGACGTCTGTTCTTTGTGGGG 31159	TG _	TCTC
			CTCCA AAGG CA TGTTT		
			GGGGT TTCT GT GCAGG		
			GT T CT__		
GAM1425	SPAG8	3'	GAATGGGGGTTTACAGGAGT 24901	A A	AT
			ACTCC TG AGGC CTCTGTTT		
			TGAGG AC TTTG GGGGTAAG		
			_ A _		
GAM1425	STK10	3'	GGATGGGGCTGTTGGTGGGGT 19986	G AG	T
			ACTCCAT A GCA CTCTGTTT		
			TGGGGTG T TGT GGGGTAGG		
			G__ C		
GAM1425	SYNGR2	3'	GGGCAGGGGTGCCCCATGG 16307	AA	
			CCATG GGCATCTCTGTTT		
			GGTAC CCGTGGGGACGGG		
			C_		
GAM1425	TAP2	3'	GGGGTGTGGTGGGGT 5029	GAAG	
			ACTCCAT GCATCTC		

			TGGGGTG TGTGGGG		
			G__		
GAM1425 TDRD1	3'	GATAGAGCTAATGGAGT	48395	GA GCAT	
		ACTCCAT AG CTCTGTT			
		TGAGGTA TC GAGATAG			
		A_ ____			
GAM1425 TEAD3	3'	AGCAGAGGCCCTGGGAGT	12206	ATGAA AT	
		ACTCC GGC CTCTGTT			
		TGAGG CCG GAGACGA			
		GTC_ _			
GAM1425 TEM6	3'	AGGCAGAGGTGCCGAGTG	42740	GAA	
		CAT GGCATCTCTGTTT			
		GTG CCGTGGAGACGGA			
		AG_			
GAM1425 TEM7	3'	GGGTGGGGAGGCGTAGGGGT	39892	ATGAAG A TG	
		ACTCC GC TCTC TTT			
		TGGGG CG AGGG GGG			
		ATG_ G GT			
GAM1425 TEM8	3'	GGGCAGAGACAGGCCTGGAGT	36331	TGAA A_	
		ACTCCA GGC TCTCTGTTT			
		TGAGGT CCG AGAGACGGG			
		____ GAC			
GAM1425 TERT	3'	GGATGGGGGTCCCTGTGGG	12227	GA C	
		TCCAT AGG ATCTCTGTTT			
		GGGTG TCC TGGGGGTAGG			
		_ C			
GAM1425 TEX15	3'	GAGTAGAGATGTTTTAAATG	48389	G_	
		CAT AAGGCATCTCTGTTT			
		GTA TTTTGTAGAGATGAG			
		AA			
GAM1425 TIAL1	3'	AGTACCGCCTTATGGAGT	42258	A ATCT	
		ACTCCATGA GGC CT			
		TGAGGTATT CCG GA			
		_ CCAT			
GAM1425 TJP1	3'	AAATGGGGGTGCATTTGAG	12293	CAT G	
		CTC GAA GCATCTCTGTTT			
		GAG TTT CGTGGGGGTAAA			
		_ A			
GAM1425 TLE1	3'	GGACAGAGGGGCCATGGG	17414	GAA AT	
		TCCAT GGC CTCTGTTT			

GGGTA CCG GAGACAGG  
 \_\_\_\_ GG  
 GAM1425 TMPRSS2 3' AAACATTTTTGTTCTTATGGGG 18962 AG TCTC  
 T ACTCCATGA GCA TGT  
 ||||| ||| ||||  
 TGGGGTATT TGT AAAAA  
 CT TTTT

GAM1425 TNFSF10 3' AGGCAGAGGTTGCAGTGTGG 13747 AAG \_  
 CCATG GCA TCTCTGTTT  
 |||| ||| |||||  
 GGTGT CGT GGAGACGGA  
 GA\_ T

GAM1425 TNR 3' AAGCAGGGATGTCGCAGGA 12352 A AA  
 TCC TG GGCATCTCTGTTT  
 ||| || |||||  
 AGG AC CTGTAGGGACGAA  
 \_ G\_

GAM1425 TOP2A 5' GGGTGGTCTCGTGGGGT 6531 A AT  
 ACTCCATGA GGC CTC  
 ||||| ||| |||  
 TGGGGTGCT CTG GGG  
 \_ GT

GAM1425 TTN 3' AGTGCAGCCAATGCCTTTGTGT 55917 TC TG CT\_ TT  
 GGT AC CA AAGGCAT CTGT  
 || || ||||| ||||  
 TG GT TTCCGTA GACG  
 GT GT ACC TGAG

GAM1425 TTN 3' AGTGCAGCCAATGCCTTTGTGT 55935 TC TG CT\_ TT  
 GGT AC CA AAGGCAT CTGT  
 || || ||||| ||||  
 TG GT TTCCGTA GACG  
 GT GT ACC TGAG

GAM1425 TTN 3' AGTGCAGCCAATGCCTTTGTGT 55947 TC TG CT\_ TT  
 GGT AC CA AAGGCAT CTGT  
 || || ||||| ||||  
 TG GT TTCCGTA GACG  
 GT GT ACC TGAG

GAM1425 TXK 5' AGATGTGTTTTTGTGAGT 12452 \_ T G  
 ACTC CA GAA GCATCT  
 |||| ||| |||||  
 TGAG GT TTT TGTA  
 T T G

GAM1425 TXNRD1 3' AGGGATGCATCCATGAAGT 12455 C AAG  
 ACTCATG GCATCTCT  
 ||| ||| |||||  
 TGA GTAC CGTAGGGA  
 A CTA

GAM1425 UBE2I 5' GGGTGGAGGAACGTGTGGAGT 12493 AAGGCA TG  
 ACTCCATG TCTC TTT  
 ||||| ||| |||

			TGAGGTGT	GGAG GGG		
			GCAA__	GT		
GAM1425	UBE2L3	3'	GAGCAGAGACCCCGTGCAGT	12501	C	AA CA
			ACT CATG GG TCTCTGTTT			
			TGA GTGC CC AGAGACGAG			
			C C_ _			
GAM1425	UBTF	3'	GGCAGGGAACATGGGG	26449	AAGGCA	
			CTCCATG TCTCTGTT			
			GGGGTAC AGGGACGG			
			A_			
GAM1425	UNG	3'	AGACGGTCTTTATTGGGT	12549	C	ATC
			ACTC ATGAAGGC TCT			
			TGGG TATTTCTG AGA			
			T GC_			
GAM1425	UNG	3'	AGACGGTCTTTATTGGGT	55153	C	ATC
			ACTC ATGAAGGC TCT			
			TGGG TATTTCTG AGA			
			T GC_			
GAM1425	VEGF	5'	AGTGACCTGCTTTTGGGGT	12585	A	_ T
			ACTCC TGAAGGCA TC CT			
			TGGGG GTTTTCGT AG GA			
			_ CC T			
GAM1425	VHL	3'	AGGCAGGGTGTGTTGTGTGGT	5056	TC TG AG	T
			AC CA A GCATC CTGTTT			
			TG GT T TGTGG GACGGA			
			GT GT G_ _			
GAM1425	WBSCR1	3'	GAGCAGAGGTGGCCGCCGTGGG	42228	AA	_
	G		CTCCATG GGC ATCTCTGTTT			
			GGGGTGC CCG TGGAGACGAG			
			CG G			
GAM1425	WBSCR1	3'	GAGCAGAGGTGGCCGCCGTGGG	49260	AA	_
	G		CTCCATG GGC ATCTCTGTTT			
			GGGGTGC CCG TGGAGACGAG			
			CG G			
GAM1425	WFS1	3'	AAACAGAGAACCCTGTGGGG	20007	GA	CA
			CTCCAT AGG TCTCTGTTT			
			GGGGTG TCC AGAGACAAA			
			_ CA			
GAM1425	WNT3A	3'	GGATGGGGCACGGCTCTGGGGT	52437	T AG AT_	
			ACTCCA GA GC CTCTGTTT			

		TGGGGT CT CG GGGGTAGG	
		— — GCAC	
GAM1425 WWOX	3'	AAGCAGGGAATTCCTGGGGT 33042	T GGCA
		ACTCCA GAA TCTCTGTTT	
		TGGGGT CTT AGGGACGAA	
		C A__	
GAM1425 ZHX1	3'	AGACAGCTGGCTTTGTGGG 23329	TG G TCT
		TCCA AAG CA CTGTTT	
		GGGT TTC GT GACAGA	
		GT G C__	
GAM1425 ZNF135	3'	GAGTGGCATCTTTATGGA 12852	__ AT
		TCCATGAAG GC CTC	
		AGGTATTC CG GAG	
		TA GT	
GAM1425 ZNF2	5'	GGATGGTAGATCTTCATGGG 40805	GC _
		TCCATGAAG ATCT CTGTTT	
		GGGTACTTC TAGA GGTAGG	
		__ T	
GAM1425 ZNF22	3'	AAATAGAGATGCTTTATAGTAG 91461	CCATG
		CT AAGGCATCTCTGTTT	
		GA TTTCGTAGAGATAAA	
		TGATA	
GAM1425 ZNF266	5'	GGATAGAGAGGACCTCCTGGGG 88323	T A CA_
T		ACTCCA GA GG TCTCTGTTT	
		TGGGGT CT CC AGAGATAGG	
		C _ AGG	
GAM1425 ZNF278	5'	GGGCGGGGGTTGGCTATGTGGG 26730	A G _
G		CTCCATG AG CA TCTCTGTTT	
		GGGGTGT TC GT GGGGGCGGG	
		A G T	
GAM1425 ZNF278	5'	GGGCGGGGGTTGGCTATGTGGG 49437	A G _
G		CTCCATG AG CA TCTCTGTTT	
		GGGGTGT TC GT GGGGGCGGG	
		A G T	
GAM1425 ZNF278	5'	GGGCGGGGGTTGGCTATGTGGG 49439	A G _
G		CTCCATG AG CA TCTCTGTTT	
		GGGGTGT TC GT GGGGGCGGG	
		A G T	
GAM1425 ZNF278	5'	GGGCGGGGGTTGGCTATGTGGG 49445	A G _
G		CTCCATG AG CA TCTCTGTTT	

GGGGTGT TC GT GGGGGCGGG  
A G T  
GAM1425 ZNF42 5' AGATGGAGTGTATTTTATGGG 12783 \_ T  
TCCATGAAG GCA CTCTGTTT  
||||||| ||| |||||||  
GGGTATTTT TGT GAGGTAGA  
A \_  
GAM1425 ZNFN2A1 5' AGATGGAGATGAGGATGGA 60735 GAAGG  
TCCAT CATCTCTGTTT  
||||| |||||||||  
AGGTA GTAGAGGTAGA  
GGA\_\_  
GAM1425 A4GALT 3' GGACAGAGGTGCCCCACGAGGG 33839 A AA  
TCC TG GGCATCTCTGTTT  
||| || |||||||||  
GGG GC CCGTGGAGACAGG  
A AC  
GAM1425 ABLIM 5' GAACAGAGAGAATTGTGGGG 9768 TG AGGCA  
CTCCA A TCTCTGTTT  
||||| | |||||||  
GGGGT T AGAGACAAG  
GT AAG\_\_  
GAM1425 AMOT 3' TAGGGAGTTTTGGGGT 55725 TGA A  
ACTCCA AGGC TCTCTG  
||||| ||| |||||  
TGGGGT TTTG AGGGAT  
\_\_\_\_\_  
GAM1425 APCL 5' GGGCAGGCTTGCTTTTATGGGG 19680 TC  
CTCCATGAAGGCA TCTGTTT  
||||||||| |||||  
GGGGTATTTTCGT GGACGGG  
TC  
GAM1425 APCL 3' GGGTGGAGGTGTCCTGAG 19682 CATGA \_ TG  
CTC AGG CATCTC TTT  
||| ||| ||||| |||  
GAG TCC GTGGAG GGG  
\_\_\_\_ T GT  
GAM1425 ARHGAP5 3' AAGTGACTGCTGCTTTTGGGG 77068 T A\_ \_ T GTTT  
CTCCA GA GGCA TC CT  
||||| || ||||| |||  
GGGGT TT TCGT AG GA  
T CG C T A  
GAM1425 ARHGEF4 3' GAGCAGGGATGGGCTGGGGAGT 52216 ATGA G\_  
ACTCC AG CATCTCTGTTT  
||||| || |||||||||  
TGAGG TC GTAGGGACGAG  
GG\_ GG  
GAM1425 ARL3 3' AATGGAGATGCAGGAG 15045 ATGAAG  
CTCC GCATCTCTGTT  
||| |||||||||

			GAGG CGTAGAGGTAA		
			A_____		
GAM1425	ASAH	3'	AAATGGAGATTCAGCGTGGGTG 15046	_	AA C
	T		AC TCCATG GG ATCTCTGTTT		
			TG GGGTGC CT TAGAGGTAAA		
			T GA _		
GAM1425	ATP5D	3'	GGGCAGGGATGCCAGGTGGG 8074		GAA
			TCCAT GGCATCTCTGTTT		
			GGGTG CCGTAGGGACGGG		
			GA_		
GAM1425	BCDO	5'	AGACAGAGATGTGAAGGAG 33825		ATGAAG
			CTCC GCATCTCTGTTT		
			GAGG TGTAGAGACAGA		
			AAG_____		
GAM1425	BICD2	3'	AGGTGGGGGTCAGAGGTGGGG 70387		GAAGGC TG
			CTCCAT ATCTC TTT		
			GGGGTG TGGGG GGA		
			GAGAC_ GT		
GAM1425	BICD2	3'	TTAGATAACTTCATCTGTATGG 70405	_____	GC CTGTTT
	GGT		CCA TGAAG ATCT		
			GGT ACTTC TAGA		
			ATGTCT AA TTT		
GAM1425	BPES	3'	GGGCGGAGGTGCGACCGGGCGT 43535		T ATGAAG
			AC CC GCATCTCTGTTT		
			TG GG CGTGGAGGCGGG		
			C GCCAG_		
GAM1425	C11orf11	3'	AGATGGGGAAGGGTGTGGAGT 93247		AAGGCA
			ACTCCATG TCTCTGTTT		
			TGAGGTGT AGGGGTAGA		
			GGA_		
GAM1425	C11orf21	3'	GGGCAGAGGTGATAGATGTGGG 26243		GAAGG_
	GT		ACTCCAT CATCTCTGTTT		
			TGGGGTG GTGGAGACGGG		
			TAGATA		
GAM1425	C17orf1A	3'	GGCAGAGAACGTGGGAGT 21088	_	AAGGCA
			ACTCC ATG TCTCTGTT		
			TGAGG TGC AGAGACGG		
			G A_____		
GAM1425	C1orf17	3'	AAACTATTTGCCTTCTGGAG 68207	T	TCTCT
			CTCCA GAAGGCA GTTT		

		GAGGT CTTCCGT CAAA	
		_ TTAT_	
GAM1425	C1orf33 3'	AGGTGGAGGTTGCCGTGAGT 32458	CATGAA _ TG
		ACTC GGCA TCTC TTT	
		TGAG CCGT GGAG GGA	
		TG____ T GT	
GAM1425	C20orf124 3'	GAGCAGCTGAGCTTCGTGGAG 45486	G A T_
		CTCCATGAAG C TC CTGTTT	
		GAGGTGCTTC G AG GACGAG	
		_ _ TC	
GAM1425	C20orf139 3'	GGGATCCCTCATGGAG 84760	A C
		CTCCATGA GG ATCTC	
		GAGGTACT CC TAGGG	
		C _	
GAM1425	C20orf172 3'	AAACAGCTGCAGGCCTTTATGG 46207	ATCT__
	A	TCCATGAAGGC CTGTTT	
		AGGTATTTCCG GACAAA	
		GACGTC	
GAM1425	C20orf21 3'	GAGTGGGCATTTTTGTGGGGT 35113	TG _ AT_
		ACTCCA AAG GC CTC	
		TGGGGT TTT CG GAG	
		GT TA GGT	
GAM1425	C20orf28 5'	AGGCAGAGGCAGTTATGGG 31222	AG AT
		TCCATGA GC CTCTGTTT	
		GGGTATT CG GAGACGGA	
		GA _	
GAM1425	C20orf39 5'	GGGCGGGGAGAGGCGTGGGG 46045	AAGGCA
		CTCCATG TCTCTGTTT	
		GGGGTGC AGGGGCGGG	
		GGAG__	
GAM1425	C20orf42 3'	AAACGCCTGTCCTTCATGGA 34579	_ TCTC
		TCCATGAAGG CA TGTTT	
		AGGTACTTCC GT GCAAA	
		T CC__	
GAM1425	C20orf97 3'	AGGCAGAAGCCTGTGTGGAGT 40962	A ATC
		ACTCCATG AGGC TCTGTTT	
		TGAGGTGT TCCG AGACGGA	
		G A__	
GAM1425	C21orf59 3'	AGACATTTTCATGGAGT 35237	CA
		ACTCCATGAAGG TCT	



			TGAGGTACTTTT AGA	
			AC	
GAM1425	C5orf6	3'	AATGGGGGTGAGTGGAG 33476	GAAGG
			CTCCAT CATCTCTGTT	
			GAGGTG GTGGGGGTAA	
			A____	
GAM1425	C9orf5	3'	GAGCAGAGGTGCCCCAGAGT 49276	CA AA
			ACTC TG GGCATCTCTGTTT	
			TGAG AC CCGTGGAGACGAG	
			__ C_	
GAM1425	CAMTA1	3'	AAACAGAGATATGTGCATG 67913	AAGGC
			CATG ATCTCTGTTT	
			GTAC TAGAGACAAA	
			GTGTA	
GAM1425	caspr5	5'	AAGCGGGGGTGGGAGGGGGT 55380	ATGAAGG
			ACTCC CATCTCTGTTT	
			TGGGG GTGGGGGCGAA	
			GAGG____	
GAM1425	caspr5	5'	AAGCGGGGGTGGGAGGGGGT 57311	ATGAAGG
			ACTCC CATCTCTGTTT	
			TGGGG GTGGGGGCGAA	
			GAGG____	
GAM1425	CDC14B	3'	GGCGTCTTTCATGGGGT 52858	_ AT
			ACTCCATGAAGG C C	
			TGGGGTACTTTC G G	
			T CG	
GAM1425	CDCA4	3'	AGGCAGGGAGTGAGCTGGGGGT 35654	ATGAAG A
			ACTCC GC TCTCTGTTT	
			TGGGG TG AGGGACGGA	
			GTCGAG _	
GAM1425	CDT6	3'	GGACAGAGTCTCTCATGGA 40945	AG CAT
			TCCATGA G CTCTGTTT	
			AGGTACT C GAGACAGG	
			CT T__	
GAM1425	CEACAM4	3'	GGACAGGGAGGGATGGGAGT 8427	ATGAAGGCA
			ACTCC TCTCTGTTT	
			TGAGG AGGGACAGG	
			GTAGGG____	
GAM1425	CEACAM4	3'	GGACGGGGAAGGACATGGAG 8428	AAGGCA
			CTCCATG TCTCTGTTT	

GAGGTAC AGGGGCAGG  
 AGGA\_\_  
 GAM1425 CEACAM7 3' GAACAGGGAGGAGTTTGTGCAG 22558 C TG GGCA  
 T ACT CA AA TCTCTGTTT  
 ||| || || |||||  
 TGA GT TT AGGGACAAG  
 C GT GAGG  
 GAM1425 CEACAM8 3' AAACAGGCTGATACCTTTGTGA 8418 C TG C \_\_  
 AGT ACT CA AAGG ATC TCTGTTT  
 ||| || |||| || |||||  
 TGA GT TTCC TAG GGACAAA  
 A GT A TC  
 GAM1425 CENTA1 3' GGACGGAGGGGACCCGTGGA 22495 AA CA\_  
 TCCATG GG TCTCTGTTT  
 ||||| || |||||  
 AGGTGC CC GGAGGCAGG  
 \_\_ AGG  
 GAM1425 CENTG1 3' GGGCAGGGGGTGGGTTGGGGT 28710 TGAAG A  
 ACTCCA GC TCTCTGTTT  
 ||||| || |||||  
 TGGGGT TG GGGGACGGG  
 TGGG\_\_  
 GAM1425 CENTG1 3' GGGTGGGGGTGCTCTCGGG 28712 A AG TG  
 CC TGA GCATCTC TTT  
 || ||| ||||| |||  
 GG GCT CGTGGGG GGG  
 \_ CT GT  
 GAM1425 CGI-57 3' GGGAGCTTATGGGGT 73881 AA A  
 ACTCCATG GGC TCTC  
 ||||| ||| |||  
 TGGGGTAT TCG AGGG  
 \_\_ \_\_  
 GAM1425 CKAP4 3' AGGTGGCTTTTCATGGATGT 22390 \_ \_\_ G  
 AC TCCATGA AG CATCT  
 || ||||| || |||||  
 TG AGGTACT TC GTGGA  
 T TT G  
 GAM1425 CL25084 5' GAGCAGAGGAGGTTGTGGCGGT 31658 \_ TG AGGCA  
 ACT CCA A TCTCTGTTT  
 ||| ||| | |||||  
 TGG GGT T GGAGACGAG  
 C GT GGA\_\_  
 GAM1425 CMG2 3' GAATGGAGGTTTCGTTGGGGT 54162 TGAA C  
 ACTCCA GG ATCTCTGTTT  
 ||||| || |||||  
 TGGGGT CT TGGAGGTAAG  
 TG\_\_  
 GAM1425 CNOT3 5' TTAGATGTTCCCTTCTTTGTGG 27221 \_ T\_ \_\_ CTGTTT  
 GT TC CA GAAGG CATCT  
 || || |||| |||||

		GG GT CTTCC GTAGA		
		T TT CTT TTT		
GAM1425 COPS7B	3'	AGACAGAGGGTGCTGTGGG	42689	GAA _
		TCCAT GGCATC TCTGTTT		
		GGGTG TCGTGG AGACAGA		
		_ G		
GAM1425 CPEB1	5'	GGGCATGATGGCTTTTCATGGA	47597	_ TC
		TCCATGAAGGC ATC TGTTT		
		AGGTACTTTTCG TAG ACGGG		
		G T_		
GAM1425 CPEB1	3'	GGTTTTGTTTTTCAGGGGGT	47598	A TCT
		ACTCC TGAAGGCA CT		
		TGGGG ACTTTTGT GG		
		G TTT		
GAM1425 CRA	3'	GGGCAGAGGGGGATCTGGGGT	21974	T AGGCA
		ACTCCA GA TCTCTGTTT		
		TGGGGT CT GGAGACGGG		
		_ AGGG_		
GAM1425 CRK7	3'	AGTAGAGAATATGGAG	33250	AAGGCA
		CTCCATG TCTCTGTT		
		GAGGTAT AGAGATGA		
		A_		
GAM1425 CRTAM	3'	AGGTGGAGATTGCAGTGAGT	38977	CATGAAG _ TG
		ACTC GCA TCTC TTT		
		TGAG CGT AGAG GGA		
		TGA_ T GT		
GAM1425 CSAGE	5'	GGATGGGGATCCAGATGGAG	86861	GAA C
		CTCCAT GG ATCTCTGTTT		
		GAGGTA CC TAGGGGTAGG		
		GA_ _		
GAM1425 CTSO	3'	GAATTTATTTTCTTTTGTGGGG	7190	TG CATCTCT
T		ACTCCA AAGG GTTT		
		TGGGGT TTTC TAAG		
		GT TTTTATT		
GAM1425 CUL4A	3'	AAACAAGGGCCCTTCATGGG	13147	CA TC
		TCCATGAAGG TC TGTTT		
		GGGTACTTCC GG ACAA		
		C_ GA		
GAM1425 CYB5-M	3'	AGTAGGGATGAATTGGGGT	94562	TGAAGG TT
		ACTCCA CATCTCTG T		

			TGGGGT	GTAGGGAT	A		
			TAA__	GG			
GAM1425	CYP2D6	5'	GGGTGGGGGGTGCCAGGTGTG	3657	AA_	TG	
			CATG GGCATCTC TTT				
			GTGT CCGTGGGG GGG				
			GGA GT				
GAM1425	DDX28	5'	AGACAGAGAGGGGTGAGGGGT	37212	ATGAAG	A_	
			ACTCC GC TCTCTGTTT				
			TGGGG TG AGAGACAGA				
			AG__ GG				
GAM1425	DDX32	3'	AAATAGAAGTTTTATTGAGT	36416	C	ATC	
			ACTC ATGAAGGC TCTGTTT				
			TGAG TATTTTTG AGATAAA				
			T A_				
GAM1425	DICER1	3'	AGTGAAACCTTCATGGA	47607	CA	T	
			TCCATGAAGG TC CT				
			AGGTACTTCC AG GA				
			AA T				
GAM1425	DIO2	3'	AGACAGAGATGTGCCAGAGT	25675	CA	AAG	
			ACTC TG GCATCTCTGTTT				
			TGAG AC TGTAGAGACAGA				
			_ CG_				
GAM1425	DIO2	3'	AGACAGAGATGTGCCAGAGT	5823	CA	AAG	
			ACTC TG GCATCTCTGTTT				
			TGAG AC TGTAGAGACAGA				
			_ CG_				
GAM1425	DIS3	3'	AAACTATCTCTGCCTTCAAGGA	30222	A	TCTCT_	
	G		CTCC TGAAGGCA GTTT				
			GAGG ACTTCCGT CAAA				
			A CTCTAT				
GAM1425	DKFZP434A0225	3'	AGTGGAGTTTTTCATGAGT	93906	C	AT T	
			ACTC ATGAAGGC C CT				
			TGAG TACTTTTG G GA				
			_ AG T				
GAM1425	DKFZP434B205	3'	AGGTGGAGATGCTTATAGCAGT	75317	CCA	A TG	
			ACT TG AGGCATCTC TTT				
			TGA AT TTCGTAGAG GGA				
			CG_ A GT				
GAM1425	DKFZP434F091	3'	AGGCGGAGGTTGCGGTGAGT	31281	C	GAAG _	
			ACTC AT GCA TCTCTGTTT				

	TGAG TG CGT GGAGGCGGA		
	_ G_ T		
GAM1425 DKFZP434G156 3'	GAGTTCTGCCTCATGGAGT 69782	A T_	
	ACTCCATGA GGCA CTC		
	TGAGGTACT CCGT GAG		
	_ CTT		
GAM1425 DKFZP434H0820 3'	TTTAGGGGGTGCCTCATGGGGT 63855	A GTTT	
	ACTCCATGA GGCATCTCT		
	TGGGGTACT CCGTGGGGG		
	_ ATTTA		
GAM1425 DKFZP434I0714 5'	AAACAGGGGTGCGGCTTGAGT 85795	CATGAAG	
	ACTC GCATCTCTGTTT		
	TGAG CGTGGGGACAAA		
	TTCGG_		
GAM1425 DKFZP434N093 3'	AAACGAACTGCTTTTCGTGGG 79941	TC T	
	TCCATGAAGGCA TC GTTT		
	GGGTGCTTTCGT AG CAAA		
	CA _		
GAM1425 DKFZP434O125 3'	AGGTGGGGGTGAGCAGGGGGT 64957	A AAGG TG	
	ACTCC TG CATCTC TTT		
	TGGGG AC GTGGGG GGA		
	G GA_ GT		
GAM1425 DKFZp547G183 3'	AGGCGGAGGTTGCAGTGAGT 38023	CATGAAG _	
	ACTC GCA TCTCTGTTT		
	TGAG CGT GGAGGCGGA		
	TGA_ T		
GAM1425 DKFZP564C103 3'	AAGCAGAGGCCCTTGGGG 31609	TGAA AT	
	CTCCA GGC CTCTGTTT		
	GGGGT CCG GAGACGAA		
	TCC_ _		
GAM1425 DKFZP564I122 3'	AAACAGGGAAAGCAAGGAGT 63172	A AAGGCA	
	ACTCC TG TCTCTGTTT		
	TGAGG AC AGGGACAAA		
	A GAA_		
GAM1425 DKFZP564L0862 5'	GAGCAGGGGGAGCATGGAGT 44023	AAGGCA	
	ACTCCATG TCTCTGTTT		
	TGAGGTAC GGGGACGAG		
	GAG_		
GAM1425 DKFZP564O0423 3'	AAATGGAACCTTTTATGGG 91672	CATC	
	TCCATGAAGG TCTGTTT		

GGGTATTTTC AGGTAAA  
A\_\_\_\_

GAM1425 DKFZP564O0463 5' GGACACCTCGTGGAGT 26281 A CA  
ACTCCATGA GG TCT  
||||||| || |||  
TGAGGTGCT CC AGG  
\_ AC

GAM1425 DKFZP564O1863 3' AAGTGGGGGTAAAGGTGGAGT 68587 GAAGGC TG  
ACTCCAT ATCTC TTT  
||||| |||| |||  
TGAGGTG TGGGG GAA  
GAAA\_ GT

GAM1425 DKFZP566G1424 3' GGGCAGCTCCTTCATGAGGT 84787 TC CATCT  
AC CATGAAGG CTGTTT  
|| ||||| |||||  
TG GTA CTTCC GACGGG  
GA TC\_

GAM1425 DKFZp586H0623 3' GAACAGAGGTGCTGCGAG 34070 CATGAA  
CTC GGCATCTCTGTTT  
||| |||||  
GAG TCGTGGAGACAAG  
CG\_

GAM1425 DKFZP586J1624 3' GGGCATCCCTCCATGGGGT 31395 A C \_  
ACTCCATG AGG AT CTC  
||||||| ||| |||  
TGGGGTAC TCC TA GGG  
C C C

GAM1425 DKFZP727G051 3' GGACGGGGGTGGGGGGTGGTAG 69472 \_ GAAGG  
T ACT CCAT CATCTCTGTTT  
||| ||| |||||  
TGA GGTG GTGGGGGCAGG  
T GGGG\_

GAM1425 DNAJA4 3' AGACAGCCTCTTTATGAGGT 37751 TC CATCT  
AC CATGAAGG CTGTTT  
|| ||||| |||||  
TG GTATTTCT GACAGA  
GA CC\_

GAM1425 DPCR1 3' AGTGGGGTTTATGGGG 55119 GGCAT TG  
CTCCATGAA CTC TT  
||||||| ||| ||  
GGGGTATTT GGG GA  
\_ GT

GAM1425 DREV1 3' AATAGTCACGACTTCATGGA 32067 GCATCT  
TCCATGAAG CTGTT  
||||||| |||||  
AGGTACTTC GATAA  
AGCACT

GAM1425 DSCR6 3' AGGCGGAGGTTGCCGTGAGT 38542 CATGAA \_  
ACTC GGCA TCTCTGTTT  
||| ||| |||||

			TGAG CCGT GGAGGCGGA		
			TG____ T		
GAM1425	DUSP10	5'	GAATGGGGGCTGAATGTGCGAG 23281	_	AA_ AT
		T	ACTC CATG GGC CTCTGTTT		
			TGAG GTGT TCG GGGGTAAG		
			C AAG _		
GAM1425	DUSP10	5'	GAATGGGGGCTGAATGTGCGAG 58561	_	AA_ AT
		T	ACTC CATG GGC CTCTGTTT		
			TGAG GTGT TCG GGGGTAAG		
			C AAG _		
GAM1425	E2F6	3'	AAATGGACAGTTCTTTGTGGA 8709	TG	CATC
			TCCA AAGG TCTGTTT		
			AGGT TTCT AGGTAAA		
			GT TGAC		
GAM1425	E2F6	3'	AGTAGTGCTTTGAGGAGT 8710	A	CT
			ACTCC TGAAGGCAT CT		
			TGAGG GTTTCTGTG GA		
			A AT		
GAM1425	EPS8R1	3'	GAGTGGGGAGGGCGTGGAG 57601	AAGGCA	TG
			CTCCATG TCTC TTT		
			GAGGTGC AGGG GAG		
			GGG____ GT		
GAM1425	EPS8R1	3'	GAGTGGGGAGGGCGTGGAG 55700	AAGGCA	TG
			CTCCATG TCTC TTT		
			GAGGTGC AGGG GAG		
			GGG____ GT		
GAM1425	EPS8R1	3'	GAGTGGGGAGGGCGTGGAG 34802	AAGGCA	TG
			CTCCATG TCTC TTT		
			GAGGTGC AGGG GAG		
			GGG____ GT		
GAM1425	ERF	3'	GGGCGGAGGAGGGTGAGGGGT 21437	ATGAAGGCA	
			ACTCC TCTCTGTTT		
			TGGGG GGAGGCGGG		
			AGTGGA__		
GAM1425	ERMAP	3'	AGGTGGAGATGTTGAATATG 37596	AA_	TG
			CATG GGCATCTC TTT		
			GTAT TTGTAGAG GGA		
			AAG GT		
GAM1425	ESM1	3'	AGATGGGGAGGGGGTGGGAGT 22875	ATGAAGGCA	
			ACTCC TCTCTGTTT		

		TGAGG	AGGGGTAGA		
		GTGGGGG__			
GAM1425	ESPL1	5'	AGGTGGGGGTGCTGCCTGG 24457	TGAA	TG
			CCA GGCATCTC TTT		
			GGT TCGTGGGG GGA		
			CCG_ GT		
GAM1425	EVI5	3'	GGGCAGGGAGGATCACTGGAGT 19005	_	AGGCA
			ACTCCA TGA TCTCTGTTT		
			TGAGGT ACT AGGGACGGG		
			C AGG__		
GAM1425	FER1L4	3'	GGCAGAGGACGTGGAG 47357	AAGGCA	
			CTCCATG TCTCTGTT		
			GAGGTGC GGAGACGG		
			A_____		
GAM1425	FKBP9	3'	GGGTGGGTTGATATATGGGGT 94066	AA__	AT_
			ACTCCATG GGC CTC		
			TGGGGTAT TTG GGG		
			ATAG GGT		
GAM1425	FLJ00026	3'	AGGCAGGGCAAACCTTGTAGGAG 64994	ATG	GCAT
	T		ACTCC AAG CTCTGTTT		
			TGAGG TTC GGGACGGA		
			ATG AAAC		
GAM1425	FLJ00060	3'	AAGCAGAGTTCTCTTGTGGAGT 61088	TG AG	CAT
			ACTCCA A G CTCTGTTT		
			TGAGGT T C GAGACGAA		
			GT CT TT_		
GAM1425	FLJ10040	3'	GGATGAATGTTTTTATAGGGT 35753	C	--
			ACTC ATGAAGGCAT C TCT		
			TGGG TATTTTGTAG G AGG		
			A A T		
GAM1425	FLJ10097	5'	AAGCGGAGGGGGAGCAGGAGT 68509	A	AAGGCA
			ACTCC TG TCTCTGTTT		
			TGAGG AC GGAGGCGAA		
			_ GAGGG_		
GAM1425	FLJ10193	3'	GGGTGGAGATGTTTTTAGCAGA 35888	CA_	TG
	G		CTC TGAAGGCATCTC TTT		
			GAG ATTTTGTAGAG GGG		
			ACG GT		
GAM1425	FLJ10300	5'	AAACAGTTCCCCTTCCAGAG 35996	CAT	CATCT
			CTC GAAGG CTGTTT		



			GAG CTTCC GACAAA		
			AC_ CCTT_		
GAM1425	FLJ10352	3'	AAGTGGAGATGTTTTTAGAG 49555	CA	TG
			CTC TGAAGGCATCTC TTT		
			GAG ATTTTGTAGAG GAA		
			__ GT		
GAM1425	FLJ10407	5'	AGGCAGAGGGCGGTTCTGGAG 36088	T	G_ A
			ACTCCA GAA GC TCTCTGTTT		
			TGAGGT CTT CG GGAGACGGA		
			C GG _		
GAM1425	FLJ10468	3'	GAGCACTTCTCTCTTATGGGGT 36147	AG	CATCTC
			ACTCCATGA G TGTTT		
			TGGGGTATT C ACGAG		
			CT TCTTC_		
GAM1425	FLJ10508	3'	GACAGAGGGAACATGGA 36199	AAGGCA	
			TCCATG TCTCTGTT		
			AGGTAC GGAGACAG		
			AAG__		
GAM1425	FLJ10520	3'	AGGCAGAGGTTGCAGTGAGT 36209	CATGAAG	_
			ACTC GCA TCTCTGTTT		
			TGAG CGT GGAGACGGA		
			TGA__ T		
GAM1425	FLJ10597	3'	GGCAGGGAGGTGGGG 36317	GAAGGCA	
			CTCCAT TCTCTGTT		
			GGGGTG AGGGACGG		
			G__		
GAM1425	FLJ10704	3'	AGACGGAGGTTACAGTGAGT 36448	C	GAAGGC
			ACTC AT ATCTCTGTTT		
			TGAG TG TGGAGGCAGA		
			_ ACAT_		
GAM1425	FLJ10748	3'	AAATGGAGAATGATTGGGG 36555	TGAAGG	_
			CTCCA CAT CTCTGTTT		
			GGGGT GTA GAGGTAAA		
			TA__ A		
GAM1425	FLJ10829	3'	GGTGAGGTCTTCATGAGT 36712	C	A T
			ACTC ATGAAGGC TC CT		
			TGAG TACTTCTG AG GG		
			_ G T		
GAM1425	FLJ10904	3'	AGACAGACTTCTTTTATGTAGT 36845	C	CATC
			ACT CATGAAGG TCTGTTT		

		TGA GTATTTTC AGACAGA		
		T TTC_		
GAM1425	FLJ10970	3' GAATGGGGGTGGGAGGGTGGAG 36922	GAAGG	
		CTCCAT CATCTCTGTTT		
		GAGGTG GTGGGGGTAAG		
		GGAGG		
GAM1425	FLJ11036	3' AGGCAGAGGGTGGGTGTGGGG 36997	AAG A	
		CTCCATG GC TCTCTGTTT		
		GGGGTGT TG GGAGACGGA		
		GGG _		
GAM1425	FLJ11198	3' GGTGGGGGTCTGGGGGGT 37158	ATGA AT TG	
		ACTCC AGGC CTC TT		
		TGGGG TCTG GGG GG		
		GG_ _ GT		
GAM1425	FLJ11267	3' GGGCAGGTTGTTATCTGCATGG 39005	A _ T T	
		GGT CTCCATG AG GCA C CTGTTT		
		GGGGTAC TC TGT G GACGGG		
		G TAT T_		
GAM1425	FLJ11726	3' AAGCAGGGGCCCGTCAGGAGT 46403	A A_ AT	
		ACTCC TGA GGC CTCTGTTT		
		TGAGG ACT CCG GGGACGAA		
		_ GC _		
GAM1425	FLJ11996	5' GGATAATTGCCTTTTATGGA 46438	_ TC_	
		TCCATGAA GGCA TCT		
		AGGTATTT CCGT AGG		
		T TAAT		
GAM1425	FLJ12171	3' GAGCAGAGGGATGTATGGAGT 44871	AAGGCA	
		ACTCCATG TCTCTGTTT		
		TGAGGTAT GGAGACGAG		
		GTAG_		
GAM1425	FLJ12229	3' AGGTAGGGGTGCGGGGTGGGG 45915	GAAG TT	
		CTCCAT GCATCTCTG T		
		GGGGTG CGTGGGGAT A		
		GGG_ GG		
GAM1425	FLJ12270	3' GGAAGTTTTTCATGGAG 47573	A	
		CTCCATGAAGGC TCT		
		GAGGTACTTTTG AGG		
		A		
GAM1425	FLJ12303	3' GTGCATTATGTTTTTCATGAGGT 72702	TC CTC TT	
		AC CATGAAGGCAT TGT		

TG GTACTTTTGT ACG  
 GA TT\_ TGG  
 GAM1425 FLJ12425 3' GAACACTTTTGTGTGTGGAG 85892 TG AG TCTC  
 T ACTCCA A GCA TGTTT  
 ||||| I ||| |||||  
 TGAGGT T TGT ACAAG  
 GT GT TTTC  
 GAM1425 FLJ12505 3' GCAGAGACCAGGAGT 45388 ATGAA CA  
 ACTCC GG TCTCTGT  
 ||||| || |||||  
 TGAGG CC AGAGACG  
 A\_\_\_\_\_  
 GAM1425 FLJ12526 3' GGATGGGGGTGTCTACG 45563 A  
 TG AGGCATCTCTGTTT  
 || |||||  
 GC TCTGTGGGGGTAGG  
 A  
 GAM1425 FLJ12529 3' AAGCAGAGAAGGCCTATGAGGT 45657 TC GA A\_  
 AC CAT AGGC TCTCTGTTT  
 || ||| ||| |||||  
 TG GTA TCCG AGAGACGAA  
 GA \_ GA  
 GAM1425 FLJ12577 3' GAATAGGGGACCCACGGGGT 48156 A AA CA  
 ACTCC TG GG TCTCTGTTT  
 ||||| || || |||||  
 TGGGG AC CC GGGGATAAG  
 C \_ A\_  
 GAM1425 FLJ12687 3' AGGTGGAGGTTGCAGTGGG 46185 GAAG \_ TG  
 TCCAT GCA TCTC TTT  
 ||||| ||| ||| |||  
 GGGTG CGT GGAG GGA  
 A\_\_ T GT  
 GAM1425 FLJ12875 5' GGTGGAGAGTCGGGGGT 44609 ATGAA A TG  
 ACTCC GGC TCTC TT  
 ||||| ||| ||| ||  
 TGGGG CTG AGAG GG  
 G\_\_\_\_ \_ GT  
 GAM1425 FLJ13119 5' AACAGGGAAATGTGGTGT 44719 T GAAGGCA  
 AC CCAT TCTCTGTT  
 || ||| |||||  
 TG GGTG AGGGACAA  
 T TAA\_\_\_\_  
 GAM1425 FLJ13181 5' GGGCAGAGGAGGGCGTGGGCGT 47240 \_ AAGGCA  
 AC TCCATG TCTCTGTTT  
 || ||||| |||||  
 TG GGGTGC GGAGACGGG  
 C GGGA\_  
 GAM1425 FLJ13215 3' AGACGACTTTTCATGGA 46565 CA \_  
 TCCATGAAGG TC TCT  
 ||||| || |||

AGGTACTTTT AG AGA  
 C\_ C  
 GAM1425 FLJ13769 3' AGGTGGAGGTTGCCAGTGAGT 46598 C GAA \_ TG  
 ACTC AT GGCA TCTC TTT  
 |||| || |||| |||| ||  
 TGAG TG CCGT GGAG GGA  
 \_ A\_ T GT  
 GAM1425 FLJ13798 3' AGGCAGGGGTGAAACATGGG 87106 AAGG  
 TCCATG CATCTCTGTTT  
 ||||| |||||  
 GGGTAC GTGGGGACGGA  
 AAA\_  
 GAM1425 FLJ13855 3' GACAGGGATTGGTGGG 43587 G AGGC  
 TCCAT A ATCTCTGTT  
 ||||| |||||  
 GGGTG T TAGGGACAG  
 G \_\_\_\_  
 GAM1425 FLJ14129 3' AGGCGGGGAGGTCTCAGGGGT 48064 A A A  
 ACTCC TGA GGC TCTCTGTTT  
 |||| |||| |||||  
 TGGGG ACT CTG AGGGGCGGA  
 \_ \_ G  
 GAM1425 FLJ14153 3' TATGTGAAGATGTTTTATGAA 42707 C CTGTTT  
 GT ACT CATGAAGGCATCT  
 || |||||  
 TGA GTATTTTGTAGA  
 A AGTGTATA  
 GAM1425 FLJ14260 3' AAGCAGAGATGTTGAAGGA 46703 ATGAA  
 TCC GGCATCTCTGTTT  
 || |||||  
 AGG TTGTAGAGACGAA  
 AAG\_  
 GAM1425 FLJ14356 5' AGTGGGTTCCCTCGTGGGGT 48029 A C \_  
 ACTCCATGA GG ATCT CT  
 ||||| || ||||  
 TGGGGTGCT CC TGGG GA  
 C T T  
 GAM1425 FLJ14356 5' GGATGGGGGTGTTTAGGGGT 48033 ATGA  
 ACTCC AGGCATCTCTGTTT  
 |||| |||||  
 TGGGG TTTGTGGGGGTAGG  
 A\_  
 GAM1425 FLJ14596 3' GGGTGGAGGTGAAGGATGGGG 51463 GAAGG TG  
 CTCCAT CATCTC TTT  
 |||| |||| ||  
 GGGGTA GTGGAG GGG  
 GGAA\_ GT  
 GAM1425 FLJ14641 3' AGGCAGAGAGTGCCGTGGAGT 51482 GAA \_  
 ACTCCAT GGCA TCTCTGTTT  
 ||||| |||||

			TGAGGTG CCGT AGAGACGGA		
			___ G		
GAM1425	FLJ20034	3'	AAATGGGGCGCTGTTGTTTGTG 34352	TG ___	AT
			GGGT CCA AA GGC CTCTGTTT		
			GGT TT TCG GGGGTAAA		
			GT GTTG C_		
GAM1425	FLJ20054	5'	AGGTGGCTTTTGTGGAG 38782	TG _	
			CTCCA AAGGC ATCT		
			GAGGT TTTCG TGGA		
			GT G		
GAM1425	FLJ20207	3'	AAGTGGAATGCTTCAGGGGT 34735	A G C	TG
			ACTCC TGAAG CAT TC TTT		
			TGGGG ACTTC GTA AG GAA		
			_ _ _ GT		
GAM1425	FLJ20280	3'	AGACGGAGGTTGCGGTGAGT 34847	C GAAG _	
			ACTC AT GCA TCTCTGTTT		
			TGAG TG CGT GGAGGCAGA		
			_ G_ T		
GAM1425	FLJ20308	3'	GGACAGAGGCTGATGCTGGAGT 66855	TGAA_	AT
			ACTCCA GGC CTCTGTTT		
			TGAGGT TCG GAGACAGG		
			CGTAG _		
GAM1425	FLJ20374	5'	AGGTGGGGGTGTTCCCCGGGG 35078	ATGAA	TG
			CTCC GGCATCTC TTT		
			GGGG TTGTGGGG GGA		
			CCCC_ GT		
GAM1425	FLJ20436	3'	GTGGGAGCTGTCTTTGTGAGT 35171	C TG	T GTTT
			ACTC A AAGGCA CTCT		
			TGAG T TTCTGT GAGG		
			_ GT C GTGG		
GAM1425	FLJ20464	5'	AAGTGGGGGTGCCGAGGAGT 35225	ATGAA	TG
			ACTCC GGCATCTC TTT		
			TGAGG CCGTGGGG GAA		
			AGG_ GT		
GAM1425	FLJ20725	3'	GGTTGTGTTTTTCATGGGG 35612	CT	
			CTCCATGAAGGCAT CT		
			GGGGTACTTTTGTG GG		
			TT		
GAM1425	FLJ20793	3'	AGTGCATGTTTTTATCGAGT 91804	C	CT_
			ACTC ATGAAGGCAT CT		

TGAG TATTTTTGTA GA  
 C CGT  
 GAM1425 FLJ21044 3' AGTAGGGATGTCTTTTC 42330 T  
 A GAAGGCATCTCTGTT  
 | |||||  
 C TTTCTGTAGGGATGA  
 T  
 GAM1425 FLJ21144 3' GAGCTTGGCTTTTATGGAG 42877 AT\_\_  
 CTCCATGAAGGC CTC  
 ||||| ||  
 GAGGTATTTTCG GAG  
 GTTC  
 GAM1425 FLJ21324 5' AGCAGGGGAACTGGAGT 91186 TGAA GCA  
 ACTCCA G TCTCTGTT  
 |||| | |||||  
 TGAGGT C GGGGACGA  
 \_\_\_\_AA\_  
 GAM1425 FLJ21324 5' AGTGGGGGCCCATGGGG 91188 AA AT TG  
 CTCCATG GGC CTC TT  
 ||||| || || ||  
 GGGGTAC CCG GGG GA  
 \_\_\_\_GT  
 GAM1425 FLJ21324 5' GAGCAGATGGTGCCTTTGTGGG 91203 TG \_  
 TCCA AAGGCATC TCTGTTT  
 ||| ||||| |||||  
 GGGT TTCCGTGG AGACGAG  
 GT T  
 GAM1425 FLJ21324 3' GGCAGAGGTGCTGACGT 91207 AA  
 ATG GGCATCTCTGTT  
 || |||||  
 TGC TCGTGGAGACGG  
 AG  
 GAM1425 FLJ21777 3' AGGCGGAGGTTGCAGTGAGT 49862 CATGAAG \_  
 ACTC GCA TCTCTGTTT  
 ||| || |||||  
 TGAG CGT GGAGGCGGA  
 TGA\_\_\_\_T  
 GAM1425 FLJ21865 3' AAGCAGAGACTGGGATTAGGGG 42801 A AGG \_  
 T ACTCC TGA CA TCTCTGTTT  
 |||| || || |||||  
 TGGGG ATT GT AGAGACGAA  
 \_ AGG C  
 GAM1425 FLJ22173 5' GGATGGGGAGGCTGCGGGGT 46748 ATGAA A  
 ACTCC GGC TCTCTGTTT  
 |||| || |||||  
 TGGGG TCG AGGGGTAGG  
 CG\_\_\_\_G  
 GAM1425 FLJ22215 3' GGGTGGGGGTGCCTAGCCAGGT 43093 T A A\_\_ TG  
 G C CC TG AGGCATCTC TTT  
 || || ||||| ||

G GG AC TCCGTGGGG GGG  
 T \_ CGA GT  
 GAM1425 FLJ22215 5' GGGTGGGGGTGCCTAGCCAGGT 96837 T A A\_\_ TG  
 G C CC TG AGGCATCTC TTT  
 ||| || ||||| |||  
 G GG AC TCCGTGGGG GGG  
 T \_ CGA GT  
 GAM1425 FLJ22349 3' AGGTGGAGGTGTGGTTGTGG 45692 TG AG TG  
 CCA A GCATCTC TTT  
 ||| | ||||| |||  
 GGT T TGTGGAG GGA  
 GT GG GT  
 GAM1425 FLJ22635 3' GACAGAGGTGGGGGAGT 46981 ATGAAGG  
 ACTCC CATCTCTGTT  
 |||| |||||  
 TGAGG GTGGAGACAG  
 GG\_\_\_\_  
 GAM1425 FLJ22729 5' GGTGGAGATGCTTTCTG 45190 T TG  
 CA GAAGGCATCTC TT  
 || ||||| ||  
 GT CTTTCGTAGAG GG  
 \_ GT  
 GAM1425 FLJ23017 3' AGATGGGGAATATTTGGAGT 43119 TGAAGGCA  
 ACTCCA TCTCTGTTT  
 |||| |||||  
 TGAGGT AGGGGTAGA  
 TTATA\_\_\_\_  
 GAM1425 FLJ23074 3' GGGCGGGGAAGAGTTAAGGAGT 46819 A AGGCA  
 ACTCC TGA TCTCTGTTT  
 |||| || |||||  
 TGAGG ATT AGGGGCGGG  
 A GAGA\_  
 GAM1425 FLJ23323 3' AAACAGAGATTCCTCAGAAAGT 45047 CCA A C  
 ACT TGA GG ATCTCTGTTT  
 || ||| |||||  
 TGA ACT CC TAGAGACAAA  
 AAG \_ T  
 GAM1425 FLJ23360 3' AAGCAGAGTGATTATGGA 43565 AGG T  
 TCCATGA CA CTCTGTTT  
 |||| || |||||  
 AGGTATT GT GAGACGAA  
 A\_\_ \_  
 GAM1425 FLJ23550 3' GGATGGGGAGAGGTGTGGAGT 46854 AAGGCA  
 ACTCCATG TCTCTGTTT  
 |||| |||||  
 TGAGGTGT AGGGGTAGG  
 GGAG\_\_  
 GAM1425 FLJ23604 5' GGAATGTATTTATGGAGT 46861 G CT  
 ACTCCATGAA GCAT C  
 ||||| ||| |

			TGAGGTATTT TGTA G		
			A AG		
GAM1425	FLJ25422	3'	AGACAGAAGTATAGTTTTCATG 58755	— — —	
			GAG TCCATGAAGGC AT CT CTGTTT		
			AGGTACTTTTG TA GA GACAGA		
			A T A		
GAM1425	FLJ30058	3'	AAGCAGAGATGTTTCTGTG 58636 GA		
			CAT AGGCATCTCTGTTT		
			GTG TTTGTAGAGACGAA		
			TC		
GAM1425	FLJ32332	3'	AGGCAGGGAGACCGTGGG 58298 GAA CA		
			TCCAT GG TCTCTGTTT		
			GGGTG CC AGGGACGGA		
			— AG		
GAM1425	GABARAPL1	3'	GGACAGAGGTGTCTTATGTAG 48602 C A		
			CT CATGA GGCATCTCTGTTT		
			GA GTATT CTGTGGAGACAGG		
			T —		
GAM1425	GABARAPL3	3'	AAATAGGGGTTAGGCATGAGGG 50796 — AAGGC		
			T ACTC CATG ATCTCTGTTT		
			TGGG GTAC TGGGGATAAA		
			A GGAT_		
GAM1425	GABARAPL3	3'	GGACAGAGATGTCTTATGTAG 50801 C A		
			CT CATGA GGCATCTCTGTTT		
			GA GTATT CTGTAGAGACAGG		
			T —		
GAM1425	GIT2	3'	GGGCAGAGGAGACTATGGGG 54083 GA GCA		
			CTCCAT AG TCTCTGTTT		
			GGGGTA TC GGAGACGGG		
			— AGA		
GAM1425	GIT2	3'	GGGCAGAGGAGACTATGGGG 54096 GA GCA		
			CTCCAT AG TCTCTGTTT		
			GGGGTA TC GGAGACGGG		
			— AGA		
GAM1425	GIT2	3'	GGGCAGAGGAGACTATGGGG 28761 GA GCA		
			CTCCAT AG TCTCTGTTT		
			GGGGTA TC GGAGACGGG		
			— AGA		
GAM1425	GK001	3'	GGTGGATGTTTCATGGAG 39498 AG —		
			CTCCATGA GCATCT CT		



			GAGGTACT TGTAGG GG		
			— T		
GAM1425	GMEB2	5'	TGATTAGAGATGCCTTTGTGAG 24740	C TG	TTT
	T		ACTC A AAGGCATCTCTG		
			TGAG T TTCCGTAGAGAT		
			_GT TAGTC		
GAM1425	GPR88	3'	AAGCAACACTGTTTTTATGTAG 41873	C	TCTC
	T		ACT CATGAAGGCA TGTTT		
			TGA GTATTTTGT ACGAA		
			T CACA		
GAM1425	GPS2	5'	AGATGAAGCCTTCATGGTGT 87150	T	A _
			AC CCATGAAGGC TC TCT		
			TG GGTACTTCCG AG AGA		
			T A T		
GAM1425	GPS2	5'	GGATGGAGAGGATATGGGG 15667		AAGGCA
			CTCCATG TCTCTGTTT		
			GGGGTAT AGAGGTAGG		
			AGG__		
GAM1425	GPS2	5'	GGGTGGGGAGCCGTGTGGGTGT 15670	_	GAA A TG
			AC TCCAT GGC TCTC TTT		
			TG GGGTG CCG AGGG GGG		
			T TG_ _ GT		
GAM1425	GRASP1	3'	GGGCAGAGGCCACCAGGGAGT 39303	A AA	AT
			ACTCC TG GGC CTCTGTTT		
			TGAGG AC CCG GAGACGGG		
			G CA _		
GAM1425	GRID1	3'	AGTAGAAGCTTTGTGGTGT 68494	T G	A _
			AC CCAT AAGGC TCT CT		
			TG GGTG TTTCG AGA GA		
			T _ A T		
GAM1425	GTF2E1	3'	GAATATATGAGCCTTGATGGA 18613	_	A TC_
	GT		ACTCCATG AAGGC TC TGTTT		
			TGAGGTAT TTCCG AG ATAAG		
			G _ TAT		
GAM1425	GZMK	3'	AAGCAGAGCACATATGGGGT 9168	AAG	ATC
			ACTCCATG GC TCTGTTT		
			TGGGGTAT CG AGACGAA		
			ACA _		
GAM1425	H105E3	3'	AAACAGACATTTCTTCCTTCAT 31927	C_	C
	GGA		TCCATGAAGG AT TCTGTTT		

			AGGTACTTCC	TA AGACAAA		
			TTCTT	C		
GAM1425	H2AFJ	3'	AAACCTCTTGCTTTTAGGGGT	36836	A	TCTCT
			ACTCC TGAAGGCA	GTTT		
			TGGGG	ATTTTCGT CAAA		
			—	TCTC—		
GAM1425	H2AFJ	3'	AGTAATGTCTTTGGGAGT	36839	A	CT
			ACTCC TGAAGGCAT	CT		
			TGAGG	GTTTCTGTA GA		
			—	AT		
GAM1425	HA-1	3'	GGATGGGGGCGGAGCTGGGGT	65555		TGAAG AT
			ACTCCA	GC CTCTGTTT		
			TGGGGT	CG GGGGTAGG		
			CGAGG	—		
GAM1425	HEMGN	3'	GAACACATACATTTTGTGGAGT	37379		TG GCATCTC
			ACTCCA	AAG TGTTT		
			TGAGGT	TTT ACAAG		
			GT	ACATAC—		
GAM1425	HIC2	3'	GAGCGGCGTCTTTTGGGG	65261	T	ATCT
			CTCCA	GAAGGC CTGTTT		
			GGGGT	TTTCTG GGCGAG		
			—	C—		
GAM1425	HNRPA0	3'	GGGTGGGGGTTGGGGTGGGG	22323		GAAGGC TG
			CTCCAT	ATCTC TTT		
			GGGGTG	TGGGG GGG		
			GGGT—	GT		
GAM1425	HS6ST	3'	GAGCAGGGATGTAGTGGGG	62027		GAAG
			CTCCAT	GCATCTCTGTTT		
			GGGGTG	TGTAGGGACGAG		
			A—			
GAM1425	HS6ST1	3'	GAGCAGGGATGTAGTGGGG	16659		GAAG
			CTCCAT	GCATCTCTGTTT		
			GGGGTG	TGTAGGGACGAG		
			A—			
GAM1425	HSA249128	3'	AAGCAGGGATGTACTAGGGG	34150		ATGAAG
			CTCC	GCATCTCTGTTT		
			GGGG	TGTAGGGACGAA		
			ATCA—			
GAM1425	HSD17B12	3'	AAATAGAAGTTGCTTTTAGGGG	32338	A	T _
			ACTCC	TGAAGGCA CT CTGTTT		

TGGGG ATTTTCGT GA GATAAA  
 \_ T A  
 GAM1425 HSPC065 3' GAGTGATTCTGCTTTTGTGTTGGG 26301 C TG \_\_\_\_ T GTTT  
 T ACTC A AAGGCA TC CT  
 ||||| ||||| ||||  
 TGGG T TTTCGT AG GA  
 T GT CTT T G  
 GAM1425 HSPC189 3' GGATGGAGGTGGGGAGTGTGGT 95277 T AAGG\_  
 GT AC CCATG CATCTCTGTTT  
 || ||||| |||||  
 TG GGTGT GTGGAGGTAGG  
 T GAGGG  
 GAM1425 IL10RB 3' GAATGGAGATGTTACATCTGG 5277 T A\_\_  
 CCA GA GGCATCTCTGTTT  
 ||| || |||||  
 GGT CT TTGTAGAGGTAAG  
 \_ ACA  
 GAM1425 JIK 3' GGACGGGGGTGGGTGGGGT 32799 GAAGG  
 ACTCCAT CATCTCTGTTT  
 ||||| |||||  
 TGGGGTG GTGGGGGCAGG  
 G\_\_\_\_  
 GAM1425 JM1 3' GCAGGGATTGTTGGGGT 25793 TGAAGGC  
 ACTCCA ATCTCTGT  
 ||||| |||||  
 TGGGGT TAGGGACG  
 T\_\_\_\_\_  
 GAM1425 KCNK16 3' GACAGAGGTGTGGGAG 49506 ATGAAG  
 CTCC GCATCTCTGTT  
 ||| |||||  
 GAGG TGTGGAGACAG  
 G\_\_\_\_\_  
 GAM1425 KCNS1 5' AGGTGGAGATCCAAGTGGAG 9571 GAA C TG  
 CTCCAT GG ATCTC TTT  
 ||||| || ||||| |||  
 GAGGTG CC TAGAG GGA  
 AA\_ \_ GT  
 GAM1425 KIAA0057 3' TTAAGCTGCCTCATTCTTTTAT 24446 \_\_\_\_\_ T CTGTTT  
 GGAGT ATGA AGGCA CT  
 ||||| ||||| |||  
 TATT TCCGT GA  
 TTCTTAC C A TTT  
 GAM1425 KIAA0089 3' GAGCAGGGACAGAGCCAGGAGT 69965 ATGAA A\_\_\_\_  
 ACTCC GGC TCTCTGTTT  
 ||||| ||| |||||  
 TGAGG CCG AGGGACGAG  
 A\_\_\_\_ AGAC  
 GAM1425 KIAA0152 3' GGGCAGGGATGCTTTC 28302  
 GAAGGCATCTCTGTTT  
 |||||

CTTTCGTAGGGACGGG

GAM1425 KIAA0189 3' AGATAGGGATGTGAGAGTGGAG 28269 GAAG  
T ACTCCAT GCATCTCTGTTT

||||| |||||  
TGAGGTG TGTAGGGATAGA  
AGAG

GAM1425 KIAA0218 3' AAGCGGAGATGACATGGAAGT 28617 \_ AAGG  
ACTCCATG CATCTCTGTTT

||| ||||| |||||  
TGA GGTAC GTAGAGGCGAA  
A A\_\_

GAM1425 KIAA0247 3' GGCAGAGGGGTGTGGAG 28405 GAAG AT  
CTCCAT GC CTCTGTT

||||| || |||||  
GAGGTG TG GAGACGG  
\_\_ GG

GAM1425 KIAA0258 3' GAACAGGGGTGTTGGCTGAG 28815 CATGAA  
CTC GGCATCTCTGTTT

||| |||||  
GAG TTGTGGGGACAAG  
TCGG\_\_

GAM1425 KIAA0295 3' GCAGGGGGCAGGGGT 68104 ATGAAG A  
ACTCC GC TCTCTGT

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TGGGG CG GGGGACG  
A\_\_ \_

GAM1425 KIAA0296 3' GAGCAGAGGGCAGGTGGGAGT 28111 ATGAAG A  
ACTCC GC TCTCTGTTT

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TGAGG CG GGAGACGAG  
GTGGA\_ \_

GAM1425 KIAA0296 3' GGGTGGGGGCTTGGCTATGGGG 28116 A\_\_ AT TG  
T ACTCCATG AGGC CTC TTT

||||| ||| ||| |||  
TGGGGTAT TTCG GGG GGG  
CGG \_ GT

GAM1425 KIAA0317 3' ACAGGGACTAGGAGT 29080 ATGA GCA  
ACTCC AG TCTCTGT

||||| || |||||  
TGAGG TC AGGGACA  
A\_\_ \_

GAM1425 KIAA0317 5' GGGTGGAGACCAACTCTGGGGT 29089 T A\_\_ CA TG  
ACTCCA GA GG TCTC TTT

||||| || || ||| |||  
TGGGGT CT CC AGAG GGG  
\_ CAA \_ GT

GAM1425 KIAA0319 5' GGGCGGGGATCCCCGGGGGT 29039 A AA C  
ACTCC TG GG ATCTCTGTTT

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TGGGG GC CC TAGGGGCGGG  
 \_ CC \_  
 GAM1425 KIAA0352 3' GAGTGGGCTCTATGGGGT 29156 AA AT\_  
 ACTCCATG GGC CTC  
 ||||| ||| |||  
 TGGGGTAT TCG GAG  
 C\_ GGT  
 GAM1425 KIAA0354 3' GAGTCATGTTTTGTGGGGT 29570 G \_  
 ACTCCAT AAGGCAT CTC  
 ||||| ||||| |||  
 TGGGGTG TTTTGTA GAG  
 \_ CT  
 GAM1425 KIAA0375 3' AGGTGGAGATGAGGATGGG 71019 GAAGG TG  
 TCCAT CATCTC TTT  
 |||| ||||| |||  
 GGGTA GTAGAG GGA  
 GGA\_ GT  
 GAM1425 KIAA0391 3' GAGTGGGGAACCATTTGTAGGGT 27913 C TG A CA TG  
 ACTC A A GG TCTC TTT  
 |||| | || |||| |||  
 TGGG T T CC AGGG GAG  
 A GT A A\_ GT  
 GAM1425 KIAA0397 3' AGGCAGGGGATGCATGGGTGT 61671 \_ GAAG \_  
 AC TCCAT GCATCTC TGTTT  
 || |||| ||||| |||||  
 TG GGGTA CGTAGGG ACGGA  
 T \_ G  
 GAM1425 KIAA0417 3' AGACAGAGGTGCCTAGGG 71241 ATGA  
 CC AGGCATCTCTGTTT  
 || |||||  
 GG TCCGTGGAGACAGA  
 GA\_  
 GAM1425 KIAA0418 3' AAATGGGGGTGGGGGGTGGGG 27550 GAAGG  
 CTCCAT CATCTCTGTTT  
 |||| |||||  
 GGGGTG GTGGGGGTAAA  
 GGGG\_  
 GAM1425 KIAA0418 3' GGATGGGGGTGCCCACACTGAG 27559 CA AA  
 T ACTC TG GGCATCTCTGTTT  
 |||| || |||||  
 TGAG AC CCGTGGGGGTAGG  
 TC AC  
 GAM1425 KIAA0444 3' GGGCAGGGGACAGGGCGTGGG 62345 AAGGCA  
 TCCATG TCTCTGTTT  
 |||| |||||  
 GGGTGC GGGGACGGG  
 GGGACA  
 GAM1425 KIAA0444 3' GGGTGGAGGTGCACACGGG 62346 A AAG TG  
 TCC TG GCATCTC TTT  
 ||| || ||||| |||

GGG AC CGTGGAG GGG  
 C A\_\_ GT  
 GAM1425 KIAA0469 3' GAGCAGGGGTGTGGGCTTGGAG 29331 TGAAG  
 CTCCA GCATCTCTGTTT  
 |||| |||||  
 GAGGT TGTGGGGACGAG  
 TCGGG  
 GAM1425 KIAA0476 5' AGCGGGGGTTGGGGGAGT 29375 ATGAAGGC  
 ACTCC ATCTCTGTT  
 |||| |||||  
 TGAGG TGGGGGCGA  
 GGGT\_\_\_\_  
 GAM1425 KIAA0478 3' AAGCAGGGATGCTATAATGAGT 29536 C GAA  
 ACTC AT GGCATCTCTGTTT  
 ||| || |||||  
 TGAG TA TCGTAGGGACGAA  
 \_ ATA  
 GAM1425 KIAA0478 3' GCAGGGACCAGGGGT 29548 ATGAA CA  
 ACTCC GG TCTCTGT  
 |||| || |||||  
 TGGGG CC AGGGACG  
 A\_\_\_\_ \_  
 GAM1425 KIAA0481 3' GAGCAGAGGTGGACATGGGGT 71847 AAGG  
 ACTCCATG CATCTCTGTTT  
 ||||| |||||  
 TGGGGTAC GTGGAGACGAG  
 AG\_\_\_\_  
 GAM1425 KIAA0493 5' AGGTGCTCTTGTTCATGGGGT 64270 \_ \_  
 ACTCCATGA AG GCATCT  
 ||||| || |||||  
 TGGGGTACT TC CGTGGA  
 GT T  
 GAM1425 KIAA0493 5' GGGCAGGGATGGTGGTGAGGGT 64278 \_ GAAGG  
 ACTC CAT CATCTCTGTTT  
 ||| || |||||  
 TGGG GTG GTAGGGACGGG  
 A GTG\_\_\_\_  
 GAM1425 KIAA0514 3' GGTAGGTTTCTGCATGGAGT 28094 A C \_  
 ACTCCATG AGG ATCT CT  
 ||||| || ||| ||  
 TGAGGTAC TCT TGGA GG  
 G T T  
 GAM1425 KIAA0574 3' GGACAGAGGGTGACATCGAGT 69282 C AAG A  
 ACTC ATG GC TCTCTGTTT  
 ||| || || |||||  
 TGAG TAC TG GGAGACAGG  
 C AG\_ \_  
 GAM1425 KIAA0618 3' GGGCAGAGGGCAGAGCAGGGGT 29174 A AAG\_ A  
 ACTCC TG GC TCTCTGTTT  
 |||| || || |||||

TGGGG AC CG GGAGACGGG  
 \_ GAGA \_  
 GAM1425 KIAA0628 3' AGACGGAGATCACAGTAGGGT 28861 C GAAGGC  
 ACTC AT ATCTCTGTTT  
 |||| || |||||  
 TGGG TG TAGAGGCAGA  
 A ACAC\_  
 GAM1425 KIAA0630 3' GGATGGAGATGGGAGATTTTCAT 89392 G\_\_\_\_  
 GGAG CCATGAAG CATCTCTGTTT  
 ||||| |||||  
 GGTACTTT GTAGAGGTAGG  
 AGAGG  
 GAM1425 KIAA0650 3' GGATTTTGGTTTTTTGTGGGGT 88239 TG C TCT  
 ACTCCA AAGG ATC GTTT  
 |||| ||| |||  
 TGGGGT TTTT TGG TAGG  
 GT \_ TTT  
 GAM1425 KIAA0662 3' GGGCAGGGGAGCCATTGTGGGG 81859 TG A AT  
 T ACTCCA A GGC CTCTGTTT  
 |||| | ||| |||||  
 TGGGGT T CCG GGGACGGG  
 GT A AG  
 GAM1425 KIAA0861 5' GGGCGGAGATGCCTTTA 88931  
 TGAAGGCATCTCTGTTT  
 |||||  
 ATTTCCGTAGAGGCGGG  
 GAM1425 KIAA0912 3' AGGCAGGGAAGGTAAGGAGT 64405 ATGAAG A\_  
 ACTCC GC TCTCTGTTT  
 |||| || |||||  
 TGAGG TG AGGGACGGA  
 AA\_\_\_\_ GA  
 GAM1425 KIAA0930 3' GGGCGGGGGTGTCTTT 70548  
 GAAGGCATCTCTGTTT  
 |||||  
 TTTCTGTGGGGGCGGG  
 GAM1425 KIAA0945 3' GGGCAGGGGCCCCCTGTGGG 30214 AA AT  
 TCCATG GGC CTCTGTTT  
 |||| ||| |||||  
 GGGTGT CCG GGGACGGG  
 CC \_  
 GAM1425 KIAA0953 3' AGCAGGGGTGCAGGGG 66777 ATGAAG  
 CTCC GCATCTCTGTT  
 ||| |||||  
 GGGG CGTGGGGACGA  
 A\_\_\_\_  
 GAM1425 KIAA0980 3' AGATGGAGGTGGGGGCTGGGG 47202 TGAAGG  
 CTCCA CATCTCTGTTT  
 |||| |||||

GGGGT GTGGAGGTAGA  
CGGGG\_  
GAM1425 KIAA1024 3' AAATGGAGATGAAATCATGGAG 69058 AGG  
CTCCATGA CATCTCTGTTT  
||||| |||||  
GAGGTACT GTAGAGGTAAA  
AAA  
GAM1425 KIAA1032 3' AGGTGGAGGTGCTTTGGGG 66150 TGA TG  
CTCCA AGGCATCTC TTT  
|||| ||||| ||  
GGGGT TTCGTGGAG GGA  
\_\_\_\_ GT  
GAM1425 KIAA1036 5' AGATGGGGGTGCTTTGTG 29810 G  
CAT AAGGCATCTCTGTTT  
|| |||||  
GTG TTTCGTGGGGGTAGA  
\_\_\_\_  
GAM1425 KIAA1036 3' GGGTGGAGATGTTTCTC 29826 \_ TG  
GA AGGCATCTC TTT  
|| ||||| ||  
CT TTTGTAGAG GGG  
C GT  
GAM1425 KIAA1036 3' GGGTGGGGGTGGGGTGGAG 29827 GAAGG TG  
CTCCAT CATCTC TTT  
|||| |||| ||  
GAGGTG GTGGGG GGG  
GG\_\_\_\_ GT  
GAM1425 KIAA1055 3' GGATGGAGGAATGTTTTCGGGG 66064 A \_  
GT ACTCC TGAAGGCAT CTCTGTTT  
|||| ||||| |||||  
TGGGG GCTTTTGTA GAGGTAGG  
\_\_\_\_ AG  
GAM1425 KIAA1055 3' GGGGTTTTTTTATGGG 66066 C  
TCCATGAAGG ATCTC  
||||| ||||  
GGGTATTTTT TGGGG  
\_\_\_\_  
GAM1425 KIAA1061 3' GGTGGGGAGTCAGGGGT 71179 ATGAA A TG  
ACTCC GGC TCTC TT  
|||| || |||| ||  
TGGGG CTG AGGG GG  
A\_\_\_\_ \_ GT  
GAM1425 KIAA1076 3' AGTGGGGGTGTTCGAG 65511 CAT AG TG  
CTC GA GCATCTC TT  
|| || ||||| ||  
GAG CT TGTGGGG GA  
\_\_\_\_ \_ GT  
GAM1425 KIAA1095 3' GGATGGAGACGGTTTGTGGA 67470 TG GGCA  
TCCA AA TCTCTGTTT  
|||| || |||||



AGGT TT AGAGGTAGG  
 GT GGC\_  
 GAM1425 KIAA1110 3' GGTGGGGGCCGTGGGG 61849 GAA AT TG  
 CTCCAT GGC CTC TT  
 ||||| ||| ||| ||  
 GGGGTG CCG GGG GG  
 \_\_\_\_ \_ GT  
 GAM1425 KIAA1196 3' GAGCAGCCTCGTGGAGT 61466 A AT  
 ACTCCATGA GGC CTC  
 ||||| ||| |||  
 TGAGGTGCT CCG GAG  
 \_ AC  
 GAM1425 KIAA1196 3' GGGCAGGGGTCAGGCAGGGAGT 61476 A AAGGC  
 ACTCC TG ATCTCTGTTT  
 ||||| || |||||  
 TGAGG AC TGGGGACGGG  
 G GGAC\_  
 GAM1425 KIAA1211 5' GGCGGAGGTGCAGGGG 68895 ATGAAG  
 CTCC GCATCTCTGTT  
 ||| |||||  
 GGGG CGTGGAGGCGG  
 A\_\_\_\_  
 GAM1425 KIAA1233 3' GGATGGAGGTTAGGTTTGGAGT 63082 TGAAGGC  
 ACTCCA ATCTCTGTTT  
 ||||| |||||  
 TGAGGT TGGAGGTAGG  
 TTGGAT\_  
 GAM1425 KIAA1238 3' AAATGGAGATGCTGCAGAG 71075 CATGAA  
 CTC GGCATCTCTGTTT  
 ||| |||||  
 GAG TCGTAGAGGTAAA  
 ACG\_\_\_\_  
 GAM1425 KIAA1247 3' GGACAGAGGCAACGTGGAG 61853 AAG AT  
 CTCCATG GC CTCTGTTT  
 ||||| || |||||  
 GAGGTGC CG GAGACAGG  
 AA\_ \_  
 GAM1425 KIAA1266 3' GGGTGGAGGTGGCAGGCAGGGG 66125 A AAG \_ TG  
 T ACTCC TG GC ATCTC TTT  
 ||||| || || ||||| |||  
 TGGGG AC CG TGGAG GGG  
 \_ GGA G GT  
 GAM1425 KIAA1277 3' AAGCAGGGAGGGTGTGGAG 64449 GAAG A\_  
 CTCCAT GC TCTCTGTTT  
 ||||| || |||||  
 GAGGTG TG AGGGACGAA  
 \_\_\_\_ GG  
 GAM1425 KIAA1297 3' AAACGGAGGCTCGGATTGTGGG 72162 TG A\_\_\_\_ AT  
 G CTCCA A GGC CTCTGTTT  
 ||||| | ||| |||||

GGGGT T TCG GAGGCAAA  
GT AGGC \_  
GAM1425 KIAA1300 3' AGGCAGGGGTGTTGAGCG 62861 AA\_  
TG GGCATCTCTGTTT  
|| |||||  
GC TTGTGGGGACGGA  
GAG  
GAM1425 KIAA1323 5' AAGTGGAGATGCTGCTCAGGGT 63036 T A A\_ TG  
AC CC TGA GGCATCTC TTT  
|| ||| ||||| |||  
TG GG ACT TCGTAGAG GAA  
\_ \_ CG GT  
GAM1425 KIAA1372 5' AGGCAGGCTGTGTTGTGGGGT 91648 TG AG T T  
ACTCCA A GCA C CTGTTT  
|||| | ||| |||||  
TGGGGT T TGT G GACGGA  
GT G\_ C\_  
GAM1425 KIAA1441 3' GGCGGGGGGGGTGGGGGGT 88412 ATGAAG AT  
ACTCC GC CTCTGTT  
|||| || |||||  
TGGGG TG GGGGCGG  
GG\_ GG  
GAM1425 KIAA1453 3' ATGGAGAGCGGGAGT 46971 ATGAAG A  
ACTCC GC TCTCTGT  
|||| || |||||  
TGAGG CG AGAGGTA  
G\_ \_  
GAM1425 KIAA1462 3' GCGCCTGGAGGTCTTTGTGGGG 91387 TG A CT TT  
T ACTCCA AAGGC TCT GT  
|||| |||| ||| ||  
TGGGGT TTCTG AGG CG  
GT G TC CGG  
GAM1425 KIAA1486 3' GGCAGAGGTGGGTGGA 67382 GAAGG  
TCCAT CATCTCTGTT  
|||| |||||  
AGGTG GTGGAGACGG  
G\_  
GAM1425 KIAA1511 3' GAGTGGGGGTGCCAAGGAG 70166 ATGAA TG  
CTCC GGCATCTC TTT  
||| ||||| |||  
GAGG CCGTGGGG GAG  
AA\_ GT  
GAM1425 KIAA1535 3' GGTGGGGAGTTCTGGGGT 79413 T AG A TG  
ACTCCA GA GC TCTC TT  
|||| || || ||| ||  
TGGGGT CT TG AGGG GG  
\_ \_ \_ GT  
GAM1425 KIAA1564 3' AGGGGAGATGTGGGG 63865 ATGAAG G  
CTCC GCATCTCT TT  
||| ||||| ||

GGGG TG TAGAGG GA  
\_\_\_\_\_ G  
GAM1425 KIAA1604 5' GCAGAGACGCGGAGT 64236 ATGAAG A  
ACTCC GC TCTCTGT  
||||| || |||||  
TGAGG CG AGAGACG  
\_\_\_\_\_ C  
GAM1425 KIAA1613 3' AATAGAGAAATAGGAGT 64810 A AAGGCA  
ACTCC TG TCTCTGTT  
||||| || |||||  
TGAGG AT AGAGATAA  
\_ AA \_  
GAM1425 KIAA1627 3' GGTGGAGATTCCAGGGGT 80754 ATGAA C TG  
ACTCC GG ATCTC TT  
||||| || ||||| ||  
TGGGG CC TAGAG GG  
A \_ T GT  
GAM1425 KIAA1634 3' GAATAAACTATTTTATGGAGT 63389 GCATCTC  
ACTCCATGAAG TGTTT  
||||||| |||||  
TGAGGTATTTT ATAAG  
ATCAA \_  
GAM1425 KIAA1655 5' AAACAGGGATGCCCTCAGG 66582 A A  
CC TGA GGCATCTCTGTTT  
|| ||| |||||  
GG ACT CCGTAGGGACAAA  
\_ C  
GAM1425 KIAA1668 3' GGGCAGGGGTGAACTGGAG 66479 TGAAGG  
CTCCA CATCTCTGTTT  
||||| |||||  
GAGGT GTGGGGACGGG  
CAA \_  
GAM1425 KIAA1679 3' GGTGGAGACTGTGGGG 70155 GA GCA TG  
CTCCAT AG TCTC TT  
||||| || ||||| ||  
GGGGTG TC AGAG GG  
\_ \_ GT  
GAM1425 KIAA1737 5' GGGCGGGGAGAGAGCTTGGAGT 67360 TGAA A \_  
ACTCCA GGC TCTCTGTTT  
||||| || |||||  
TGAGGT TCG AGGGGCGGG  
\_ AGAG  
GAM1425 KIAA1755 3' AAGTGGGGGTGCATTTGGGG 61336 TGAAG TG  
CTCCA GCATCTC TTT  
||||| ||||| |||  
GGGGT CGTGGGG GAA  
TTA \_ GT  
GAM1425 KIAA1796 5' AAATGGAGGTGCCGCGCCTGGA 91453 TGAA \_  
TCCA GGCATCTCTGTTT  
||| |||||

		AGGT CCGTGGAGGTAAA		
		CCGCG		
GAM1425 KIAA1808	3'	GGATGGAGATAGGATGGAG 85867	GAAGGC	
		CTCCAT ATCTCTGTTT		
		GAGGTA TAGAGGTAGG		
		GGA__		
GAM1425 KIAA1808	3'	GGATGGAGATAGGATGGAG 85868	GAAGGC	
		CTCCAT ATCTCTGTTT		
		GAGGTA TAGAGGTAGG		
		GGA__		
GAM1425 KIAA1904	3'	GGCAGAGAAGCCAGGGGT 73494	ATGAA A	
		ACTCC GGC TCTCTGTT		
		TGGGG CCG AGAGACGG		
		A__ A		
GAM1425 KIAA1950	3'	GATCCTGGGTGCTTCTCGTGGA 92592	_ CTGTTT	
GT		ACTCCATGA AGGCATCT		
		TGAGGTGCT TTCGTGGG		
		C TCCTAG		
GAM1425 KIAA1972	3'	GGGCAGAAGTCTTTATGGAG 91758	ATC	
		CTCCATGAAGGC TCTGTTT		
		GAGGTATTTCTG AGACGGG		
		A__		
GAM1425 KIAA1981	3'	AACGGAGGCAGCAGGAGT 88338	A AAG AT	
		ACTCC TG GC CTCTGTT		
		TGAGG AC CG GAGGCAA		
		_ GA_ _		
GAM1425 KIAA1981	3'	AGTGGAGGCCATGGGG 88340	GAA AT TG	
		CTCCAT GGC CTC TT		
		GGGGTA CCG GAG GA		
		_ _ GT		
GAM1425 KLF5	3'	GGGTGGGGGTGAAGGGGAGT 8185	ATGAAGG TG	
		ACTCC CATCTC TTT		
		TGAGG GTGGGG GGG		
		GGAA__ GT		
GAM1425 Kv6.3	3'	GGGCGGAGATGTCTTTTAGGGG 56039	AT	
		CTCC GAAGGCATCTCTGTTT		
		GGGG TTTCTGTAGAGGCGGG		
		AT		
GAM1425 LGI2	3'	AGTGAATGCCTTTAGGGGT 36396	A _T	
		ACTCC TGAAGGCAT C CT		

			TGGGG ATTTCCGTA G GA		
			— A T		
GAM1425	LMOD1	3'	GATGGAGAGGCATGGGG 24044	AAGGCA	
			CTCCATG TCTCTGTT		
			GGGGTAC AGAGGTAG		
			GG_____		
GAM1425	LY75	3'	AAACAGAGAAAGGGTCCATGAA 9831	C AA A_____	
	G		CTCATG GGC TCTCTGTTT		
			GA GTAC CTG AGAGACAAA		
			A _ GGAA		
GAM1425	MADHIP	3'	GGACAGAGGTGTTTTT 23638		
			GAAGGCATCTCTGTTT		
			TTTTTGTGGAGACAGG		
GAM1425	MAIL	3'	GATGGGGAGTTACGGAGT 48651	ATGAA A	
			ACTCC GGC TCTCTGTT		
			TGAGG TTG AGGGGTAG		
			CA_____		
GAM1425	MAPK13	3'	GGATGGAGGTGTTGGCAGGG 10856	A AA	
			TCC TG GGCATCTCTGTTT		
			GGG AC TTGTGGAGGTAGG		
			_ GG		
GAM1425	MAPK8IP3	3'	AAGCAGAGCCACTCGGGAGT 52975	A A_ ATC	
			ACTCC TGA GGC TCTGTTT		
			TGAGG GCT CCG AGACGAA		
			_ CA _____		
GAM1425	MDS018	3'	GAGTAGAGGTGCCTTGAGGGG 41534	ATG	
			CTCC AAGGCATCTCTGTTT		
			GGGG TTCCGTGGAGATGAG		
			AG_		
GAM1425	MGC10561	3'	GGGCAGAGGCAGTGTGGG 51000	AAG AT	
			TCCATG GC CTCTGTTT		
			GGGTGT CG GAGACGGG		
			GA_ _____		
GAM1425	MGC10771	3'	AGGCAGAGGTTGCAGTGAGT 44450	CATGAAG _	
			ACTC GCA TCTCTGTTT		
			TGAG CGT GGAGACGGA		
			TGA_____ T		
GAM1425	MGC13071	3'	GAGCAACAACCTTATGGAGT 51088	A CATCTC	
			ACTCCATGA GG TGTTT		

			TGAGGTATT CC	ACGAG		
			_ AACA_			
GAM1425	MGC13204	3'	AGATATGTTTTCTGGAGT	48836	T	C
			ACTCCA GAAGGCAT TCT			
			TGAGGT CTTTTGTA AGA			
			_ T			
GAM1425	MGC15416	5'	AGATGGAGGTGCTTCTGTGGGG	56539		GA
			CTCCAT AGGCATCTCTGTTT			
			GGGGTG TTCGTGGAGGTAGA			
			TC			
GAM1425	MGC15827	3'	GGGCTGCTTGTTTTTGTGGAG	51805	TG	TCTCT
			CTCCA AAGGCA GTTT			
			GAGGT TTTTGT CGGG			
			GT TCGT_			
GAM1425	MGC16142	3'	AGGCAGAGATCGCAGTGAGT	51289		CATGAAG _
			ACTC GC ATCTCTGTTT			
			TGAG CG TAGAGACGGA			
			TGA_ C			
GAM1425	MGC17330	3'	AGACAGGGGTTAGTGGGG	53526		GAAGGC
			CTCCAT ATCTCTGTTT			
			GGGGTG TGGGGACAGA			
			AT_			
GAM1425	MGC17998	3'	GGGCTCGTCTTCTGGGGT	58743	T	AT_
			ACTCCA GAAGGC CTC			
			TGGGGTCTTCTG GGG			
			_ CTC			
GAM1425	MGC1842	3'	GAGTGGCCTTCATGGAG	65650		AT
			CTCCATGAAGGC CTC			
			GAGGTACTTCCG GAG			
			GT			
GAM1425	MGC19604	3'	GGACAGGGCCCCTAGTGGGGT	54725		GA CAT
			ACTCCAT AGG CTCTGTTT			
			TGGGGTG TCC GGGACAGG			
			A_ CC_			
GAM1425	MGC20496	3'	GGATGGAGATGCTGATGAG	53432		CATGAA
			CTC GGCATCTCTGTTT			
			GAG TCGTAGAGGTAGG			
			TAG_			
GAM1425	MGC2376	3'	GGCATGTGCCTTCATGTAGT	43705	C	CTC
			ACT CATGAAGGCAT TGTT			

TGA GTACTTCCGTG ACGG  
 T T\_\_  
 GAM1425 MGC2508 3' GAGTGGGGGTAGCAATTGGAGT 44255 TGAAG \_ TG  
 ACTCCA GC ATCTC TTT  
 ||||| || ||||| ||  
 TGAGGT CG TGGGG GAG  
 TAA\_\_ A GT  
 GAM1425 MGC2641 3' AGCAGAGAACTGTGGGG 50941 GAA CA  
 CTCCAT GG TCTCTGTT  
 ||||| || |||||  
 GGGGTG TC AGAGACGA  
 \_\_ A\_  
 GAM1425 MGC2650 3' AGGTGGGGGTGTCAGAGGAG 44101 ATGAA TG  
 CTCC GGCATCTC TTT  
 ||| ||||| ||  
 GAGG CTGTGGGG GGA  
 AGA\_\_ GT  
 GAM1425 MGC2668 3' GGGTAGAGATGAGGGGAGGGAG 60577 ATGAAGG TT  
 T ACTCC CATCTCTG T  
 |||| | ||||| |  
 TGAGG GTAGAGAT G  
 GAGGGGA GG  
 GAM1425 MGC2835 3' GGGCCTGCATTTATGGAGT 43963 G T\_  
 ACTCCATGAA GCA CTC  
 ||||| || ||  
 TGAGGTATTT CGT GGG  
 A CC  
 GAM1425 MGC3413 5' GATGGGGGCCCTGGGGGT 51048 ATGAA AT  
 ACTCC GGC CTCTGTT  
 |||| || |||||  
 TGGGG CCG GGGGTAG  
 GTC\_\_ \_\_  
 GAM1425 MGC4342 3' GAATGGAGCAAGTTCAGGGGT 44267 A GGCAT  
 ACTCC TGAA CTCTGTTT  
 |||| || |||||  
 TGGGG ACTT GAGGTAAG  
 \_ GAAC\_  
 GAM1425 MGC4737 5' AGGCAGGGATGCTGCAGGA 48843 A AA  
 TCC TG GGCATCTCTGTTT  
 || || |||||  
 AGG AC TCGTAGGGACGGA  
 \_ G\_  
 GAM1425 MGC9753 3' AAATGGGGATGGCTGGGG 53044 TGAA G  
 CTCCA G CATCTCTGTTT  
 |||| | |||||  
 GGGGT C GTAGGGGTAAA  
 \_\_ G  
 GAM1425 MMP24 3' GGCAGGGAATTATGGGG 21945 AGGCA  
 CTCCATGA TCTCTGTT  
 ||||| |||||

GGGGTATT AGGGACGG  
A\_\_\_\_  
GAM1425 MMPL1 3' AGATGGAGGAAGACCTGGGGT 14716 TGAA CA\_\_\_\_  
ACTCCA GG TCTCTGTTT  
||||| || |||||  
TGGGGT CC GGAGGTAGA  
\_\_\_\_ AGAA  
GAM1425 MRF2 3' AACAGAGATGACTGGA 76517 TGAAGG  
TCCA CATCTCTGTT  
|||| |||||  
AGGT GTAGAGACAA  
CA\_\_\_\_  
GAM1425 MRF2 3' AACAGAGATGACTGGA 76517 TGAAGG  
TCCA CATCTCTGTT  
|||| |||||  
AGGT GTAGAGACAA  
CA\_\_\_\_  
GAM1425 MRPS18B 3' AGGCGGAGGTTGCAGTGAGT 25905 CATGAAG \_  
ACTC GCA TCTCTGTTT  
|||| ||| |||||  
TGAG CGT GGAGGCGGA  
TGA\_\_\_\_ T  
GAM1425 MRPS7 5' GGCAGTCCTTGTGGGGT 31996 G CATCT  
ACTCCAT AAGG CTGTT  
||||| ||| ||||  
TGGGGTG TTCC GACGG  
\_ T\_\_\_\_  
GAM1425 MTCH1 3' GGATGGGGAAAGGCTAATGGGG 26780 GAA A\_\_\_\_  
T ACTCCAT GGC TCTCTGTTT  
||||| ||| |||||  
TGGGGTA TCG AGGGGTAGG  
A\_\_ GAA  
GAM1425 MYO3B 3' GAATGGAGAATACATGGAG 57306 AAGGCA  
CTCCATG TCTCTGTTT  
||||| |||||  
GAGGTAC AGAGGTAAG  
ATA\_\_\_\_  
GAM1425 NDRG4 3' AGGCAGGGGCGTCAAGGGGT 43285 A AG AT  
ACTCC TGA GC CTCTGTTT  
||||| ||| |||||  
TGGGG ACT CG GGGACGGA  
A G\_ \_\_  
GAM1425 NDRG4 3' AGGCAGGGGCGTCAAGGGGT 39982 A AG AT  
ACTCC TGA GC CTCTGTTT  
||||| ||| |||||  
TGGGG ACT CG GGGACGGA  
A G\_ \_\_  
GAM1425 NLI-IF 3' GGGACCTTCTGTGGGGT 41052 \_ CA  
ACTCCAT GAAGG TCTC  
||||| |||| |||



		TGGGGTG CTTCC AGGG	
		T _	
GAM1425 NRF	3'	GAGTAAGTCTCATGGGGT 34082	A AT_
		ACTCCATGA GGC CTC	
		TGGGGTACT CTG GAG	
		_ AAT	
GAM1425 OAZ2	3'	GGACGGGGATGTCAGGGAG 10307	ATGAA
		CTCC GGCATCTCTGTTT	
		GAGG CTGTAGGGGCAGG	
		GA _	
GAM1425 OPN4	5'	AAGCAGGGGTGCTGAGGATGGA 52715	GAA_
G		CTCCAT GGCATCTCTGTTT	
		GAGGTA TCGTGGGGACGAA	
		GGAG	
GAM1425 ORMDL3	3'	GAATAGAGACTCCATGGAGT 74311	A GCA
		ACTCCATG AG TCTCTGTTT	
		TGAGGTAC TC AGAGATAAG	
		C _	
GAM1425 OSBPL5	3'	AGGTGGAGGTGTTGTGGG 72683	GA G TG
		TCCAT AG CATCTC TTT	
		GGGTG TT GTGGAG GGA	
		_ G GT	
GAM1425 PACSIN2	3'	GGGTGGGGGGAACGTGGGG 23343	AAGGCA TG
		CTCCATG TCTC TTT	
		GGGGTGC GGGG GGG	
		AAG _ GT	
GAM1425 PAFAH2	3'	AAGCTCTGGATGTCTTTGGGGG 4756	A CT_
T		ACTCC TGAAGGCATCT GTTT	
		TGGGG GTTTCTGTAGG CGAA	
		_ TCT	
GAM1425 PAFAH2	3'	AGGCGGAGGTTGCAGTGAGT 4759	CATGAAG _
		ACTC GCA TCTCTGTTT	
		TGAG CGT GGAGGCGGA	
		TGA _ T	
GAM1425 PAPOLG	5'	AAATAGAGCCGTTTGTGGTG 43169	T G AT_
T		AC CCAT AAGGC CTCTGTTT	
		TG GGTG TTTTG GAGATAAA	
		T _ GCC	
GAM1425 PARVA	3'	AGATAGAGGTGGGGCTTGTGG 36651	TG AGG_
		CCA A CATCTCTGTTT	

GGT T GTGGAGATAGA  
GT CGGG  
GAM1425 PIP5K1C 3' GGGCAGAGGTCAGAAGGGGT 70765 ATGAA AT  
ACTCC GGC CTCTGTTT  
||||| ||| |||||  
TGGGG CTG GAGACGGG  
AAGA\_ \_  
GAM1425 PLCL1 3' GGTGCCCTATATGGGGT 20636 AA\_  
ACTCCATG GGCATC  
||||| |||||  
TGGGGTAT CCGTGG  
ATC  
GAM1425 PMX2B 3' GCGGTGTCTTTATGGTGT 14084 T C  
AC CCATGAAGGCAT TC  
|| ||||| ||  
TG GGTATTTCTGTG GG  
T C  
GAM1425 PP1628 5' GGGTGGAGACCCCTGTGGGG 47304 GA CA TG  
CTCCAT AGG TCTC TTT  
||||| ||| ||| |||  
GGGGTG TCC AGAG GGG  
\_ CC GT  
GAM1425 PPP1R13B 3' GGCAGAGGAGCTGGGGT 31008 TGAAG AT  
ACTCCA GC CTCTGTT  
||||| || |||||  
TGGGGT CG GAGACGG  
\_ AG  
GAM1425 PRDM14 3' GGCAGAGGTGGGTGGA 44449 GAAGG  
TCCAT CATCTCTGTT  
||||| |||||  
AGGTG GTGGAGACGG  
G\_  
GAM1425 PRDM8 3' CGCAGCGCCTTCGTGGAG 39570 ATCT TT  
CTCCATGAAGGC CTGT  
||||||| |||  
GAGGTGCTTCCG GACG  
C\_ CG  
GAM1425 PRO1855 3' AAACAAGTAGCATCATGGAG 37543 AG AT C  
CTCCATGA GC CT TGTTT  
||||| || |||||  
GAGGTACT CG GA ACAA  
A\_ AT \_  
GAM1425 PRO2730 3' AGGCGGAGGTTGCGGTGAGT 47409 C GAAG \_  
ACTC AT GCA TCTCTGTTT  
||| || ||| |||||  
TGAG TG CGT GGAGGCGGA  
\_ G\_ T  
GAM1425 PRPF8 3' GGATACCTATATGGGGT 61194 A C  
ACTCCATG AGG ATCT  
||||| ||| |||

			TGGGGTAT TCC TAGG		
			A A		
GAM1425 PSMD3	3'	GGTGGGGGTGCTGGGAG	10973	ATGAA	TG
		CTCC GGCATCTC TT			
		GAGG TCGTGGGG GG			
		G_____ GT			
GAM1425 PTPRR	3'	AGGTATATGCCTTCAGGA	11137	A	C__
		TCC TGAAGGCAT TCT			
		AGG ACTTCCGTA GGA			
		_____ TAT			
GAM1425 PTPRR	3'	AGGTATATGCCTTCAGGA	55614	A	C__
		TCC TGAAGGCAT TCT			
		AGG ACTTCCGTA GGA			
		_____ TAT			
GAM1425 R32184_3	3'	AGGCGGAGGTGTGGAGGAG	53061	ATGAAG	
		CTCC GCATCTCTGTTT			
		GAGG TGTGGAGGCGGA			
		AGG_____			
GAM1425 RAI17	3'	AAACAGAGATGGTCCT	91272	__	
		AGG CATCTCTGTTT			
		TCC GTAGAGACAAA			
		TG			
GAM1425 RBT1	3'	GGGTGTGTGTTTTTGTGGGG	25354	TG	__
		CTCCA AAGGCAT CTC			
		GGGGT TTTTGTG GGG			
		GT TGT			
GAM1425 RGS11	3'	GGGCCAGTCTTCTGTGGGGT	13826	_	AT__
		ACTCCAT GAAGGC CTC			
		TGGGGTG CTTCTG GGG			
		T ACCC			
GAM1425 RNAC	3'	GAGTGGCAGCTCTTCATGAGT	19312	C	_ AT__
		ACTC ATGAAG GC CTC			
		TGAG TACTTC CG GAG			
		_____ T ACGGT			
GAM1425 RNPC1	3'	GGGCGGGGGGCAGCGGGGGGT	33992	A AAG A	
		ACTCC TG GC TCTCTGTTT			
		TGGGG GC CG GGGGGCGGG			
		G GA_ _			
GAM1425 ROBO4	3'	AGCCAGAGGTGCCTTTGTGGAG	38789	TG	TTT
		CTCCA AAGGCATCTCTG			

			GAGGT TTCCGTGGAGAC		
			GT CGAG		
GAM1425	RODH-4	5'	AGGCAGAGAGAAACCAGGAGT 13528	A	AAGGCA
			ACTCC TG TCTCTGTTT		
			TGAGG AC AGAGACGGA		
			_ CAAAG_		
GAM1425	SBB103	5'	GAGTGGAGGCATCAGGGGGT 19359	A	AG AT TG
			ACTCC TGA GC CTC TTT		
			TGGGG ACT CG GAG GAG		
			G A_ _ GT		
GAM1425	SDC3	3'	GAGCAGACCCTCTGCCTCATGG 27752	A	TC_
	GGT		CTCCATGA GGCA TCTGTTT		
			GGGGTACT CCGT AGACGAG		
			_ CTCCC		
GAM1425	SDC3	3'	GGGCAGGGAGGGGGGCATGTGGT 27758	TC	AAGGCA
			AC CATG TCTCTGTTT		
			TG GTAC AGGGACGGG		
			GT GGGGG_		
GAM1425	SEMA5B	3'	AGATGGAGATGGGACAGTGGAG 63124		GAAGG
			CTCCAT CATCTCTGTTT		
			GAGGTG GTAGAGGTAGA		
			ACAGG		
GAM1425	SEPT3	3'	AGTAGGGGGCAGGGAGT 38882	ATGAAG	A
			ACTCC GC TCTCTGTT		
			TGAGG CG GGGGATGA		
			GA_ _		
GAM1425	SLAC2-B	3'	AGGTAGGGATGATAACAGTGGG 30508	GAAGG_	TT
	G		CTCCAT CATCTCTG T		
			GGGGTG GTAGGGAT A		
			ACAATA GG		
GAM1425	SLC31A2	3'	AATGGAGATAACAGGGGT 60127	A	AAGGC
			ACTCC TG ATCTCTGTT		
			TGGGG AC TAGAGGTAA		
			_ AA_		
GAM1425	SMCR5	5'	GACAGGGAAGTGTGGGG 58595	GAA	CA
			CTCCAT GG TCTCTGTT		
			GGGGTG TC AGGGACAG		
			_ A_		
GAM1425	SSR3	3'	AGGCAGAGGTTGCAGTGAGT 23037	CATGAAG	_
			ACTC GCA TCTCTGTTT		

			TGAG	CGT GGAGACGGA		
			TGA_____	T		
GAM1425	STAT5A	3'	AGGTGGGGATGAGAAGAGGGGT	12010	ATGAAGG	TG
			ACTCC	CATCTC TTT		
			TGGGG	GTAGGG GGA		
			AGAAGA_	GT		
GAM1425	STIM2	3'	AGGTGGGGGGATATGGGG	40469	AAGGCA	TG
			CTCCATG	TCTC TTT		
			GGGGTAT	GGGG GGA		
			AG_____	GT		
GAM1425	STK16	3'	GAGTGGGGGTGGGTGGGG	72118	GAAGG	TG
			CTCCAT	CATCTC TTT		
			GGGGTG	GTGGGG GAG		
			G_____	GT		
GAM1425	STK29	3'	AAACAGAGACACCCTGCGG	87572	ATGA	CA_
			CC	AGG TCTCTGTTT		
			GG	TCC AGAGACAAA		
			CG_	CAC		
GAM1425	SV2B	3'	AAACAGGGGTGTGGGTTGGGG	29290	TGAAG	
			CTCCA	GCATCTCTGTTT		
			GGGGT	TGTGGGGACAAA		
			TGGG_			
GAM1425	SV2B	3'	AACAGAGTCCATTGGAGT	29291	TGAA	CAT
			ACTCCA	GG CTCTGTT		
			TGAGGT	CC GAGACAA		
			TA_	T_		
GAM1425	TAO1	3'	GGCAGGGGTGGGTGGAG	16548	GAAGG	
			CTCCAT	CATCTCTGTT		
			GAGGTG	GTGGGGACGG		
			G_____			
GAM1425	TFB2M	5'	GGATACCCTGCGTGGGGT	42308	A	C_
			ACTCCATG	AGG ATCT		
			TGGGGTGC	TCC TAGG		
			G	CA		
GAM1425	TIP120A	3'	TAGGATTTTATGGAGT	37428	GGC	T
			ACTCCATGAA	ATC CTG		
			TGAGGTATTT	TAG GAT		
			_____	_____		
GAM1425	TJP4	5'	AAGTGGAGGGGCCGTGGG	54606	GAA	AT TG
			TCCAT	GGC CTC TTT		

		GGGTG CCG GAG GAA		
		___ GG GT		
GAM1425 TMG3	3'	GGTAGGGACCGCATGAGT 43993	C AA_ CA	TT
		ACTC ATG GG TCTCTG T		
		TGAG TAC CC AGGGAT G		
		_ GCA ___ GG		
GAM1425 TOR2A	3'	AAGTGGAGCGTTTTTCAGTGGAG 55311	_ AT TG	
T		ACTCCA TGAAGGC CTC TTT		
		TGAGGT ACTTTTG GAG GAA		
		G C_ GT		
GAM1425 TPC2	3'	AGGTGGGGATGCTGGTGG 57445	GAA TG	
		CCAT GGCATCTC TTT		
		GGTG TCGTAGGG GGA		
		G___ GT		
GAM1425 TPD52	3'	AAATGGGGGTGGCAAGTGGGGT 17416	GAAG _	
		ACTCCAT GC ATCTCTGTTT		
		TGGGGTG CG TGGGGGTAAA		
		AA___ G		
GAM1425 TPD52	5'	AGGCGGGGGTGCTGCAGAG 17422	CATGAA	
		CTC GGCATCTCTGTTT		
		GAG TCGTGGGGGCGGA		
		ACG___		
GAM1425 TRIM31	3'	GAGTGGAGATGGGGGCGGGGGT 91000	A AAGG TG	
		ACTCC TG CATCTC TTT		
		TGGGG GC GTAGAG GAG		
		_ GGGG GT		
GAM1425 TRIP3	3'	TTAGGTGGCAAGTCCTTTATGG 78221	_____ CTGTTT	
AG		CCATGAAGG CATCT		
		GGTATTTC GTGGA		
		TGAACG TTT		
GAM1425 UHRF2	3'	GGACAGAAAAGATTTATGGGG 73450	GGCATC	
		CTCCATGAA TCTGTTT		
		GGGGTATTT AGACAGG		
		AGAAA_		
GAM1425 UNC5D	3'	GGGGGAGGTGGGGAGT 55140	ATGAAGG G	
		ACTCC CATCTCT TT		
		TGAGG GTGGAGG GG		
		G_____ G		
GAM1425 UNC5D	3'	GGTGGGGAGTTGGGGAGT 55143	ATGAA A TG	
		ACTCC GGC TCTC TT		

		TGAGG	TTG AGGG GG		
		GG	GT		
GAM1425 VILL	5'	GACAGGGAACGTGGTGGT	68413	AAGGCA	
		ACT CCATG	TCTCTGTT		
		TGG GGTGC	AGGGACAG		
		T	A		
GAM1425 WDF2	5'	AGCAGGGAGCGCGGAGT	53660	ATGAAG A	
		ACTCC	GC TCTCTGTT		
		TGAGG	CG AGGGACGA		
			CG		
GAM1425 YKT6	3'	AAATGGAGGTATGAATTTGGGG	21594	TGAAGGC	
T		ACTCCA	ATCTCTGTTT		
		TGGGGT	TGGAGGTAAA		
			TTAAGTA		
GAM1425 YKT6	3'	GGGCGGGGAGTGTGTGGG	21605	GAAG	
		TCCAT	GCA TCTCTGTTT		
		GGGTG	TGT AGGGGCGGG		
			G		
GAM1425 ZNF337	3'	GAACAGAGATGCCAGTTGAG	68089	C GAA	
		CTC AT	GGCATCTCTGTTT		
		GAG TG	CCGTAGAGACAAG		
		T	A		
GAM1425 ZNF384	3'	AAACAGGGGTGTTGCGGAG	55982	ATGAA	
		CTCC	GGCATCTCTGTTT		
		GAGG	TTGTGGGGACAAA		
			CG		
GAM1425 LOC115207	3'	ATGCCACTTTTCATGCAGT	56597	C	
		ACT CATGAA	GGCAT		
		TGA G	TACTT CCGTA		
		C	TCA		
GAM1425 LOC120071	3'	GGGCAGAGCATCTGTGGGGT	74000	GA CAT	
		ACTCCAT AGG	CTCTGTTT		
		TGGGGT	TCT GAGACGGG		
			AC		
GAM1425 LOC121133	5'	GAGCAGGGATGCATCTGGAG	75992	T AG	
		CTCCA GA	GCATCTCTGTTT		
		GAGGT CT	CGTAGGGACGAG		
			A		
GAM1425 LOC121838	5'	GGTAGAGAGAAGCAGGGGT	76002	A AAGGCA	TT
		ACTCC TG	TCTCTG T		

		TGGGG AC AGAGAT G	
		_ GAAG_ GG	
GAM1425	LOC123242 5'	AAGCAGGGGGCTGGTGGGGT 75588	GAA A
		ACTCCAT GGC TCTCTGTTT	
		TGGGGTG TCG GGGGACGAA	
		G_ _	
GAM1425	LOC123397 5'	GGGCAGAGGTGTTAAGTGAG 75609	C GAA
		CTC AT GGCATCTCTGTTT	
		GAG TG TTGTGGAGACGGG	
		_ AA_	
GAM1425	LOC123435 5'	AGGCAGAGGTTTCAGGTGAGAGT 74206	_ GAA C
		ACTC CAT GG ATCTCTGTTT	
		TGAG GTG CT TGGAGACGGA	
		A GA_ _	
GAM1425	LOC123855 5'	ATCATCGGTGCTTGCGTGGAGT 75626	A TCTGTTT
		ACTCCATG AGGCATC	
		TGAGGTGC TTCGTGG	
		G CTACTAG	
GAM1425	LOC124216 5'	AAGCGGAGGTGTGGTGGGG 74258	GAAG
		CTCCAT GCATCTCTGTTT	
		GGGGTG TGTGGAGGCGAA	
		G_ _	
GAM1425	LOC124222 3'	AGGCAGAGAAGACCATGGGAGT 74269	ATGAA CA_
		ACTCC GG TCTCTGTTT	
		TGAGG CC AGAGACGGA	
		GTA_ AGA	
GAM1425	LOC124977 5'	GGTGGGGGGTGCCAGGAG 76063	ATGAA TG
		CTCC GGCATCTC TT	
		GAGG CCGTGGGG GG	
		A_ GT	
GAM1425	LOC126006 5'	GGATGATCTTTATGGGG 74429	_
		CTCCATGAAGG CATCT	
		GGGGTATTTCT GTAGG	
		A	
GAM1425	LOC126129 5'	GGGCGGGGGTGGACTCGGG 74447	A A G_
		CC TGA G CATCTCTGTTT	
		GG GCT C GTGGGGGCGGG	
		_ _AG	
GAM1425	LOC126669 3'	GGGTAGGGTGTTCTTTTATGG 75412	T _ T TT
	TGT	C CCATGAAG GCATC CTG T	



G GGTATTTT TGTGG GAT G  
 T TCT \_ GG  
 GAM1425 LOC127281 5' AGCGGGGAACAGGGAGT 74643 A AAGGCA  
 ACTCC TG TCTCTGTT  
 ||||| || |||||  
 TGAGG AC AGGGGCGA  
 G A\_\_\_\_  
 GAM1425 LOC130612 3' GATGGGGGTGGGGGGGT 74959 ATGAAGG  
 ACTCC CATCTCTGTT  
 ||||| |||||  
 TGGGG GTGGGGGTAG  
 GG\_\_\_\_  
 GAM1425 LOC130617 3' GGGCAGAGACAAGCGGGAGT 57137 A AAGGCA  
 ACTCC TG TCTCTGTTT  
 ||||| || |||||  
 TGAGG GC AGAGACGGG  
 \_ GAAC\_\_\_\_  
 GAM1425 LOC132166 3' TAAATGGGTTTATTTGCCTTTC 75040 \_ TC\_\_\_\_  
 ATGGGGT ATGAA GGCA TCTGTTT A  
 ||||| ||||| |  
 TACTT CCGT GGGTAAA T  
 T TTATTT  
 GAM1425 LOC134147 3' AGGCAGAGGTTGCAGTGAGT 57156 CATGAAG \_  
 ACTC GCA TCTCTGTTT  
 ||||| || |||||  
 TGAG CGT GGAGACGGA  
 TGA\_\_\_\_ T  
 GAM1425 LOC135818 3' GGACAGTCTTTATGGAG 75240 ATC  
 CTCCATGAAGGC TCT  
 ||||| ||||| ||  
 GAGGTATTTCTG AGG  
 AC\_\_\_\_  
 GAM1425 LOC143425 3' GGCAGAGACCACTGGAGT 87638 TGAA CA  
 ACTCCA GG TCTCTGTT  
 ||||| || |||||  
 TGAGGT CC AGAGACGG  
 CA\_\_\_\_  
 GAM1425 LOC143465 5' AATGGGGGGCGGGGGGT 82959 ATGAAG A  
 ACTCC GC TCTCTGTT  
 ||||| || |||||  
 TGGGG CG GGGGGTAA  
 GG\_\_\_\_  
 GAM1425 LOC143872 3' AGCTATGCCTTCTGAAGT 76649 C T CT  
 ACT CA GAAGGCAT CT  
 ||||| || ||||| ||  
 TGA GT CTTCCGTA GA  
 A \_ TC  
 GAM1425 LOC144395 3' GAGTGCCTACATGGGGT 76826 A T  
 ACTCCATG AGGCA CTC  
 ||||| ||||| ||

TGGGGTAC TCCGT GAG  
 A \_  
 GAM1425 LOC144473 3' AGATGGTTCTGTGGAGT 83066 GA G  
 ACTCCAT AG CATCT  
 ||||| || |||||  
 TGAGGTG TT GTAGA  
 TC G  
 GAM1425 LOC144600 3' GGGCGGGGGTGTCTTT 83161  
 GAAGGCATCTCTGTTT  
 |||||  
 TTTCTGTGGGGGCGGG  
  
 GAM1425 LOC144742 5' AAATGGAGACCCGTTTCTTTAT 76937 CA\_\_\_\_  
 GGA CCATGAAGG TCTCTGTTT  
 ||||| |||||  
 GGTATTCT AGAGGTAAA  
 TTGCCC  
 GAM1425 LOC144845 3' AGGCGGAGGTTGCAGTGAGGT 56657 TC GAAG \_  
 AC CAT GCA TCTCTGTTT  
 || || || |||||  
 TG GTG CGT GGAGGCGGA  
 GA A\_\_ T  
 GAM1425 LOC145438 5' GACGGAGGTGCGAGGGG 83337 ATGAAG  
 CTCC GCATCTCTGTT  
 ||| |||||  
 GGGG CGTGGAGGCAG  
 AG\_\_\_\_  
 GAM1425 LOC145693 5' AAATGGAGGTGGTCAGTGGA 77345 GAAGG  
 TCCAT CATCTCTGTTT  
 |||| |||||  
 AGGTG GTGGAGGTAAA  
 ACTG\_  
 GAM1425 LOC145693 5' AGCAGAGATGCCTGGTG 77346 GA  
 CAT AGGCATCTCTGTT  
 || |||||  
 GTG TCCGTAGAGACGA  
 G\_  
 GAM1425 LOC145725 5' GGGCGGGGAGGGGTGTGGAG 77412 AAGGCA  
 CTCCATG TCTCTGTTT  
 ||||| |||||  
 GAGGTGT AGGGGCGGG  
 GGGG\_  
 GAM1425 LOC145732 5' GGGCGGGGAGGGGTGTGGAG 77434 AAGGCA  
 CTCCATG TCTCTGTTT  
 ||||| |||||  
 GAGGTGT AGGGGCGGG  
 GGGG\_  
 GAM1425 LOC145757 3' AGTGGGGATCTTGGGG 77453 TGAA C TG  
 CTCCA GG ATCTC TT  
 |||| || |||| ||

GGGGT TC TAGGG GA  
\_\_\_\_ \_ GT  
GAM1425 LOC145826 5' GACAGAGAAGTGTGGG 83530 TGA G A  
TCCA A GC TCTCTGTT  
|||| | || |||||  
GGGT T TG AGAGACAG  
\_\_\_\_ G A  
GAM1425 LOC145868 5' ATGTTAATTTTTATGGGG 83560 \_\_\_\_  
CTCCATGAAG GCAT  
||||||| |||  
GGGGTATTTT TGTA  
TAAT  
GAM1425 LOC145921 3' AAACAGAGATCCCATCTTGGAG 76014 T A C  
T ACTCCA GA GG ATCTCTGTTT  
||||| || || |||||  
TGAGGT CT CC TAGAGACAAA  
T A C  
GAM1425 LOC145921 3' AAACAGAGATCCCATCTTGGAG 76014 T A C  
T ACTCCA GA GG ATCTCTGTTT  
||||| || || |||||  
TGAGGT CT CC TAGAGACAAA  
T A C  
GAM1425 LOC146159 5' GGGTGGGGGTGCTAAATAGGG 77685 C GAA TG  
CTC AT GGCATCTC TTT  
||| || ||||| |||  
GGG TA TCGTGGGG GGG  
A AA\_ GT  
GAM1425 LOC146237 3' TAGAGATGCCCAGAG 83634 CA AA  
CTC TG GGCATCTCTG  
||| || |||||  
GAG AC CCGTAGAGAT  
\_\_\_\_\_  
GAM1425 LOC146332 5' GGGTGGGGGGGCACGTGGGG 77829 AAG A TG  
CTCCATG GC TCTC TTT  
||||| || ||| |||  
GGGGTGC CG GGGG GGG  
A\_ \_ GT  
GAM1425 LOC146337 3' GGTGGGGCCTCAGGGGT 83662 A A AT T  
ACTCC TGA GGC C CT  
||||| ||| ||| |||  
TGGGG ACT CCG G GG  
\_ \_ GG T  
GAM1425 LOC146506 3' GAGCTGGTGGATGTCTTTGTGG 77933 TG \_ \_  
AG CTCCA AAGGCATCT CT GTTT  
||||| ||||| || |||  
GAGGT TTCTGTAGG GG CGAG  
GT T T  
GAM1425 LOC146714 5' AAATGGGGATGAAGATGGCGT 83737 T GAAGG  
AC CCAT CATCTCTGTTT  
|| ||| |||||

		TG GGTA GTAGGGGTAAA	
		C GAA__	
GAM1425	LOC146714 5'	AACAGAGAAGGTGTGGA 83738	AAGGCA
		TCCATG TCTCTGTT	
		AGGTGT AGAGACAA	
		GGA__	
GAM1425	LOC146733 3'	GAATGGGGAGCAAGCCAGGGGT 83764	A AAG_ A
		ACTCC TG GC TCTCTGTTT	
		TGGGG AC CG AGGGGTAAG	
		_ CGAA _	
GAM1425	LOC146839 5'	GAGTGGAAATGGTCTTTGTGT 83812	TC TG _ C TG
	GGT	AC CA AAGG CAT TC TTT	
		TG GT TTCT GTA AG GAG	
		GT GT TG A GT	
GAM1425	LOC146880 3'	GAATAGAGGTCAATGTGGAG 78157	AA AT
		CTCCATG GGC CTCTGTTT	
		GAGGTGT CTG GAGATAAG	
		AA _	
GAM1425	LOC146957 3'	GACAGGGATGCGGCGAGT 78204	CAT AAG
		ACTC G GCATCTCTGTT	
		TGAG C CGTAGGGACAG	
		_ GG_	
GAM1425	LOC147004 3'	GGTAGGGGTCTTTGTGGG 83904	TG AT TT
		TCCA AAGGC CTCTG T	
		GGGT TTCTG GGGAT G	
		GT _ GG	
GAM1425	LOC147136 3'	GGGCAGAGAGTATTGTGGGG 78267	TG AG A
		CTCCA A GC TCTCTGTTT	
		GGGGT T TG AGAGACGGG	
		GT A_ _	
GAM1425	LOC147136 3'	AGTGGAGGTGCTCAGG 78257	A AG TG
		CC TGA GCATCTC TT	
		GG ACT CGTGGAG GA	
		_ _ GT	
GAM1425	LOC147645 5'	AGGCAGAGGTGGCACTGGAG 78419	TGAAG _
		CTCCA GC ATCTCTGTTT	
		GAGGT CG TGGAGACGGA	
		CA__ G	
GAM1425	LOC147929 3'	AGATAAGCCTTTATGTGGAGT 78573	_ ATC
		ACTCCAT GAAGGC TCT	

		TGAGGTG TTTCCG AGA		
		TA AAT		
GAM1425	LOC148014 3'	GGGGATGACAGGGGT 78610	A AAGG	
		ACTCC TG CATCTCT		
		TGGGG AC GTAGGGG		
		_ A _		
GAM1425	LOC148113 3'	AGTGGGGGTGTGGGGT 78666	ATGAAG TG	
		ACTCC GCATCTC TT		
		TGGGG TGTGGGG GA		
		_____ GT		
GAM1425	LOC148114 5'	GGGCAGAGGGCATGTGGG 78661	GAAG A	
		TCCAT GC TCTCTGTTT		
		GGGTG CG GGAGACGGG		
		TA _ _		
GAM1425	LOC148824 3'	AAATGTAGATGCCTCCATGAGT 84224	C A CT	
		ACTC ATG AGGCATCT GTTT		
		TGAG TAC TCCGTAGA TAAA		
		_ C TG		
GAM1425	LOC148936 5'	GGGCAGGGCCCTCATGGAG 84299	A ATC	
		CTCCATGA GGC TCTGTTT		
		GAGGTACT CCG GGACGGG		
		C _		
GAM1425	LOC148938 5'	GAGCAGGGCCCTCATGGAG 84273	A ATC	
		CTCCATGA GGC TCTGTTT		
		GAGGTACT CCG GGACGAG		
		C _		
GAM1425	LOC149073 5'	GGACAGATAACCTTTTGTGTG 84326	TC _ CATC	
	GT	AC CAT GAAGG TCTGTTT		
		TG GTG TTTCC AGACAGG		
		GT TT AAT _		
GAM1425	LOC149076 5'	AGGCGGAGAACCCGGGGGGT 79147	ATGAA CA	
		ACTCC GG TCTCTGTTT		
		TGGGG CC AGAGGCGGA		
		GG _ CA		
GAM1425	LOC149157 3'	GGACAGGGATGGAGCTGGAG 79202	TGAAGG	
		CTCCA CATCTCTGTTT		
		GAGGT GTAGGGACAGG		
		CGAG _		
GAM1425	LOC149422 3'	AGACAGAGCTGGTTTCATGGG 79347	G T	
		TCCATGAAG CA CTCTGTTT		

	GGGTACTTT GT GAGACAGA	
	G C	
GAM1425 LOC149466 3'	GGACAGAGGTGGCTGGGG 79397	TGAA G
	CTCCA G CATCTCTGTTT	
	GGGGT C GTGGAGACAGG	
	___ G	
GAM1425 LOC149570 3'	CTCCTTGGGGCCTTTATGGGGT 84499	A CTGTTT
	ACTCCATGAAGGC TCT	
	TGGGGTATTTCCG GGG	
	_ TTCCTCG	
GAM1425 LOC149832 5'	GAATGGGGGTGGGGAGTTGGGG 84699	TGAAGG
	CTCCA CATCTCTGTTT	
	GGGGT GTGGGGGTAAG	
	TGAGGG	
GAM1425 LOC149837 3'	GAATGGGGGTGGATTTGGGT 84734	CAT GG
	ACTC GAA CATCTCTGTTT	
	TGGG TTT GTGGGGGTAAG	
	___ AG	
GAM1425 LOC149837 3'	GATGGGGGTGGATGGGG 84738	GAAGG
	CTCCAT CATCTCTGTT	
	GGGGTA GTGGGGGTAG	
	G___	
GAM1425 LOC149844 3'	AGTAGAGGTGGTTATGGA 79513	AGG TT
	TCCATGA CATCTCTG T	
	AGGTATT GTGGAGAT A	
	G_ GG	
GAM1425 LOC149844 5'	GTGCCTTTTTATGTGGAGT 79520	___
	ACTCCAT GAAGGCAT	
	TGAGGTG TTTCCGTG	
	TATT	
GAM1425 LOC150113 5'	GAGCAGGGACAACATGGA 87212	AAGGCA
	TCCATG TCTCTGTTT	
	AGGTAC AGGGACGAG	
	AAC___	
GAM1425 LOC150113 5'	GAGTGGGGACAACCTGTGGG 87213	GA CA_ TG
	TCCAT AGG TCTC TTT	
	GGGTG TCC AGGG GAG	
	_ AAC GT	
GAM1425 LOC150225 3'	GCCTGTGATGTTTCTGTGGGGT 84998	GA TCTGTTT
	ACTCCAT AGGCATC	

TGGGGTG TTTGTAG  
 TC TGTCCGA  
 GAM1425 LOC150299 3' AGGCAGAGGTCGCAGTGAGT 84967 CATGAAG \_  
 ACTC GC ATCTCTGTTT  
 ||| || |||||  
 TGAG CG TGGAGACGGA  
 TGA\_\_ C  
 GAM1425 LOC150311 5' GGGTGGGGAAGGGGTCGTGGTG 79757 T AGGCA TG  
 T AC CCATGA TCTC TTT  
 || ||||| ||| ||  
 TG GGTGCT AGGG GGG  
 T GGGGA GT  
 GAM1425 LOC150889 3' GGGTGGAGACCCATGCTGGGGT 80029 TGAA CA TG  
 ACTCCA GG TCTC TTT  
 ||||| || ||| ||  
 TGGGGT CC AGAG GGG  
 CGTA C\_ GT  
 GAM1425 LOC151162 5' AAATGGAGATGCTTTTCAT 85236 \_  
 ATGAAG GCATCTCTGTTT  
 ||||| |||||  
 TACTTT CGTAGAGGTAAA  
 T  
 GAM1425 LOC151465 3' GGATGTCTCCACAGAGT 62779 CA A  
 ACTC TG AGGCATCT  
 ||| || |||||  
 TGAG AC TCTGTAGG  
 AC C  
 GAM1425 LOC151568 5' GAGTGGAGGTGCCTGGGAG 56693 ATGA TG  
 CTCC AGGCATCTC TTT  
 ||| ||||| ||  
 GAGG TCCGTGGAG GAG  
 G\_\_ GT  
 GAM1425 LOC151904 3' AAGCAGGGAGGGCTGTGGTGT 80383 T GAA A\_  
 AC CCAT GGC TCTCTGTTT  
 || ||| || |||||  
 TG GGTG TCG AGGGACGAA  
 T \_\_ GG  
 GAM1425 LOC151904 5' AGTAGAGGCTTTGTGGGG 80385 TG GCA TT  
 CTCCA AAG TCTCTG T  
 |||| || ||||| |  
 GGGGT TTC GGAGAT A  
 GT \_\_ GG  
 GAM1425 LOC152008 5' AGGTAGAGATGCCTTC 80432 TT  
 GAAGGCATCTCTG T  
 ||||| ||| |  
 CTTCCGTAGAGAT A  
 GG  
 GAM1425 LOC152215 3' AAACAGTAGCTTTGTTTTTAGG 80486 A T\_\_ \_  
 GGGT TCC TGAAGGCA CT CTGTTT  
 ||| ||||| || |||||

	GGG ATTTTGT GA GACAAA	
	G TTC T	
GAM1425 LOC152283 5'	GGACGGGGGCAGTGTGGGG 85683	AAG AT
	CTCCATG GC CTCTGTTT	
	GGGGTGT CG GGGGCAGG	
	GA_ _	
GAM1425 LOC152317 3'	GGCAGAGAACCATGAGT 85645	C AAGGCA
	ACTC ATG TCTCTGTT	
	TGAG TAC AGAGACGG	
	_ CA_ _	
GAM1425 LOC152447 5'	AGACAGTTGTCTTATGGAGT 80585	A TCT
	ACTCCATGA GGCA CTGTTT	
	TGAGGTATT CTGT GACAGA	
	_ T_ _	
GAM1425 LOC152790 5'	AGGCAGGGAAGAGGCATGAGT 85873	C AAGGCA
	ACTC ATG TCTCTGTTT	
	TGAG TAC AGGGACGGA	
	_ GGAGA_	
GAM1425 LOC153020 3'	AACAGCTCTTCGTGGGG 80761	CATCT
	CTCCATGAAGG CTGTT	
	GGGGTGCTTCT GACAA	
	C_ _	
GAM1425 LOC153139 5'	AAATAGAGAAAATGTGGAG 85923	GAAGGCA
	CTCCAT TCTCTGTTT	
	GAGGTG AGAGATAAA	
	TAAA_ _	
GAM1425 LOC153146 5'	GGATGGGGATGTTGGGGAGGAG 85930	ATGAA
	CTCC GGCATCTCTGTTT	
	GAGG TTGTAGGGGTAGG	
	AGGGG	
GAM1425 LOC153222 3'	AGATGGAAAAATTATGGGGT 80781	AGG_ _
	ACTCCATGA CATCT	
	TGGGGTATT GTAGA	
	AAAAAG	
GAM1425 LOC153592 3'	AGGCAGAGATGGAAGTTGGA 86064	TGAAGG
	TCCA CATCTCTGTTT	
	AGGT GTAGAGACGGA	
	TGAAG_	
GAM1425 LOC153733 5'	AGGCAGAGGTGTTCCAGTG 80919	GA_
	CAT AGGCATCTCTGTTT	



	GTG TTTGTGGAGACGGA		
	ACC		
GAM1425 LOC153811 3'	AGGTGGAGGTGCAGTGGGG 80941	GAAG	TG
	CTCCAT GCATCTC TTT		
	GGGGTG CGTGGAG GGA		
	A___ GT		
GAM1425 LOC154089 3'	AGTGGTTATTTTCATGGA 81034	C_	T
	TCCATGAAGG ATC CT		
	AGGTACTTTT TGG GA		
	AT T		
GAM1425 LOC154184 5'	AAATAGAGAAAATGTGGAG 86177	GAAGGCA	
	CTCCAT TCTCTGTTT		
	GAGGTG AGAGATAAA		
	TAAA___		
GAM1425 LOC154215 3'	GGACAGGTCATTTATGGG 81055	_	ATCT
	TCCATGAA GGC CTGTTT		
	GGGTATTT CTG GACAGG		
	A _____		
GAM1425 LOC154790 5'	GAGTGTGTCTTCGTGGAG 81150	_	
	CTCCATGAAGGCAT CTC		
	GAGGTGCTTCTGTG GAG		
	T		
GAM1425 LOC154834 3'	GAGCAGAGGGAGGGCTTTGTGG 86266	TG	GCA___
A	TCCA AAG TCTCTGTTT		
	AGGT TTC GGAGACGAG		
	GT GGGAG		
GAM1425 LOC157254 5'	AGGTCGCCTGCGTGGGGT 81382	A	_
	ACTCCATG AGGC ATCT		
	TGGGGTGC TCCG TGGA		
	G C		
GAM1425 LOC157376 3'	AGACAGGGGCTGTCAGGAGT 81429	A A	AT
	ACTCC TGA GGC CTCTGTTT		
	TGAGG ACT TCG GGGACAGA		
	_ G _		
GAM1425 LOC157506 3'	AGGTGACTTTTTCATGGTGT 81437	T	__ _
	AC CCATGAA GG CATCT		
	TG GGTACTT TC GTGGA		
	T TT A		
GAM1425 LOC158170 5'	GGGCAGAGGGGCGCTCGTAGGG 81765	C	AG AT
T	ACTC ATGA GC CTCTGTTT		

	TGGG TGCT CG GAGACGGG		
	A CG GG		
GAM1425 LOC158191 3'	GGGTGTCCTTTTGGGG 81782 T _		
	CTCCA GAAGG CATCT		
	GGGGT TTTCC GTGGG		
	T T		
GAM1425 LOC158257 3'	AAACATGGGCCTTCATGGG 86708 AT C		
	TCCATGAAGGC CT TGTTT		
	GGGTACTTCCG GG ACAA		
	_ T		
GAM1425 LOC158257 3'	AAACATGGGCCTTCATGGG 86708 AT C		
	TCCATGAAGGC CT TGTTT		
	GGGTACTTCCG GG ACAA		
	_ T		
GAM1425 LOC158373 5'	AGATGGAGAGACTGTGGAGT 71041 GA GCA		
	ACTCCAT AG TCTCTGTTT		
	TGAGGTG TC AGAGGTAGA		
	_ AG_		
GAM1425 LOC158696 3'	AGGTGGAGGACTGAATCATGGG 81971 AGG _ TG		
G	CTCCATGA CA TCTC TTT		
	GGGGTACT GT GGAG GGA		
	AA_ CA GT		
GAM1425 LOC158819 5'	GAGCAGGGGTCTTTTCATGTGG 86907 TC C		
T	AC CATGAAGG ATCTCTGTTT		
	TG GTACTTTC TGGGGACGAG		
	GT T		
GAM1425 LOC158856 5'	GGGTGGGGGTGCCCAGTG 86918 GAA TG		
	CAT GGCATCTC TTT		
	GTG CCGTGGGG GGG		
	AC_ GT		
GAM1425 LOC158954 3'	GAGTGGCATCTTTATGGA 60435 _ AT		
	TCCATGAAG GC CTC		
	AGGTATTTC CG GAG		
	TA GT		
GAM1425 LOC158969 3'	AAACGGGGGTCTCCAGGAGT 82056 A A C		
	ACTCC TG AGG ATCTCTGTTT		
	TGAGG AC TCC TGGGGGCAAA		
	_ C _		
GAM1425 LOC158997 3'	AAGTGGAGATGGGATGGGG 82078 GAAGG TG		
	CTCCAT CATCTC TTT		

	GGGGTA GTAGAG GAA	
	GG___ GT	
GAM1425 LOC159199 5'	AGGTGGAGTACCTCATGGAGT 82180	A CAT TG
	ACTCCATGA GG CTC TTT	
	TGAGGTACT CC GAG GGA	
	_ AT_ GT	
GAM1425 LOC160777 3'	GGATGCTCTTTATGGA 82241	_
	TCCATGAAG GCATCT	
	AGGTATTTT CGTAGG	
	T	
GAM1425 LOC164714 5'	AGGTGCCTTTGGGGAGT 87222	AT
	ACTCC GAAGGCATCT	
	TGAGG TTTCCGTGGA	
	GG	
GAM1425 LOC170261 3'	AAGCGGCTATCTTTTGGGGT 82581	T CATCT
	ACTCCA GAAGG CTGTTT	
	TGGGGT TTTCT GCGCAA	
	_ ATC_	
GAM1425 LOC196478 5'	AGACGGGGATTACAATGGAG 87724	GAAGGC
	CTCCAT ATCTCTGTTT	
	GAGGTA TAGGGGCAGA	
	ACAT_	
GAM1425 LOC196955 5'	AGCAGGGATAGGTGGG 77361	GAAGGC
	TCCAT ATCTCTGTT	
	GGGTG TAGGGACGA	
	GA_	
GAM1425 LOC196957 5'	GGGCGGGGAGGGGTGTGGAG 87828	AAGGCA
	CTCCATG TCTCTGTTT	
	GAGGTGT AGGGGCGGG	
	GGGG_	
GAM1425 LOC196961 5'	GGGCGGGGAGGGGTGTGGAG 87849	AAGGCA
	CTCCATG TCTCTGTTT	
	GAGGTGT AGGGGCGGG	
	GGGG_	
GAM1425 LOC196985 5'	GGGCAGAGGTGCTATCTGGG 89664	T A
	TCCA GA GGCATCTCTGTTT	
	GGGT CT TCGTGGAGACGGG	
	_ A	
GAM1425 LOC196986 5'	GGGCAGAGGTGCTATCTGGG 89659	T A
	TCCA GA GGCATCTCTGTTT	

GGGT CT TCGTGGAGACGGG  
 \_ A  
 GAM1425 LOC196993 5' GGGCGGAGGCAAAGCGGGGAGT 89670 A AAG\_ AT  
 ACTCC TG GC CTCTGTTT  
 ||||| || || |||||  
 TGAGG GC CG GAGGCGGG  
 G GAAA \_

GAM1425 LOC197135 5' GGGTGGGTGTTTATGGCAGT 87895 \_ G AT\_  
 ACT CCATGAA GC CTC  
 ||| ||||| || |||  
 TGA GGTATTT TG GGG  
 C G GGT

GAM1425 LOC197138 5' GGGCGGGGAGGGGTGTGGAG 87922 AAGGCA  
 CTCCATG TCTCTGTTT  
 ||||| |||||  
 GAGGTGT AGGGGCGGG  
 GGGG\_

GAM1425 LOC197322 5' AGACAGGGGACACCGTGGTGT 89738 T AAGGCA  
 AC CCATG TCTCTGTTT  
 || ||||| |||||  
 TG GGTGC GGGGACAGA  
 T CACA\_

GAM1425 LOC199221 5' GAGTGGACCAAAC TTTATGGGG 80349 GCATC TG  
 CTCCATGAAG TC TTT  
 ||||| || |||  
 GGGGTATTC AG GAG  
 AAACC GT

GAM1425 LOC199837 5' ATATGGTTGATGTCTTCATGGA 88405 T\_ TT  
 TCCATGAAGGCATC CTGT  
 ||||| ||||| |||||  
 AGGTACTTCTGTAG GGTA  
 TT TAG

GAM1425 LOC199858 5' AGATAGGGATGCTTCTTGGAG 88415 T G  
 CTCCA GAAG CATCTCTGTTT  
 |||| |||| |||||  
 GAGGT CTTC GTAGGGATAGA  
 T \_

GAM1425 LOC199858 5' AGTAGGGGCTTATGGAG 88416 AA AT \_  
 CTCCATG GGC CT CT  
 ||||| ||| |||  
 GAGGTAT TCG GA GA  
 \_ GG T

GAM1425 LOC199858 5' GGATGGAGGTTACGCATGGG 88422 AAGGC  
 TCCATG ATCTCTGTTT  
 ||||| |||||  
 GGGTAC TGGAGGTAGG  
 GCAT\_

GAM1425 LOC199906 3' GAATAGGGTGATTTGTGAAGT 88484 C TG GG T  
 ACT CA AA CATC CTGTTT  
 ||| || ||| |||||

		TGA GT TT GTGG GATAAG		
		A GT A_ _		
GAM1425	LOC199986 5'	GGGTGGAGATGTCTAGGGG	89907	ATGA TG
		CTCC AGGCATCTC TTT		
		GGGG TCTGTAGAG GGG		
		A_ _ GT		
GAM1425	LOC200169 3'	GGTGGTGCTTCTGGGGT	89956	T G T
		ACTCCA GAAG CATC CT		
		TGGGGT CTTC GTGG GG		
		_ _ T		
GAM1425	LOC200225 5'	GAGCGGAAGCAGTTCATGGG	89966	G_ ATC
		TCCATGAA GC TCTGTTT		
		GGGTACTT CG AGGCGAG		
		GA A_		
GAM1425	LOC200720 5'	GGACAATCCATCGTGGAGT	90111	A CATC
		ACTCCATGA GG TCT		
		TGAGGTGCT CC AGG		
		A TAAC		
GAM1425	LOC200953 5'	GGTGGGGACTCAGGAGT	90210	A A GCA TG
		ACTCC TGA G TCTC TT		
		TGAGG ACT C AGGG GG		
		_ _ _ GT		
GAM1425	LOC201164 3'	GGGGTGCTTTCATGAGT	88121	C
		ACTC ATGAAGGCATCTC		
		TGAG TACTTTCGTGGGG		
		_		
GAM1425	LOC201229 3'	GGGCCTTGCCTTCAGGGAGT	88146	A T_
		ACTCC TGAAGGCA CTC		
		TGAGG ACTTCCGT GGG		
		G TCC		
GAM1425	LOC201242 5'	AGATGGGGAGACTGTGGA	87359	GA GCA
		TCCAT AG TCTCTGTTT		
		AGGTG TC AGGGGTAGA		
		_ AG_		
GAM1425	LOC201510 5'	AGCAGATTACGTGGAGT	88249	A GCATC
		ACTCCATG AG TCTGTT		
		TGAGGTGC TT AGACGA		
		A _ _ _		
GAM1425	LOC201549 3'	GCGGAGGTGTGGCGT	90231	T ATGAAG
		AC CC GCATCTCTGT		

		TG GG TGTGGAGGCG	
		C _____	
GAM1425	LOC201689 5'	GAACAAACGAATGCCTTTGTGG 67145	TG C ____
		GGT CTCCA AAGGCAT TC TGTTT	
		GGGGT TTCCGTA AG ACAAG	
		GT _ CAA	
GAM1425	LOC201705 5'	AGATGGAGGTGCAGGCAGTGG 90250	GAAG_
		CCAT GCATCTCTGTTT	
		GGTG CGTGGAGGTAGA	
		ACGGA	
GAM1425	LOC202934 3'	GGGCAGGGCACTCATGGAG 90422	AG ATC
		CTCCATGA GC TCTGTTT	
		GAGGTACT CG GGACGGG	
		CA ____	
GAM1425	LOC203377 5'	AAATGGAGATGCTTTTCAT 90574	_
		ATGAAG GCATCTCTGTTT	
		TACTTT CGTAGAGGTAAA	
		T	
GAM1425	LOC203378 3'	GAGCTTTCAGCCTTCGTGGG 90605	ATCTCT
		TCCATGAAGGC GTTT	
		GGGTGCTTCCG CGAG	
		ACTTT_	
GAM1425	LOC203504 5'	GGGTGGGGGTGCCAGTG 90640	GAA TG
		CAT GGCATCTC TTT	
		GTG CCGTGGGG GGG	
		AC_ GT	
GAM1425	LOC205418 5'	AGTGGAGAGCGTGGAG 90680	GAAG A TG
		CTCCAT GC TCTC TT	
		GAGGTG CG AGAG GA	
		____ _ GT	
GAM1425	LOC219300 5'	GACAGAGAACAAGGGGT 94312	A AAGGCA
		ACTCC TG TCTCTGTT	
		TGGGG AC AGAGACAG	
		A A_____	
GAM1425	LOC219513 5'	AAGCAGGGATCTGTCGTGGGGT 94321	A C
		ACTCCATGA GG ATCTCTGTTT	
		TGGGGTGCT TC TAGGGACGAA	
		G _	
GAM1425	LOC219722 5'	AGGCAGAGGTTGCAGTGAGGT 93079	TC GAAG _
		AC CAT GCA TCTCTGTTT	

	TG GTG CGT GGAGACGGA		
	GA A___ T		
GAM1425 LOC219940 5'	AGATCAGCTTTATGTGGAGT 93353	_	ATC
	ACTCCATG AAGGC TCT		
	TGAGGTGT TTTCG AGA		
	A ACT		
GAM1425 LOC220282 5'	AGCAGAGATAAGTGGAG 94318	GAAGGC	
	CTCCAT ATCTCTGTT		
	GAGGTG TAGAGACGA		
	AA___		
GAM1425 LOC220513 3'	AGTAGGCTTTTCATGGGG 60448	_	AT_
	CTCCATGAAG GC CT		
	GGGGTACTTT CG GA		
	T GAT		
GAM1425 LOC220514 3'	GGGTGGGGGGAACGTGGGG 60447	AAGGCA	TG
	CTCCATG TCTC TTT		
	GGGGTGC GGGG GGG		
	AAG___ GT		
GAM1425 LOC220705 3'	GTCCTGGGTCTTTCATGGGGT 91229	C	CTGTTT
	ACTCCATGAAGG ATCT		
	TGGGGTACTTTC TGGG		
	_ TCCTGG		
GAM1425 LOC220766 5'	GACAGAGATCAGTGAGT 90798	CA	AGGCA
	ACTC TGA TCTCTGTT		
	TGAG ACT AGAGACAG		
	TG _____		
GAM1425 LOC221088 5'	GAGCGGGGATGATGAGGAGT 93265	ATGAAGG	
	ACTCC CATCTCTGTTT		
	TGAGG GTAGGGGCGAG		
	AGTA___		
GAM1425 LOC221092 3'	AACAGGGGCTGTCGGGGT 93240	ATGAA	_
	ACTCC GGCA TCTCTGTT		
	TGGGG CTGT GGGGACAA		
	___ C		
GAM1425 LOC221322 5'	AAACAGAATATTCTCTTCGTGA 91929	C	CATC___
AGT	ACT CATGAAGG TCTGTTT		
	TGA GTGCTTCT AGACAAA		
	A CTTATA		
GAM1425 LOC221322 5'	AAACAGAATATTCTCTTCGTGA 91929	C	CATC___
AGT	ACT CATGAAGG TCTGTTT		

	TGA GTGCTTCT	AGACAAA	
	A	CTTATA	
GAM1425 LOC221336 5'	GAATAGCATCATCTTCATGGG	92272	CATCT
	TCCATGAAGG	CTGTTT	
	GGGTACTTCT	GATAAG	
	ACTAC		
GAM1425 LOC221399 5'	AGGCAGAGGAAAGACATGGTGT	93844	T AAGGCA
	AC CCATG	TCTCTGTTT	
	TG GGTAC	GGAGACGGA	
	T	AGAAA_	
GAM1425 LOC221477 3'	AAGTGGAGACTTTTATGGA	92147	CA TG
	TCCATGAAGG	TCTC TTT	
	AGGTATTTTC	AGAG GAA	
	_	GT	
GAM1425 LOC221601 5'	AAATAGAGAAAATGTGGAG	93645	GAAGGCA
	CTCCAT	TCTCTGTTT	
	GAGGTG	AGAGATAAA	
	TAAA_		
GAM1425 LOC221662 3'	AGACAGGTTAGCATTTTATGG	92400	_ ATC
A	TCCATGAAG	GC TCTGTTT	
	AGGTATTTT	CG GGACAGA	
	TA	ATT	
GAM1425 LOC221922 5'	GGATGGAGGTGGAAGGCTGGAG	92698	TGAAGG
	CTCCA	CATCTCTGTTT	
	GAGGT	GTGGAGGTAGG	
	CGGAAG		
GAM1425 LOC221935 3'	AGGCAGGGATGCTAAGGTGT	92616	T ATGAA
	AC CC	GGCATCTCTGTTT	
	TG GG	TCGTAGGGACGGA	
	T	AA_	
GAM1425 LOC222169 3'	GATACAGACAGATGTTTTTTGG	94086	T _ TT
GGT	CTCCA	GAAGGCATC TCTGT	
	GGGGT	TTTTTG TAG AGACA	
	_	AC TAGA	
GAM1425 LOC222228 3'	GAGCAGGGGTGGGGGGAGGGGG	94298	ATGAAGG
	CTCC	CATCTCTGTTT	
	GGGG	GTGGGGACGAG	
	GAGGGGG		
GAM1425 LOC222233 5'	GAATAGAGGGATGTGGAGT	94254	GAAGGCA
	ACTCCAT	TCTCTGTTT	



	TGAGGTG	GGAGATAAG	
	TAG_____		
GAM1425 LOC222233 3'	GAGCAGGGGTGGGGGGAGGGGG	94255	ATGAAGG
	CTCC CATCTCTGTTT		
	GGGG GTGGGGACGAG		
	GAGGGGG		
GAM1425 LOC222865 3'	GGGCAGGGGAGGACTGTGGGGT	92866	GA GCA_
	ACTCCAT AG TCTCTGTTT		
	TGGGGTG TC GGGGACGGG		
	___ AGGA		
GAM1425 LOC253001 5'	AAGCAGGGGGCTGGTGGGGT	96248	GAA A
	ACTCCAT GGC TCTCTGTTT		
	TGGGGTG TCG GGGGACGAA		
	G_ _		
GAM1425 LOC253392 5'	AGCAGGGGGCGCCGTGGG	96448	GAA AT
	TCCAT GGC CTCTGTT		
	GGGTG CCG GGGACGA		
	___ CG		
GAM1425 LOC253816 3'	GGATGCCTTTAGGAGT	94388	A
	ACTCC TGAAGGCATCT		
	TGAGG ATTTCCGTAGG		
	—		
GAM1425 LOC253866 5'	GGGCAGGGGTGTGGAGAGGGGG	95588	ATGAAG
T	ACTCC GCATCTCTGTTT		
	TGGGG TGTGGGGACGGG		
	GAGAGG		
GAM1425 LOC253982 5'	GACAGGGGAAGTGGGGT	95078	TGAA GCA
	ACTCCA G TCTCTGTT		
	TGGGGT C GGGGACAG		
	___ AA_		
GAM1425 LOC254085 3'	GGGTAGGGGTGCATATTGGA	96119	TGAAG TT
	TCCA GCATCTCTG T		
	AGGT CGTGGGGAT G		
	TATA_ GG		
GAM1425 LOC254110 3'	AACAGCCATGCCTTCTGGA	95106	T CT
	TCCA GAAGGCAT CTGTT		
	AGGT CTTCCGTA GACAA		
	_ CC		
GAM1425 LOC254128 3'	GAGTAGGGATGACATGGAG	95637	AAGG
	CTCCATG CATCTCTGTTT		

	GAGGTAC GTAGGGATGAG	
	A__	
GAM1425 LOC254221 5'	AAACAGAATAAATTCATGGA 97600	GGCATC
	TCCATGAA TCTGTTT	
	AGGTACTT AGACAAA	
	AAATA_	
GAM1425 LOC254381 5'	AAACAGAGAGCACCTTCCGGAG 97457	AT CA_
	CTCC GAAGG TCTCTGTTT	
	GAGG CTTCC AGAGACAAA	
	C_ ACG	
GAM1425 LOC254876 3'	GAGCAGGGGTGGGGTGGGGT 96052	GAAGG
	ACTCCAT CATCTCTGTTT	
	TGGGGTG GTGGGGACGAG	
	GG__	
GAM1425 LOC255271 5'	AGGCAGAGTCCTTCTGGAGT 95498	T CAT
	ACTCCA GAAGG CTCTGTTT	
	TGAGGT CTTCC GAGACGGA	
	_ T__	
GAM1425 LOC255465 3'	GGATGGGGATGCCAGGAAGT 97296	_ ATGAA
	ACT CC GGCATCTCTGTTT	
	TGA GG CCGTAGGGGTAGG	
	A A__	
GAM1425 LOC255465 3'	GGGCAGGGCACTCATGGAG 97298	AG ATC
	CTCCATGA GC TCTGTTT	
	GAGGTACT CG GGACGGG	
	CA _	
GAM1425 LOC255588 5'	GGACAGAGCTGTCGGGGAGT 96979	ATGAA T
	ACTCC GGCA CTCTGTTT	
	TGAGG CTGT GAGACAGG	
	GG__ C	
GAM1425 LOC255645 3'	GAATGGGGGCACCTATGGA 96652	GA CA
	TCCAT AGG TCTCTGTTT	
	AGGTA TCC GGGGGTAAG	
	_ AC	
GAM1425 LOC255650 3'	GAACAGGGAACGGAACAGGAGT 96712	A AAGGCA
	ACTCC TG TCTCTGTTT	
	TGAGG AC AGGGACAAG	
	_ AAGGCA	
GAM1425 LOC255749 3'	GAATGGGGGTGCCTTCATGAG 96447	C
	CTC ATGAAGGCATCTCTGTTT	

GAG TACTTCCGTGGGGGTAAG

GAM1425 LOC256112 5' GGCCTGATGCCTTCAGGAAGT 96367 \_ A TCT  
ACT CC TGAAGGCATC GTT  
||| || ||||| |||  
TGA GG ACTTCCGTAG CGG  
A \_ TC\_  
GAM1425 LOC256158 5' AGGTGGAGGTGTCTGTGCATG 97646 A\_\_ TG  
CATG AGGCATCTC TTT  
||| ||||| |||  
GTAC TCTGTGGAG GGA  
GTG GT  
GAM1425 LOC256306 3' AGGCAGGAATATTCATGGAG 96679 GGCA T  
CTCCATGAA TC CTGTTT  
||| || |||  
GAGGTACTT AG GACGGA  
ATA\_ \_  
GAM1425 LOC256530 3' AGCAGGGATAATGGGG 96813 GAAGGC  
CTCCAT ATCTCTGTT  
||| |||||  
GGGGTA TAGGGACGA  
A\_\_\_\_  
GAM1425 LOC256790 5' GGACAGGGGTGTCATGCCTGGA 94835 TGAA\_  
G CTCCA GGCATCTCTGTTT  
||| |||||  
GAGGT CTGTGGGGACAGG  
CCGTA  
GAM1425 LOC256867 5' GGGCGGGGGGAGTTCTGGGGT 94866 T GGCA  
ACTCCA GAA TCTCTGTTT  
||| || |||||  
TGGGGT CTT GGGGGCGGG  
\_ GAG\_  
GAM1425 LOC257051 3' AAGCGGCTATCTTTTGGGGT 96315 T CATCT  
ACTCCA GAAGG CTGTTT  
||| ||| |||  
TGGGGT TTTCT GGCGAA  
\_ ATC\_  
GAM1425 LOC257054 3' GGGCGGGGGTGTTCGGGTGG 95668 GAA  
CCAT GGCATCTCTGTTT  
||| |||||  
GGTG TTGTGGGGGCGGG  
GCG  
GAM1425 LOC257128 5' GAATGGAGGAAAACTGTGGAG 96086 GA GCA\_  
CTCCAT AG TCTCTGTTT  
||| || |||||  
GAGGTG TC GGAGGTAAG  
\_ AAAA  
GAM1425 LOC257177 3' AAACAGGGAAATTTTGGGGT 95381 T GGCA  
ACTCCA GAA TCTCTGTTT  
||| || |||||

TGGGGT TTT AGGGACAAA  
 \_ AA\_  
 GAM1425 LOC257438 3' GGGCAGAGGCCTGCCTTCAAGG 93973 A \_  
 AGT ACTCC TGAAGGCA TCTCTGTTT  
 ||||| ||||| |||||  
 TGAGG ACTTCCGT GGAGACGGG  
 A CC  
 GAM1425 LOC257608 3' GAGTGGAGATGGGGGCGGGGGT 97828 A AAGG TG  
 ACTCC TG CATCTC TTT  
 ||||| || ||||| ||  
 TGGGG GC GTAGAG GAG  
 \_ GGGG GT  
 GAM1425 LOC51279 3' GGGTAGGGGTTGGGGGTGGGG 33317 GAAGGC TT  
 CTCCAT ATCTCTG T  
 ||||| ||||| |  
 GGGGTG TGGGGAT G  
 GGGGT\_ GG  
 GAM1425 LOC51291 3' GGACAGGGGTGCTTTT 33363  
 GAAGGCATCTCTGTTT  
 ||||| |||||  
 TTTTCGTGGGGACAGG  
  
 GAM1425 LOC51596 5' GGGCATTCTTCGGGGGT 31926 A CAT  
 ACTCC TGAAGG CTC  
 ||||| ||||| ||  
 TGGGG GCTTCT GGG  
 \_ TAC  
 GAM1425 LOC51706 3' GAGCAGTCTCTTCCATGGAGT 70316 \_ CATCT  
 ACTCCATG AAGG CTGTTT  
 ||||| ||||| |||||  
 TGAGGTAC TTCT GACGAG  
 C CT\_  
 GAM1425 LOC56270 3' GCGGGGACGGGGGGT 39020 A AAGGCA  
 ACTCC TG TCTCTGT  
 ||||| || |||||  
 TGGGG GC AGGGGCG  
 G \_  
 GAM1425 LOC56930 5' AGACGGGATAGTTTATGGAGT 62058 GGC T  
 ACTCCATGAA ATC CTGTTT  
 ||||| ||||| |||||  
 TGAGGTATTT TAG GGCAGA  
 GA\_ \_  
 GAM1425 LOC58525 3' GGTGGGGGCCAGTGGGGT 78650 GAA AT TG  
 ACTCCAT GGC CTC TT  
 ||||| || |||||  
 TGGGGTG CCG GGG GG  
 A\_ \_ GT  
 GAM1425 LOC89135 3' AGTAGAGGTGGTTATGGA 60315 AGG TT  
 TCCATGA CATCTCTG T  
 ||||| ||||| |

AGGTATT GTGGAGAT A  
 G\_\_ GG  
 GAM1425 LOC89135 5' GTGCCTTTTTATGTGGAGT 60318 \_\_\_\_  
 ACTCCAT GAAGGCAT  
 ||||| |||||  
 TGAGGTG TTTCCGTG  
 TATT  
 GAM1425 LOC89919 3' GAGCATCTTTCAGGGGT 60723 A C \_  
 ACTCC TGAAGG AT CTC  
 |||| ||||| || |||  
 TGGGG ACTTTC TA GAG  
 \_ \_ C  
 GAM1425 LOC90148 3' AAGCGGGGATGCCTTCCACAGG 61661 AT\_\_  
 CC GAAGGCATCTCTGTTT  
 || |||||  
 GG CTTCCGTAGGGGCGAA  
 ACAC  
 GAM1425 LOC90342 5' AGGCGGGGGTGGTCTGGAGT 62352 T AGG  
 ACTCCA GA CATCTCTGTTT  
 ||||| || |||||  
 TGAGGT CT GTGGGGGCGGA  
 \_ G\_  
 GAM1425 LOC90525 3' GGGCAGAGGGAAGTGTGCAGT 63156 C GA GCA  
 ACT CAT AG TCTCTGTTT  
 ||| || |||||  
 TGA GTG TC GGAGACGGG  
 C \_ AAG  
 GAM1425 LOC90625 3' GGGCAGAGGATGGTTCATGGGG 63611 GG \_  
 T ACTCCATGAA CATC TCTGTTT  
 ||||| ||| |||||  
 TGGGGTACTT GTAG AGACGGG  
 G\_ G  
 GAM1425 LOC90750 5' AAGTGGAGGTGTGCATGGTGT 63910 T AAG TG  
 AC CCATG GCATCTC TTT  
 || |||| ||||| |||  
 TG GGTAC TGTGGAG GAA  
 T G\_ GT  
 GAM1425 LOC90785 3' GAATGGGGGTGCCTGGTGAG 64017 C GA  
 CTC AT AGGCATCTCTGTTT  
 ||| || |||||  
 GAG TG TCCGTGGGGGTAAG  
 \_ G\_  
 GAM1425 LOC91050 3' GCAGGGAGCAGGAGT 64746 ATGAAG A  
 ACTCC GC TCTCTGT  
 |||| || |||||  
 TGAGG CG AGGGACG  
 A\_\_\_\_ \_  
 GAM1425 LOC91069 3' AGCAGGGATCAGGGAGT 64772 A AGGCA  
 ACTCC TGA TCTCTGTT  
 |||| || |||||

	TGAGG ACT AGGGACGA	
	G _____	
GAM1425 LOC91097 5'	AGTGGGGGCCCATGGGG 64834	AA AT TG
	CTCCATG GGC CTC TT	
	GGGGTAC CCG GGG GA	
	___ _ GT	
GAM1425 LOC91097 3'	GAGCAGATGGTGCCTTTGTGGG 64837	TG _
	TCCA AAGGCATC TCTGTTT	
	GGGT TTCCGTGG AGACGAG	
	GT T	
GAM1425 LOC91149 3'	GGGTGCAGCTTCATGGGGT 65081	___
	ACTCCATGAAG GCATCT	
	TGGGGTACTTC CGTGGG	
	GA	
GAM1425 LOC91170 5'	AACAGCCTTTTATGGGG 65132	CATCT
	CTCCATGAAGG CTGTT	
	GGGGTATTTTC GACAA	
	C_____	
GAM1425 LOC91266 5'	GAGCAGAGGCAGGCGTGGGG 65415	AAG AT
	CTCCATG GC CTCTGTTT	
	GGGGTGC CG GAGACGAG	
	GGA _	
GAM1425 LOC91355 5'	GGTGGTTGCTTCATGGGGT 65718	G _ T
	ACTCCATGAAG CA TC CT	
	TGGGGTACTTC GT GG GG	
	_ T T	
GAM1425 LOC91397 5'	GGATGGGGATGCCCGGGAG 65912	ATGAA
	CTCC GGCATCTCTGTTT	
	GAGG CCGTAGGGGTAGG	
	GC_____	
GAM1425 LOC91461 3'	GGACAATCCATCGTGGAGT 66134	A CATC
	ACTCCATGA GG TCT	
	TGAGGTGCT CC AGG	
	A TAAC	
GAM1425 LOC91661 3'	AGACAGAGGTGCCTGGGTGG 56397	GA
	CCAT AGGCATCTCTGTTT	
	GGTG TCCGTGGAGACAGA	
	GG	
GAM1425 LOC91663 3'	GAGTTTTCTTTATGGAGT 56407	CAT
	ACTCCATGAAGG CTC	

			TGAGGTATTTCT	GAG	
			TTT		
GAM1425	LOC91813	5'	GGGTGGAGGCTGGGCTGGGGAG	67258	ATGAA A___ TG
		T	ACTCC GGC TCTC TTT		
			TGAGG TCG GGAG GGG		
			GG___ GGTC GT		
GAM1425	LOC91828	5'	AGGCGGAGGGCGCGTCGGG	67274	A AG A_
			CC TGA GC TCTCTGTTT		
			GG GCT CG GGAGGCGGA		
			_ G_ CG		
GAM1425	LOC92080	3'	GAGCAGAGGGGGTCATGCAGT	68051	C AGGCA
			ACT CATGA TCTCTGTTT		
			TGA GTACT GGAGACGAG		
			C GGG___		
GAM1425	LOC92249	5'	AAGTGGAGAGTGACATGCAGT	68563	C AAG A TG
			ACT CATG GC TCTC TTT		
			TGA GTAC TG AGAG GAA		
			C AG_ _ GT		
GAM1425	LOC92303	3'	AAACAGGGGCCCTCAGAAGT	68817	CCA A AT
			ACT TGA GGC CTCTGTTT		
			TGA ACT CCG GGGACAAA		
			AG_ C _		
GAM1425	LOC92340	3'	GGATGGAGGCTGGACTGTGTGG	68996	A G_ _
			CCATG AG CA TCTCTGTTT		
			GGTGT TC GT GGAGGTAGG		
			G AG C		
GAM1425	LOC92597	5'	AATAGAGATGATGTGGA	69969	GAAGG
			TCCAT CATCTCTGTT		
			AGGTG GTAGAGATAA		
			TA___		
GAM1425	LOC93017	3'	AACAGAGATAGTGGA	71151	GAAGGC
			TCCAT ATCTCTGTT		
			AGGTG TAGAGACAA		
			A_____		
GAM1425	LOC93259	5'	GAACGGGGGGCACCCGTGGA	71820	AA CA
			TCCATG GG TCTCTGTTT		
			AGGTGC CC GGGGGCAAG		
			_ AC		
GAM1425	LOC93626	3'	GGGCAGGGGTGCCTGCCCCAG	72772	CCATGA
			CT AGGCATCTCTGTTT		

			GA	TCCGTGGGGACGGG		
				CCCCG_		
GAM1425	LOC96597	5'	GACAGGGAATCAGGAGT	66914	A	AGGCA
			ACTCC TGA	TCTCTGTT		
			TGAGG ACT	AGGGACAG		
			_ A _			
GAM1426	BDKRB2	3'	AGCTCCGTGGAGCAGAATCAGT	5263	A	GA A
	A		TACTGAT CTGT	TCAC GAGCT		
			ATGACTA GACG	GGTG CTCGA		
			A A_ C			
GAM1426	COL4A1	3'	AGCTCTGTTGAATCACAGTATC	8460	-	-
	AGTA		TACTGATACTGTGAT	CA CAGAGCT		
			ATGACTATGACACTA	GT GTCTCGA		
			A T			
GAM1426	DNAJB9	5'	AGCTCTGTGGAGGAGCAGCAGT	24677	ATA	GA_
	A		TACTG CTGT	TCACAGAGCT		
			ATGAC GACG	GGTGTCTCGA		
			_ AGGA			
GAM1426	GRM6	3'	CTCTGTGATTCAGAATCAG	5933	A	T
			CTGAT CTG	GATCACAGAG		
			GACTA GAC	TTAGTGTCTC		
			A _			
GAM1426	MGA	3'	AGCTCATTTACAGTACCAG	62804	A	TCACA
			CTG TACTGTGA	GAGCT		
			GAC ATGACACT	CTCGA		
			C TTA_			
GAM1426	NR2E1	3'	AGCTCTGTGTATAACATCGTA	12322	T	AC AT
			TAC GAT TGTG	CACAGAGCT		
			ATG CTA ATAT	GTGTCTCGA		
			_ CA _			
GAM1426	SCN3A	3'	CTCTGTGAAGCAGGGTATCA	22631	G	A_
			TGATACT TG	TCACAGAG		
			ACTATGG AC	AGTGTCTC		
			G GA			
GAM1426	UBE2L3	3'	AGCCCTATAATCACAGGTCTGT	12497	T	A CAC A
	G		TAC GAT CTGTGAT	AG GCT		
			GTG CTG GACACTA	TC CGA		
			T _ ATA C			
GAM1426	FLJ14054	3'	GCTCTGTGATATATCAGTG	44660	CTGTG	
			TACTGATA	ATCACAGAGC		



			GTGACTAT TAGTGTCTCG		
			A____		
GAM1426	MUC16	5'	AGCTCTGTACCCACCACCAG 60525	ATACT ATC	
			CTG GTG ACAGAGCT		
			GAC CAC TGTCTCGA		
			CAC__ CCA		
GAM1426	MYO3B	3'	CTCCATGAGGCTATCAGTG 57305	CT GA CA	
			TACTGATA GT TCA GAG		
			GTGACTAT CG AGT CTC		
			__ G_ AC		
GAM1426	ZNF-U69274	3'	GCTCTGTGGATACCATGT 26989	CT A	
			ATA GTG TCACAGAGC		
			TGT CAT GGTGTCTCG		
			AC A		
GAM1426	LOC150299	3'	AGCTCTGTAATCAGGCAG 84966	__ C	
			CTGT GAT ACAGAGCT		
			GACG CTA TGTCTCGA		
			GA A		
GAM1426	LOC51277	3'	CTCTGTAATTATAGTA 80042	C	
			TACTGTGAT ACAGAG		
			ATGATATTA TGTCTC		
			A		
GAM1427	CDH5	3'	GCATCTTCCACTGGA 8387	A CT	
			TCCAGTG AGGA TGT		
			AGGTCAC TTCT ACG		
			C __		
GAM1427	COL1A1	3'	ACCAGCCCCCTCACTGGG 3600	A A T	
			TCCAGTGA GG CT GT		
			GGGTCAC CT GA CA		
			C C C		
GAM1427	ICMT	3'	CAAGGCCCCCACTGGAG 24808	AA A	
			CTCCAGTG GG CTTG		
			GAGGTCAC CC GAAC		
			C_ G		
GAM1427	ITK	3'	ATCTGATGTCTGCACCAGA 18673	CA AA TT	
			TC GTG GGAC GTCAGAT		
			AG CAC TCTG TAGTCTA		
			AC G_ __		
GAM1427	PDE1B	3'	CTGACACCCCACTGGGGT 6243	AA ACT	
			ACTCCAGTG GG TGTCAG		

TGGGGTCAC CC ACAGTC

GAM1427 PLAU 3' CAATCCTCACTGGG 68967 A C  
TCCAGTGA GGA TTG  
||||||| ||| |||  
GGGTCACT CCT AAC

GAM1427 PRKG1 3' CTGAGTCCTTCACTGG 20746 TTG  
CCAGTGAAGGAC TCAG  
||||||| |||  
GGTCACTTCCTG AGTC

GAM1427 TEAD3 3' ATCTGACAAACCCTTGGTGGG 12208 G G AC  
TCCA T AAGG TTGTCAGAT  
||| | ||| |||||  
GGGT G TTCC AACAGTCTA  
\_ G CA

GAM1427 20D7-FC4 3' TTGATCCCTCACCGGA 60911 A A CTTG  
TCC GTGA GGA TCAG  
||| ||| ||| |||  
AGG CACT CCT AGTT  
C C \_

GAM1427 C20orf142 3' CTGACTGGCTTCACTGAAG 74773 C GA T  
CT CAGTGAAG CT GTCAG  
|| ||||| || |||||  
GA GTCACTTC GG CAGTC  
A \_ T

GAM1427 CNNM4 5' ATCTGATCTCCTTCACCGAG 39474 CA CTT  
CTC GTGAAGGA GTCAGAT  
||| ||||| |||||  
GAG CACTTCCT TAGTCTA  
C\_ C\_

GAM1427 FLJ13305 5' GGTAATCCCATCACTGGAG 90132 A\_ C GT  
CTCCAGTGA GGA TT C  
||||||| ||| |||  
GAGGTCACT CCT AA G  
AC A TG

GAM1427 FLJ20400 3' ATCCAATCCCTCTTCACTGG 66510 ACTT CA  
CCAGTGAAGG GT GAT  
||||||| || |||  
GGTCACTTCT CA CTA  
CCCT AC

GAM1427 FLJ20533 5' ATCTGACAAATCAGAAGATGGA 35356 GTGAAG C  
TCCA GA TTGTCAGAT  
||| || |||||  
AGGT CT AACAGTCTA  
AGAAGA A

GAM1427 FLJ23045 3' ATCTGGTTTCCTCTTTCAC 45230 CTTG\_  
GTGAAGGA TCAGAT  
||||||| |||||

CACTTTCT GGTCTA  
 CCTTT  
 GAM1427 HCNGP 3' TTTGGCGATTCTCCACTGGAG 25155 A C  
 CTCCAGTG AGGA TTGTCAGA  
 ||||| ||| |||||  
 GAGGTCAC TCTT AGCGGTTT  
 C \_  
 GAM1427 KCNH8 3' TAAGCACCTTCACTAAAGT 58258 CC A\_  
 ACT AGTGAAGG CTTG  
 || ||||| |||  
 TGA TCACTTCC GAAT  
 AA AC  
 GAM1427 KIAA0182 3' TCTGGTTCCTCACTG 72036 A CTTG  
 CAGTGA GGA TCAGA  
 ||||| ||| |||||  
 GTCACT CCT GGTCT  
 \_ T\_\_  
 GAM1427 KIAA0939 3' CTGACAGGCCTCTGGAG 62012 TGA A  
 CTCCAG AGG CTTGTCAG  
 ||||| ||| |||||  
 GAGGTC TCC GGACAGTC  
 \_ \_  
 GAM1427 KIAA1879 5' CTGACAAGCAGGAGCTGGA 73568 GAAGGA  
 TCCAGT CTTGTCAG  
 ||||| |||||  
 AGGTCG GAACAGTC  
 AGGAC\_  
 GAM1427 NT5C1B 5' CTGACAAAACAGGAGT 71228 A GAAGGAC  
 ACTCC GT TTGTCAG  
 ||||| || |||||  
 TGAGG CA AACAGTC  
 A A\_\_\_\_\_  
 GAM1427 PJA1 5' CTGACAGTCACTGGA 42322 AGGAC  
 TCCAGTGA TTGTCAG  
 ||||| |||||  
 AGGTCACT GACAGTC  
 \_  
 GAM1427 LOC144932 3' GGTCCCTTCACTGAGT 76977 C  
 ACTC AGTGAAGGACT  
 ||| |||||  
 TGAG TCACTTCCTGG  
 \_  
 GAM1427 LOC148223 3' CTGAGGGCCCCACTGGGGT 78739 AA A G  
 ACTCCAGTG GG CTT TCAG  
 ||||| || ||| |||  
 TGGGGTCAC CC GGG AGTC  
 C\_ \_ \_  
 GAM1427 LOC150503 5' ATCTACATTACCTTAAGTGGAG 79908 G ACT C  
 T  
 ACTCCAGT AAGG TGT AGAT  
 ||||| ||| ||| |||

			TGAGGTCA TTCC ACA TCTA		
			A ATT _		
GAM1427	LOC150504	5'	ATCTACATTACCTTAACTGGAG 59348	G	ACT C
		T	ACTCCAGT AAGG TGT AGAT		
			TGAGGTCA TTCC ACA TCTA		
			A ATT _		
GAM1427	LOC150605	5'	ACAGCCCCTCACTGGG 85081	A	AC
			TCCAGTGA GG TTGT		
			GGGTCACT CC GACA		
			_ CC		
GAM1427	LOC150759	3'	GCAGTCCTTCACTACAGT 80005	CC	T
			ACT AGTGAAGGACT GT		
			TGA TCACTTCCTGA CG		
			CA _		
GAM1427	LOC157867	5'	TCTAACAAGTCTCTGAG 86559	C	TGAA C
			CTC AG GGACTTGT AGA		
			GAG TC TCTGAACA TCT		
			_ _ _ _ A		
GAM1427	LOC164862	5'	AGTTCCTCACTGGAGT 87181	A	
			ACTCCAGTGA GGACT		
			TGAGGTCACT CTTGA		
			C		
GAM1427	LOC203080	3'	CTGTTACATCGTTCACTGGA 89265	G	CT T
			TCCAGTGAA GA TG CAG		
			AGGTCACTT CT AT GTC		
			G AC T		
GAM1428	ALDH8A1	3'	CTTGGAATCTCCAGAT 42608	AAATCTG	
			ATCTGGG TCTCAAG		
			TAGACCT AGGGTTC		
			CTA _ _ _		
GAM1428	APOL1	3'	TGAGAACCCAACTTCCCAGAG 13354	A	ATCTG _ _
		A	TC TCTGGGAA TCTCA		
			AG AGACCCTT AGAGT		
			_ CAAACCCA		
GAM1428	ATM	5'	TTGAGACAGAATTCCCA 56297	A	
			TGGGAA TCTGTCTCAA		
			ACCCTT AGACAGAGTT		
			A		
GAM1428	ATM	5'	TTGAGACAGAATTCCCA 56309	A	
			TGGGAA TCTGTCTCAA		

			ACCCTT AGACAGAGTT		
			A		
GAM1428	CLNS1A	3'	TCTTGAGACAGACTATACTGAG 7098	G	AAA__
	A		TCT GG TCTGTCTCAAGA		
			AGA TC AGACAGAGTTCT		
			G ATATC		
GAM1428	HOXC13	3'	CTTAGGCAAGATTTCCCAG 59683	_	C
			CTGGGAAATCT GTCT AAG		
			GACCCTTTAGA CGGA TTC		
			A _		
GAM1428	STK38	3'	AGACAGATCTTGCCGTGG 23441	CT G	_
			TCAT GG AA ATCTGTCT		
			GGTG CC TT TAGACAGA		
			_ G C		
GAM1428	ZNF256	5'	CTTGAGACAGATTTTGCA 19318	G	
			TG GAAATCTGTCTCAAG		
			AC TTTTAGACAGAGTTC		
			G		
GAM1428	acmsd	5'	TGAGACAAGGATTCAGATG 56356	AAA	_
			CATCTGGG TCT GTCTCA		
			GTAGACTT GGA CAGAGT		
			A__ A		
GAM1428	APOL2	3'	TGAGAACCCAACTTCCCAGAG 48056	A	ATCTG__
	A		TC TCTGGGAA TCTCA		
			AG AGACCCTT AGAGT		
			_ CAAACCCA		
GAM1428	ATP6V1G3	3'	TCTCAGAATAATCTCTCAGATG 55820	A	CTG CA
	A		TCATCTGGGA AT TCT AGA		
			AGTAGACTCT TA AGA TCT		
			C ATA C_		
GAM1428	DKFZp434A171	3'	TAGATTCCCCAGATGA 50011	A	
			TCATCTGGG AATCTG		
			AGTAGACCC TTAGAT		
			C		
GAM1428	DKFZP762D096	3'	TCTTGAGGTTTACTTCTCAAAT 65581	C	ATCTG
	GA		TCAT TGGGAA TCTCAAGA		
			AGTA ACTCTT GGAGTTCT		
			A CATT		
GAM1428	FLJ10665	3'	GGACCACATTTCCCAAAGGA 36393	ATC	CT_
			TC TGGGAAAT GTCT		

AG ACCCTTTA CAGG  
 GAA CAC  
 GAM1428 FLJ13117 3' CTTGATCTTTCCCAGTGA 43540 T TCTGTC  
 TCA CTGGGAAA TCAAG  
 ||| ||||| ||||  
 AGT GACCCTTT AGTTC  
 \_ CT\_\_\_\_  
 GAM1428 FLJ20716 3' CTAAGGACAATTTCCCAGCTGA 35603 T C CA  
 TCA CTGGGAAAT TGTCT AG  
 ||| ||||| |||| ||  
 AGT GACCCTTTA ACAGG TC  
 C \_ AA  
 GAM1428 GBA2 5' AGACAGATTTATGGTTG 71021 T GG  
 CA CTG AAATCTGTCT  
 || ||| |||||  
 GT GGT TTAGACAGA  
 T A\_  
 GAM1428 KIAA0215 3' TGAGGCAGTTTCCCA 28422 T  
 TGGGAAA CTGTCTCA  
 ||||| |||||  
 ACCCTTT GACGGAGT  
 \_  
 GAM1428 KIAA0318 3' CTCGAGACAGAGAAACGGA 68954 GGAAA A  
 TCTG TCTGTCTC AG  
 ||| ||||| ||  
 AGGC AGACAGAG TC  
 AAAG\_ C  
 GAM1428 KIAA1128 3' CAAATTCCTCCAGACTGA 68473 \_ A C  
 TCA TCTGGG AAT TG  
 ||| ||||| ||| ||  
 AGT AGACCC TTA AC  
 C C A  
 GAM1428 LNX 3' CTTGACCTTTTCTCAGAT 50919 TCTGTC  
 ATCTGGGAAA TCAAG  
 ||||| ||||  
 TAGACTCTTT AGTTC  
 TCC\_\_\_\_  
 GAM1428 NAV3 3' CTTAAAACAGATTTCTATGA 29771 CTG CTC  
 TCAT GGAAATCTGT AAG  
 ||| ||||| |||  
 AGTA TCTTTAGACA TTC  
 \_ AAA  
 GAM1428 PALM 3' CTTGATTTTCCCAGAGA 10412 A TCTGTC  
 TC TCTGGGAAA TCAAG  
 || ||||| ||||  
 AG AGACCCTTT AGTTC  
 \_ T\_\_\_\_  
 GAM1428 ROBO4 3' TGAGACTTCCCAGACGG 38792 A ATCT  
 TC TCTGGGAA GTCTCA  
 || ||||| ||||

		GG AGACCCTT CAGAGT		
		C _ _ _		
GAM1428	STAF65(gamma) 3'	TGAACAATTCCCCAGATGA	29448	A C C
		TCATCTGGG AAT TGT TCA		
		AGTAGACCC TTA ACA AGT		
		C _ _		
GAM1428	TCL6 5'	TCTTGAGACACTCCAGATGA	40149	AAATC
		TCATCTGGG TGTCTCAAGA		
		AGTAGACCT ACAGAGTTCT		
		C _ _		
GAM1428	TCL6 5'	TCTTGAGACACTCCAGATGA	40164	AAATC
		TCATCTGGG TGTCTCAAGA		
		AGTAGACCT ACAGAGTTCT		
		C _ _		
GAM1428	TTY2 5'	CTCGAATTTGATTCCCAGAGGA	87003	A A TGTC A
		TC TCTGGGAA TC TC AG		
		AG AGACCCTT AG AG TC		
		G _ TTTA C		
GAM1428	LOC135818 3'	CTTGAGACAACTGAGGGA	75236	A G AAATC
		TC TCT GG TGTCTCAAG		
		AG GGA TC ACAGAGTTC		
		_ G AA _ _		
GAM1428	LOC145497 5'	TGGGATGCCCCCAGATGA	77218	AAATCT
		TCATCTGGG GTCTCA		
		AGTAGACCC TAGGGT		
		CCG _ _		
GAM1428	LOC150482 3'	TAGATTCCCCAGATGA	63075	A
		TCATCTGGG AATCTG		
		AGTAGACCC TTAGAT		
		C		
GAM1428	LOC151568 5'	TCTTTGGAAATCTCCCAGGTGA	56704	AATCTG C
		TCATCTGGGA TCT AAGA		
		AGTGGACCCT AGG TTCT		
		CTAA _ T		
GAM1428	LOC158327 3'	GACTTTCCCAGAAGA	81881	A TCT
		TC TCTGGGAAA GTC		
		AG AGACCCTTT CAG		
		A _ _		
GAM1428	LOC159148 5'	CTCGAATTTGATTCCCAGAGGA	87012	A A TGTC A
		TC TCTGGGAA TC TC AG		

AG AGACCCTT AG AG TC  
 G \_ TTTA C  
 GAM1428 LOC169426 5' AGGCAGAGATTTCCCAGAT 87285 \_  
 ATCTGGGAAA TCTGTCT  
 ||||| |||||  
 TAGACCCTTT AGACGGA  
 AG  
 GAM1428 LOC200014 5' TGAGACAGACCCTCCAG 88544 AAA  
 CTGGG TCTGTCTCA  
 |||| |||||  
 GACCT AGACAGAGT  
 CCC  
 GAM1428 LOC202986 5' TCCTGAGAACATCCCGGATGA 90445 AATC \_ A  
 TCATCTGGGA TGT CTCA GA  
 ||||| || |||||  
 AGTAGGCCCT ACA GAGT CT  
 \_ A C  
 GAM1428 LOC220115 5' TCTTAAGGATATTTCCAGATGG 91745 ATC C\_  
 TCATCTGGGAA TGTCT AAGA  
 ||||| |||||  
 GGTAGACCCTT ATAGG TTCT  
 \_ AA  
 GAM1428 LOC221756 5' CTCTGGACTCCTCAGATGA 92139 \_ AATCT CA  
 TCATCTG GGA GTCT AG  
 ||||| || |||||  
 AGTAGAC CCT CAGG TC  
 T \_ TC  
 GAM1428 LOC254228 3' TTTGGGACCTCCCAAGTGA 95962 TC AATCT  
 TCA TGGGA GTCTCAAG  
 || ||||| |||||  
 AGT ACCCT CAGGGTTT  
 GA C\_  
 GAM1428 LOC51145 3' TCTTAAGCTGATTTCCCA 32399 T T C  
 TGGGAAATC G CT AAGA  
 ||||| || |||||  
 ACCCTTTAG C GA TTCT  
 T \_ A  
 GAM1428 LOC90322 3' CTTGAGGCCTGCCAAATGA 62266 C GAAATCT  
 TCAT TGG GTCTCAAG  
 |||| || |||||  
 AGTA ACC CGGAGTTC  
 A GTC\_  
 GAM1428 LOC90632 5' GAGACCCCCAGATGG 63647 AAATCT  
 TCATCTGGG GTCTC  
 ||||| |||||  
 GGTAGACCC CAGAG  
 C\_  
 GAM1429 SOST 3' CAAACTCACAGACCAGCA 47468 AA T  
 TGC GTCTGTGA TTG  
 || ||||| |||||



ACG CAGACACT AAAC  
 AC C  
 GAM1429 FLJ21596 3' AGAACCACAGACTTGCA 45697 A  
 TGCAAGTCTGTG TTTT  
 |||||  
 ACGTTCAGACAC AAGA  
 C  
 GAM1429 SEPT3 3' CATAAAATCACAAAAC 38888 C\_  
 AGT TGTGATTTTGTG  
 ||| |||||  
 TCA AACTAAAATAC  
 AA  
 GAM1429 LOC147958 5' AATTCAGAAACACAGACCTGCA 87175 A A T  
 TGCA GTCTGTG TTTTG GTT  
 ||| ||||| ||| |||  
 ACGT CAGACAC AAGAC TAA  
 C A T  
 GAM1429 LOC158377 3' CAGGAAATCACAGAACTGCA 86792 AG G  
 TGCA TCTGTGATTTT TG  
 ||| ||||| ||  
 ACGT AGACACTAAAG AC  
 CA G  
 GAM1429 LOC201824 3' CAAACACAACAATGACTCAC 89070 CT G \_  
 GT GT ATT TTGTGTTTG  
 || || || |||||  
 CA CA TAA AACACAAAC  
 CT G C  
 GAM1429 LOC253573 3' AAAGTACCACAGACTTCCA 97044 C \_  
 TG AAGTCTGTG ATTTT  
 || ||||| ||||  
 AC TTCAGACAC TGAAA  
 C CA  
 GAM1429 LOC91263 5' AAATAATACAGACTTGCA 65375 ATT T  
 TGCAAGTCTGTG TTG GTTT  
 ||||| ||| |||  
 ACGTTCAGACAT AAT CAAA  
 \_ \_  
 GAM1430 ABCB1 5' CCAGAACATTCTCCTGGAA 6247 CTGT CT  
 TTCC GG ATGTTCTGG  
 ||| || |||||  
 AAGG CC TACAAGACC  
 TCCT T\_  
 GAM1430 AGT 3' CCAGAACACAGTGCCTGGCA 3454 \_ TA\_  
 TGT GGC TGTCTGG  
 ||| || |||||  
 ACG CCG ACAAGACC  
 GT TGAC  
 GAM1430 ALDOB 3' CCAGAATACCCACCCAAGAA 68087 CCT\_ CTA  
 TTC GTGG TGTCTGG  
 ||| ||| |||||

			AAG CACC ATAAGACC		
			AACC C__		
GAM1430	ARL4	3'	CCAGAACACAGTTGTGGGAA 19198	T TG A	
			TTCCC G GCT TGTTCCTGG		
			I		
			AAGGG T TGA ACAAGACC		
			_GT C		
GAM1430	B3GAT1	3'	CCAGAACAAAGGACAGAGAA 53972	C GG A	
			TTC CTGT CT TGTTCCTGG		
			AAG GACA GA ACAAGACC		
			A G_ A		
GAM1430	B3GAT1	3'	CCAGAACAAAGGACAGAGAA 37827	C GG A	
			TTC CTGT CT TGTTCCTGG		
			AAG GACA GA ACAAGACC		
			A G_ A		
GAM1430	CD79B	3'	CCAGAAGAGCCACAGG 5271	ATG	
			CCTGTGGCT TTCTGG		
			GGACACCGA AAGACC		
			G__		
GAM1430	CD79B	3'	CCAGAAGAGCCACAGG 41207	ATG	
			CCTGTGGCT TTCTGG		
			GGACACCGA AAGACC		
			G__		
GAM1430	CDH3	3'	CCAAACGTCAGGCCACAG 8380	__ C	
			CTGTGGCT ATGTT TGG		
			GACACCGG TGCAA ACC		
			AC _		
GAM1430	COL5A1	5'	GCCAGAACAGCCGCCACAA 3634	CC TA__	
	AGAA		C TGTGGC TGTTCCTGG C		
			G ACACCG ACAAGACC G		
			AA CCGCCG		
GAM1430	CRIM1	3'	CCAGAACAAAGGCAG 33173	GG A	
			CTGT CT TGTTCCTGG		
			GACG GA ACAAGACC		
			_ A		
GAM1430	DIAPH2	3'	CCAAAACAAGTCTAGCAGGGAA 22063	_ A C	
			TTCCCTGT GGCT TGT TGG		
			AAGGGACG CTGA ACAA ACC		
			AT _ A		
GAM1430	DMD	3'	AGAAAATATAGTCACAGG 14414	_	
			CCTGTGGCTATGT TCT		

			GGACACTGATATA AGA		
			AA		
GAM1430 ED1	3'	TTGGAACAATCACAGGGAA	7376	CTA	TG
		TTCCCTGTGG TGTTC G			
		AAGGGACACT ACAAG T			
		A__ GT			
GAM1430 EXTL3	3'	CCAAAACATGCCCGCAGGGAG	7528	T	C
		TTCCCTGTGGC ATGTT TGG			
		GAGGGACGCCG TACAA ACC			
		- A			
GAM1430 FCRH3	3'	CCAGAGTGGCCCACAGG	53630	-	GT
		CCTGTGG CTAT TCTGG			
		GGACACC GGTG AGACC			
		C -			
GAM1430 FECH	3'	CGTGGTGCCACAGGGAA	3753	-	
		TTCCCTGTGGC TATG			
		AAGGGACACCG GTGC			
		TG			
GAM1430 FGFR1	3'	CCAGAACATACAAGGA	41619	C	GGCT
		TCC TGT ATGTTCTGG			
		AGG ACA TACAAGACC			
		A -			
GAM1430 GATA4	3'	CCAGAACAACAACCTGGGAA	9004	T	GGCTA
		TTCCC GT TGTTCTGG			
		AAGGG CA ACAAGACC			
		T ACA-			
GAM1430 GNRH1	5'	CCATCACCAGCCACAGAGA	5883	C	AT TC
		TC CTGTGGCT GT TGG			
		AG GACACCGA CA ACC			
		A C_ CT			
GAM1430 HAMP	3'	CCAGAACATAGGTCTTGGAA	40991	CTGT	-
		TTCC GGC TATGTTCTGG			
		AAGG CTG ATACAAGACC			
		TT_ G			
GAM1430 IPP	3'	TAGTTTGAGCCACAGAGAA	19729	C	ATGTT
		TTC CTGTGGCT CTG			
		AAG GACACCGA GAT			
		A GTTT_			
GAM1430 ITGB1	3'	CCAGTGTGGCCCAGGGAA	53369	T	GTT
		TTCCCTG GGCTAT CTGG			

			AAGGGAC CCGGTG GACC		
			— T—		
GAM1430 KCNQ1	3'	CCAGCTGCTGAGCCGCAGAGAA 4021	C	AT T—	
		TTC CTGTGGCT GT CTGG			
		AAG GACGCCGA CG GACC			
		A GT TC			
GAM1430 KDR	3'	CAGAATACCACAAAGAA 9591	CC	CTA	
		TTC TGTGG TGTTCCTG			
		AAG ACACC ATAAGAC			
		AA —			
GAM1430 LEP	3'	CCAGGGGCCCCACAGGGAA 4047	—	ATGT	
		TTCCCTGTGG CT TCTGG			
		AAGGGACACC GG GGACC			
		C —			
GAM1430 MKI67	3'	CCAGTGACCAGCCACAGGAGA 10041	—	AT —	
		TC CCTGTGGCT GTT CTGG			
		AG GGACACCGA CAG GACC			
		A C— T			
GAM1430 NEFH	3'	CCGGAACAGCCAAAG 40780	G	AT	
		CT TGGCT GTTCTGG			
		GA ACCGA CAAGGCC			
		A —			
GAM1430 NXF2	5'	CCAGAACATCACCAAG 35136	G	CT	
		CT TGG ATGTTCTGG			
		GA ACC TACAAGACC			
		— AC			
GAM1430 PDE6D	3'	CCAGCATACACACAGGGAA 10489	GC	TT	
		TTCCCTGTG TATG CTGG			
		AAGGGACAC ATAC GACC			
		AC —			
GAM1430 PHEMX	5'	CCAGCTGGAACACAGGGAG 57364		CTATGTT	
		TTCCCTGTGG CTGG			
		GAGGGACACC GACC			
		AAAGGTC			
GAM1430 PHEMX	5'	CCAGCTGGAACACAGGGAG 57359		CTATGTT	
		TTCCCTGTGG CTGG			
		GAGGGACACC GACC			
		AAAGGTC			
GAM1430 PODXL	3'	CCAGAATGACACAAAGGA 18230	C—	GCTAT	
		TCC TGTG GTTCTGG			

AGG ACAC TAAGACC  
 AA AG\_\_\_\_  
 GAM1430 PRODH 3' CTGGGACAGCCACTGGAA 32925 CT AT TG  
 TTCC GTGGCT GTTC G  
 |||| ||||| ||| |  
 AAGG CACCGA CAGG C  
 T\_ \_ GT  
 GAM1430 RANBP2L1 3' CCAGAATAAAACCACCAGGAA 17313 CT CTA  
 TTCC GTGG TGTTCCTGG  
 |||| ||| |||||  
 AAGG CACC ATAAGACC  
 AC AAA  
 GAM1430 REGL 3' CCAGAACATGAATTCAGG 21486 TGGC  
 CCTG TATGTTCTGG  
 |||| |||||  
 GGAC GTACAAGACC  
 TTAA  
 GAM1430 SLC19A1 5' CCAGAAATGCATCCAGAGGGAA 11755 G CTA  
 TTCCCT TGG TGTTCCTGG  
 ||||| ||| |||||  
 AAGGGA ACC GTAAGACC  
 G TAC  
 GAM1430 ST14 3' CCAGAACATACACTGTGAA 41765 CCT GC  
 TTC GTG TATGTTCTGG  
 ||| ||| |||||  
 AAG CAC ATACAAGACC  
 TGT \_  
 GAM1430 TBL2 3' CCAGAACAACTAGAGAA 24926 C T CTA  
 TTC CTG GG TGTTCCTGG  
 ||| ||| ||| |||||  
 AAG GAT CC ACAAGACC  
 A \_ A\_  
 GAM1430 TBL2 3' CCAGAACAACTAGAGAA 52182 C T CTA  
 TTC CTG GG TGTTCCTGG  
 ||| ||| ||| |||||  
 AAG GAT CC ACAAGACC  
 A \_ A\_  
 GAM1430 TCFL4 3' CCAGGATAAGACCACAGGGAA 63461 \_ A  
 TTCCCTGTGG CT TGTTCCTGG  
 ||||| ||| |||||  
 AAGGGACACC GA ATAGGACC  
 A \_  
 GAM1430 TFAP4 3' CCGGGGCAGCCACAGGGAG 12237 AT  
 TTCCCTGTGGCT GTTCTGG  
 ||||| |||||  
 GAGGGACACCGA CGGGGCC  
 \_  
 GAM1430 UBE2L6 3' CCAGGGGGAGCCACGG 14873 ATG  
 CTGTGGCT TTCTGG  
 ||||| |||||

GGCACCGA GGGACC  
GG\_

GAM1430 UBQLN3 3' CAAAACATAGTGGAG 33926 CTGTG C  
TTCC GCTATGTT TG  
|||| ||||| ||  
GAGG TGATACAA AC  
\_\_\_\_\_ A

GAM1430 UMOD 3' CCAGTGCTCCAGCCACAG 12548 AT\_ T  
CTGTGGCT GT CTGG  
||||| || |||  
GACACCGA CG GACC  
CCT T

GAM1430 WBSCR5 3' CCAGAACAGGGCAGAG 26256 G G A  
CT TG CT TGTTCTGG  
|| || || |||||  
GA AC GG ACAAGACC  
G G \_

GAM1430 WBSCR5 3' CCAGAACAGGGCAGAG 41856 G G A  
CT TG CT TGTTCTGG  
|| || || |||||  
GA AC GG ACAAGACC  
G G \_

GAM1430 WBSCR5 3' CCAGAACAGGGCAGAG 50610 G G A  
CT TG CT TGTTCTGG  
|| || || |||||  
GA AC GG ACAAGACC  
G G \_

GAM1430 ZNF134 3' CAGTTTAAGCCACAGGGAA 12846 A TT  
TTCCCTGTGGCT TG CTG  
||||||| || |||  
AAGGGACACCGA AT GAC  
\_ TT

GAM1430 ZNF36 3' CCTTCGTAGCCACAAGG 93960 C TTCT  
CC TGTGGCTATG GG  
|| ||||| ||  
GG ACACCGATGC CC  
A TT\_

GAM1430 ABCA9 5' CAGAACATGCAGAGA 54410 C GGCT  
TC CTGT ATGTTCTG  
|| ||| |||||  
AG GACG TACAAGAC  
A \_\_\_\_\_

GAM1430 ADAMTSL1 3' CCTCAAATAGCACAGGGAA 57686 G GTTCT  
TTCCCTGTG CTAT GG  
||||||| ||| ||  
AAGGGACAC GATA CC  
\_ AACT\_

GAM1430 BAIAP1 3' CCAGAACGGCAGCAGG 16449 G AT  
CCTGT GCT GTTCTGG  
|||| ||| |||||

GGACG CGG CAAGACC  
A \_  
GAM1430 BCKDK 3' CCAGAACTTGGAGCAGGGAA 59793 GG T  
TTCCCTGT CTA GTTCTGG  
||||||| ||| |||||||  
AAGGGACG GGT CAAGACC  
A\_ T  
GAM1430 C11orf25 3' CCAAATTAGGGCCACAG 48639 AT\_ C  
CTGTGGCT GTT TGG  
||||||| ||| |||  
GACACCGG TAA ACC  
GAT \_  
GAM1430 C20orf112 3' CCAGTGCTGCCACAGGGA 54640 TAT T  
TCCCTGTGGC GT CTGG  
||||||| || |||||  
AGGGACACCG CG GACC  
T\_ T  
GAM1430 C6orf26 3' CCAAACACAGAGCAGG 47509 GG A C  
CCTGT CT TGTT TGG  
||||| || ||||| |||  
GGACG GA ACAA ACC  
A\_ C A  
GAM1430 CGGBP1 5' CTGGCACCACAGGGAA 13362 CTA CT  
TTCCCTGTGG TGTT G  
||||||| |||| |  
AAGGGACACC ACGG C  
\_ T\_  
GAM1430 DKFZP566G1424 5' CCAGTGCTGCCACAGGGA 84779 TAT T  
TCCCTGTGGC GT CTGG  
||||||| || |||||  
AGGGACACCG CG GACC  
T\_ T  
GAM1430 DKFZp586I021 5' CCAGACGTCACCACAGGGA 50088 CT T  
TCCCTGTGG ATGT CTGG  
||||||| |||| |||||  
AGGGACACC TGCA GACC  
AC \_  
GAM1430 DKFZP727M111 5' CCAATCTGGTCACAGGGAA 31407 T TC  
TTCCCTGTGGCTA GT TGG  
||||||| || |||  
AAGGGACACTGGT TA ACC  
C \_  
GAM1430 ELF4 3' CCGTGGATCAGCCACAGGGA 7431 AT \_  
TCCCTGTGGCT GTTC TGG  
||||||| |||| |||  
AGGGACACCGA TAGG GCC  
C\_ T  
GAM1430 ERG-1 3' CCAGGATGCCAAAGG 41842 G TAT  
CCT TGGC GTTCTGG  
||| |||| |||||||

GGA ACCG TAGGACC  
 A \_\_\_\_  
 GAM1430 FLJ00058 5' CCAGAAATGCCAGCAGGGAA 78765 \_ TATG  
 TTCCCTG TGGC TTCTGG  
 ||||| ||| |||||  
 AAGGGAC ACCG AAGACC  
 G TA\_\_  
 GAM1430 FLJ12816 3' CCAGAACAGGACGACAGTGAA 41932 C GGCTA  
 TTC CTGT TGTTCTGG  
 ||| ||| |||||  
 AAG GACA ACAAGACC  
 T GCAGG  
 GAM1430 FLJ13315 3' CCAGAACATAATACA 46568 GC  
 TGTG TATGTTCTGG  
 ||| |||||  
 ACAT ATACAAGACC  
 A\_  
 GAM1430 FLJ20010 3' CCAGAACGATTGGAACAGG 38716 GG \_\_\_\_  
 CCTGT CTA TGTTCTGG  
 |||| | |||||  
 GGACA GGT GCAAGACC  
 A\_ TA  
 GAM1430 FLJ22369 5' ATGGCGCGACAGGGAA 49918 --  
 TTCCCTGT G GCTAT  
 ||||| | |||||  
 AAGGGACA C CGGTA  
 G G  
 GAM1430 FLJ23563 3' CCAGAATGCTACAAAAGAA 67593 CC\_ TAT  
 TTC TGTGGC GTTCTGG  
 ||| ||||| |||||  
 AAG ACATCG TAAGACC  
 AAA \_\_\_\_  
 GAM1430 FLJ32332 3' CACAGCACACAGGGAA 58299 \_ A  
 TTCCCTGTG GCT TG  
 ||||| ||| ||  
 AAGGGACAC CGA AC  
 A C  
 GAM1430 GRIN3A 3' CCAAGTGAAGCAGCCACAGGGA 55968 ATG \_\_\_\_  
 TCCCTGTGGCT TTC TGG  
 ||||| ||| |||  
 AGGGACACCGA AAG ACC  
 CG\_ TGA  
 GAM1430 HSPC166 3' CCAGAACACATGGAGGGAA 26366 G GCTA  
 TTCCCT TG TGTTCTGG  
 |||| || |||||  
 AAGGGA GT ACAAGACC  
 G AC\_\_  
 GAM1430 HSPC251 3' CCAGGCTAGAGCCACAGAGA 33249 C A TT  
 TC CTGTGGCT TG CTGG  
 || ||||| || |||



AG GACACCGA AT GACC  
 A G CG  
 GAM1430 IGF2AS 3' CCAGGGTGCAACAGAGAA 33095 C G TAT TT  
 TTC CTGT GC G CTGG  
 ||| ||| || | |||  
 AAG GACA CG T GACC  
 A A \_\_ GG  
 GAM1430 ILF3 3' CCAAAACACGCTGGGAA 15722 T GCTA C  
 TTCCC GTG TGT TGG  
 ||||| ||| ||| |||  
 AAGGG CGC ACAA ACC  
 T \_\_ A  
 GAM1430 KIAA0040 3' CCAAAGTTTCCAGCAGGGAA 27780 \_ CT GTTC  
 TTCCCTG TGG AT TGG  
 ||||| ||| ||| |||  
 AAGGGAC ACC TG ACC  
 G TT AA\_\_  
 GAM1430 KIAA0254 3' CAGACAGTCACAGGGAA 28596 ATGT  
 TTCCCTGTGGCT TCTG  
 ||||| ||| ||| |||  
 AAGGGACACTGA AGAC  
 C\_\_  
 GAM1430 KIAA0336 3' CCAGAATAAAACCACCAGGAA 27589 CT CTA  
 TTCC GTGG TGT TCTGG  
 ||| ||| ||||| |||  
 AAGG CACC ATAAGACC  
 AC AAA  
 GAM1430 KIAA0494 3' CCAGAACACATTTGGG 28740 T\_ GCTA  
 CCC GTG TGT TCTGG  
 ||| ||| ||||| |||  
 GGG TAC ACAAGACC  
 TT \_\_  
 GAM1430 KIAA0537 3' CCAGAACAGCCTACAGGGGA 29244 \_ AT  
 TTCCCTGT GGCT GTTCTGG  
 ||||| ||| ||||| |||  
 AGGGGACA CCGA CAAGACC  
 T \_\_  
 GAM1430 KIAA0774 5' CGGGATGCCACAAGGAA 91752 C TAT TG  
 TTCC TGTGGC GTTC G  
 ||| ||||| ||| |  
 AAGG ACACCG TAGG C  
 A \_\_ GT  
 GAM1430 KIAA0828 3' CCATGAAAGCCACAGAGGA 81194 \_ ATG \_  
 TCC CTGTGGCT TTC TGG  
 ||| ||||| ||| |||  
 AGG GACACCGA AAG ACC  
 A \_\_ T  
 GAM1430 KIAA1118 3' CCAGAGGCCACAGGGA 69606 \_ ATGT  
 TCCCTGTGG CT TCTGG  
 ||||| ||| ||| |||

			AGGGACACC GG AGACC		
			C ____		
GAM1430	KIAA1742	3'	CAGATCCACAGGGAG 77657		CTATGT
			TTCCCTGTGG TCTG		
			GAGGGACACC AGAC		
			T ____		
GAM1430	KIAA1944	5'	CCAACCTAGCCACAGGGA 75558		T TC
			TCCCTGTGGCTA GT TGG		
			AGGGACACCGAT CA ACC		
			C ____		
GAM1430	KIAA1981	3'	CGGAACAGCACAAGGAA 88342	C G AT TG	
			TTCC TGTG CT GTTC G		
			AAGG ACAC GA CAAG C		
			A _ _ GT		
GAM1430	NXPH3	3'	ACGGAGCCACAGAGAG 65747	C A	
			TTC CTGTGGCT TGT		
			GAG GACACCGA GCA		
			A G		
GAM1430	PP5395	3'	TCAGGATAGCACAGGGAA 72110	G AT	
			TTCCCTGTG CT GTTCTGG		
			AAGGGACAC GA TAGGACT		
			— —		
GAM1430	PRDM7	3'	CCAGAAGGGCCACAGAGAA 53788	C ATG	
			TTC CTGTGGCT TTCTGG		
			AAG GACACCGG AAGACC		
			A G__		
GAM1430	PRDM9	3'	CCAGAAGGGCCACAGAGAA 39575	C ATG	
			TTC CTGTGGCT TTCTGG		
			AAG GACACCGG AAGACC		
			A G__		
GAM1430	PXR2b	3'	ATATAGCCCAAGGAA 33337	C T	
			TTCC TG GGCTATGT		
			AAGG AC CCGATATA		
			A _		
GAM1430	RAB33B	3'	CCAGCTTAGCCACAAAGAA 48490	CC TGTT	
			TTC TGTGGCTA CTGG		
			AAG ACACCGAT GACC		
			AA TC__		
GAM1430	SH120	3'	CCAGAACATGAGAGGGAG 32920	GTGGC	
			TTCCCT TATGTTCTGG		

			GAGGGA GTACAAGACC		
			GA__		
GAM1430	SH120	3'	CCAGAACATGAGAGGGAG 94606	GTGGC	
			TTCCCT TATGTTCTGG		
			GAGGGA GTACAAGACC		
			GA__		
GAM1430	SLC2A12	3'	CCAGAACACACAGTGTGGA 59078	__ GCTA	
			TCC CTGTG TGTCTGG		
			AGG GACAC ACAAGACC		
			TGT ____		
GAM1430	SP329	3'	CCAGAGTGCTCCACAGGGA 47924	CTA GT	
			TCCCTGTGG T TCTGG		
			AGGGACACC G AGACC		
			TC_ TG		
GAM1430	SSH2	3'	TCAGTAAGCCCACAGGGAA 62213	_ ATGTT	
			TTCCCTGTGG CT CTGG		
			AAGGGACACC GA GACT		
			C AT__		
GAM1430	SYTL4	5'	CCAGTCAGCCACAGGGAA 54939	ATGTT	
			TTCCCTGTGGCT CTGG		
			AAGGGACACCGA GACC		
			CT__		
GAM1430	TNRC4	3'	CCAGTCAGCCACAGAGA 23221	C ATGTT	
			TC CTGTGGCT CTGG		
			AG GACACCGA GACC		
			A CT__		
GAM1430	UBE3B	3'	CCAGACTGTGACACAGGGAA 76919	G _ GT	
			TTCCCTGTG CT AT TCTGG		
			AAGGGACAC GA TG AGACC		
			_ C TC		
GAM1430	VPS4A	3'	CCTTGCAGCCACAGAGA 25102	C AT TCT	
			TC CTGTGGCT GT GG		
			AG GACACCGA CG CC		
			A _ TT_		
GAM1430	XYLT1	5'	CCAACAGCAGCCACGGGAA 77847	T A_ TC	
			TTCCC GTGGCT TGT TGG		
			AAGGG CACCGA ACA ACC		
			_ CG _		
GAM1430	ZFP100	3'	CCAGAAAGCCAAAAAGAA 70050	CCTG ATG	
			TTC TGGCT TTCTGG		

		AAG ACCGA AAGACC		
		AAAA ____		
GAM1430	ZNF213	5' CAGCTACCACAGGGGA	65091	C TGT
		TTCCCTGTGG TA CTG		
		AGGGGACACC AT GAC		
		_ C__		
GAM1430	LOC112609	3' CCAGTGTGGCACAGGGAA	72837	G GTT
		TTCCCTGTG CTAT CTGG		
		AAGGGACAC GGTG GACC		
		_ T__		
GAM1430	LOC115073	5' CCAGGCGTCAAACCACAGGGA	73204	CT__ T
		TCCCTGTGG ATGT CTGG		
		AGGGACACC TGCG GACC		
		AAAC _		
GAM1430	LOC122962	5' CCAGACAGTGGCCACTGAGAA	75587	CCT GT
		TTC GTGGCTAT TCTGG		
		AAG CACCGGTG AGACC		
		AGT AC		
GAM1430	LOC124044	3' CCAGAACACTCAGAGGGA	76025	G CTA
		TCCCT TGG TGTTCTGG		
		AGGGA ACT ACAAGACC		
		G C__		
GAM1430	LOC143308	5' CCAAATTTGGCCACAG	82936	T C
		CTGTGGCTA GTT TGG		
		GACACCGGT TAA ACC		
		T _		
GAM1430	LOC145314	3' CCAGAACACATCACCTGAG	77086	CCT CTA
		TTC GTGG TGTTCTGG		
		GAG CACT ACAAGACC		
		TC_ AC_		
GAM1430	LOC146420	3' CCAGAACCAGTTACAG	83667	AT
		CTGTGGCT GTTCTGG		
		GACATTGA CAAGACC		
		C_		
GAM1430	LOC146445	3' CCAGAGCCACCACAGGGA	83678	CTAT
		TCCCTGTGG GTTCTGG		
		AGGGACACC CGAGACC		
		AC__		
GAM1430	LOC147178	3' CCAGCCAGCCACGGAGAA	61323	C ATGTT
		TTC CTGTGGCT CTGG		

AAG GGCACCGA GACC  
 A CC\_\_\_\_  
 GAM1430 LOC148529 5' CACAGCCACAGGAGAA 84166 \_ A  
 TTC CCTGTGGCT TG  
 ||| ||||| ||  
 AAG GGACACCGA AC  
 A C  
 GAM1430 LOC148930 5' CCAGGGGCAGACCACGGGGAA 79093 CTA \_  
 TTCCCTGTGG TGTTC TGG  
 ||||| |||||  
 AAGGGGCACC ACGGG ACC  
 AG\_ G  
 GAM1430 LOC149950 5' CCAGAACATGATCTCAGG 79551 T GC  
 CCTG G TATGTTCTGG  
 ||| | |||||  
 GGAC C GTACAAGACC  
 T TA  
 GAM1430 LOC150378 5' CCAGAAACAAGCCACGGGAA 79742 T ATG  
 TTCCC GTGGCT TTCTGG  
 |||| |||| ||||  
 AAGGG CACCGA AAGACC  
 \_ ACA  
 GAM1430 LOC150951 5' CCAGGGCCACACAGGGAA 85167 GCTAT  
 TTCCCTGTG GTTCTGG  
 ||||| |||||  
 AAGGGACAC CGGGACC  
 AC\_\_\_\_  
 GAM1430 LOC151429 3' CCAGGAGACCACAGGGA 85347 \_ ATGT  
 TCCCTGTGG CT TCTGG  
 ||||| || ||||  
 AGGGACACC GA GGACC  
 A \_\_\_\_  
 GAM1430 LOC158434 3' CCAGAATAAACCACCTGGGAA 86819 T CTA  
 TTCCC GTGG TGTTCCTGG  
 |||| ||| |||||  
 AAGGG CACC ATAAGACC  
 T AA\_  
 GAM1430 LOC170106 5' CCAAGGCAGTCAGCCACAGG 82571 A\_\_ TC  
 CCTGTGGCT TGT TGG  
 ||||| ||| |||  
 GGACACCGA ACG ACC  
 CTG GA  
 GAM1430 LOC196446 3' CGGAAAGCCACAGAGAA 87708 C ATG TG  
 TTC CTGTGGCT TTC G  
 ||| ||||| ||| |  
 AAG GACACCGA AAG C  
 A \_ GT  
 GAM1430 LOC197136 3' CCAGAACACTCAGAGGGA 89728 G CTA  
 TCCCT TGG TGTTCCTGG  
 |||| ||| |||||

	AGGGA ACT ACAAGACC		
	G C_		
GAM1430 LOC197342 3'	CCAGGAGAAGCCACAGGGGA 87993	ATG	
	TTCCCTGTGGCT TTCTGG		
	AGGGGACACCGA AGGACC		
	AG_		
GAM1430 LOC200734 3'	CCATCCGCAGCCACAGGGGA 88860	A TTC	
	TTCCCTGTGGCT TG TGG		
	AGGGGACACCGA GC ACC		
	C CT_		
GAM1430 LOC201102 3'	CCTGACCAGCCACAGGAGA 88090	_ AT CT	
	TC CCTGTGGCT GTT GG		
	AG GGACACCGA CAG CC		
	A C_ T_		
GAM1430 LOC201283 3'	CCAGAACACAGTCGTGAGGA 60413	CT A	
	TCC GTGGCT TGTCTGG		
	AGG TGCTGA ACAAGACC		
	AG C		
GAM1430 LOC202915 3'	CCACACGCCAGCCACAGGGGA 90388	A_ TC	
	TTCCCTGTGGCT TGT TGG		
	AGGGGACACCGA GCA ACC		
	CC C_		
GAM1430 LOC204965 5'	CAGAGTGCACAGAGAA 90647	C G TATG	
	TTC CTGTG C TTCTG		
	AAG GACAC G GAGAC		
	A _ T_		
GAM1430 LOC205418 3'	CACAGCCAGCAGGGAA 90681	_ A	
	TTCCCTG TGGCT TG		
	AAGGGAC ACCGA AC		
	G C		
GAM1430 LOC220692 3'	CCAGAATAAAACCACCAGGAA 91220	CT CTA	
	TTCC GTGG TGTCTGG		
	AAGG CACC ATAAGACC		
	AC AAA		
GAM1430 LOC222631 5'	CCAGAACACAGCTGGAA 92838	CTGT A	
	TTCC GGCT TGTCTGG		
	AAGG TCGA ACAAGACC		
	_ C		
GAM1430 LOC253039 3'	CCAAATACATCTACAGGGAA 96153	CT TC_	
	TTCCCTGTGG ATGT TGG		

		AAGGGACATC TACA ACC	
		___ TAA	
GAM1430	LOC253841 5'	CCAGAATGTAGCCACAG 96342	
		CTGTGGCTATGTTCTGG	
		GACACCGATGTAAGACC	
GAM1430	LOC254028 3'	CCAGAACAGAAGCACCAAGAA 96539	CC TG A_
		TTC TG GCT TGTCTGG	
		AAG AC CGA ACAAGACC	
		A_ CA AG	
GAM1430	LOC257449 3'	CAGATCCACAGGGAG 62718	CTATGT
		TTCCCTGTGG TCTG	
		GAGGGACACC AGAC	
		T_____	
GAM1430	LOC89231 3'	GGACAGCACAGGGAA 92733	G AT
		TTCCCTGTG CT GTTC	
		AAGGGACAC GA CAGG	
GAM1430	LOC90550 3'	CCAGAACACAAATCAGAGGGA 73090	G CTA_
		TCCCT TGG TGTCTGG	
		AGGGA ACT ACAAGACC	
		G AAAC	
GAM1430	LOC91373 3'	CCAGCAAGGCCACAG 65834	A TT
		CTGTGGCT TG CTGG	
		GACACCGG AC GACC	
		A _	
GAM1430	LOC91445 3'	CCAGAACCTGCCACAGG 60547	TAT
		CCTGTGGC GTTCTGG	
		GGACACCG CAAGACC	
		TC_	
GAM1431	ABCC1 3'	TTGACTAGAAATAGAGACTGAG 39129	GC _ A
	AG	CTTTCAGTCTTTATTT AG CAA	
		GAGAGTCAGAGATAAA TC GTT	
		GA A	
GAM1431	ABCC1 3'	TTGACTAGAAATAGAGACTGAG 39137	GC _ A
	AG	CTTTCAGTCTTTATTT AG CAA	
		GAGAGTCAGAGATAAA TC GTT	
		GA A	
GAM1431	ABCC1 3'	TTGACTAGAAATAGAGACTGAG 17184	GC _ A
	AG	CTTTCAGTCTTTATTT AG CAA	

			GAGAGTCAGAGATAAA TC GTT		
			GA A		
GAM1431	ABCD2	3'	TAGATAAAGGCTCAAAG 17700	C	
			CTTT AGTCTTTATTTG		
			GAAA TCGGAAATAGAT		
			C		
GAM1431	ABP1	5'	GCAAAGGCTGGAAG 63110	TATT	
			CTTTCAGTCTT TGC		
			GAAGGTCGGAA ACG		
GAM1431	ACK1	3'	TGCCCTGGGTGACAGACTGGGA 19348	TT	_ TT CA AA
	G		CT CAGTCT TTAT G GCA		
			GA GTCAGA AGTG T CGT		
			GG C GG CC		
GAM1431	ACO1	3'	GCAAGTGAGCACTGAGGG 9352	C	
			CTTTCAGT TTTATTTGC		
			GGGAGTCA GAGTGAACG		
			C		
GAM1431	ACVR1	3'	TTGCAAAGGTAGGGACTGGAGG 6614		GCA
			CTTTCAGTCTTTATTT GCAA		
			GGAGGTCAGGGATGGA CGTT		
			AA_		
GAM1431	ADAMTS5	3'	TTTGTTGTGAAACACTGCAAAG 22897	_	CTTTA TG
			CTTT CAGT TT CAGCAA		
			GAAA GTCA AA GTTGTTT		
			C CA__ GT		
GAM1431	ADCY7	3'	GTAAATGAAGCTGAAAG 6643	T	
			CTTTCAG CTTTATTTGC		
			GAAAGTC GAAGTAAATG		
GAM1431	ADD2	3'	TTGTTCCCAAGGGCTGATGG 33939	T	ATTT
			CT TCAGTCTTT GCAG		
			GG AGTCGGGAA TGTT		
			T CCCT		
GAM1431	ADD2	3'	TTGTTCCCAAGGGCTGATGG 33950	T	ATTT
			CT TCAGTCTTT GCAG		
			GG AGTCGGGAA TGTT		
			T CCCT		
GAM1431	ADD2	3'	TTGTTCCCAAGGGCTGATGG 33956	T	ATTT
			CT TCAGTCTTT GCAG		



			GG AGTCGGGAA TGTT		
			T CCCT		
GAM1431	ADD2	3'	TTGTTCCCAAGGGCTGATGG 33967	T	ATTT
			CT TCAGTCTTT GCAG		
			GG AGTCGGGAA TGTT		
			T CCCT		
GAM1431	AES	3'	CAAATAAAGATGAGGG 6675	G	
			CTTTCA TCCTTATTTG		
			GGGAGT AGAAATAAAC		
			—		
GAM1431	AHCY	3'	TGACAGCTAGGGGTTGAGAG 5478	GT	T _
			CTTTCA CTTTA TTG CA		
			GAGAGT GGGAT GAC GT		
			TG C A		
GAM1431	AIM1	5'	TGAGTAAGACTGAGGG 91831	T	
			CTTTCAGTCTT ATTTG		
			GGGAGTCAGAA TGAGT		
			—		
GAM1431	ALS2	3'	TAAAGGGAGGATTGAAAG 40508	A_	
			CTTTCAGTCTTT TTTG		
			GAAAGTTAGGAG AAAT		
			GG		
GAM1431	APAF1	3'	TTGTTGCCAGGCTGGAG 25050	TTATTT	
			TTTCAGTCT GCAGCAA		
			GAGGTCGGA CGTTGTT		
			C_____		
GAM1431	APAF1	3'	TTGTTGCCAGGCTGGAG 6741	TTATTT	
			TTTCAGTCT GCAGCAA		
			GAGGTCGGA CGTTGTT		
			C_____		
GAM1431	ARNT2	3'	TTTGCTGTGATCCATTGAAAG 29466	CTTTAT TG	
			CTTTCAGT T CAGCAAA		
			GAAAGTTA A GTCGTTT		
			CCT__ GT		
GAM1431	ASNS	3'	GTGTTGGATGGGGACTGTGGG 8032	TT	TG AA
			CT CAGTCTTTATT CAGCA		
			GG GTCAGGGGTAG GTTGT		
			GT _ GC		
GAM1431	ASNS	3'	GTGTTGGATGGGGACTGTGGG 55941	TT	TG AA
			CT CAGTCTTTATT CAGCA		

		GG GTCAGGGGTAG GTTGT	
		GT     _     GC	
GAM1431	B4GALT5	3' CTTTGGGTGGGGATTGAGGG 16501	TT C
		CTTTCAGTCTTTAT G AG	
		GGGAGTTAGGGGTG T TC	
		GG T	
GAM1431	B4GALT5	3' TGGGTGGGGATTGAGGG 16516	TT
		CTTTCAGTCTTTAT G	
		GGGAGTTAGGGGTG T	
		GG	
GAM1431	BAX	3' TTTCTGGGAGGGGTGGGGATTG 57039 TT	_ G CAAA
		GGGG CAGTCTTTAT TT CAG	
		GTTAGGGGTG AG GTC	
		GG GGG G TTT	
GAM1431	BAX	3' TTTCTGGGAGGGGTGGGGATTG 57041 TT	_ G CAAA
		GGGG CAGTCTTTAT TT CAG	
		GTTAGGGGTG AG GTC	
		GG GGG G TTT	
GAM1431	BAX	3' TTTCTGGGAGGGGTGGGGATTG 57043 TT	_ G CAAA
		GGGG CAGTCTTTAT TT CAG	
		GTTAGGGGTG AG GTC	
		GG GGG G TTT	
GAM1431	BAX	3' TTTCTGGGAGGGGTGGGGATTG 57045 TT	_ G CAAA
		GGGG CAGTCTTTAT TT CAG	
		GTTAGGGGTG AG GTC	
		GG GGG G TTT	
GAM1431	BAZ2A	3' TTTGAAGAAGTGGGGGCTGGAG 25615	GCAG
		TTTCAGTCTTTATTT CAAA	
		GAGGTCGGGGGTGAA GTTT	
		GAA_	
GAM1431	BCL2L2	3' AGGCCAGGTAGGCGATTGGAAG 14463	_ CA AAA
		CTTTCAGTC TTTATTTG GC	
		GAAGGTTAG GGATGGAC CG	
		C _ GAT	
GAM1431	BDKRB2	3' TTGTGTAAGGATTGAGGG 5266	TT
		CTTTCAGTCTTTAT GCAG	
		GGGAGTTAGGAATG TGTT	
		_	
GAM1431	BLVRB	5' CAGATGGGGGCAGAGAG 5545 A	
		CTTTC GTCTTTATTTG	

GAGAG CGGGGGTAGAC  
 A  
 GAM1431 BMP6 5' AGATAAGGACTGAGGG 8164  
 CTTTCAGTCTTTATTT  
 |||||  
 GGGAGTCAGGAATAGA

GAM1431 BSN 3' CTGAGCAAGGGCTGAGGG 12919 ATTTG  
 CTTTCAGTCTTT CAG  
 ||||| ||  
 GGGAGTCGGGAA GTC  
 CGA\_\_

GAM1431 C14orf1 3' CAGATGCATGAGGGTTGGAAG 23173 GT TT GCAAA  
 CTTTCA CTTTA TGCA  
 |||| |||| ||  
 GAAGGT GGAGT ACGT  
 TG \_\_ AGACA

GAM1431 C7 3' TTTGTTGCCAGGCTGGAG 5171 TTATTT  
 TTTTCAGTCT GCAGCAAA  
 ||||| |||||  
 GAGGTCGGA CGTTGTTT  
 CC\_\_

GAM1431 CABC1 3' GCAGATGAAGATGAAAG 39655 G  
 CTTTCA TCTTTATTTGC  
 |||| |||||  
 GAAAGT AGAAGTAGACG

GAM1431 CDH18 5' GCAGTGGAGATTGAGAG 17033 T  
 CTTTCAGTCTTTATT GC  
 ||||| ||  
 GAGAGTTAGAGGTGA CG

GAM1431 CDK5R2 3' TTTGCTGGGCGTGGAGTGGGGA 14134 A G\_\_\_\_  
 CGGAAG GTCTTTATTT CAGCAAA  
 ||||| |||||  
 CAGGGGTGAG GTCGTTT  
 GTGCGG

GAM1431 CELSR2 3' TTTGCTGTGATGTGGGTGGGGG 7413 TT G TTTAT TG  
 CT CA TC T CAGCAAA  
 || || | |||||  
 GG GT GG A GTCGTTT  
 GG G TGT\_\_GT

GAM1431 CHST1 3' TGCGGGTGGGGGCGGGAG 13336 TT A  
 CT C GTCTTTATTTGCA  
 || | |||||  
 GA G CGGGGGTGGGCGT  
 GG\_

GAM1431 CLIC3 5' TTTGTCAAGGCGAGTGAGGACG 16243 T A A\_\_\_\_  
 GGGAG C GTCTTTATTTGC GCAAA  
 | ||||| ||||

			G CAGGAGTGAGCG	TGTTT	
			G G	GAAC	
GAM1431	CMRF35	5'	TTTGCCAGACGTCAGGGTTGAG	21931	GT TA__ CA
	AG		CTTTCA CTT	TTTG GCAAA	
			GAGAGT GGA	AGAC CGTTT	
			TG CTGC	__	
GAM1431	CNR1	3'	TGCAGATGAAGGCTCAGGG	32216	C
			CTTT AGTCTTTATTTGCA		
			GGGA TCGGAAGTAGACGT		
			C		
GAM1431	COL4A4	5'	GTGGATTGGGGCTGGAGG	3628	TT TG
			CTTTCAGTCT ATT C		
			GGAGGTCGGG TAG G		
			GT GT		
GAM1431	COX15	3'	TTCCATTAGGTGAAGATTGAAA	54323	CAGCAAA
	G		CTTTCAGTCTTTATTTG		
			GAAAGTTAGAAGTGGAT		
			TACCTT		
GAM1431	CPD	3'	TGAATGAAGCTGAGAG	7131	T
			CTTTCAG CTTTATTTG		
			GAGAGTC GAAGTAAGT		
			—		
GAM1431	CRHR1	3'	TTTGTGAGAAGATGGGGGCTGG	15216	GCA_
	AGG		CTTTCAGTCTTTATTT	GCAAA	
			GGAGGTCGGGGGTAGA	TGTTT	
			AGAG		
GAM1431	CSF3	3'	CCTTGCTGGATGGGGACTGGGG	5664	TT TG A
			T CAGTCTTTATT CAGCAA		
			G GTCAGGGGTAG GTCGTT		
			GG	__ CCG	
GAM1431	CSPG3	3'	TTTGTTTGCGGGGGGCTGGGG	15243	TT ATT _
			T CAGTCTTT	TGCAG CAAA	
			G GTCGGGGG GCGTT GTTT		
			GG	__ T	
GAM1431	CTSL	5'	GCCGGACAGGGACTGGAAG	8588	A CA
			CTTTCAGTCTTT TTTG GC		
			GAAGGTCAGGGA AGGC CG		
			C	__	
GAM1431	CXorf6	3'	GAGCCCAGATGAAGACTGGG	18515	CA AAA
			TTCAGTCTTTATTTG GC		

			GGGTCAGAAGTAGAC CG		
			C_ AGT		
GAM1431	CYLN2	3'	TTGTCAGTGGAGGCAGAGGG 12641	A	T
			CTTTC GTCTTTATT GCAG		
			GGGAG CGGAGGTGA TGTT		
			A C		
GAM1431	DDX20	3'	TTGGGACATAGAGCTGAAAG 23275	T	_ G
			CTTTCAG CTTTAT TT CAG		
			GAAAGTC GAGATA AG GTT		
			_ C G		
GAM1431	DFFB	3'	TTTGTTGCCCAGGCTGGAG 87403	TTATTT	
			TTTCAGTCT GCAGCAAA		
			GAGGTCGGA CGTTGTTT		
			CC_____		
GAM1431	DHCR7	5'	GCAAGAGGCTGGAGG 7234	TAT	
			CTTTCAGTCTT TTGC		
			GGAGGTCGGAG AACG		
			_____		
GAM1431	DHFR	5'	TGCACAAATAGGGACGAGGG 5818	A	CA
			CTTTC GTCTTTATTTG GCA		
			GGGAG CAGGGATAAAC CGT		
			_ A_		
GAM1431	DMPK	5'	TTGTGAGGGGTTAAGGCTGGGA 15328	TT	T GCA A
	G		CT CAGTCTT ATTT GCAA		
			GA GTCGGAA TGGG TGTT		
			GG T GAG		
GAM1431	DPYS	3'	GTTGCTGCATAAGATTGAAGG 7287	TATT	A
			CTTTCAGTCTT TGCAGCAA		
			GGAAGTTAGAA ACGTCGTT		
			T_____ GT		
GAM1431	DUSP3	3'	TCCCTGAGATGGGGGCTCAGAG 14564	C	G CAAA
			CTTT AGTCTTTATTT CAG		
			GAGA TCGGGGGGTAGA GTC		
			C _ CCTT		
GAM1431	ECT2	3'	TTTGCAAATTGAGATAAGGACA 36137	A	G _____
	GAAAG		C GTCTTTATTT CA GCAAA		
			G CAGGAATAGA GT CGTTT		
			A _ TAAA		
GAM1431	EEF1B2	3'	TAAATAAAAGATTGAAAG 40881	_	
			CTTTCAGTCTTT ATTTG		

			GAAAGTTAGAAA TAAAT		
			A		
GAM1431	EEF1B2	3'	TAAATAAAAGATTGAAAG 8731	—	
			CTTTCAGTCTTT ATTTG		
			GAAAGTTAGAAA TAAAT		
			A		
GAM1431	EGFL5	3'	TTGTGTAAGGATTGGAA 86631	TT	
			TTTCAGTCTTTAT GCAG		
			AAGGTTAGGAATG TGTT		
			—		
GAM1431	EGLN2	5'	CAAGTGGAGGCGGAGG 53852	A	
			CTTTC GTCTTTATTTG		
			GGAGG CGGAGGTGAAC		
			—		
GAM1431	EGLN2	3'	TTTGCTGCCCCATCATGGGGGC 53856	TT_____	
			TGGGG CAGTCTTTAT GCAGCAAA		
			GTCGGGGGTA CGTCGTTT		
			CTACCC		
GAM1431	EGLN2	5'	CAAGTGGAGGCGGAGG 54926	A	
			CTTTC GTCTTTATTTG		
			GGAGG CGGAGGTGAAC		
			—		
GAM1431	EGLN2	3'	TTTGCTGCCCCATCATGGGGGC 54933	TT_____	
			TGGGG CAGTCTTTAT GCAGCAAA		
			GTCGGGGGTA CGTCGTTT		
			CTACCC		
GAM1431	EGLN2	3'	TTTGCTGCCCCATCATGGGGGC 34106	TT_____	
			TGGGG CAGTCTTTAT GCAGCAAA		
			GTCGGGGGTA CGTCGTTT		
			CTACCC		
GAM1431	EIF2B2	5'	GCCGGTGAAGGCTGAAGG 26453	TT	
			CTTTCAGTCTTTAT GC		
			GGAAGTCGGAAGTG CG		
			GC		
GAM1431	EPHB3	3'	TTGTCCTGGGGGCTGAGGG 15458	TTT	
			CTTTCAGTCTTTA GCAG		
			GGGAGTCGGGGGT TGTT		
			CC_		
GAM1431	ESPN	3'	GTGAATAGAGGATGAGGG 48921	GT TG	
			CTTTCA CTTTATT C		

		GGGAGT GAGATAA G	
		AG GT	
GAM1431 EYA4	5'	TTTGTGTGGGGTGGCCGAAGG 14615	A TTTA TG
		CTTTC GTC TT CAGCAAA	
		GGAAG CGG GG GTTGTTT	
		C TG__ GT	
GAM1431 F8	3'	GTAAAGGGGGCTGGAGG 3731	A
		CTTTCAGTCTTT TTTGC	
		GGAGGTCGGGGG AAATG	
		—	
GAM1431 FAAH	3'	TTTGCTGCGGAGCTATTTAAAG 44197	C CTTTA
		CTTT AGT TTTGCAGCAAA	
		GAAA TTA AGGCGTCGTTT	
		T TCG__	
GAM1431 FACL5	3'	TTGCTGCTGAGCTGGAAG 64190	T TATTT
		CTTTCAG CTT GCAGCAA	
		GAAGGTC GAG CGTCGTT	
		— T__	
GAM1431 FCGR2A	3'	TAAATGGAGACTGGAA 79264	
		TTTCAGTCTTTATTTG	
		AAGGTCAGAGGTAAAT	
		—	
GAM1431 FEZ1	3'	TTTGTATTTTGAGTAGAGATGG 42584	TT G CA__
		GAG T CA TCTTTATTTG GCAAA	
		A GT AGAGATGAGT TGTTT	
		GG _ TTTA	
GAM1431 FGF1	3'	TTTGTTCTCGAAAGGCTGGAG 52457	ATTTGC
		G CTTTCAGTCTTT AGCAAA	
		GGAGGTCGGAAA TTGTTT	
		GGTCC_	
GAM1431 FGF1	3'	TTTGTTCTCGAAAGGCTGGAG 52460	ATTTGC
		G CTTTCAGTCTTT AGCAAA	
		GGAGGTCGGAAA TTGTTT	
		GGTCC_	
GAM1431 FGF2	3'	TTTGCTGTTTTATAGGTTTGAA 8877	T TATTT
		TTCAG CTT GCAGCAAA	
		AAGTT GGA TGTCGTTT	
		T TATTT	
GAM1431 FKBP1B	3'	GAGTGAAGGCAGGAAG 54009	A
		CTTTC GTCTTTATTT	

GAAGG CGGAAGTGAG

A

GAM1431 FOSB 3' ATTTTGTGAGTGAGACTGAG 22101 T TG CAAA  
GG CTTTCAGTCTT ATT CAG

||||||| ||| |||

GGGAGTCAGAG TGA GTT

\_ GT TTTTAT

GAM1431 FRAT2 3' TTTGCTGTGGGGTTCCTGGGAG 23884 TT TCTTTA TG  
CT CAG TT CAGCAAA

|| ||| || |||||

GA GTC GG GTCGTTT

GG CTTG\_ GT

GAM1431 FRG1 5' TGGGTGAAGACGGAGG 15580 A TT  
CTTTC GTCTTTAT G

||||| ||||| |

GGAGG CAGAAGTG T

\_ GG

GAM1431 FZD4 3' TTTGCTGCAGACTTTGGAA 24160 TCTTTA  
TTTCAG TTTGCAGCAAA

||||| |||||

AAGGTT AGACGTCGTTT

TC\_

GAM1431 G6PC 3' TAAATCACGGATGGCAGATTGG 3832 \_ CAGCAAA  
AGG CTTTCAGTCT TTATTTG

||||||| |||||

GGAGGTTAGA GGTAGGC

C ACTAAATT

GAM1431 GAC1 3' TGGGCAAGGGCTGAAGG 20946 TTAT AG  
CTTTCAGTCT TTGC CA

||||||| ||| ||

GGAAGTCGGG AACG GT

\_ G\_

GAM1431 GARP 3' TTGTGGGGTGAGATTGGGGG 18605 TT TA TG  
CT CAGTCTT TT CAG

|| ||||| || |||

GG GTTAGAG GG GTT

GG TG GT

GAM1431 GBF1 3' GCAGGTGGGGGCTGGG 14833  
TTCAGTCTTTATTTGC

|||||||

GGGTCGGGGGTGGACG

GAM1431 GCK 5' CTGGGGAAGGCTGAGGG 3870 ATT G  
CTTTCAGTCTTT T CAG

||||||| | |||

GGGAGTCGGAAG G GTC

\_ G

GAM1431 GJA1 3' TGGAATGCAAGAGAGGTTGAAA 3907 GT A GCAAA  
G CTTTCA CTTT TTTGCA

||||| ||| |||||



			GAAAGT GAGA GAACGT		
			TG _ AAGGTT		
GAM1431	GLRA2	3'	TTTGACAGAGGAGAAGATTGAG 9035	A__ _ CAAA	
	GG		TTTCAGTCTTT TTTG CAG		
			GGAGTTAGAAG AGAC GTT		
			AGG A T		
GAM1431	GPRK2L	5'	TGTAGATTGGGACTGAAGG 94475	TT	
			CTTTCAGTCT ATTTGCA		
			GGAAGTCAGG TAGATGT		
			GT		
GAM1431	GRB10	3'	GCTGAAGACTGGAGG 17981	TATTTG	
			CTTTCAGTCTT CAGC		
			GGAGGTCAGAA GTCG		
GAM1431	GRIK3	3'	GCAAAGGAGATTGGAAG 5888	A	
			CTTTCAGTCTTT TTTGC		
			GAAGGTTAGAGG AAACG		
GAM1431	GRIN2B	3'	TGAGTGAAGCTGGGAG 5908	TT T	
			CT CAG CTTTATTTG		
			GA GTC GAAGTGAGT		
			GG _		
GAM1431	GRIN2B	3'	TGCCAAGCAGAGGTTGGGAG 5909	TT GT A CA	
			CT CA CTTT TTTG GCA		
			GA GT GAGA GAAC CGT		
			GG TG C _		
GAM1431	GRPR	3'	TGGTGTAGGTGGGGGTGGGGAG 18002	TT AG G	
			CT C TCTTTATTTGCA CA		
			GA G GGGGGTGGATGT GT		
			GG GT G		
GAM1431	HDAC7A	5'	GCCTGAGGGAGGCTGAGGG 31211	ATTTG _	
			CTTTCAGTCTTT CAG C		
			GGGAGTCGGAGG GTC G		
			GA__ C		
GAM1431	HDAC7A	5'	GCCTGAGGGAGGCTGAGGG 33452	ATTTG _	
			CTTTCAGTCTTT CAG C		
			GGGAGTCGGAGG GTC G		
			GA__ C		
GAM1431	HMG20A	3'	TTATTGTAAGTGAAGAACTGAGG 36545	C CAAA	
	G		CTTTCAGT TTTATTTGCAG		

			GGGAGTCA AAGTGAATGTT		
			A A T T T		
GAM1431	HOXD4	3'	TGAATTTGCAAATGAAGGTTGG 27531	GT	CAAA
	A		TTCA CTTTATTTGCAG		
			AGGT GAAGTAAACGTT		
			TG TAAGTT		
GAM1431	IL11	3'	GGGTGGGGACGGAGG 5331 A		
			CTTTC GTCTTTATTT		
			GGAGG CAGGGGTGGG		
			—		
GAM1431	IL13RA1	3'	TTGAAGTCAGATTGAGGCTGGG 7783	TT	T _AG A
	AG		CT CAGTCTT ATTTG C CAA		
			GA GTCGGAG TAGAC G GTT		
			GG T TAA		
GAM1431	IL18RAP	5'	CTGAAATAAGGACTTGAAG 13903	C	G
			CTTT AGTCTTTATTT CAG		
			GAAG TCAGGAATAAA GTC		
			T —		
GAM1431	IL4R	3'	CTGCAGATGAGGACTAGGG 4700	C	
			CTTT AGTCTTTATTTGCAG		
			GGGA TCAGGAGTAGACGTC		
			—		
GAM1431	IL9R	3'	CTGGATGGAGGCTGGAGG 9317		TG
			CTTTCAGTCTTTATT CAG		
			GGAGGTCGGAGGTAG GTC		
			—		
GAM1431	IL9R	3'	TGTCTGGATGGAGGCTGGAGG 9319		TG _
			CTTTCAGTCTTTATT CAG CA		
			GGAGGTCGGAGGTAG GTC GT		
			— T		
GAM1431	ITGB2	3'	TTGCATGGAGACTTGAGG 3993	C	TT
			CTTT AGTCTTTA TGCAG		
			GGAG TCAGAGGT ACGTT		
			T —		
GAM1431	KCNK4	5'	CAGACAGGGGCTGAGGG 52807		A
			CTTTCAGTCTTT TTTG		
			GGGAGTCGGGGA AGAC		
			C		
GAM1431	KNSL2	3'	CGGGTGAGGGGTGGGAG 73849	TT	G
			CT CA TCTTTATTTG		

			GA GT GGGAGTGGGC		
			GG G		
GAM1431	LFNG	3'	TTTGCTGTGAATAAAGG 92646	TG	
			TCTTTATT CAGCAA		
			GGAAATAA GTCGTTT		
			GT		
GAM1431	LFNG	3'	TTTGCTTGGGAGGGTGGGGGTG 92647	TT G TA_ G _	
			GGGG T CA TCTT TTT CA GCAA		
			G GT GGGG GAG GT CGTTT		
			GG G TGG G T		
GAM1431	MAP1A	3'	TGAATGGGGACTGAGG 9903		
			TTTCAGTCTTTATTTG		
			GGAGTCAGGGGTAAGT		
GAM1431	MAPRE1	3'	TTTGCTGCTTAGAGTTGGAAG 24663	T TTT	
			CTTTCAG CTTTA GCAGCAA		
			GAAGGTT GAGAT CGTCGTTT		
			_ T_		
GAM1431	MDM1	3'	GTAGGAAAGGACTGAGAG 39273	A	
			CTTTCAGTCTTT TTTGC		
			GAGAGTCAGGAA GGATG		
			A		
GAM1431	MDS1	5'	GCGAGTGTGGATTGAGAG 17161	T	
			CTTTCAGTCT TATTTGC		
			GAGAGTTAGG GTGAGCG		
			T		
GAM1431	MFAP4	3'	TGGGAGTGGGTAGGGACTGAAG 69258	TG AGCAA	
	G		CTTTCAGTCTTTATT C		
			GGAAGTCAGGGATGG G		
			GT AGGGT		
GAM1431	MLANA	3'	TTTGTTGCCAGGCTGGAG 18591	TTATTT	
			TTTCAGTCT GCAGCAA		
			GAGGTCGGA CGTTGTTT		
			CC_		
GAM1431	MS4A4A	3'	GCAAATAAGGTTTGGAAG 43782	T	
			CTTTCAG CTTTATTTGC		
			GAAGGTT GGAATAAACG		
			T		
GAM1431	MSL3L1	3'	TTTGCTGATTCTTTGAAGATTG 54371	TT TTTG_	
	GGA		T CAGTCTTTA CAGCAA		

			A GTTAGAAGT GTCGTTT		
			GG TTCTTA		
GAM1431	MTAP	3'	TTTGCAACAATAAAGGGTGGAG 10131	G	___ CAAA
	G		CTTTCA TCTTTATT TGCAG		
			GGAGGT GGAAATAA ACGTT		
			G CA T		
GAM1431	MTMR3	3'	TTTGCTGCTGGGGAGGCTGGAA 40817		ATTT
	G		CTTTCAGTCTTT GCAGCAAA		
			GAAGGTCGGAGG CGTCGTTT		
			GGT_		
GAM1431	MUC12	3'	TGCTGGGGAAGGCTGGGGG 94242	TT	ATT G
			CT CAGTCTTT T CAGCA		
			GG GTCGGAAG G GTCGT		
			GG ___ G		
GAM1431	MXI1	3'	TGAGTATGGATTGGGGG 55264	TT	T
			CT CAGTCT TATTTG		
			GG GTTAGG ATGAGT		
			GG T		
GAM1431	MXI1	3'	TGAGTATGGATTGGGGG 19903	TT	T
			CT CAGTCT TATTTG		
			GG GTTAGG ATGAGT		
			GG T		
GAM1431	MYB	3'	TTTGTTGTGGTACAACAGTTGA 59542	T	TTAT__ TG
	GAG		TTTCAG CT T CAGCAAA		
			AGAGTT GA G GTTGTTT		
			_ CAACAT GT		
GAM1431	MYEOV	3'	TCAGCTGGTTAGAGGCTGGGAG 57054	TT	TTTG AAA
			CT CAGTCTTTA CAGC		
			GA GTCGGAGAT GTCG		
			GG TG__ ACTC		
GAM1431	MYO1D	3'	TTGAGGGAAGTAGAGGCTGGGA 71773	TT	GCAG A
	G		CT CAGTCTTTATTT CAA		
			GA GTCGGAGATGAA GTT		
			GG GGG A		
GAM1431	MYO1E	3'	GCAGGTCAGGGGCTGGGGG 17188	TT	_
			CT CAGTCTTT ATTTGC		
			GG GTCGGGGA TGGACG		
			GG C		
GAM1431	NESH	5'	TGCTGGGTGGGATTGGGGG 33149	TT	TATTTG
			CT CAGTCTT CAGCA		

			GG GTTAGGG	GTCGT		
			GG	TGG___		
GAM1431	NFKBIL1	3'	TTGTAACAAGTGGGGGTGGGGG	17198	TT G	CA A
			CT CA TCTTTATTTG	GCAA		
			GG GT GGGGGTGAAC	TGTT		
			GG _	AA		
GAM1431	NFKBIL2	5'	GGCTATTGTGGATGAGGAGCTG	25526	_	TG CAAA
			GAGG	TTTCAG TCTTTATT	CAG	
			GAGGTC AGGAGTAG	GTT		
			G	GT ATCGGT		
GAM1431	NLGN3	3'	GCACTGGATGGAGCTGGAGG	38600	T	TT CA
			CTTTCAG CTTTAT	G GC		
			GGAGGTC GAGGTA	T CG		
			_	GG CA		
GAM1431	NR2E3	3'	TGGGTGAAGGTAAGGAATGAGG	32973	G	GCA AAA
			G	CTTTCATCTTTATTT	GC	
			GGGAGT AGGAATGGA	TG		
			A	AG_ GGTT		
GAM1431	NR5A2	3'	TTCAAAACAAAAAGAGATTGGG	13792	TT	A CAGCAAA
			GG	CT CAGTCTTT TTTG		
			GG GTTAGAGA	AAAC		
			GG	A AAAACTTT		
GAM1431	NRCAM	3'	TTGCTGTGAAACTGAAA	17210	CTTTA	TG
			TTTCAGT	TT CAGCAA		
			AAAGTCA	AA GTCGTT		
			_____	GT		
GAM1431	PAX5	3'	TTGAATGTGAGGGCTGGA	33639	TTG	
			TTCAGTCTTTAT	CAG		
			AGGTCGGGAGTG	GTT		
			TAA			
GAM1431	PCDHA11	5'	CAAGGGAGACTGAAAG	38198	A	
			CTTTCAGTCTTT	TTTG		
			GAAAGTCAGAGG	GAAC		
			-			
GAM1431	PCDHA11	5'	CAAGGGAGACTGAAAG	49032	A	
			CTTTCAGTCTTT	TTTG		
			GAAAGTCAGAGG	GAAC		
			-			
GAM1431	PDE4A	3'	TTGGAGGTGGGGGCTGGGG	20590	TT	G
			T	CAGTCTTTATTT	CAG	

			G GTCGGGGGTGGA GTT			
			GG G			
GAM1431	PIK3CD	3'	TTTGTATTTTAGTAGAGACGGG 17254	TT A		TGCA_
	GG		CT C GTCTTTATT GCAAA			
			GG G CAGAGATGA TGTTT			
			GG_ TTTTA			
GAM1431	PIN1L	3'	CCGCACGGAGTGAGGATTGGGG 20620	TT		GCA AAA
	G		CT CAGTCTTTATTT GC			
			GG GTTAGGAGTGAG CG			
			GG GCA CCT			
GAM1431	PK428	5'	GCGGGGGAGGGCTGGAAG 13211	A		
			CTTTCAGTCTTT TTTGC			
			GAAGGTCGGGAG GGGCG			
			G			
GAM1431	PPARGC1	3'	CATGTGAGGACTGGGGG 25159	TT		T
			CT CAGTCTTTAT TG			
			GG GTCAGGAGTG AC			
			GG T			
GAM1431	PPP3CB	3'	CTGGATGGAGGCTTGAGG 40898	C		TG
			CTTT AGTCTTTATT CAG			
			GGAG TCGGAGGTAG GTC			
			T _			
GAM1431	PRDM4	3'	TAAGTGGTGGACTGGGAG 24825	TT		_
			CT CAGTCT TTATTTG			
			GA GTCAGG GGTGAAT			
			GG T			
GAM1431	PRKG1	3'	TTTCTTCAAGTGAAGGCTGTGG 20751	TT		C CAAA
	G		CT CAGTCTTTATTTG AG			
			GG GTCGGAAGTGAAC TC			
			GT T TTT			
GAM1431	PRX	3'	CGGGTGGGGGCTGAGG 40529			
			TTTCAGTCTTTATTTG			
			GGAGTCGGGGGTGGGC			
GAM1431	PTGER2	5'	TCCTCCCAGGTAAAGGCCGGA 6309	TT A		CAGCAAA
	G		CT C GTCTTTATTTG			
			GA G CGGAAATGGAC			
			GG C CCTCCTT			
GAM1431	PTPN7	3'	CTGAGATGGGGATGAAGG 54550	G		G
			CTTTCA TCTTTATTT CAG			

GGAAGT AGGGGTAGA GTC

GAM1431 PTPN7 3' CTGAGATGGGGATGAAGG 54561 G G  
CTTTCA TCTTTATTT CAG  
||||| ||||||| |||  
GGAAGT AGGGGTAGA GTC

GAM1431 PTPN7 3' CTGAGATGGGGATGAAGG 11068 G G  
CTTTCA TCTTTATTT CAG  
||||| ||||||| |||  
GGAAGT AGGGGTAGA GTC

GAM1431 PTPRO 5' TTTGCTGTGGGTGGAAGAGGGA 47705 AG \_ TG  
G TTC TCTTT ATT CAGCAAA  
||| ||||| ||| |||||||  
GAG AGAAG TGG GTCGTTT  
GG G GT

GAM1431 PTPRO 5' TTTGCTGTGGGTGGAAGAGGGA 47710 AG \_ TG  
G TTC TCTTT ATT CAGCAAA  
||| ||||| ||| |||||||  
GAG AGAAG TGG GTCGTTT  
GG G GT

GAM1431 PTPRO 5' TTTGCTGTGGGTGGAAGAGGGA 47720 AG \_ TG  
G TTC TCTTT ATT CAGCAAA  
||| ||||| ||| |||||||  
GAG AGAAG TGG GTCGTTT  
GG G GT

GAM1431 PUM2 3' TTTGCTTTTTCATAGAGGCAGA 31018 A TTGC\_  
AAG CTTTC GTCTTTAT AGCAAA  
||||| ||||||| |||||  
GAAAG CGGAGATA TCGTTT  
A CTTTT

GAM1431 RAB5A 3' TTTGTTGTTTGGGGTGGGG 14782 TT G TTATTT  
T CA TCT GCAGCAAA  
| ||||| |||||||  
G GT GGG TGTTGTTT  
GG G TT\_\_\_\_

GAM1431 RAD54L 5' TTTGGGAACAGGAAGGTTGAGA 13120 GT A\_\_ G CAAA  
G CTTTCA CTTT TTT CAG  
||||| ||||| ||| |||  
GAGAGT GAAG AAG GTT  
TG GAC G T

GAM1431 RB1 3' ATTTGCTTTTAATTAAATAAAA 90914 TC C\_\_\_\_  
GCTGGAAG G TTTATTTG AGCAAA T  
| ||||||| ||||| |  
C AAATAAAT TCGTTT A  
GA TAATTT

GAM1431 RBM3 5' TTGTTCTAGGGGGTGGAGG 70491 G TTT  
CTTTCA TCTTTA GCAG  
||||| ||||||| |||||

			GGAGGT GGGGAT TGTT		
			G CT_		
GAM1431	RECQL5	3'	TTGTTGTGGGTCTGAGG 14932	T	TTAT TG
			TTTCAG CT T CAGCAA		
			GGAGTC GG G GTTGTT		
			T ____ GT		
GAM1431	RFPL2	3'	TATGAGTTAAATAAAGATTGGA 21726		CAG AA
	A		TTTCAGTCTTTATTTG CA		
			AAGGTTAGAAATAAAT GT		
			TGA ATT		
GAM1431	RPH3AL	3'	TTTGTTGCCCAGGCTGGGG 22759	TT	TTATTT
			T CAGTCT GCAGCAAA		
			G GTCGGA CGTTGTTT		
			GG CC____		
GAM1431	RPN1	3'	TTTGCTGTGGCAGGCAGATTGG 11393		TTAT_ TG
	G		TTTCAGTCT T CAGCAAA		
			GGGTTAGA G GTCGTTT		
			CGGAC GT		
GAM1431	RPP30	3'	TTGTTGCTCAGGCTGGAG 21177		TTATTT
			TTTCAGTCT GCAGCAA		
			GAGGTCGGA CGTTGTT		
			CT____		
GAM1431	RPS6KA2	3'	GCTGGAGGCTGGAGG 40907		TATTTG
			CTTTCAGTCTT CAGC		
			GGAGGTCGGAG GTCG		
			_____		
GAM1431	RRM2B	3'	TGTAAGTGAAGATGGAAG 67829	G	
			CTTTCA TCTTTATTTGCA		
			GAAGGT AGAAGTGAATGT		
			_____		
GAM1431	RTN1	3'	TTTGTTGTATGGGATTGGTGG 40912	T	TATT
			CT TCAGTCTT TGCAGCAAA		
			GG GGTTAGGG ATGTTGTTT		
			T T____		
GAM1431	RTN3	3'	TTGAAAGGGGAAAGATTGGAGG 73903		A GCAG
			CTTTCAGTCTTT TTT CAA		
			GGAGGTTAGAAA GGG GTT		
			G AAA_		
GAM1431	SCGB3A2	3'	GTGGATGGGGATGGAAG 53965	G	TG
			CTTTCA TCTTTATT C		



GAAGGT AGGGGTAG G  
 \_ GT  
 GAM1431 SEPN1 3' TTGTGGGGTGAAGAATGGAGG 66384 G \_TG  
 CTTTCA TCTTTAT T CAG  
 ||||| ||||| | |||  
 GGAGGT AGAAGTG G GTT  
 A G GT  
 GAM1431 SERPINA4 3' GCAGGGGAGGGCTGGGAG 20612 TT A  
 CT CAGTCTTT TTTGC  
 || ||||| |||||  
 GA GTCGGGAG GGACG  
 GG G  
 GAM1431 SET 3' TTTGCTCTGCTGGAAGCTGGAG 11561 T ATTT \_  
 G CTTTCAG CTTT GCA GCAAA  
 ||||| ||| ||| |||||  
 GGAGGTC GAAG CGT CGTTT  
 \_ GT\_ CT  
 GAM1431 SMCX 5' TTGTTGTGGTGTGGGGA 14827 \_TG  
 TCTTTAT T CAGCAA  
 ||||| | |||||  
 AGGGGTG G GTTGTT  
 T GT  
 GAM1431 SNL 3' TGGCGGGCGGGTAGGGGTGTGG 11854 TT \_ A\_ AAA  
 GGG T CA GTCTTTATTTGC GC  
 | || ||||| ||||| ||  
 G GT TGGGGATGGGCG CG  
 GG G GG GT  
 GAM1431 SOCS5 3' TTAAAGCAAAATGGGGATTGA 25804 \_ AGCAAA  
 AGG CTTTCAGTCTTTATTT GC  
 ||||| ||||| ||||| ||  
 GGAAGTTAGGGGTAAA CG  
 A AAATTT  
 GAM1431 SOD3 5' TTTGTTGCAGGAATGCAGGAGG 11867 A C AT  
 CTTTC GT TTT TTGCAGCAAA  
 |||| || ||| ||||| |||||  
 GGAGG CG AAG GACGTTGTTT  
 A T \_  
 GAM1431 SOST 3' TTGTAAAATGAGGGTGGAGG 47472 G TA  
 CTTTCA TCTT TTTGCAG  
 ||||| ||| |||||  
 GGAGGT GGAG AAATGTT  
 G TA  
 GAM1431 SPRR1B 3' TGAATGAAGCTGAAGG 87407 T  
 CTTTCAG CTTTATTTG  
 ||||| ||||| |||||  
 GGAAGTC GAAGTAAGT  
 \_  
 GAM1431 SRRM2 3' TGCAGATGGGAGTTGGGGG 32917 TT TC  
 CT CAG TTTATTTGCA  
 || ||| ||||| |||||

GG GTT GGGTAGACGT  
GG GA  
GAM1431 STC1 3' TTTGCTGCAGAGTGATTCGGGG 12034 TT\_ TTTA  
G CT C AGTC TTTGCAGCAAA  
|| |||| |||||  
GG G TTAG AGACGTCGTTT  
GG C TG\_\_  
GAM1431 STXBP1 3' GCAGCTGTGGGTGGAGGCTGGG 12047 TT TG AAA  
G T CAGTCTTTATT CAGC  
| ||||| ||||  
G GTCGGAGGTGG GTCG  
GG GT ACGT  
GAM1431 SULT1A3 3' TTGGGAAGCAGAGGCTGGAGG 12057 A\_ G  
CTTTCAGTCTTT TTT CAG  
||||||| ||||  
GGAGGTCGGAGA AAG GTT  
CG G  
GAM1431 SUPT5H 3' TGAGTAGAGTCTGGGGG 12066 TT T  
CT CAG CTTTATTTG  
|| |||||  
GG GTC GAGATGAGT  
GG T  
GAM1431 SYT5 5' TTTGTTGTGCGTG GGGGCTCAAA 12076 C T T  
G CTTT AGTCTT AT TGCAGCAAA  
|||| |||| |||||  
GAAA TCGGGG TG GTGTTGTTT  
C \_ C  
GAM1431 TCF15 3' TTGTGTAGGGACCGGGG 16042 TT A TT  
CT C GTCTTTAT GCAG  
|| ||||| ||||  
GG G CAGGGATG TGTT  
GG C \_  
GAM1431 TDGF1 3' TTTGTATTTTAGTAGAGATGGG 12205 TT G TGCA\_  
GG CT CA TCTTTATT GCAAA  
|| ||||| ||||  
GG GT AGAGATGA TGTTT  
GG \_ TTTTA  
GAM1431 TIC 3' TGGCATGAGTGAGGGCTGGG 24939 GCA AAA  
TTCAGTCTTTATTT GC  
||||||| ||  
GGGTCGGGAGTGAG CG  
TA\_ GT  
GAM1431 TNFAIP6 3' TTTGAGCTAAAGGAGACTGGAA 59466 TA T AG  
G CTTTCAGTCTT TT GC CAAA  
||||||| || ||||  
GAAGGTCAGAG AA CG GTTT  
GA T A\_  
GAM1431 TNFSF15 3' CGGGTCAGGATTGAAAG 17591 T  
CTTTCAGTCTT ATTTG  
||||||| ||||

			GAAAGTTAGGA TGGGC		
			C		
GAM1431 TOX	3'	AAGAATTGAACTAGGGGCTGGA 28287		T G	CAAA
AG		CTTTCAGTCTTTA TT CAG			
		GAAGGTCGGGGAT AA GTT			
		C _ AAGAAT			
GAM1431 TP53	3'	TTTGTTGCCAGGCTGGAG 5044		TTATTT	
		TTTCAGTCT GCAGCAAA			
		GAGGTCGGA CGTTGTTT			
		CC _			
GAM1431 TP53	3'	TTTGTTGTGGGGAGGAGGATGG 5045	TT A	AT _	TG
GGAG		T C GTCTTT T CAGCAAA			
		A G TAGGAG G GTTGTTT			
		GG G GAGG GT			
GAM1431 VEGFB	3'	TTGGAAGAGGAGACTGGGAG 12592	TT	TA	G
		CT CAGTCTT TTT CAG			
		GA GTCAGAG GAA GTT			
		GG GA G			
GAM1431 VTN	5'	TTTGCTGCAGCAGCCGCTGGAG 5317		CTTTAT	
G		CTTTCAGT TTGCAGCAAA			
		GGAGGTCG GACGTCGTTT			
		CCGAC _			
GAM1431 ZNF215	3'	TTGCTGTTGAATGGAGACTAGA 25121	C	_	A
G		CTTT AGTCTTTATTTG CAGCAA			
		GAGA TCAGAGGTAAGT GTCGTT			
		_ T			
GAM1431 ZNF219	3'	TTTGTACAAGGGGTGAGGGTGG 33135	TT G	TA _	CA
GGG		T CA TCTT TTTG GCAAA			
		G GT GGAG GAAC TGTTT			
		GG G TGGG A _			
GAM1431 ZNF76	3'	CTCAGGTAGAGATTGGGG 12810	TT		C
		T CAGTCTTTATTTG AG			
		G GTTAGAGATGGAC TC			
		GG _			
GAM1431 ABTB1	3'	CAGGAAGGGCTGGGGG 50727	TT	A	
		CT CAGTCTTT TTTG			
		GG GTCGGGAA GGAC			
		GG _			
GAM1431 ACTR1A	3'	TTTGTTTCAGTTAGGGGCTGGAG 62970		T C	
		TTTCAGTCTTTA TTG AGCAAA			

GAGGTCGGGGAT GAC TTGTTT  
 T \_  
 GAM1431 AKR1D1 3' TTTGCTGCACCTTGAGTTGAGA 19980 T TATT  
 G CTTTCAG CTT TGCAGCAAA  
 ||||| ||| |||||  
 GAGAGTT GAG ACGTCGTTT  
 \_ TTCC  
 GAM1431 AMOT 3' TGTTAGGTAAGGGTTGGGGG 55729 TT GT \_  
 CT CA CTTTATTTG CA  
 || || ||||| ||  
 GG GT GGAATGGAT GT  
 GG TG T  
 GAM1431 APCL 3' GCGGGGGAGGCTGGGAG 19678 TT A  
 CT CAGTCTTT TTTGC  
 || ||||| ||||  
 GA GTCGGAGG GGGCG  
 GG \_  
 GAM1431 APELIN 3' TTTGTGTGTGTGGGGACGGGGG 33788 TT A T G  
 CT C GTCTTTAT TGCA CAAA  
 || | ||||| ||| ||||  
 GG G CAGGGGTG GTGT GTTT  
 GG \_ T \_  
 GAM1431 APOA5 3' TGGGTGGAGGGTGAAG 53731 G TT  
 CTTTCA TCCTTAT G  
 ||||| ||||| |  
 GAAGGT GGAGGTG T  
 G GG  
 GAM1431 APOL4 5' TTTGCTGTGCTTGATTGTGAG 47633 T TTTATTT  
 CTT CAGTC GCAGCAAA  
 ||| |||| |||||  
 GAG GTTAG TGTCGTTT  
 T TTCG\_\_  
 GAM1431 ARAP3 5' TTGGAGGAAGATTGGAGG 42506 AT G  
 CTTTCAGTCTTT TT CAG  
 ||||| ||| |||  
 GGAGGTTAGAAG GA GTT  
 \_ G  
 GAM1431 ARHGEF2 3' TTGATGGAATAAAGGTTGGGG 16366 TT GT G G  
 T CA CTTTATTT CA CAA  
 | || ||||| ||| |||  
 G GT GAAATAAG GT GTT  
 GG TG \_ A  
 GAM1431 ARHGEF9 3' TTTGATGTGGTAGAGTTGGGAG 30826 TT T T TG G  
 CT CAG CTTTA T CA CAAA  
 || ||| |||| | ||| |||  
 GA GTT GAGAT G GT GTTT  
 GG \_ \_GT A  
 GAM1431 ART4 5' CGGATGAGACTGAAAG 40775 T  
 CTTTCAGTCTT ATTTG  
 ||||| ||||| |||||

GAAAGTCAGAG TAGGC

GAM1431 ASPN 3' TTGATACATAAGGGTTGAGAG 34604 GT T \_  
CTTTCA CTTTAT TG CAG  
||||| ||||| || |||  
GAGAGT GGAATA AT GTT  
TG C A

GAM1431 BC008967 5' CCAAGGCAGAAGGGGTTGAAGG 60765 GT A AGCAAA  
CTTTCA CTTT TTTGC  
||||| ||| |||||  
GGAAGT GGGG AGACG  
TG \_ GAACCT

GAM1431 BMF 3' GGCTTGCTGAGGGTGGGGGTTG 53161 TT GT TG A  
GGAG CT CA CTTTATT CAGCAA  
|| || ||||| |||||  
GA GT GGGGTGG GTCGTT  
GG TG GA CGGT

GAM1431 BOP 5' AAGTGAAGCTGAGAG 85048 T  
CTTTCAG CTTTATTT  
||||| |||||  
GAGAGTC GAAGTGAA

GAM1431 BRAP 3' CAAGTGAGGACGAAGG 22248 A  
CTTTC GTCTTTATTTG  
||||| |||||  
GGAAG CAGGAGTGAAC

GAM1431 BRD2 3' TTAAAGCTAGGTAAGGCTGGGG 17539 TT T \_ AGCAAA  
G CT CAGTCTT ATTT GC  
|| ||||| ||| ||  
GG GTCGGAA TGGA CG  
GG \_ T AATTT

GAM1431 BRD4 3' TAGATAAGGAGTGGGAG 26667 TT G  
CT CA TCTTTATTTG  
|| || |||||  
GA GT AGGAATAGAT  
GG G

GAM1431 BTBD3 3' AAATAAGGAACTGGGGG 30303 TT \_  
CT CAGT CTTTATTT  
|| ||| |||||  
GG GTCA GGAATAAA  
GG A

GAM1431 BTN3A2 3' CGAGTGAAGATTGAAA 22910  
TTTCAGTCTTTATTTG  
|||||  
AAAGTTAGAAGTGAGC

GAM1431 C11orf16 5' AGGCTGAGGTGGAGGCTGGGAG 40216 TT G AAA  
CT CAGTCTTTATTT CAGC  
|| ||||| |||

			GA GTCGGAGGTGGA GTCG		
			GG _ GAG		
GAM1431	C14orf4	3'	TTTGTTGCAAGTTTGTGAGGG 67343	GTCTTT	
			CTTTCA ATTTGCAGCAAA		
			GGGAGT TGAACGTTGTTT		
			GTT__		
GAM1431	C1orf24	3'	GCCTGGGTAAGACTGAAAG 53721	T TT CA	
			CTTTCAGTCTT AT G GC		
			GAAAGTCAGAA TG T CG		
			_ GG C_		
GAM1431	C20orf121	3'	TGACCAAATGTGAGACTGGGAG 44277	TT _ CAG	
			CT CAGTCTT TATTTG CA		
			GA GTCAGAG GTAAAC GT		
			GG T CA_		
GAM1431	C20orf124	5'	GCTGGTAGGGGCTGGGAG 45487	TT TTG	
			CT CAGTCTTTAT CAGC		
			GA GTCGGGGATG GTCG		
			GG _		
GAM1431	C20orf151	3'	CAAGAGGGGCTGGAGG 88696	A	
			CTTTCAGTCTTT TTTG		
			GGAGGTCGGGGA GAAC		
			_		
GAM1431	C20orf54	3'	TTGCTGGTGGGGCTGGGG 53011	TT TATTTG	
			T CAGTCTT CAGCAA		
			G GTCGGGG GTCGTT		
			GG TG__		
GAM1431	C20orf60	3'	GCCGAGTAGGGGTGGGGG 53734	TT G CA	
			CT CA TCTTTATTTG GC		
			GG GT GGGGATGAGC CG		
			GG _ _		
GAM1431	C20orf98	3'	TGGGTGAAGAAGGCTGGAGG 71518	A TG AG	
			CTTTCAGTCTTT TT C CA		
			GGAGGTCGGAAG AA G GT		
			_ GT G_		
GAM1431	C22orf5	3'	TTGCGTGGAGGGTGGGGG 24350	TT G TT	
			CT CA TCTTTAT GCAG		
			GG GT GGAGGTG CGTT		
			GG G _		
GAM1431	C3IP1	3'	TTTGCCTTGAATGGGGGTGAAA 41287	G CA	
G			CTTTCA TCTTTATTTG GCAAA		

			GAAAGT GGGGGTAAGT CGTTT			
			— TC			
GAM1431	C5orf5	3'	TTTCTGGGGGGTGGGGGGTGAG 33474	G	_ G	CAAA
	GG		CTTTCA TCTTTATT T CAG			
			GGGAGT GGGGGTGG G GTC			
			G G G TTT			
GAM1431	C5orf6	5'	CAAGTGAGGTCTGGAAG 33478	T		
			CTTTCAG CTTTATTTG			
			GAAGGTC GGAGTGAAC			
			T			
GAM1431	C6.1A	3'	TTGCCAGGGATAGGGACTGGAG 44287		GCA	A
	G		CTTTCAGTCTTTATTT GCAA			
			GGAGGTCAGGGATAGG CGTT			
			GAC			
GAM1431	C8orf14	5'	CTGTGGATGGAGGCAGGGGG 53998	TT A	TG	
			CT C GTCTTTATT CAG			
			GG G CGGAGGTAG GTC			
			GG A GT			
GAM1431	C9orf5	3'	TTTGTGTGAATGAAGACT 49285	TG		
			AGTCTTTATT CAGCAAA			
			TCAGAAGTAA GTTGTTT			
			GT			
GAM1431	CCR8	3'	TAAGTAGAGACTGAAA 17784			
			TTTCAGTCTTTATTTG			
			AAAGTCAGAGATGAAT			
GAM1431	CDA08	5'	GCGGGCGGGGGCTGAGGG 47907	TA		
			CTTTCAGTCTT TTTGC			
			GGGAGTCGGGG GGGCG			
			GC			
GAM1431	CDK5RAP3	5'	TTTCCCTGAGTGAGTGCTGGG 47287	TT _		CAGCAAA
	GG		CT CAGT CTTTATTTG			
			GG GTCG GAGGTGAGT			
			GG T CCCTTT			
GAM1431	CDT6	3'	TGAGGGCAGATGAGGACAGGAA 40946	A	AG_	AA
	G		CTTTC GTCTTTATTTGC CA			
			GAAGG CAGGAGTAGACG GT			
			A GGA			
GAM1431	CENPH	3'	TTGTAGTGGGATTGAAAG 43281	TAT		
			CTTTCAGTCTT TTGCAG			

GAAAGTTAGGG GATGTT  
 T\_\_  
 GAM1431 CENPH 3' TTTGTTGCCAGACTGGAGG 43282 TTATTT  
 CTTTCAGTCT GCAGCAA  
 ||||| |||||  
 GGAGGTCAGA CGTTGTTT  
 CC\_\_  
 GAM1431 CEZANNE 3' TTTGGTGTGTGGGGGTGGGAG 39514 TT G TT G  
 CT CA TCTTTAT GCA CAAA  
 || || ||||| || ||||  
 GA GT GGGGGTG TGT GTTT  
 GG \_ \_ G  
 GAM1431 CSR1 3' TTGGGCCTGAGTGGAGATGGGA 32691 TT G \_ AG A  
 G CT CA TCTTTATTT GC CAA  
 || || ||||| || ||||  
 GA GT AGAGGTGAG CG GTT  
 GG \_ TC G\_  
 GAM1431 DAMS 5' TGTAAAAAAGACTGAGGG 41823 A  
 CTTTCAGTCTTT TTTGCA  
 ||||| |||||  
 GGGAGTCAGAAA AAATGT  
 -  
 GAM1431 DGKD 3' TTGTAGATGGGGGTGGCAG 59413 T GT  
 CT TCA CTTTATTTGCAG  
 || || ||||| |||||  
 GA GGT GGGGTAGATGTT  
 C TG  
 GAM1431 DIO2 3' CAACTGAAGGAAGGCTGAAGG 5827 ATTTG CAAA  
 CTTTCAGTCTTT CAG  
 ||||| |||||  
 GGAAGTCGGAAG GTC  
 GAA\_ AACG  
 GAM1431 DIO2 3' CAACTGAAGGAAGGCTGAAGG 25679 ATTTG CAAA  
 CTTTCAGTCTTT CAG  
 ||||| |||||  
 GGAAGTCGGAAG GTC  
 GAA\_ AACG  
 GAM1431 DJ667H12.2 3' GTAGATGAGATTGGGGG 38988 TT T  
 CT CAGTCTT ATTTGC  
 || ||||| |||||  
 GG GTTAGAG TAGATG  
 GG \_  
 GAM1431 DKFZP434C171 3' AAGGCCAGAGTAGGGGTGGGG 31550 TT GT GCA AAA  
 G CT CA CTTTATTT GC  
 || || ||||| |||||  
 GG GT GGGATGAG CG  
 GG TG AC\_ GAAG  
 GAM1431 DKFZP434F091 5' CTGTAGGTGGGAGTTGGGAG 31282 TT TC  
 CT CAG TTTATTTGCAG  
 || || ||||| |||||



GA GTT GGGTGGATGTC  
 GG GA  
 GAM1431 DKFZP434K1172 5' CTGTGAGTCAGGACTGAAAG 48443 T TG  
 CTTTCAGTCTT ATT CAG  
 ||||| ||| |||  
 GAAAGTCAGGA TGA GTC  
 C GT  
 GAM1431 DKFZp434K1815 3' TTTGGGCCGATGGGGGTGGGGG 94266 TT G T AG  
 CT CA TCTTTATT GC CAAA  
 || || ||||| || |||  
 GG GT GGGGGTAG CG GTTT  
 GG \_ C G\_  
 GAM1431 DKFZP434N161 3' TTGTTGCCAGATTTGAAAG 78523 \_ TTATTT  
 CTTTCAG TCT GCAGCAA  
 ||||| ||| |||||  
 GAAAGTT AGA CGTTGTT  
 T C\_\_\_\_  
 GAM1431 DKFZP434P211 3' TTGAGGAATAGGGATGGGGAG 27271 TT A G\_  
 CT C GTCTTTATTT CAG  
 || | ||||| |||  
 GA G TAGGGATAAG GTT  
 GG G GA  
 GAM1431 DKFZp547A023 5' AGCCGCTGTGGATGGGGAGTGG 72615 G TG AAA  
 AGG CTTTCA TCTTTATT CAGC  
 ||||| ||||| |||  
 GGAGGT AGGGGTAG GTCG  
 G GT CCGAC  
 GAM1431 DKFZp547G183 3' TTGCGGGACAAATAGAGACGGG 38027 TT A CA\_\_ A  
 AG CT C GTCTTTATTTG GCAA  
 || | ||||| |||  
 GA G CAGAGATAAAC CGTT  
 GG \_ AGGG  
 GAM1431 DKFZp761F2014 3' CTCAAGGAAGGGCTGGGGG 39537 TT A C  
 CT CAGTCTTT TTTG AG  
 || ||||| ||| ||  
 GG GTCGGGAA GAAC TC  
 GG G \_  
 GAM1431 DKFZP762N2316 3' TTGTTGCGGAATATGGAAG 67130 GTCTTTA  
 CTTTCA TTTGCAGCAA  
 ||||| |||||  
 GAAGGT AGGCGTTGTT  
 ATA\_\_\_\_  
 GAM1431 DMTF1 3' GTTGAGTGGAGGCTGGGAG 40942 TT TG  
 CT CAGTCTTTATT CAGC  
 || ||||| ||| |||  
 GA GTCGGAGGTGA GTTG  
 GG \_  
 GAM1431 DNAH7 3' CTGAAATAAATAAAGACTAAAG 38158 C CAG AA  
 CTTT AGTCTTTATTTG CA  
 ||| ||||| ||| ||

			GAAA TCAGAAATAAAT	GT		
			— AAA CT			
GAM1431	DUSP10	5'	GTGAATGGGGGCTGAA	23283	TG	
			TTCAGTCTTTATT C			
			I			
			AAGTCGGGGGTAA G			
			GT			
GAM1431	DUSP10	5'	GTGAATGGGGGCTGAA	58563	TG	
			TTCAGTCTTTATT C			
			I			
			AAGTCGGGGGTAA G			
			GT			
GAM1431	DUSP9	3'	TTGCGGGATGGGGGTGGGGG	7346	TT G TA	
			CT CA TCTT TTTGCAG			
			GG GT GGGG GGGCGTT			
			GG G TA			
GAM1431	E	3'	TGTGAGTGAAGATTAGAG	40390	C TG	
			CTTT AGTCTTTATT CA			
			GAGA TTAGAAGTGA GT			
			— GT			
GAM1431	EAT2	3'	TTGTGTCAGGTGAAGGTGAGGG	79284	G CA	
			CTTTCA TCTTTATTTG GCAA			
			GGGAGT GGAAGTGGAC TGTT			
			— TG			
GAM1431	EFA6R	3'	TTGCCTTTGAAGGCTGAGG	30991	TTT	
			TTTCAGTCTTTA GCAG			
			GGAGTCGGAAGT CGTT			
			TTC			
GAM1431	EFA6R	3'	TTTGTTTGCTAAAGGATGGGGG	30992	TT GT TTT _	
			CT CA CTTTA GCAG CAAA			
			GG GT GAAAT CGTT GTTT			
			GG AG _ T			
GAM1431	ERG-1	5'	GTAGGTGGAGGTGGGAG	41843	TT G	
			CT CA TCTTTATTTGC			
			GA GT GGAGGTGGATG			
			GG _			
GAM1431	EZF-2	3'	TTGGTGAAGCAGAGGCTGAAGG	37106	A G G	
			CTTTCAGTCTTT TTT CA CAA			
			GGAAGTCGGAAGA GAA GT GTT			
			C _ G			
GAM1431	FADS2	3'	AGGTGGGGGCTGGAGG	14951		
			CTTTCAGTCTTTATTT			

GGAGGTCGGGGGTGGA

GAM1431 FAM3C 3' TAGAGTGAGGCTGGAGG 29687 TA  
CTTTCAGTCTT TTG  
||||||| |||  
GGAGGTCGGAG AGAT  
TG

GAM1431 FBXO9 3' TTGCACTAAAGGCTCAAAG 53108 C TT  
CTTT AGTCTTTA TGCAG  
||| ||||| ||||  
GAAA TCGGAAAT ACGTT  
C C\_

GAM1431 FENS-1 3' AAATAAGACTGAAGG 40436 T  
CTTTCAGTCTT ATTT  
||||||| |||  
GGAAGTCAGAA TAAA

GAM1431 FENS-1 3' TTTGTACAGATAGGGATTAAGG 40446 C CA  
CTTT AGTCTTTATTTG GCAAA  
||| ||||| ||||  
GGAA TTAGGGATAGAC TGTTT  
\_ A\_

GAM1431 FKBP9 3' TGAGATAAATAGGGCTGGGGG 94071 TT T CAG  
CT CAGTCTT ATTTG CA  
|| ||||| |||| ||  
GG GTCGGGA TAAAT GT  
GG \_ AGA

GAM1431 FLB6421 3' TTTGCTGTGGATTCTTTTGGG 39235 TCTTT TG  
TTCAG ATT CAGCAAA  
|||| | |||||  
GGGTT TAG GTCGTTT  
TTCT\_ GT

GAM1431 FLJ10081 3' TTGCTAAAGACTGGAG 35804 TTT  
TTTCAGTCTTTA GCAG  
||||||| |||  
GAGGTCAGAAAT CGTT

GAM1431 FLJ10099 3' TTGAGAGAGACTGAGAG 35814 ATTTG  
CTTTCAGTCTTT CAG  
||||||| |||  
GAGAGTCAGAGA GTT  
GA\_

GAM1431 FLJ10460 3' TTTGCTGCTGGTAATACTGAAA 36135 CT TT  
G CTTTCAGT TTAT GCAGCAAA  
||||| ||| |||||  
GAAAGTCA AATG CGTCGTTT  
T\_ GT

GAM1431 FLJ10508 5' TGGAAGCAGAAAGAGGCTGGAA 36203 A AGCAAA  
G CTTTCAGTCTTT TTTGC  
||||||| ||||

		GAAGGTCGGAGA AGACG	
		A AAGGT	
GAM1431	FLJ10521	3' TGACCAGGAGGAGGCTGAGGG 36221	TA CAG
		CTTTCAGTCTT TTTG CA	
		GGGAGTCGGAG GGAC GT	
		GA CA_	
GAM1431	FLJ10700	3' TAAGTGGGGACAGAAGG 36429 A	
		CTTTC GTCTTTATTTG	
		GGAAG CAGGGGTGAAT	
		A	
GAM1431	FLJ10751	3' TTGGGGGCAAGTGGGGGCTGAA 36573	AG_ A
	G	TTTCAGTCTTTATTTGC CAA	
		GAAGTCGGGGGTGAACG GTT	
		GGG	
GAM1431	FLJ10751	3' TTGGGGGCAAGTGGGGGCTGAA 36734	AG_ A
	G	TTTCAGTCTTTATTTGC CAA	
		GAAGTCGGGGGTGAACG GTT	
		GGG	
GAM1431	FLJ10774	3' TTGCTCGCAGGGGTGAGGG 45088	G TTATT _
		CTTTCA TCT TGC AGCAA	
		GGGAGT GGG ACG TCGTT	
		G _ _ _ C	
GAM1431	FLJ10898	3' TGCTGGAAGAGGTTGAGAG 59438	GT TAT G
		CTTTCA CTT TT CAGCA	
		GAGAGT GAG AA GTCGT	
		TG _ _ G	
GAM1431	FLJ11722	3' TGAATGGGGGCTGGAG 46400	
		TTTCAGTCTTTATTTG	
		GAGGTCGGGGGTAAGT	
GAM1431	FLJ12057	3' TTGATGACTAGGAAAGGCTGAG 45443	ATTG_ G A
	GG	CTTTCAGTCTTT CA CAA	
		GGGAGTCGGAAA GT GTT	
		GGATCA A	
GAM1431	FLJ12190	3' TTGGGGAGGGGACTGAGGG 46877	TA G
		CTTTCAGTCTT TTT CAG	
		GGGAGTCAGGG AGG GTT	
		_ G	
GAM1431	FLJ12592	3' TTGAGGTGGGGTGGAGGTGGGG 49702	TT AG _TG AG A
	AG	CT C TCTTTAT T C CAA	

		GA G GGAGGTG G G GTT		
		GG GT G GT GA		
GAM1431	FLJ12592	3' TTTGTTGTGAGAATTGCTGAAG 49703	CT A TG	
		TTTCAGT TT TT CAGCAAA		
		GAAGTCG AA GA GTTGTTT		
		TT _ GT		
GAM1431	FLJ12691	3' AGATGAAGAATGGAGG 44700 G		
		CTTTCA TCTTTATTT		
		GGAGGT AGAAGTAGA		
		A		
GAM1431	FLJ12716	5' TTGTGTAAGAAAAAGATTGGAA 41657	A_ G A	
	G	CTTTCAGTCTTT TTTGCA CAA		
		GAAGGTTAGAAA GAATGT GTT		
		AA _		
GAM1431	FLJ12800	3' TTGGGAGGTTGAGGCTGGAAG 43239	TA_ G	
		CTTTCAGTCTT TTT CAG		
		GAAGGTCGGAG GAG GTT		
		TTG G		
GAM1431	FLJ12838	3' TTGCTGTGAACCTGAAA 44971	TCTTTA TG	
		TTTCAG TT CAGCAA		
		AAAGTC AA GTCGTT		
		C_ GT		
GAM1431	FLJ12934	3' TTTCCAAAGGTAAAGATGGAAG 43203	G GCAGCAAA	
		CTTTCA TCTTTATTT		
		GAAGGT AGAAATGGA		
		_ AACCTT		
GAM1431	FLJ13102	3' CTGAGGAGGATTGAGGG 46009	ATTTG	
		CTTTCAGTCTTT CAG		
		GGGAGTTAGGAG GTC		
		GA_		
GAM1431	FLJ13111	3' GTAGAAGAGGCTGAGGG 46939	A	
		CTTTCAGTCTTT TTTGC		
		GGGAGTCGGAGA AGATG		
		_		
GAM1431	FLJ13441	3' CTGCAGATAGAGCTGGGAG 43662	TT T	
		CT CAG CTTTATTTGCAG		
		GA GTC GAGATAGACGTC		
		GG _		
GAM1431	FLJ13909	3' GCCTGTTTCAGATGGGGATTGGG 47067	TT C AA	
	GG	CT CAGTCTTTATTTG AGCA		

GG GTTAGGGGTAGAC TTGT  
GG \_ CCGG  
GAM1431 FLJ14009 5' TTGCTGCGGAGTTGGAGA 45413 \_  
TCTTTA TTTGCAGCAA  
||||| |||||||  
AGAGGT AGGCGTCGTT  
TG  
GAM1431 FLJ14346 3' GTGGAGAGGGGCTGAGGG 46719 A TG  
CTTTCAGTCTTT TT C  
||||||||| || |  
GGGAGTCGGGGA AG G  
G GT  
GAM1431 FLJ14442 3' CAGGTGAGGATGGAGG 51363 G  
CTTTCA TCTTTATTTG  
||||| |||||||  
GGAGGT AGGAGTGGAC  
—  
GAM1431 FLJ14486 3' TGGTGGTGGGGGCTGGGGG 51397 TT TTG G  
CT CAGTCTTTAT CA CA  
|| ||||||| || ||  
GG GTCGGGGGTG GT GT  
GG \_ G  
GAM1431 FLJ14624 3' CGAATGAGGAATGGAAG 71323 G  
CTTTCA TCTTTATTTG  
||||| |||||||  
GAAGGT AGGAGTAAGC  
A  
GAM1431 FLJ14834 3' GCACTGGGTGGGGCTGGGGG 51654 TT T TT CA  
CT CAGTCTT AT G GC  
|| ||||||| || | ||  
GG GTCGGGG TG T CG  
GG \_ GG CA  
GAM1431 FLJ20060 3' TAAGTGAAGACTGGGG 34452 TT  
T CAGTCTTTATTTG  
| |||||||||||  
G GTCAGAAGTGAAT  
GG  
GAM1431 FLJ20308 3' TTTGTTGCCTGTTAGGGCTGAA 66860 T TT  
G TTTTCAGTCTT AT GCAGCAAA  
||||||||| || |||||||  
GAAGTCGGGA TG CGTTGTTT  
T TC  
GAM1431 FLJ20337 3' TTGGTAGTGGAGGGTGGGGG 34970 TT G TG  
CT CA TCTTTATT CAG  
|| || ||||||| |||  
GG GT GGAGGTGA GTT  
GG G TG  
GAM1431 FLJ20345 3' TTCTGAGTAAGTGAAGGCTGAA 35025 AGCAAA  
GG CTTTCAGTCTTTATTTGC  
|||||||||||||||

GGAAGTCGGAAGTGAATG  
 AGTCTTT  
 GAM1431 FLJ21791 3' GCAAATAAGGGCTTGGAG 61439 TC  
 CTT AGTCTTTATTTGC  
 ||| |||||  
 GAG TCGGGAATAAACG  
 GT  
 GAM1431 FLJ22329 3' GCAAGGGCTGGAGG 45070 TTAT  
 CTTTCAGTCT TTGC  
 ||||| |||  
 GGAGGTCGGG AACG  
  
 GAM1431 FLJ22551 5' GGTGAGTGTAGAGGAGGCTGAA 45239 A G\_ AA  
 AG CTTTCAGTCTTT TTTGCA CA  
 ||||| ||||| ||  
 GAAAGTCGGAGG AGATGT GT  
 \_ GA GGT  
 GAM1431 FLJ22593 5' TTGCCTGGTGAGGCTGGAGG 45229 TATTT  
 CTTTCAGTCTT GCAG  
 ||||| |||  
 GGAGGTCGGAG CGTT  
 TGGTC  
 GAM1431 FLJ22684 3' TTGGGGATAAGGGTTGCGGG 46800 TT GT G  
 CT CA CTTTATTT CAG  
 || || ||||| |||  
 GG GT GGAATAGG GTT  
 GC TG G  
 GAM1431 FLJ23185 5' TTGGGGTAAGGATTGAG 46836 G  
 TTCAGTCTTTATTT CAG  
 ||||| |||  
 GAGTTAGGAATGGG GTT  
  
 GAM1431 FLJ23322 3' GCACGTGAGGGCTGAAAG 88787 T  
 CTTTCAGTCTTTAT TGC  
 ||||| |||  
 GAAAGTCGGGAGTG ACG  
 C  
 GAM1431 FLJ23476 3' TGGATAAAGATTGAAG 44964 TT  
 TTTTCAGTCTTTAT G  
 ||||| |||  
 GAAGTTAGAAATA T  
 GG  
 GAM1431 FLJ23519 3' TGCCAAGCTGGGGGCTGGGAG 49972 TT \_ CA  
 CT CAGTCTTTA TTTG GCA  
 || ||||| ||| |||  
 GA GTCGGGGGT GAAC CGT  
 GG C \_  
 GAM1431 FLJ23563 3' AAATAAAGAATGAAGG 67580 G  
 CTTTCA TCTTTATTT  
 ||||| |||||

GGAAGT AGAAATAAA

A

GAM1431 FLJ30525 5' TCTCTCAAATAGAGCTTGAAGG 58065 T C CAAA

CTTTCAG CTTTATTTG AG

||||| ||||||| ||

GGAAGTT GAGATAAAC TC

C \_ TCTT

GAM1431 FLJ30927 3' TGCTGGGAAAGGTTGGGAG 58414 TT GT TAT G

CT CA CTT TT CAGCA

|| || || || ||||

GA GT GAA AG GTCGT

GG TG \_ G

GAM1431 FLJ31153 3' TTTGCTGTAAATAAAACAAAGA 58133 CA C

G

CTTT GT TTTATTTGCAGCAAA

|||| || |||||||||||

GAGA CA AAATAAATGTCGTTT

AA \_

GAM1431 FLJ31300 3' TTTGCTGGCCCCTGAGGCTGGA 58288 TATTTG

G

TTTCAGTCTT CAGCAAA

||||||| |||||

GAGGTCGGAG GTCGTTT

TCCCCG

GAM1431 FLJ31528 3' TTTGGTGCATGTGGGTTGAGGG 58379 GT TTATT G

CTTTCA CT TGCA CAAA

||||| || ||| ||||

GGGAGT GG ACGT GTTT

TG TGT\_ G

GAM1431 FOXP1 3' TTGTTGTACAGTCTGGAGG 51076 T TTATT

CTTTCAG CT TGCAGCAA

||||| || |||||||

GGAGGTC GA ATGTTGTT

T C \_

GAM1431 GBA2 3' TGTGCCAGTAAATGGGGGTTGA 71026 GT A\_ AA

GGG

CTTTCA CTTTATTTGC GCA

||||| ||||||| |||

GGGAGT GGGGTAAATG CGT

TG AC GTT

GAM1431 GDF11 3' GCAGGTGGGAATTGAGGG 19441 CT

CTTTCAGT TTATTTGC

||||| |||||||

GGGAGTTA GGTGGACG

AG

GAM1431 GOLGA3 3' TTTGTTGCCCAGGCTGGAG 19723 TTATTT

TTTCAGTCT GCAGCAAA

||||||| |||||||

GAGGTCGGA CGTTGTTT

CC\_

GAM1431 GPT2 3' TTGGGGTAGATGCTGGGGG 55961 TT CTTT AG

CT CAGT ATTTGC CAA

|| ||| ||||| |||



			GG GTCG TAGATG GTT		
			GG ____ GG		
GAM1431	GTF2F2	3'	GAATAGGGGTTGGAGG 14679	GT	
			CTTTCA CTTTATTT		
			GGAGGT GGGATAAG		
			TG		
GAM1431	GTF2H3	3'	TTGTTGGGAAGACTGAAA 7710	TTAT G	
			TTTCAGTCT TT CAGCAA		
			AAAGTCAGA AG GTTGTT		
			____ G		
GAM1431	GW112	3'	TTTGCTGTGGATGAGAATGGA 21195	G T TG	
			TTCA TCTT ATT CAGCAAA		
			AGGT AGAG TAG GTCGTTT		
			A _ GT		
GAM1431	HEMK	3'	ATGGGCAGAGGCTGGAAG 32427	TATT AG AA	
			CTTTCAGTCTT TGC CA		
			GAAGGTCGGAG ACG GT		
			____ G_ AA		
GAM1431	HIC2	3'	TTTGTTGCAGGCGGCTTGAG 65272	TC TTTA	
			CTT AGTC TTTGCAGCAAA		
			GAG TCGG GGACGTTGTTT		
			GT C__		
GAM1431	HIC2	3'	TTTGTTTAATTGGAAGTGAAG 65273	C T C	
			CTTTCAGT TTTA TTG AGCAAA		
			GAAGGTCA AGGT AAT TTGTTT		
			_ T _		
GAM1431	HOMER-3	3'	GTCCTGGAAGGGACTGGGGG 16718	TT TA G CAAA	
			CT CAGTCTT TTT CAG		
			GG GTCAGGG AAA GTC		
			GG _ G CTGC		
GAM1431	HSMPP8	3'	TTTGCTGCCCTTGAAAGGGTTG 93487	TT GT ATTT__	
	GGAG		T CA CTTT GCAGCAAA		
			A GT GGAA CGTCGTTT		
			GG TG AGTTCC		
GAM1431	HSPC043	3'	TGTAAGTGAAAGCTGAAAG 67723	TC	
			CTTTCAG TTTATTTGCA		
			GAAAGTC AAGTGAATGT		
			GA		
GAM1431	HSPC052	5'	TTTGAAGCCGTGGAGGCAGAGG 26261	A TT AG	
	G		CTTTC GTCTTTAT GC CAAA		

GGGAG CGGAGGTG CG GTTT  
 A C\_ AA  
 GAM1431 HSPC189 3' TTGACTGGATGGAGGTGGGGAG 95280 TT AG TG \_  
 CT C TCTTTATT CAG CAA  
 || | ||||| ||| |||  
 GA G GGAGGTAG GTC GTT  
 GG GT \_ A  
 GAM1431 HSPC216 5' TTGCCGTAGGGGTTGAAA 33212 GT TT  
 TTTCA CTTTAT GCAG  
 |||| |||| |||  
 AAAGT GGGATG CGTT  
 TG C\_  
 GAM1431 HTATIP 3' TTGTAAAGTAGAAGTTGGGGG 21110 TT TC \_  
 CT CAG TTTATTT GCAG  
 || ||| ||||| |||  
 GG GTT AGATGAA TGTT  
 GG GA A  
 GAM1431 HTMP10 3' TTGAAAGTAAAGATGGGGG 52614 TT G G  
 CT CA TCTTTATTT CAG  
 || || ||||| |||  
 GG GT AGAAATGAA GTT  
 GG \_ A  
 GAM1431 ICT1 3' TTGGAATGAAGGCTGCAGG 7751 T G  
 CTT CAGTCTTTATTT CAG  
 ||| ||||| |||  
 GGA GTCGGAAGTAAG GTT  
 C \_  
 GAM1431 ING4 3' TTGTATTTAAGGACTGGGG 59706 TT TT  
 T CAGTCTTTA TGCAG  
 | ||||| ||||  
 G GTCAGGAAT ATGTT  
 GG TT  
 GAM1431 jdp2 3' TTTGCTGTGGGCACTGAGGC 55328 TA\_\_ TG  
 GTCTT TT CAGCAA  
 |||| || |||||  
 CGGAG GG GTCGTTT  
 TCAC GT  
 GAM1431 KCNS1 5' CAAGTGGAGGTGGGAG 9573 TT G  
 CT CA TCTTTATTTG  
 || || ||||| |||  
 GA GT GGAGGTGAAC  
 GG \_  
 GAM1431 KIAA0056 3' TTGCTGTGGAACACGAGAG 91556 A CTTTA TG  
 CTTTC GT TT CAGCAA  
 |||| || || |||||  
 GAGAG CA AG GTCGTT  
 \_ CA\_\_ GT  
 GAM1431 KIAA0057 3' TTCATGTAAAAAAGGGTTGGGG 24447 TT GT A GCAAA  
 G CT CA CTTT TTTGCA  
 || || ||| |||||

			GG GT GGAA AAATGT		
			GG TG A ACTTT		
GAM1431	KIAA0189	3'	TTGGCATAGATAGGGATGTGAG 28277	—	CA AAA
		AG	CTTTCA GTCTTTATTTG GC		
			GAGAGT TAGGGATAGAT CG		
			G A_ GTTT		
GAM1431	KIAA0194	3'	TTAATGGAGGGGAGGCTGAGGG 65989		A G GCAAA
			CTTTCAGTCTTT TTT CA		
			GGGAGTCGGAGG GGA GT		
			— G AATTT		
GAM1431	KIAA0212	3'	GTGGGTGAGACTGAGGG 27941		T TG
			CTTTCAGTCTT ATT C		
			GGGAGTCAGAG TGG G		
			— GT		
GAM1431	KIAA0212	3'	TTGTTAGAGGATTGAGA 27945		ATTT
			TTTCAGTCTTT GCAG		
			AGAGTTAGGAG TGTT		
			AT__		
GAM1431	KIAA0232	3'	GTAAAAAAGGATTGAAAG 72755		A
			CTTTCAGTCTTT TTTGC		
			GAAAGTTAGGAA AAATG		
			A		
GAM1431	KIAA0237	3'	GTGGGTAAGGGCAGGAAG 28535	A	TG
			CTTTC GTCTTTATT C		
			GAAGG CGGGAATGG G		
			A GT		
GAM1431	KIAA0247	3'	GCGAGTGAGGCTGGGAG 28403	TT	T
			CT CAGTCTT ATTTGC		
			GA GTCGGAG TGAGCG		
			GG —		
GAM1431	KIAA0256	3'	TAAATGAAAGGCTGAGGG 64424	—	
			CTTTCAGTCTT TATTTG		
			GGGAGTCGGAA GTAAAT		
			A		
GAM1431	KIAA0286	3'	CAAGAAGGATTGAAGG 68319		A
			CTTTCAGTCTTT TTTG		
			GGAAGTTAGGAA GAAC		
			—		
GAM1431	KIAA0408	3'	TTTGTTGCAAGTGGCAGAAAG 28144	A	TTT
			CTTTC GTC ATTTGCAGCAAA		

GAAAG CGG TGAACGTTGTTT  
 A \_\_\_\_  
 GAM1431 KIAA0410 3' TTGTTCTGAAGGCTGCAGAG 28783 \_ TTT  
 CTTT CAGTCTTTA GCAG  
 |||| ||||| ||||  
 GAGA GTCGGAAGT TGTT  
 C CT\_  
 GAM1431 KIAA0435 3' TATTTGCAGGTGGAGACGGGGG 28984 TT A CAAA  
 CT C GTCTTTATTTGCAG  
 || | ||||| |||||  
 GG G CAGAGGTGGACGTT  
 GG \_ TATT  
 GAM1431 KIAA0446 5' CAAGTGGGGATTGACAG 68855 T  
 CT TCAGTCTTTATTTG  
 || ||||| |||||  
 GA AGTTAGGGGTGAAC  
 C  
 GAM1431 KIAA0446 5' TTTGCTGGAGGAAGGGGAGGTT 68887 GT AT\_\_ G  
 GAGGG TCA CTTT TT CAGCAAA  
 ||| ||| || |||||  
 AGT GAGG GA GTCGTTT  
 TG GGAAG G  
 GAM1431 KIAA0450 3' GGGTGAAGAGTGAGGG 27645 G  
 CTTTCA TCTTTATTT  
 ||||| |||||  
 GGGAGT AGAAGTGGG  
 G  
 GAM1431 KIAA0459 3' TTTGTTGCCCAGGCTGGAG 61014 TTATTT  
 TTTCAGTCT GCAGCAAA  
 ||||| |||||  
 GAGGTCGGA CGTTGTTT  
 CC\_\_  
 GAM1431 KIAA0475 3' TTTGTTGTAAGTCAGGATTGGA 29506 T  
 G TTTCAGTCTT ATTTGCAGCAAA  
 ||||| |||||  
 GAGGTTAGGA TGAATGTTGTTT  
 C  
 GAM1431 KIAA0478 3' AAGTAGAGTCTGAAAG 29537 T  
 CTTTCAG CTTTATTT  
 ||||| |||||  
 GAAAGTC GAGATGAA  
 T  
 GAM1431 KIAA0513 3' TTTGCTCATGAAATAGAGGTGG 28385 TT G GC\_\_  
 GGG T CA TCTTTATTT AGCAAA  
 | || ||||| |||||  
 G GT GGAGATAAA TCGTTT  
 GG \_ GTAC  
 GAM1431 KIAA0515 3' TTCCTGCTGCTGAGGTAGGGAT 63818 TT \_ AA  
 TGGGGG CAGTCTTTATTT GCAGCA  
 ||||| |||||

			GTTAGGGATGGA CGTCGT		
			GG GT CCTTT		
GAM1431	KIAA0527	3'	TTGGGTAAAATAAAGCCTGAAG 95811	T	_ AG A
	G		CTTTCAG CTTTATTT GC CAA		
			GGAAGTC GAAATAAA TG GTT		
			C A G_		
GAM1431	KIAA0599	3'	TTAGGGAGATGGAGACATGGAG 77194	_	GCAGCAAA
	G		CTTTCAGTCTTTATTT		
			GGAGGT CAGAGGTAGA		
			A GGGATT		
GAM1431	KIAA0712	3'	TTGCTGCATAATTGAGAG 28200	CTTTATT	
			CTTTCAGT TGCAGCAA		
			GAGAGTTA ACGTCGTT		
			AT_____		
GAM1431	KIAA0748	3'	AAACTGGGAAGAGGCTGGAAG 28927	TA G CAAA	
			CTTTCAGTCTT TTT CAG		
			GAAGGTCGGAG AAG GTC		
			_ G AAAA		
GAM1431	KIAA0766	3'	TTGAGAGAAAGACTGGAAG 29008	A G	
			CTTTCAGTCTTT TTT CAG		
			GAAGGTCAGAAA AGA GTT		
			G _		
GAM1431	KIAA0769	3'	TTTCTATGAGAAAGGACTGAAG 29099	A GC CAAA	
	G		CTTTCAGTCTTT TTT AG		
			GGAAGTCAGGAA GAG TC		
			A TA TTT		
GAM1431	KIAA0773	3'	TTTGGAGTGAGAAGGTTGAGAG 28064	GT AT TG AG	
			CTTTCAGTCTTT TTT C CAAA		
			GAGAGT GAAG A G GTTT		
			TG _ GT AG		
GAM1431	KIAA0790	3'	CTGGTAGAGGCTGGGAG 68694	TT TTG	
			CT CAGTCTTTAT CAG		
			GA GTCGGAGATG GTC		
			GG _		
GAM1431	KIAA0795	3'	AGTGCCAGATAAGGACTGGAA 46587	CA AA	
			TTTCAGTCTTTATTTG GCA		
			AAGGTCAGGAATAGAC CGT		
			_ GAA		
GAM1431	KIAA0830	3'	TTGAGGTAGAGGTTGGGG 69706	TT GT G	
			T CA CTTTATTT CAG		

G GT GAGATGGA GTT  
 GG TG \_  
 GAM1431 KIAA0831 3' TTTGTATTTTGGTAGAGACGGG 29985 TT A TGCA\_  
 GG CT C GTCTTTATT GCAAA  
 || | ||||| ||||  
 GG G CAGAGATGG TGTTT  
 GG \_ TTTTA  
 GAM1431 KIAA0864 3' GCAGTGGGGGCTGGGAG 63250 TT T  
 CT CAGTCTTTATT GC  
 || ||||| ||  
 GA GTCGGGGGTGA CG  
 GG \_  
 GAM1431 KIAA0937 3' TAGATGGGAACTGGAGG 91589 CT  
 CTTTCAGT TTATTTG  
 ||||| |||||  
 GGAGGTCA GGTAGAT  
 AG  
 GAM1431 KIAA0939 3' TCAGGATGAGTGAAGGCTGGAG 62019 CAGCAAA  
 TTTTCAGTCTTTATTTG  
 ||||| |||||  
 GAGGTCGGAAGTGAGT  
 AGGACTT  
 GAM1431 KIAA0945 3' TGCTGGGAGAGGGTTGGGGG 30217 TT GT AT G  
 CT CA CTTT TT CAGCA  
 || || ||| || ||||  
 GG GT GGAG AG GTCGT  
 GG TG \_ G  
 GAM1431 KIAA0945 3' TGGGTGAGGCCTGGAGG 30219 T TT  
 CTTTCAG CTTTAT G  
 ||||| ||||| |  
 GGAGGTC GGAGTG T  
 C GG  
 GAM1431 KIAA0971 3' TTTGTTGCCAGAAAAGGCTGGA 30005 A T  
 TTCAGTCTTT TT GCAGCAAA  
 ||||| || |||||  
 AGGTCGGAAA GA CGTTGTTT  
 A C  
 GAM1431 KIAA0980 3' TGGAGGTGGGGGCTGGGGG 47206 TT G  
 CT CAGTCTTTATTT CA  
 || ||||| ||  
 GG GTCGGGGGTGGA GT  
 GG G  
 GAM1431 KIAA0982 3' TTGCTGGGAAGACTGTGAG 25853 T TTAT G  
 CTT CAGTCT TT CAGCAA  
 || ||||| || |||||  
 GAG GTCAGA AG GTCGTT  
 T \_ G  
 GAM1431 KIAA1017 3' TTGGAAGGTAAAGACGGGAG 23306 TT A G\_  
 CT C GTCTTTATTT CAG  
 || | ||||| |||

			GA G CAGAAATGGA GTT		
			GG _ AG		
GAM1431	KIAA1018	3'	TTGCTGTAAACTGGAGA 30356	_	
			TCTTTA TTTGCAGCAA		
			AGAGGT AAATGTCGTT		
			C		
GAM1431	KIAA1032	3'	AGGTGAAGAATGAGAG 66149	G	
			CTTTCA TCTTTATTT		
			GAGAGT AGAAGTGGA		
			A		
GAM1431	KIAA1055	3'	TTTGTGTGAACACACTGAGA 66072	CTTTA TG	
			TTTCAGT TT CAGCAAA		
			AGAGTCA AA GTTGTTT		
			CAC__ GT		
GAM1431	KIAA1058	3'	TTGAAGATGAAGATGGAAAG 82257	A G	
			CTTTC GTCTTTATTT CAG		
			GAAAG TAGAAGTAGA GTT		
			G A		
GAM1431	KIAA1079	3'	TTTGCTGACATGAGATTGGGAG 29884	TT TATTTG	
			CT CAGTCTT CAGCAAA		
			GA GTTAGAG GTCGTTT		
			GG TACA__		
GAM1431	KIAA1102	3'	TTGTTGTTAAGACTGGGG 69018	TT TATTT	
			T CAGTCTT GCAGCAA		
			G GTCAGAA TGTTGTT		
			GG T__		
GAM1431	KIAA1128	3'	TTTGCTGCAGCAATTTGAGAG 68491	TCTTTAT	
			CTTTCAG TTGCAGCAAA		
			GAGAGTT GACGTCGTTT		
			TAAC__		
GAM1431	KIAA1145	3'	CACCTGGATGAAGATTGAGAG 65620	TG CAAA	
			CTTTCAGTCTTTATT CAG		
			GAGAGTTAGAAGTAG GTC		
			_ CACT		
GAM1431	KIAA1155	3'	CTGGGGAAAGGCTGGGAG 62232	TT TA G	
			CT CAGTCTT TTT CAG		
			GA GTCGGAA AGG GTC		
			GG _ G		
GAM1431	KIAA1165	3'	TTTGAGTGTGAACTGGGGATTG 67411	_ TG G_	
	GAAG		TTTCAGTCTTTA TT CA CAAA		

AAGGTTAGGGGT AA GT GTTT  
 C GT GA  
 GAM1431 KIAA1193 3' CGGGTGGGGGCTGGGG 67638 TT  
 T CAGTCTTTATTTG  
 | |||||  
 G GTCGGGGGTGGGC  
 GG  
 GAM1431 KIAA1199 3' TTACAGGAATGAAGGCTGGGGG 72522 TT GCAGCAAA  
 CT CAGTCTTTATTT  
 || |||||  
 GG GTCGGAAGTAAG  
 GG GACATT  
 GAM1431 KIAA1277 3' TGTGGGTGGGGACTAGGGG 64462 TC TG  
 CTT AGTCTTTATT CA  
 ||| ||||| ||  
 GGG TCAGGGGTGG GT  
 GA GT  
 GAM1431 KIAA1280 5' TTTGTTGCCCAGGCTGGAG 69736 TTATTT  
 TTTCAGTCT GCAGCAAA  
 ||||| |||||  
 GAGGTCGGA CGTTGTTT  
 CC\_\_\_\_  
 GAM1431 KIAA1287 3' CAGATGAGGATTTAAAG 78325 C  
 CTTT AGTCTTTATTTG  
 ||| |||||  
 GAAA TTAGGAGTAGAC  
 T  
 GAM1431 KIAA1320 5' CTGAAGAAAGGCTGAAAG 69302 ATTTG  
 CTTTCAGTCTTT CAG  
 ||||| |||  
 GAAAGTCGGA GTC  
 GAA\_\_\_\_  
 GAM1431 KIAA1336 3' TTGAAGGGAGTAGGGAGTGGGG 72327 TT G GCAG A  
 G CT CA TCTTTATTT CAA  
 || || ||||| |||  
 GG GT AGGGATGAG GTT  
 GG G GGAA  
 GAM1431 KIAA1416 3' TAAATAAAGAGTGAGAG 86462 G  
 CTTTCA TCTTTATTTG  
 |||| |||||  
 GAGAGT AGAAATAAAT  
 G  
 GAM1431 KIAA1432 5' TTGCAGATGGAGGTTTAGAG 66755 C GT  
 CTTT A CTTTATTTGCAG  
 ||| | |||||  
 GAGA T GAGGTAGACGTT  
 T TG  
 GAM1431 KIAA1462 3' CAAATAAGGGCTGAGG 91383  
 TTTCAGTCTTTATTTG  
 |||||



GGAGTCGGGAATAAAC

GAM1431 KIAA1483 3' AAGTAAGGACTGAAGG 69871  
CTTTCAGTCTTTATTT  
|||||||  
GGAAGTCAGGAATGAA

GAM1431 KIAA1484 3' TAAGTGAGACTGAAGG 69980 T  
CTTTCAGTCTT ATTTG  
||||||| ||||  
GGAAGTCAGAG TGAAT

GAM1431 KIAA1500 3' GCAGATGGAGATGAGAG 64120 G  
CTTTCA TCTTTATTTGC  
||||| |||||  
GAGAGT AGAGGTAGACG

GAM1431 KIAA1535 3' TTCTCCAGGTAGGGGCAGGAG 79415 A CAGCAAA  
G CTTTC GTCTTTATTTG  
||||| |||||  
GGAGG CGGGGATGGAC  
A CCTCTT

GAM1431 KIAA1602 3' CTGGAAGGGACTGGGGG 64629 TT TTA G  
CT CAGTCT TTT CAG  
|| ||||| ||| |||  
GG GTCAGG GAA GTC  
GG \_ G

GAM1431 KIAA1602 3' TTGTGGGAGTCAGGGCTGAGGG 64637 T G G  
CTTTCAGTCTT ATTT CA CAA  
||||||| |||| || |||  
GGGAGTCGGGA TGAG GT GTT  
C G \_

GAM1431 KIAA1679 3' TTGGAGGGTGGAGACTGTGGG 70158 TT G\_  
CT CAGTCTTTATTT CAG  
|| ||||| ||| |||  
GG GTCAGAGGTGGG GTT  
GT AG

GAM1431 KIAA1737 5' TTTGCTGTGAGGGGCGTGGGAG 67367 TT \_ TTA TG  
CT CA GTCT TT CAGCAAA  
|| || ||| || |||||  
GA GT CGGG GA GTCGTTT  
GG G \_ GT

GAM1431 KIAA1765 3' AACACGTGAAAGAGGCTGGAAG 70606 A TG AGCAAA  
CTTTCAGTCTTT TT C  
||||||| || |  
GAAGGTCGGAGA AA G  
\_ GT CACAAG

GAM1431 KIAA1786 3' TGGGAGGAGACTGGGAG 66042 TT TA G  
CT CAGTCTT TTT CA  
|| ||||| ||| ||

		GA GTCAGAG GAG GT		
		GG _ G		
GAM1431 KIAA1786	3'	TTTGTCTTTACATGGAGGTTG 66046	GT	T CA__
		AAGG TTTCA CTTTAT TG GCAAA		
		GAAGT GAGGTA AC TGTTT		
		TG C TTTC		
GAM1431 KIAA1853	3'	TTGCAACTTAGGTGGGGGTTGG 69399	GT	CA__ A
		AG TTTCA CTTTATTTG GCAA		
		GAGGT GGGGTGGAT CGTT		
		TG TCAA		
GAM1431 KIAA1870	3'	TAGAAGTGGGTGGGGGTAGGAG 49662	AG	TG AGCAAA
		G CTTTC TCTTTATT C		
		GGAGG GGGGGTGG G		
		AT GT AAGAT		
GAM1431 KIAA1941	3'	TGGAGCAGGTGGAGGCTGAAGG 74847		AGCAAA
		CTTTCAGTCTTTATTTGC		
		GGAAGTCGGAGGTGGACG		
		AGGT		
GAM1431 KIAA1954	3'	TTGTACAGATGAAGACTGAAAG 77723		CA
		CTTTCAGTCTTTATTTG GCAA		
		GAAAGTCAGAAGTAGAC TGTT		
		A_		
GAM1431 KIF1C	3'	GTGGGAGAGGACTGAGAG 61227	A	TG
		CTTTCAGTCTTT TT C		
		GAGAGTCAGGAG GG G		
		A GT		
GAM1431 KRT6IRS	3'	TTTAAGAAAAGGAGGACTGAAG 53090	A	GCAGCAAA
		G CTTTCAGTCTTT TTT		
		GGAAGTCAGGAG AAA		
		G AGAATT		
GAM1431 LAMP3	3'	CTGGAAGGAGACTGAGGG 59490	TA	G
		CTTTCAGTCTT TTT CAG		
		GGGAGTCAGAG GAA GTC		
		_ G		
GAM1431 LGI2	3'	GCAATGAAGATTGAGA 36399	T	
		TTTCAGTCTTTATT GC		
		AGAGTTAGAAGTAA CG		
		-		
GAM1431 LGI3	3'	CGGGTGGGGGCTGGTGG 57742	T	
		CT TCAGTCTTTATTTG		

			GG GGTCTGGGGGTGGGC			
			T			
GAM1431	LIP8	5'	TTGGGGACTGAGGACTGGAAG 88152		_ G	
			CTTTCAGTCTTTA TTT CAG			
			GAAGGTCAGGAGT AGG GTT			
			C G			
GAM1431	LSR68	5'	TGAATGCAGATGGATGCTGGGA 37936	TT C	GCAAA	
	G		CT CAGT TTTATTTGCA			
			GA GTCG AGGTAGACGT			
			GG T AAGT			
GAM1431	MADHIP	3'	TTGCACTTTAAACTGGAAG 23641	C TT_		
			CTTTCAGT TTTA TGCAG			
			GAAGGTCA AAAT ACGTT			
			_ TTC			
GAM1431	MADHIP	3'	TTGCACTTTAAACTGGAAG 16625	C TT_		
			CTTTCAGT TTTA TGCAG			
			GAAGGTCA AAAT ACGTT			
			_ TTC			
GAM1431	MAP3K3	3'	TTGCTGCATGGCAGGGGG 10001	TT A TTTATT		
			CT C GTC TGCAGCAA			
			GG G CGG ACGTCGTT			
			GG A T_____			
GAM1431	MAPK6	3'	TTTGACACAAAAATAAAGACT 10838	C	GCA_____	
	AGAG		TT AGTCTTTATTT GCAAA			
			GA TCAGAAATAAA CGTTT			
			_ AACACA			
GAM1431	MGC10848	3'	TAGGGGTGGGTAGGGGCGGGAA 47545	A	TG AGCAAA	
	G		CTTTC GTCTTTATT C			
			GAAGG CGGGGATGG G			
			G GT GGGAT			
GAM1431	MGC11335	3'	CAGGTGGGGACTGGGG 48018	TT		
			T CAGTCTTTATTTG			
			G GTCAGGGGTGGAC			
			GG			
GAM1431	MGC13251	3'	TTTGACACCGTGGATGGAGCT 51150	T	TG A_____	
	GGAGG		CAG CTTTATT C GCAAA			
			GTC GAGGTAG G CGTTT			
			_ GT CCACA			
GAM1431	MGC14376	3'	GCAAATAGAGCTGGAAG 51848	T		
			CTTTCAG CTTTATTTGC			

GAAGGTC GAGATAAACG

GAM1431 MGC15606 5' GCAAATGAAACTGAAAG 58876 C  
CTTTCAGT TTTATTTGC  
||||||| |||||||  
GAAAGTCA AAGTAAACG

GAM1431 MGC17303 3' TTGTGGGGAGAGGCTGGGGG 57503 TT A TG  
CT CAGTCTTT TT CAG  
|| ||||||| || |||  
GG GTCGGAGA GG GTT  
GG G GT

GAM1431 MGC20253 5' GTAAGAGAAGACTGGAAG 58061 A  
CTTTCAGTCTTT TTTGC  
||||||||| |||||  
GAAGGTCAGAAG GAATG  
A

GAM1431 MGC2217 3' TGAACAAGTAAAGACTGAA 44179 CAG  
TTCAGTCTTTATTTG CA  
||||||||| ||  
AAGTCAGAAATGAAC GT  
AA\_

GAM1431 MGC2721 3' TTTGCCTTGGGTGGAGCTGGGG 51225 TT T TT CA  
G CT CAG CTTTAT G GCAA  
|| || ||||| | |||||  
GG GTC GAGGTG T CGTTT  
GG \_ GG TC

GAM1431 MGC29898 3' TTTGTTGCCAGACTGGAG 58931 TTATTT  
TTTCAGTCT GCAGCAA  
||||||| |||||||  
GAGGTCAGA CGTTGTTT  
CC\_

GAM1431 MGC35558 3' CAGAGGAGGGCTGGAGG 58777 A  
CTTTCAGTCTTT TTTG  
||||||||| |||||  
GGAGGTCGGGAG AGAC  
G

GAM1431 MGC35558 3' TGGCTGTGCGTGGGGGCTGAGG 58788 T AAA  
G CTTTCAGTCTTTAT TGCAGC  
||||||||| |||||  
GGGAGTCGGGGGTG GTGTCTG  
C GT

GAM1431 MGC4251 3' AGATGGAGATTGGAAG 50455  
CTTTCAGTCTTTATTT  
|||||||||  
GAAGGTTAGAGGTAGA

GAM1431 MGC4643 3' TTTGCTATAGATGAAGGTAGAG 51161 AG C  
GG CTTTC TCTTTATTTG AGCAA  
|||| ||||||| |||||

GGGAG GGAAGTAGAT TCGTTT  
AT A  
GAM1431 MGC5395 5' TCCCGACGAGAGAGACTGAGGG 43934 A CAGCAAA  
CTTTCAGTCTTT TTTG  
||||||| |||  
GGGAGTCAGAGA GAGC  
\_ AGCCCTT  
GAM1431 MLLT10 5' TTAGCGGCCGGGTGGAGGTGGG 16171 TT AG \_ A AAA  
GAG CT C TCTTTATTTG C GC  
|| | ||||| | ||  
GA G GGAGGTGGGC G CG  
GG GT C G ATT  
GAM1431 MR 5' GTGGATGGAGTTGGAGG 48325 T TG  
CTTTCAG CTTTATT C  
||||| ||||| |  
GGAGGTT GAGGTAG G  
\_ GT  
GAM1431 MRPL13 5' TTGCTGCCGTGGAGAAGACTGG 26018 ATTT\_ A  
AGG TTTTCAGTCTTT GCAGCAA  
||||||| |||||  
GAGGTCAGAAG CGTCGTT  
AGGTGC  
GAM1431 MRPL15 3' CTGGAATAGGGGCTGAAGG 26347 G  
CTTTCAGTCTTTATTT CAG  
||||||| ||||| |||  
GGAAGTCGGGGATAAG GTC  
\_ \_  
GAM1431 MSTP031 3' TAGGTACAGGATTGGGAG 49344 TT \_  
CT CAGTCTT TATTTG  
|| ||||| |||||  
GA GTTAGGA ATGGAT  
GG C  
GAM1431 MT-ACT48 3' GCCGATGGGGCTGAGGG 24690 T CA  
CTTTCAGTCTT ATTTG GC  
||||||| ||||| ||  
GGGAGTCGGGG TAGGC CG  
\_ \_  
GAM1431 MYT1 3' TTTGTCTGTCTGAGGCTGGGAG 15783 TT TATTT \_  
CT CAGTCTT GCAG CAAA  
|| ||||| ||||| |||||  
GA GTCGGAG TGTC GTTT  
GG C\_ T  
GAM1431 NASP 3' GTGAAGGAGGCTGAAGG 67970 A TG  
CTTTCAGTCTTT TT C  
||||||| || |  
GGAAGTCGGAGG AA G  
\_ GT  
GAM1431 NIBAN 3' GCCTGGGTAAGACTGAAAG 42002 T TT CA  
CTTTCAGTCTT AT G GC  
||||||| || | ||

GAAAGTCAGAA TG T CG  
 \_ GG C\_  
 GAM1431 NXPH3 3' GGATGGATGGCTGAGAG 65765 \_  
 CTTTCAGTC TTTATTT  
 ||||| |||||  
 GAGAGTCGG AGGTAGG  
 T  
 GAM1431 OBSCN 3' GTGGGTGGAGGTGGAGG 70656 G TG  
 CTTTCA TCTTTATT C  
 ||||| ||||| |  
 GGAGGT GGAGGTGG G  
 \_ GT  
 GAM1431 OPRL1 3' CAGGTGGGGGCTGGCAG 6194 T  
 CT TCAGTCTTTATTTG  
 || ||||| |||||  
 GA GGTCTGGGGGTGGAC  
 C  
 GAM1431 OSBPL10 3' CCTGCTGGATGGGGGTGGCAG 35047 T GT TG AA  
 CT TCA CTTTATT CAGCA  
 || ||| ||||| |||||  
 GA GGT GGGGTAG GTCGT  
 C TG \_ CCT  
 GAM1431 OSBPL11 3' TTTGCTGCGAAATGCACTGAAA 42895 CTTTA  
 TTTCAGT TTTGCAGCAAA  
 ||||| ||||| |||||  
 AAAGTCA AAGCGTCGTTT  
 CGTA\_  
 GAM1431 OSBPL2 3' TTTGTAGCTTTGGAAGCTGGAA 57876 T ATTT A  
 G CTTTCAG CTTT GC GCAAA  
 ||||| ||| || |||||  
 GAAGGTC GAAG CG TGTTT  
 \_ GTTT A  
 GAM1431 OSBPL2 3' TTTGTAGCTTTGGAAGCTGGAA 29225 T ATTT A  
 G CTTTCAG CTTT GC GCAAA  
 ||||| ||| || |||||  
 GAAGGTC GAAG CG TGTTT  
 \_ GTTT A  
 GAM1431 OSMR 3' AACTCTGTGGGTGGGGGCGGGG 14342 TT A TG CAAA  
 G CT C GTCTTTATT CAG  
 || | ||||| |||  
 GG G CGGGGGTGG GTC  
 GG \_ GT TCAAT  
 GAM1431 P101-PI3K 3' TGCAATGAGCAGGGGCTGGGAG 26680 TT AT\_\_  
 CT CAGTCTTT TTGCA  
 || ||||| |||  
 GA GTCGGGGA AACGT  
 GG CGAGT  
 GAM1431 p25 3' TGCCCCAGAGGGGGCTGGGGG 22857 TT A CA  
 CT CAGTCTTT TTTG GCA  
 || ||||| ||| |||

GG GTCGGGGG AGAC CGT  
GG \_ CC  
GAM1431 PADI1 3' TTGCAGAGATAGGGCTGGGGG 62001 TT TA\_  
CT CAGTCTT TTTGCAG  
|| ||||| |||||  
GG GTCGGGA AGACGTT  
GG TAG  
GAM1431 PCSK7 3' GGGTAGAGGCTGGGAG 16336 TT  
CT CAGTCTTTATTT  
|| |||||  
GA GTCGGAGATGGG  
GG  
GAM1431 PDE11A 3' TTTGATTAAAGTAAGGGTGGAA 33779 G GCAG  
G CTTTCA TCTTTATTT CAAA  
||||| ||||| |||  
GAAGGT GGAATGAA GTTT  
\_ ATTA  
GAM1431 PDZD2 5' TTTGCTGTGGATGAGAGTAC 80883 \_ \_ TG  
GT CTTT ATT CAGCAA  
|| ||| ||| |||||  
CA GAGA TAG GTCGTTT  
T G GT  
GAM1431 PEX11A 3' TTTGCTGAATGAATAAAAATTG 13890 C G\_  
AAAG TTTCAGT TTTATTT CAGCAA  
||||| ||||| |||||  
AAAGTTA AAATAAG GTCGTTT  
A TAA  
GAM1431 PHRET1 3' TGGGCTGGGGTGGAGGCTGGGA 41065 TT G AAA  
T CAGTCTTTATTT CAGC  
| ||||| |||  
A GTCGGAGGTGGG GTCG  
GG \_ GGTT  
GAM1431 PIPPIN 3' CTGTGAGTAAACTGGGGG 79695 TT C TG  
CT CAGT TTTATT CAG  
|| ||| ||||| |||  
GG GTCA AAATGA GTC  
GG \_ GT  
GAM1431 PLA2G12 3' TGACAGATGAAGATGGAAG 48027 G \_  
CTTTCA TCTTTATTTG CA  
||||| ||||| ||  
GAAGGT AGAAGTAGAC GT  
\_ A  
GAM1431 PP591 5' CTGTGGCTGGAGGCTGGGAG 47368 TT T TG  
CT CAGTCTTTA T CAG  
|| ||||| | |||  
GA GTCGGAGGT G GTC  
GG C GT  
GAM1431 PPAP2A 3' CAAGTAGAGGCTGGCAG 67833 T  
CT TCAGTCTTTATTTG  
|| ||||| |||||

GA GGTCTGGAGATGAAC  
C

GAM1431 PPP1R13B 3' TTGGGGTTGGGGCTGGGGG 31013 TT TAT G  
CT CAGTCTT TT CAG  
|| ||||| ||||  
GG GTCGGGG GG GTT  
GG TT\_ G

GAM1431 PPP1R14C 3' TTGGTGTGAAGGTGGGGG 48204 TT G ATTT G  
CT CA TCTTT GCA CAA  
|| ||||| ||||  
GG GT GGAAG TGT GTT  
GG \_ \_ \_ G

GAM1431 PRDM11 3' TCTAGAAGGATGGAGAGTGAGG 39583 G GCAGCAAA  
G CTTTCA TCTTTATTT  
||||| |||||  
GGGAGT AGAGGTAGG  
G AAGATCTT

GAM1431 PREI3 3' GATAAAGCACTGGAGG 66323 \_  
CTTTCAGT CTTTATT  
||||| |||||  
GGAGGTCA GAAATAG  
C

GAM1431 PRO0461 5' TGCCTGAATCGGGGCTGGAGG 48377 TT GCA  
CTTTCAGTCT ATTT GCA  
||||||| |||||  
GGAGGTCGGG TAAG CGT  
GC TC\_

GAM1431 PRO0628 5' TGTAGAGGGGGTTGGAGG 26209 GT A  
CTTTCA CTTT TTTGCA  
||||| ||||| |||||  
GGAGGT GGGG AGATGT  
TG \_

GAM1431 PRO1483 3' CAAATGGAGAATGGAGG 37718 G  
CTTTCA TCTTTATTTG  
||||| |||||  
GGAGGT AGAGGTAAAC  
A

GAM1431 PRO1598 5' GAAAAGTAAATGGGGGTTGAGG 37536 GT AGCAAA  
G CTTTCA CTTTATTTGC  
||||| |||||  
GGGAGT GGGGTAAATG  
TG AAAAGT

GAM1431 PRO2266 3' GGGTGAAGAATGAAAG 37582 G  
CTTTCA TCTTTATTT  
||||| |||||  
GAAAGT AGAAGTGGG  
A

GAM1431 PRO2266 3' TAGATGAGACTGGGAG 37583 TT T  
CT CAGTCTT ATTTG  
|| ||||| |||||



			GA GTCAGAG TAGAT		
			GG _		
GAM1431	PRO2289	5'	TTTGCAACAACGTGGATGGAAC 37797	C	TG A_____
			TGAAGG AGT TTTATT C GCAAA		
			TCA AGGTAG G CGTTT		
			_ GT CAACAA		
GAM1431	PTBP2	3'	AGATGAAGATTGGGGG 41032 TT		
			CT CAGTCTTTATTT		
			GG GTTAGAAGTAGA		
			GG		
GAM1431	QSCN6	3'	TTGGCTTCAGGGTGGGGTTTGG 11044	T	GC_ AAA
			AAG CTTTCAG CTTTATTT AGC		
			GAAGGTT GGGGTGGG TCG		
			T ACT GTTT		
GAM1431	RAB25	5'	TTTGAGAGCTGAGGGTTGAGGG 72882	GT	TTT AG_
			CTTTCA CTTTA GC CAAA		
			GGGAGT GGAGT CG GTTT		
			TG _ AGA		
GAM1431	RBAK	3'	GCAAAATGATGGATTGAAAG 40975	_	
			CTTTCAGTCT TTATTTGC		
			GAAAGTTAGG AGTAAACG		
			T		
GAM1431	RBBP4	3'	TAAGTAAAGGCTAGAG 18826 C		
			CTTT AGTCTTTATTTG		
			GAGA TCGGAAATGAAT		
			_		
GAM1431	RGS10	3'	TTTGTTATTTGTAAGGACTGAA 11333		TTGC
			A TTTCAGTCTTTAT AGCAAA		
			AAAGTCAGGAATG TTGTTT		
			TTTA		
GAM1431	RHOBTB2	3'	TTTGCCCATCTGGAGACTGCAG 60946	T	TT CA
			G CTT CAGTCTTTA TG GCAAA		
			GGA GTCAGAGGT AC CGTTT		
			C CT C_		
GAM1431	RNF20	3'	TCTAATGAAATAAAGATTGAAG 38968		G GCAAA
			TTTCAGTCTTTATTT CA		
			GAAGTTAGAAATAAA GT		
			_ AATCTT		
GAM1431	RNF34	3'	TTTGACTACTAAGTGGGGACAG 47096	A	C_ _
			AAAG TTTC GTCTTTATTTG AG CAAA		

			AAAG CAGGGGTGAAT TC GTTT		
			A CA A		
GAM1431	RNPS1	3'	TTGTTGTGTAGAGTGGAAG 22009	G	TTATTT
			CTTTCA TCT GCAGCAA		
			GAAGGT AGA TGTTGTT		
			G TG_____		
GAM1431	RNPS1	3'	TTGTTGTGTAGAGTGGAAG 54581	G	TTATTT
			CTTTCA TCT GCAGCAA		
			GAAGGT AGA TGTTGTT		
			G TG_____		
GAM1431	RTP801	3'	TTGGGGTGGAGACTAGAG 38800	C	G
			CTTT AGTCTTTATTT CAG		
			GAGA TCAGAGGTGGG GTT		
			— —		
GAM1431	SART3	3'	TTGTATCTTAAAGACTGAGG 28173		TT_
			TTTCAGTCTTTA TGCAG		
			GGAGTCAGAAAT ATGTT		
			TCT		
GAM1431	SDF1	3'	TTGAAAAAATAGAGCCTGAGGG 90865	T	GCAG
			CTTTCAG CTTTATTT CAA		
			GGGAGTC GAGATAAA GTT		
			C AAA_		
GAM1431	SDS3	3'	TGAAGTAAATGGGGTTGGGGG 69235	TT T	AG
			CT CAG CTTTATTTGC CA		
			GG GTT GGGGTAAATG GT		
			GG _ AA		
GAM1431	SEC14L2	3'	GCAGACTAGGGGCTGGGGG 24873	TT	_
			CT CAGTCTTTA TTTGC		
			GG GTCGGGGAT AGACG		
			GG C		
GAM1431	SEC6	3'	TTTGTTGCAGTGTTGAAAG 71597	GT	TTTAT
			CTTTCA C TTGCAGCAAA		
			GAAAGT G GACGTTGTTT		
			TG T_____		
GAM1431	SIRPB1	3'	CAGATGAGGTTGGAAG 20245	T	
			CTTTCAG CTTTATTTG		
			GAAGGTT GGAGTAGAC		
			—		
GAM1431	SLAM	3'	AAAGAGTGAATAGAGGCCGAAG 11707	A	TG AGCAAA
	G		CTTTC GTCTTTATT C		

			GGAAG CGGAGATAA G		
			C GT AGAAAT		
GAM1431	SLC12A5	3'	GCTGCAATAAAGGTTGGGAG 40383	TT GT	T
			CT CA CTTTATT GCAGC		
			GA GT GAAATAA CGTCG		
			GG TG _		
GAM1431	SLC26A7	3'	TTTGCTGTGAATATTGGAA 53420	CTTT TG	
			TTTCAGT ATT CAGCAAA		
			AAGGTTA TAA GTCGTTT		
			_ GT		
GAM1431	SLC6A14	3'	TTGGTGGGGGCTGGGGG 23362	TT	ATTTG G
			CT CAGTCTTT CA CAA		
			GG GTCGGGGG GT GTT		
			GG _ G		
GAM1431	SRPUL	3'	TAGAAGCTAGGTAGGGACTGAG 27100	_	AGCAAA
	G		TTTCAGTCTTTATTT GC		
			GGAGTCAGGGATGGA CG		
			T AAGAT		
GAM1431	SSH1	3'	TTTGCTGCGTCAGGCTGGG 38610	TTATT	
			TTTCAGTCT TGCAGCAAA		
			GGGTCGGA GCGTCGTTT		
			CT_		
GAM1431	ST13	3'	AGGACCTGGGTAGGGATTGGAA 14114	TT	CAGCAAA
	G		CTTTCAGTCTTTAT G		
			GAAGGTTAGGGATG T		
			GG CCAGGAT		
GAM1431	STAB1	3'	TGGGGCAGGAGGGGCTGAGGG 65432	A	AG
			CTTTCAGTCTTT TTTGC CA		
			GGGAGTCGGGGA GGACG GT		
			_ GG		
GAM1431	STX3A	3'	CTGGATGAATACTGGGAG 14804	TT C	TG
			CT CAGT TTTATT CAG		
			GA GTCA AAGTAG GTC		
			GG T _		
GAM1431	SV2B	3'	TCAAACAACATGGGGACTGAGG 29300	_	CAGCAAA
	G		CTTTCAGTCTTTAT TTG		
			GGGAGTCAGGGGTA AAC		
			C AAAT		
GAM1431	SYT13	3'	TTTGTTGCCAGGCTGGAG 93463	TTATTT	
			TTTCAGTCT GCAGCAAA		

			GAGGTCGGA CGTTGTTT		
			CC_____		
GAM1431	TANK	3'	TTTCAAGTAAAATAAAGGCTGA 56013		_ AGCAAA
	GG		TTTCAGTCTTTATTT GC		
			GGAGTCGGAAATAAA TG		
			A AACTTT		
GAM1431	TEX27	3'	TCCAGGTGGGTGAGGGCAGGAG 41665	A	TG AGCAAA
	G		CTTTC GTCTTTATT C		
			GGAGG CGGGAGTGG G		
			A GT GACCT		
GAM1431	TIX1	3'	TAGTAAGGGTGAAGGCTGGAGG 61749		GCA AAA
			CTTTCAGTCTTTATTT GC		
			GGAGGTCGGAAGTGGG TG		
			AA_ ATT		
GAM1431	TM4SF11	3'	TTAATAAAAATAAAGATGAGAG 32038	G	GCAGCAAA
			CTTTCA TCCTTTATTT		
			GAGAGT AGAAATAAA		
			_ AATAATTT		
GAM1431	TOR1B	3'	AAATCGGGGCTGGAGG 27193	TT	
			CTTTCAGTCT ATTT		
			GGAGGTCGGG TAAA		
			GC		
GAM1431	USP22	3'	TTTGTTGCCCAGGCTGGAG 68035	TTATTT	
			TTTCAGTCT GCAGCAAA		
			GAGGTCGGA CGTTGTTT		
			CC_____		
GAM1431	UXS1	5'	TTGTTGTAAATGGAAGG 46892	_	
			TCTTT ATTTGCAGCAA		
			GGAAG TAAATGTTGTT		
			G		
GAM1431	WIRE	5'	CAAATAAAGACGGAGAG 78299	A	
			CTTTC GTCTTTATTTG		
			GAGAG CAGAAATAAAC		
			G		
GAM1431	XLKD1	3'	TTCCAACAAGAAGGGACTGAGA 21951	A	CAGCAAA
	G		CTTTCAGTCTTT TTTG		
			GAGAGTCAGGGA GAAC		
			A AACCTTT		
GAM1431	XPO5	3'	TTGCTGCTGGGCTGGCAG 91239	T	TTATTT
			CT TCAGTCT GCAGCAA		

			GA GGTCGGG	CGTCGTT		
			C	T_____		
GAM1431	ZDHC3	3'	GTGGATAGAGGTGAAGG	33457	G	TG
			CTTTCA TCCTTTATT	C		
				I		
			GGAAGT GGAGATAG	G		
			—	GT		
GAM1431	ZIN	3'	GCAGGTGGGGCTGAGGG	25491	T	
			CTTTCAGTCTT ATTTGC			
			GGGAGTCGGGG	TGGACG		
			—			
GAM1431	ZNF259	3'	TAGTATTGGATGAAGGCGAAGG	72620	A	TT CA AAA
			CTTTC GTCTTTAT	G GC		
				I II		
			GGAAG CGGAAGTA	T TG		
			—	GG TA ATT		
GAM1431	ZNF262	3'	CAAATGAGGACTGTGGG	17483	TT	
			CT CAGTCTTTATTTG			
			II			
			GG GTCAGGAGTAAAC			
			GT			
GAM1431	ZNF262	3'	TGCAAATGAAAATTGAAGG	17491	C	
			CTTTCAGT TTTATTTGCA			
			GGAAGTTA AAGTAAACGT			
			A			
GAM1431	LOC114971	3'	TTCTCCTAAGTAAAGCCTGAAG	73156	T	CAGCAAA
	G		CTTTCAG CTTTATTTG			
			GGAAGTC GAAATGAAT			
			C	CCTCTT		
GAM1431	LOC115708	3'	TTTCCCAAAGTGGGGACAGAGG	73557	A	GCAGCAAA
	G		CTTTC GTCTTTATTT			
			GGGAG CAGGGGTGAA			
			A	ACCCTTT		
GAM1431	LOC116150	3'	TAAGTAGGATTGAAGG	56636	T	
			CTTTCAGTCTT ATTTG			
			GGAAGTTAGGA	TGAAT		
			—			
GAM1431	LOC118987	3'	CAAATTGAGACTGGAAG	73955	T	
			CTTTCAGTCTT ATTTG			
			GAAGGTCAGAG	TAAAC		
			T			
GAM1431	LOC121219	5'	TTTGGTGTTGGGGGTTGGGGG	74052	TT GT	TTT G
			CT CA CTTTA	GCA CAAA		
			II II	III		

		GG GT GGGGT TGT GTTT			
		GG TG ____ G			
GAM1431	LOC122210 5'	TACATTGTGGATGGAGATGGAG	74120	G	TG CAAA
		G CTTTCA TCTTTATT CAG			
		GGAGGT AGAGGTAG GTT			
		_ GT ACATT			
GAM1431	LOC123876 5'	CTGTGTGGAGACTGGAAG	74245	TT	
		CTTTCAGTCTTTAT GCAG			
		GAAGGTCAGAGGTG TGTC			
		_____			
GAM1431	LOC124460 3'	GCTGGGGTGGGGGCTGAGGG	76046	G	
		CTTTCAGTCTTTATTT CAGC			
		GGGAGTCGGGGGTGGG GTCG			
		_____			
GAM1431	LOC124944 3'	TGCACGAGAGAGGGCTGAAAG	74375	A	CA
		CTTTCAGTCTTT TTTG GCA			
		GAAAGTCGGGAG GAGC CGT			
		A A_			
GAM1431	LOC126327 3'	GAATGGAGACAGAAAG	74498	A	
		CTTTC GTCTTTATTT			
		GAAAG CAGAGGTAAG			
		A			
GAM1431	LOC126520 3'	CTGGGGGAGGGCTGGGGG	74522	TT	AT G
		CT CAGTCTTT TT CAG			
		GG GTCGGGAG GG GTC			
		GG ____ G			
GAM1431	LOC126906 3'	TGCATGAATGAGGGTTGAAG	75434	GT	GCA
		TTTCA CTTTATTT GCA			
		GAAGT GGAGTAAG CGT			
		TG TA_			
GAM1431	LOC126917 3'	GCGTTGGGAGAGGGTTGGGAG	74588	TT GT	AT G AAA
		CT CA CTTT TT CAGC			
		GA GT GGAG AG GTTG			
		GG TG ____ G CGT			
GAM1431	LOC126917 3'	GGGTGGGGATCTGAGGG	74592	_	
		CTTTCAG TCTTTATTT			
		GGGAGTC AGGGGTGGG			
		T			
GAM1431	LOC126917 3'	TTGGGAGTGAGGACTTGGGG	74598	TC	G
		CTT AGTCTTTATTT CAG			

GGG TCAGGAGTGAG GTT  
GT G  
GAM1431 LOC128208 5' TTGAGAGTAAAGACTGTGGG 75465 TT TG  
CT CAGTCTTTATT CAG  
|| ||||| |||  
GG GTCAGAAATGA GTT  
GT GA  
GAM1431 LOC129080 3' AGGCTGAGCAAGGGCTGAGAG 55978 ATTTG AAA  
CTTTCAGTCTTT CAGC  
||||||| |||  
GAGAGTCGGGAA GTCG  
CGA\_\_ GAG  
GAM1431 LOC132200 5' CAGGTGAAGTTGAGAG 57155 T  
CTTTCAG CTTTATTTG  
||||| |||||  
GAGAGTT GAAGTGGAC  
—  
GAM1431 LOC137541 5' TTGTGGGGTGGAGGCTGGCAG 75940 T \_TG  
CT TCAGTCTTTAT T CAG  
|| ||||| | |||  
GA GGTCGGAGGTG G GTT  
C G GT  
GAM1431 LOC138639 5' TTTGTTCCACCAGAAGGCTGAAA 75366 ATT C  
TTTCAGTCTTT TG AGCAAA  
||||||| || |||||  
AAAGTCGGAAG AC TTGTTT  
ACC \_  
GAM1431 LOC138649 5' GGGGCTGGGTGGGGGTGGAAAG 75358 AG TG AAA  
CTTTC TCTTTATT CAGC  
|||| ||||| |||  
GAAAG GGGGGTGG GTCG  
GT \_ GGGT  
GAM1431 LOC142927 3' TTTGCCCTTCAGGGGGGACTGGG 76435 TT ATTTGCA  
GG CT CAGTCTTT GCAAA  
|| ||||| |||||  
GG GTCAGGGG CGTTT  
GG GACTTCC  
GAM1431 LOC142948 3' TCTGGGTCGGGTGGGGACTTGG 82892 TC \_AG AA  
AG CTT AGTCTTTATTTG C CA  
||| ||||| ||| | |||  
GAG TCAGGGGTGGGC G GT  
GT T G\_ CTT  
GAM1431 LOC143146 5' CCAGTTGGATGGACACTGAAGG 60133 C TG AAA  
CTTTCAGT TTTATT CAGC  
||||| ||||| |||  
GGAAGTCA AGGTAG GTTG  
C \_ ACCA  
GAM1431 LOC143286 5' TTTGCTGTAAGAAAGTGGCTGA 82949 \_ A  
GGG CTTTCAGTC TTT TTTGCAGCAAA  
||||||| ||| ||||| |||||

GGGAGTCGG GAA GAATGTCGTTT  
 T A  
 GAM1431 LOC143310 3' TAGGAAGGGGCTGGAAG 76540 A  
 CTTTCAGTCTTT TTTG  
 |||||  
 GAAGGTCGGGGA GGAT  
 A  
 GAM1431 LOC144266 5' TAATATCAAGTGGGGCTGGAAG 76763 T CAGCAAA  
 CTTTCAGTCTT ATTTG  
 |||||  
 GAAGGTCGGGG TGAAC  
 \_ TATAATT  
 GAM1431 LOC144512 5' TTTGCTGGACAGTGGCTGAAGG 83117 TTTATTTG  
 CTTTCAGTC CAGCAAA  
 |||||  
 GGAAGTCGG GTCGTTT  
 TGACAG\_  
 GAM1431 LOC144776 3' AAGCCAGAAGAGACTGGGGG 76957 TT A CA AAA  
 CT CAGTCTTT TTTG GC  
 || |||||  
 GG GTCAGAGA AGAC CG  
 GG \_ \_ AAC  
 GAM1431 LOC145009 3' TTGTGTGGGTGAGGATGGAAG 60355 G TG G  
 CTTTCA TCTTTATT CA CAA  
 ||||| |||||  
 GAAGGT AGGAGTGG GT GTT  
 \_ GT \_  
 GAM1431 LOC145098 5' TTTGCAGTGTCAATGAGATTGA 76996 T T \_  
 GGG TTTTCAGTCTT ATT GCA GCAAA  
 ||||| |||||  
 GGAGTTAGAG TAA TGT CGTTT  
 \_ C GA  
 GAM1431 LOC145173 3' TTAGAGCGAAAAAGGACTGAAA 77043 A AGCAAA  
 G CTTTCAGTCTTT TTTGC  
 |||||  
 GAAAGTCAGGAA AAGCG  
 A AGATT  
 GAM1431 LOC145231 3' GTGAGGAGAGACTGAAGG 83294 A TG  
 CTTTCAGTCTTT TT C  
 |||||  
 GGAAGTCAGAGA GA G  
 G GT  
 GAM1431 LOC145482 3' TGTACATAGGGACTGGGGG 77233 TT T  
 CT CAGTCTTTAT TGCA  
 || |||||  
 GG GTCAGGGATA ATGT  
 GG C  
 GAM1431 LOC145601 3' TTGGGAGAGGAAAGGCTGGAAG 83373 AT\_ G  
 CTTTCAGTCTTT TT CAG  
 ||||| |||||



		GAAGGTCGAAA	AG GTT		
		GGAG G			
GAM1431	LOC145676 5'	AAGTAGATGATTGAGAG	77329	—	
		CTTTCAGTC TTTATTT			
		GAGAGTTAG AGATGAA			
		T			
GAM1431	LOC145719 5'	TGGTGTAGGGGCTGGGAG	83458	TT TTAT G	
		CT CAGTCT TTGCA CA			
		GA GTCGGG GATGT GT			
		GG — G			
GAM1431	LOC145720 5'	TGGTGTAGGGGCTGGGAG	83440	TT TTAT G	
		CT CAGTCT TTGCA CA			
		GA GTCGGG GATGT GT			
		GG — G			
GAM1431	LOC145826 5'	TTTGTGGTGAAAGTGGCTGGA	83534	TTTA TG _	
	AG	CTTTCAGTC TT C AGCAAA			
		GAAGGTCGG AA G TTGTTT			
		TGA_ GT G			
GAM1431	LOC146237 5'	TTGTAGGGTGGGGGCGGGGG	83638	TT A _	
		CT C GTCTTTATT TGCAG			
		GG G CGGGGGTGG ATGTT			
		GG_ G			
GAM1431	LOC146287 5'	GTGGGGGAAGACTGAGAG	83653	A TG	
		CTTTCAGTCTTT TT C			
		GAGAGTCAGAAG GG G			
		G GT			
GAM1431	LOC146316 3'	CTGGATGGAGGCTGGAGG	60871	TG	
		CTTTCAGTCTTTATT CAG			
		GGAGGTCGGAGGTAG GTC			
		—			
GAM1431	LOC146316 3'	TGTCTGGATGGAGGCTGGAGG	60875	TG _	
		CTTTCAGTCTTTATT CAG CA			
		GGAGGTCGGAGGTAG GTC GT			
		— T			
GAM1431	LOC146488 3'	GACACCCGGACAGAGGCTGGAG	70812	A CAGCAAA	
	G	CTTTCAGTCTTT TTTG			
		GGAGGTCGGAGA AGGC			
		C CCACAGT			
GAM1431	LOC146556 3'	GTAGGTGGGGGCCGGGAG	77983	TT A	
		CT C GTCTTTATTTGC			

		GA G CGGGGGTGGATG		
		GG C		
GAM1431	LOC146728 5'	TAAAGAGGTGAGTAAGGGCTGG	83752	TT TG AGCAAA
		GGG CT CAGTCTTTATT C		
		GG GTCGGAATGA G		
		GG GT GAGAAATT		
GAM1431	LOC147299 3'	TTTGCTGGGGAAGGCTGCAGG	78351	T ATT G
		CTT CAGTCTTT T CAGCAAA		
		GGA GTCGGAAG G GTCGTTT		
		C _ G		
GAM1431	LOC147976 5'	TTGCTGACAGGCTGAAGG	78591	TTATTTG
		CTTTCAGTCT CAGCAA		
		GGAAGTCGGA GTCGTT		
		CA _		
GAM1431	LOC148195 3'	TGAAGTAGATAGGGGCTAGAG	84138	C AG
		CTTT AGTCTTTATTTGC CA		
		GAGA TCGGGGATAGATG GT		
		_ AA		
GAM1431	LOC148354 3'	TTAGCGGTGAGTGGGGGCTGGG	78803	TT TG A AAA
		G T CAGTCTTTATT C GC		
		G GTCGGGGGTGA G CG		
		GG GT G ATTT		
GAM1431	LOC148710 3'	TGCTGGGAACTGAAAG	84198	CTTTAT G
		CTTTCAGT TT CAGCA		
		GAAAGTCA AG GTCGT		
		_ G		
GAM1431	LOC148894 3'	TTGTAATAGCAAGTAAAGGCTG	84262	A_ A
		GAGG TCAGTCTTTATTTGC GCAA		
		GGTCGGAAATGAACG TGTT		
		ATAA		
GAM1431	LOC148894 3'	TTGTATTTTAAAGATTGAGAG	84263	TT_
		CTTTCAGTCTTTA TGCAG		
		GAGAGTTAGAAAT ATGTT		
		TTT		
GAM1431	LOC149113 5'	GCAGGTGAGGCTGAAAG	79166	T
		CTTTCAGTCTT ATTTGC		
		GAAAGTCGGAG TGGACG		
		_		
GAM1431	LOC149302 3'	TTTGCTGTAAATAAAGAC	79274	
		GTCTTTATTTGCAGCAAA		

CAGAAATAAATGTCGTTT

GAM1431	LOC149577	3'	TTTGTGCCCAGGCTGGAG	84525	TTATTT
			TTTCAGTCT GCAGCAAA		
			GAGGTCGGA CGTTGTTT		
			CC____		
GAM1431	LOC149734	3'	CCCAAGTAGATGGGACTGAAAG	84633	T AGCAAA
			CTTTCAGTCTT ATTTGC		
			GAAAGTCAGGG TAGATG		
			— AACCT		
GAM1431	LOC149827	5'	TGAATGCGGACTGGAGG	84770	T
			CTTTCAGTCT TATTTG		
			GGAGGTCAGG GTAAGT		
			C		
GAM1431	LOC150170	5'	TTTGCTGTGTGCAGATGGAGG	79594	G T TT
			CTTTCA TCT TAT GCAGCAAA		
			GGAGGT AGA GTG TGTCGTTT		
			— C —		
GAM1431	LOC150175	5'	TTTGCTGTGTGCAGATGGAGG	79635	G T TT
			CTTTCA TCT TAT GCAGCAAA		
			GGAGGT AGA GTG TGTCGTTT		
			— C —		
GAM1431	LOC150215	5'	TTTGCTGTGTGCAGATGGAGG	79643	G T TT
			CTTTCA TCT TAT GCAGCAAA		
			GGAGGT AGA GTG TGTCGTTT		
			— C —		
GAM1431	LOC150218	5'	TTTGCTGTGTGCAGATGGAGG	79724	G T TT
			CTTTCA TCT TAT GCAGCAAA		
			GGAGGT AGA GTG TGTCGTTT		
			— C —		
GAM1431	LOC150225	3'	TTGCAGGTGAAGGTGGGAG	85017	TT G
			CT CA TCTTTATTTGCAG		
			GA GT GGAAGTGGACGTT		
			GG _		
GAM1431	LOC150372	3'	TGAGTGGGGACTGGAG	79809	
			TTTCAGTCTTTATTTG		
			GAGGTCAGGGGTGAGT		
GAM1431	LOC150935	3'	TCTGGGTCAGGTGGGGACTTGG	80038	TC _ AG AA
			AG CTT AGTCTTTATTTG C CA		

GAG TCAGGGGTGGAC G GT  
 GT T G\_ CTT  
 GAM1431 LOC151121 5' TGAATAGAGACTTGAAG 80122 C  
 CTTT AGTCTTTATTTG  
 ||| |||||  
 GAAG TCAGAGATAAGT  
 T  
 GAM1431 LOC151304 3' GCAGGTGGGGACTGTGGG 85309 TT  
 CT CAGTCTTTATTTGC  
 || |||||  
 GG GTCAGGGGTGGACG  
 GT  
 GAM1431 LOC151414 3' GCATATGGGGGTGGAGG 80238 G T  
 CTTTCA TCTTTAT TGC  
 |||| |||||  
 GGAGGT GGGGGTA ACG  
 \_ T  
 GAM1431 LOC151438 3' TGAGCTGGGTGGGGATTGAAA 85372 TG AAA  
 TTTCAGTCTTTATT CAGC  
 ||||| |||||  
 AAAGTTAGGGGTGG GTCG  
 \_ AGTC  
 GAM1431 LOC151556 5' GCGAAGAGGGCTGGGGG 80276 TT A  
 CT CAGTCTTT TTTGC  
 || ||||| |||||  
 GG GTCGGGAG AAGCG  
 GG \_  
 GAM1431 LOC151584 3' GCAGCTGGAGGCTGGAGG 85448 T  
 CTTTCAGTCTTTA TTGC  
 ||||| |||||  
 GGAGGTCGGAGGT GACG  
 C  
 GAM1431 LOC151877 3' TTTGCTGCAAACCTCTGCAGG 85511 T TCTTTA  
 CTT CAG TTTGCAGCAA  
 ||| ||| |||||  
 GGA GTC AAACGTCGTTT  
 C TCC\_  
 GAM1431 LOC152273 5' CGAGAGAGGCTGGGGG 80536 TT A  
 CT CAGTCTTT TTTG  
 || ||||| |||||  
 GG GTCGGAGA GAGC  
 GG \_  
 GAM1431 LOC152317 5' GCAAGGAGGAGGCTGGGAG 85642 TT A\_  
 CT CAGTCTTT TTTGC  
 || ||||| |||||  
 GA GTCGGAGG GAACG  
 GG AG  
 GAM1431 LOC152330 5' TTTGTTTCTCAAGAGACTGGGA 80541 TT ATTTGC  
 T CAGTCTTT AGCAA  
 | ||||| |||||

	A GTCAGAGA TTGTTT		
	GG ACTCT_		
GAM1431 LOC152402 3'	TTGGGGAGGGGCTGGAGG 85709	TA	G
	CTTTCAGTCTT TTT CAG		
	GGAGGTCGGGG AGG GTT		
	_ G		
GAM1431 LOC152890 3'	TTGGTGAATAAGTGAAGACAGA 80721	A	_ G A
AGG	TTTC GTCTTTATTTG CA CAA		
	GAAG CAGAAGTGAAT GT GTT		
	A AA G		
GAM1431 LOC152905 3'	TTGAAAGGGGAAAGATTGGAGG 60480	A	GCAG
	CTTTCAGTCTTT TTT CAA		
	GGAGGTTAGAAA GGG GTT		
	G AAA_		
GAM1431 LOC153027 3'	TTGTTGTGTAGAGTGGAAG 67435	G	TTATTT
	CTTTCA TCT GCAGCAA		
	GAAGGT AGA TGTTGTT		
	G TG_____		
GAM1431 LOC153606 3'	TTTGTTCCTTCTAAGTTGAGA 86078	T	TATTT
G	CTTTCAG CTT GCAGCAAA		
	GAGAGTT GAA CGTTGTTT		
	_ TCTTC		
GAM1431 LOC153688 3'	GTAAATAGGACTGAAAG 86118	T	
	CTTTCAGTCTT ATTTGC		
	GAAAGTCAGGA TAAATG		
	-		
GAM1431 LOC153811 3'	CAGATGGAGGTGGAAG 80944	G	
	CTTTCA TCTTTATTTG		
	GAAGGT GGAGGTAGAC		
	-		
GAM1431 LOC153811 3'	TTGGAAGAAGAGAGGCTGAGAG 80961	A	GCAG
	CTTTCAGTCTTT TTT CAA		
	GAGAGTCGGAGA AAG GTT		
	G AAG_		
GAM1431 LOC154007 3'	AGGGGTGCAAATCAGGATTGGG 81012	TT	T GCAAA
AG	CT CAGTCTT ATTTGCA		
	GA GTTAGGA TAAACGT		
	GG C GGGGAT		
GAM1431 LOC154403 5'	GCAGGTGAGGCTGAAAG 81072	T	
	CTTTCAGTCTT ATTTGC		

GAAAGTCGGAG TGGACG

GAM1431 LOC154641 5' TAGGTAAAGAATGGAAG 81099 G  
CTTTCA TCTTTATTTG  
||||| |||||||  
GAAGGT AGAAATGGAT

A

GAM1431 LOC154992 5' GCAGGTGAGGCTGAAAG 81216 T  
CTTTCAGTCTT ATTTGC  
||||||| |||||  
GAAAGTCGGAG TGGACG

GAM1431 LOC157381 3' TGATAAATGAAGATTGAG 86440 \_  
TTCAGTCTTTATTTG CA  
||||||| ||  
GAGTTAGAAGTAAAT GT

A

GAM1431 LOC157562 5' TTGGGAGGTCTGAGGCTGGAGG 86479 TA\_ G  
CTTTCAGTCTT TTT CAG  
||||||| ||| ||  
GGAGGTCGGAG GAG GTT

CTG G

GAM1431 LOC157653 5' TGGGCTAGGGACTGAGGG 81532 TTT AG  
CTTTCAGTCTTTA GC CA  
||||||| || ||  
GGGAGTCAGGGAT CG GT

\_\_\_ G\_

GAM1431 LOC157860 3' TGTGTGTGGGGGCTGGGGG 86572 TT T  
CT CAGTCTTTAT TGCA  
|| ||||||| ||||  
GG GTCGGGGGTG GTGT

GG T

GAM1431 LOC158014 5' TTTGTATGTGGTGGGGATGGGA 81662 TT G T TG \_  
G CT CA TCTTTA T CA GCAAA  
|| || ||||| | || |||||  
GA GT AGGGGT G GT TGTTT

GG \_ \_ GT A

GAM1431 LOC158062 3' TGGGTGGGGCTGGAGG 86680 T TT  
CTTTCAGTCTT AT G  
||||||| || |  
GGAGGTCGGGG TG T

\_ GG

GAM1431 LOC158972 5' CTGAGGTAGGGATGGGAG 86949 TT G G  
CT CA TCTTTATTT CAG  
|| || ||||||| |||  
GA GT AGGGATGGA GTC

GG \_ \_

GAM1431 LOC159053 3' CAAATGGAAGTAAAG 86977 C  
CTTTCAGT TTTATTTG  
||||||| |||||||

GAAAGTCA AGGTAAAC

GAM1431 LOC162333 5' CAGATAAAGACTGAAG 87122  
TTTCAGTCTTTATTTG  
|||||  
GAAGTCAGAAATAGAC

GAM1431 LOC169611 3' TTTGTTGCCCGGGCTGGAA 82781 TTATTT  
TTTCAGTCT GCAGCAAA  
||||| |||||  
AAGGTCGGG CGTTGTTT  
CC\_\_

GAM1431 LOC170372 3' TTTGCTCACAAAAGTAAAGACT 76364 C GC\_\_  
AGAG TT AGTCTTTATTT AGCAAA  
|| ||||| |||||  
GA TCAGAAATGAA TCGTTT  
AACAC

GAM1431 LOC196510 3' TTGCATGGAGACTGAGA 87751 TT  
TTTCAGTCTTTA TGCAG  
||||| |||||  
AGAGTCAGAGGT ACGTT

GAM1431 LOC196694 5' CGAGTGGCGACTGAAGG 89581 T  
CTTTCAGTC TTATTTG  
||||| |||||  
GGAAGTCAG GGTGAGC  
C

GAM1431 LOC196932 5' TGACGGGTGGGGAATGGGGG 87808 TT G \_  
CT CA TCTTTATTTG CA  
|| || ||||| ||  
GG GT AGGGGTGGGC GT  
GG A A

GAM1431 LOC196955 5' GGGTGAAGGCTGCAAAG 77386 \_  
CTTT CAGTCTTTATTT  
||| |||||  
GAAA GTCGGAAGTGGG  
C

GAM1431 LOC196955 3' TCCAAGTGAGTAGGGGCTGAA 77389 TG AGCAAA  
TTCAGTCTTTATT C  
||||| |  
AAGTCGGGGATGA G  
GT AACCT

GAM1431 LOC197114 5' TGGTGTAGGGGCTGGGAG 89710 TT TTAT G  
CT CAGTCT TTGCA CA  
|| |||| | |||| ||  
GA GTCGGG GATGT GT  
GG \_ G

GAM1431 LOC197117 5' TGGTGTAGGGGCTGGGAG 89726 TT TTAT G  
CT CAGTCT TTGCA CA  
|| |||| | |||| ||

		GA GTCGGG GATGT GT		
		GG ____ G		
GAM1431	LOC197342 3'	TTGTGACAGTGAGGGTTGAGGG 88010	GT	T CA
		CTTTCA CTTTATT G GCAA		
		GGGAGT GGAGTGA C TGTT		
		TG _AG		
GAM1431	LOC199675 3'	TGAATAGGACTGAGAG 88269	T	
		CTTTCAGTCTT ATTTG		
		GAGAGTCAGGA TAAGT		
		—		
GAM1431	LOC199870 3'	TAAGTAAGGGCAGAAAG 88432	A	
		CTTTC GTCTTTATTTG		
		GAAAG CGGGAATGAAT		
		A		
GAM1431	LOC199883 5'	CAGGTGAAGGCTCAAGG 89870	C	
		CTTT AGTCTTTATTTG		
		GGAA TCGGAAGTGGAC		
		C		
GAM1431	LOC200020 5'	CAGGTGAAGGCTCAAGG 89928	C	
		CTTT AGTCTTTATTTG		
		GGAA TCGGAAGTGGAC		
		C		
GAM1431	LOC200035 5'	TGGGTGTGGGCTGAGGG 73255	T TT	
		CTTTCAGTCT TAT G		
		GGGAGTCGGG GTG T		
		T GG		
GAM1431	LOC200220 3'	TTGCATGGAGACTGAGA 88640	TT	
		TTTCAGTCTTTA TGCAG		
		AGAGTCAGAGGT ACGTT		
		—		
GAM1431	LOC200471 5'	TTTGGCAAATAGGGGTGGAGG 90056	G TA	AGCAAA
		CTTTCA TCTT TTTGC		
		GGAGGT GGGA AAACG		
		G TA GTTT		
GAM1431	LOC200933 3'	CTGGCTAAAGATTGAAGG 90196	TTTG	
		CTTTCAGTCTTTA CAG		
		GGAAGTTAGAAAT GTC		
		CG__		
GAM1431	LOC200982 3'	TTTGTGACCAGTGGGGATGGGG 90230	TT G	TGCA
	G	CT CA TCTTTATT GCAAA		



		GG GT AGGGGTGA TGT		
		GG _ CCAG		
GAM1431	LOC201685 5'	TTTGCTAATCACGGGGCTGGGA	90249	TT TATTTGC
	G	CT CAGTCTT AGCAAA		
		GA GTCGGGG TCGTTT		
		GG CACTAA_		
GAM1431	LOC201868 5'	GCAGGTGAGGCTGAAAG	89078	T
		CTTTCAGTCTT ATTTGC		
		GAAAGTCGGAG TGGACG		
		-		
GAM1431	LOC201911 3'	GGGCGCGGGGAAGACTGAGGG	90264	A A AAA
		CTTTCAGTCTTT TTTGC GC		
		GGGAGTCAGAAG GGGCG CG		
		- _ GGT		
GAM1431	LOC202052 3'	CAGGTAAAGATTGGGGG	90307	TT
		CT CAGTCTTTATTTG		
		GG GTTAGAAATGGAC		
		GG		
GAM1431	LOC202134 5'	CAGGTAGAGGCTGAGG	90319	
		TTTCAGTCTTTATTTG		
		GGAGTCGGAGATGGAC		
GAM1431	LOC203429 3'	TGGCAGTAAATGAGGCATTGAG	89367	_ A AAA
	AG	CTTTCAGT CTTTATTTGC GC		
		GAGAGTTA GGAGTAAATG CG		
		C A GT		
GAM1431	LOC204084 5'	TTTGTTGTAGGTACACCTATGG	89451	GTCTT_
	AA	TTTCA TATTTGCAGCAAA		
		AAGGT ATGGATGTTGTTT		
		ATCCAC		
GAM1431	LOC205418 5'	TTGCTGTAGTGATTGAGA	90691	TTTAT
		TTTCAGTC TTGCAGCAA		
		AGAGTTAG GATGTCGTT		
		T__		
GAM1431	LOC219445 5'	TTTGTTGCCAGGCTGGAG	91582	TTATTT
		TTTCAGTCT GCAGCAAA		
		GAGGTCGGA CGTTGTTT		
		CC__		
GAM1431	LOC219854 5'	GAGGTGTGAGTAGAGCCTGGGG	91485	TT T TG GCAAA
	G	CT CAG CTTTATT CA		

GG GTC GAGATGA GT  
GG C GT GGAGT  
GAM1431 LOC221302 5' TGAATGAGGTACTGGGGG 59005 TT \_  
CT CAGT CTTTATTTG  
|| ||| |||||  
GG GTCA GGAGTAAGT  
GG T  
GAM1431 LOC221337 3' AAGTGAAAAGTGGGAAG 92105 C  
CTTTCAGT TTTATTT  
||||| |||||  
GAAGGTCA AAGTGAA  
A  
GAM1431 LOC221416 3' TGCTGGAAGAGACTGGGAG 93771 TT TAT G  
CT CAGTCTT TT CAGCA  
|| ||||| || |||||  
GA GTCAGAG AA GTCGT  
GG \_ G  
GAM1431 LOC221418 3' TTGACAGTGGAGACAGAGAG 93637 A TG  
CTTTC GTCTTTATT CAG  
||||| ||||| |||  
GAGAG CAGAGGTGA GTT  
A CA  
GAM1431 LOC221683 3' TTAGGGTTAGATGAGGGCATGA 93720 \_ CAGCAAA  
GGG CTTTCA GTCTTTATTTG  
||||| |||||  
GGGAGT CGGGAGTAGAT  
A TGGGATT  
GAM1431 LOC222001 3' TAAGTGAAGACTGGGG 92907 TT  
T CAGTCTTTATTTG  
| |||||  
G GTCAGAAAGTGAAT  
GG  
GAM1431 LOC222031 3' TTGCCTCTAGAGCACTGAGAG 94032 \_ TTT  
CTTTCAGT CTTTA GCAG  
||||| ||||| |||  
GAGAGTCA GAGAT CGTT  
C CTC  
GAM1431 LOC222134 5' GCAGATGAAAGTTGGAAG 94138 TC  
CTTTCAG TTTATTTGC  
||||| |||||  
GAAGGTT AAGTAGACG  
GA  
GAM1431 LOC222161 5' GCAGATGGAGCTGGAGG 92797 T  
CTTTCAG CTTTATTTGC  
||||| |||||  
GGAGGTC GAGGTAGACG  
\_  
GAM1431 LOC222681 5' CAGATAAAAGTGGGAAG 92850 C  
CTTTCAGT TTTATTTG  
||||| |||||

GAAGGTCA AAATAGAC

GAM1431 LOC222962 3' GGAACGTAGGGAGGGGCTGGGG 92874 TT A AGCAAA  
G CT CAGTCTTT TTTGC

|| ||||| ||||

GG GTCGGGGA GGATG

GG G CAAGGT

GAM1431 LOC245812 3' CTGGGGTGGAGGGTGGGG 93953 TT G G

CT CA TCTTTATTT CAG

|| || ||||| |||

GG GT GGAGGTGGG GTC

GG G

GAM1431 LOC253461 3' GCAAATGGAGGCTTGAAG 96282 C

CTTT AGTCTTTATTTGC

|||| |||||

GAAG TCGGAGGTAAACG

T

GAM1431 LOC253626 5' TGGGTGAGGGGTGGAAG 97220 G TT

CTTTCA TCTTTAT G

|||| ||||| |

GAAGGT GGGAGTG T

G GG

GAM1431 LOC253714 3' TAAATAAGGAACTGAAGG 95950

CTTTCAGT CTTTATTTG

||||| |||||

GGAAGTCA GGAATAAAT

A

GAM1431 LOC254042 3' CTGGAGGGGACTGGAGG 95691 TAT G

CTTTCAGTCTT TT CAG

||||||| || |||

GGAGGTCAGGG GA GTC

\_\_\_ G

GAM1431 LOC254085 5' TTTGTTGTGAGTTACTAGGAG 96122 TC CTTT TG

CTT AGT ATT CAGCAAA

||| ||| ||| |||||

GAG TCA TGA GTTGTTT

GA T\_\_\_ GT

GAM1431 LOC254143 5' TTTGCTGGACAGTGGCTGAAGG 96499 TTTATTTG

CTTTCAGTC CAGCAAA

||||||| |||||

GGAAGTCGG GTCGTTT

TGACAG\_\_\_

GAM1431 LOC254413 5' TTCAAATCAAGTGAGGGCAGAA 97125 A CAGCAAA

GG

CTTTC GTCTTTATTTG

|||| |||||

GGAAG CGGGAGTGAAC

A TAACTTT

GAM1431 LOC255285 3' CTGCAGATCAGGACTGGAAG 96274 T

CTTTCAGTCTT ATTTGCAG

||||||| |||||

		GAAGGTCAGGA TAGACGTC		
		C		
GAM1431	LOC255308 3'	CGGATGGAGCTGGAAG	94535	T
		CTTTCAG CTTTATTTG		
		GAAGGTC GAGGTAGGC		
		—		
GAM1431	LOC255328 3'	CAGGTGAGGAGTGAAGG	96558	G
		CTTTCA TCCTTATTTG		
		GGAAGT AGGAGTGGAC		
		G		
GAM1431	LOC255413 3'	CGGATGGAGGTGGAGAG	97575	AG
		CTTTC TCCTTATTTG		
		GAGAG GGAGGTAGGC		
		GT		
GAM1431	LOC255995 5'	TTTGCTTTTGTCTCGGGAGATTGA	96978	ATTTGC_
	AAG	CTTTCAGTCCTT	AGCAAA	
		GAAAGTTAGAGG	TCGTTT	
		GCTGTTT		
GAM1431	LOC256369 3'	TTGGACAAAATGGAGACTGTAA	94936	T GCAG A
	G	CTT CAGTCCTTTATTT	CAA	
		GAA GTCAGAGGTAAA	GTT	
		T ACAG		
GAM1431	LOC256940 3'	TCAGTGATAGAGGAAGACTGGG	96495	TT A CA AAA
	AG	CT CAGTCCTT TTTG	GC	
		GA GTCAGAAG AGAT	TG	
		GG G AG ACTT		
GAM1431	LOC257106 3'	TTTGTTAAAGTGAAGACTGGAG	95392	GC
		TTTCAGTCCTTTATTT	AGCAAA	
		GAGGTCAGAAGTGAA	TTGTTT	
		A_		
GAM1431	LOC257160 5'	GCAAATGGGGTTGAAGG	94849	T
		CTTTCAG CTTTATTTGC		
		GGAAGTT GGGGTAAACG		
		—		
GAM1431	LOC257396 5'	CGAGTGGGGACTTGGAG	97136	TC
		CTT AGTCCTTATTTG		
		GAG TCAGGGGTGAGC		
		GT		
GAM1431	LOC257406 5'	CTGCGGGTGGAAGTGAAG	97440	C
		CTTTCAGT TTTATTTGCAG		

GAAGGTCA AGGTGGGCGTC

GAM1431 LOC257464 3' GGGTAAAGACATGAAAG 89672 \_  
CTTTCA GTCTTTATTT  
||||| |||||||  
GAAAGT CAGAAATGGG

A

GAM1431 LOC257507 5' CAGATAAAACTGGAAG 97772 C  
CTTTCAGT TTTATTTG  
||||| |||||||  
GAAGGTCA AAATAGAC

GAM1431 LOC257625 5' CAGATAAAACTGGAAG 97903 C  
CTTTCAGT TTTATTTG  
||||| |||||||  
GAAGGTCA AAATAGAC

GAM1431 LOC51020 3' TGCCATGGATGAACACTGGAGG 32160 C TT CA  
CTTTCAGT TTTAT G GCA  
||||| |||| | |||  
GGAGGTCA AAGTA T CGT  
C GG AC

GAM1431 LOC51207 3' AAACAGCAAGTGGGGGCTGAGG 33033 AGCAAA  
TTTCAGTCTTTATTTGC  
||||| |||||||  
GGAGTCGGGGGTGAACG  
ACAAAT

GAM1431 LOC51236 3' AGGCTCCAGTAAGGATTGGAGG 33198 T C AAA  
CTTTCAGTCTTTATT G AGC  
||||| ||||||| | |||  
GGAGGTTAGGAATGA C TCG  
\_ C GAT

GAM1431 LOC51279 3' AACACTGGGGTAGGGGTTGGGG 33305 TT GT G CAAA  
G CT CA CTTTATTT CAG  
|| || ||||||| |||  
GG GT GGGATGGG GTC  
GG TG \_ ACAAG

GAM1431 LOC54466 5' TTGCAGGGGATTGGGAG 38657 TT TAT  
CT CAGTCTT TTGCAG  
|| ||||||| |||||||  
GA GTTAGGG GACGTT  
GG \_

GAM1431 LOC56961 5' GTGAAGGGGGATTGGAGG 62911 TA TG  
CTTTCAGTCTT TT C  
||||| || |||  
GGAGGTTAGGG AA G  
GG GT

GAM1431 LOC56964 5' TAGATAGGGAGTGGGAG 62570 TT G  
CT CA TCTTTATTTG  
|| || |||||||

	GA GT AGGGATAGAT	
	GG G	
GAM1431 LOC89890 3'	TTTGTTGTAAGTATTGAAA 60581	TTAT
	TTTCAGTCT TTGCAGCAAA	
	AAAGTTAGA AATGTTGTTT	
	TC__	
GAM1431 LOC89932 5'	CTGAGTCGGAGGCTGAGAG 60797	AT G
	CTTTCAGTCTTT TT CAG	
	GAGAGTCGGAGG GA GTC	
	CT _	
GAM1431 LOC89985 5'	TTTGCTGTGCCTGTGCTGAGAG 61021	CTTTATTT
	CTTTCAGT GCAGCAAA	
	GAGAGTCG TGTCGTTT	
	TGTCCG__	
GAM1431 LOC90110 5'	TAAATGTAAGATTGGAAG 61512	_
	CTTTCAGTCTT TATTTG	
	GAAGGTTAGAA GTAAAT	
	T	
GAM1431 LOC90170 5'	CTGGGGATGGAGGCTGGAG 61706	G
	TTTCAGTCTTTATTT CAG	
	GAGGTCGGAGGTAGG GTC	
	G	
GAM1431 LOC90550 3'	TAAAGCATTGCAGGTGGAAGCT 73093	TT TC _ AAA
	GGGAG CAG TTTATTTGCA GC	
	GTC AGGTGGACGT CG	
	GG GA TA AAATT	
GAM1431 LOC90564 3'	TTGAATGTAAAGACTGGAAG 63245	TTG
	CTTTCAGTCTTTAT CAG	
	GAAGGTCAGAAATG GTT	
	TAA	
GAM1431 LOC91012 3'	GTGAGCTGAGGGCTGGAGG 64642	_ TG
	CTTTCAGTCTTTA TT C	
	GGAGGTCGGGAGT GA G	
	C GT	
GAM1431 LOC91149 5'	CAGAAAAGGCTGGAGG 65071	A
	CTTTCAGTCTTT TTTG	
	GGAGGTCGGAAA AGAC	
	_	
GAM1431 LOC91263 3'	TTGGAGGGTAGGGCTGAAAG 65385	TA G
	CTTTCAGTCTT TTT CAG	

			GAAAGTCGGGA GGA GTT		
			TG G		
GAM1431	LOC91286	3'	GTGGGTAGAGGGTGAGGG 65454	G	TG
			CTTTCA TCTTTATT C		
			GGGAGT GGAGATGG G		
			G GT		
GAM1431	LOC91301	5'	CGGGAAGGGGCTGGGGG 65542	TT	A
			CT CAGTCTTT TTTG		
			GG GTCGGGGA GGCG		
			GG A		
GAM1431	LOC91582	3'	GAGCCGAGTGGAGGCTGGAA 66537		CA AAA
			TTTCAGTCTTTATTTG GC		
			AAGGTCGGAGGTGAGC CG		
			__ AGT		
GAM1431	LOC91694	5'	TGATTGTAAATGAAGATGGAAG 66966	G	_
			CTTTCA TCTTTATTTGCAG CA		
			GAAGGT AGAAGTAAATGTT GT		
			_ A		
GAM1431	LOC91828	5'	CAGGTCGGGGGCTGGGAG 67275	TT	_
			CT CAGTCTTT ATTTG		
			GA GTCGGGGG TGGAC		
			GG C		
GAM1431	LOC91960	3'	TGAATGGGGCTGAGGG 67667	T	
			CTTTCAGTCTT ATTTG		
			GGGAGTCGGGG TAAGT		
			_		
GAM1431	LOC92078	3'	TAAATAGAGGATTGGAGG 67988		_
			CTTTCAGTC TTTATTTG		
			GGAGGTTAG AGATAAAT		
			G		
GAM1431	LOC92170	3'	TTTGCTGTGCAATGACTGGAAG 68371		TTTATTT
			CTTTCAGTC GCAGCAA		
			GAAGGTCAG TGTCGTTT		
			TAACG__		
GAM1431	LOC92270	5'	TAGATGGGGTCTGAGAG 68634	T	
			CTTTCAG CTTTATTTG		
			GAGAGTC GGGGTAGAT		
			T		
GAM1431	LOC93048	5'	CAAATTGAGACTGGAAG 71248	T	
			CTTTCAGTCTT ATTTG		

GAAGGTCAGAG TAAAC  
T  
GAM1431 LOC93297 3' TTGAAGTGAGGATTAGAAG 71951 TC G  
CTT AGTCTTTATTT CAG  
||| ||||| |||  
GAA TTAGGAGTGAA GTT  
GA \_  
GAM1432 CKB 5' CGTCGCTCCGGGAGCTGC 8434 AGC T T  
GCAGCTCCC G GA CGACG  
||| ||| | |||  
CGTCGAGGG C CT GCTGC  
\_ \_ C  
GAM1432 CLASP1 5' CACCTGATAACCGGGGCCGCA 65298 A \_ \_ C  
TGC GCTCC CAG GTG  
||| ||| ||| |||  
ACG CGGGG GTC CAC  
C CCAATA \_  
GAM1432 DDX11 3' ATCAGGTCTGCAGAGCTGCA 47647 C \_ \_ G  
TGCAGCTC CAG C TGAT  
||| ||| ||| |||  
ACGTCGAG GTC G ACTA  
AC T G  
GAM1432 ESR1 5' GCGTTCGCTCCTGGGAGCTGCA 3703 CGT C  
TGCAGCTCCCAG GAT GACGC  
||| ||| ||| |||  
ACGTCGAGGGTC CTG TTGCG  
\_ C  
GAM1432 PPP2R2B 5' ATCCTCGCTGGGAACTG 15905 C T\_  
CAG TCCCAGCG GAT  
||| ||| ||| |||  
GTC AGGGTCGC CTA  
A TC  
GAM1432 SLC39A4 5' TGAGCACGCTGGGAGCTG 55631 A  
CAGCTCCCAGCGTG TCG  
||| ||| ||| |||  
GTCGAGGGTCGCAC AGT  
G  
GAM1432 STAC 3' GCGTCAACCCAAAGGAGCTGC 11992 CAGCG ATC\_  
GCAGCTCC TG GACGC  
||| ||| ||| |||  
CGTCGAGG AC CTGCG  
AA \_ CCAA  
GAM1432 SURF5 3' CATGCTGGGAGCCACA 22182 CA  
TG GCTCCCAGCGTG  
|| ||| ||| |||  
AC CGAGGGTCGTAC  
AC  
GAM1432 TNFSF11 3' ATCATGCTGGAACCTGCA 13511 CTC  
TGCAG CCAGCGTGAT  
||| ||| ||| |||



ACGTC GGTCGTACTA  
 CAA  
 GAM1432 TNFSF11 3' ATCATGCTGGAACCTGCA 52239 CTC  
 TGCAG CCAGCGTGAT  
 |||| |||||  
 ACGTC GGTCGTACTA  
 CAA  
 GAM1432 ABHD2 5' GCGCCGCTGGCAGCCGGGGAGC 22807 A\_ G AT\_ A  
 TGC GCAGCTCCC GC TG CG CGC  
 ||||| || || ||  
 CGTCGAGGG CG AC GC GCG  
 GC \_ GGTC C  
 GAM1432 Apg4B 3' GCGCCGCTGTGCTGGGAGCTGC 25287 TGAT A  
 A TGCAGCTCCCAGCG CG CGC  
 ||||| || ||  
 ACGTCGAGGGTCGT GC GCG  
 GTC\_ C  
 GAM1432 DDX12 3' ATCAGGTCTGCAGAGCTGCA 59693 C\_ \_ G  
 TGCAGCTC CAG C TGAT  
 ||||| || | |||  
 ACGTCGAG GTC G ACTA  
 AC T G  
 GAM1432 DKFZp547C176 5' CGCCGCCGCGCGCCGGGAGCTG 67221 A AT\_ A  
 C GCAGCTCCC GCGTG CG CG  
 ||||| ||| || ||  
 CGTCGAGGG CGCGC GC GC  
 C GCC C  
 GAM1432 FLJ20359 3' TACAGCTGGGGCTGCA 35046 T \_  
 TGCAGC CCCAGC GTG  
 ||||| ||||| ||  
 ACGTCG GGGTCG CAT  
 \_ A  
 GAM1432 FREQ 3' GCGCCTAAGGCTGGGAGCTG 26581 GTGATCGA  
 CAGCTCCCAGC CGC  
 ||||| ||  
 GTCGAGGGTCG GCG  
 GAATCC\_  
 GAM1432 HA-1 5' GCGGCCAGCGCCGGGAGCTGCA 65554 A GATCGA  
 TGCAGCTCCC GCGT CGC  
 ||||| ||| ||  
 ACGTCGAGGG CGCG GCG  
 C ACCG\_  
 GAM1432 HSZFP36 5' GCGTCTGTCGCGCTGGGA 63483 C  
 TCCCAGCGTGAT GACGC  
 ||||| ||||  
 AGGGTCGCGCTG CTGCG  
 T  
 GAM1432 KIAA0977 5' CGCCGCCTGGGAGCTG 29749 C ATCGA  
 CAGCTCCCAG GTG CG  
 ||||| || ||

GTCGAGGGTC CGC GC  
 \_ C\_  
 GAM1432 KIAA1529 5' TCGGCTGGGAGCTCCA 70600 C G  
 TG AGCTCCCAGC TGA  
 || ||||| ||  
 AC TCGAGGGTCG GCT  
 C \_  
 GAM1432 KIAA1924 3' ATCATCCGGGAGCTGC 73665 AGC  
 GCAGCTCCC GTGAT  
 ||||| ||||  
 CGTCGAGGG TACTA  
 CC\_  
 GAM1432 KIAA1957 3' GCGTCTGCAGCTGGGAGCGACA 75717 CA G ATC  
 TG GCTCCCAGC TG GACGC  
 || ||||| || ||||  
 AC CGAGGGTCG AC CTGCG  
 AG \_ GT\_  
 GAM1432 MGC10966 5' TCGACTCGTCATGGGAGCTGC 48901 \_ TGA  
 GCAGCTCCCA GCG TCGA  
 ||||| || ||||  
 CGTCGAGGGT TGC AGCT  
 AC TC\_  
 GAM1432 MGC26914 5' GCGTCTGGCGCGCTGGGACCTG 58667 C ATC  
 CA TGCAG TCCCAGCGTG GACGC  
 |||| ||||| ||||  
 ACGTC AGGGTCGCGC CTGCG  
 C GGT  
 GAM1432 MGC4170 5' GCGTCCGTCGCCGGAGCTGCA 44224 CAGC C  
 TGCAGCTCC GTGAT GACGC  
 ||||| |||| ||||  
 ACGTCGAGG CGCTG CTGCG  
 C\_ C  
 GAM1432 PDZD2 5' CGAACACTGGGAGCCCCA 80867 CA C GA  
 TG GCTCCCAG GT TCG  
 || ||||| || ||  
 AC CGAGGGTC CA AGC  
 CC A \_  
 GAM1432 RAD51 5' CGTGCAGCTGGGAACTGCA 56015 C G ATCG  
 TGCAG TCCCAGC TG ACG  
 |||| ||||| || ||  
 ACGTC AGGGTCG AC TGC  
 A \_ G\_  
 GAM1432 RAD51 5' CGTGCAGCTGGGAACTGCA 11221 C G ATCG  
 TGCAG TCCCAGC TG ACG  
 |||| ||||| || ||  
 ACGTC AGGGTCG AC TGC  
 A \_ G\_  
 GAM1432 RODH-4 5' GCATCAGTCACACTGGGAGCTG 13533 C C C  
 CA TGCAGCTCCCAG GTGAT GA GC  
 ||||| |||| || ||

	ACGTCGAGGGTC CACTG CT CG	
	A A A	
GAM1432 LOC124977 5'	GTCTCAGGCCAAGAGCTGCA 76064	CCA G TC
	TGCAGCTC GC TGA GAC	
	ACGTCGAG CG ACT CTG	
	AAC G _	
GAM1432 LOC146315 5'	ATCAGGTCTCCAGAGCTGCA 60885	CC_ _ G
	TGCAGCTC AG C TGAT	
	ACGTCGAG TC G ACTA	
	ACC T G	
GAM1432 LOC146823 3'	GCATATGATACACCAGAGCTGC 83797	CCAGC _ AC_
A	TGCAGCTC GTG ATCG GC	
	ACGTCGAG CAC TAGT CG	
	AC_ _ A ATA	
GAM1432 LOC169369 5'	GCGCTGCACAGGGAGCTGCA 87284	_____
	TGCAGCTCCC AGCGT	
	ACGTCGAGGG TCGCG	
	ACACG	
GAM1432 LOC170254 5'	GCGCCTTCAAAACGGTAAGAGC 87249	___ AGCG TCGA
TGC	GCAGCTC CC TGA CGC	
	CGTCGAG GG ACT GCG	
	AAT CAAA TCC_	
GAM1432 LOC207089 5'	GCGCCTTCAAAACGGTAAGAGC 89516	___ AGCG TCGA
TGC	GCAGCTC CC TGA CGC	
	CGTCGAG GG ACT GCG	
	AAT CAAA TCC_	
GAM1432 LOC255426 5'	GCGCCGAGGCTCGCACCGGGAG 97160	A_ TGA_ A
CTGC	GCAGCTCCC GCG TCG CGC	
	CGTCGAGGG CGC AGC GCG	
	CCA TCGG C	
GAM1432 LOC257095 5'	GCTTCCCACACTGGGAGC 96940	C ATC C
	GCTCCCAG GTG GA GC	
	CGAGGGTC CAC CT CG	
	A C_ _ T	
GAM1432 LOC257101 5'	GCACGAGCCACCAGGGCTGCA 96906	CCAGC A_ AC
	TGCAGCTC GTG TCG GC	
	ACGTCGGG CAC AGC CG	
	AC_ _ CG A_	
GAM1432 LOC257203 5'	GCGCCAGGTTATGCTGGGGCTG 96932	T GA_
CA	TGCAGC CCCAGCGTGATC CGC	

				ACGTCG GGGTCGTATTGG GCG			
				— ACC			
GAM1432	LOC91373	3'	GCGTCCTGGAGCTGGGGGCTAC	65840	C		GTGATC
	A		TG AGCTCCCAGC GACGC				
			AC TCGGGGGTCG CTGCG				
			A AGGTC_				
GAM1432	LOC92017	5'	CATGTTTCCTGGGAGCCACA	67886	CA		—
			TG GCTCCCAG CGTG				
			AC CGAGGGTC GTAC				
			AC CTT				
GAM1433	ADH1B	3'	CTTAGACATAAAGTAAAAT	72644	C		CAC
			ATTT ACTTT TGTCTGAG				
			TAAA TGAAA ACAGATTC				
			A T_				
GAM1433	AHR	3'	ATCTCAGATGTTAAATAAATG	7875	CAC	C	T
			CATTT TTT AC GTCTGAGAT				
			GTAAA AAA TG TAGACTCTA				
			TA_ T _				
GAM1433	FDFT1	3'	TAGGAAAGTGAAATG	15518		A	
			CATTTCACTTTC CTG				
			GTAAAGTGAAAG GAT				
			—				
GAM1433	JTB	3'	ATCTCAGACAGTGAAAGTGAAA	21959			
	TG		CATTTCACTTTCACTGTCTGAGAT				
			GTAAAGTGAAAGTGACAGACTCTA				
GAM1433	KLF4	3'	TCCCAGACAGTGGATATG	14891	CT		A
			CA TTCACTGTCTG GA				
			GT AGGTGACAGAC CT				
			AT C				
GAM1433	PHYH	3'	ACAGTAAAAGTGAAAT	20608		C	
			ATTTCACTTT ACTGT				
			TAAAGTGAAA TGACA				
			A				
GAM1433	PKD2	3'	TCCAGGTTGAAAGTGAAA	60096		CTG	A
			TTTCACTTTCA TCTG GA				
			AAAGTGAAAGT GGAC CT				
			T_ _				
GAM1433	WRN	3'	GGGCAGTGAAAATGAAA	5098		C	
			TTTCA TTTCACTGTCT				

			AAAGT AAAGTGACGGG	
			A	
GAM1433	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA CTG
			TTTCACTTT CTGT AGAT	
			AAAGTGAAA GACA TCTA	
			C_ CG_	
GAM1433	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT CT
			TTCACCTTTCA GT GAG	
			AAGTGAAAGT CA CTC	
			CT _	
GAM1433	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G T_
			CTTTCACT TC GAGAT	
			GAAAGTGA AG TTCTA	
			G TC	
GAM1433	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT 45802	ACTTTCACT
	G		CATTTTC GTCTGAGAT	
			GTAAAG CAGACTCTA	
			AAACATTT_	
GAM1433	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281	CTT
			CATTTCA TCACTGTCTGAGAT	
			GTAAAGT AGTGACAGACTCTA	
			C_	
GAM1433	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C TC
			TTCA TTTCACTG TGAG	
			AAGT AAAGTGAC GTTT	
			A CT	
GAM1433	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A _
			TTTC CTG TCTGAGAT	
			AAAG GAC AGACTCTA	
			_ G	
GAM1433	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T
			ATT CACTTTCACTGT	
			TAA GTGAAAGTGACG	
			C	
GAM1433	PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA 53598	CA G
			TTCACCTTT CT TCTGAGAT	
			AAGTGAAA GG AGACTCTA	
			CC G	
GAM1433	PP35	3'	ATCTCAGACTGAAA 22814	CT
			TTTCA GTCTGAGAT	

AAAGT CAGACTCTA

GAM1433 PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148 TCAC C\_  
CATTTCACCTT TGT TGAG  
||||||| ||| |||  
GTAAAGTGAA ACG ACTC  
TA\_\_ TT

GAM1433 SEP15 3' TCCTACAGTAAGAGTGAAA 14934 C CT  
TTTCACTTT ACTGT GA  
||||||| ||||| ||  
AAAGTGAGA TGACA CT  
A TC

GAM1433 SFXN2 3' CTCAGGGGAAAAAAGTGAAA 73941 CACTG  
TTTCACTTT TCTGAG  
||||||| |||||  
AAAGTGAAA GGA CTC  
AAAGG

GAM1433 LOC149703 3' ATCTCAGACAGCCGTTTGAAA 84647 ACTTTCA  
TTTC CTGTCTGAGAT  
||| |||||  
AAAG GACAGACTCTA  
GTTTGCC

GAM1433 LOC154007 3' ATCTCAAACCCTTTAGTGAAA 81015 TTCACT C  
TTTCACT GT TGAGAT  
||||| || |||||  
AAAGTGA CA ACTCTA  
TTTCC\_ A

GAM1433 LOC155004 3' TCATTTAAGTGAAAGGAAA 81226 A GTC\_  
TTTC CTTTCACT TGA  
||| ||||| |||  
AAAG GAAAGTGA ACT  
\_ ATTT

GAM1433 LOC222134 5' ACAGTGAAGTGAAATG 94136 T  
CATTTCACCTT CACTGT  
||||||| |||||  
GTAAAGTGAA GTGACA

GAM1434 B3GALT2 5' TGCTCAAAATCCTT 13685 ATAG  
AAGGATTTT GGGCA  
||||||| |||||  
TTCCTAAAA CTCGT

GAM1434 CCBL1 3' ACATGCCCGCAGAGATCCT 14483 ATAG  
AGGATTTT GGGCATGT  
||||||| |||||  
TCCTAGAG CCCGTACA  
ACG\_

GAM1434 IL1A 3' ACATGAAGAAGCTAAATCCTTT 62463 TATAGGGG  
AAAGGATTT CATGT  
||||||| |||||

		TTTCCTAAA GTACA		
		TCGAAGAA		
GAM1434 MME	3'	ACAGTCCTTCAAAATCCTT 23483	AT	A
		AAGGATTTT AGGGGC TGT		
		TTCCTAAAA TTCCTG ACA		
		C_ _		
GAM1434 MME	3'	ACAGTCCTTCAAAATCCTT 23493	AT	A
		AAGGATTTT AGGGGC TGT		
		TTCCTAAAA TTCCTG ACA		
		C_ _		
GAM1434 MME	3'	ACAGTCCTTCAAAATCCTT 6136	AT	A
		AAGGATTTT AGGGGC TGT		
		TTCCTAAAA TTCCTG ACA		
		C_ _		
GAM1434 MME	3'	ACAGTCCTTCAAAATCCTT 23503	AT	A
		AAGGATTTT AGGGGC TGT		
		TTCCTAAAA TTCCTG ACA		
		C_ _		
GAM1434 NRXN1	3'	ATATGTTTATATAAAATCC 57029	GG	
		GGATTTTATA GGCATGT		
		CCTAAAATAT TTGTATA		
		AT		
GAM1434 NRXN1	3'	ATATGTTTATATAAAATCC 16630	GG	
		GGATTTTATA GGCATGT		
		CCTAAAATAT TTGTATA		
		AT		
GAM1434 PCSK2	3'	ACACTGTGCTATAAATCCTTT 10463	TATA G _	
		AAAGGATTT GG GCA TGT		
		TTTCCTAAA TC TGT ACA		
		TA_ G C		
GAM1434 SLC4A4	3'	ACAGTTAATATCAAAATCCTTT 13633	T GG A	
		AAAGGATTT ATA GGC TGT		
		TTTCCTAAA TAT TTG ACA		
		C AA _		
GAM1434 UQCRC1	3'	CCACCAATAAAATCCT 12553	A _	
		AGGATTTTAT GG GG		
		TCCTAAAATA CC CC		
		A A		
GAM1434 XKRY	5'	ACATGCCACACAAATCACTT 16252	_ TATAG	
		AAG GATTT GGGCATGT		

TTC CTAA CCGTACA  
 A CACA\_  
 GAM1434 XKRY 5' ACATGCCCCACACAAATCACTT 60013 \_ TATAG  
 AAG GATT GGGCATGT  
 ||| ||| |||||  
 TTC CTAA CCGTACA  
 A CACA\_  
 GAM1434 C13orf1 3' TCCTGCAAAATCCTTT 39978 A  
 AAAGGATTTT TAGGG  
 ||||| |||  
 TTTCTAAAA GTCCT  
 C  
 GAM1434 dJ309H15.1 3' ACATATTTTATAAAATCTTTT 56795 GC  
 AAAGGATTTTATAGGG ATGT  
 ||||| |||  
 TTTTCTAAAATATTTT TACA  
 A\_  
 GAM1434 DKFZp434A1010 3' ACATGCCCCACTAAACC 71341 A TATA  
 GG TTT GGGGCATGT  
 || ||| |||||  
 CC AAA CCGGTACA  
 \_ TCA\_  
 GAM1434 DKFZp547F072 5' ACATGCCCCCTACACTCCTCC 50092 A TTTTATA  
 A AGGA GGGGCATGT  
 | ||| |||||  
 C TCCT CCGGTACA  
 C CACATC\_  
 GAM1434 DKFZp762L0311 3' ACATGCTAGAAAATCCTCA 38051 A ATAGG  
 A AGGATTTT GGCATGT  
 | ||||| |||||  
 A TCCTAAAA TCGTACA  
 C GA\_  
 GAM1434 GRIP1 3' ACATGGTGCTAAAAATCCTTT 70624 A GGG  
 AAAGGATTTT TAG CATGT  
 ||||| ||| |||  
 TTTCTAAAA ATC GTACA  
 \_ GTG  
 GAM1434 LAK-4P 5' ACATGCCCCTGGCCTACCT 23434 ATTTTA  
 AGG TAGGGGCATGT  
 || |||||  
 TCC GTCCCGTACA  
 ATCCG\_  
 GAM1434 MGC16491 3' ACATACCCCCAGCTGTGAAGCC 53636 A \_ C  
 TT AAGG TTTTATA GGGG ATGT  
 ||| ||||| ||| |||  
 TTCC GAAGTGT CCCC TACA  
 \_ CGAC A  
 GAM1434 MIC2L1 3' ACATGCCTGGAAGACCC 48817 A ATAG  
 GG TTTT GGGCATGT  
 || ||| |||||



			CC AGAA TCCGTACA		
			C GG__		
GAM1434	OLFM3	3'	CTCTATAAGACCCCTT	82144	A_
			AAGG TTTTATAGGG		
			TTCC AGAATATCTC		
			CC		
GAM1434	PDE1C	3'	TCCTCAAAATCCTTT	17221	AT
			AAAGGATTTT AGGG		
			TTTCCTAAAA TCCT		
			C_		
GAM1434	SCDGF-B	3'	CTCTTAAATCCTTT	52449	T
			AAAGGATTTTA AGGG		
			TTTCCTAAAAT TCTC		
			-		
GAM1434	SCDGF-B	3'	CTCTTAAATCCTTT	47377	T
			AAAGGATTTTA AGGG		
			TTTCCTAAAAT TCTC		
			-		
GAM1434	ZNF220	3'	CATGCACAAAATCTTTT	22225	ATAGGG
			AAAGGATTTT GCATG		
			TTTTCTAAAA CGTAC		
			CA__		
GAM1434	LOC113763	3'	ACATACCCCCACACACCAGTCT	56575	TTATA__ C
		TTT	AAAGGATT GGGG ATGT		
			TTTTCTGA CCCC TACA		
			CCACACAC A		
GAM1434	LOC130355	5'	ACATGCCCCTGTGTTACTTT	74928	GATTT
			AAAG TATAGGGGCATGT		
			TTTC GTGTCCCCGTACA		
			ATT__		
GAM1434	LOC149684	3'	CCTCTGCTCAAAATCCTTT	84612	A__
			AAAGGATTTT TAGGGG		
			TTTCCTAAAA GTCTCC		
			CTC		
GAM1434	LOC157556	3'	CTGCTTTAAATCCTT	86484	T G
			AAGGATTTTA AG GG		
			TTCTAAAAT TC TC		
			T G		
GAM1434	LOC157567	3'	CAGTCAGAAAATCCTTT	81478	ATAGG A
			AAAGGATTTT GGC TG		

TTTCTAAAA CTG AC  
 GA\_\_ \_  
 GAM1434 LOC253017 5' TCTTTATAAAATTCCTT 95843 \_  
 AAGGA TTTTATAGGGG  
 ||||| |||||  
 TTCCT AAAATATTTCT  
 T  
 GAM1434 LOC255126 5' ACATACCCCTAACTTTCTCA 97470 A TTTTA C  
 A AGGA TAGGGG ATGT  
 | ||| ||||| |||||  
 A TCTT ATCCCC TACA  
 C TCA\_\_ A  
 GAM1434 LOC256158 5' ACATGCCCCCGAGTATCCTT 97641 T ATA  
 AAGGAT TT GGGGCATGT  
 ||||| || |||||  
 TTCCTA GA CCCC GTACA  
 T GC\_  
 GAM1434 LOC92578 3' ACATGCCCTTGAATTCCTCC 69821 A T TA  
 A AGGA TTTA GGGGCATGT  
 | ||| ||| |||||  
 C TCCT AAGT TCCCGTACA  
 C T \_  
 GAM1434 LOC93259 3' CATACCCCTGTCCTT 71807 TTTAT C  
 AAGGAT AGGGG ATG  
 ||||| ||||| |||  
 TTCCTG TCCCC TAC  
 \_\_\_\_\_ A  
 GAM1434 LOC96652 3' CCCCTAAAAACCCTTT 65465 A A  
 AAAGG TTTT TAGGGG  
 ||||| ||| |||||  
 TTTCC AAAA ATCCCC  
 C \_  
 GAM1435 AQP3 3' TTCACGATCCACCCTTTC 59593 T\_ \_  
 GAAA GTGG TCGTGAA  
 ||| ||| |||||  
 CTTT CACC AGCACTT  
 CC T  
 GAM1435 ARSB 3' TCACGACTCTTGTC 3502 AATGTG  
 GACAAGA GTCGTGA  
 ||||| |||||  
 CTGTTCT CAGCACT  
 \_\_\_\_\_  
 GAM1435 B4GALT5 3' TTTTCACAAAAATAGTCCTTTG 16519 AAA\_ GGTC  
 TCA TGACAAG TGT GTGAAAA  
 ||||| || |||||  
 ACTGTTT ATA CACTTTT  
 CCTG AAAA  
 GAM1435 CHRNA3 3' TCGTTACCCATTTCTT 5610 T CG  
 AAGAAATG GGT TGA  
 ||||| ||| |||

			TTCTTTAC CCA GCT		
			— TT		
GAM1435	DRD1	3'	TTACAACCACATTTCTGGCCA 5840	ACA	C
			TG AGAAATGTGGT GTGA		
			AC TCTTTACACCA CATT		
			CGG A		
GAM1435	FUT1	3'	TCTGATCACATCCCCTGTC 3798	AGAA	T
			GACA ATGTGGTCTG GA		
			CTGT TACACTAGT CT		
			CCCC —		
GAM1435	IRF1	3'	GCCACATTTCTGATCA 64345	CA	
			TGA AGAAATGTGGT		
			ACT TCTTTACACCG		
			AG		
GAM1435	MAP3K8	5'	TCACGACCACCTCATG 17791	A AAT	
			CA GA GTGGTCTGTA		
			GT CT CACCAGCACT		
			A C__		
GAM1435	NGFR	3'	TTCTGACCACACTTCCTGTC 10231	A A	T
			GACA GAA TGTGGTCTG GAA		
			CTGT CTT ACACCAGT CTT		
			C C —		
GAM1435	OLR1	3'	TTCACAACAGTTCTTGTTA 10341	ATGTG	C
			TGACAAGAA GT GTGAA		
			ATTGTTCTT CA CACTT		
			GA__ A		
GAM1435	POU4F1	3'	CACTGAAAACATTTTGTCA 20660	A GG	_
			TGACAAGAA TGT TC GTG		
			ACTGTTTTT ACA AG CAC		
			_ AA T		
GAM1435	SMP1	3'	TTTCACATGAATAATTTTGTGTC 26705	A GGTC	
	A		TGACAAGAA TGT GTGAAA		
			ACTGTTTTT ATA CACTTT		
			A AGTA		
GAM1435	ZNF264	3'	TTCTATTAACATTTCTTTTCA 12769	C	GGTCGT
			TGA AAGAAATGT GAA		
			ACT TTCTTTACA CTT		
			T ATTAT_		
GAM1435	C20orf175	3'	CGAGCTCCACGTTTCCTGCCA 55063	A A	__
			TG CA GAAATGTGG TCG		

AC GT CTTTGCACC AGC  
 C C TCG  
 GAM1435 CAPNS2 3' TTTCACAACCCTACATATTCT 50323 CA \_\_\_\_ C  
 GATCA TGA AGAAATGT GGT GTGAAA  
 ||| ||||| ||| |||||  
 ACT TCTTTATA CCA CACTTT  
 AG CATC A  
 GAM1435 CLDN6 3' TTTACACTCACATTTTTATCA 41041 CA \_ C  
 TGA AGAAATGTG GT GTGAA  
 ||| ||||| || |||||  
 ACT TTTTACAC CA CATT  
 A\_ T\_  
 GAM1435 DKFZP564L0864 3' GCACCAATTTCTTGCCA 72555 A G C  
 TG CAAGAAAT TGGT GT  
 || ||||| |||| ||  
 AC GTTCTTTA ACCA CG  
 C \_ \_  
 GAM1435 DKFZP566B183 3' TTTCCATAAACATTTCTTTTCA 31330 C GGTCGT  
 TGA AAGAAATGT GAAA  
 ||| ||||| ||||  
 ACT TTCTTTACA CTTT  
 T AATAC\_  
 GAM1435 GTF2E1 3' TACAGACCTCTTGTC 18616 AATGT \_  
 TGACAAGA GGTC GTG  
 ||||| |||| ||  
 ACTGTTCT CCAG CAT  
 \_\_\_\_ A  
 GAM1435 KIAA0089 3' TTTTAATTCACATTTCTT 69967 TCG  
 AAGAAATGTGG TGAAA  
 ||||| ||||  
 TTCTTTACACT ATTTT  
 TA\_  
 GAM1435 KIAA0373 5' TTTTCAAAGTAACATTTCTT 28015 GGTCG  
 AAGAAATGT TGAAAA  
 ||||| ||||  
 TTCTTTACA ACTTTT  
 ATGAA  
 GAM1435 KIAA1813 3' TTTTCACACTGTAAATTTCTTG 70314 \_\_ TG C  
 T ACAAGAAAT G GT GTGAAAA  
 ||||| | || |||||  
 TGTTCTTTA T CA CACTTTT  
 AA GT \_  
 GAM1435 KIAA1951 3' TTCCAGGCTTCTCTTGTC 73766 AATGT GT  
 TGACAAGA GGTC GAA  
 ||||| |||| ||  
 ACTGTTCT TCGG CTT  
 CT\_\_ AC  
 GAM1435 MGC4170 3' TTCACCATTTCTTGTC 44227 TGGTC  
 GACAAGAAATG GTGAA  
 ||||| ||||

CTGTTCTTTAC CACTT

GAM1435 NRN1 3' CACTGCACATTTCTCCTCA 33432 CA GTC  
TGA AGAAATGTG GTG  
||| ||||| |||  
ACT TCTTTACAC CAC  
CC GT\_

GAM1435 PLA2G12 3' TTTTCACAACCACATTT 48028 C  
AAATGTGGT GTGAAAA  
||||||| |||||  
TTTACACCA CACTTTT  
A

GAM1435 PPY2 3' CACTCCACATTCCTGGCCA 40819 ACA A TC  
TG AG AATGTGG GTG  
|| ||||| |||  
AC TC TTACACC CAC  
CGG C T\_

GAM1435 ZNF31 3' TTTGTAGACCACATTTCTGTT 64992 A \_TG  
A TGACA GAAATGTGGTC G AA  
||||| ||||| ||| ||  
ATTGT CTTTACACCAG T TT  
C A GT

GAM1435 LOC115219 3' CACGACAACGGGTCCTCA 73295 CAA AA G  
TGA GA TGT GTCGTG  
||| || ||| |||||  
ACT CT GCA CAGCAC  
C\_ GG A

GAM1435 LOC120376 5' TTCAGAGCATTTCTTTCA 75986 C GG G  
TGA AAGAAATGT TC TGAA  
||| ||||| || |||||  
ACT TTCTTTACG AG ACTT

GAM1435 LOC133418 3' TTTTCATATACATTTTGTGCCA 75094 A GTC  
TG CAAGAAATGTG GTGAAA  
|| ||||| |||||  
AC GTTTTACAT TACTTT  
C A\_

GAM1435 LOC151199 3' TTAAAACCACAGCTCTTGCCA 80174 A AA CG  
TG CAAGA TGTGGT TGA  
|| |||| ||||| |||  
AC GTTCT ACACCA ATT  
C CG AA

GAM1435 LOC152317 5' TCACACTGACTTTTGTCA 85649 AATG C  
TGACAAGA TGGT GTGA  
||||| ||| |||||  
ACTGTTTT GTCA CACT  
CA\_ \_

GAM1435 LOC152674 3' TTCAACCCACCCTCTTGTC 85841 AAT TCG  
TGACAAGA GTGG TGAA  
||||| ||| |||||

ACTGTTCT CACC ACTT  
 CC\_ CA\_  
 GAM1435 LOC152845 5' CATGACCACATTTTTCA 60330 CAA  
 TGA GAAATGTGGTCGTG  
 ||| |||||  
 ACT TTTTACACCAGTAC  
 —  
 GAM1435 LOC154743 3' TTTAGTCCACATTGTCTTGTCA 81118 \_ TCG  
 TGACAAGA AATGTGG TGAA  
 ||||| ||||| |||  
 ACTGTTCT TTACACC ATTT  
 G TG\_  
 GAM1435 LOC165476 5' TTCACGGCACCTTCT 87201 AT G  
 AGAA GTG TCGTGAA  
 ||| ||| |||||  
 TCTT CAC GGCACCT  
 C\_ —  
 GAM1435 LOC254266 5' TTTTCGGTCACACATCTTATCA 97356 C AA GT T  
 TGA AAGA TGTG CG GAA  
 ||| ||| ||| |||  
 ACT TTCT ACAC GC TTT  
 A AC TG T  
 GAM1435 LOC255919 3' TTTCATTCTTACATTTCTAATC 95043 CA TC  
 A  
 TGA AGAAATGTGG GTGAAA  
 ||| ||||| |||||  
 ACT TCTTTACATT TACTTT  
 AA CT  
 GAM1435 LOC51754 5' CACGGCCACATCTCTGTCA 71027 A A  
 TGACA GA ATGTGGTCGTG  
 ||||| ||| |||||  
 ACTGT CT TACACCGGCAC  
 \_ C  
 GAM1435 LOC55862 3' ACCTCATTTCTTGCCA 37485 A T  
 TG CAAGAAATG GGT  
 || ||||| |||  
 AC GTTCTTTAC CCA  
 C T  
 GAM1435 LOC55954 3' CACGTGGTCACTTTTCTCATCA 38877 CA T GT \_  
 TGA AGAAA GTG C GTG  
 ||| ||||| ||| | |||  
 ACT TCTTT CAC G CAC  
 AC T TG TG  
 GAM1436 AGTR1 5' GATGAAGAAAATGAATCACA 49008 CTC GG  
 TGTG CGT TCTTCATC  
 |||| ||| |||||  
 ACAC GTA AGAAGTAG  
 TAA AA  
 GAM1436 AGTR1 5' GGATGAAGAAAATGAATCACA 16709 CTC GG  
 TGTG CGT TCTTCATCC  
 |||| ||| |||||

			ACAC GTA AGAAGTAGG		
			TAA AA		
GAM1436 ASB2	3'	GATGAAGACGTGGCCCA	32356	T TC GTG	
		TG GC C GTCTTCATC			
		AC CG G CAGAAGTAG			
		C GT ____			
GAM1436 BAALC	3'	GGATTTCACGGAGACA	45665	G TC	
		TGT CTCCGTGG TTC			
		ACA GAGGCACT AGG			
		— TT			
GAM1436 C1orf1	3'	GAGCTCCAGGGAGCACA	6860	G TC	
		TGTGCTCC TGG TTC			
		ACACGAGG ACC GAG			
		G TC			
GAM1436 C4orf1	3'	ATGAAGACATCTCAGTACA	59505	CCGTG	
		TGTGCT GTCTTCAT			
		ACATGA CAGAAGTA			
		CTCTA			
GAM1436 CD58	3'	GATGAAGACAACAGCATA	8353	CC G	
		TGTGCT GT GTCTTCATC			
		ATACGA CA CAGAAGTAG			
		— A			
GAM1436 CDH3	3'	GATGAAGGGTGAGGACA	8381	G CGT G	
		TGT CTC G TCTTCATC			
		ACA GAG T GGAAGTAG			
		G — G			
GAM1436 COX7A2L	3'	GGATGAAGGCTGAACACA	16353	C CGT	
		TGTG TC GGTCTTCATCC			
		ACAC AG TCGGAAGTAGG			
		A —			
GAM1436 CXCL6	3'	GATGAAGAAGCCCCAAAAACA	11465	GCTCCG —	
		TGT TGG TCTTCATC			
		ACA ACC AGAAGTAG			
		AAA— CGA			
GAM1436 CYP4B1	3'	ATGAAGACTGTACA	5759	TCCGT	
		TGTGC GGTCTTCAT			
		ACATG TCAGAAGTA			
		—			
GAM1436 DMD	3'	GATGAAGAAGGAGCA	14406	GTGG	
		TGCTCC TCTTCATC			

		ACGAGG AGAAGTAG		
		A__		
GAM1436 DMD	3'	GATGAAGAAGGAGCA	14383	GTGG
		TGCTCC TCTTCATC		
		ACGAGG AGAAGTAG		
		A__		
GAM1436 DMD	3'	GATGAAGAAGGAGCA	14388	GTGG
		TGCTCC TCTTCATC		
		ACGAGG AGAAGTAG		
		A__		
GAM1436 DMD	3'	GATGAAGAAGGAGCA	14395	GTGG
		TGCTCC TCTTCATC		
		ACGAGG AGAAGTAG		
		A__		
GAM1436 DMD	3'	GATGAAGAAGGAGCA	14357	GTGG
		TGCTCC TCTTCATC		
		ACGAGG AGAAGTAG		
		A__		
GAM1436 DMD	3'	GATGAAGAAGGAGCA	14363	GTGG
		TGCTCC TCTTCATC		
		ACGAGG AGAAGTAG		
		A__		
GAM1436 DMD	3'	GATGAAGAAGGAGCA	14369	GTGG
		TGCTCC TCTTCATC		
		ACGAGG AGAAGTAG		
		A__		
GAM1436 DMD	3'	GATGAAGAAGGAGCA	14377	GTGG
		TGCTCC TCTTCATC		
		ACGAGG AGAAGTAG		
		A__		
GAM1436 DMD	3'	GATGAAGAAGGAGCA	14401	GTGG
		TGCTCC TCTTCATC		
		ACGAGG AGAAGTAG		
		A__		
GAM1436 DMD	3'	GATGAAGAAGGAGCA	3665	GTGG
		TGCTCC TCTTCATC		
		ACGAGG AGAAGTAG		
		A__		
GAM1436 DSC3	3'	ATGAAGACCGCATGCCA	44338	T TCC
		TG GC GTGGTCTTCAT		



			AC CG CGCCAGAAGTA		
			_ TA_		
GAM1436	DUOX2	3'	GATAAAGACCACTCCTCAC	26021	CTCC C
			GTG GTGGTCTT ATC		
			CAC CACCAGAA TAG		
			TCCT A		
GAM1436	FEZ1	3'	GAATTCAGGAGCACA	42572	G TC
			TGTGCTCC TGG TTC		
			ACACGAGG ACT AAG		
			_ TT		
GAM1436	FST	3'	GATGAAGACCAAGACTACA	20957	C G
			TGTG TCC TGGTCTTCATC		
			ACAT AGG ACCAGAAGTAG		
			C _		
GAM1436	GAGED2	3'	ATGAAGACAAGCTGAAACA	55928	GC C G_
			TGT TC GT GTCTTCAT		
			ACA AG CG CAGAAGTA		
			A_ T AA		
GAM1436	GAS41	5'	GAATGGCCTTCAGGAGCACA	21520	GT__ _
			TGTGCTCC GGTC TTC		
			ACACGAGG CCGG AAG		
			ACTT T		
GAM1436	GFPT2	5'	GGAGCCCACGGAGCCCA	17578	T T
			TG GCTCCGTGG CTTC		
			AC CGAGGCACC GAGG		
			C C		
GAM1436	GLRX	3'	GGATGAATTTGGGGGCACA	9037	GTGGTC
			TGTGCTCC TTCATCC		
			ACACGGGG AAGTAGG		
			GTTT__		
GAM1436	GRAF	3'	GGATGAAGAGGGTTAAACA	30570	GCT__ GTGG
			TGT CC TCTTCATCC		
			ACA GG AGAAGTAGG		
			AAATT G__		
GAM1436	IL12RB2	3'	GATGAAGACATAAAAGACA	7769	G CCGTG
			TGT CT GTCTTCATC		
			ACA GA CAGAAGTAG		
			_ AAATA		
GAM1436	IL1A	3'	GATGAAGGCAAAGCACG	62467	CCGTG
			TGTGCT GTCTTCATC		

			GCACGA	CGGAAGTAG		
			AA__			
GAM1436	IL21R	3'	GGACTCACGGAGCTCA	41430	T	_
			TG GCTCCGTG GTCT			
			AC CGAGGCAC CAGG			
			T T			
GAM1436	IQGAP1	3'	GGATGAAGGAAAGAAGCAC	69040		CCGTGG
			GTGCT TCTTCATCC			
			CACGA GGAAGTAGG			
			AGAAA_			
GAM1436	ITGBL1	3'	ATGAAGACAAGCAC	16573		CCGTG
			TGTGCT GTCTTCAT			
			ACACGA CAGAAGTA			
			A__			
GAM1436	MAML1	3'	GATGGAGAGAGCAC	28590		CGTGG
			GTGCTC TCTTCATC			
			CACGAG AGAGGTAG			
			_____			
GAM1436	MAPK8IP1	3'	GGATGTCCGTTCCAGGAGCACA	18405	G	TCTT__
			TGTGCTCC TGG CATCC			
			ACACGAGG ACC GTAGG			
			_ TTGCCT			
GAM1436	MATK	5'	ATGAGGAAACGGAGCA	57818		GG
			TGCTCCGT TCTTCAT			
			ACGAGGCA AGGAGTA			
			A_			
GAM1436	MATK	5'	ATGAGGAAACGGAGCA	57815		GG
			TGCTCCGT TCTTCAT			
			ACGAGGCA AGGAGTA			
			A_			
GAM1436	NOL3	3'	GACAAAGGCCACACACA	14156	CTCC	CA
			TGTG GTGGTCTT TC			
			ACAC CACCGGAA AG			
			A__ AC			
GAM1436	PCTK3	3'	AGATCACATGGAGCACA	72963		__
			TGTGCTCC GTGGTCT			
			ACACGAGG CACTAGA			
			TA			
GAM1436	SLC13A4	3'	GGACCACCAGGAGCACA	24921		__
			TGTGCTCC GTGGTCT			

			ACACGAGG CACCAGG		
			AC		
GAM1436	TEM7	3'	GGATAAACCACGGAGCA 39888	CTTC	
			TGCTCCGTGGT ATCC		
			ACGAGGCACCA TAGG		
			AA__		
GAM1436	TTID	5'	AAGCCAGGAGCACA 22301	G T	
			TGTGCTCC TGG CTT		
			ACACGAGG ACC GAA		
			- -		
GAM1436	TXNRD1	5'	GACAAAGCCGCGAGCCCA 12459	T C T CA	
			TG GCTC GTGG CTT TC		
			AC CGAG CGCC GAA AG		
			C - - AC		
GAM1436	UVRAG	3'	GATGAAGAAGCAGCATA 12561	CC GG	
			TGTGCT GT TCTTCATC		
			ATACGA CG AGAAGTAG		
			- A-		
GAM1436	WISP2	3'	GGATGAAGAGAAGGCACA 13936	CCGTGG	
			TGTGCT TCTTCATCC		
			ACACGG AGAAGTAGG		
			AAG__		
GAM1436	A2BP1	5'	GGACGGCGGACGGAGCCCA 38061	T G_ -	
			TG GCTCCGT GTC TTC		
			AC CGAGGCA CGG AGG		
			C GG C		
GAM1436	AP1G2	5'	GGACCGCACGGAGCAC 14045	-	
			GTGCTCCGT GGTCT		
			CACGAGGCA CCAGG		
			CG		
GAM1436	AP1G2	5'	GGACCGCACGGAGCAC 54501	-	
			GTGCTCCGT GGTCT		
			CACGAGGCA CCAGG		
			CG		
GAM1436	ARTS-1	3'	GATGGAGAAAAGCACA 33185	CCGTGG	
			TGTGCT TCTTCATC		
			ACACGA AGAGGTAG		
			AA__		
GAM1436	C12orf3	3'	ATGCAGTCAGGAGCACA 39807	G T T	
			TGTGCTCC TGG CT CAT		

ACACGAGG ACT GA GTA  
     — — C  
 GAM1436 C21orf51 3' ATGAAGACGTGGACA 54197 C G  
     TG TCCGTG TCTTCAT  
     || ||||| |||||  
     AC AGGTGC AGAAGTA

    — —  
 GAM1436 CACNA1H 3' GGACGAAGACCGGGCAC 40842 CGT A  
     GTGCTC GGTCTTC TCC  
     ||||| ||||| |||  
     CACGGG CCAGAAG AGG

    — — C  
 GAM1436 CDK5RAP3 3' GGATGAAGATGATAGCCA 47284 T CC G  
     TG GCT GT GTCTTCATCC  
     || ||| || |||||  
     AC CGA TA TAGAAGTAGG

    — — G  
 GAM1436 CDT6 3' AAGTCTCCAAGGAGCACA 40943 G T\_\_  
     TGTGCTCC TGG CTT  
     ||||||| ||| |||  
     ACACGAGG ACC GAA  
     A TCT

GAM1436 DKFZp547C176 5' GATGAAGACCACGCCGCCG 67224 T TC  
     TG GC CGTGGTCTTCATC  
     || || |||||  
     GC CG GCACCAGAAGTAG  
     — CC

GAM1436 DKFZp547G183 3' GATGAAGAAACAGCTCA 38026 T CC GG  
     TG GCT GT TCTTCATC  
     || ||| || |||||  
     AC CGA CA AGAAGTAG  
     T — A\_

GAM1436 DKFZP564A1164 3' GATGAAGATGAAGAGCATA 70978 CGTG  
     TGTGCTC GTCTTCATC  
     ||||| |||||  
     ATACGAG TAGAAGTAG  
     AAG\_

GAM1436 DKFZP566M1046 5' GGATGAAGCAGACTGGAGACA 49538 G \_ G\_ T  
     TGT CTCC GT G CTTCATCC  
     ||| ||| || | |||||  
     ACA GAGG CA C GAAGTAGG  
     — T GA\_

GAM1436 ELF4 3' ATGTCAGCCACGGAAACA 7428 GC CTT  
     TGT TCCGTGGT CAT  
     ||| ||||| |||  
     ACA AGGCACCG GTA  
     A\_ ACT

GAM1436 FLJ10232 3' GAACCCAGGAGCACA 35925 G TC  
     TGTGCTCC TGG TTC  
     ||||||| ||| |||

ACACGAGG ACC AAG  
 \_ C\_  
 GAM1436 FLJ10743 3' GATGAAGGTCAAGAGCACA 36548 CG GT  
 TGTGCTC TG CTTCATC  
 ||||| || |||||  
 ACACGAG AC GAAGTAG  
 A\_ TG  
 GAM1436 FLJ11560 5' GGACCCACGGA ACTACA 47217 C\_ \_  
 TGTG TCCGTGG TCT  
 ||| ||||| |||  
 ACAT AGGCACC AGG  
 CA C  
 GAM1436 FLJ12998 3' GACAGCCACGGAGCTCA 42837 T CT  
 TG GCTCCGTGGT TC  
 || ||||| ||  
 AC CGAGGCACCG AG  
 T AC  
 GAM1436 FLJ13441 3' GGACCTGCACGAAGCACA 43665 C \_  
 TGTGCT CGT GGTCT  
 ||||| ||| |||||  
 ACACGA GCA CCAGG  
 A CGT  
 GAM1436 FLJ20154 3' GGATGAAGAAGGAAAC 72931 GC GTGG  
 GT TCC TCTTCATCC  
 || ||| |||||  
 CA AGG AGAAGTAGG  
 A\_ A\_  
 GAM1436 FLJ20511 3' GATGAAGAAGAAGGCACA 35324 CCGTGG  
 TGTGCT TCTTCATC  
 ||||| |||||  
 ACACGG AGAAGTAG  
 AAGA\_  
 GAM1436 FLJ20618 3' GGATGAAGTAGTGAAGCA 35458 C TG T  
 TGCT CG G CTTCATCC  
 ||| || | |||||  
 ACGA GT T GAAGTAGG  
 A GA\_  
 GAM1436 FLJ20725 3' GGATGAAGACTCACCAC 35610 CTCC \_  
 GTG GTG GTCTTCATCC  
 ||| ||| |||||  
 CAC CAC CAGAAGTAGG  
 \_ T  
 GAM1436 FLJ21820 3' GATGAAGATGAGCCCA 41624 T CGTG  
 TG GCTC GTCTTCATC  
 || ||| |||||  
 AC CGAG TAGAAGTAG  
 C \_  
 GAM1436 FLJ31951 3' GGATAAAGAGCATGAGGACA 58555 G C G C  
 TGT CTC GTG TCTT ATCC  
 ||| ||| ||| ||| |||

			ACA GAG TAC AGAA TAGG		
			G _ G A		
GAM1436	FLJ32312	3'	GGACATCCATGGAGCACA	58496	TC_
			TGTGCTCCGTGG TTC		
			ACACGAGGTACC AGG		
			TAC		
GAM1436	GMPPB	5'	ATGAAGGCACAGGAGCA	95722	GTG
			TGCTCC GTCTTCAT		
			ACGAGG CGGAAGTA		
			ACA		
GAM1436	GNG10	3'	ATGAAGACCAGAAAGTACA	14675	CCG
			TGTGCT TGGTCTTCAT		
			ACATGA ACCAGAAGTA		
			AAG		
GAM1436	KIAA0169	3'	GATGAAGAGGTCAACAGCA	72819	CCG _
			TGCT TGG TCTTCATC		
			ACGA ACT AGAAGTAG		
			CA_ GG		
GAM1436	KIAA0446	5'	GGATACACTGGAGCACA	68874	_ _
			TGTGCTCC GTG GTCT		
			ACACGAGG CAC TAGG		
			T A		
GAM1436	KIAA0543	5'	GGACGAGGGCCAGAGCCA	68938	T CG A
			TG GCTC TGGTCTTC TCC		
			AC CGAG ACCGGGAG AGG		
			_ _ C		
GAM1436	KIAA0561	3'	GATGAAGTTCAAGCCA	65885	T CCG GT
			TG GCT TG CTTCATC		
			AC CGA AC GAAGTAG		
			_ _ TT		
GAM1436	KIAA0711	5'	GGACAGCCTCCAGGAGCACA	29523	G TCTTCA
			TGTGCTCC TGG TCC		
			ACACGAGG ACC AGG		
			_ TCCGAC		
GAM1436	KIAA0923	3'	GGATGCTACGGACACA	25837	C C
			TGTG TCCGTGGT TTC		
			ACAC AGGCATCG AGG		
			_ T		
GAM1436	KIAA1018	3'	AGACTTCACGGAGCCA	30346	T _
			TG GCTCCGTG GTCT		

AC CGAGGCAC CAGA  
 \_ TT  
 GAM1436 KIAA1041 5' GATGAAGAAGCAAGACA 30133 G CC GG  
 TGT CT GT TCTTCATC  
 ||| || || |||||  
 ACA GA CG AGAAGTAG  
 \_ A\_ A\_  
 GAM1436 KIAA1077 3' GATGAAGACCCAAGGCATA 72906 CCGT  
 TGTGCT GGTCTTCATC  
 ||||| |||||  
 ATACGG CCAGAAGTAG  
 AAC\_  
 GAM1436 KIAA1237 3' GGATGAAGTGAGGGGAATACA 80472 C GTGGT  
 TGTG TCC CTTCATCC  
 ||| ||| |||||  
 ACAT AGG GAAGTAGG  
 A GGAGT  
 GAM1436 KIAA1253 3' ATGAAGACACTGAAATACA 91895 C\_ C G  
 TGTG TC GTG TCTTCAT  
 ||| || ||| |||||  
 ACAT AG CAC AGAAGTA  
 AA T \_  
 GAM1436 KIAA1416 3' ATGAAGACGAGAACA 86456 G CGTG  
 TGT CTC GTCTTCAT  
 ||| ||| |||||  
 ACA GAG CAGAAGTA  
 A \_  
 GAM1436 KIAA1511 3' GAATAAATCATGGATCACA 70164 C C\_  
 TGTG TCCGTGGT TTC  
 ||| ||||| |||  
 ACAC AGGTACTA AAG  
 T AAT  
 GAM1436 KIAA1649 3' GATGAAGGTTGAGCCA 50263 T CGT GT  
 TG GCTC G CTTCATC  
 || ||| | |||||  
 AC CGAG T GAAGTAG  
 \_ \_ TG  
 GAM1436 KIAA1706 3' GGATGCTACCAGGGAGCACA 92790 G CTT  
 TGTGCTCC TGGT CATCC  
 ||||| ||| |||||  
 ACACGAGG ACCA GTAGG  
 G TC\_  
 GAM1436 KIAA1719 3' GATGAGGAAACAGGCACA 68163 CC GG  
 TGTGCT GT TCTTCATC  
 ||||| || |||||  
 ACACGG CA AGGAGTAG  
 A\_ A\_  
 GAM1436 KIAA1954 3' GATGAAGACTGAAAGCCA 77720 T CCG  
 TG GCT TGGTCTTCATC  
 || ||| |||||

AC CGA GTCAGAAGTAG  
 \_ AA\_  
 GAM1436 KIAA1981 3' GATGAAACCATGGAAGCCA 88343 T \_ C  
 TG GCT CCGTGGT TTCATC  
 || ||| ||||| |||||  
 AC CGA GGTACCA AAGTAG  
 \_ A \_  
 GAM1436 KIAA1987 3' GGATGAAGCTGAAAAGACA 88020 G CCG T  
 TGT CT TGG CTTTCATCC  
 ||| || ||| |||||  
 ACA GA GTC GAAGTAGG  
 \_ AAA \_  
 GAM1436 KLHL6 3' ATGAATCATGGAAACA 55300 GC CT  
 TGT TCCGTGGT TCAT  
 ||| ||||| |||  
 ACA AGGTACTA AGTA  
 A\_ \_  
 GAM1436 LRBA 3' ATGAGGCGGAGCCA 22052 T TGGT  
 TG GCTCCG CTTTCAT  
 || ||||| |||||  
 AC CGAGGC GGAGTA  
 \_ \_  
 GAM1436 MBD2 3' GATGAAGACATCAGGAAACA 31718 GC GTG\_  
 TGT TCC GTCTTCATC  
 ||| ||| |||||  
 ACA AGG CAGAAGTAG  
 A\_ ACTA  
 GAM1436 MEGF11 3' GAAGCCTGCCATGGAACACA 50580 C \_  
 TGTG TCCGTGGT CTTC  
 |||| ||||| |||  
 ACAC AGGTACCG GAAG  
 A TCC  
 GAM1436 MGC15873 3' GATGAGGACACAGACACA 51903 C C G  
 TGTG TC GTG TCTTCATC  
 |||| || ||| |||||  
 ACAC AG CAC AGGAGTAG  
 \_ A \_  
 GAM1436 MGC5508 3' GGATAAAGGGTGGGGAAACA 44038 GC G G C  
 TGT TCC TG TCTT ATCC  
 ||| ||| || ||||| |||  
 ACA AGG GT GGAA TAGG  
 A\_ G G A  
 GAM1436 PEG10 3' ATGATACCTGGAGCACA 30518 T CT  
 TGTGCTCCG GGT TCAT  
 ||||| ||| |||  
 ACACGAGGT CCA AGTA  
 \_ T\_  
 GAM1436 PLA2G12 3' GATGAAGATGGAAGAACA 48024 GC\_ GTG  
 TGT TCC GTCTTCATC  
 ||| ||| |||||



ACA AGG TAGAAGTAG  
 AGA \_\_\_\_  
 GAM1436 RBM9 3' GATGAAGAGGAAAAACA 26681 GC\_ GTGG  
 TGT TCC TCTTCATC  
 ||| ||| |||||  
 ACA AGG AGAAGTAG  
 AAA \_\_\_\_  
 GAM1436 RHOBTB2 3' AAGGCCACAGGACACA 60940 C \_  
 TGTG TCC GTGGTCTT  
 |||| ||| |||||  
 ACAC AGG CACCGGAA  
 \_ A  
 GAM1436 SCYB5 3' GATGAAGAAGCTAGAAAACA 11468 GC C\_ GG  
 TGT TC GT TCTTCATC  
 ||| || || |||||  
 ACA AG CG AGAAGTAG  
 AA AT A\_  
 GAM1436 SEC24C 3' GGATAAAACATATAGGTGCACA 16998 T GTG\_\_ C C  
 TGTGC CC GT TT ATCC  
 |||| || || |||||  
 ACACG GG CA AA TAGG  
 T ATATA A \_  
 GAM1436 SPC12 3' GATGGGGAACAGAACACA 95825 C C GG  
 TGTG TC GT TCTTCATC  
 |||| || || |||||  
 ACAC AG CA AGGGGTAG  
 A A \_  
 GAM1436 SS18L1 3' GATGAAGAACTGAGGCACA 65346 TC TGG  
 TGTGC CG TCTTCATC  
 |||| || |||||  
 ACACG GT AGAAGTAG  
 GA CA\_  
 GAM1436 TTTY9 5' GATGAAGAAGAGGACA 49185 G CGTGG  
 TGT CTC TCTTCATC  
 ||| ||| |||||  
 ACA GAG AGAAGTAG  
 G A\_\_\_\_  
 GAM1436 ust3 3' GATAAAGACCACCCTGGCCA 93228 T CC\_ C  
 TG GCT GTGGTCTT ATC  
 || ||| ||||| |||  
 AC CGG CACCAGAA TAG  
 \_ TCC A  
 GAM1436 LOC115110 3' ATGAACCGTGGACACA 71710 C CT  
 TGTG TCCGTGGT TCAT  
 |||| ||||| |||  
 ACAC AGGTGCCA AGTA  
 \_ \_  
 GAM1436 LOC116123 5' GGATGAAGATCTGGAGCCCA 57087 T T  
 TG GCTCCG GGTCTTCATCC  
 || ||||| ||||| |||

AC CGAGGT CTAGAAGTAGG  
 C \_  
 GAM1436 LOC126549 5' GATGAAGACGCGCTGGCCCA 75710 T CC \_  
 TG GCT GTG GTCTTCATC  
 || ||| ||| |||||  
 AC CGG CGC CAGAAGTAG  
 C T\_ G  
 GAM1436 LOC127703 3' GGATGGGGACAGAGGACA 74679 G CGTG  
 TGT CTC GTCTTCATCC  
 ||| ||| |||||  
 ACA GAG CAGGGGTAGG  
 G A\_\_  
 GAM1436 LOC130666 5' GGAGCGGTCCAGGAGCACA 75757 G T TCA  
 TGTGCTCC TGG CT TCC  
 ||||| ||| |||  
 ACACGAGG ACC GG AGG  
 \_ T CG\_  
 GAM1436 LOC144262 5' GAAGGCCACAAAGAACA 76749 G CC  
 TGT CT GTGGTCTTC  
 ||| ||| |||||  
 ACA GA CACCGGAAG  
 A AA  
 GAM1436 LOC144766 3' GGATGAAGCTAGGTGAAGCA 76955 \_ G T  
 TGCT CC TGG CTTCATCC  
 ||| ||| ||| |||||  
 ACGA GG ATC GAAGTAGG  
 AGT \_ \_  
 GAM1436 LOC146445 3' GGAGGCCTCCACGGAGCACA 83679 \_  
 TGTGCTCCGT GGTCTTC  
 ||||| |||||  
 ACACGAGGCA CCGGAGG  
 CCT  
 GAM1436 LOC148354 3' GATGGAGAGAGAGCACA 78800 CGTGG  
 TGTGCTC TCTTCATC  
 ||||| |||||  
 ACACGAG AGAGGTAG  
 AG\_\_  
 GAM1436 LOC149296 3' GATAAAGGCGAGCAC 79258 CGTG C  
 GTGCTC GTCTT ATC  
 ||||| ||||| |||  
 CACGAG CGGAA TAG  
 \_ A  
 GAM1436 LOC149422 3' GATACCGCGGAGCACA 79350 CT  
 TGTGCTCCGTGGT TC  
 ||||| ||||| |||  
 ACACGAGGCGCCA AG  
 T\_  
 GAM1436 LOC149703 3' GATGAAGAGACATGAGGACA 84653 G C G\_  
 TGT CTC GTG TCTTCATC  
 ||| ||| ||| |||||

	ACA GAG TAC AGAAGTAG	
	G _ AG	
GAM1436 LOC149935 3'	GGATGAAGATGACAGCCA	60301 T CC G
	TG GCT GT GTCTTCATCC	
	AC CGA CA TAGAAGTAGG	
	_ _ G	
GAM1436 LOC152273 3'	GATGAAGATGTGGAAAC	80538 GC GTG
	GT TCC GTCTTCATC	
	CA AGG TAGAAGTAG	
	A_ TG_	
GAM1436 LOC152445 3'	GGATGAAGAATTCAGACA	85756 G CCGTGG
	TGT CT TCTTCATCC	
	ACA GA AGAAGTAGG	
	_ CTTA_	
GAM1436 LOC152925 3'	AAGGCCATAGCACA	80732 CC
	TGTGCT GTGGTCTT	
	ACACGA TACCGGAA	
	_	
GAM1436 LOC157421 5'	AGGGCCACGAAGTACA	86442 C
	TGTGCT CGTGGTCTT	
	ACATGA GCACCGGGA	
	A	
GAM1436 LOC163426 5'	GATGAAGATGAAGCCCA	82139 T C GTG
	TG GCT C GTCTTCATC	
	AC CGA G TAGAAGTAG	
	C A _	
GAM1436 LOC170409 3'	GATGAAGGAGGAACATA	82862 C GTGG
	TGTG TCC TCTTCATC	
	ATAC AGG GGAAGTAG	
	A A_	
GAM1436 LOC201911 3'	GGACGAAGGGAGGGAGCA	90262 GTGG A
	TGCTCC TCTTC TCC	
	ACGAGG GGAAG AGG	
	GAG_ C	
GAM1436 LOC203246 3'	ATGAAGATGACAGCAC	89302 CC G
	GTGCT GT GTCTTCAT	
	CACGA CA TAGAAGTA	
	_ G	
GAM1436 LOC220038 5'	ATGAGGACAGAGACA	91719 G CGTG
	TGT CTC GTCTTCAT	

ACA GAG CAGGAGTA  
 \_ A\_\_\_\_  
 GAM1436 LOC220753 5' GATGAAGAAGTGGGAGACA 92942 G GTGG  
 TGT CTCC TCTTCATC  
 ||| ||| |||||  
 ACA GAGG AGAAGTAG  
 \_ GTGA  
 GAM1436 LOC221466 5' GATGAAGAAGCTGAAGCCCA 93687 T \_ C GG  
 TG GCT C GT TCTTCATC  
 || ||| || |||||  
 AC CGA G CG AGAAGTAG  
 C A T A\_  
 GAM1436 LOC221712 5' GGATAACAATGGAGCA 93625 G CTTC  
 TGCTCCGT GT ATCC  
 ||||| || |||  
 ACGAGGTA CA TAGG  
 A AA\_\_\_\_  
 GAM1436 LOC222182 5' GGACGAAGACCACTGAGCAT 94192 C A  
 GTGCTC GTGGTCTTC TCC  
 ||||| ||||| |||  
 TACGAG CACCAGAAG AGG  
 T C  
 GAM1436 LOC253216 3' GATGAAGGGCAAGGACA 94958 C G G  
 TG TCC TG TCTTCATC  
 || ||| || |||||  
 AC AGG AC GGAAGTAG  
 \_ A G  
 GAM1436 LOC255271 5' GATGAAGAGATACCAGCCA 95501 T CC G\_  
 TG GCT GTG TCTTCATC  
 || ||| || |||||  
 AC CGA CAT AGAAGTAG  
 \_ C\_ AG  
 GAM1436 LOC255411 3' GATGGAGAAAGCACA 94882 CCGTGG  
 TGTGCT TCTTCATC  
 ||||| |||||  
 ACACGA AGAGGTAG  
 A\_\_\_\_  
 GAM1436 LOC255849 3' GGATGAGGAGACAGAAAACA 96444 GC C GG  
 TGT TC GT TCTTCATCC  
 ||| ||| |||||  
 ACA AG CA AGGAGTAGG  
 AA A G\_  
 GAM1436 LOC256789 5' GGACAGGGCACAGAGACA 97447 G C G TCA  
 TGT CTC GTG TCT TCC  
 ||| ||| ||| ||| |||  
 ACA GAG CAC GGA AGG  
 \_ A G C\_  
 GAM1436 LOC256995 5' ATGATTTCAGGAGCACA 97588 G TCT  
 TGTGCTCC TGG TCAT  
 ||||| ||| |||

			ACACGAGG ACT AGTA		
			_ T _		
GAM1436	LOC51652	3'	GGAGCTGACCAGGAGCACA 32194	G	TTCA
			TGTGCTCC TGGTC TCC		
			ACACGAGG ACCAG AGG		
			_ TCG _		
GAM1436	LOC90494	5'	ATGAAAGTCCAGGAGCATA 63052	G T	_
			TGTGCTCC TGG CTT CAT		
			ATACGAGG ACC GAA GTA		
			_ T A		
GAM1436	LOC90835	5'	GGATGAAGACCCCGGAGCCA 64132	T	T
			TG GCTCCG GGTCTTCATCC		
			AC CGAGGC CCAGAAGTAGG		
			_ C		
GAM1436	LOC91133	3'	GATCTGCCATGGAGCACA 65012	CT	_
			TGTGCTCCGTGGT TC		
			ACACGAGGTACCG AG		
			TCT		
GAM1436	LOC91522	3'	GATGAAGGTAGAAGCAC 66314	CCGTG	
			GTGCT GTCTTCATC		
			CACGA TGGAAGTAG		
			AGA _		
GAM1436	LOC92228	3'	GATGAAGAGAGGAGGACA 68542	G	GTGG
			TGT CTCC TCTTCATC		
			ACA GAGG AGAAGTAG		
			G AG _		
GAM1436	LOC92539	5'	ATGAAGGTGGAGCCA 69629	T	TGG
			TG GCTCCG TCTTCAT		
			AC CGAGGT GGAAGTA		
			_ _		
GAM1437	FTSJ2	3'	CCAAAAAGAGATGACAAACT 25434	T	ACAA
			AGTTTT TCATCTCT TGG		
			TCAAAA AGTAGAGA ACC		
			C AAA _		
GAM1437	LDHB	5'	CCATTTTGGAGATGAAGAACT 9708	C	
	GA		TCAGTTTTTTCATCTCTA AATGG		
			AGTCAAAGAAGTAGAGGT TTACC		
			T		
GAM1437	MYCL1	3'	CCATTAACAGATGGAAAACTG 18161	CTAC	
	A		TCAGTTTTTTCATCT AATGG		

			AGTCAAAAAGGTAGA	TTACC	
			CAA_		
GAM1437	NT5E	3'	CCACCTGTCAGATGAAAAAACT	10280	CT A_
	GA		TCAGTTTTTTTCATCT	ACA TGG	
			AGTCAAAAAGGTAGA	TGT ACC	
			C_ CC		
GAM1437	PTGIS	3'	CCACTTCATAGATGAGAAAACT	6327	CTACAA
	GA		TCAGTTTTTTTCATCT	TGG	
			AGTCAAAAGAGTAGA	ACC	
			TACTTC		
GAM1437	ZNF83	3'	TTGAGAGAAACAAAAACACTGA	36982	_ CA_ A
			TCAGT TTTT	TCTCT CAA	
			AGTCA AAAAA	AGAGA GTT	
			C CAA	_	
GAM1437	KIAA0040	5'	CCATTTTGGAGATGAAGAACT	27782	C
	GA		TCAGTTTTTTTCATCTCTA	AATGG	
			AGTCAAAGAAGTAGAGGT	TTACC	
			T		
GAM1437	KIAA1922	5'	CCTTTTAGAGATGAGAAAACTG	73623	C T
	A		TCAGTTTTTTTCATCTCTA	AA GG	
			AGTCAAAAGAGTAGAGAT	TT CC	
			T	_	
GAM1437	KRTAP1-3	3'	AGAAATGAAAAAGCCGA	48237	A C
			TC GTTTTTTCAT	TCT	
			AG CGAAAAAGTA	AGA	
			C A		
GAM1437	SGP28	3'	AGTAATGAAAAAACTGA	20227	CT
			TCAGTTTTTTTCAT	CT	
			AGTCAAAAAGTA	GA	
			AT		
GAM1437	SIAT4A	5'	TGGAGATGAAGAACTGA	11677	
			TCAGTTTTTTTCATCTCTA		
			AGTCAAAGAAGTAGAGGT		
GAM1437	LOC113146	3'	AGAGATGCAAAAAACT	72970	_
			AGTTTTTT	CATCTCT	
			TCAAAAAA	GTAGAGA	
			C		
GAM1437	LOC151720	5'	CCATTTACAGATGAAGAACTG	80338	C C
	A		TCAGTTTTTTTCATCT	TA AATGG	

AGTCAAAGAAGTAGA AT TTACC  
 C \_  
 GAM1437 LOC152580 3' CCAGGTTT TAGATGAAAACT 85775 T CT AA  
 AGTTTTT CATCT AC TGG  
 ||||| |||| || |||  
 TCAAAAA GTAGA TG ACC  
 \_ TT G\_  
 GAM1437 LOC158696 3' CCATTGTATCTTGGAAATAACT 81972 T ATCTC  
 AGTT TTTC TACAATGG  
 ||| ||| |||||  
 TCAA AAAG ATGTTACC  
 T GTTCT  
 GAM1437 LOC253805 3' CCATTTTCCAGATGAAGAAACT 96427 CTAC  
 GA TCAGTTTTTTCATCT AATGG  
 ||||| |||||  
 AGTCAAAGAAGTAGA TTACC  
 CCTT  
 GAM1437 LOC92078 5' CCATTTTACAGATGAGAAAACT 67979 C C  
 GA TCAGTTTTTTCATCT TA AATGG  
 ||||| ||||| |||||  
 AGTCAAAGAGTAGA AT TTACC  
 C T  
 GAM1438 ABCA3 5' GAAACTCTTCCACTGTGA 6562 C AACC CA  
 TCAC AGTGGA AG TTTC  
 ||| |||| || |||  
 AGTG TCACCT TC AAAG  
 \_ \_\_\_\_ TC  
 GAM1438 CARPX 3' GAAATGCTACAACGTGTGA 39422 C GGAAACC  
 TCAC AGT AGCATTTC  
 ||| ||| |||||  
 AGTG TCA TCGTAAAG  
 \_ ACA\_\_\_\_  
 GAM1438 DEK 3' AAATGCTGATATTTACTGG 12956 AAC  
 CCAGTGGA CAGCATTT  
 ||||| |||||  
 GGTCATTT GTCGTAAA  
 ATA  
 GAM1438 DGKB 3' AAATGCTGGAAAGCGAGTGA 92530 CA GGAAA  
 TCAC GT CCAGCATTT  
 ||| || |||||  
 AGTG CG GGTGTAAG  
 AG AAA\_\_\_\_  
 GAM1438 HTR7 3' AAATGCTGACTACTGTAGA 39097 AC AAAC  
 TC CAGTGG CAGCATTT  
 || |||| |||||  
 AG GTCATC GTCGTAAA  
 AT A\_\_\_\_  
 GAM1438 KDR 3' GAAATGCTGGGAACAATG 9593 G GAAA  
 CA TG CCAGCATTTT  
 || || |||||

			GT AC GGTCGTAAAG		
			A AAG_		
GAM1438 KMO	3'	TGACAGTGATTCA	CCACTGGTG 13459	AAACCAG	_
A		TCACCAGTGG	CATT TCA		
		AGTGGTCACC	GTGA AGT		
		ACTTA_	C		
GAM1438 LAMA4	3'	GCAATTCCTACTGGTGA	9669	_	ACCA
		TCACCAGT GGAA	GC		
		AGTGGTCA CCTT	CG		
		T AA_			
GAM1438 LEP	3'	TGACGGTCCCACACTGGTGA	4059	GAA_	AG
		TCACCAGTG	ACC CA		
		AGTGGTCAC	TGG GT		
		ACCC	CA		
GAM1438 LPIN2	3'	AGGTCTTGGTCTCCATTGGCGA	27703	A	A C
		TC CCAGTGGA	ACCAG ATTT		
		AG GGTACCT	TGGTT TGGA		
		C	C C		
GAM1438 MBNL	5'	AAATGAACCCACTGGTG	40723	AAACCAG	
		CACCAGTGG	CATTT		
		GTGGTCACC	GTAAA		
		CAA_			
GAM1438 PPARGC1	3'	AAATGTTGATCTTCCACTG	25156	AC_	
		CAGTGGAA	CAGCATTT		
		GTCACCTT	GTTGTAAA		
		CTA			
GAM1438 PRSS7	3'	TGAAATGCTAGGGGGCCAGGG	10916	AG	AAA _
		CC TGG	CC AGCATTTCA		
		GG ACC	GG TCGTAAAGT		
		G_	GGG A		
GAM1438 SELL	3'	TGAAATGCTAGCTGCAAGTGA	5394	CA TG	AAACC
		TCAC G G	AGCATTTCA		
		AGTG C C	TCGTAAAGT		
		AA GT GA_			
GAM1438 TBL1X	3'	TGGTTTCCACTGAGGA	18940	AC	
		TC CAGTGGAA	ACCA		
		AG GTCACCTTTGGT			
		GA			
GAM1438 TNFAIP1	5'	TGAGGCTCTGGCCTCCACTGG	40926	AA	CA
		CCAGTGGAA	CCAG TTCA		



GGTCACCT GGTC GGAGT  
CC TC

GAM1438 ZNF14 3' GAAAGAATTCCCACTGGTGA 40715 AAACCAGCA  
TCACCA GTG TTT  
||||||| |||  
AGTGGTCACC AAAG  
CTTAAG\_\_

GAM1438 ARPP-19 3' TGAAATGCTAAGTGCCCA 21806 AA C\_  
TGG AC AGCATTTC  
||| || |||||  
ACC TG TCGTAAAGT  
CG AA

GAM1438 C20orf97 3' TGTCGGCCTCCACTGATG 40965 C AA A  
CA CAGTGGA CC GCA  
|| ||||| |||  
GT GTCACCT GG TGT  
A CC C

GAM1438 CLDN8 3' TGAAATGCCAGTCCATTACACT 24035 GAA\_\_ CA  
G CAGTG AC GCATTTC  
||||| || |||||  
GTCAC TG CGTAAAGT  
ATTACC AC

GAM1438 EKI1 3' TGAAATGCCAGTCATTGACTG 37810 G A\_ CA  
CAGT GA AC GCATTTC  
||||| || |||||  
GTCA TT TG CGTAAAGT  
G AC AC

GAM1438 FLJ10618 3' AAATGTTTTGGTTTCCACTGCT 36343 C \_  
GA TCA CAGTGGAACCA GCATT  
||| |||||  
AGT GTCACCTTTGGT TGTA  
C TT

GAM1438 FLJ12443 3' CTGGTTTCCATGGTGA 45728 G  
TCACCA TGGAAACCAG  
||||| |||||  
AGTGGT ACCTTTGGTC

GAM1438 FLJ12649 3' TGAAATGCTGGGAGTCC 44787 AA\_  
GGA CCAGCATTTC  
||| |||||  
CCT GGTCTGTAAGT  
GAG

GAM1438 FLJ14397 3' TGAAACCCTGTTTCCACT 51329 C CA  
AGTGGAAC AG TTCA  
||||| || |||  
TCACCTTTG TC AAAGT  
\_ CC

GAM1438 FLJ20209 3' TGACATGGGTTTCCATGGTGA 85519 G AG T  
TCACCA TGGAAACC CAT TCA  
||||| ||||| ||| |||

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AGTGGT ACCTTTGG GTA AGT
      _ _ C
GAM1438 FRB 3' TGAAATGCCATCTCCACT 19092 AACCA
            AGTGGA GCATTTCA
            ||||| |||||
            TCACCT CGTAAAGT
            CTAC_
GAM1438 GNB4 3' AAATACTGGTTTCTAAGTGG 41265 G_ C
            CCA TGGAAACCAG ATTT
            ||| ||||| |||
            GGT ATCTTTGGTC TAAA
            GA A
GAM1438 HT010 3' TGAAAATCTTTTCCACTGGAGA 37474 A CC CA
            TC CCAGTGGAAA AG TTTCA
            || ||||| || |||
            AG GGTACCTTT TC AAAGT
            A _ TA
GAM1438 KIAA1046 3' TGAAATGGCTGTTTCCAC 29999 C _
            GTGGAAAC AGC ATTTCA
            ||||| || |||||
            CACCTTTG TCG TAAAGT
            _ G
GAM1438 PLP1 3' GGTACTTCCACTGATGG 5009 C _
            TCA CAGTGGAA ACC
            ||| ||||| |||
            GGT GTCACCTT TGG
            A CA
GAM1438 RGS13 5' AAATGCTGGGTGTCTCAC 58574 _ AA_
            GTG GA CCAGCATTT
            ||| || |||||
            CAC CT GGTCGTAAA
            T GTG
GAM1438 RGS13 5' AAATGCTGGGTGTCTCAC 11337 _ AA_
            GTG GA CCAGCATTT
            ||| || |||||
            CAC CT GGTCGTAAA
            T GTG
GAM1438 SBI31 3' GAAATGCTGGCACCAGG 25876 AG AAA
            CC TGG CCAGCATTT
            || ||| |||||
            GG ACC GGTCGTAAAG
            _ AC_
GAM1438 SYT6 3' TGAAATGCTGCGTCTCCA 78775 A _
            TGG AC CAGCATTTCA
            ||| || |||||
            ACCT TG GTCGTAAAGT
            C C
GAM1438 TIEG 3' AAATGCTTCCACTG 18955 AACC
            CAGTGGAG AGCATTT
            ||||| |||||

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GTCACCT TCGTAAA

GAM1438 TOR1B 3' GTTGGTTCCCATGGTGA 27203 G A  
TCACCA TGG AACCAGC  
||||| ||| |||||  
AGTGGT ACC TTGGTTG

— C  
GAM1438 ZNF297B 3' TGAAATGCTGGCCAT 25789 AAA  
GTGG CCAGCATTTCA  
||| |||||  
TACC GGTCTGTAAAGT

—  
GAM1438 LOC145231 3' GAAATGCTAGCCAGGGTG 83284 AG AAACC  
CACC TGG AGCATTTTC  
||| ||| |||||  
GTGG ACC TCGTAAAG  
G\_ GA\_

GAM1438 LOC147042 3' TGTTAATTTCCACTGG 83915 CC  
CCAGTGGAAA AGCA  
||||||| |||  
GGTCACCTTT TTGT  
AA

GAM1438 LOC147947 5' TGAGAGAATTCACACTGGTGA 78583 \_ ACCAGCA  
TCACCAGTG GAA TTTCA  
||||||| ||| |||||  
AGTGGTCAC CTT AGAGT  
A AAG\_

GAM1438 LOC150998 3' TGAAATGCTAGCTGTGACACTG 85187 GAA C\_  
CAGTG AC AGCATTTCA  
||||| || |||||  
GTCAC TG TCGTAAAGT  
AG\_ TCGA

GAM1438 LOC151521 3' TGAAATGCCGGCCCCCTTGAGT 85440 \_ T AAA A  
AC CAG GG CC GCATTTCA  
|| ||| || |||||  
TG GTT CC GG CGTAAAGT  
A C CC\_ C

GAM1438 LOC153442 3' TGAAATACCAGTGGTTTCTA 86041 GC\_  
TGGAACCA ATTTCA  
||||||| |||||  
ATCTTTGGT TAAAGT  
GACCA

GAM1438 LOC154282 3' TGCAGCCTCCGCTGGTGA 86212 AACCA  
TCACCAGTGGA GCA  
||||||| |||  
AGTGGTCGCCT CGT  
CCGA\_

GAM1438 LOC159089 3' TGAAATGCTGGCCTTGTGT 86988 \_ T AAA  
AC CAG GG CCAGCATTTCA  
|| ||| || |||||

		TG GTT CC GGT	CGTAAAGT		
		T _ _ _			
GAM1438	LOC196424	3'	TGAAATGCTAATGTCAACT	87703	G AACC
			AGT GA AGCATTTCA		
			TCA CT TCGTAAAGT		
			A GTAA		
GAM1438	LOC255535	3'	GCCTGGTTTCCAGTGGTGA	95707	G _
			TCACCA TGGAAACCAG C		
			AGTGGT ACCTTTGGTC G		
			G C		
GAM1438	LOC257048	3'	AGTGTCCCCACTGGTGA	96215	AAACCA
			TCACCAGTGG GCATT		
			AGTGGTCACC TGTGA		
			CC _ _		
GAM1438	LOC51152	3'	GAAATGCTAAATCTAGTGG	32452	G AACC
			CCA TGA AGCATTTT		
			GGT ATCT TCGTAAAG		
			G AAA _		
GAM1438	LOC55885	3'	AAATGCTGAGAACTAGTGA	37811	C GGAAAC
			TCAC AGT CAGCATTT		
			AGTG TCA GTCGTAAA		
			A AGA _ _		
GAM1438	LOC57146	3'	AGGTGTAGTTTCCACTG	39911	CA
			CAGTGGAAAC GCATT		
			GTCACCTTTG TGTGGA		
			A _		
GAM1438	LOC90826	3'	GAAAGGCTTCCACTG	64093	AACC A
			CAGTGGA AGC TTTC		
			GTCACCT TCG AAAG		
			_ _ G		
GAM1439	CDS2	3'	TTTCTAGAAATCCCTGCT	13779	AAAT CA
			AGCAGG GG TCTAGAAA		
			TCGTCC CT AGATCTTT		
			_ _ AA		
GAM1439	CLCN6	3'	TCTTCCCCTCCTGCT	41393	A CATCT
			AGCAGGAA TGG AGA		
			TCGTCCTT ACC TCT		
			C CT _ _		
GAM1439	CLCN6	3'	TCTTCCCCTCCTGCT	41408	A CATCT
			AGCAGGAA TGG AGA		

		TCGTCCTT ACC	TCT	
		C CT__		
GAM1439	CLCN6	3' TCTTCCCACTTCCTGCT	7086	A CATCT
		AGCAGGAA TGG	AGA	
		TCGTCCTT ACC	TCT	
		C CT__		
GAM1439	CLDN5	3' TTCCCAGAGGCTCCTGCTG	12347	AATG A A_
		TAGCAGGA GC TCT	GAA	
		GTCGTCCT CG AGA	CTT	
		___ G CC		
GAM1439	COL18A1	3' TCCAGGATTTCCTGCT	47578	GGCA A
		AGCAGGAAAT TCT	GA	
		TCGTCCTTTA GGA	CT	
		___ C		
GAM1439	COL18A1	3' TCCAGGATTTCCTGCT	55290	GGCA A
		AGCAGGAAAT TCT	GA	
		TCGTCCTTTA GGA	CT	
		___ C		
GAM1439	COL18A1	3' TCCAGGATTTCCTGCT	55294	GGCA A
		AGCAGGAAAT TCT	GA	
		TCGTCCTTTA GGA	CT	
		___ C		
GAM1439	CREBL2	3' TTCCCAGACATGAATTCCTG	7148	GG __ A_
		CAGGAAAT CA TCT	GAA	
		GTCCTTTA GT AGA	CTT	
		A_ AC CC		
GAM1439	DAB2	3' TTCTCCCATTTCTTGCTA	7199	CATCT
		TAGCAGGAAATGG	AGAA	
		ATCGTTCTTTACC	TCTT	
		C__		
GAM1439	ESRRBL1	3' TTTCTAGATGTATTCC	35852	ATG
		GGAA GCATCTAGAAA		
		CCTT TGTAGATCTTT		
		A__		
GAM1439	EYA1	3' TTTTCTAAAATTTTTCCTGC	4958	TGGCATC
		GCAGGAAA TAGAAAA		
		CGTCCTTT ATCTTTT		
		TTTAAA_		
GAM1439	F8	3' TCTACTAATTTTCCTGCTG	3735	GGCATC
		TAGCAGGAAAT TAGA		

GTCGTCCTTTA ATCT  
 ATC\_\_\_\_  
 GAM1439 FIGF 5' TTCTCTGCATTTTCTGC 15559 G TCT  
 GCAGGAAATG CA AGAA  
 ||||| || |||  
 CGTCTTTTAC GT TCTT  
 \_ C\_  
 GAM1439 GLTSCR1 3' TCTTCCCATTTCCTGGC 31678 \_ CATCT  
 GC AGGAAATGG AGA  
 || ||||| |||  
 CG TCCTTTACC TCT  
 G CT\_\_\_\_  
 GAM1439 GNB3 3' TTCCGGGTGCCATTCCCACTA 9081 CA A TA  
 TAG GGAA TGGCATC GAA  
 ||| ||| ||||| |||  
 ATC CCTT ACCGTGG CTT  
 AC \_ GC  
 GAM1439 GUCY1B3 3' TTCTAGATATATCTCTCACTA 5968 CA A GC  
 TAG GGA ATG ATCTAGAA  
 ||| ||| ||| |||||  
 ATC TCT TAT TAGATCTT  
 AC C A\_  
 GAM1439 H1F5 5' TTCTAGCAGTTTCTTGC 18018 GGCAT  
 GCAGGAAAT CTAGAA  
 ||||| |||||  
 CGTTCTTTG GATCTT  
 AC\_\_\_\_  
 GAM1439 HIP1 3' TTCTAGATGGACCCAGC 18067 A AAAT \_\_\_\_  
 GC GG GG CATCTAGAA  
 || || || |||||  
 CG CC CC GTAGATCTT  
 A \_\_\_\_ AG  
 GAM1439 IL1RL1LG 3' TTTTAGTTTCCTGC 22472 TGGCAT  
 GCAGGAAA CTAGAA  
 ||||| |||||  
 CGTCCTTT GATTTT  
 \_\_\_\_\_  
 GAM1439 IL27 3' TTCTCAGTTCCTCCTGCT 64693 A CAT \_  
 G TAGCAGGAA TGG CT AGAA  
 ||||| ||| || |||  
 GTCGTCCTT ACC GA TCTT  
 C CTT C  
 GAM1439 LPIN2 3' TCTGGTCGCCTCATTTCTGCT 27712 \_ AT  
 A TAGCAGGAAAT GGC CTAGA  
 ||||| ||| |||||  
 ATCGTCCTTTA CCG GGTCT  
 CT CT  
 GAM1439 LSP1 3' GATGCCATCCGCTG 9810 A AA  
 TAGC GGA TGGCATC  
 ||| ||| |||||

GTCG CCT ACCGTAG

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      — —
GAM1439 MKKS  5' TTTTCTAGATCTTGA CTCCCTG 38140  AAAT__ C
      C              GCAGG  GG ATCTAGAAAA
                ||||  || |||||
                CGTCC  TC TAGATCTTTT
                CTCAGT _
GAM1439 MYO1D  3' TCTGGACCACCTCCCGCTG 71771  A AA CA
                TAGC GGA TGG TCTAGA
                |||| ||| ||| |||||
                GTCG CCT ACC AGGTCT
                C CC _
GAM1439 NR1I2  3' CTAGGGAATTCCTGCTA 41828  ATGGCA
                TAGCAGGAA TCTAG
                ||||| ||||
                ATCGTCCTT GGATC
                AAG__
GAM1439 NR1I2  3' CTAGGGAATTCCTGCTA 13968  ATGGCA
                TAGCAGGAA TCTAG
                ||||| ||||
                ATCGTCCTT GGATC
                AAG__
GAM1439 OPCML  3' TTTCTGGGACACTATCCTACTA 10349  C AA CA_
                TAG AGGA TGG TCTAGAAA
                ||| ||| ||| |||||
                ATC TCCT ATC GGGTCTTT
                A _ ACA
GAM1439 PDHB  3' CTAGATGCCATGCT 87419  GGAAA
                AGCA TGGCATCTAG
                ||| |||||
                TCGT ACCGTAGATC
      — —
GAM1439 PPP1R2  3' TCTTCTGTCA TTTGCTGCTA 20696  G TCT
                TAGCAG AAATGGCA AGA
                |||| ||||| |||
                ATCGTC TTTACTGT TCT
                G CT_
GAM1439 RS1  3' CTAGGGCTACCATTTTCCTAGC 4391  _ CA__
                GC AGGAAATGG TCTAG
                || ||||| ||||
                CG TCCTTTACC GGATC
                A ATCG
GAM1439 SEL1L  3' TTTTCTAGTCTGTCTTCCTGC 17369  AT T_
                GCAGGAA GGCA CTAGAAAA
                ||||| ||| |||||
                CGTCCTT CTGT GATCTTTT
                _ CT
GAM1439 TCL1B  3' TTCTAGATGCCACTCC 16988  AA
                GGA TGGCATCTAGAA
                ||| |||||
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			CCT ACCGTAGATCTT		
			C_		
GAM1439	AKAP11	3'	TCTACATTTCTACTA	32714	C GCATC
			TAG AGGAAATG TAGA		
			ATC TCCTTTAC ATCT		
			A		
GAM1439	CALN1	3'	CTAGATGTCAGCCACTACTA	48865	C GAAA
			TAG AG TGGCATCTAG		
			ATC TC ACTGTAGATC		
			A ACCG		
GAM1439	CBX6	3'	TCTAGCTTGCTTCCTGCT	26626	AAT T_
			AGCAGGA GGCA CTAGA		
			TCGTCCT TCGT GATCT		
			TC		
GAM1439	CLDN4	3'	TTCCCAAGGCCGCTCCTGCTA	7138	AA ATCTA
			TAGCAGGA TGGC GAA		
			ATCGTCCT GCCG CTT		
			CC GAACC		
GAM1439	DKFZp434G118	3'	TTTCCAGGCTTCTTTCTGCT	50059	T_ AT A
			AGCAGGAAA GGC CT GAAA		
			TCGTCCTTT TCG GA CTTT		
			CT _ C		
GAM1439	DKFZP586I2223	3'	TTCTGGGGGCCATTTCC	54914	A
			GGAAATGGC TCTAGAA		
			CCTTTACCG GGGTCTT		
			-		
GAM1439	DKFZP586I2223	3'	TTCTGGGGGCCATTTCC	54923	A
			GGAAATGGC TCTAGAA		
			CCTTTACCG GGGTCTT		
			-		
GAM1439	DKFZP586I2223	3'	TTCTGGGGGCCATTTCC	31273	A
			GGAAATGGC TCTAGAA		
			CCTTTACCG GGGTCTT		
			-		
GAM1439	DKFZP727G051	3'	TTCTCTTCCACTTTCCTGC	69484	_ CATCT
			GCAGGAAA TGG AGAA		
			CGTCCTTT ACC TCTT		
			C TTC_		
GAM1439	DKFZp761H2121	5'	TTTTCTAGACACCAGAATAGGC	56374	AGGAAA CA
			GC TGG TCTAGAAAA		



		CG ACC AGATCTTTT		
		GATAAG AC		
GAM1439	DNAL4	3' AGGGCCTTTTCCTGC	19212	T A
		GCAGGAAA GGC TCT		
		CGTCCTTT CCG GGA		
		T _		
GAM1439	FLJ13105	3' ATGCATTTTCCTGCTA	46543	G
		TAGCAGGAAATG CAT		
		ATCGTCCTTTAC GTA		
		-		
GAM1439	FLJ22789	3' TTTTCTAAACATATATGTCCTG	94871	A GCATC_
		TTA TAGCAGGA ATG TAGAAAA		
		ATTGTCCT TAT ATCTTTT		
		G ATACAA		
GAM1439	GNG4	3' TCTCCAAATGCCACCTCTTCCT	15628	A__ CT__
		GCT AGCAGGAA TGGCAT AGA		
		TCGTCCTT ACCGTA TCT		
		CTCC AACC		
GAM1439	KIAA0026	5' TTTCTAGGTTGTATCTCCCACT	24412	CA AATG _
		AG GGA GCA TCTAGAAA		
		TC CCT TGT GGATCTTT		
		AC CTA_ T		
GAM1439	KIAA0258	3' TTTCTCACCCTCTCCTGCTA	28827	AA_ CATCT
		TAGCAGGA TGG AGAAA		
		ATCGTCCT ACC TCTTT		
		CTC AC__		
GAM1439	KIAA0451	3' TTCTCTGTGCACTTCTGCTA	29121	AATG CT
		TAGCAGGA GCAT AGAA		
		ATCGTCCT CGTG TCTT		
		CA__ TC		
GAM1439	KIAA1040	3' TCCAGAATATTTCTGT	72234	GCA A
		GCAGGAAATG TCT GA		
		TGTCCTTTAT AGA CT		
		A__ C		
GAM1439	KIAA1041	3' TTTTCTAGACACCAAATAGCT	30147	AGGAAA CA
		G TAGC TGG TCTAGAAAA		
		GTCG ACC AGATCTTTT		
		ATAAA_ AC		
GAM1439	KIAA1557	3' TTTCTAGACTTTCTGT	61141	TGGCA
		GCAGGAAA TCTAGAAA		

			TGTCCTTT	AGATCTTT		
			C___			
GAM1439	KIF1C	3'	TTCCAGGCCTCCTGCTA	61228	AAT	AT A
			TAGCAGGA	GGC CT GAA		
			ATCGTCCT	CCG GA CTT		
			___ _	C		
GAM1439	MAPK8IP3	3'	TCCAGAAGCTTACTTCCTGCTG	52994	AT_	A A
			TAGCAGGAA	GGC TCT GA		
			GTCGTCCTT	TCG AGA CT		
			CAT	A C		
GAM1439	MGC11082	3'	TTCTTTCCATTTCTGC	51104	G	CATCT
			GCAG AAATGG	AGAA		
			CGTC TTTACC	TCTT		
			_	TT___		
GAM1439	MGC4415	3'	TTCTAGATGTGCCTTCCCGCT	48957	A	ATG
			AGC GGAA	GCATCTAGAA		
			TCG CCTT	TGTAGATCTT		
			C	CCG		
GAM1439	NAG73	5'	TTCTAAGCCATTTCC	50809	ATC	
			GGAAATGGC	TAGAA		
			CCTTTACCG	ATCTT		
			A_			
GAM1439	NRF	5'	TTAGACATTTCTGC	34085	GCA	
			GCAGGAAATG	TCTAG		
			CGTCCTTTAC	AGATT		
			___			
GAM1439	PRO2086	5'	TTCTAGATGCCCTCCTAGC	26072	_	AAT
			GC AGGA	GGCATCTAGAA		
			CG TCCT	CCGTAGATCTT		
			A	C_		
GAM1439	SCAMP-4	3'	TTTCCTTCATCATTTCTGC	54404		CATCTA
			GCAGGAAATGG	GAAA		
			CGTCCTTTACT	CTTT		
			ACTTC_			
GAM1439	SIRPB1	3'	GTCATGCTTCCTGTTA	20261	___	
			TAGCAGGAA	ATGGC		
			ATTGTCCTT	TACTG		
			CG			
GAM1439	SLC7A3	5'	TTCTTCAATTCCTGCTA	51431	A	CATCT
			TAGCAGGAA	TGG AGAA		

		ATCGTCCTT ACT TCTT	
		A _____	
GAM1439	SSBP4	3' TTTTCTGTATGGACCCTTCCTG 50936	AT __ C
	C	GCAGGAA GG CAT TAGAAAA	
		CGTCCTT CC GTA GTCTTTT	
		C_ AG T	
GAM1439	STK39	3' TTTCTGCCCATTTCCT 25080	CATC
		AGGAAATGG TAGAAA	
		TCCTTTACC GTCTTT	
		C____	
GAM1439	LOC112687	3' TCTTGAAACCATTCCT 72871	CA T
		AGGAAATGG TC AGA	
		TCCTTTACC AG TCT	
		AA T	
GAM1439	LOC129285	3' TTTCCAGACCTGCTCCTGCTG 74869	AAT CA A
		TAGCAGGA GG TCT GAAA	
		GTCGTCCT CC AGA CTTT	
		CGT __ C	
GAM1439	LOC146909	3' AGACATCCATCCTGCTA 78166	AA CA_
		TAGCAGGA TGG TCT	
		ATCGTCCT ACC AGA	
		__ TAC	
GAM1439	LOC148894	5' TCTCCTATGAATTCCTGGC 84259	_ GG CT_
		GC AGGAAAT CAT AGA	
		CG TCCTTTA GTA TCT	
		G A_ TCC	
GAM1439	LOC150319	3' AGATGCCACCTCCTGC 79646	AA
		GCAGGA TGGCATCT	
		CGTCCT ACCGTAGA	
		CC	
GAM1439	LOC150368	3' TTCTCTCCTTCCTGCTA 79704	AT CATCT
		TAGCAGGAA GG AGAA	
		ATCGTCCTT CC TCTT	
		__ TC__	
GAM1439	LOC151996	5' TTCTCTGGCTTTCCTGCTA 85540	AT ATCT
		TAGCAGGAA GGC AGAA	
		ATCGTCCTT TCG TCTT	
		__ GTC_	
GAM1439	LOC158263	3' GGAAGCCTTCCTGCT 81850	AT A
		AGCAGGAA GGC TCT	

	TCGTCCTT CCG AGG	
	___ A	
GAM1439 LOC158476 5'	TCTAGTTTAACTCTTGCTA 86857	AAT CAT__
	TAGCAGGA GG CTAGA	
	ATCGTTCT CC GATCT	
	___ AATTT	
GAM1439 LOC158835 5'	TTCTCCAAGATATTTCTGGC 82014	_ GCATCT
	GC AGGAAATG AGAA	
	CG TCCTTTAT TCTT	
	G AGAACC	
GAM1439 LOC200576 3'	TTTTCTAACATTTTTCTGCT 88827	TGGCATC
G	TAGCAGGAAA TAGAAAA	
	GTCGTCCTTT ATCTTTT	
	TTTACA_	
GAM1439 LOC200830 3'	TTCCAGTCATGCTTCCTGTTA 90152	AAT __ A
	TAGCAGGA GGCAT CT GAA	
	ATTGTCCT TCGTA GA CTT	
	___ CT C	
GAM1439 LOC204084 5'	TTTCTTGTAACACCTCCTGCTG 89449	AA C CT
	TAGCAGGA TGG AT AGAAA	
	GTCGTCCT ACC TG TCTTT	
	CC A T_	
GAM1439 LOC219793 5'	TCTTGCTCCTTCCTGCTA 91377	AT TCT
	TAGCAGGAA GGCA AGA	
	ATCGTCCTT TCGT TCT	
	CC ___	
GAM1439 LOC221922 5'	TCTCCAGCCCTCCTGCTG 92705	AAT ATCT
	TAGCAGGA GGC AGA	
	GTCGTCCT CCG TCT	
	C_ ACC_	
GAM1439 LOC254228 3'	TTTGCGAACCATTTCTT 95961	CA _
	AGGAAATGG TC TAGA	
	TCCTTTACC AG GTTT	
	A_ C	
GAM1439 LOC255833 5'	TTCTAGCAGTTTCTTGC 94630	GGCAT
	GCAGGAAAT CTAGAA	
	CGTTCTTTG GATCTT	
	AC___	
GAM1439 LOC256849 5'	TTTTCTAGGGACTTTCCTGT 96953	AT CA
	GCAGGAA GG TCTAGAAAA	

			TGTCCTT TC GGATCTTTT		
			___ AG		
GAM1439	LOC90139	3'	TCTAATCTCCTCCTGCTG 55404	AAT	CATC
			TAGCAGGA GG TAGA		
			GTCGTCCT CC ATCT		
			___ TCTA		
GAM1439	LOC90557	3'	TCTATAGCATTTCTG 57063	G	ATC
			CAGGAAATG C TAGA		
			GTCCTTTAC G ATCT		
			_AT_		
GAM1439	LOC91409	3'	TCTATAGCATTTCTG 65960	G	ATC
			CAGGAAATG C TAGA		
			GTCCTTTAC G ATCT		
			_AT_		
GAM1440	LILRB4	3'	TGCCCAGCTGCACAGCTT 22436	A	ACT
			AAGCTGTGCAGC TG GCA		
			TTCGACACGTCG AC CGT		
			_ C_		
GAM1440	NCOA4	3'	GTCATTGCCATACAGCTTCA 18370	CA	_
			TGAAGCTGTG GCA TGAC		
			ACTTCGACAT CGT ACTG		
			AC T		
GAM1440	PTPN7	3'	GCAACTGCACAGCCCCA 54551	AA	CATGAC
			TG GCTGTGCAG TGC		
			AC CGACACGTC ACG		
			CC A_____		
GAM1440	PTPN7	3'	GCAACTGCACAGCCCCA 54562	AA	CATGAC
			TG GCTGTGCAG TGC		
			AC CGACACGTC ACG		
			CC A_____		
GAM1440	PTPN7	3'	GCAACTGCACAGCCCCA 11069	AA	CATGAC
			TG GCTGTGCAG TGC		
			AC CGACACGTC ACG		
			CC A_____		
GAM1440	SLA2	3'	CAGCCATGCTGTTTCAG 49891	T_	A
			CTG GCAGCATG CTG		
			GAC TGTCGTAC GAC		
			TT C		
GAM1440	XRCC2	3'	TCACGCTACCCAGCTTCA 18329	TGC	A
			TGAAGCTG AGC TGA		

ACTTCGAC TCG ACT  
 CCA C  
 GAM1440 DKFZP434C212 3' ATACTGCACAGCATCA 68904 A C  
 TGA GCTGTGCAG AT  
 ||| ||||| ||  
 ACT CGACACGTC TA  
 A A  
 GAM1440 DKFZP434D146 3' CAGTGAGTTTGCACAGCTCA 31522 A C G\_  
 TGA GCTGTGCAG AT ACTG  
 ||| ||||| || |||  
 ACT CGACACGTT TG TGAC  
 \_ \_ AG  
 GAM1440 DKFZP434P211 3' CAGGTGCTGCACGCTCCA 27261 A T GA  
 TG AGC GTGCAGCAT CTG  
 || ||| ||||| |||  
 AC TCG CACGTCGTG GAC  
 C \_ \_  
 GAM1440 FLJ22969 3' CAGTCATGACAGCTCA 68647 A GCAG  
 TGA GCTGT CATGACTG  
 ||| ||| |||||  
 ACT CGACA GTACTGAC  
 \_ \_  
 GAM1440 HSPC117 3' GCAGTCATACTGATCTTTA 26676 CTGTG C  
 TGAAG CAG ATGACTGC  
 |||| ||| |||||  
 ATTTG GTC TACTGACG  
 TA\_\_ A  
 GAM1440 KIAA1550 3' TGCAGTCATACACACT 66569 C CAGC  
 AG TGTG ATGACTGCA  
 || ||| |||||  
 TC ACAC TACTGACGT  
 \_ A\_\_  
 GAM1440 MGC9564 3' GCCCAAAGTGCACAGCCCCA 54741 AA CA ACT  
 TG GCTGTGCAG TG GC  
 || ||||| || ||  
 AC CGACACGTC AC CG  
 CC AA C\_\_  
 GAM1440 RNF9 3' TGCTATGCTGCACTGCCTCA 53414 A T ACT  
 TGA GC GTGCAGCATG GCA  
 ||| || ||||| |||  
 ACT CG CACGTCGTAT CGT  
 C T \_  
 GAM1440 TRAF3 3' ATGCAGTTCTAGGCACAGC 59734 AGCAT  
 GCTGTGC GACTGCAT  
 ||||| |||||  
 CGACACG TTGACGTA  
 GATC\_  
 GAM1440 LOC150174 3' CAGGTGCTGCACGCTCCA 79605 A T GA  
 TG AGC GTGCAGCAT CTG  
 || ||| ||||| |||

			AC TCG CACGTCGTG GAC			
			C _ _			
GAM1440	LOC150213	3'	CAGGTGCTGCACGCTCCA	74852	A T	GA
			TG AGC GTGCAGCAT CTG			
			AC TCG CACGTCGTG GAC			
			C _ _			
GAM1440	LOC150236	5'	CAGGTGCTGCACGCTCCA	79684	A T	GA
			TG AGC GTGCAGCAT CTG			
			AC TCG CACGTCGTG GAC			
			C _ _			
GAM1440	LOC157421	5'	TATGCTGCCAGCCTCA	86445	A T	
			TGA GCTG GCAGCATG			
			ACT CGAC CGTCGTAT			
			C _			
GAM1440	LOC253933	3'	ATGCCAGCTGCACAACTT	96039	C	A ACT
			AAG TGTGCAGC TG GCAT			
			TTC ACACGTCG AC CGTA			
			A _ C _			
GAM1440	LOC51001	5'	ATGCTGCACAACTCA	31950	A C	
			TGA G TGTGCAGCAT			
			ACT C ACACGTCGTA			
			_ A			
GAM1440	LOC51314	3'	CAACCATTGTCACAGCTTC	33520		AGC AC
			GAAGCTGTGC ATG TG			
			CTTCGACACG TAC AC			
			GTT CA			
GAM1441	BACE	3'	CCCCCAAATCTTCCTCTGGAGC	57287	G TT_	C
	TT		AAGCT CCA GAAGAT TGGGGG			
			TTCGA GGT CTTCTA ACCCCC			
			_ CTC A			
GAM1441	BACE	3'	CCCCCAAATCTTCCTCTGGAGC	23977	G TT_	C
	TT		AAGCT CCA GAAGAT TGGGGG			
			TTCGA GGT CTTCTA ACCCCC			
			_ CTC A			
GAM1441	C5R1	3'	CCCAGCCTCCCCCAATGGCA	8202	AA_ T_	
			TGCCATTG GA CTGGG			
			ACGGTAAC CT GACCC			
			CCC CC			
GAM1441	CHRNA4	3'	CCCCCAGACCCCATCCAGC	5615	CCAT AAGA	
			GCTG TG TCTGGGGG			

CGAC AC AGACCCCC  
 CT\_\_ CCC\_  
 GAM1441 EZH1 3' CCCAGGCCCAACGGCAGC 8816 A AAGA  
 GCTGCC TTG TCTGGG  
 ||||| ||| |||||  
 CGACGG AAC GGACCC  
 C CCC\_  
 GAM1441 GORASP1 3' CCTGTATCCCCAGTGGCAACT 49109 C AA CT  
 AG TGCCATTG GAT GGG  
 || ||||| ||| |||  
 TC ACGGTGAC CTA TCC  
 A CC TG  
 GAM1441 GPR62 5' CCCCCAAGAGGATGGCAGC 89519 GAAGA \_  
 GCTGCCATT TCT GGGGG  
 ||||| ||| |||||  
 CGACGGTAG AGA CCCCC  
 G\_\_ A  
 GAM1441 MHC2TA 3' CCTGTGTCTTGCAATGGCAGC 4170 \_ CT  
 GCTGCCATTG AAGAT GGG  
 ||||| ||||| ||| |||  
 CGACGGTAAC TTCTG TCC  
 G TG  
 GAM1441 POLS 3' CCATCTTCAAGAACAGCT 22791 CCA TC  
 AGCTG TTGAAGA TGG  
 |||| ||||| |||  
 TCGAC AACTTCT ACC  
 AAG \_  
 GAM1441 PSCD4 3' CCCCCAGAAGGAACCGCAGCT 25404 CATTGAAGA  
 AGCTGC TCTGGGGG  
 |||| |||||  
 TCGACG AGACCCCC  
 CCAAGGA\_  
 GAM1441 SELL 3' CCCCCAGACCTTTTATCCACTT 5390 C CCATT A  
 AAG TG GAAG TCTGGGGG  
 ||| || ||||| |||||  
 TTC AC TTTC AGACCCCC  
 \_ CTAT\_ C  
 GAM1441 SLC1A5 5' CCCCAGATTCTGGCA 78536 TTGAA  
 TGCCA GATCTGGGG  
 |||| |||||  
 ACGGT TTAGACCCC  
 C\_  
 GAM1441 SLC1A5 5' CCCCAGATTCTGGCA 18845 TTGAA  
 TGCCA GATCTGGGG  
 |||| |||||  
 ACGGT TTAGACCCC  
 C\_  
 GAM1441 TIMP4 5' CCCCAGACCTCACAGGC 12290 AT A A  
 GCC TGA G TCTGGGG  
 ||| ||| |||||



CGG ACT C AGACCCC  
AC \_ C

GAM1441 ABLIM 3' CCTCCTGCAATGGCAGC 9764 A ATCT  
GCTGCCATTG AG GGGG  
||||||| || |||  
CGACGGTAAC TC CTCC  
G \_\_\_\_

GAM1441 ABLIM 3' CCTCCTGCAATGGCAGC 22025 A ATCT  
GCTGCCATTG AG GGGG  
||||||| || |||  
CGACGGTAAC TC CTCC  
G \_\_\_\_

GAM1441 C11orf9 3' CCCCCAGATGGTATTGCAGCTT 25210 CAT AAG  
AAGCTGC TG ATCTGGGGG  
||||| || |||||  
TTCGACG AT TAGACCCCC  
TT\_ GG\_

GAM1441 C16orf5 3' CCCCTGGGACCAACAGCAGC 25446 CA AAGA TG  
GCTGC TTG TC GGGG  
|||| ||| || |||  
CGACG AAC GG CCCC  
AC CA\_ GT

GAM1441 CLSTN3 3' CCCCCAATGGCAGCT 28206 TGAAGATC  
AGCTGCCAT TGGGGG  
||||||| |||||  
TCGACGGTA ACCCCC

GAM1441 DEPP 5' CCCCCAGACCTCCTCAGCT 22821 CCATT A A  
AGCTG GA G TCTGGGGG  
|||| ||| |||||  
TCGAC CT C AGACCCCC  
TC\_ \_ C

GAM1441 DKFZp547E052 3' CCCTTCCCAGTGGCAGCTT 50097 AA TCT  
AAGCTGCCATTG GA GGGG  
||||||| || |||  
TTCGACGGTGAC CT TCCC  
C\_ \_\_\_\_

GAM1441 FLJ12788 3' CCCCCAGATTACTCACAGCT 42543 CCAT A\_  
AGCTG TGA GATCTGGGGG  
|||| ||| |||||  
TCGAC ACT TTAGACCCCC  
\_\_\_\_ CA

GAM1441 FLJ32332 3' CCATCTTCAAGACAGC 58301 CCA TC  
GCTG TTGAAGA TGG  
|||| ||||| |||  
CGAC AACTTCT ACC  
AG\_ \_\_\_\_

GAM1441 FREQ 3' CCCCCAGACCCTTGAGCGCT 26572 T CAT G A\_  
AGC GC T AAG TCTGGGGG  
||| || | ||| |||||

TCG CG A TTC AGACCCCC  
 \_ \_ \_ G CC

GAM1441 KIAA0321 5' CCCCCAGAGAGACTGGCAGC 62392 TTGAAGA  
 GCTGCCA TCTGGGGG  
 ||||| |||||  
 CGACGGT AGACCCCC  
 CAGAG\_

GAM1441 KIAA0346 3' CCCTTCCACCCCATTGGCAGCT 68362 T AAGATCT  
 AGCTGCCA TG GGGG  
 ||||| || |||  
 TCGACGGT AC TCCC  
 T CCCACCT

GAM1441 KIAA0773 3' CCCCCAGACCACGGTGGACAGC 28052 \_ AAGA  
 T AGCTG CCATTG TCTGGGGG  
 |||| |||| |||||  
 TCGAC GGTGGC AGACCCCC  
 A ACC\_

GAM1441 KIAA1538 3' CCCCAAATCCAGTGAGCT 71536 GC AA C  
 AGCT CATTG GAT TGGGG  
 ||| |||| |||||  
 TCGA GTGAC CTA ACCCC  
 \_ \_ A

GAM1441 MGC2941 3' CCCCAAATCTGGAGAGC 44158 G\_ TTGAA C  
 GCT CCA GAT TGGGG  
 ||| ||| |||||  
 CGA GGT CTA ACCCC  
 GA \_ \_ A

GAM1441 PALM 3' CCCCATGTCACGGCAGCTT 10411 ATTGAA C  
 AAGCTGCC GAT TGGGG  
 ||||| |||||  
 TTCGACGG CTG ACCCC  
 CA\_ T

GAM1441 PRO1489 3' CCTATCATCTTCAATAACA 37723 CC CTG  
 TG ATTGAAGAT GGG  
 || ||||| |||  
 AC TAACTTCTA TCC  
 AA CTA

GAM1441 TRIAD3 3' CCCCCAGGCCACCAACGGCAGT 94502 A A AAGA  
 CC A GCTGCC TTG TCTGGGGG  
 | |||| || |||||  
 C TGACGG AAC GGACCCCC  
 C C CACC

GAM1441 LOC136442 3' CCCCAGACGCTGGCGCT 54284 T T AAGA  
 AGC GCCA TG TCTGGGG  
 ||| ||| || |||||  
 TCG CGGT GC AGACCCC  
 \_ C \_

GAM1441 LOC138835 5' CCATCTCCACGGCAGCTT 75954 AT A TC  
 AAGCTGCC TG AGA TGG  
 ||||| || ||| |||

		TTCGACGG AC TCT ACC	
		C_ C _	
GAM1441	LOC143451 3'	CCCCCAGAATCACAGCAG 76562	CAT AGA
		CTGC TGA TCTGGGGG	
		GACG ACT AGACCCCC	
		AC_ A_	
GAM1441	LOC144577 3'	AGATCCTCATGGCAGCTT 76900	T A
		AAGCTGCCAT GA GATCT	
		TTCGACGGTA CT CTAGA	
		_ C	
GAM1441	LOC145125 3'	CCCCCAGAATCACAGCAG 77004	CAT AGA
		CTGC TGA TCTGGGGG	
		GACG ACT AGACCCCC	
		AC_ A_	
GAM1441	LOC147136 5'	CCCCCAGAGCAAAAGGCA 78261	A GAAGA
		TGCC TT TCTGGGGG	
		ACGG AA AGACCCCC	
		A ACG_	
GAM1441	LOC149113 3'	CCCCCAGAAGGAATGCAGC 79163	C GAAGA
		GCTGC ATT TCTGGGGG	
		CGACG TAA AGACCCCC	
		_ GGA_	
GAM1441	LOC151996 3'	CCCAGATCCCACAGT 85531	CCAT AA
		GCTG TG GATCTGGG	
		TGAC AC CTAGACCC	
		_ C_	
GAM1441	LOC154992 3'	CCCCCAGAAGGAATGCAGC 81213	C GAAGA
		GCTGC ATT TCTGGGGG	
		CGACG TAA AGACCCCC	
		_ GGA_	
GAM1441	LOC158809 3'	CCCTCAGATCCTCAACAG 86896	CCA A
		CTG TTGA GATCTGGGGG	
		GAC AACT CTAGACTCCC	
		_ C	
GAM1441	LOC161244 3'	CCCCCAGATCTCCCCGTCAGC 87083	CCATT A
		GCTG GA GATCTGGGGG	
		CGAC CT CTAGACCCCC	
		TGCCC _	
GAM1441	LOC161244 3'	CCCCCAGATCTCCCCGTCAGC 87084	CCATT A
		GCTG GA GATCTGGGGG	

CGAC CT CTAGACCCCC  
 TGCCC \_  
 GAM1441 LOC196955 5' CCCCCACCCTCAATGGCAGCT 77371 A ATC  
 AGCTGCCATTGA G TGGGGG  
 ||||| |||||  
 TCGACGGTAACT C ACCCCC  
 \_CC\_  
 GAM1441 LOC201868 3' CCCCCAGAAGGAATGCAGCT 89076 C GAAGA  
 AGCTGC ATT TCTGGGGG  
 ||||| ||| |||||  
 TCGACG TAA AGACCCCC  
 \_ GGA\_  
 GAM1441 LOC219940 3' CCCCCAGACCCCTTACAA 93355 \_ A\_  
 TTG AAG TCTGGGGG  
 ||| ||| |||||  
 AAC TTC AGACCCCC  
 A CCC  
 GAM1441 LOC220739 3' CCCCAGAAGTAAGCAGCT 92928 CA AAGA  
 AGCTGC TTG TCTGGGG  
 ||||| ||| |||||  
 TCGACG AAT AGACCCC  
 \_ GA\_  
 GAM1441 LOC221405 5' CCCAAGGCCCCACTGGCAGCTT 93881 T AAGA G  
 AAGCTGCCA TG TCT GGG  
 ||||| || ||| |||  
 TTCGACGGT AC GGA CCC  
 C CCC\_ A  
 GAM1441 LOC254440 3' CCCCCAGAATCACAGCAG 97064 CAT AGA  
 CTGC TGA TCTGGGGG  
 |||| ||| |||||  
 GACG ACT AGACCCCC  
 AC\_ A\_  
 GAM1442 PCDH11X 3' CAATCATATTCTACAG 27238 CC C  
 CTGTAGAA TGA TTG  
 ||||| ||| |||  
 GACATCTT ACT AAC  
 AT \_  
 GAM1442 RTN4R 3' CGCCAAGCCAGCCGGG 43432 TAGAAC A  
 CCTG CTG CTTGGCG  
 |||| ||| |||||  
 GGGC GAC GAACCGC  
 C\_ C  
 GAM1442 DKFZP564B147 5' CCGCTAGGGTCTCCACAGG 82082 A \_ GACT  
 CCTGT GA ACCT TGGCGG  
 |||| || ||| |||||  
 GGACA CT TGGG ATCGCC  
 C C \_  
 GAM1442 KIAA1260 3' GTCAGGTTGCACAGGTG 60028 AG  
 CACCTGT AACCTGAC  
 ||||| |||||

		GTGGACA TTGGACTG		
		CG		
GAM1442 KIAA1485	3'	TGCCAGGCTCTGCAGG	89263	A GACTT
		CCTGTAGA CCT GGCG		
		GGACGTCT GGA CCGT		
		C _____		
GAM1442 KIAA1643	3'	TCAGGTTCCCAGGTG	64554	TA
		CACCTG GAACCTGA		
		GTGGAC CTTGGACT		
		C_		
GAM1442 KIAA1674	3'	CCGCCAAGCCATGTGACAGAGT	68776	_ AGA C A
G		CAC CTGT AC TG CTTGGCGG		
		GTG GACA TG AC GAACCGCC		
		A G_ T C		
GAM1442 MGC10981	3'	CTGAGTCGATCCCACAGGTG	51017	A_ ACC TG
		CACCTGT GA TGA CT G		
		GTGGACA CT GCTGA C		
		CC A_ GT		
GAM1442 MGC11324	3'	CCAGAGGCAGAACCTACAGGTG	51166	AAC A _
		CACCTGTAG CTG CT TGG		
		GTGGACATC GAC GA ACC		
		CAA G G		
GAM1442 MGC20470	3'	TGCCAATCTACAGG	58965	ACCTGAC
		CCTGTAGA TTGGCG		
		GGACATCT AACCGT		
		_____		
GAM1442 RAB3D	3'	CCGTGGCTGCCAGGTTCTCAG	15006	TA ACTTG_
G		CCTG GAACCTG GCGG		
		GGAC CTTGGAC TGCC		
		TC CGTCGG		
GAM1442 TRIM6	5'	CCACAGATTCCAGGATTCTACA	54136	_ A_ _
GG		CCTGTAGAA CCTG CT TGG		
		GGACATCTT GGAC GA ACC		
		A CTTA C		
GAM1442 LOC122955	5'	TGCTGTCTCAGTTCTACAG	75586	C TT
		CTGTAGAAC TGAC GGCG		
		GACATCTTG ACTG TCGT		
		_ _		
GAM1442 LOC126549	5'	AGGCAAGCTCTACAGGTG	75707	AC GA
		CACCTGTAGA CT CTT		

		GTGGACATCT GA GGA	
		C_ AC	
GAM1442	LOC145919 3'	CCACCTGGCTTACAGGTG 77568	AA TGA CT
		CACCTGTAG CC TGG	
		GTGGACATT GG ACC	
		C_ TCC__	
GAM1442	LOC149386 5'	CAAGTCAGGTCCACA 84404	A A
		TGT GA CCTGACTTG	
		ACA CT GGA CTGAAC	
		C _	
GAM1442	LOC150197 5'	GCCAGGTCCTACGG 79597	AACCT
		CTGTAG GACTTGGC	
		GGCATC CTGGACCG	
		_____	
GAM1442	LOC151878 5'	CCACTAGTTCAGACTCTAAGG 80373	G AC C C
		CCT TAGA CTGA TTGG GG	
		GGA ATCT GACT GATC CC	
		_ CA T A	
GAM1442	LOC153146 5'	TGCCAGAGCCTACAGGT 85936	AAC GAC
		ACCTGTAG CT TTGGCG	
		TGGACATC GA GACCGT	
		C_ _	
GAM1442	LOC153205 3'	CGTAACCATGTTCTACAG 85944	C ACTTG
		CTGTAGAAC TG GCG	
		GACATCTTG AC TGC	
		T CAA__	
GAM1442	LOC153592 3'	CCGCCCTGATTCCACAGATG 86066	C A CCTGACTT
		CA CTGT GAA GGCGG	
		GT GACA CTT CCGCC	
		A C AGTC__	
GAM1442	LOC169026 3'	CCACCAAGTTGTTGCCACAG 82723	AG_ CT C
		CTGT AAC GACTTGG GG	
		GACA TTG TTGAACC CC	
		CCG _ A	
GAM1442	LOC254076 5'	CCGCCAAGCCAAGCTCAAC 97197	A ACC A
		GT GA TG CTTGGCGG	
		CA CT AC GAACCGCC	
		A CGA C	
GAM1443	PCDH11X 3'	CAATCATATTCTACAG 27238	CC C
		CTGTAGAA TGA TTG	

GACATCTT ACT AAC  
 AT \_  
 GAM1443 RTN4R 3' CGCCAAGCCAGCCGGG 43432 TAGAAC A  
 CCTG CTG CTTGGCG  
 |||| ||| |||||  
 GGGC GAC GAACCGC  
 C\_\_\_\_\_ C  
 GAM1443 DKFZP564B147 5' CCGCTAGGGTCTCCACAGG 82082 A \_ GACT  
 CCTGT GA ACCT TGGCGG  
 ||||| || |||| |||||  
 GGACA CT TGGG ATCGCC  
 C C \_\_\_\_\_  
 GAM1443 KIAA1260 3' GTCAGGTTGCACAGGTG 60028 AG  
 CACCTGT AACCTGAC  
 ||||| |||||  
 GTGGACA TTGGACTG  
 CG  
 GAM1443 KIAA1485 3' TGCCAGGCTCTGCAGG 89263 A GACTT  
 CCTGTAGA CCT GGCG  
 ||||| ||| |||  
 GGACGTCT GGA CCGT  
 C \_\_\_\_\_  
 GAM1443 KIAA1643 3' TCAGGTTCCCAGGTG 64554 TA  
 CACCTG GAACCTGA  
 ||||| |||||  
 GTGGAC CTTGGACT  
 C\_  
 GAM1443 KIAA1674 3' CCGCCAAGCCATGTGACAGAGT 68776 \_ AGA C A  
 G CAC CTGT AC TG CTTGGCGG  
 ||| ||| || || |||||  
 GTG GACA TG AC GAACCGCC  
 A G\_ T C  
 GAM1443 MGC10981 3' CTGAGTCGATCCCACAGGTG 51017 A\_ ACC TG  
 CACCTGT GA TGA CT G  
 ||||| || |||| |  
 GTGGACA CT GCTGA C  
 CC A\_ GT  
 GAM1443 MGC11324 3' CCAGAGGCAGAACCTACAGGTG 51166 AAC A \_  
 CACCTGTAG CTG CT TGG  
 ||||| ||| || |||  
 GTGGACATC GAC GA ACC  
 CAA G G  
 GAM1443 MGC20470 3' TGCCAATCTACAGG 58965 ACCTGAC  
 CCTGTAGA TTGGCG  
 ||||| |||||  
 GGACATCT AACCGT  
 \_\_\_\_\_  
 GAM1443 RAB3D 3' CCGTGGCTGCCAGGTTCTCAG 15006 TA ACTTG\_  
 G CCTG GAACCTG GCGG  
 ||| ||||| |||

		GGAC CTTGGAC TGCC	
		TC CGTCGG	
GAM1443 TRIM6	5'	CCACAGATTCCAGGATTCTACA 54136	_ A__ _
	GG	CCTGTAGAA CCTG CT TGG	
		GGACATCTT GGAC GA ACC	
		A CTTA C	
GAM1443 LOC122955	5'	TGCTGTCAGTTCTACAG 75586	C TT
		CTGTAGAAC TGAC GGCG	
		GACATCTTG ACTG TCGT	
		— —	
GAM1443 LOC126549	5'	AGGCAAGCTCTACAGGTG 75707	AC GA
		CACCTGTAGA CT CTT	
		GTGGACATCT GA GGA	
		C_ AC	
GAM1443 LOC145919	3'	CCACCTGGCTTACAGGTG 77568	AA TGACT
		CACCTGTAG CC TGG	
		GTGGACATT GG ACC	
		C_ TCC__	
GAM1443 LOC149386	5'	CAAGTCAGGTCCACA 84404	A A
		TGT GA CCTGACTTG	
		ACA CT GGACTGAAC	
		C _	
GAM1443 LOC150197	5'	GCCAGGTCCTACGG 79597	AACCT
		CTGTAG GACTTGGC	
		GGCATC CTGGACCG	
		— — —	
GAM1443 LOC151878	5'	CCACTAGTTCAGACTCTAAGG 80373	G AC C C
		CCT TAGA CTGA TTGG GG	
		GGA ATCT GACT GATC CC	
		_ CA T A	
GAM1443 LOC153146	5'	TGCCAGAGCCTACAGGT 85936	AAC GAC
		ACCTGTAG CT TTGGCG	
		TGGACATC GA GACCGT	
		C_ _	
GAM1443 LOC153205	3'	CGTAACCATGTTCTACAG 85944	C ACTTG
		CTGTAGAAC TG GCG	
		GACATCTTG AC TGC	
		T CAA__	
GAM1443 LOC153592	3'	CCGCCCTGATTCCACAGATG 86066	C A CCTGACTT
		CA CTGT GAA GGCGG	



		GT GACA CTT    CCGCC	
		A   C   AGTC_____	
GAM1443	LOC169026 3'	CCACCAAGTTGTTGCCACAG    82723	AG_   CT    C
		CTGT   AAC   GACTTGG GG	
		GACA   TTG   TTGAACC CC	
		CCG   _    A	
GAM1443	LOC254076 5'	CCGCCAAGCCAAGCTCAAC    97197	A   ACC   A
		GT GA   TG   CTTGGCGG	
		CA CT   AC   GAACCGCC	
		A   CGA   C	
GAM1444	ABCA4    3'	TTGTCTGTGTGTCTGCGTTGT    67093	GG   TT
		GCAATGCAGACA   AC   GGCAG	
		TGTTGCGTCTGT   TG   CTGTT	
		G_   T_	
GAM1444	ACTN1    3'	GTCTTGTTTTGTTGC    6591    C	
		GCAATG   AGACAGGAC	
		CGTTGT   TTTGTTCTG	
		—	
GAM1444	ADAR    3'	CTGCTGAGTCCTCAGGTTGTTT    31749	T   AC_    TG
	G	CAA GCAG   AGGACT   GCAG	
		GTT TGTT   TCCTGA   CGTC	
		_   GGAC    GT	
GAM1444	ADAR    3'	CTGCTGAGTCCTCAGGTTGTTT    31759	T   AC_    TG
	G	CAA GCAG   AGGACT   GCAG	
		GTT TGTT   TCCTGA   CGTC	
		_   GGAC    GT	
GAM1444	ADAR    3'	CTGCTGAGTCCTCAGGTTGTTT    6624	T   AC_    TG
	G	CAA GCAG   AGGACT   GCAG	
		GTT TGTT   TCCTGA   CGTC	
		_   GGAC    GT	
GAM1444	AGRN    3'	CTGCTGGGCACAGCTCTGCGTT    78835	CAGGA_   TG
	GC	GCAATGCAGA    CT   GCAG	
		CGTTGCGTCT    GG   CGTC	
		CGACAC   GT	
GAM1444	AMPH    3'	TTGTCAATAACAGGTTTGTGTTG    7908	T   AGGAC_
	T	GCAA GCAGAC    TTGGCAG	
		TGTT TGTTTG    AACTGTT	
		_    GACAAT	
GAM1444	AP2B1    3'	CTGCTCTGTGTCTGTGTTGT    7061	AGG   TT
		GCAATGCAGAC   AC   GGCAG	

TGTGTGTCTG TG TCGTC  
 \_\_\_\_ TC  
 GAM1444 APXL 3' CTGCCAGGTTTTGTCCCTGC 7927 \_\_\_\_  
 GCA GACAGGACTTGGCAG  
 ||| |||||  
 CGT CTGTTTTGGACCGTC  
 CC  
 GAM1444 ARNTL 3' TTGGATTCTGTTTGTGTTG 6785 C TG  
 CAATGCAGACAGGA T G  
 ||||| ||| |  
 GTTGTGTTTGTCTT G T  
 A GT  
 GAM1444 ATP6V1C1 3' CTGTCCTTGTGTTTGTGTGT 8090 A G CTT  
 GCA TGCAGACA GA GGCAG  
 ||| ||||| || ||||  
 TGT GTGTTTGT TT CTGTC  
 \_ G C\_  
 GAM1444 ATRN 3' GGTATTTTTTGTATTGTA 57801 CAGG  
 TGCAATGCAGA ACT  
 ||||| |||  
 ATGTTATGTTT TGG  
 TTTA  
 GAM1444 B4GALT5 3' TTGTTTGTGTTTGTGTTTGT 16517 T ACTT  
 GCAA GCAGACAGG GGCAG  
 ||| ||||| ||||  
 TGTT TGTTTGTGTT TTGTT  
 \_ GT\_  
 GAM1444 BAAT 5' TTGCTAGGTTTTGAGGTTTTGC 8115 T AGA  
 GCAA GC CAGGACTTGGCAG  
 ||| || |||||  
 CGTT TG GTTTTGGATCGTT  
 T GA\_  
 GAM1444 BACH2 3' TTGTTTTTTCTTGTGTTGTGT 41495 A CTT  
 GCA TGCAGACAGGA GGCAG  
 ||| ||||| ||||  
 TGT GTGTTTGTGTTCT TTGTT  
 \_ TTT  
 GAM1444 BCL9 3' TTGCCATCGGTCATGTGTTGCA 15071 \_ AG CT  
 TGCAATGCA GAC GA TGGCAG  
 ||||| ||| || |||||  
 ACGTTGTGT CTG CT ACCGTT  
 A G\_ \_  
 GAM1444 CD3Z 3' TGTTGAGTCTGTTTTGTA 5595 CA TG  
 TGCAGA GGACT GCA  
 ||||| |||| |||  
 ATGTTT TCTGA TGT  
 TG GT  
 GAM1444 CLCN6 3' CTGTTTGCAGTGTGTTTGTGTA 41384 T GACTT  
 TGCAA GCAGACAG GGCAG  
 ||||| ||||| ||||

			ATGTT TGT TTGTC	TTGTC		
			— ACGT—			
GAM1444	CLCN6	3'	CTGTTTGC	ACTGTTTGTA 41399	T	GACTT
			TGCAA GCAGACAG	GGCAG		
			ATGTT TGT TTGTC	TTGTC		
			— ACGT—			
GAM1444	CLCN6	3'	CTGTTTGC	ACTGTTTGTA 7077	T	GACTT
			TGCAA GCAGACAG	GGCAG		
			ATGTT TGT TTGTC	TTGTC		
			— ACGT—			
GAM1444	COX15	3'	CTGCTGAGTTCT	TGGTCTGTTGC 15194	AT	— TG
			GCA GCAGAC	AGGACT GCAG		
			CGT TGTCTG	TCTTGA CGTC		
			— G	GT		
GAM1444	CREBL2	3'	TTGCTGGGTCTCT	ATGTTTTG 7149	T	GACA TG
			CAA GCA	GGACT GCAG		
			GTT TGT	TCTGG CGTT		
			T ATC—	GT		
GAM1444	CRP	3'	CTGGTTTTTGT	TGCTTGCA 71628	T	C TG
			TGCAA GCAGACAGGA	T G		
			ACGTT CGTTTGT	TTT G C		
			— T	GT		
GAM1444	CUTL1	3'	TTGGGCCTGTCT	GCACTGC 8592	A	A TG
			GCA TGCAGACAGG	CT G		
			CGT ACGTCTGTCC	GG T		
			C	— GT		
GAM1444	D8S2298E	3'	TGTTGGGTGTG	CATTACA 19036	C	GACAGG TG
			TG AATGCA	ACT GCA		
			AC TTACGT	TGG TGT		
			A G—	GT		
GAM1444	DDX6	3'	TTGTTCCACTTGT	TGCACTGT 15294	A	ACTT
			GCA TGCAGACAGG	GGCAG		
			TGT ACGTTTGTTC	TTGTT		
			C	ACC—		
GAM1444	DLC1	3'	TGTTGAGGGTCT	GTATTCA 20337	C	AGGA TG
			TG AATGCAGAC	CT GCA		
			AC TTATGTCTG	GA TGT		
			— G—	GT		
GAM1444	DMRT1	3'	TGTTAATATTTG	CATTG 41701		CAGGAC
			CAATGCAGA	TTGGCA		

GTTACGTTT AATTGT  
 TAT\_\_\_  
 GAM1444 DPYSL2 3' TTGCTGACTTGTGTTGCATTGT 7306 \_ AC TG  
 A TGCAATGCAG ACAGG T GCAG  
 ||||| ||| | |||  
 ATGTTACGTT TGTTT A CGTT  
 G \_ GT  
 GAM1444 DRD5 3' TTGTTCACTCACTTGTGTTGT 5851 C \_ TG  
 TTG G AATGCAGACA G GACT GCAG  
 | ||||| | ||| |||  
 G TTGTGTTTGT C CTGA TGTT  
 T T A CT  
 GAM1444 DUOX2 3' TTGCTGAGTAGTATTCTATTGT 26023 GC CAGG\_ TG  
 A TGCAAT AGA ACT GCAG  
 |||| | ||| |||  
 ATGTTA TCT TGA CGTT  
 \_ TATGA GT  
 GAM1444 DUSP11 5' CTGCCGAGTCTTTTCCTGT 13133 AC\_  
 GCAG AGGACTTGGCAG  
 ||| |||||  
 TGTC TTCTGAGCCGTC  
 CTT  
 GAM1444 EFG1 3' TCTTGTTTGTGTTCA 94631 C  
 TG AATGCAGACAGGA  
 || |||||  
 AC TTGTGTTTGTCT  
 \_  
 GAM1444 EIF2C1 3' CTGTGTACTTGTGTTGCATTG 24174 C \_ TTG  
 G AATGCAGACAGG AC GCAG  
 | ||||| || |||  
 G TTACGTTTGTTC TG TGTC  
 T A \_  
 GAM1444 EIF4A2 3' ATGCATTTTGTGTTTGGTATTGTA 8754 \_ CTTG G  
 TGCAATGC AGACAGGA GCA  
 ||||| ||||| |||  
 ATGTTATG TTTGTTTT CGT  
 G A\_ AA  
 GAM1444 EN2 3' CTGCCACTTTGTTTGTGTTG 7462 ACT  
 CAATGCAGACAGG TGGCAG  
 ||||| |||||  
 GTTGTGTTTGTGTT ACCGTC  
 C\_  
 GAM1444 ERBB2IP 3' TTGTTAGGTTTTTAAACATAGC 37990 A CAGAC  
 A TGC ATG AGGACTTGGCAG  
 ||| ||| |||||  
 ACG TAC TTTTGGATTGTT  
 A AAAT\_  
 GAM1444 FASN 3' GGTGTTTGTCTGTGTTT 14635 C \_  
 G AATGCAGACAGG ACT  
 | ||||| |||

G TTGTGTCTGTTT TGG  
 T G  
 GAM1444 FBP2 3' TTCTGTTTGTTTTGCA 13843 T  
 TGCAA GCAGACAGGA  
 ||||| |||||  
 ACGTT TGTTTGTCTT  
 T  
 GAM1444 FMR1 3' TTGTTTTTGTGTTTTGTTTGT 8943 C \_TT\_  
 GCA GCAATG AGACAGGA C GGCAG  
 ||||| ||||| | |||||  
 CGTTGT TTTGTTTT G TTGTT  
 \_ T TTT  
 GAM1444 FOXG1B 3' TTGCCTTCAGTTTGTGTTGT 17903 A CTT  
 GCAATGCAGAC GGA GGCAG  
 ||||| ||||| || |||||  
 TGTGTGTTTG CTT CCGTT  
 A \_  
 GAM1444 G22P1 5' TTGAGGCCTGTCTGCGTTTG 7604 C A TG  
 G AATGCAGACAGG CT G  
 | ||||| || ||  
 G TTGCGTCTGTCC GA T  
 T G GT  
 GAM1444 GRAF 3' GGATCTGTTTGCATGCA 30569 A A  
 TGCA TGCAGACAGG CT  
 |||| ||||| ||  
 ACGT ACGTTTGTCT GG  
 \_ A  
 GAM1444 HOXA7 3' CTGCTAAGGGCACTGCACTGTA 22571 A ACAGGA  
 TGCA TGCAG CTTGGCAG  
 |||| |||| |||||  
 ATGT ACGTC GAATCGTC  
 C ACGG\_  
 GAM1444 HOXD1 3' TTGCTGAGTTCTGTCTGCA 44431 A TG  
 TGC GACAGGACT GCAG  
 || ||||| |||||  
 ACG CTGTCTTGA CGTT  
 A GT  
 GAM1444 ICAM1 3' TTGTCCTCTTGTCTGTTTGCA 71581 TT\_\_ \_  
 TTTCA AATGCAGACAGGAC GG CAG  
 ||||| ||||| || |||||  
 TTACGTTTGTCTG CC GTT  
 TTCT T  
 GAM1444 IMMP2L 3' TTGTTGGGTTTTGATTTTG 50733 \_ TG  
 CAGA CAGGACT GCAG  
 |||| ||||| |||||  
 GTTT GTTTTGG TGTT  
 TA GT  
 GAM1444 IRF2 3' TTGTTTTGTTGTTTGTGTA 9359 T GG TT  
 TGCAA GCAGACA AC GGCAG  
 |||| ||||| || |||||

			ATGTT TGTTTGT TG TTGTT		
			— — TT		
GAM1444	IRS1	5'	CTGCCTCCAGCCCTGTTTGCAT 18663	A	A T__
	GT		GCA TGCAGACAGG CT GGCAG		
			TGT ACGTTTGTCC GA CCGTC		
			— C CCT		
GAM1444	ITGA1	3'	TTGTTGAGGTTTGTGTGTGT 63538	G	GA TG
			ATGCA ACAG CT GCAG		
			TGTGT TGTT GA TGTT		
			G TG GT		
GAM1444	ITGA6	3'	GGTCTGTTTGCATTTG 3986	C	G
			G AATGCAGACAG ACT		
			G TTACGTTTGTGTC TGG		
			T —		
GAM1444	ITPKB	3'	TTGTTGGGTTTTAAATTGCA 9439	GCAGAC	TG
			TGCAAT AGGACT GCAG		
			ACGTTA TTTTGG TGTT		
			AAA__ GT		
GAM1444	KCNA7	3'	TTGTTGGGTCTTGGGTTGTGT 49065	A_	TG
			ATGCAG CAGGACT GCAG		
			TGTGTT GTTCTGG TGTT		
			GG GT		
GAM1444	KIF3B	3'	TTGCCTTTTGTCTGTATTG 16615	CTT	
			CAATGCAGACAGGA GGCAG		
			GTTATGTCTGTTTT CCGTT		
			—		
GAM1444	LARGE	3'	CTGCTGGGCTGTTTGTATTG 16435	GA	TG
			CAATGCAGACAG CT GCAG		
			GTTATGTTTGTGTC GG CGTC		
			— GT		
GAM1444	LARGE	3'	CTGCTGGGCTGTTTGTATTG 56109	GA	TG
			CAATGCAGACAG CT GCAG		
			GTTATGTTTGTGTC GG CGTC		
			— GT		
GAM1444	LILRB4	3'	TGTTAGGAATTGCATTG 22438	ACAGGA	
			CAATGCAG CTTGGCA		
			GTTACGTT GGATTGT		
			AA__		
GAM1444	MGAT5	5'	GGTTTATTTTGTCTGTATTGT 10027	A	CTT AG
			GCAATGCAG CAGGA GGC		

			TGTTATGTC GTTTT TTG		
			_ AT_ GT		
GAM1444	NAP1L3	3'	GTTTTCTTTGTATTGT 15796	C	
			GCAATGCAGA AGGAC		
			TGTTATGTTT TTTTG		
			C		
GAM1444	NCOA6	3'	CTGTTGAGCCCTTTTGGTGTG 25963	A C A TG	
	C		GCAATGC GA AGG CT GCAG		
			CGTTGTG TT TCC GA TGTC		
			G T C GT		
GAM1444	NEDD4L	3'	CTGTTTAGTCTCCTGTTTGTAT 30950	A	__ TG
	GC		GCA TGCAGACAGGA CT GCAG		
			CGT ATGTTTGTCT GA TGTC		
			_ CT TT		
GAM1444	NOTCH2	3'	TCTTGTCTGTGTGCA 44315	A	
			TGCA TGCAGACAGGA		
			ACGT GTGTCTGTTCT		
			_		
GAM1444	NPTX1	3'	CTGCCCGGTTCTGTGTTGT 10262	CA_ ACTT	
			GCAATGCAGA GG GGCAG		
			TGTTGTGTCT CC CCGTC		
			TGG ____		
GAM1444	PBP	3'	GTGCTGTTTGCTTGTA 10383	T G	
			TGCAA GCAGACAG AC		
			ATGTT CGTTTGTC TG		
			_ G		
GAM1444	PDGFRB	3'	CTGTTGAGTTTTTCTATCTGT 65976	C __ TG	
			GCAGA AG GACT GCAG		
			TGTCT TC TTGA TGTC		
			A TTT GT		
GAM1444	PEA15	3'	TGCTCTTCTGTCTGCAGTGT 13656	A	CTT G
			GCA TGCAGACAGGA GGCA		
			TGT ACGTCTGTCTT TCGT		
			G C_ G		
GAM1444	PPM1D	3'	GTA CTGCTTGCTTGTA 13250	GA _	
			TGCAATGCA CAGG AC		
			ATGTTATGT GTTC TG		
			TC A		
GAM1444	PPP1R12A	3'	TTGTATTATTGATTGTATTGTA 10181	A	GA CTTG
			TGCAATGCAG CAG GCAG		

ATGTTATGTT GTT TGTT  
 A ATTA\_\_  
 GAM1444 PPP1R2 3' CTGTTGAGTTTCTTTGTGTTTA 20692 C CA TG  
 G AATGCAGA GGA CT GCAG  
 ||||| |||| ||||  
 A TTGTGTTT TTTGA TGTC  
 T C\_ GT  
 GAM1444 PTHR2 3' TTTTGTTTGTAAATGTA 17307 A  
 TGCA TGCAGACAGGA  
 ||| |||||  
 ATGT ATGTTTGTTTT  
 A  
 GAM1444 PTPRM 3' TGTCAGATTTGTATTGT 11126 CAGGAC  
 GCAATGCAGA TTGGCA  
 ||||| ||||  
 TGTTATGTTT GACTGT  
 A\_\_\_\_  
 GAM1444 RAD54B 3' TGTCAGGTTCTGCCTTCA 56235 C A  
 TG AG CAGGACTTGGCA  
 || || |||||  
 AC TC GTCTTGGACTGT  
 T C  
 GAM1444 RAF1 3' TTTTGTTTTATTGCA 80531 C  
 TGCAATG AGACAGGA  
 ||||| |||||  
 ACGTTAT TTTGTTTT  
 T  
 GAM1444 RARG 3' TTGCTGAGTTTCTATTTTGC 6384 TGC\_ CA TG  
 A TGCAA AGA GGA CT GCAG  
 |||| || |||| ||||  
 ACGTT TCT TTTGA CGTT  
 TTTA \_ GT  
 GAM1444 RECQL5 3' CTGCTGGTATGTCTGTATTG 14929 GG T  
 CAATGCAGACA ACT GGCAG  
 ||||| || |||||  
 GTTATGTCTGT TGG TCGTC  
 A\_ \_  
 GAM1444 SACS 3' TGCTTTATGTTTGTGTGTA 94916 A GGACTT  
 TGCA TGCAGACA GGCA  
 ||| ||||| |||  
 ATGT GTGTTTGT TCGT  
 \_ ATT\_\_\_\_  
 GAM1444 SART2 3' TTGCTAAGTCCTGGTATGATGG 25330 AATG GA\_  
 T GC CA CAGGACTTGGCAG  
 || || |||||  
 TG GT GTCCTGAATCGTT  
 GTA\_ ATG  
 GAM1444 SCN1A 3' TTGTATCCACTGTTTGCATTTC 88854 C GACTTG  
 A TG AATGCAGACAG GCAG  
 || ||||| |||



Accession	Gene	Position	Sequence	Length	Quality	Notes
GAM1444	SEL1L	3'	CTGCTGCGGAACACTTGCATTTC	17358	C	ACAGGA TG
GAM1444	SF3A1	3'	CTGTCAAGTCCCTGC	19653	ACA	
GAM1444	SH3BP4	3'	TGCCAAACTCTGCATTTC	27236	C	CAGGAC
GAM1444	SH3GL1	3'	CTGCTGGGTCTCCTGCATTCCA	11622	C	ACA TG
GAM1444	SHB	3'	TGGCTGTGTCGTTTGTGTTGT	11644		AG T AG
GAM1444	SLC9A3R1	3'	TTGTAAAGAGTGCAGTATTGCA	70424		AGA GGA
GAM1444	SMARCD2	3'	TGCTGGGTTTGCATGT	11827	A	GACAG TG
GAM1444	SNX6	3'	TGTTGAGTTTCCGTTGC	41162		CA CAG TG
GAM1444	SOS2	3'	AGTTTTGTTTATATTGTA	68535	C	
GAM1444	SPR	3'	TTGTCAGGAGTCTGTGCTGT	11934	AT	AGGA

			TGT TGTCTG GGACTGTT		
			CG A__		
GAM1444 STX7	3'	TTGTTAAGTTTTGGGCCACATT 13110	CAGA_		
GC		GCAATG CAGGACTTGGCAG			
		CGTTAC GTTTTGAATTGTT			
		ACCGG			
GAM1444 TACC1	3'	CTGCTATCAGGATTGTGTTGT 20798	ACAG CT		
		GCAATGCAG GA TGGCAG			
		TGTTGTGTT CT ATCGTC			
		AGGA _			
GAM1444 TACC1	3'	TGCTGAGTTTGGGTTTGT 20801	A_ TG		
		GCAGAC GGACT GCA			
		TGTTTG TTTGA CGT			
		GG GT			
GAM1444 TAF4	3'	TGCTAAGAGACTGTATGCA 12093	G GA_		
		TGCA ACAG CTTGGCA			
		ACGT TGTC GAATCGT			
		A AGA			
GAM1444 TAF5	3'	TGTTGAGTTTGGAGTGCA 22714	GA TG		
		TGCA CAGGACT GCA			
		ACGT GTTTTGA TGT			
		GA GT			
GAM1444 TAF5	3'	TGTTGAGTTTGGAGTGCA 57403	GA TG		
		TGCA CAGGACT GCA			
		ACGT GTTTTGA TGT			
		GA GT			
GAM1444 TAF7	3'	CTGTTAAGTTCTTTTCATTTGTT 18908	T C__		
TGTA		CAA GCAGA AGGACTTGGCAG			
		GTT TGTTT TCTTGAATTGTC			
		_ ACTT			
GAM1444 TDRD1	5'	CTGTTAAGGGGGAAGTTTGTAT 48394	AGGA__		
TGC		GCAATGCAGAC CTTGGCAG			
		CGTTATGTTTG GAATTGTC			
		AAGGGG			
GAM1444 TEC	3'	TGTCAAGACTGTGTGTGT 12225	G GA		
		ATGCA ACAG CTTGGCA			
		TGTGT TGTC GAACTGT			
		G A_			
GAM1444 TERF2	3'	TTTTGTACTGTGTTGT 18951	_		
		GCAATGCAG ACAGGA			

			TGTTGTGTC TGTTTT		
			A		
GAM1444	TIMP3	3'	GTCTGTGTCTGCATGTA 4516	A	_
			TGCA TGCAGACA GGAC		
			ATGT ACGTCTGT TCTG		
			_ G		
GAM1444	TIMP3	3'	TGTCTGTCTGTGTCTGCA 4522	_	TT
			TGCAGACA GGAC GGCA		
			ACGTCTGT TCTG CTGT		
			G T_		
GAM1444	TNFRSF1B	3'	TTGTGTCTGCGTCTGTGTTGC 6528	A_	TTG
			GCAATGCAGAC GGAC GCAG		
			CGTTGTGTCTG TCTG TGTT		
			CG _		
GAM1444	TRIM37	3'	TTGCCAAACTTTGCCATTGT 30975	_	CAGGAC
			GCAATG CAGA TTGGCAG		
			TGTTAC GTTT AACCGTT		
			C CA_		
GAM1444	UBB	5'	TTGTTGGGTGAGCTTGTTTGT 38495	_	TG
			GCAGACAGG ACT GCAG		
			TGTTTGTTT TGG TGTT		
			GAG GT		
GAM1444	UBE2I	3'	GTTTTGTCTGTGTTGC 12494		
			GCAATGCAGACAGGAC		
			CGTTGTGTCTGTTTTG		
GAM1444	VIL2	3'	TTGCTTGTGTTTGTGTTTGTGTTGC 12602	T	ACTT
	A		TGCAA GCAGACAGG GGCAG		
			ACGTT TGTTTGTTT TCGTT		
			_ GTGT		
GAM1444	WRB	3'	TTGTTGAGCAAGAGTTGTATAG 16128	A	ACAGGA TG
	TA		TGC ATGCAG CT GCAG		
			ATG TATGTT GA TGTT		
			A GAGAAC GT		
GAM1444	ZNF135	3'	GTCTTGTCTGTGTGTA 12854	A	
			TGCA TGCAGACAGGAC		
			ATGT GTGTCTGTTCTG		
			_		
GAM1444	ABLIM	3'	GTCCTGCTGTGTTGCA 9775	A	
			TGCAATGCAG CAGGAC		

ACGTTGTGTC GTCCTG

GAM1444 ABLIM 3' GTCCTGCTGTGTTGCA 22036 A  
TGCAATGCAG CAGGAC  
||||||| |||||  
ACGTTGTGTC GTCCTG

GAM1444 ADMP 3' TTGCACCCTTGTGTTGTGTT 58871 ACTTG  
AATGCAGACAGG GCAG  
||||||| |||  
TTGTGTTTGTTC CGTT

GAM1444 AKAP9 3' GTGCTTTTGTATTGT 19241 C G  
GCAATGCAGA AG AC  
||||||| |||  
TGTTATGTTT TC TG

GAM1444 ALLC 5' TTGCTAAGCAGGGTGGTGTGTTGT 37374 AG AGGA  
A TGCAATGC AC CTTGGCAG  
||||||| || |||||  
ATGTTGTG TG GAATCGTT  
G\_ GGAC

GAM1444 APOL3 3' CTGCTGAGTGCCCTGTGTGTA 26813 G \_ TG  
TGCA ACAGG ACT GCAG  
||| ||||| ||| |||||  
ATGT TGTCC TGA CGTC  
G CG GT

GAM1444 APOL4 3' TTGCTGAGTGCCCTGTGTGTA 47632 G \_ TG  
TGCA ACAGG ACT GCAG  
||| ||||| ||| |||||  
ATGT TGTCC TGA CGTT  
G CG GT

GAM1444 AQP9 3' TTGCTAAGTCTTGATCTTGC 40611 \_ \_  
GCA GA CAGGACTTGGCAG  
||| || ||||| |||||  
CGT CT GTTCTGAATCGTT  
T A

GAM1444 ARHGAP5 3' CTGTAAAGTTCTAGGTATTGTA 77075 AGAC  
TGCAATGC AGGACTTGGCAG  
||||||| ||||| |||||  
ATGTTATG TCTTGAATTGTC  
GA\_

GAM1444 BCL2L1 3' TTGTTAAGCGTGTCTGTATTTA 56809 C GGA  
G AATGCAGACA CTTGGCAG  
| ||||| |||||  
A TTATGTCTGT GAATTGTT  
T GC\_

GAM1444 BHLHB2 3' CTGCAAGATTGTTGCATTGT 13379 A GA G  
GCAATGCAG CAG CTTG CAG  
||||||| ||| ||| |||

			TGTTACGTT GTT GAAC GTC		
			— A —		
GAM1444	BRAG	3'	TTGCACAGACTGTCTGTATTCA 29479	C	GA TG
			TG AATGCAGACAG CT GCAG		
			AC TTATGTCTGTC GA CGTT		
			— A CA		
GAM1444	BTN3A1	3'	TTGTCAAGTTCTAGTTGT 22930	AC	
			GCAG AGGACTTGGCAG		
			TGTT TCTTGAAGTGT		
			GA		
GAM1444	BTN3A3	3'	TTGTCAAGTTCTAGTTGT 22773	AC	
			GCAG AGGACTTGGCAG		
			TGTT TCTTGAAGTGT		
			GA		
GAM1444	C1orf25	3'	TCCTGTTTGTAGTGTA 72539	A	
			TGCA TGCAGACAGGA		
			ATGT ATGTTTGTCT		
			G		
GAM1444	C1orf9	3'	TTGTTAGGTTTTGAAGCTGCA 32641	AC	—
			TGCAG AGGACTTGGCAG		
			ACGTC TTTTGGATTGTT		
			GAAGT		
GAM1444	C20orf110	3'	CTGTTGGGTGTTTGTGTTG 79545		CA G TG
			CAATGCAGA G ACT GCAG		
			GTTGTGTTT T TGG TGTC		
			— G GT		
GAM1444	C21orf51	5'	TGTTGGGGGCTTGTGTTG 54200		GAC GA TG
			CAATGCA AG CT GCA		
			GTTGTGT TC GG TGT		
			— GG GT		
GAM1444	C8orf17	5'	CTGTCAGAGAAATTCTGTGTTG 39598		CAGGAC
			CAATGCAGA TTGGCAG		
			GTTGTGTCT GACTGTC		
			TAAAGA		
GAM1444	C8orf2	3'	CTGGCATTCTTGTCTGCATGT 23161	A	CT G
			GCA TGCAGACAGGA TG CAG		
			TGT ACGTCTGTTCT AC GTC		
			— T G		
GAM1444	C8orf2	3'	CTGGCATTCTTGTCTGCATGT 23162	A	CT G
			GCA TGCAGACAGGA TG CAG		

			TGT ACGTCTGTTCT AC GTC		
			— T_ G		
GAM1444 CDC10	3'	CTGTATTTTTTGT	TTTGTATTGT 91111	CTTG	
A			TGCAATGCAGACAGGA GCAG		
			ATGTTATGTTTGT	TTT TGTC	
			TTA_		
GAM1444 CHCR	3'	GTGTTGTATTGT	GTTGT 37237	_ G	
			GCAATGCAG ACAG AC		
			TGTTGTGTT TGTT TG		
			A G		
GAM1444 CHCR	3'	TCTTGTGTTGT	TATTGT 37238	_	
			GCAATGCAG ACAGGA		
			TGTTATGTT TGTTCT		
			G		
GAM1444 CHST3	3'	TTGCTATTTTCATGTCTGCATGG	14984 A	G CT	
TA			TGC ATGCAGACA GA TGGCAG		
			ATG TACGTCTGT CT ATCGTT		
			G A TT		
GAM1444 CLDN8	3'	TTGTCAAGGGGCTTTGCATTCA	24036 C	CAGGA	
			TG AATGCAGA CTTGGCAG		
			AC TTACGTTT GAACTGTT		
			_ CGGG_		
GAM1444 CNNM2	3'	CTGCCAAGTCTGTGCATCACTGT	34459 A CA G		
			GCA TG GACAG ACTTGGCAG		
			TGT AC CTGTC TGAACCGTC		
			C TA _		
GAM1444 CPEB1	3'	TTGTCAGGTTTTGTTTTCA	47603 C		
			TG AGACAGGACTTGGCAG		
			AC TTTGTTTTGGACTGTT		
			T		
GAM1444 CRSP3	3'	CTAGATTTTGT	TGCATTGTA 60634	A C	
			TGCAATGCAG CAGGA TTGG		
			ATGTTACGTT GTTTT GATC		
			_ A		
GAM1444 CTPS2	3'	TGCCTTTGCTGTGTTGTA	39090 A	ACTT	
			TGCAATGCAG CAGG GGCA		
			ATGTTGTGTC GTTT CCGT		
			_ _		
GAM1444 DATF1	5'	CTGCCAGGGTTTTTGGTTGTA	42068 G	CAGGA	
			TGCAAT CAGA CTTGGCAG		

			ATGTTG GTTT GGACCGTC		
			_ TTG__		
GAM1444	DATF1	5'	CTGCCAGGGTTTTGGTTGTA 55004	G	CAGGA
			TGCAAT CAGA CTTGGCAG		
			ATGTTG GTTT GGACCGTC		
			_ TTG__		
GAM1444	DATF1	5'	CTGCCAGGGTTTTGGTTGTA 55008	G	CAGGA
			TGCAAT CAGA CTTGGCAG		
			ATGTTG GTTT GGACCGTC		
			_ TTG__		
GAM1444	DDM36	3'	TTGCTCATTTATTTGTCTGTAT 40581	C	ACT_ _
	TTA		G AATGCAGACAGG TG GCAG		
			A TTATGTCTGTTT AC CGTT		
			T ATTT T		
GAM1444	DIS3	3'	TTGTTGGCTATGGTCTGTATTG 30237		AGGAC TG
	CA		TGCAATGCAGAC T GCAG		
			ACGTTATGTCTG G TGTT		
			GTATC GT		
GAM1444	DKFZP434C212	3'	TTCATAGTTTGGTTTGCATTGT 68922		AG _ CAG
	A		TGCAATGCAGAC GACT TGG		
			ATGTTACGTTTG TTGA ACT		
			GT T T		
GAM1444	DKFZP434D1335	3'	TTGTTCAAGTGCTGTTTGCTTGC 65117	T	G TG
	A		TGCAA GCAGACAG ACT GCAG		
			ACGTT CGTTTGTC TGA TGTT		
			_ G CT		
GAM1444	DKFZP434F0318	3'	CTGTTAGGTTCTGGGGCTTGCA 48009	T	AGA
			TGCAA GC CAGGACTTGGCAG		
			ACGTT CG GTCTTGATTGTC		
			_ GG_		
GAM1444	DKFZP434F0318	3'	TGTTTAGTGTTTGCATTTA 48016	C	AGG TG
			G AATGCAGAC ACT GCA		
			A TTACGTTTG TGA TGT		
			T _ TT		
GAM1444	DKFZP434L0117	3'	TTGTTATGTCCATTGTTTGTA 42923		_ T
	TTGC		AATGCAGACA GGAC TGGCAG		
			TTATGTTTGT CCTG ATTGTT		
			TTA T		
GAM1444	DKFZP564F0522	3'	TTGCTGGGTTTTGTACATGTA 68585	A_	CAG TG
			TGCA TGCAGA GACT GCAG		

	ATGT ATGTTT TTGG CGTT		
	AC ____ GT		
GAM1444 DKFZP564K0822 3'	GGCCATTCTTGTTCATTGT 94048	C	CT AG
	GCAATG AGACAGGA TGGC		
	TGTTAC TTTGTTCT ACCG		
	C T_ GT		
GAM1444 DKFZP566B183 3'	TTGTTGAGTTTGAATTGTGT 31328	ACA	TG
	ATGCAG GGA CT GCAG		
	TGTGTT TTTGA TGTT		
	AAG GT		
GAM1444 DKFZP586A011 3'	TTGCCAGCAAAGTCTGTGTGTA 31221	A	AGGAC
	TGCA TGCAGAC TTGGCAG		
	ATGT GTGTCTG GACCGTT		
	_ AAAC_		
GAM1444 DKFZP586B2420 5'	TTGCCAAGGACCGCTGCGTGGT 74999	A	ACA A_
	GC ATGCAG GG CTTGGCAG		
	TG TGCCTC CC GAACCGTT		
	G G_ AG		
GAM1444 DKFZP586I2223 3'	CTGCCAGGTGGAGTGTATGT 31268	G	GG_
	GCA ACA ACTTGGCAG		
	TGT TGT TGGACCGTC		
	A GAGG		
GAM1444 DKFZP586I2223 3'	CTGCCAGGTGGAGTGTATGT 54910	G	GG_
	GCA ACA ACTTGGCAG		
	TGT TGT TGGACCGTC		
	A GAGG		
GAM1444 DKFZP586I2223 3'	CTGCCAGGTGGAGTGTATGT 54919	G	GG_
	GCA ACA ACTTGGCAG		
	TGT TGT TGGACCGTC		
	A GAGG		
GAM1444 DKFZP586N0721 5'	AGTTGTCCTTATGTTGTCTGTG 31202	_____	TTGGCAG
TTGTA	TGCAGACA GGAC		
	GTGTCTGT CCTG		
	TGTATT TT GAC		
GAM1444 DKFZp761D0614 3'	GTTAGTCTGCATGCA 87557	A	AG
	TGCA TGCAGAC GAC		
	ACGT ACGTCTG TTG		
	_ A_		
GAM1444 DKFZp761G2113 3'	GGCATGTCCTGTCTGTGTGCA 69907	A	TTG AG
	TGCA TGCAGACAGGAC GC		



ACGT GTGTCTGTCCTG CG  
 \_ TA\_ GG  
 GAM1444 Dlc2 3' TGCTGGGACTGTTTTGCA 54761 \_ GA TG  
 TGCAGA CAG CT GCA  
 ||||| ||| || |||  
 ACGTTT GTC GG CGT  
 T A\_ GT  
 GAM1444 DNAJC5 3' CTGTTCCATGTCTGTGTTGT 61454 \_ CTTG  
 GCAATGCAGACA GGA GCAG  
 ||||| ||| |||  
 TGTGTGTCTGT CCT TGTC  
 A \_  
 GAM1444 DORFIN 3' TTGTATATTTGTTTGCATTCCA 31263 C ACTTG  
 TG AATGCAGACAGG GCAG  
 || ||||| |||  
 AC TTACGTTTGT TT GTT  
 C ATA\_  
 GAM1444 EIF3S1 3' TTGCCAGGTCCTTATGTTGT 63169 AT GAC  
 GCA GCA AGGACTTGGCAG  
 ||| ||| |||||  
 TGT TGT TCCTGGACCGTT  
 \_ AT\_  
 GAM1444 EIF3S8 5' TGTCAGGGCCTGCGGTGT 13632 AGA A  
 ATGC CAGG CTTGGCA  
 ||| ||| |||||  
 TGTG GTCC GGA CTGT  
 GC\_ G  
 GAM1444 EIF5 3' TTGTTAGTCTCTGGGGCTGCA 8764 AT AGA  
 TGCA GC CAGGACTTGGCAG  
 ||| || |||||  
 ACGT CG GTCCTGGATTGTT  
 \_ GG\_  
 GAM1444 ELL2 3' GTATTGTCTTATTGTA 23873 C G  
 TGCAATG AGACAG AC  
 ||||| ||||| ||  
 ATGTTAT TCTGTT TG  
 \_ A  
 GAM1444 FLJ10242 3' TTGCAGACATGTTCTGTTGTGT 35937 A TTG\_  
 TGCA CAATGCAG CAGGAC GCAG  
 ||||| ||||| |||  
 GTTGTGTT GTCTTG CGTT  
 \_ TACAGA  
 GAM1444 FLJ10546 3' TTGCTAAGTTATATGTGTTAGT 59483 \_ GACAG  
 GC AATGCA GACTTGGCAG  
 || ||||| |||||  
 TG TTGTGT TTGAATCGTT  
 A ATA\_  
 GAM1444 FLJ10619 3' TTCTGTCTGCCTTGTA 36355 T  
 TGCAA GCAGACAGGA  
 ||||| |||||

ATGTT CGTCTGTCTT  
 C  
 GAM1444 FLJ10851 3' CTGCTGGGTGATTTGTTTGC 36764 \_\_\_ TG  
 GCAGACAGG ACT GCAG  
 ||||| ||| |||  
 CGTTTGTTT TGG CGTC  
 AG GT  
 GAM1444 FLJ11011 3' TGTAAAGTTTTTCTTGTA 36979 \_ C  
 TGCA GA AGGACTTGGA  
 ||| || |||||  
 ATGT CT TTTTGAATTGT  
 T T  
 GAM1444 FLJ11053 3' CTGTCAGAGATCTGTGTTGC 88730 CAGGAC  
 GCAATGCAGA TTGGCAG  
 ||||| |||||  
 CGTTGTGTCT GACTGTC  
 AGA\_\_\_  
 GAM1444 FLJ11113 3' CTAGCTTTTGTTTGATTCA 37068 C C  
 TG AATGCAGACAGGA TTGG  
 || ||||| |||||  
 AC TTATGTTTGTTT GATC  
 \_ C  
 GAM1444 FLJ11274 3' TGTCAAGTTCTCCTTTGCA 37202 C\_  
 TGCAGA AGGACTTGGA  
 ||||| |||||  
 ACGTTT TCTTGAAGTGT  
 CC  
 GAM1444 FLJ12668 3' TTTTGTTTGTTTGCA 46530 T  
 TGCAA GCAGACAGGA  
 ||||| |||||  
 ACGTT TGTGTTGTTT  
 T  
 GAM1444 FLJ13102 3' CTGTTGAGTCCTGTCTCCTGGG 46010 AATGC TG  
 T GC AGACAGGACT GCAG  
 || ||||| |||||  
 TG TCTGTCCTGA TGTC  
 GTCC GT  
 GAM1444 FLJ13385 5' CTGCTGGGTTTTGGAGGCTGC 45849 AT AGA TG  
 GCA GC CAGGACT GCAG  
 ||| || ||||| |||||  
 CGT CG GTTTTG CGTC  
 \_ GAG GT  
 GAM1444 FLJ14075 3' TGCCTGTGTTTGTGTTTA 46050 C GGACTT  
 G AATGCAGACA GGCA  
 | ||||| |||||  
 A TTGTGTTTGT CCGT  
 T GT\_\_\_  
 GAM1444 FLJ20032 3' TTGTCAAGTTACCGATGCTTGT 67899 T GACAG  
 GCAA GCA GACTTGGA  
 ||||| |||||

			TGTT CGT TTGAACTGTT		
			_ AGCCA		
GAM1444	FLJ20184	3'	TTGCTGGGAGCTCTGCTTTGCA 34695	T	CAGGA TG
			TGCAA GCAGA CT GCAG		
			ACGTT CGTCT GG CGTT		
			T CGA__ GT		
GAM1444	FLJ20445	3'	TTGCTAAGTAATCTGTTTGCA 35182	—	
			TGCAGACAGG ACTTGGCAG		
			ACGTTTGTCT TGAATCGTT		
			AA		
GAM1444	FLJ20445	3'	TTGTTTTTCATTGTTTGTATGTA 35183	A	GACTT
			TGCA TGCAGACAG GGCAG		
			ATGT ATGTTTGTT TTGTT		
			_ ACTT_		
GAM1444	FLJ20507	3'	CTGTTAAGTCCTGAGTTTGTCA 35285	T	—
			A GCAGAC AGGACTTGGCAG		
			A TGTTTG TCCTGAATTGTC		
			C AG		
GAM1444	FLJ20507	3'	CTGTTAAGTCCTGAGTTTGTCA 60220	T	—
			A GCAGAC AGGACTTGGCAG		
			A TGTTTG TCCTGAATTGTC		
			C AG		
GAM1444	FLJ20511	3'	TGCCAGGCACTGCTTGTA 35333	GA	GA
			TGCA CAG CTTGGCA		
			ATGT GTC GGACCGT		
			TC AC		
GAM1444	FLJ20716	3'	CTAAGATTTTGTTTGCTTGT 35602	T	—
			GCAA GCAGACAGGA CTTGG		
			TGTT CGTTTGTTTT GAATC		
			_ A		
GAM1444	FLJ20972	3'	TGTTAAAAATCTGCATTTA 46730	C	CAGGAC
			G AATGCAGA TTGGCA		
			A TTACGTCT AATTGT		
			T AAA__		
GAM1444	FLJ21415	3'	TTTTGTTTGTATTTG 45358	C	
			TG AATGCAGACAGGA		
			GC TTATGTTTGTTTT		
			T		
GAM1444	FLJ21952	3'	TTGCCAGGAGCATCTGCATGT 42558	A	CAGGA
			GCA TGCAGA CTTGGCAG		

			TGT ACGTCT	GGACCGTT		
			_	ACGA_		
GAM1444	FLJ22009	3'	TTGCTGTATTGTCTGTATT	60287	G	TT
			AATGCAGACAG AC	GGCAG		
			TTATGTCTGTT TG	TCGTT		
			A	_		
GAM1444	FLJ22479	3'	TGTTGTGTGTCTGTGTGC	46081	G	_ T
			GCA ACAGG AC	TGGCA		
			CGT TGTCT TG	GTTGT		
			G	G T		
GAM1444	FLJ22593	3'	CTGTATTTTTTCTGTATTGTA	45224	C	CTTG
			TGCAATGCAGA AGGA	GCAG		
			ATGTTATGTCT TTTT	TGTC		
			T	TA_		
GAM1444	FLJ22639	5'	TGCCAGATCTGCGTCTGT	45611	A_	C
			GCAGAC GGA	TTGGCA		
			TGTCTG TCT	GACCGT		
			CG	A		
GAM1444	FLJ22756	3'	TGCCTGTGTTTGTGTTG	45584		GGACTT
			CAATGCAGACA	GGCA		
			GTTGTGTTTGT	CCGT		
			GT_			
GAM1444	FLJ23186	3'	GAGTTTGTGCTGTATTGT	60404		_
			GCAATGCAG ACAGGACTT			
			TGTTATGTC TGTTTTGAG			
			G			
GAM1444	FLJ31153	3'	CTGTAATTTGTTTGTACTGC	58122	A	ACTTG
			GCA TGCAGACAGG	GCAG		
			CGT ATGTTTGT	TGTC		
			C	AA_		
GAM1444	FLJ31978	3'	TGCCAGGTCCAATGTT	58353		_
			GACA GGA	CTTGGCA		
			TTGT CCTGGACCGT			
			AA			
GAM1444	GL004	3'	TTGTTTCTGTCTCTGCATTGTA	65997	CAG	TT_
			TGCAATGCAGA GAC	GGCAG		
			ATGTTACGTCT CTG	TTGTT		
			_	TCT		
GAM1444	GTF2A1	5'	TTGCCCCCTCTTGTGTGTTG	31832		CTT
			GCAATGCAGACAGGA	GGCAG		

			TGTTGTGTTTGTCT	CCGTT			
			CCC				
GAM1444	HAT	3'	TTGCAAAGTCTGTATGCA	14936	G	G	G
			TGCA ACAG ACTT GCAG				
			ACGT TGTC TGAA CGTT				
			A _ A				
GAM1444	HEY2	3'	TTGTCAAGTTAGTGATTGCATT	24322	C	A	G_
	TG		G AATGCAG CA GACTTGGCAG				
			G TTACGTT GT TTGAACTGTT				
			T A GA				
GAM1444	HIF1AN	3'	CTGTGTGTTTGTGTGTGT	61973	A	G	TTG
			GCA TGCAGACAG AC GCAG				
			TGT GTGTTTGTGTT TG TGTC				
			_ _ TG_				
GAM1444	HIF1AN	3'	TTGTCATCATGTCTGTGTGTA	61983	A	G	CT
			TGCA TGCAGACA GA TGGCAG				
			ATGT GTGTCTGT CT ACTGTT				
			_ A _				
GAM1444	HNRPA3	3'	TCCTGTTTGTACTGTA	19261	A		
			TGCA TGCAGACAGGA				
			ATGT ATGTTTGCCT				
			C				
GAM1444	HNRPA3	3'	TTGCTGAGTCCTAGCTGTGTTT	19264	C	AC	TG
	A		G AATGCAG AGGACT GCAG				
			A TTGTGTC TCCTGA CGTT				
			T GA GT				
GAM1444	HSPC055	3'	GTA CTGTTGGTATTGT	26270	A	G	
			GCAATGC GACAG AC				
			TGTTATG TTGTC TG				
			G A				
GAM1444	IBTK	3'	TGCCAAGTATGTGTTGTTG	67491	T	_	GG
			A GCAG ACA ACTTGGCA				
			G TGTT TGT TGAACCGT				
			T G A_				
GAM1444	IPLA2(GAMMA)	5'	CTGCTGCGCCAGTGTTTGTGTT	60690			__ ACT
	G		CAATGCAGACA GG TGGCAG				
			GTTGTGTTTGT CC GTCGTC				
			GA GC_				
GAM1444	JAM1	3'	TTGTTGAGCTTGTGTGTGTGTT	57906	G	G	_ TG
	GT		GCAATGCA ACA GA CT GCAG				

			TGTTGTGT TGT TT GA TGTT	
			G G C GT	
GAM1444	JAM1	3'	TTGTTGAGCTTGTGTGTGTGTT 57937	G G _ TG
	GT		GCAATGCA ACA GA CT GCAG	
			TGTTGTGT TGT TT GA TGTT	
			G G C GT	
GAM1444	JAM1	3'	TTGTTGAGCTTGTGTGTGTGTT 57961	G G _ TG
	GT		GCAATGCA ACA GA CT GCAG	
			TGTTGTGT TGT TT GA TGTT	
			G G C GT	
GAM1444	JAM1	3'	TTGTTGAGCTTGTGTGTGTGTT 33768	G G _ TG
	GT		GCAATGCA ACA GA CT GCAG	
			TGTTGTGT TGT TT GA TGTT	
			G G C GT	
GAM1444	KIAA0061	3'	TGCCAAGTTCTACATGT 68294	GAC
			GCA AGGACTTGGCA	
			TGT TCTTGAACCGT	
			ACA	
GAM1444	KIAA0095	3'	GGTTTGTCTTCTGTTGT 90918	C
			GCAATG AGACAGGACT	
			TGTTGT TTTGTTTGG	
			C	
GAM1444	KIAA0164	3'	CTGCCAAAGGAAGTATGTATTG 28449	G AGGAC
	CA		TGCAATGCA AC TTGGCAG	
			ACGTTATGT TG AACCGTC	
			A AAGGA	
GAM1444	KIAA0218	3'	CTGTTATGTTGTCTGTGCTGCA 28619	AT GG T
			TGCA GCAGACA AC TGGCAG	
			ACGT TGTCTGT TG ATTGTC	
			CG _ T	
GAM1444	KIAA0298	5'	CTGAACATTTTTTTCTGCATTG 76577	C CTTGG
	T		GCAATGCAGA AGGA CAG	
			TGTTACGTCT TTTT GTC	
			T TACAA	
GAM1444	KIAA0323	3'	CTGCCAGGTCCCCGATGTGT 63263	GACA
			ATGCA GGACTTGGCAG	
			TGTGT CCTGGACCGTC	
			AGCC	
GAM1444	KIAA0332	3'	CTGGGGTTTTTTGTTTGTGTTGT 62699	T _ TG CAG
			GCAA GCAGACAGGA CT G	

		TGTT TGTTTGTTTT GG C	
		— TTG GT	
GAM1444 KIAA0410	3'	CTGTCAAGGGTTTGTGTGTGT 28774	G A_
		ATGCA ACAGG CTTGGCAG	
		TGTGT TGTTT GAACTGTC	
		G GG	
GAM1444 KIAA0433	3'	CTGTTAAGTTAGTAAGTATT 30837	AG AG
		AATGC AC GACTTGGCAG	
		TTATG TG TTGAATTGTC	
		AA A_	
GAM1444 KIAA0446	5'	CTGCTGTATTTGTCTGTGTTG 68866	ACT
		CAATGCAGACAGG TGGCAG	
		GTTGTGTCTGTTT GTCGTC	
		AT_	
GAM1444 KIAA0451	3'	TGCTGGGGATTCCATTGTA 29118	CAGAC GA TG
		TGCAATG AG CT GCA	
		ATGTTAC TT GG CGT	
		C___ AG GT	
GAM1444 KIAA0459	3'	TCCTGTCTGTTTTGTA 61008	T
		TGCAA GCAGACAGGA	
		ATGTT TGTCTGTCCT	
		T	
GAM1444 KIAA0478	3'	AGTCCTGTCTGCGTGT 29540	A
		GCA TGCAGACAGGACT	
		TGT GCGTCTGTCCTGA	
		—	
GAM1444 KIAA0495	3'	TTGCTTAGGTGTTTTGTGTTGT 62601	CA G _
		GCAATGCAGA G ACTTG GCAG	
		TGTTGTGTTT T TGGAT CGTT	
		___G T	
GAM1444 KIAA0825	3'	TGTCACCAGTTTGTTTGCA 61034	T A ACT
		TGCAA GCAGAC GG TGGCA	
		ACGTT TGTTTG CC ACTGT	
		— A ___	
GAM1444 KIAA0826	3'	GTTGGTTTGTGTTGTA 82640	AG
		TGCAATGCAGAC GAC	
		ATGTTGTGTTTG TTG	
		G_	
GAM1444 KIAA0826	5'	TTGCTAAGTTTTCAAGCTGT 82644	AC___
		GCAG AGGACTTGGCAG	

		TGTC TTTTGAATCGTT			
		GAAC			
GAM1444	KIAA0888	3' CTGTTAAGTATATATTGTGTTG 63230		ACAGG	
	C	GCAATGCAG ACTTGGCAG			
		CGTTGTGTT TGAATTGTC			
		ATATA			
GAM1444	KIAA0895	3' GTATTGTTTGTGTTTGTGTA 92726	T	G	
		TGCAA GCAGACAG AC			
		ATGTT TGTTTGTGTT TG			
		T A			
GAM1444	KIAA0903	3' TGTTGGGTCTCAACATTG 71408	CA	CAG	TG
		CAATG GA GACT GCA			
		GTTAC CT CTGG TGT			
		AA ___ GT			
GAM1444	KIAA1014	3' TTGTATTATTGTTTGTGTTTGT 65355	T		GACTTG
		GCAA GCAGACAG GCAG			
		TGTT TGTTTGTGTT TGTT			
		T ATTA__			
GAM1444	KIAA1029	3' TGCTGGGTCCCTTGTAGCA 23482	AA	ACA	TG
		TGC TGCAG GGACT GCA			
		ACG ATGTT CCTGG CGT			
		___ C___ GT			
GAM1444	KIAA1030	3' CTGCTGGGTCCCTGGGGAGATGC 93334		ATGCAGA	TG
	A	TGCA CAGGACT GCAG			
		ACGT GTCCTGG CGTC			
		AGAGGG_ GT			
GAM1444	KIAA1076	3' TTGTCAGACCGTCTGCGTGT 65519	A	A	AC
		GCA TGCAGAC GG TTGGCAG			
		TGT GCGTCTG CC GACTGTT			
		_ _ A_			
GAM1444	KIAA1077	3' TTGCTTGTTTGTGTTTGTGTTTGTGTA 72913	T		ACTT
		TGCAA GCAGACAGG GGCAG			
		ATGTT TGTTTGTGTT TCGTT			
		T GT__			
GAM1444	KIAA1126	3' TGCCAGGTGAATGTTTGT 71943		GG_	
		GCAGACA ACTTGGCA			
		TGTTTGT TGGACCGT			
		AAG			
GAM1444	KIAA1229	3' TTGTTGAGTAAACTCATTGTA 62071		C ACAGG	TG
		TGCAATG AG ACT GCAG			



		ATGTTAC TC TGA TGTT	
		_ AAAA_ GT	
GAM1444 KIAA1340	3'	CTGCTAGGCATTCTGTATTGT 69181	CAGGA
		GCAATGCAGA CTTGGCAG	
		TGTTATGTCT GGATCGTC	
		TAC__	
GAM1444 KIAA1371	3'	TTGTTGGGTGTAATGTGTGTA 89049	G GG__ TG
		TGCA ACA ACT GCAG	
		ATGT TGT TGG TGTT	
		G AATG GT	
GAM1444 KIAA1615	3'	TTCAATATCTTTTCTGCATTGT 68739	C C_ CAG
A		TGCAATGCAGA AGGA TTGG	
		ATGTTACGTCT TTCT AACT	
		T AT T	
GAM1444 KIAA1649	3'	TTGCTGGGAGGGGGCTGTGTTG 66985	ACAGGA TG
T		GCAATGCAG CT GCAG	
		TGTTGTGTC GG CGTT	
		GGGGGA GT	
GAM1444 KIAA1674	3'	TTGTTGGGTACATTGTTTTGT 68799	T ACAGG TG
		GCAA GCAG ACT GCAG	
		TGTT TGTT TGG TGTT	
		T ACA__ GT	
GAM1444 KIAA1715	3'	TGCTCTTGTGTTGTATT 68129	CTTG
		AATGCAGACAGGA GCA	
		TTATGTTTGTCT CGT	
		_____	
GAM1444 KIAA1857	3'	TTTTGTTTGTATTCA 50722	C
		TG AATGCAGACAGGA	
		AC TTATGTTTGT	
		_____	
GAM1444 KIAA1866	3'	TTTTGTTTGTGTTGTA 60939	T
		TGCAA GCAGACAGGA	
		ATGTT TGTTTGT	
		_____	
GAM1444 KIAA1937	3'	TCCTGTCTGCTTTGCA 73700	T
		TGCAA GCAGACAGGA	
		ACGTT CGTCTGTCCT	
		T	
GAM1444 LAPTM4A	3'	TTGTAAAGTCTTTTACATT 28194	C CA
		AATG AGA GGA CTGGCAG	

TTAC TTT TCTGAATTGTT  
 A \_\_\_\_  
 GAM1444 LEPROTL1 3' TTGTTAAGGATATTTGTTTGTA 31064 GA\_\_\_\_  
 TGCAGACAG CTTGGCAG  
 ||||| |||||  
 ATGTTTGTT GAATTGTT  
 TATAG  
 GAM1444 LGI2 3' TTGTTGAGTTGCTGCTATTGCA 36402 \_ A GG TG  
 TGCAAT GCAG CA ACT GCAG  
 ||||| ||||| || |||||  
 ACGTTA CGTC GT TGA TGTT  
 T \_ \_ GT  
 GAM1444 MARCKS 5' CTGTTGAGTTTCTTTGTTG 9866 C CAG TG  
 CAATG AGA GACT GCAG  
 ||||| ||||| |||||  
 GTTGT TCT TTGA TGTC  
 T \_ \_ GT  
 GAM1444 MGC10067 3' TGTTTTTGTCTCATTGT 58942 C CTTG  
 GCAATG AGACAGGA GCA  
 ||||| ||||| |||||  
 TGTTAC TCTGTTTT TGT  
 \_ \_ \_  
 GAM1444 MGC10981 3' CTGCCACTTGCTTGTCTGCATG 51018 A ACT\_  
 T GCA TGCAGACAGG TGGCAG  
 ||||| ||||| |||||  
 TGT ACGTCTGTTC ACCGTC  
 \_ GTTC  
 GAM1444 MGC11386 3' TGTCAGGATGTGTGTTGC 51957 AG GGA  
 GCAATGC ACA CTTGGCA  
 ||||| ||||| |||||  
 CGTTGTG TGT GGA CTGT  
 \_ A \_  
 GAM1444 MGC12466 3' TTGTTGGGGCCTTTTGCATTGA 79038 C C A TG  
 G AATGCAGA AGG CT GCAG  
 | ||||| ||||| |||||  
 A TTACGTTT TCC GG TGTT  
 T \_ \_ G GT  
 GAM1444 MGC12921 3' TGTTGAGTTCTTGCTGT 63780 A \_ TG  
 GCAG CAGGA CT GCA  
 ||||| ||||| |||||  
 TGTC GTTCT GA TGT  
 G T GT  
 GAM1444 MGC13057 5' TGCCGGGCAACGTGTTGT 50309 AGACAGGA  
 GCAATGC CTTGGCA  
 ||||| ||||| |||||  
 TGTTGTG GGGCCGT  
 CAAC\_\_\_\_  
 GAM1444 MGC15619 5' TCTTGTTTTATTGCA 50423 C  
 TGCAATG AGACAGGA  
 ||||| ||||| |||||

ACGTTAT TTTGTTCT

GAM1444 MGC15827 3' TGCAGCTTCTGTGTTGT 51807 CA ACTTG  
GCAATGCAGA GG GCA  
||||||| || |||  
TGTTGTGTCT TC CGT  
\_\_ GA\_\_

GAM1444 MGC16384 3' CTGCCTGCGGCCTGTCTGTGTT 53866 C ACTT\_  
TG G AATGCAGACAGG GGCAG  
| ||||| ||||  
G TTGTGTCTGTCC CCGTC  
T GCGT  
GAM1444 MGC20255 3' TGTTTATGTCTGCGCTGT 53448 A GGACTT  
GCA TGCAGACA GGCA  
||| ||||| |||  
TGT GCGTCTGT TTGT  
C AT\_\_

GAM1444 MGC2217 3' TGCTGTTGGCTGTGTTGT 44180 ACAG TT  
GCAATGCAG GAC GGCA  
||||||| ||| |||  
TGTTGTGTC TTG TCGT  
GG\_\_ \_\_

GAM1444 MGC2641 3' GTGCTGTTTGTATTGT 50943 C G  
G AATGCAGACAG AC  
| ||||| |||  
G TTATGTTTGTGTC TG  
T G

GAM1444 MGC2747 3' TGTTGAGTTTTTTGTTGT 44090 AT CA TG  
GCA GCAGA GGACT GCA  
||| ||||| ||||| |||  
TGT TGTTT TTTGA TGT  
\_\_ \_\_ GT

GAM1444 MTCH1 3' TTGCTGAGTCTGTCTTGTGCA 26782 ATGC G TG  
TGCA AGACAG ACT GCAG  
||| ||||| ||| |||||  
ACGT TCTGTC TGA CGTT  
GT\_\_ \_ GT

GAM1444 MTHFD2 3' TTGTAAATTTTTGTATTGTA 21812 CAG C  
TGCAATGCAGA GA TTGGCAG  
||||||| || |||||  
ATGTTATGTTT TT AATTGTT  
\_\_ A

GAM1444 MY014 3' TTGCTTTACTGCTGTCTGTATG 48146 A GACTT\_  
T GCA TGCAGACAG GGCAG  
||| ||||| |||||  
TGT ATGTCTGTC TCGTT  
\_ GTCATT

GAM1444 NCKX3 3' TGTTTCTGTCTGTGGTGC 40357 AT CTTG G  
GCA GCAGACAGGA GCA  
||| ||||| |||

			CGT TGTCTGTCTT TGT		
			GG _____ A		
GAM1444	NSAP1	5'	CTGCCGGTAGGCGTCTGTGTGC 21042	A	AGG_ T
			GCA TGCAGAC ACT GGCAG		
			CGT GTGTCTG TGG CCGTC		
			_ CGGA _		
GAM1444	NUP160	3'	TGTATTTTCTGTATTGTA 87597		CAGGACTTG
			TGCAATGCAGA GCA		
			ATGTTATGTCT TGT		
			TTTA_____		
GAM1444	OPRL1	3'	CTGTGTGCTGTTTGCATGGCA 6197	A	G TTG
			TGC ATGCAGACAG AC GCAG		
			ACG TACGTTTGTG TG TGTC		
			G G _		
GAM1444	OSBPL3	3'	TGTTCTTGCTTTGTGTTGT 31442	_	CTTG G
			GCAATGCAGA CAGGA GCA		
			TGTTGTGTTT GTTCT TGT		
			C _ A		
GAM1444	pcnp	3'	TTGTTTTGTATTTTGTATTGT 39790		CAGG TT
	A		TGCAATGCAGA AC GGCAG		
			ATGTTATGTTT TG TTGTT		
			TTA_ TT		
GAM1444	PFTK1	3'	TTGTAATTTGTCTGTATT 24762		ACTTG
			AATGCAGACAGG GCAG		
			TTATGTCTGTTT TGTT		
			AA_____		
GAM1444	PHCA	3'	TGCCAAGGGTTGCATGT 37181	A	ACAGGA
			GCA TGCAG CTTGGCA		
			TGT ACGTT GAACCGT		
			_ GG_____		
GAM1444	POLR2B	3'	GTCTTGTTTCTATTGT 6265	C	
			GCAATG AGACAGGAC		
			TGTTAT TTTGTTCTG		
			C		
GAM1444	PPIL3	5'	TTGCTGAGTTCTGTGTTGC 55663	_	TG
			GCAG ACAGGACT GCAG		
			CGTT TGTCTTGA CGTT		
			G GT		
GAM1444	PRO2389	3'	CTGCCAGGTCTTCACGTTG 63737	CA	CA
			CAATG GA GGA CTGGCAG		

GTTGC CT TCTGGACCGTC  
 A\_ \_  
 GAM1444 PRO2900 3' TGCCAGGTCTTCCTTGCA 37807 AC  
 TGCAG AGGACTTGGCA  
 |||| |||||  
 ACGTT TTCTGGACCGT  
 CC  
 GAM1444 RA-GEF-2 3' TTGTTGTGGTTTTGTTTGTATT 32962 C TG\_  
 TG G AATGCAGACAGGACT GCAG  
 | ||||| ||||  
 G TTATGTTTGTGTTTGG TGTT  
 T TGT  
 GAM1444 RAB10 3' TTGCTGAGTCTTGTTTTAAGTG 85181 ATGC TG  
 CA AGACAGGACT GCAG  
 || ||||| ||||  
 GT TTTGTTCTGA CGTT  
 GAAT GT  
 GAM1444 RAB34 3' CTGCTGGGCCCTTTGTGTTTG 49192 C CA A TG  
 G AATGCAGA GG CT GCAG  
 | ||||| || ||||  
 G TTGTGTTT CC GG CGTC  
 T C\_ \_ GT  
 GAM1444 RNPC2 3' GAAATAGGTTTTGTCTGGTTGC 16922 G GCAG  
 A TGCAAT CAGACAGGACTTG  
 ||||| |||||  
 ACGTTG GTCTGTTTTGGAT  
 \_ AAAGA  
 GAM1444 SCN12A 3' TTCTGTTTGTGTTCCA 26225 C  
 TG AATGCAGACAGGA  
 || |||||  
 AC TTGTGTTTGTCTT  
 C  
 GAM1444 SCYA13 3' CTGCTGGCAGTGGGTTTGTATT 18256 C AGGAC\_ TG  
 CG G AATGCAGAC T GCAG  
 | ||||| | ||||  
 G TTATGTTT G CGTC  
 C GGTGAC GT  
 GAM1444 SDF1 3' TTGCCAAGGGCTTTGTTTGTGCA 90866 T AC GA  
 TGCAA GCAG AG CTTGGCAG  
 |||| |||| || |||||  
 ACGTT TGTT TC GAACCGTT  
 T \_ GG  
 GAM1444 SFRS10 3' CTGCTGAGAAGTTTCTATTGTA 15976 C AGGA TG  
 TGCAATG AGAC CT GCAG  
 ||||| |||| || ||||  
 ATGTTAT TTTG GA CGTC  
 C AA\_ GT  
 GAM1444 SKRP1 5' CTGCTGGATTTGTTTGTATTTG 55145 C AC TG  
 G AATGCAGACAGG T GCAG  
 | ||||| |||| | ||||

G TTATGTTTGT TT G CGTC  
 T A\_ GT  
 GAM1444 SMARCF1 3' TTGCCAAGCGCTGCGTCTGT 37447 A\_ A\_  
 GCAGAC GG CTTGGCAG  
 ||||| || |||||  
 TGTCTG TC GAACCGTT  
 CG GC  
 GAM1444 STX3A 3' TTGATTTTTCTCTGTGTTGTA 14808 C C TG  
 TGCAATGCAGA AGGA T G  
 ||||| ||||| ||  
 ATGTTGTGTCT TTTT A T  
 C T GT  
 GAM1444 TED 3' CTGCTTTCTGTTTGTTCATT 31636 A TT\_\_  
 GT GCAATGCAG CAGGAC GGCAG  
 ||||| ||||| |||||  
 TGTACGTT GTTTTG TCGTC  
 \_ TCTT  
 GAM1444 TGIF2 3' TGCTGTGGTTTGCATTCA 41459 C AGGACT  
 TG AATGCAGAC TGGCA  
 || ||||| |||||  
 AC TTACGTTTG GTCGT  
 \_ GT\_\_\_\_  
 GAM1444 TSGA14 3' TTGTTGGGTCTCTCTGTGTTGT 38048 CA TG  
 GCAATGCAGA GGACT GCAG  
 ||||| ||||| |||||  
 TGTGTGTCT TCTGG TGTT  
 C\_ GT  
 GAM1444 WSB1 5' TGTTGGGTCCGCATCGTA 56143 A AGACA TG  
 TGC ATGC GGACT GCA  
 ||| ||||| ||||| |||  
 ATG TACG CCTGG TGT  
 C \_\_\_\_\_ GT  
 GAM1444 WSB1 5' TGTTGGGTCCGCATCGTA 56149 A AGACA TG  
 TGC ATGC GGACT GCA  
 ||| ||||| ||||| |||  
 ATG TACG CCTGG TGT  
 C \_\_\_\_\_ GT  
 GAM1444 ZF 3' GCCAGGCTCCGTTGTA 41087 A A \_  
 TGCAG C GGA CTTGGC  
 ||||| ||||| |||||  
 ATGTT G CCT GGACCG  
 \_ \_ C  
 GAM1444 ZFP95 3' TTGTTGACCATATGTGTTGTA 59028 GACA AC TG  
 TGCAATGCA GG T GCAG  
 ||||| ||||| |||||  
 ATGTTGTGT CC A TGTT  
 ATA\_ \_ GT  
 GAM1444 ZFP95 3' TTGTTGACCATATGTGTTGTA 27384 GACA AC TG  
 TGCAATGCA GG T GCAG  
 ||||| ||||| |||||

		ATGTTGTGT CC A TGTT		
		ATA_ _GT		
GAM1444	ZNF238	3' GTCTTTGTTTGCATTGTA 20966		_
		TGCAATGCAGACAG GAC		
		ATGTTACGTTTGTGTT CTG		
		T		
GAM1444	ZNF340	3' TTGTTTGTGTCTGTTTGTATT 84567		ACTT
		AATGCAGACAGG GGCAG		
		TTATGTTTGTCT TTGTT		
		GTGT		
GAM1444	ZNF397	3' TTGCTAAGTCCAAGGACATTG 50357		CAGACA
		CAATG GGACTIONGGCAG		
		GTTAC CCTGAATCGTT		
		AGGAA_		
GAM1444	ZNRD1	3' TTGTCCATCCTGTCTGGTTGCA 96002	G	CT _
		TGCAAT CAGACAGGA TGG CAG		
		ACGTTG GTCTGTCCT ACC GTT		
		_ _ T		
GAM1444	ZNRD1	3' TTGTCCATCCTGTCTGGTTGCA 27474	G	CT _
		TGCAAT CAGACAGGA TGG CAG		
		ACGTTG GTCTGTCCT ACC GTT		
		_ _ T		
GAM1444	ZWINT	3' TTGTTGAGTCCTTTCTTTGT 22937	TGC C	TG
		GCAA AGA AGGACT GCAG		
		TGTT TCT TCCTGA TGTT		
		_ T GT		
GAM1444	LOC113523	3' TTGTTGATGGCCTTTTGTGTTG 73053		C AC_ TG
	T	GCAATGCAGA AGG T GCAG		
		TGTTGTGTTT TCC A TGTT		
		_ GGT GT		
GAM1444	LOC116411	5' CTGCCGAGTGCCTGCGATTGCA 73864		_ A AGG
		TGCAAT GCAG C ACTTGGCAG		
		ACGTTA CGTC G TGAGCCGTC		
		G C _		
GAM1444	LOC118812	5' GTCTTTATCTGCGTTGCA 73934		C_
		TGCAATGCAGA AGGAC		
		ACGTTGCGTCT TTCTG		
		AT		
GAM1444	LOC120448	5' TGCTATTGGCTGTGTTGT 75551		A GACT
		GCAATGCAG CAG TGGCA		

		TGTTGTGTC GTT ATCGT		
		G ____		
GAM1444	LOC125228 3'	TTGATTTCTGTTTGTGCA 74404	C	C TG
		TGCAATG AGACAGGA T G		
		ACGTTGT TTTGTCTT A T		
		_ T GT		
GAM1444	LOC126669 3'	TTGTCAAGTTCTTAGCCGTTCA 75426	C	CAGAC
		TG AATG AGGACTTGGCAG		
		AC TTGC TCTTGAAGTGT		
		_ CGAT_		
GAM1444	LOC127829 3'	TCCTGTTTTTATTGTA 57118	C	
		TGCAATG AGACAGGA		
		ATGTTAT TTTGTCCT		
		T		
GAM1444	LOC128977 3'	TGTTAGATTTGTGTGTA 74830	G	C
		TGCA ACAGGA TTGGCA		
		ATGT TGTTTT GATTGT		
		G A		
GAM1444	LOC130355 5'	TGCTGTGTGTTTGTGTTCTG 74932	C	GGACT
		G AATGCAGACA TGGCA		
		G TTGTGTTTGT GTCGT		
		C GT__		
GAM1444	LOC131034 3'	CTGTAAAGCCCTTGATTGT 55520	GAC	A
		GCAATGCA AGG CTTGGCAG		
		TGTTATGT TCC GAATTGTC		
		_ C		
GAM1444	LOC137593 5'	CTGCCAGGTCGACGTTTTGCGT 75270	C	_ AG_
	TTA	G AATGCAGA C GACTTGGCAG		
		A TTGCGTTT G CTGGACCGTC		
		T T CAG		
GAM1444	LOC144486 3'	TTGCTGAGCATTGTGTGGCA 83088	A	CAGGA TG
		TGC ATGCAGA CT GCAG		
		ACG TGTGTTT GA CGTT		
		G AC__ GT		
GAM1444	LOC144747 5'	CTGTTGTTTGCATTGTA 76953	_____	
		TGCAATGCA GACAG		
		ATGTTACGT TTGTC		
		TTTG		
GAM1444	LOC144932 3'	CTGTTAGGAACCTGCATAGCA 76975	A	ACAGGA
		TGC ATGCAG CTTGGCAG		



ACG TACGTC GGATTGTC  
 A CAA\_\_\_\_  
 GAM1444 LOC145082 5' TGCTGGCCGTTTGCATTCA 83249 C A AC TG  
 TG AATGCAGAC GG T GCA  
 || ||||| || | |||  
 AC TTACGTTTG CC G CGT  
 \_ \_ \_ GT  
 GAM1444 LOC145801 3' GTTAGGTTTTTGTGTG 77499 G \_  
 CA ACAGGA CTTGGC  
 || ||||| |||||  
 GT TGTTTT GGATTG  
 G T  
 GAM1444 LOC146445 3' GGCCTGTCTGTGCTGCA 83680 AT A  
 TGCA GCAGACAGG CT  
 ||| ||||| ||  
 ACGT TGTCTGTCC GG  
 CG \_  
 GAM1444 LOC147276 5' TGTAGCTGTTTGTGCTGCA 78341 AT GACTTG  
 TGCA GCAGACAG GCA  
 ||| ||||| |||  
 ACGT TGTTTGTC TGT  
 CG GA\_\_\_\_  
 GAM1444 LOC148223 3' TGCCGGGCACTGCATGCA 78745 GA GA  
 TGCA CAG CTTGGCA  
 ||| || |||||  
 ACGT GTC GGGCCGT  
 AC AC  
 GAM1444 LOC148887 3' TGTCTGTCTCTGTGTTGT 84250 CAG TT  
 GCAATGCAGA GAC GGCA  
 ||||| || |||  
 TGTTGTGTCT CTG CTGT  
 \_ T\_  
 GAM1444 LOC149703 3' CTGTCAGGTTATATTATTGTA 84652 CAGACAG  
 TGCAATG GACTTGGCAG  
 ||||| |||||  
 ATGTTAT TTGGA CTGTC  
 TATA\_\_\_\_  
 GAM1444 LOC150319 3' CTGCTGAGCCACTGCCTTGCA 79654 T ACA A TG  
 TGCAA GCAG GG CT GCAG  
 ||||| ||| || |||  
 ACGTT CGTC CC GA CGTC  
 C A \_ \_ GT  
 GAM1444 LOC151632 3' TGCTTTGTCTGTGTTACA 85472 C GACTT  
 TG AATGCAGACAG GGCA  
 || ||||| |||  
 AC TTGTGTCTGTT TCGT  
 A \_\_\_\_\_  
 GAM1444 LOC151720 5' TTGTTGAGGATTCTGGGTTGCA 80342 G CA GA TG  
 TGCAAT CAGA G CT GCAG  
 ||||| ||| | || |||

ACGTTG GTCT T GA TGTT  
 G \_\_ AG GT  
 GAM1444 LOC152271 3' TGCTTTGTCTGTGTTACA 80521 C GACTT  
 TG AATGCAGACAG GGCA  
 || ||||| ||||  
 AC TTGTGTCTGTT TCGT  
 A \_\_\_\_\_  
 GAM1444 LOC152627 5' TGTTAAGTGTGTGTGT 80633 G G  
 GCA ACAG ACTTGGCA  
 ||| ||| |||||  
 TGT TGTT TGAATTGT  
 G G  
 GAM1444 LOC153077 3' TGTTGAGTTCTGTGCCTG 85920 \_\_ TG  
 CAG ACAGGACT GCA  
 ||| ||||| |||  
 GTC TGTCTTGA TGT  
 CG GT  
 GAM1444 LOC153396 3' CTGCTGACTACCTGTATGTATT 80819 G AC\_TG  
 GTA TGCAATGCA ACAGG T GCAG  
 ||||| |||| | ||||  
 ATGTTATGT TGTCC A CGTC  
 A ATC GT  
 GAM1444 LOC153743 3' CTGTTGAGTTTCTTTGTGTTTA 60512 C CA TG  
 G AATGCAGA GGACT GCAG  
 | ||||| |||| ||||  
 A TTGTGTTT TTTGA TGTC  
 T C\_ GT  
 GAM1444 LOC153810 3' CTGTTGGGTTTCAGACTTGCA 80934 TGCA CAG TG  
 TGCAA GA GACT GCAG  
 |||| | |||| ||||  
 ACGTT CT TTGG TGTC  
 CAGA \_\_ GT  
 GAM1444 LOC155435 3' TTGTTGATGTGTTTGTGTGTA 81356 A GGAC TG  
 TGC ATGCAGACA T GCAG  
 ||| ||||| | ||||  
 ATG TGTGTTTGT A TGTT  
 \_ GT\_\_ GT  
 GAM1444 LOC157507 5' TTGTTGGGTTCTTTGTATT 81464 CA TG  
 AATGCAGA GGACT GCAG  
 ||||| |||| ||||  
 TTATGTTT CTTGG TGTT  
 C\_ GT  
 GAM1444 LOC157627 3' TGCCAGGTTTCTGCTGCA 81508 A \_  
 TGCAG CAGGA CTTGGCA  
 |||| |||| |||||  
 ACGTC GTCTT GGACCGT  
 \_ T  
 GAM1444 LOC157739 3' CTGCTCACATGTTTGTGTGT 81582 A GGACTT  
 GCA TGCAGACA GGCAG  
 ||| ||||| ||||

		TGT GTGTTTGT	TCGTC		
		— ACAC—			
GAM1444	LOC158117 3'	TTGTCAAGCACCTTCTGTGTT	81714	C	A_
		AATGCAGA AGG CTTGGCAG			
		TTGTGTCT TCC GAACTGTT			
		— AC			
GAM1444	LOC159110 3'	TGTCAAAAATCTGTATTCA	82101	C	CAGGAC
		TG AATGCAGA TTGGCA			
		AC TTATGTCT AACTGT			
		— AAA—			
GAM1444	LOC159116 3'	TGTCAAAAATCTGTATTCA	82096	C	CAGGAC
		TG AATGCAGA TTGGCA			
		AC TTATGTCT AACTGT			
		— AAA—			
GAM1444	LOC169611 3'	TTGCTGAGATATCTGTTTTGCA	82780	T	CAGGA TG
		TGCAA GCAGA CT GCAG			
		ACGTT TGTCT GA CGTT			
		T ATA__ GT			
GAM1444	LOC170409 3'	CTGTTAGGGCTTTTTGTGTGT	82861	A	C GA
		GCA TGCAGA AG CTTGGCAG			
		TGT GTGTTT TC GGATTGTC			
		— T G_			
GAM1444	LOC196500 3'	CTGTCCTGGCTGTCTGTGTGT	87741	A	GA T_
		GCA TGCAGACAG CT GGCAG			
		TGT GTGTCTGTC GG CTGTC			
		— __ TC			
GAM1444	LOC197358 3'	TGCAGCTGTTTGTGTTG	88054		GACTTG
		CAATGCAGACAG GCA			
		GTTGTGTTTGTGTC CGT			
		GA__			
GAM1444	LOC200298 3'	CTGCTGGGTCCCTCCACATTGC	89972	CA CA	TG
		GCAATG GA GGACT GCAG			
		CGTTAC CT CCTGG CGTC			
		AC C_ GT			
GAM1444	LOC200904 3'	TGCTTTGTCTGTGTTACA	90189	C	GACTT
		TG AATGCAGACAG GGCA			
		AC TTGTGTCTGTT TCGT			
		A _____			
GAM1444	LOC202934 5'	TTGATTCTGTTTGTGTGGTA	90437	A	C TG
		TGC ATGCAGACAGGA T G			

ATG TGTGTTTGTCTT A T  
 G T GT  
 GAM1444 LOC202934 5' TTTTGTCTCTGTTGCA 90438 C  
 TGCAATG AGACAGGA  
 ||||| |||||  
 ACGTTGT TCTGTTTT  
 C  
 GAM1444 LOC203083 3' TGCTTTGTCTGTGTTACA 90465 C GACTT  
 TG AATGCAGACAG GGCA  
 || ||||| ||||  
 AC TTGTGTCTGTT TCGT  
 A \_\_\_\_\_  
 GAM1444 LOC203275 3' TTGTCAAGCACCTTCTGTGTTC 89330 C C A\_  
 A TG AATGCAGA AGG CTTGGCAG  
 || ||||| || |||||  
 AC TTGTGTCT TCC GAACTGTT  
 - - AC  
 GAM1444 LOC205143 5' TTGCCGGGTTCTGGAGC 90666 AGA  
 GC CAGGACTTGGCAG  
 || ||||| |||||  
 CG GTCTTGGGCCGTT  
 AG\_  
 GAM1444 LOC219919 3' TGCTTTGTCTGTGTTACA 93295 C GACTT  
 TG AATGCAGACAG GGCA  
 || ||||| ||||  
 AC TTGTGTCTGTT TCGT  
 A \_\_\_\_\_  
 GAM1444 LOC220824 5' TGCCAGATCTGCGTCTGT 90808 A\_ C  
 GCAGAC GGA TTGGCA  
 ||||| || |||||  
 TGTCTG TCT GACCGT  
 CG A  
 GAM1444 LOC220988 3' TTGCTGAGTCCTAGCTGTGTTT 90850 C AC TG  
 A G AATGCAG AGGACT GCAG  
 | ||||| ||||| ||||  
 A TTGTGTC TCCTGA CGTT  
 T GA GT  
 GAM1444 LOC221035 3' TCCTTTTGTGTTGTA 93172 C  
 TGCAATGCAGA AGGA  
 ||||| ||||| ||||  
 ATGTTGTGTTT TCCT  
 -  
 GAM1444 LOC221178 3' CTGCTAGAGTTGTTTGTATGTA 93533 A GG \_  
 TGCA TGCAGACA ACT TGGCAG  
 |||| ||||| || |||||  
 ATGT ATGTTTGT TGA ATCGTC  
 - - G  
 GAM1444 LOC221466 5' TTGTCAGTGTCTGTGTCTGT 93699 - -  
 GCAGACA GGAC TTGGCAG  
 ||||| ||||| |||||

	TGTCTGT TCTG GACTGTT		
	G T		
GAM1444 LOC221608 3'	TTGTCAAGTTCTAGTTGT 92189	AC	
	GCAG AGGACTTGGCAG		
	TGTT TCTTGAAGTGT		
	GA		
GAM1444 LOC221795 3'	TGCTTTGTCTGTGTTACA 92480	C	GACTT
	TG AATGCAGACAG GGCA		
	AC TTGTGTCTGTT TCGT		
	A		
GAM1444 LOC221865 3'	CTGCCGAGGGCTTGCAGTGT 92487	A	GAC GA
	GCA TGCA AG CTTGGCAG		
	TGT ACGT TC GAGCCGTC		
	G ___ GG		
GAM1444 LOC253866 5'	CTGCTAAGTCTGCGCTGCTGCA 95586	AT	ACA
	TGCA GCAG GGACTTGGCAG		
	ACGT CGTC TCTGAATCGTC		
	___ GCG		
GAM1444 LOC254057 3'	CTGCTGAGTCCAGGCTTACTTG 97000	TGC ACA	TG
CA	TGCAA AG GGACT GCAG		
	ACGTT TC CCTGA CGTC		
	CAT GGA GT		
GAM1444 LOC254176 3'	TGCTTTGTCTGTGTTACA 97342	C	GACTT
	TG AATGCAGACAG GGCA		
	AC TTGTGTCTGTT TCGT		
	A		
GAM1444 LOC254746 5'	TTGTTGGGTGAGGTTGTTGT 95143	GCA AGG	TG
	GCAAT GAC ACT GCAG		
	TGTTG TTG TGG TGTT		
	___ GAG GT		
GAM1444 LOC255465 5'	TTGATTTCTGTTTGTGTGGTA 97308	A	C TG
	TGC ATGCAGACAGGA T G		
	ATG TGTGTTTGTCTT A T		
	G T GT		
GAM1444 LOC255465 5'	TTGCATTTTTTTTGTCTCTGTT 97309	C	CTTG_
GCA	TGCAATG AGACAGGA GCAG		
	ACGTTGT TCTGTTTT CGTT		
	C TTTTA		
GAM1444 LOC256515 3'	TGCTTTGTCTGTGTTACA 96466	C	GACTT
	TG AATGCAGACAG GGCA		

		AC TTGTGTCTGTT	TCGT		
		A			
GAM1444	LOC256594 3'	TGCTTTGTCTGTGTTACA	97081	C	GA
		TG AATGCAGACAG	GGCA		
		AC TTGTGTCTGTT	TCGT		
		A			
GAM1444	LOC257295 3'	GTTAGGTTTTGTGTG	94969	G	
		CA ACAGGA CTTGGC			
		GT TGTTTT GGATTG			
		G T			
GAM1444	LOC51141 3'	CTGTTGGGTTCTGTCTTCTATT	68590	C_	TG
	G	CAATG AGACAGGACT GCAG			
		GTTAT TCTGTCTTGG TGTC			
		CT GT			
GAM1444	LOC51313 3'	TTGTTGGATTGTGTTTGTGTGT	33514	A	G C TG
		GCA TGCAGACA GA T GCAG			
		TGT GTGTTTGT TT G TGTT			
		_ G A GT			
GAM1444	LOC51320 3'	TTTTGTTGCATTGTA	33549	A	
		TGCAATGCAG CAGGA			
		ATGTTACGTT GTTTT			
GAM1444	LOC57018 3'	GGTTTGTCTGCATGT	39698	A	G
		GCA TGCAGACAG ACT			
		TGT ACGTCTGTT TGG			
GAM1444	LOC80298 3'	CTGCTTAGCTTCTGTGTTGTA	47289		CA A T
		TGCAATGCAGA GG CT GGCAG			
		ATGTTGTGTCT TC GA TCGTC			
		_ _ T			
GAM1444	LOC90288 3'	AGCTGTCTTGTCTGTGTT	62077		TT AG
		AATGCAGACAGGAC GGC			
		TTGTGTCTGTTCTG TCG			
		_ AG			
GAM1444	LOC90906 3'	CTGCTAGGAGCTGCAGTTGTA	64297		ACAGGA
		TGCAA TGCAG CTTGGCAG			
		ATGTT ACGTC GGATCGTC			
		G GA_			
GAM1444	LOC91582 5'	CTGCCAGGTCGGAAGTAGTGT	66536	A	AGACAG
		GCA TGC GACTTGGCAG			

			TGT ATG	CTGGACCGTC		
			G	AAGG__		
GAM1444	LOC91923	5'	GTTGTTGTTGCATTGCA	67554	A	_
			TGCAATGCAG CAG GAC			
			ACGTTACGTT GTT TTG			
			_	G		
GAM1444	LOC92360	3'	CTGTTAGGTACTTCTGTGTTG	69072	C	G
			CAATGCAGA AG ACTTGGCAG			
			GTTGTGTCT TC TGGATTGTC			
			_	A		
GAM1444	LOC92606	3'	TCAACCTTCTGTCTGGTTGT	69990	G	C_
			GCAAT CAGACAGGA TTGG			
			TGTTG GTCTGTCTT AACT			
			_	CC		
GAM1444	LOC93259	5'	CTGTCAGGGAGCTTGTGCTGT	71817	_	A__
			GCAG ACAGG CTTGGCAG			
			TGTC TGTTT GGA CTGTC			
			G	GAG		
GAM1445	AMPD3	3'	CTGGATTCCTTATTCC	4897	CTA	A
			GGA GAG GAAATCCAG			
			CCT TTC CTTTAGGTC			
			TA_ _			
GAM1445	CDK10	3'	CTGAGCTGGATCCCTGCTC	13401	_	AA
			GAG AG ATCCAGCTCAG			
			CTC TC TAGGTCGAGTC			
			G	CC		
GAM1445	CDK10	3'	CTGAGCTGGATCCCTGCTC	53768	_	AA
			GAG AG ATCCAGCTCAG			
			CTC TC TAGGTCGAGTC			
			G	CC		
GAM1445	CDK10	3'	CTGAGCTGGATCCCTGCTC	53777	_	AA
			GAG AG ATCCAGCTCAG			
			CTC TC TAGGTCGAGTC			
			G	CC		
GAM1445	CLTCL1	3'	CTGAGCTGGCCATCCTCTACTC	63671	C	A AAT
	C		GGA TAGAG GA CCAGCTCAG			
			CCT ATCTC CT GGTCGAGTC			
			C	_ ACC		
GAM1445	MCL1	3'	CTGA ACTCTTTCTAGCC	41717	A	AATC
			GG CTAGAGAGA CAG			

			CC GATCTTTCT GTC		
			— CAA—		
GAM1445	MDM1	3'	CTGAGCTGACTTCTACCTAGCC 39271	A AG ATC	
			GG CTAG AGAA CAGCTCAG		
			CC GATC TCTT GTCGAGTC		
			— CA CA—		
GAM1445	PML	3'	CTGAGCTGCCTCCTCCAGCCC 52661	A A A AATC	
			GG CT GAG GA CAGCTCAG		
			CC GA CTC CT GTCGAGTC		
			C C — CC—		
GAM1445	PML	3'	CTGAGCTGCCTCCTCCAGCCC 52667	A A A AATC	
			GG CT GAG GA CAGCTCAG		
			CC GA CTC CT GTCGAGTC		
			C C — CC—		
GAM1445	PML	3'	CTGAGCTGCCTCCTCCAGCCC 52673	A A A AATC	
			GG CT GAG GA CAGCTCAG		
			CC GA CTC CT GTCGAGTC		
			C C — CC—		
GAM1445	SHOX	3'	TGAGCTGAACTGTAGATCC 4839	— G AGAAATC	
			GGA CTA AG CAGCTCA		
			CCT GAT TC GTCGAGT		
			A G AA—		
GAM1445	TRPM1	5'	CTGAGCTGTGCCCTCTCCATTC 10057	CTA AAATC	
	C		GGA GAGAG CAGCTCAG		
			CCT CTCTC GTCGAGTC		
			TAC CCGT—		
GAM1445	ELOVL1	5'	GGA CTGAGAGAGAA TCC 43062	A A	
			CC GGTCTCTCTT AGG		
			— C		
GAM1445	FLJ20296	5'	CTGACGCGTTTCTCTCCATTCC 34890	CTA CCA —	
			GGA GAGAGAAAT GC TCAG		
			CCT CTCTCTTTG CG AGTC		
			TAC — C		
GAM1445	FLJ20721	3'	GACTTCTCTCTAGTGC 35609	G A	
			G ACTAGAGAGAA TC		
			C TGATCTCTCTT AG		
			G C		
GAM1445	KIAA0265	3'	AGCGACCTCTTCTCTAGTCC 69874	— AA CA	
			GGA CTAGAGA GA TC GCT		



CCTGATCTCT CT AG CGA  
 T CC \_\_\_\_  
 GAM1445 KIAA0285 3' GCTAGATGCCCTCTCTAGTCC 29018 AA\_ C  
 GGACTAGAGAG ATC AGC  
 ||||| |||||  
 CCTGATCTCTC TAG TCG  
 CCG A  
 GAM1445 KIAA0820 3' CTGAGCTGAATCTTAAAAAGCC 69023 ACTAGA AATC  
 GG GAGA CAGCTCAG  
 || ||| |||||  
 CC TTCT GTCGAGTC  
 GAAAAA AA\_  
 GAM1445 KIAA1274 3' GGCATCTCTCTCTGTCC 91367 T A \_  
 GGAC AGAGAGA AT CC  
 ||| ||||| ||||  
 CCTG TCTCTCT TA GG  
 \_ C C  
 GAM1445 KIAA1831 3' CTGAGCTGCTGTGGCTCCCTAG 63782 A A AA C\_  
 CC GG CTAG GAG AT CAGCTCAG  
 || ||| ||| |||||  
 CC GATC CTC TG GTCGAGTC  
 \_ C GG TC  
 GAM1445 MGC2560 5' CTGAGCTGGATTGACATAGCC 48781 A GAGAGA  
 GG CTA AATCCAGCTCAG  
 || ||| |||||  
 CC GAT TTAGGTCGAGTC  
 \_ ACAG\_  
 GAM1445 Rab11-FIP3 3' CTGAGCTGGATTGCGGACTC 28125 AGA\_  
 GAG AATCCAGCTCAG  
 ||| |||||  
 CTC TTAGGTCGAGTC  
 AGGGC  
 GAM1445 UGT2B10 3' CTGAGCTGGAGCCTCCATGCC 6541 ACTAGA AAA  
 GG GAG TCCAGCTCAG  
 || ||| |||||  
 CC CTC AGGTCGAGTC  
 GTAC\_ CG\_  
 GAM1445 LOC145815 5' GGATTTCTCCCTGACCC 83519 AC A  
 GG TAG GAGAAATCC  
 || ||| |||||  
 CC GTC CTCTTTAGG  
 CA C  
 GAM1445 LOC146745 5' TGAGCTGAGGCTGCAGTCC 78091 AG AGAAATC  
 GGACT AG CAGCTCA  
 |||| || |||||  
 CCTGA TC GTCGAGT  
 CG GGA\_  
 GAM1445 LOC201243 5' TGAGCTGAGGCTGCAGTCC 88163 AG AGAAATC  
 GGACT AG CAGCTCA  
 |||| || |||||

				CTGA TC	GTGAGT		
				CG GGA____			
GAM1445	LOC221929	3'	CTGAGCTGGACTTCCTCCTCC	92675		CTA A A	
			GGA GAG GAA TCCAGCTCAG				
			CCT CTC CTT AGGTCGAGTC				
			C__ _ C				
GAM1445	LOC51042	5'	GAGCGCACTCTCTAGCC	31854	A	AAATCCA	
			GG CTAGAGAG GCTC				
			CC GATCTCTC CGAG				
			_ ACG____				
GAM1445	LOC56912	3'	TGAGCTGGCCCCTCTGCC	39337	AC	AGAAAT	
			GG TAGAG CCAGCTCA				
			CC GTCTC GGTCGAGT				
			_ CCC____				
GAM1446	DGAT2	3'	TCTGCCACCCCTACCTCACC	50792	CA T T CA		
			GG TGA GT GG GTGGCAGA				
			CC ACT CA CC CACCGTCT				
			_ C T C_				
GAM1446	EGLN2	5'	TCCACTGCCAGCCCT	54931	CATGAT	C	
			AGG GTTGGCAGTGG A				
			TCC CGACCGTCACC T				
			_____ A				
GAM1446	FANCA	3'	CTGCCACTGCACACCAGCC	3747	A A TG		
			GGC TG TGT GCAGTGGCAG				
			CCG AC ACA CGTCACCGTC				
			_ C _				
GAM1446	FANCG	3'	TCTGCCACCACCAAGTCATTGA	16143	GC_ G CA		
	CT		AG ATGAT TTGG GTGGCAGA				
			TC TACTG AACC CACCGTCT				
			AGT _ AC				
GAM1446	FES	3'	CTGCCACCAGCATCCACACT	8862	GCAT CAG		
			AG GATGTTGG TGGCAG				
			TC CTACGACC ACCGTC				
			ACAC _____				
GAM1446	GLRX2	5'	TCTGCCACCATCCTCATGC	32162	TGTT CA_		
			GCATGA GG GTGGCAGA				
			CGTACT CC CACCGTCT				
			_____ TAC				
GAM1446	GLS	3'	CTGCCACTGCCCTCCCATTACC	29788	CA TT_		
	T		AGG TGATG GGCAGTGGCAG				

			TCC ATTAC CCGTCACCGTC	
			— CCTC	
GAM1446 IHPK1	3'	TCTGCCACTGCTTTCTCCCTGC 95765	TGATGTT	
C		GGCA GGCAGTGGCAGA		
		CCGT TCGTCACCGTCT		
		CCCTCTT		
GAM1446 IHPK3	5'	CCACCACCACCATCTGCC 54023	T T CA	
		GGCA GATG TGG GTGG		
		CCGT CTAC ACC CACC		
		— C AC		
GAM1446 JPH2	3'	CTGCCACTGCTGGCTGCC 94446	TGAT TG	
		GGCA GT GCAGTGGCAG		
		CCGT CG CGTCACCGTC		
		— GT		
GAM1446 LIMK1	3'	CTGCCACTGGGCCACAGCT 33646	ATGA T —	
		GGC TGT GGC AGTGGCAG		
		TCG ACA CCG TCACCGTC		
		— C GG		
GAM1446 PAX8	3'	CCACTGCCACGGCCT 25643	ATGA T	
		AGGC TGT GGCAGTGG		
		TCCG GCA CCGTCACC		
		— —		
GAM1446 PAX8	3'	CCACTGCCACGGCCT 25644	ATGA T	
		AGGC TGT GGCAGTGG		
		TCCG GCA CCGTCACC		
		— —		
GAM1446 PAX8	3'	CCACTGCCACGGCCT 25691	ATGA T	
		AGGC TGT GGCAGTGG		
		TCCG GCA CCGTCACC		
		— —		
GAM1446 PCTP	3'	CCACTGTTCAGCCT 41096	A TGTTG	
		AGGC TGA GCAGTGG		
		TCCG ACT TGTCACC		
		— —		
GAM1446 PHKB	3'	CTGCCACTGCACACCAGCCT 4306	A A TG	
		AGGC TG TGT GCAGTGGCAG		
		TCCG AC ACA CGTCACCGTC		
		— C —		
GAM1446 SCAP1	3'	TCTGCCACCCACCAACGCCT 13574	ATGAT CA—	
		AGGC GTTGG GTGGCAGA		

TCCG CAACC CACCGTCT  
 \_\_\_\_\_ ACCC  
 GAM1446 SORBS1 3' TCTGCCACTACCAGCAGCAACC 31163 CA A C  
 GG TG TGTTGG AGTGGCAGA  
 || || ||||| |||||  
 CC AC ACGACC TCACCGTCT  
 A\_ G A  
 GAM1446 STAR 5' CCACTGCCACATTTGCC 4444 T T  
 GGCA GATGT GGCAGTGG  
 ||| ||||| |||||  
 CCGT TTACA CCGTCACC  
  
 GAM1446 TRIM9 3' CCACTGCCACATTCCT 53756 CAT T  
 AGG GATGT GGCAGTGG  
 ||| ||||| |||||  
 TCC TTACA CCGTCACC  
 \_\_\_\_\_ C  
 GAM1446 UBE2G2 3' GCCACTGCACTCCAGCCT 64858 A AT TG  
 AGGC TG GT GCAGTGGC  
 |||| || || |||||  
 TCCG AC CA CGTCACCG  
 \_ CT \_  
 GAM1446 ZNF264 3' CTACCCTGCTGAACATCATAGC 12750 \_ \_ T C  
 C GGC ATGATGTT GGCAG GG AG  
 ||| ||||| |||| || ||  
 CCG TACTACAA TCGTC CC TC  
 A G \_ A  
 GAM1446 BMF 3' CCACCTCAACATCAAGCCT 53152 A CA  
 AGGC TGATGTTGG GTGG  
 |||| ||||| ||||  
 TCCG ACTACAACT CACC  
 A C\_  
 GAM1446 BTBD3 3' TGCCAACATATGCCT 30314 A  
 AGGCATG TGTTGGCA  
 ||||| |||||  
 TCCGTAT ACAACCGT  
  
 GAM1446 C1QTNF2 3' CTGCCACTGCACTCCAGCCT 49125 A AT TG  
 AGGC TG GT GCAGTGGCAG  
 |||| || || |||||  
 TCCG AC CA CGTCACCGTC  
 \_ CT \_  
 GAM1446 DKFZp434E169 3' GCCACTGCAGCCAGCCT 50061 A A TG  
 AGGC TG TGT GCAGTGGC  
 |||| || || |||||  
 TCCG AC GCA CGTCACCG  
 \_ C \_  
 GAM1446 DPYSL4 3' CCACCACCACTGCCT 21214 \_ GT CA  
 AGGCA TGAT TGG GTGG  
 |||| |||| || ||||

TCCGT ACTG ACC CACC  
 C \_ AC  
 GAM1446 FLJ10379 3' C TACTTGCCAACATCTGCCT 36081 T \_  
 AGGCA GATGTTGGCA GTGG  
 |||| |||||  
 TCCGT CTACAACCGT CATC  
 \_ T  
 GAM1446 FLJ10803 3' CTGCCACTGCACTCCAGCCT 36663 A AT TG  
 AGGC TG GT GCAGTGGCAG  
 ||| || || |||||  
 TCCG AC CA CGTCACCGTC  
 \_ CT \_  
 GAM1446 FLJ10898 3' CCACTGCCCACCCCACCCC 59426 CA AT T  
 GG TG GT GGCAGTGG  
 || || || |||||  
 CC AC CA CCGTCACC  
 CC CC C  
 GAM1446 FLJ13621 3' GCCACTGCACTCCAGCCT 46580 A AT TG  
 AGGC TG GT GCAGTGGC  
 ||| || || |||||  
 TCCG AC CA CGTCACCG  
 \_ CT \_  
 GAM1446 FLJ20671 3' CTGGGCAACATCATACCT 35523 C G\_  
 AGG ATGATGTTG CAG  
 || ||||| ||  
 TCC TACTACAAC GTC  
 A GG  
 GAM1446 FLJ21628 3' TCTGCCACTGCCTTGGACA 47604 \_  
 TGTT GGCAGTGGCAGA  
 ||| |||||  
 ACAG CCGTCACCGTCT  
 GTT  
 GAM1446 FLJ25467 3' CTGCCAACACCTGCCT 58528 TGA  
 AGGCA TGTTGGCAG  
 |||| |||||  
 TCCGT ACAACCGTC  
 CC\_  
 GAM1446 HSPC023 3' TGCAGGCCAACATCCCACC 25911 CAT AGTG  
 GG GATGTTGGC GCA  
 || ||||| ||  
 CC CTACAACCG CGT  
 ACC GA\_  
 GAM1446 HUMNPIIY20 3' TGCCACTACCACATC 83348 T C  
 GATGT GG AGTGGCA  
 |||| || |||||  
 CTACA CC TCACCGT  
 \_ A  
 GAM1446 IMP13 5' CTGCCACTAGGATCCCCGCCT 27732 AT\_ G GGC  
 AGGC GAT TT AGTGGCAG  
 ||| ||| || |||||

		TCCG CTA GA TCACCGTC		
		CCC G ____		
GAM1446 KIAA0285	5'	CCACGCCCCAGCATCACACCT 29014	CA	CA_
		AGG TGATGTTGG GTGG		
		TCC ACTACGACC CACC		
		AC CCG		
GAM1446 KIAA0672	3'	CTGCCACTGCCAACACGAGGTT 29408	ATGA	
		GGC TGTTGGCAGTGGCAG		
		TTG ACAACCGTCACCGTC		
		GAGC		
GAM1446 KIAA0773	3'	CTGCCACTGCCCAGGTAGCC 28054	ATGA TT	
		GGC TG GGCAGTGGCAG		
		CCG AC CCGTCACCGTC		
		ATGG ____		
GAM1446 KIAA1055	3'	CCACTGCCTGGAACATC 66059	____	
		GATGTT GGCAGTGG		
		CTACAA CCGTCACC		
		GGT		
GAM1446 KIAA1130	3'	CTGCCACTGGCTAGCCTGCCT 62419	TGAT _	
		AGGCA GTTGGC AGTGGCAG		
		TCCGT CGATCG TCACCGTC		
		C____ G		
GAM1446 MRPL10	3'	CTGCCACTGCCACAGTAGCT 59152	ATGA T	
		GGC TGT GGCAGTGGCAG		
		TCG ACA CCGTCACCGTC		
		ATG_ _		
GAM1446 NEUROG3	3'	TCTGCCACCACCCATAATCC 40658	C G TT CA	
		GG AT ATG GG GTGGCAGA		
		CC TA TAC CC CACCGTCT		
		_ A C_ AC		
GAM1446 PEG10	3'	CTACCACTGAACCCCATTTGCC 30524	_ AT GG C	
		GGCA TG GTT CAGTGG AG		
		CCGT AC CAA GTCACC TC		
		T CC _ A		
GAM1446 SEZ6	3'	CTGGCATGCCAACATCAGCCT 74363	A G G	
		AGGC TGATGTTGGCA TG CAG		
		TCCG ACTACAACCGT AC GTC		
		_ _ G		
GAM1446 SMCR8	3'	TCTGCCACCACCTGCACCTGCC 58600	TGA T CA	
T		AGGCA TGT GG GTGGCAGA		

TCCGT ACG CC CACCGTCT  
 CC\_ T AC  
 GAM1446 THG-1 5' GCCACTGCCCATGGCC 48186 \_ ATGTT  
 GGC ATG GGCAGTGGC  
 ||| ||| |||||  
 CCG TAC CCGTCACCG  
 G \_  
 GAM1446 VIT1 3' CTGCCATTGTAACATCATAACT 37972 GC G  
 AG ATGATGTTG CAGTGGCAG  
 || ||||| |||||  
 TC TACTACAAT GTTACCGTC  
 AA \_  
 GAM1446 ZNF271 3' TCTGCCACTGCATTCCAGCCT 95256 A ATGTTG  
 AGGC TG GCAGTGGCAGA  
 ||| || |||||  
 TCCG AC CGTCACCGTCT  
 \_ CTTA\_  
 GAM1446 LOC112609 3' CTGCCACTACTATGCTCTACCT 72838 CAT T \_ C  
 AGG GA GT TGG AGTGGCAG  
 || || || || |||||  
 TCC CT CG ATC TCACCGTC  
 AT\_ \_ T A  
 GAM1446 LOC127841 5' ACTGCCAACCACGCC 74692 A AT  
 GGC TG GTTGGCAGT  
 ||| || |||||  
 CCG AC CAACCGTCA  
 C C\_  
 GAM1446 LOC129138 3' CTGCCACTGCCCCACCCTGCC 57120 TGA TT  
 GGCA TG GGCAGTGGCAG  
 ||| || |||||  
 CCGT AC CCGTCACCGTC  
 CCC C\_  
 GAM1446 LOC130643 5' TTTGCACTGCAACATCATGCCT 74963 G G  
 AGGCATGATGTTG CAGTG CAGA  
 ||||| ||||| |||||  
 TCCGTACTACAAC GTCAC GTTT  
 \_ \_  
 GAM1446 LOC132203 5' TCTGCAGCCCCAACATCCACCT 75042 CAT CA G  
 AGG GATGTTGG GT GCAGA  
 || ||||| || |||||  
 TCC CTACAACC CG CGTCT  
 AC\_ C\_ A  
 GAM1446 LOC135892 3' CTGCCACTTGCTAACCATGCT 75244 AT \_  
 GGCATG GTTGGCA GTGGCAG  
 ||||| ||||| |||||  
 TCGTAC CAATCGT CACCGTC  
 \_ T  
 GAM1446 LOC145438 3' GCCACTGCACTCCAGCCT 83339 A AT TG  
 AGGC TG GT GCAGTGGC  
 |||| || || |||||

	TCCG AC CA CGTCACCG	
	_ CT _	
GAM1446 LOC146745 5'	TCTGCCACCACCCTCTCTCTAC 78090	CAT TGTT CA_
CT	AGG GA GG GTGGCAGA	
	TCC CT CC CACCGTCT	
	AT_ CTCT CAC	
GAM1446 LOC146756 3'	GCCACTGCACTCCAGCCT 83779	A AT TG
	AGGC TG GT GCAGTGGC	
	TCCG AC CA CGTCACCG	
	_ CT _	
GAM1446 LOC148902 3'	TCTGCCACTGGCTTTTCATGCC 84265	TGTT _
	GGCATGA GGC AGTGGCAGA	
	CCGTACT TCG TCACCGTCT	
	T_ G	
GAM1446 LOC149721 5'	GCCACTGCATTCCACAGCCT 79498	A A TTG_
	AGGC TG TG GCAGTGGC	
	TCCG AC AC CGTCACCG	
	_ _ CTTA	
GAM1446 LOC151005 3'	CTGCCACTCCAGCTCATACC 80097	C T C
	GG ATGA GTTGG AGTGGCAG	
	CC TACT CGACC TCACCGTC	
	A _ _	
GAM1446 LOC157983 3'	TCTGCCACTGCACTCCAGCCT 81641	A AT TG
	AGGC TG GT GCAGTGGCAGA	
	TCCG AC CA CGTCACCGTCT	
	_ CT _	
GAM1446 LOC158235 3'	CTGCCACTGTACTCCAGCCT 86701	A AT TG
	AGGC TG GT GCAGTGGCAG	
	TCCG AC CA TGTCACCGTC	
	_ CT _	
GAM1446 LOC166206 3'	CCACTGCCCCACCACC 82623	CA A TT
	GG TG TG GGCAGTGG	
	CC AC AC CCGTCACC	
	_ C C_	
GAM1446 LOC200213 5'	CTGCCACTACTACAGCC 88633	ATGA T C
	GGC TGT GG AGTGGCAG	
	CCG ACA TC TCACCGTC	
	_ _ A	
GAM1446 LOC200301 5'	TCTGCCACAGGACACCACACC 88754	CA A GGCA
	GG TG TGTT GTGGCAGA	



	CC AC ACAG CACCGTCT	
	AC C GA__	
GAM1446 LOC201243 5'	TCTGCCACCACCCTCTCTCTAC 88162	CAT TGTT CA_
CT	AGG GA GG GTGGCAGA	
	TCC CT CC CACCGTCT	
	AT_ CTCT CAC	
GAM1446 LOC203289 3'	TCTGCCACTGCACTCCAGCCT 89332	A AT TG
	AGGC TG GT GCAGTGGCAGA	
	TCCG AC CA CGTCACCGTCT	
	_ CT _	
GAM1446 LOC221490 3'	GCCACTGCACTGCAGCCT 93661	ATGA TG_
	AGGC TGT GCAGTGGC	
	TCCG ACG CGTCACCG	
	_____ TCA	
GAM1446 LOC222166 3'	TCTGAAATCCAAAATCATGCCT 94099	G CA GG
	AGGCATGAT TTGG GT CAGA	
	TCCGTACTA AACC TA GTCT	
	A _ AA	
GAM1446 LOC255975 5'	CTACAGTCCCAACATCTGCCT 95890	T CA__
	AGGCA GATGTTGG GTGG	
	TCCGT CTACAACC CATC	
	_ CTGA	
GAM1446 LOC255987 5'	CTACAGTCCCAACATCTGCCT 96065	T CA__
	AGGCA GATGTTGG GTGG	
	TCCGT CTACAACC CATC	
	_ CTGA	
GAM1446 LOC256544 3'	TCTGCCACTGCACTCCAGCCT 96202	A AT TG
	AGGC TG GT GCAGTGGCAGA	
	TCCG AC CA CGTCACCGTCT	
	_ CT _	
GAM1446 LOC257476 3'	TCTGCCACTGCTTTCTCCCTGC 61260	TGATGTT
C	GGCA GGCAGTGGCAGA	
	CCGT TCGTCACCGTCT	
	CCCTCTT	
GAM1446 LOC56920 3'	CTGCCACTGCCCACCGCCT 39384	ATGAT T
	AGGC GT GGCAGTGGCAG	
	TCCG CA CCGTCACCGTC	
	C__ C	
GAM1446 LOC90768 3'	TCTGCCACTGAATTTCACTT 63959	CA TGTTGG
	AGG TGA CAGTGGCAGA	

TTC ACT GTCACCGTCT  
 AC TTAA\_\_  
 GAM1446 LOC91663 5' GCCACTGCCGCCCCGCACCCC 56408 CA ATGT  
 GG TG TGGCAGTGGC  
 || || |||||  
 CC AC GCCGTCACCG  
 CC GCCC  
 GAM1446 LOC91748 3' CTACTCCAACATCACCCC 67054 CA C  
 GG TGATGTTGG AGTGG  
 || ||||| ||||  
 CC ACTACAACC TCATC  
 CC \_  
 GAM1446 LOC91862 3' GCCACTGCACTCCAGCC 53465 A AT TG  
 GGC TG GT GCAGTGGC  
 ||| || || |||||  
 CCG AC CA CGTCACCG  
 \_ CT \_  
 GAM1446 LOC93082 3' CGCTGCCAACACCCGCCT 56442 ATGA  
 AGGC TGTTGGCAGTG  
 ||| |||||  
 TCCG ACAACCGTCGC  
 CCC\_  
 GAM1447 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
 GTA GGAT GGGTTGTTT  
 ||| ||| |||||  
 CGT CCTA CCCAACAAA  
 C CGTG\_  
 GAM1447 LCT 3' AACCGTAAAAATCCTT 9697 G  
 AAGGATTTTTTA GGTT  
 ||||| ||||  
 TTCCTAAAAAT CCAA  
 G  
 GAM1447 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
 GTAAGGATTTTTAGGGTTGTTT  
 |||||  
 CATTCTAAAAATCCCAACAAA  
 GAM1447 FBXO30 3' AACTAAAAAAATCCTGAC 49573 A AG  
 GT AGGATTTTT GGTT  
 || ||||| |||  
 CA TCCTAAAAA TCAA  
 G AA  
 GAM1447 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTT  
 GTAAG AGGGTTGTT  
 ||| |||||  
 CATT TCCCAACAA  
 AT\_\_\_\_  
 GAM1447 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
 TAAG TTTT GGGTTGTTT  
 ||| ||| |||||

		GTTC AAAA CCCAACAAA		
		___ C		
GAM1447	SMT3H2	3' AACAAACATAAAAAATCCTTGC	22670	GG
		GTAAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1447	LOC120103	3' AACCTATGAAAAATCCTTGC	74002	A__
		GTAAAGGATTTTTT GGGTT		
		CGTTCCTAAAAA TCCAA		
		GTA		
GAM1447	LOC129831	3' AAACAACCCCAATGTCC	74889	TT A
		GGAT TT GGGTTGTTT		
		CCTG AA CCCAACAAA		
		T_ C		
GAM1447	LOC133088	5' AAACAAAATAGAAAAATCCCTG	75075	A AGGG_
	C	GTA GGATTTTTT TTGTTT		
		CGT CCTAAAAA AACAAA		
		C GATAA		
GAM1447	LOC148089	3' GGCCCTAAAAATTCCTAC	78637	A
		GTA GGATTTTTTAGGGTT		
		CAT CTTAAAAATCCCGG		
		C		
GAM1447	LOC154547	3' AACAAACATAAAAAATCCTTGC	76050	GG
		GTAAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1447	LOC158104	3' ACAGCCAAAAATCCTTA	60313	AG
		TAAGGATTTTTT GGTTGT		
		ATTCCTAAAAA CCGACA		
		—		
GAM1447	LOC205880	5' AAACAACCATCATCCTGAC	90709	A TTTTAG
		GT AGGAT GGTGTTT		
		CA TCCTA CCAACAAA		
		G CTA__		
GAM1447	LOC221561	3' AACAAACATAAAAAATCCTTGC	92130	GG
		GTAAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1447	LOC257591	3' AACAAACATAAAAAATCCTTGC	97840	GG
		GTAAAGGATTTTTTA GTTGTT		

		CGTTCCTAAAAAT CAACAA	
		A_	
GAM1447	LOC51145	3' AGCTAAAATCCTTAC 32393 TAG	
		GTAAGGATTTT GGTT	
		CATTCCTAAAA TCGA	
GAM1448	APAF1	3' AAGCCTTGAATGGCCCTTGTCT 6724 _ C_	
	TA	TAAGGCAAGG TTA CAAGGCTT	
		ATTCTGTTCC GGT GTTCCGAA	
		C AA	
GAM1448	APAF1	3' AAGCCTTGAATGGCCCTTGTCT 25033 _ C_	
	TA	TAAGGCAAGG TTA CAAGGCTT	
		ATTCTGTTCC GGT GTTCCGAA	
		C AA	
GAM1448	CD7	3' GGAAGCCTTCCCTGCCAGCC 20429 AA TACC	
		GGC GGT AAGGCTTCC	
		CCG CCG TTCCGAAGG	
		AC TCCC	
GAM1448	ELMO3	5' GAAGCCCTGAGGCGCCTTG 45251 TAC_ A	
		CAAGGT CA GGCTTC	
		GTTCCG GT CCGAAG	
		CGGA C	
GAM1448	FKRP	3' AGCCCTGATAACCTCGCCTT 44183 A C A	
		AAGGC AGGTTA CA GGCT	
		TTCCG TCCAAT GT CCGA	
		C A C	
GAM1448	FZD1	3' GGATGCCTGGCAACCTTGCCTT 13037 A A T	
		AAGGCAAGGTT CCA GGC TCC	
		TTCCGTTCCAA GGT CCG AGG	
		C _ T	
GAM1448	KRTHA4	3' GAAACCTCATCTTGCCT 40669 TACCA C	
		AGGCAAGGT AGG TTC	
		TCCGTTCTA TCC AAG	
		C_ A	
GAM1448	LPP	3' GCTATTAACCTTGCCTTA 18749 CCAA	
		TAAGGCAAGGTTA GGC	
		ATTCCGTTCCAAT TCG	
		TA_	
GAM1448	LZTS1	3' GAAGCCTTGGAACCAGCC 40690 AA A	
		GGC GGTT CCAAGGCTTC	

CCG CCAA GGTTCGAAG  
A\_ \_  
GAM1448 MAPK10 3' GGAAGCCTCGGCAGGACCCCT 57292 CAA A\_ A  
AGG GGTT CC AGGCTTCC  
||| ||| || |||||  
TCC CCAG GG TCCGAAGG  
\_ GAC C  
GAM1448 MVK 3' GAAGCCTTCCCCTACCCCT 60649 CAA TACC\_  
AGG GGT AAGGCTTC  
||| ||| |||||  
TCC CCA TTCCGAAG  
\_ TCCCC  
GAM1448 PDYN 3' AAGCTTAAACATTGCCTTA 44319 G ACCA  
TAAGGCAA GTT AGGCTT  
||||| ||| |||||  
ATTCCGTT CAA TTCGAA  
A A\_  
GAM1448 RAD51L3 3' AAGCCTCTAACTTGCCTT 56064 G CCA  
AAGGCAAG TTA AGGCTT  
||||| ||| |||||  
TTCCGTTT AAT TCCGAA  
\_ C\_  
GAM1448 RAD51L3 3' AAGCCTCTAACTTGCCTT 56072 G CCA  
AAGGCAAG TTA AGGCTT  
||||| ||| |||||  
TTCCGTTT AAT TCCGAA  
\_ C\_  
GAM1448 RAD51L3 3' AAGCCTCTAACTTGCCTT 56078 G CCA  
AAGGCAAG TTA AGGCTT  
||||| ||| |||||  
TTCCGTTT AAT TCCGAA  
\_ C\_  
GAM1448 RAD51L3 3' AAGCCTCTAACTTGCCTT 11232 G CCA  
AAGGCAAG TTA AGGCTT  
||||| ||| |||||  
TTCCGTTT AAT TCCGAA  
\_ C\_  
GAM1448 SLC9A5 5' GGAAGCCTTGAGGTGTGCC 59770 AGGTTAC  
GGCA CAAGGCTTCC  
||| |||||  
CCGT GTTCCGAAGG  
GTGGA\_  
GAM1448 ZNFN1A3 3' GGAAGCCTCACCCCTTCTGCC 60242 \_ TTACCA  
GGCA AGG AGGCTTCC  
||| ||| |||||  
CCGT TCC TCCGAAGG  
CT CAC\_  
GAM1448 ARHF 3' GAAGCCTTCTGAGACCCTCCCC 38741 CAA\_ ACC\_  
GG GGTT AAGGCTTC  
|| ||| |||||

CC CCAG TTCCGAAG  
 CCTC AGTC  
 GAM1448 BDG-29 3' GAACTGACACAACCTTGCCTTA 72354 ACCAA C  
 TAAGGCAAGGTT GG TTC  
 ||||| || ||  
 ATTCCGTTTCAA TC AAG  
 CACAG \_  
 GAM1448 DKFZP586N0721 3' GAAGCCTTCACTCACCTTCA 31203 C TACC\_  
 G AAGGT AAGGCTTC  
 | ||| |||||  
 A TTCCA TTCCGAAG  
 C CTCAC  
 GAM1448 DKFZp762K2015 3' GAAGCCCCTACCTTGCT 72476 TACCAA  
 GGCAAGGT GGCTTC  
 ||||| |||||  
 TCGTTCCA CCGAAG  
 TCC\_\_  
 GAM1448 FLJ11110 3' TCTCTGGCAACCTTGCC 37062 A \_  
 GGCAAGGTT CCA AGG  
 ||||| || ||  
 CCGTTCCAA GGT TCT  
 C C  
 GAM1448 FLJ12610 3' GGAAGCCTTGTCTACCTTTCCC 45514 C\_ TAC  
 T AGG AAGGT CAAGGCTTCC  
 || |||| |||||  
 TCC TTCCA GTTCCGAAGG  
 CT TCT  
 GAM1448 FLJ21415 3' GGAAACCTTGGCTTTGACC 45355 \_ TTA C  
 GG CAAGG CCAAGG TTCC  
 || |||| ||||| |||||  
 CC GTTTC GGTTC AAGG  
 A \_ A  
 GAM1448 FLJ21736 3' GAAGCCTTCCCTGCCTT 46228 A TTACC  
 AAGGCA GG AAGGCTTC  
 ||||| || |||||  
 TTCCGT CC TTCCGAAG  
 C \_\_\_\_  
 GAM1448 FLJ21777 3' GAAGCCTTGACAACCCCAGCTC 49864 A AA\_ AC  
 A A GGC GGTT CAAGGCTTC  
 | ||| ||||| |||||  
 A TCG CCAA GTTCCGAAG  
 C ACC CA  
 GAM1448 KIAA0229 3' GGAAGCCTTGGCTAGTCTGCTC 92429 \_ A GT \_  
 T AG GCA G TA CCAAGGCTTCC  
 || ||| | |||||  
 TC CGT C AT GGTTCGAAGG  
 T \_TG C  
 GAM1448 KIAA0352 3' AGCAGCAGCCTTGCCTTA 29153 ACCAAG  
 TAAGGCAAGGTT GCT  
 ||||| || ||

ATTCCGTTCCGA CGA  
 CGA\_\_\_\_  
 GAM1448 KIAA0471 3' GAAGCCTTGTGCAGTTGCCTTA 29394 G\_ TAC  
 TAAGGCAA GT CAAGGCTTC  
 ||||| || |||||  
 ATTCCGTT CG GTTCCGAAG  
 GA T\_\_\_\_  
 GAM1448 MGC13170 3' AAGCCTTGGGCACTACCCT 51143 CAA TA  
 AGG GGT CCAAGGCTT  
 ||| ||| |||||  
 TCC TCA GGTTCGAA  
 CA\_ CG  
 GAM1448 MGC26744 3' GGAAGCCTCCCACGGCCCGCC 58312 AA ACCA\_  
 GGC GGTT AGGCTTCC  
 ||| ||| |||||  
 CCG CCGG TCCGAAGG  
 C\_ CACCC  
 GAM1448 MGC33345 3' GGAAGCCTTTCTGTGCCTTGCC 58277 TACC\_  
 GGCAAGGT AAGGCTTCC  
 ||||| |||||  
 CCGTTCCG TTCCGAAGG  
 TGTCT  
 GAM1448 NIR3 3' GAAGCCTTAGTCCCACTCCC 66239 CAA\_ TT C  
 GG GG AC AAGGCTTC  
 || || || |||||  
 CC CC TG TTCCGAAG  
 CTCA C\_ A  
 GAM1448 PDZD2 3' GAAGCCTTCCACCTGCGTC 80870 A\_ TACC  
 GGC AGGT AAGGCTTC  
 ||| ||| |||||  
 CTG TCCA TTCCGAAG  
 CG CC\_  
 GAM1448 RPH3A 3' GGAAGCCTCAGCCAAAGCCT 30246 AA\_ ACCA  
 AGGC GGTT AGGCTTCC  
 ||| ||| |||||  
 TCCG CCGA TCCGAAGG  
 AAA C\_  
 GAM1448 SPRY1 5' GAAACCTTGGTGGGCCACCC 65004 CAA \_ C  
 GG GGTT ACCAAGG TTC  
 || ||| ||||| |||  
 CC CCGG TGGTTCC AAG  
 CA\_ G A  
 GAM1448 THEA 3' GAAGCCTTCTCTTATCT 66283 GC TTACC  
 AG AAGG AAGGCTTC  
 || ||| |||||  
 TC TTCT TTCCGAAG  
 TA CC\_  
 GAM1448 ZNF213 3' GGAAGCCTTCCCCTCCCGCC 65102 AA TTACC  
 GGC GG AAGGCTTCC  
 ||| || |||||

CCG CC TTCCGAAGG  
 C\_ TCCCC  
 GAM1448 LOC145125 3' GAAGCCTTAGCAACACTGCT 77006 AG ACC  
 GGCA GTT AAGGCTTC  
 ||| ||| |||||  
 TCGT CAA TTCCGAAG  
 CA CGA  
 GAM1448 LOC149478 3' GAAACCTGGATCTCATCCTTGC 79378 TTA\_\_\_\_ A C  
 CTTA TAAGGCAAGG CCA GG TTC  
 ||||| ||| |||  
 ATTCCGTTCC GGT CC AAG  
 TACTCTA \_ A  
 GAM1448 LOC149672 5' GAAACCTTTTCCTTGCCTTG 79511 TTACC C  
 TAAGGCAAGG AAGG TTC  
 ||||| ||| |||  
 GTTCCGTTCC TTCC AAG  
 TT\_\_\_\_ A  
 GAM1448 LOC150481 5' AAGCCTTGGAGCTCCCC 79879 CAA A  
 GG GGTT CCAAGGCTT  
 || ||| |||||  
 CC TCGA GGTTCGAA  
 CCC \_  
 GAM1448 LOC158191 5' AAGCCTTGGAGATCCCC 81768 CAA A  
 GG GGTT CCAAGGCTT  
 || ||| |||||  
 CC CTAG GGTTCGAA  
 CC\_ A  
 GAM1448 LOC196500 3' AAGCCTTGCACACTCACCT 87738 CA \_ TAC  
 AGG AG GT CAAGGCTT  
 ||| ||| |||||  
 TCC TC CA GTTCCGAA  
 AC A C\_  
 GAM1448 LOC256714 3' GAAACCTTGAACTTTTACCTT 96313 C\_ AC C  
 G TAAGG AAGGTT CAAGG TTC  
 |||| |||| |||||  
 GTTCC TTTCAA GTTCC AAG  
 AC A\_ A  
 GAM1448 LOC91170 5' GAAACCTCAAGCCCTTGCTT 65136 TTACCA C  
 AGGCAAGG AGG TTC  
 ||||| ||| |||  
 TTCGTTCC TCC AAG  
 CGAAC\_ A  
 GAM1449 DMRT2 3' CACAACAAGCAACAAGAACA 21614 CTATC\_  
 TGTTC CTTGTTGTG  
 |||| |||||  
 ACAAG GAACAACAC  
 AACAAC  
 GAM1449 F8 3' CACAACAAAAATGTAACAGGG 3725 G CC CC  
 CCC TGTT TAT TTGTTGTG  
 ||| ||| ||| |||||



GGG ACAA GTA AACAAACAC  
\_ T\_ AA  
GAM1449 GJB3 3' TAAGAGACAGGAACACAGG 43770 C A \_  
CC GTGTTTCCT TC CTTG  
|| ||||| || ||||  
GG CACAAGGA AG GAAT  
A C A  
GAM1449 SH3BP2 3' CAAGGACAGGAACACTGGT 11593 C A  
ACC GTGTTTCCT TCCTTG  
||| ||||| |||||  
TGG CACAAGGA AGGAAC  
T C  
GAM1449 TEM8 3' CACCCAGGGATAAAAACA 49851 CC TT  
TGTT TATCCTTG GTG  
||| ||||| |||  
ACAA ATAGGGAC CAC  
AA C\_  
GAM1449 ZNF216 3' CACAGATAATAGGAACA 20018 CCTTG  
TGTTTCCTAT TTGTG  
|||||| ||||  
ACAAGGATA GACAC  
ATA\_  
GAM1449 C20orf142 3' AAGGAGCAGAAACACAGGT 74763 C C A\_  
ACC GTGTT CT TCCTT  
||| |||| || ||||  
TGG CACAA GA AGGAA  
A A CG  
GAM1449 C20orf59 3' CACACGAGCAGAGAGGAACAC 41991 A \_ T  
GTGTTTCCT TC CTTGT GTG  
|||||| || ||||| |||  
CACAAGGA AG GAGCA CAC  
G AC \_  
GAM1449 CLSTN2 3' CACAACAAGGACAACAAGGACA 42126 T A\_\_\_\_  
C GTGT CCT TCCTTGTTGTG  
||| ||| ||||| |||||  
CACA GGA AGGAACAACAC  
\_ ACAAC  
GAM1449 CLSTN2 3' CACAACAAGGACAGTCACAAC 42127 \_ TC A  
GT GT CT TCCTTGTTGTG  
|| || || ||||| |||||  
CA CA GA AGGAACAACAC  
A CT C  
GAM1449 CLSTN2 3' CACAACAAGGACAGTCACAACA 42128 CG\_\_ TC A  
AGG CC TGT CT TCCTTGTTGTG  
|| || || ||||| |||||  
GG ACA GA AGGAACAACAC  
AACA CT C  
GAM1449 FLJ10101 5' CGGGGAGACAGGAACACGGG 45264 A\_  
CCCGTGTTTCCT TCCTTG  
||||||| |||||

			GGGCACAAGGA AGGGGC		
			CAG		
GAM1449	HEYL	3'	CACTCAGGACAGGAACAAGG 27391	G	A TTT
			CC TG TTCCT TCCT G GTG		
			GG ACAAGGA AGGA C CAC		
			A C _T_		
GAM1449	INPP4B	3'	TAATAAACAGGAACAC 13915	ATCC	
			GTG TTCCT TTGTTG		
			CACAAGGA AATAAT		
			CA__		
GAM1449	KIAA0391	3'	CAAGAGACAGGAACAC 27906	A _	
			GTG TTCCT TC CTTG		
			CACAAGGA AG GAAC		
			C A		
GAM1449	KIAA1376	3'	CACAACAAGGAACAAAACA 63621	CCTA	
			TGTT TCCTTGTTGTG		
			ACAA AGGAACAACAC		
			AACA		
GAM1449	KIAA1494	3'	CACAACAAAGTAGCAC 68457	C ATCC	
			GTGTT CT TTGTTGTG		
			CACGA GA AACAACAC		
			T ____		
GAM1449	LOC147639	3'	CACAATAACAGGGACAC 78378	ATCC	
			GTG TTCCT TTGTTGTG		
			CACAGGGA AATAACAC		
			C__		
GAM1449	LOC219529	3'	ACAGGATAACAGGAACAC 92964	__ T	
			GTG TTCCT ATCCT GT		
			CACAAGGA TAGGA CA		
			CAA _		
GAM1450	ARHGEF6	3'	CAAACCTGAAGCCAGGC 68197	ACCA	
			GCCTGG CAAGTTTG		
			CGGACC GTTCAAAC		
			GAA_		
GAM1450	CNTN2	3'	GTCACAACCCAGGTGA 17411	ACCACAA _	
			TCGCCTGG GTT TGAC		
			AGTGGACC CAA ACTG		
			_____ C		
GAM1450	CORO2A	3'	AAACTGTGGTCCAGAGA 53398	GC A	
			TC CTGGACCACA GTTT		

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AG GACCTGGTGT CAAA
A_ _
GAM1450 CORO2A 3' AAACGTGTGGTCCAGAGA 12642 GC A
TC CTGGACCACA GTTT
|| ||||| |||
AG GACCTGGTGT CAAA
A_ _
GAM1450 GRLF1 3' AGGTCAGAAAGTGGCCCAGG 78551 A AAG
CCTGG CCAC TTTGACCT
||||| ||| |||||
GGACC GGTG AGACTGGA
C AA_
GAM1450 LAPTM5 3' AGGCTTGTGGTCAAGC 22199 CTG
GC GACCACAAGTTT
|| ||||| |||
CG CTGGTGTTTCGGA
AA_
GAM1450 POU2AF1 3' AGATTTACAGTCCAGGC 20647 CAC
GCCTGGAC AAGTTT
||||| |||
CGGACCTG TTTAGA
ACA
GAM1450 PTGS1 3' GTCTCCTGTCTTATGGTCCAG 6355 C TTT__
CTGGACCA AAG GAC
||||| ||| |||
GACCTGGT TTC CTG
A TGTCT
GAM1450 PTGS1 3' GTCTCCTGTCTTATGGTCCAG 54574 C TTT__
CTGGACCA AAG GAC
||||| ||| |||
GACCTGGT TTC CTG
A TGTCT
GAM1450 TRIM34 5' AGGTCAAGTTGAGCCCAG 55224 ACCA G
CTGG CAA TTTGACCT
||| ||| |||||
GACC GTT GAACTGGA
CGA_ _
GAM1450 TRIM9 5' AGGCCAGGCAAGTCCAGGC 30749 CACAA A
GCCTGGAC GTTTG CCT
||||| ||| |||
CGGACCTG CGGAC GGA
AA__ C
GAM1450 ABLIM 5' GATATGTAACCCAGGCGG 22030 ACC A
TCGCTGG ACA GTT
||||| ||| |||
GGCGGACC TGT TAG
CAA A
GAM1450 AMOT 3' AGGCATCTTCATGGTCCAGGGA 55716 G C_ TT A
TC CCTGGACCA AAG TG CCT
|| ||||| ||| |||

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		AG GGACCTGGT TTC AC GGA		
		— AC T_ _		
GAM1450	DKFZp434D177 5'	TTAGACCCAGGCGA	79443	ACCACAA
		TCGCCTGG GTTTGA		
		AGCGGACC CAGATT		
		—————		
GAM1450	DKFZp434D177 5'	TTAGACCCAGGCGA	50056	ACCACAA
		TCGCCTGG GTTTGA		
		AGCGGACC CAGATT		
		—————		
GAM1450	FLJ23420 3'	CAAGTGGGTCCAGGC	46845	A AG
		GCCTGGACC CA TTTG		
		CGGACCTGG GT GAAC		
		— —		
GAM1450	HSA249128 5'	GGCGCGGTCCAGGCGG	34152	ACAA
		TCGCCTGGACC GTT		
		GGCGGACCTGG CGG		
		CG_		
GAM1450	MGC15668 5'	AGACCCGGTGGTCCAGACG	51277	C AA_
		CG CTGGACCAC GTTT		
		GC GACCTGGTG CAGA		
		A GCC		
GAM1450	MGC22014 3'	AGGTCCCGAGTGTAACCCAGGT	64486	ACC AGTTT
	GA	TCGCCTGG ACA GACCT		
		AGTGGACC TGT CTGGA		
		CAA GAGCC		
GAM1450	SDCCAG10 5'	AGAGTTGTGGTCCAAAGA	19641	GCC G
		TC TGGACCACAA TTT		
		AG ACCTGGTGTT AGA		
		AA_ G		
GAM1450	LOC115442 3'	AGGTCAGGGATGGTCCAG	72676	CAAG
		CTGGACCA TTTGACCT		
		GACCTGGT GGA CTGGA		
		AG_		
GAM1450	LOC129011 5'	AGACCTGCGGTCCAGGC	74862	A A
		GCCTGGACC CA GTTT		
		CGGACCTGG GT CAGA		
		C C		
GAM1450	LOC130536 5'	GCAAAGTCCAGGCG	75746	CACAAG A
		CGCCTGGAC TTTG C		

GCGGACCTG    AAAC G  
                   \_\_\_\_\_ C  
 GAM1450 LOC149108 3' AGACTTCACTGTGGTCCA    84357    \_\_\_\_\_  
                   TGGACCACA    AGTTT  
                   |||||||    |||||  
                   ACCTGGTGT    TCAGA  
                   CACT  
 GAM1450 LOC221688 5' AGACTCGGGCCCCAGACGA    93674    C    A    ACA  
                   TCG CTGG CC    AGTTT  
                   ||| ||||| ||    |||||  
                   AGC GACC GG    TCAGA  
                   A    C    GC\_  
 GAM1450 LOC256228 5' AGACTTGTGGTCAAAGC    96233    CTG  
                   GC    GACCACAAGTTT  
                   ||    |||||||||  
                   CG    CTGGTGTTTCAGA  
                   AAA  
 GAM1450 LOC257441 5' TTAGACCCAGGCGA    95566    ACCACAA  
                   TCGCCTGG    GTTTGA  
                   |||||||    |||||  
                   AGCGGACC    CAGATT  
  
 GAM1450 LOC91960 3' AGGTGCCTCTCGTGGTCCAAGC 67657    C    A    TTTG  
                   GC TGGACCAC AG    ACCT  
                   ||    ||||||| ||    |||||  
                   CG ACCTGGTG TC    TGA  
                   A    C    TCCG  
 GAM1450 LOC92840 3' GTCCCTCGGGTCCAGGC    56435    ACA    TTT  
                   GCCTGGACC AG    GAC  
                   ||||||| ||    |||  
                   CGGACCTGG TC    CTG  
                   GC\_ C\_  
 GAM1451 ADH1B    3' CTTAGACATAAAGTAAAAT 72644    C    CAC  
                   ATTT ACTTT TGTCTGAG  
                   |||| ||||| |||||||  
                   TAAA TGAAA ACAGATTC  
                   A    T\_  
 GAM1451 AHR    3' ATCTCAGATGTATAAATAAATG 7875    CAC    C    T  
                   CATTT TTT AC GTCTGAGAT  
                   ||||| ||| || |||||||  
                   GTAAA AAA TG TAGACTCTA  
                   TA\_ T \_  
 GAM1451 FDFT1    3' TAGGAAAGTGAAATG    15518    A  
                   CATTTCACTTTC CTG  
                   ||||||||| |||  
                   GTAAAGTGAAAG GAT  
  
 GAM1451 JTB    3' ATCTCAGACAGTGAAAGTGAAA 21959  
                   TG    CATTTCACTTTCACTGTCTGAGAT  
                   |||||||||||||||||

GTAAAGTGAAAGTGACAGACTCTA

GAM1451	KLF4	3'	TCCCAGACAGTGGATATG	14891	CT	A
			CA TTCACTGTCTG GA			
			GT AGGTGACAGAC CT			
			AT C			
GAM1451	PHYH	3'	ACAGTAAAAGTGAAAT	20608		C
			ATTTCACTTT ACTGT			
			TAAAGTGAAA TGACA			
			A			
GAM1451	PKD2	3'	TCCAGGTTGAAAGTGAAA	60096	CTG	A
			TTTCACTTTCA TCTG GA			
			AAAGTGAAAGT GGAC CT			
			T__ _			
GAM1451	WRN	3'	GGGCAGTGAAAATGAAA	5098		C
			TTTCA TTTCACTGTCT			
			AAAGT AAAGTGACGGG			
			A			
GAM1451	ZNF216	3'	ATCTGCACAGCAAAGTGAAA	20017	CA	CTG
			TTTCACTTT CTGT AGAT			
			AAAGTGAAA GACA TCTA			
			C_ CG_			
GAM1451	CG012	5'	CTCACTCTGAAAGTGAA	83218	CT	CT
			TTCAC TTTCA GT GAG			
			AAGTGAAAGT CA CTC			
			CT _			
GAM1451	EIF2C2	3'	ATCTTCTGAGAGTGAAAG	71946	G	T_
			CTTTCACT TC GAGAT			
			GAAAGTGA AG TTCTA			
			G TC			
GAM1451	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT	45802	ACTTTCACT	
	G		CATTTT GTCTGAGAT			
			GTAAAG CAGACTCTA			
			AAACATTT_			
GAM1451	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG	45281	CTT	
			CATTTCA TCACTGTCTGAGAT			
			GTAAAGT AGTGACAGACTCTA			
			C_			
GAM1451	KIAA0984	3'	TTTGTCCAGTGAAAATGAA	65534	C	TC
			TTCA TTTCACTG TGAG			

			AAGT AAAGTGAC GTTT		
			A CT		
GAM1451	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A _	
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1451	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T	
			ATT CACTTTCACTGT		
			TAA GTGAAAGTGACG		
			C		
GAM1451	PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA 53598	CA G	
			TTCAC TTT CT TCTGAGAT		
			AAGTGAAA GG AGACTCTA		
			CC G		
GAM1451	PP35	3'	ATCTCAGACTGAAA 22814	CT	
			TTTCA GTCTGAGAT		
			AAAGT CAGACTCTA		
			—		
GAM1451	PRTD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148	TCAC C_	
			CATTTCACTT TGT TGAG		
			GTAAAGTGAA ACG ACTC		
			TA__ TT		
GAM1451	SEP15	3'	TCCTACAGTAAGAGTGAAA 14934	C CT	
			TTTCACTTT ACTGT GA		
			AAAGTGAGA TGACA CT		
			A TC		
GAM1451	SFXN2	3'	CTCAGGGGAAAAAAGTGAAA 73941	CACTG	
			TTTCACTTT TCTGAG		
			AAAGTGAAA GGA CTC		
			AAAGG		
GAM1451	LOC149703	3'	ATCTCAGACAGCCGTTTGAAA 84647	ACTTTCA	
			TTTC CTGTCTGAGAT		
			AAAG GACAGACTCTA		
			GTTTGCC		
GAM1451	LOC154007	3'	ATCTCAAACCCTTTAGTGAAA 81015	TTCAC T C	
			TTTCACT GT TGAGAT		
			AAAGTGA CA ACTCTA		
			TTTCC_ A		
GAM1451	LOC155004	3'	TCATTTAAGTGAAAAGGAAA 81226	A GTC_	
			TTTC CTTTCACT TGA		

			AAAG GAAAGTGA	ACT	
			—	ATTT	
GAM1451	LOC222134	5'	ACAGTGAAGTCAAATG	94136	T
			CATTTCACTT	CACTGT	
			GTAAAGTGAA	GTGACA	
			—		
GAM1452	ARNT2	3'	GCTCCACTCTCCCCTGCA	29463	C A _
			TGC AG	GGAGAGTG AGC	
			ACG TC	CCTCTCAC TCG	
			—	C C	
GAM1452	CASP10	3'	CTACACTTTGCTCCTCTGGC	52101	— _
			GCCAGAGGAG	AGTG AG	
			CGGTCTCCTC	TCAC TC	
			GTT	A	
GAM1452	CASP10	3'	CTACACTTTGCTCCTCTGGC	52118	— _
			GCCAGAGGAG	AGTG AG	
			CGGTCTCCTC	TCAC TC	
			GTT	A	
GAM1452	FGF1	3'	ATTGTGCTTGGCCCCTGGTA	52455	A AGAGT
			TGCCAG GG	GAGCACAAT	
			ATGGTC CC	TTCGTGTTA	
			C GG	—	
GAM1452	FGF1	3'	ATTGTGCTTGGCCCCTGGTA	52458	A AGAGT
			TGCCAG GG	GAGCACAAT	
			ATGGTC CC	TTCGTGTTA	
			C GG	—	
GAM1452	FGF1	3'	ATTGTGCTTGGCCCCTGGTA	5855	A AGAGT
			TGCCAG GG	GAGCACAAT	
			ATGGTC CC	TTCGTGTTA	
			C GG	—	
GAM1452	LHX3	3'	CTGGCCCCTCCTCTGACA	27373	C A_ G
			TG CAGAGGAG	GT AG	
			AC GTCTCCTC	CG TC	
			A	CC G	
GAM1452	MFRP	3'	TGCCCTGCCTCTCCTCTGGC	48707	TG CA
			GCCAGAGGAGAG	AG CA	
			CGGTCTCCTCTC	TC GT	
			CG	CC	
GAM1452	NT5C	3'	GTGCTGGTGCCTCTGGC	27473	AGAG G
			GCCAGAGG	T AGCAC	



CGGTCTCC G TCGTG  
GT\_\_G  
GAM1452 PPP1R3C 3' TTCACTCTCCTCTAGC 18251 C  
GC AGAGGAGAGTGAG  
|| |||||  
CG TCTCCTCTCACTT  
A  
GAM1452 RAB36 3' CACTGCCCTCCTCTGGCA 16949 \_\_\_\_  
TGCCAGAGGAG AGTG  
||||||| |||  
ACGGTCTCCTC TCAC  
CCG  
GAM1452 SH3BP2 3' TCACTCTCCCTGGCA 11612 A  
TGCCAG GGAGAGTGA  
||||| |||||  
ACGGTC CCTCTCACT  
—  
GAM1452 STK38 3' TGCTTTTCCTCTCACA 23444 CC GTG  
TG AGAGGAGA AGCA  
|| ||||| |||  
AC TCTCCTTT TCGT  
AC \_\_\_\_  
GAM1452 AKAP3 3' TGCTTTCCCTCTTCTGGCA 21212 AGT\_  
TGCCAGAGGAG GAGCA  
||||||| |||  
ACGGTCTTCTC TTCGT  
CCCT  
GAM1452 BBX 3' TGTAGCTCACCCAGCA 39590 CAGA AGA \_  
TGC GG GTGAGC ACA  
||| || ||||| |||  
ACG CC CACTCG TGT  
A\_\_ \_\_ A  
GAM1452 BET1 5' CTCTCTCTCCTCTGGCA 19640 T  
TGCCAGAGGAGAG GAG  
||||||| |||  
ACGGTCTCCTCTC CTC  
T  
GAM1452 CHST4 3' TCACTTCCCCTCTGCA 19305 C A\_  
TGC AGAGG GAGTGA  
||| ||||| |||||  
ACG TCTCC TTCACT  
— CC  
GAM1452 FHOD2 3' CTTACTCTCCTCTGACA 73825 C  
TG CAGAGGAGAGTGAG  
|| |||||  
AC GTCTCCTCTCATTC  
A  
GAM1452 FLJ12438 3' GCCTCTCCCCTCTGGCA 41644 A TGA  
TGCCAGAGG GAG GC  
||||||| ||| ||

			ACGGTCTCC CTC CG		
			C TC_		
GAM1452	FLJ12592	5'	ATTGTGCAACCTCTGGCA 49695	AGAGTGA	
			TGCCAGAGG GCACAAT		
			ACGGTCTCC CGTGTTA		
			AA_____		
GAM1452	FLJ12800	5'	TGCAGACTCTCCTCTG 43237	GA	
			CAGAGGAGAGT GCA		
			GTCTCCTCTCA CGT		
			GA		
GAM1452	FLJ13909	5'	TGTCACCTCTTCTGGCA 47070	A G	
			TGCCAGAGGAG GTGA CA		
			ACGGTCTTCTC CACT GT		
			- -		
GAM1452	FLJ20445	3'	TTTACTCTCCTCTTGCA 35184	C	
			TGC AGAGGAGAGTGAG		
			ACG TCTCCTCTCATTT		
			T		
GAM1452	FLJ20716	3'	ATTGTGCTTAACCCAGCA 35600	CAGA AGAG	
			TGC GG TGAGCACAAT		
			ACG CC ATTCGTGTTA		
			A__ CCA_		
GAM1452	FLJ21596	3'	TGTGCTCATGGCGTGGCA 45705	GAGGAGA	
			TGCCA GTGAGCACA		
			ACGGT TACTCGTGT		
			GCGG__		
GAM1452	GPR74	3'	TGAAAGCCCTCTCTGGCA 53837	G A GAG	
			TGCCAGAG AG GT CA		
			ACGGTCTC TC CG GT		
			_ C AAA		
GAM1452	HABP2	3'	GCCCACTCTCCTTGCA 14697	G A	
			TGCCA AGGAGAGTG GC		
			ACGGT TCCTCTCAC CG		
			- C		
GAM1452	KIAA1155	3'	GCCACTCTCCTCTGG 62234	A	
			CCAGAGGAGAGTG GC		
			GGTCTCCTCTCAC CG		
			-		
GAM1452	KIAA1586	5'	ATTGTGCTCTACCCTGGGCA 92327	AG AGAGT	
			TGCC AGG GAGCACAAT		

		ACGG TCC CTCGTGTTA		
		G_ CAT__		
GAM1452	MGC20576	3' GTGCCACTCTCTCTGGCA 58415	G	A
		TGCCAGAG AGAGTG GCAC		
		ACGGTCTC TCTCAC CGTG		
		— —		
GAM1452	NPGPR	3' TGAAAGCCCTCTCTGGCA 16879	G	A GAG
		TGCCAGAG AG GT CA		
		ACGGTCTC TC CG GT		
		— C AAA		
GAM1452	PDE4DIP	3' TGCTGGAGCTCCTCTGGCA 95440		AGTG
		TGCCAGAGGAG AGCA		
		ACGGTCTCCTC TCGT		
		GAGG		
GAM1452	PRO0902	5' TGCACAGTACCTCTGGCA 53899		AGAG A
		TGCCAGAGG TG GCA		
		ACGGTCTCC AC CGT		
		ATG_ A		
GAM1452	RASD2	3' TGTGCTCGTTCTCAAGCA 26691	CA	AG
		TGC GAGGAG TGAGCACA		
		ACG CTCCTT GCTCGTGT		
		AA —		
GAM1452	SIAT4B	5' TGGCTCCCCTCCTCTGGCA 22657		AGT A
		TGCCAGAGGAG GAGC CA		
		ACGGTCTCCTC CTCG GT		
		CC_ —		
GAM1452	ZMPSTE24	3' ATTGTGCTCACACCT 19593		AGA
		AGG GTGAGCACAAT		
		TCC CACTCGTGTTA		
		A_		
GAM1452	ZNF340	5' TTCACCCCCTCCTCTGGCA 84566		A_
		TGCCAGAGGAG GTGAG		
		ACGGTCTCCTC CACTT		
		CCC		
GAM1452	LOC123096	3' ATTGTGCTCCTGCCCTGCA 74198	C	A AG T
		TGC AG GG AG GAGCACAAT		
		ACG TC CC TC CTCGTGTTA		
		— — G_ —		
GAM1452	LOC143888	3' TGCATAATTTCTCCTTTACA 76661	CC	TGA_
		TG AGAGGAGAG GCA		

		AC TCTCCTCTT CGT		
		AT TAATA		
GAM1452	LOC150225 3'	TGCACACCCCTCTGGCA	85015	AGA A
		TGCCAGAGG GTG GCA		
		ACGGTCTCC CAC CGT		
		C__ A		
GAM1452	LOC151429 3'	TGTGACCTCCTCTG	85361	A GAG
		CAGAGGAG GT CACA		
		GTCTCCTC CA GTGT		
		- - -		
GAM1452	LOC157381 3'	CTCACTCTCCTCTGGCA	86438	
		TGCCAGAGGAGAGTGAG		
		ACGGTCTCCTCTCACTC		
GAM1452	LOC200205 3'	TGTGCTTGCTTCCAGCA	88630	CAGA G TG
		TGC GGA AG AGCACA		
		ACG CCT TC TCGTGT		
		A__ _ GT		
GAM1452	LOC204285 5'	TATTGTGCTCACCATT	89459	GA
		GA GTGAGCACAATA		
		TT CACTCGTGTTAT		
		AC		
GAM1452	LOC253664 3'	GTAGCCCTACTCTGGCA	94813	G A GA
		TGCCAGAG AG GT GC		
		ACGGTCTC TC CG TG		
		A C A_		
GAM1452	LOC254018 5'	TGTGCCCAGCCTCCAGCA	96970	CAGA AG A
		TGC GGAG TG GCACA		
		ACG CCTC AC CGTGT		
		A__ CG C		
GAM1452	LOC56996 3'	GCCACCTCCTTTGGCA	39648	A A
		TGCCAGAGGAG GTG GC		
		ACGGTTTCCTC CAC CG		
		- C		
GAM1452	LOC89932 5'	GCCCATCTCCTCTGACA	60802	C G A
		TG CAGAGGAGA TG GC		
		AC GTCTCCTCT AC CG		
		A _ C		
GAM1452	LOC91464 5'	GCCACTCTCCACTGGCA	66140	A A
		TGCCAG GGAGAGTG GC		

		ACGGTC CCTCTCAC CG			
		A _			
GAM1453	ADH1B	3'	CTTAGACATAAAAGTAAAAT 72644	C	CAC
		ATTT ACTTT TGTCTGAG			
		TAAA TGAAA ACAGATTC			
		A T_			
GAM1453	AHR	3'	ATCTCAGATGTTAAAATAAATG 7875	CAC	C T
		CATTT TTT AC GTCTGAGAT			
		GTAAA AAA TG TAGACTCTA			
		TA_ T _			
GAM1453	FDFT1	3'	TAGGAAAGTGAAATG 15518	A	
		CATTTCACTTTC CTG			
		GTAAAGTGAAAG GAT			
		_			
GAM1453	JTB	3'	ATCTCAGACAGTGAAAGTGAAA 21959		
	TG		CATTTCACTTTCACTGTCTGAGAT		
		GTAAAGTGAAAGTGACAGACTCTA			
GAM1453	KLF4	3'	TCCCAGACAGTGGATATG 14891	CT	A
		CA TTCACTGTCTG GA			
		GT AGGTGACAGAC CT			
		AT C			
GAM1453	PHYH	3'	ACAGTAAAAGTGAAAT 20608	C	
		ATTTCACTTT ACTGT			
		TAAAGTGAAA TGACA			
		A			
GAM1453	PKD2	3'	TCCAGGTTGAAAGTGAAA 60096	CTG	A
		TTTCACTTTCA TCTG GA			
		AAAGTGAAAGT GGAC CT			
		T_ _			
GAM1453	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
		TTTCA TTTCACTGTCT			
		AAAGT AAAGTGACGGG			
		A			
GAM1453	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA	CTG
		TTTCACTTT CTGT AGAT			
		AAAGTGAAA GACA TCTA			
		C_ CG_			
GAM1453	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT	CT
		TTCACTTTCA GT GAG			

AAGTGAAAGT CA CTC  
 CT \_  
 GAM1453 EIF2C2 3' ATCTTCTGAGAGTGAAAAG 71946 G T\_  
 CTTTCACT TC GAGAT  
 ||||| || ||||  
 GAAAGTGA AG TTCTA  
 G TC  
 GAM1453 FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802 ACTTTCACT  
 G CATTTC GTCTGAGAT  
 |||| | |||||  
 GTAAAG CAGACTCTA  
 AAACATT\_ \_  
 GAM1453 FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281 CTT  
 CATTTC TCACTGTCTGAGAT  
 |||| | |||||  
 GTAAAGT AGTGACAGACTCTA  
 C\_ \_  
 GAM1453 KIAA0984 3' TTTGTCCAGTGAAAATGAA 65534 C TC  
 TTCA TTTCACTG TGAG  
 ||| ||||| |||  
 AAGT AAAGTGAC GTTT  
 A CT  
 GAM1453 KLHL6 3' ATCTCAGAGCAGGAAA 55299 A \_  
 TTTC CTG TCTGAGAT  
 ||| ||| |||||  
 AAAG GAC AGACTCTA  
 \_ G  
 GAM1453 NIR3 3' GCAGTGAAAGTGCAAT 66242 T  
 ATT CACTTTCACTGT  
 ||| |||||  
 TAA GTGAAAGTGACG  
 C  
 GAM1453 PORIMIN 3' ATCTCAGAGGGCCAAAGTGAA 53598 CA G  
 TTCACTTT CT TCTGAGAT  
 ||||| || |||||  
 AAGTGAAA GG AGACTCTA  
 CC G  
 GAM1453 PP35 3' ATCTCAGACTGAAA 22814 CT  
 TTTC GTCTGAGAT  
 |||| | |||||  
 AAAGT CAGACTCTA  
 \_  
 GAM1453 PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148 TCAC C\_  
 CATTTCAC TT TGT TGAG  
 ||||| || |||  
 GTAAAGTGAA ACG ACTC  
 TA\_ TT  
 GAM1453 SEP15 3' TCCTACAGTAAGAGTGAAA 14934 C CT  
 TTTCAC TTT ACTGT GA  
 ||||| |||| ||

		AAAGTGAGA TGACA CT		
		A TC		
GAM1453	SFXN2	3' CTCAGGGGAAAAAAGTGAAA 73941		CACTG
		TTTCACTTT TCTGAG		
		AAAGTGAAA GGA CTC		
		AAAGG		
GAM1453	LOC149703	3' ATCTCAGACAGCCGTTTGAAAA 84647		ACTTTCA
		TTTC CTGTCTGAGAT		
		AAAG GACAGACTCTA		
		GTTTGCC		
GAM1453	LOC154007	3' ATCTCAAACCCTTTAGTGAAA 81015		TTCACT C
		TTTCACT GT TGAGAT		
		AAAGTGA CA ACTCTA		
		TTTCC_ A		
GAM1453	LOC155004	3' TCATTTAAGTGAAAGGAAA 81226	A	GTC_
		TTTC CTTTCACT TGA		
		AAAG GAAAGTGA ACT		
		_ ATTT		
GAM1453	LOC222134	5' ACAGTGAAGTGAAATG 94136		T
		CATTTCACTT CACTGT		
		GTAAAGTGAA GTGACA		
		-		
GAM1454	ABCD3	3' AATCAGTTTCTCAAACCTGAGCT 11154		AG C
	T	AAGCTCAGTTTGA AACTG ATT		
		TTCGAGTCAAACCT TTGAC TAA		
		CT -		
GAM1454	CARD15	3' GCCTCTTCAAAATGAGC 42215	G	ACT
		GCTCA TTTGAAGA GC		
		CGAGT AAACCTTCT CG		
		A C_		
GAM1454	EBAF	3' AATGCAGCTCAGATGCTGAGCT 65420		TTGAA A
		AGCTCAGT GA CTGCATT		
		TCGAGTCG CT GACGTAA		
		TAGA_ C		
GAM1454	RP1	3' TTCTTCAAAATGAACTT 20774	C G	
		AAG TCA TTTGAAGAA		
		TTC AGT AAACCTTCTT		
		A A		
GAM1454	SLC2A5	3' AATGCAGTCCTCATCTCCAGC 11722		CAGTT A A
		GCT TGA GA CTGCATT		

CGA ACT CT GACGTAA  
CCTCT C \_

GAM1454 BCMP1 3' CAGTTCTTCTTTCAGCTT 48734 CAGTTT  
AAGCT GAAGAACTG  
||||| |||||  
TTCGA CTTCTTGAC  
CTTT\_

GAM1454 BRAG 3' AATGCACAAGCTGAACTT 29467 C AAGAAC  
AAG TCAGTTTG TGCATT  
||| ||||| |||||  
TTC AGTCGAAC ACGTAA  
A \_

GAM1454 C20orf142 3' AGCCTTTCAAACTGAGC 74767 AA  
GCTCAGTTTGAAG CT  
||||||| ||  
CGAGTCAAACCTT GA  
CC

GAM1454 CARD14 3' AATGCAGTCCTGTTCTCAGC 44104 C TTTGA A  
GCT AG AG ACTGCATT  
||| || |||||  
CGA TC TC TGACGTAA  
C CTTG\_ C

GAM1454 DKFZP434A0225 3' AATGCAGTCCTCTATTTAGC 93903 C TT A A  
GCT AGT GA GA CTGCATT  
||| ||| || |||||  
CGA TTA CT CT GACGTAA  
T T\_ C \_

GAM1454 FLJ22865 5' TTCCTCCAGAACTGAGC 47073 \_ A  
GCTCAGTTT GA GAA  
||||||| || |||  
CGAGTCAAG CT CTT  
AC C

GAM1454 FLJ23604 3' GCAAAGTGGAGACTGAGCTT 46859 GAAGAAC  
AAGCTCAGTTT TGC  
||||||| |||  
TTCGAGTCAGA ACG  
GGTGAA\_

GAM1454 KIAA1641 5' AGTCCTCAAAACTGAGCT 80205 GA A  
AGCTCAGTTT AG ACT  
||||||| || |||  
TCGAGTCAAA TC TGA  
AC C

GAM1454 SIPL 3' AATGCAGTTCCTTAGATGC 36849 TCA A  
GC GTTTGA GAACTGCATT  
|| ||||| |||||  
CG TAGATT CTTGACGTAA  
\_ C

GAM1454 LOC121536 3' AGTATCTTCAAACCTGA 74083 \_  
TCAGTTTGAAGA ACT  
||||||| |||



AGTCAAACCTTCT TGA  
 A  
 GAM1454 LOC122210 5' CAGTTCTTTTGGTGATCTT 74117 C G TT  
 AAG TCA T GAAGAACTG  
 ||| ||| | |||||  
 TTC AGT G TTTCTTGAC  
 T \_ GT  
 GAM1454 LOC168667 3' TGGTTCTTCAACTAAGCT 92761 C T  
 AGCT AGTT GAAGAACTG  
 ||| ||| |||||  
 TCGA TCAA CTTCTTGGT  
 A \_  
 GAM1454 LOC200830 3' TGCCTCCCCAAACTGGACT 90150 CT AA ACT  
 AG CAGTTTG GA GCA  
 || ||||| || |||  
 TC GTCAAAC CT CGT  
 AG CC C\_\_  
 GAM1454 LOC257446 5' AGTCCTCAAACTGAGCT 79998 GA A  
 AGCTCAGTTT AG ACT  
 ||||| || |||  
 TCGAGTCAAA TC TGA  
 AC C  
 GAM1454 LOC51125 3' AGTTCTCAAAGCTGAAGCT 32247 \_ A  
 AGCT CAGTTTGA GAACT  
 ||| ||||| |||||  
 TCGA GTCAAAGCT CTTGA  
 A C  
 GAM1455 ADAMTS8 5' TCGGGCCGCCAGCACCTG 22886 \_ ATAAG  
 CAG TGCTGGC CTGA  
 ||| ||||| |||||  
 GTC ACGACCG GGCT  
 C CCG\_\_  
 GAM1455 BAP1 3' TCAGGGACCCAGCACTGG 16219 CATAAG  
 CCAGTGCTGG CTGA  
 ||||| |||||  
 GGTCACGACC GACT  
 CAGG\_\_  
 GAM1455 BF 5' TTCAGCTTGGACACTG 8140 CTGGCA  
 CAGTG TAAGCTGAA  
 |||| |||||  
 GTCAC GTTCGACTT  
 AG\_\_  
 GAM1455 C1QB 3' TTCAACTCTGTGTCCCAGCACT 4923 A \_ \_ C  
 GGC G CCAGTGCTGG CATA AG TGAA  
 | ||||| ||| || |||||  
 C GGTCACGACC GTGT TC ACTT  
 \_ CT C A  
 GAM1455 CHC1 3' CAGCCCTGAGCACTGTGTC 7020 \_ \_ CATAA  
 GAC CAGTGCT GG GCTG  
 ||| ||||| || |||||

			CTG GTCACGA CC CGAC		
			T GT _____		
GAM1455	CMRF35	5'	CAGAGCTGTCAGCACCGG	21929	A TAAG
			CC GTGCTGGCA CTG		
			GG CACGACTGT GAC		
			C CGA_		
GAM1455	EPHB6	3'	TCAGCCCTGGACACTGGTC	15466	_ TG CATAA
			GACCAGTG C G GCTGA		
			CTGGTCAC G C CGACT		
			A GT C_____		
GAM1455	EVPL	5'	CAGCCTGAGCCAGCACT	8803	A A
			AGTGCTGGC TA GCTG		
			TCACGACCG GT CGAC		
			A C		
GAM1455	GARP	3'	CAGCCCAGCACTGG	18594	CATAA
			CCAGTGCTGG GCTG		
			GGTCACGACC CGAC		
			_____		
GAM1455	GJB5	3'	CAGCTCGACGGCACTGG	17945	GCATA
			CCAGTGCTG AGCTG		
			GGTCACGGC TCGAC		
			AGC_		
GAM1455	GPR81	3'	CTTACCAGCATTAGTC	50757	C CA
			GAC AGTGCTGG TAAG		
			CTG TTACGACC ATTC		
			A _		
GAM1455	IFI16	5'	AGCAAGCCAGCACTAGTC	71221	C ATAA
			GAC AGTGCTGGC GCT		
			CTG TCACGACCG CGA		
			A AA_		
GAM1455	KRT4	3'	CAGCTGGGCCAGCACTGGT	9635	_ ATA
			ACCAGTGCTGG C AGCTG		
			TGGTCACGACC G TCGAC		
			C GG_		
GAM1455	MAP3K9	3'	TTCAGCTTCCCAAACACCAGT	60709	CA C_ CAT
			AC GTG TGG AAGCTGAA		
			TG CAC ACC TTCGACTT		
			AC AA C_		
GAM1455	MGAT5	5'	TCAGCTTACAGTTCCTG	10028	T_ GCA
			CAG GCTG TAAGCTGA		

GTC TGAC ATTCGACT  
 CT \_\_\_\_  
 GAM1455 MOCS1 3' TTCAGCTTAACAGTTGCCCGGT 92037 A\_ \_ GCA  
 C GACC GTG CTG TAAGCTGAA  
 |||| |||| ||||  
 CTGG CGT GAC ATTCGACTT  
 CC T A\_\_  
 GAM1455 P23 3' TCAGCTTATACCCGGGCT 21719 G C\_  
 AGT CTGG ATAAGCTGA  
 |||| |||| ||||  
 TCG GGCC TATTCGACT  
 \_ CA  
 GAM1455 PFKFB4 3' TCAGCCACATGCAACACTGTGT 15874 \_ CTG AA\_  
 C GAC CAGTG GCAT GCTGA  
 |||| |||| ||||  
 CTG GTCAC CGTA CGACT  
 T AA\_ CAC  
 GAM1455 PTPRK 3' TTCAGCCTGTGGCCAGCACTG 11125 \_ A  
 GTC GACCAGTGCTGG CATA GCTGAA  
 |||| |||| ||||  
 CTGGTCACGACC GTGT CGACTT  
 CG C  
 GAM1455 RNPEPL1 3' CGGATGCCAGCACCTG 36676 \_ AAG  
 CAG TGCTGGCAT CTG  
 |||| |||| ||||  
 GTC ACGACCGTA GGC  
 C \_\_\_\_  
 GAM1455 UBE2L3 3' TCAGCCCTGGCACTGGC 12507 A TG CATAA  
 G CCAGTGC G GCTGA  
 | |||| | ||||  
 C GGTACAG C CGACT  
 \_ GTC\_\_\_\_  
 GAM1455 APXL2 5' CAGCCTCAGCACTCATC 75185 CC CATAA  
 GA AGTGCTGG GCTG  
 || |||| ||||  
 CT TCACGACT CGAC  
 AC C\_\_\_\_  
 GAM1455 ARHGEF9 3' TTCAGCTTACCAAGCA 30824 \_ CA  
 TGCT GG TAAGCTGAA  
 |||| || ||||  
 ACGA CC ATTCGACTT  
 A \_\_\_\_  
 GAM1455 CEGP1 3' TTCAGCTTCCTCTAGCCCGG 40589 AGT CAT  
 CC GCTGG AAGCTGAA  
 || |||| ||||  
 GG CGATC TTCGACTT  
 CC\_ TCC  
 GAM1455 DKFZp547D155 3' CAGCCCTGAGACCACTGGTC 70435 CTGG TAA  
 GACCAGTG CA GCTG  
 |||| || ||||

CTGGTCAC GT CGAC  
 CAGA CC\_  
 GAM1455 DKFZP727G051 3' TTCAGCCCATCAACCAGCATTG 69483 CATAA\_\_  
 GTC GACCAGTGCTGG GCTGAA  
 ||||| ||||  
 CTGGTTACGACC CGACTT  
 AACTACC  
 GAM1455 DUSP14 5' CACTGTCACCAGCACTGCTC 22834 C CATA C  
 GA CAGTGCTGG AG TG  
 || ||||| ||  
 CT GTCACGACC TC AC  
 C ACTG \_  
 GAM1455 FLJ10206 5' CAGCTTATGCCAGGAGTC 35898 CAGTG  
 GAC CTGGCATAAGCTG  
 || |||||  
 CTG GACCGTATTCGAC  
 AG\_\_  
 GAM1455 FLJ20967 5' GGCGCCAGCACTGGTT 41962 CATAA  
 GACCAGTGCTGG GCT  
 ||||| ||  
 TTGGTCACGACC CGG  
 CG\_\_  
 GAM1455 FLJ22569 3' TTCAGCTTACTAACTG 43679 GC CA  
 CAGT TGG TAAGCTGAA  
 ||| || |||||  
 GTCA ATC ATTCGACTT  
 A\_ \_  
 GAM1455 FOXN4 3' TTCAGCTTGGACACACTGG 75574 C GCA  
 CCAGTG TG TAAGCTGAA  
 |||| || |||||  
 GGTCAC AC GTTCGACTT  
 \_ AG\_  
 GAM1455 GW112 3' TTCAACTGAAGCCAGCACTGGT 21194 ATA C  
 T GACCAGTGCTGGC AG TGAA  
 ||||| || ||||  
 TTGGTCACGACCG TC ACTT  
 AAG A  
 GAM1455 HOOK2 3' CAGCTCACATGGCGCCAGCAC 25256 \_\_\_\_ A\_  
 TGG CCAGTGCTGG CAT AGCTG  
 ||||| || ||||  
 GGTCACGACC GTA TCGAC  
 CGCG CAC  
 GAM1455 jdp2 3' TTCAGCACAGCCAGCAT 55327 ATAA  
 GTGCTGGC GCTGAA  
 ||||| ||||  
 TACGACCG CGACTT  
 ACA\_  
 GAM1455 KIAA0767 3' TCTGCTGCCAGCACAGG 60632 A TAA T  
 CC GTGCTGGCA GC GA  
 || ||||| ||

		GG CACGACCGT CG CT	
		A     _ T	
GAM1455 KIAA0923	3'	TCAGCTTGATGCATGGTC 25838	G TGGCA
		GACCA TGC TAAGCTGA	
		CTGGT ACG GTTCGACT	
		_ TA_	
GAM1455 KIAA0982	3'	TTCAGTGTGGCCAGCAC 25852	TA_ C
		GTGCTGGCA AG TGAA	
		CACGACCGT TC ACTT	
		TTG _	
GAM1455 KIAA1000	3'	TTCAGCTTTGCAAAGTACTGG 65281	G_ T
		CCAGTGCT GCA AAGCTGAA	
		GGTCATGA CGT TTCGACTT	
		AA _	
GAM1455 MAP3K3	3'	TCAGCCTGGGCGCTGGTC 9999	GG TAA
		GACCAGTGCT CA GCTGA	
		CTGGTCGCGG GT CGACT	
		_ C_	
GAM1455 MGC16037	5'	CTTGTCCAGCACTAGTC 51821	C C
		GAC AGTGCTGG ATAAG	
		CTG TCACGACC TGTC	
		A _	
GAM1455 MIDORI	3'	TCAGCTTATCCTGCAACT 73792	_ T C
		AGT GC GG ATAAGCTGA	
		TCA CG CC TATTCGACT	
		A T _	
GAM1455 MtFMT	5'	CAGTGGCGAGCACTGG 57651	G ATAA
		CCAGTGCT GC GCTG	
		GGTCACGA CG TGAC	
		G G_	
GAM1455 PCDH16	5'	TCAGTTCCAACCACTGG 72826	C_ CATA
		CCAGTG TGG AGCTGA	
		GGTCAC ACC TTGACT	
		CA _	
GAM1455 QKI	3'	CAGCTTATCAACTCGTC 65439	C GCTGGC
		GAC AGT ATAAGCTG	
		CTG TCA TATTCGAC	
		C AC_	
GAM1455 TNRC6	3'	CAACTTTTAGCACTG 70506	CAT C
		CAGTGCTGG AAG TG	

GTCACGATT TTC AC  
 \_\_\_\_ A  
 GAM1455 TOB2 3' CAGCCCAGGCCAGCACTG 95618 ATAA  
 CAGTGCTGGC GCTG  
 ||||| |||  
 GTCACGACCG CGAC  
 GACC  
 GAM1455 TU12B1-TY 3' TCAGCCCACAGCACTGTC 33406 C GCATAA  
 GAC AGTGCTG GCTGA  
 || ||||| |||  
 CTG TCACGAC CGACT  
 \_ ACC\_  
 GAM1455 TUSP 3' TCAGCCTAAGAGCGCAGCACTG 39641 \_ A\_ A  
 CAGTGCTG GC TA GCTGA  
 ||||| || |||||  
 GTCACGAC CG AT CGACT  
 G AGA C  
 GAM1455 USP19 3' TCAGCTTATGCATCTGGT 88959 TGCTG  
 ACCAG GCATAAGCTGA  
 |||| |||||  
 TGGTC CGTATTCGACT  
 TA\_  
 GAM1455 ZD52F10 3' CAGCCTGTGCCAGCCCTGG 52819 T A  
 CCAG GCTGGCATA GCTG  
 |||| ||||| |||  
 GGTC CGACCGTGT CGAC  
 C C  
 GAM1455 LOC145268 3' TCAGCTTACAAGAGCCACTG 77062 \_ GGCA  
 CAGTG CT TAAGCTGA  
 |||| || |||||  
 GTCAC GA ATTCGACT  
 C GAAC  
 GAM1455 LOC149296 5' CAGCTTATGGGCAGCA 79256 G\_  
 TGCTG CATAAGCTG  
 |||| |||||  
 ACGAC GTATTCGAC  
 GG  
 GAM1455 LOC161877 5' TCAGGGCAGGCCAGCGCTGG 82326 ATAAG  
 CCAGTGCTGGC CTGA  
 ||||| |||  
 GGTCGCGACCG GACT  
 GACGG  
 GAM1455 LOC163115 5' TCAGCCCCTGACAGCACTGG 82413 G TAA  
 CCAGTGCTG CA GCTGA  
 ||||| || |||  
 GGTCACGAC GT CGACT  
 A CCC  
 GAM1455 LOC196500 3' TCAGCTCACTCAGTGGTC 87744 AGT CATA  
 GACC GCTGG AGCTGA  
 ||| |||| |||||

CTGG TGA CT TCGACT  
 \_\_\_\_ CAC\_  
 GAM1455 LOC197287 3' TCAGCTCATGTGTTTTGCACTG 60865 T\_ \_  
 CAGTGC GGCATA AGCTGA  
 ||||| ||||| |||||  
 GTCACG TTGTGT TCGACT  
 TT AC  
 GAM1455 LOC200470 5' TCAGCCTGCGGCGCTGG 90069 G TAA  
 CCAGTGCTG CA GCTGA  
 ||||| || |||||  
 GGTCGCGGC GT CGACT  
 \_ C\_  
 GAM1455 LOC221584 3' CAGCTTATGTGGCAC 93828 G  
 GTGCTG CATAAGCTG  
 ||||| |||||  
 CACGGT GTATTTCGAC  
 \_  
 GAM1455 LOC51716 3' CAGCTCATGGCCCTAGCA 32787 \_ A  
 TGCTGG CAT AGCTG  
 ||||| || |||||  
 ACGATC GTA TCGAC  
 CCG C  
 GAM1455 LOC92196 5' CAGAGCACCAGCACTGGC 68456 A CATAAG  
 G CCAGTGCTGG CTG  
 | ||||| |||||  
 C GGTACGACC GAC  
 \_ ACGA\_  
 GAM1456 RRM2 3' TTAAATATAAACCTGGCACTT 6411 TA\_ C  
 AAGTGCCAG TGTAT TAA  
 ||||| ||||| |||||  
 TTCACGGTC ATATA ATT  
 CAA A  
 GAM1456 DKFZP564D172 3' ATTTAGATATAACACACTTAA 49384 CCA A  
 TTAAGTG GT TGTATCTAAAT  
 ||||| || |||||  
 AATTCAC CA ATATAGATTTA  
 A\_ \_  
 GAM1456 TLOC1 3' ATTTAGATATTTCTCAACACTT 12310 CC\_ TAT  
 AA TTAAGTG AG GTATCTAAAT  
 ||||| || |||||  
 AATTCAC TC TATAGATTTA  
 AAC TT\_  
 GAM1456 LOC158969 5' TTAGATAAATGGCATTAA 82064 GTATG  
 TTAAGTGCCA TATCTAA  
 ||||| |||||  
 AATTTACGGT ATAGATT  
 AA\_  
 GAM1456 LOC51195 3' TTGGGCACCTGGCACT 32951 TAT AT  
 AGTGCCAG GT CTAA  
 ||||| || |||||

		TCACGGTC CA GGTT		
		___ CG		
GAM1457	SPAP1	5' ATTCCCCTCAAACGTCTAA 57036	CG	AA T
		TTAGACGT TGA GG AGT		
		AATCTGCA ACT CC TTA		
		A_ CC _		
GAM1457	SPAP1	5' ATTCCCCTCAAACGTCTAA 57037	CG	AA T
		TTAGACGT TGA GG AGT		
		AATCTGCA ACT CC TTA		
		A_ CC _		
GAM1458	CDC2L2	5' GCGGGAGGCCCGCAGGGA 53198	AGA	T
		TCCCTGT CCTCCC GT		
		AGGGACG GGAGGG CG		
		CCC _		
GAM1458	CLCA1	5' GAATCACAGGGAGATGTACAG 7070	GAC	
		CTGTA CTCCCTGTGATTC		
		GACAT GAGGGACACTAAG		
		GTA		
GAM1458	CTSH	3' AGTTGTGGGGAGATCCACTGGG 15247	T A C	TG
	A	TCCC GT GA CTCCCTG ATT		
		AGGG CA CT GAGGGGT TGA		
		T C A GT		
GAM1458	DSC2	3' ATCCAAGGAGGTCTACAGAGA 17063	C	C T
		TC CTGTAGACCTCC TG GAT		
		AG GACATCTGGAGG AC CTA		
		A A _		
GAM1458	DSC2	3' ATCCAAGGAGGTCTACAGAGA 44332	C	C T
		TC CTGTAGACCTCC TG GAT		
		AG GACATCTGGAGG AC CTA		
		A A _		
GAM1458	ED1	3' AATTTGAGGTCTAGAGAGA 7361	C G	CCTGT
		TC CT TAGACCTC GATT		
		AG GA ATCTGGAG TTAA		
		A G T___		
GAM1458	GDF5	3' GAATCACAGAGGGGTCAGG 5103	GTA	C
		CCT GACCTC CTGTGATTC		
		GGA CTGGGG GACACTAAG		
		___ A		
GAM1458	LZTR1	3' GAAGACACAGGTCCACAGGGA 22238	A	CCCT A_
		TCCCTGT GACCT GTG TTC		



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AGGGACA CTGGA CAC AAG
C ____ AG
GAM1458 PCDHB13 5' ACCTGGAAGTCCACGGGGA 38426 A C CT
TCCCTGT GAC TCC GT
||||| ||| ||| ||
AGGGGCA CTG AGG CA
C A TC
GAM1458 PCDHB8 5' ACCTGGAAGTCCACGGGGA 38951 A C CT
TCCCTGT GAC TCC GT
||||| ||| ||| ||
AGGGGCA CTG AGG CA
C A TC
GAM1458 PHEMX 5' CACAGGGAGGGGAAGGGA 57358 GTAGA
TCCCT CCTCCCTGTG
||||| |||||||
AGGGA GGAGGGACAC
AGG__
GAM1458 PHEMX 5' CACAGGGAGGGGAAGGGA 57362 GTAGA
TCCCT CCTCCCTGTG
||||| |||||||
AGGGA GGAGGGACAC
AGG__
GAM1458 DKFZp434F1819 3' GAACATACAGAGACCTACAGGG 50006 AC CC A
A TCCCTGTAG CTC TGTG TTC
||||| ||| ||| |||
AGGGACATC GAG ATAC AAG
CA AC _
GAM1458 EFA6R 3' GAATCAGCTGCTCTACAGG 30985 CCTCCCTG
CCTGTAGA TGATTC
||||| |||||
GGACATCT ACTAAG
CGTCG__
GAM1458 ESDN 3' GCAAGAGGTCTATAG 55174 CC
CTGTAGACCTC TGT
||||| |||
GATATCTGGAG ACG
A_
GAM1458 FLJ10415 3' AGAAAGATCTGCAGGGA 36093 C CC
TCCCTGTAGA CT CT
||||| || ||
AGGGACGTCT GA GA
A AA
GAM1458 FLJ10458 3' AATCGAAGGTCACAGG 36123 A CCCTG
CCTGT GACCT TGATT
||||| |||||
GGACA CTGGA GCTAA
_ A__
GAM1458 FLJ10512 3' CACAGGGAGGTTTCA 36207 T
TG AGACCTCCCTGTG
|| |||||||||

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AC TTTGGAGGGACAC

GAM1458 FLJ10535 3' GAATTACAGGGAAGTTACAGGG 36238 A C  
A TCCCTGT GAC TCCCTGTGATTC

||||| ||| |||||||||  
AGGGACA TTG AGGGACATTAAG

\_ A

GAM1458 FLJ20209 3' CAGATGAGATCTTACAGGGA 85518 \_ C C\_  
TCCCTGTA GA CTC CTG

||||| || ||| |||  
AGGGACAT CT GAG GAC

T A TA

GAM1458 KIAA0377 3' AATCACAGATTGTTAAAGG 27791 GTA CTCC  
CCT GAC CTGTGATT

||| ||| |||||||  
GGA TTG GACACTAA

AA\_ TTA\_

GAM1458 KIAA0408 5' GAATCACAAAGATGGTCTGAG 28135 G \_ CC  
CT TAGACC TC TGTGATTC

|| ||||| || |||||||  
GA GTCTGG AG AACTAAG

\_ T AA

GAM1458 KIAA1199 3' AATCACAGAGAGGTAAAATGGA 72507 CTGTAG C  
TCC ACCTC CTGTGATT

||| ||||| |||||||  
AGG TGGAG GACACTAA

TAAAA\_ A

GAM1458 KIAA1393 3' GAATCACAGAGAAGATCTGCG 72098 C \_ C  
TGTAGA CT C CTGTGATTC

||||| || | |||||||  
GCGTCT GA G GACACTAAG

A A A

GAM1458 KIAA1979 3' GAACCAAGCTGGGTCTATAAGG 88280 C CC G A  
A TCC TGTAGACCT CT TG TTC

||| ||||||| || || |||  
AGG ATATCTGGG GA AC AAG

A TC \_ C

GAM1458 MGC19556 5' AATCTTTGAGACCTCAGGGA 53224 T AC CCTGT  
TCCCTG AG CTC GATT

||||| || ||| |||||  
AGGGAC TC GAG CTAA

\_ CA TTT\_

GAM1458 MGC2705 3' ACGGGGAGGCCAGCAGGGA 51111 AGA\_  
TCCCTGT CCTCCCTGT

||||| |||||||  
AGGGACG GGAGGGGCA

ACCC

GAM1458 PP2447 5' GAGTTCAGGGAGGCCTTCAAGG 47320 C T A T  
A TCC TG AG CCTCCCTG GATTC

||| || || ||||||| |||||

AGG AC TC GGAGGGAC TTGAG  
 A T C \_  
 GAM1458 PRO1853 5' AATTTTCAGAAAACACCACAGGG 37770 AGACCTCC T  
 A TCCCTGT CTG GATT  
 ||||| |||||  
 AGGGACA GAC TTAA  
 CCACAAAA T  
 GAM1458 SLC26A1 3' GCAGGGAGACCTGCAGG 41866 AC  
 CCTGTAG CTCCCTGT  
 ||||| |||||  
 GGACGTC GAGGGACG  
 CA  
 GAM1458 SRPK1 3' AATCACAATTGTGGAATTACAG 11964 A\_ TCCC\_  
 G CCTGTAG CC TGTGATT  
 ||||| || |||||  
 GGACATT GG AACTAA  
 AA TGTTA  
 GAM1458 SYNJ2 3' GAATCACAAAAAAGTTACGAGG 61768 C ACCTCCC  
 A TCC TGTAG TGTGATTC  
 || ||||| |||||  
 AGG GCATT AACTAAG  
 A GAAAAA\_  
 GAM1458 TACTILE 5' GCAGGGGAGGTCCAGAGA 19473 C TA \_  
 TC CTG GACCTCCC TGT  
 || ||| ||||| |||  
 AG GAC CTGGAGGG ACG  
 A \_ G  
 GAM1458 LOC124460 3' GAATCACAGAGCATACAAAGGA 76044 C\_ GAC CC  
 TCC TGTA CTC TGTGATTC  
 ||| |||| ||| |||||  
 AGG ACAT GAG AACTAAG  
 AA AC\_ \_  
 GAM1458 LOC139231 3' AATCAGAAACCAACAGGGA 75372 AGACC CCTG  
 TCCCTGT TC TGATT  
 ||||| || |||||  
 AGGGACA AG ACTAA  
 ACCAA \_  
 GAM1458 LOC154760 5' AGGGAGACTACAGGGA 86243 AC  
 TCCCTGTAG CTCCCT  
 ||||| |||||  
 AGGGACATC GAGGGA  
 A\_  
 GAM1458 LOC160379 5' GTCAGGAGGAAGTCACAGGGA 87063 A C \_ G  
 TCCCTGT GAC TCC CT TGAT  
 ||||| ||| ||| ||| |||  
 AGGGACA CTG AGG GG ACTG  
 \_ A A \_  
 GAM1458 LOC203221 5' AATCACAGGAAGAGTC 89546 \_ C  
 GAC CT CCTGTGATT  
 ||| || |||||

CTG GA GGACACTAA  
 A A  
 GAM1458 LOC253573 3' CAGGGATGGAAATTACAGAGA 97046 C A\_\_ \_  
 TC CTGTAG CC TCCCTG  
 || ||||| || |||||  
 AG GACATT GG AGGGAC  
 A AAA T  
 GAM1458 LOC86651 5' ATAGAAAGGCTACAAGGA 68755 C A CC  
 TCC TGTAG CCT CTGT  
 ||| ||||| ||| ||||  
 AGG ACATC GGA GATA  
 A \_ AA  
 GAM1458 LOC93134 3' GAATTGTGGAGAGGTCTTCAGG 71520 T C TG  
 GA TCCCTG AGACCTC CTG ATTC  
 ||||| ||||| ||| ||||  
 AGGGAC TCTGGAG GGT TAAG  
 T A GT  
 GAM1459 CRADD 3' GGCTCAACAATTCTTTGTTTT 13739 TC CA  
 AAAACAGA AAT TTGAGCC  
 ||||| ||| |||||  
 TTTTGTTT TTA AACTCGG  
 C\_ AC  
 GAM1459 GPM6A 3' GGCATTACAATTAATCTGTTTT 17952 C CAT \_  
 GT ATAAAACAGAT AAT TGA GCC  
 ||||| ||| ||| |||  
 TGTTTTGTCTA TTA ATT CGG  
 A AC\_ A  
 GAM1459 HIPK3 3' GCTCAATGATACAAACATTTG 19197 CA\_\_\_\_  
 CAGAT ATCATTGAGC  
 |||| |||||  
 GTTTA TAGTAACTCG  
 CAAACA  
 GAM1459 KCNJ10 3' GCCCAGAGAAGATCTGTTT 9538 AA A A  
 AACAGATC TC TTG GC  
 ||||| || ||| ||  
 TTTGTCTAG AG GAC CG  
 A\_ A C  
 GAM1459 LTA 3' GCCCAAAGCTGTTGGTCTGT 5175 CA\_\_ A  
 ACAGATCAAT TTG GC  
 ||||| ||| ||  
 TGTCTGGTTG AAC CG  
 TCGA C  
 GAM1459 MSN 3' GCTCACTTGGTGATATGTCCTA 60253 AA G A T\_  
 T ATA ACA ATCA TCA TGAGC  
 ||| ||| ||| ||| ||||  
 TAT TGT TAGT GGT ACTCG  
 CC A \_ TC  
 GAM1459 PCDH9 5' GCAAAGTGATCTGTTTTAT 82798 ATCATTGA  
 ATAAAACAGATCA GC  
 ||||| ||| ||

TATTTTGTCTAGT CG  
 GAAA\_\_\_\_  
 GAM1459 PEPD 3' GGCTCCACCTTTAATCTGTTT 59910 C TCATT\_  
 TAT ATAAACAGAT AA GAGCC  
 ||||| || ||||  
 TATTTTGTCTA TT CTCGG  
 A TCCACC  
 GAM1459 RECQL5 3' CTCAACGCATCTGTTT 14928 CAATCA  
 TAAACAGAT TTGAG  
 ||||| ||||  
 ATTTTGTCTA AACTC  
 CGC\_\_\_\_  
 GAM1459 ARP5 3' GGCTCAGTGCCAATGTGT 71573 G CAAT  
 ACA AT CATTGAGCC  
 ||| || |||||  
 TGT TA GTGACTCGG  
 G ACC\_  
 GAM1459 DKFZP564G202 3' GCTCAGCCAAATCTTGTTTTAT 65290 \_ CAATCA  
 ATAAACA GAT TTGAGC  
 ||||| || ||||  
 TATTTTGT CTA GACTCG  
 T AACC\_\_\_\_  
 GAM1459 FKBP3 3' GGCTCAATAAAAATTGATC 8896 C\_\_\_\_  
 GATCAAT ATTGAGCC  
 ||||| |||||  
 CTAGTTA TAACTCGG  
 AAAA  
 GAM1459 FLJ20275 3' GCTCAGTGCACCTGCTTTA 34823 A A AAT  
 TAAA CAG TC CATTGAGC  
 ||| ||| || |||||  
 ATTT GTC AG GTGACTCG  
 C C C\_\_\_\_  
 GAM1459 FLJ22055 3' GGCTGGACTGATCTGT 45498 ATCA G  
 ACAGATCA TT AGCC  
 ||||| || ||||  
 TGTCTAGT AG TCGG  
 C\_\_\_\_ G  
 GAM1459 GPR77 3' GCTCAATGATGTCTTCATTTTA 37491 C\_\_ CA  
 T ATAAAA AGAT ATCATTGAGC  
 ||||| ||| |||||  
 TATTTT TCTG TAGTAACTCG  
 ACT \_\_\_\_  
 GAM1459 KIAA1678 3' GCTCAGTGGCCTGTTT 72306 ATCAA  
 AAACAG TCATTGAGC  
 ||||| |||||  
 TTTGTC GGTGACTCG  
 C\_\_\_\_  
 GAM1459 MAP2K4 3' CTCAAGAGGAATCTGTTT 11547 CAA A  
 AAACAGAT TC TTGAG  
 ||||| || ||||

		TTTGTCTA AG AACTC	
		AGG _	
GAM1459	PARG1	3' GGTGATCGGATCTGTTT 16683	A_
		AAACAGATC ATCATT	
		TTTGTCTAG TAGTGG	
		GC	
GAM1459	SNIP1	5' GCTCAACTGATCTGTTTT 45213	ATCA
		AAAACAGATCA TTGAGC	
		TTTTGTCTAGT AACTCG	
		C__	
GAM1459	ZDHC4	5' GGTGTTGAATTGATCTGT 36158	_ TTGA
		ACAGATCAAT CA GCC	
		TGTCTAGTTA GT TGG	
		A TG__	
GAM1459	LOC144571	3' GGCTCAATCCTCCTGCTTTA 83155	A ATCAATC
		TAAA CAG ATTGAGCC	
		ATTT GTC TAACTCGG	
		C CTCC__	
GAM1459	LOC152445	3' GGCTCAATGATTCTCCTGT 85757	ATC
		ACAG AATCATTGAGCC	
		TGTC TTAGTAACTCGG	
		CTC	
GAM1459	LOC157867	5' TGATTGATCTGTCTTA 86560	A
		TAA ACAGATCAATCA	
		ATT TGTCTAGTTAGT	
		C	
GAM1459	LOC158156	3' GCCCATGTCGGATCTGTTT 81726	AAT T A
		AAACAGATC CAT G GC	
		TTTGTCTAG GTA C CG	
		GCT _ C	
GAM1459	LOC197131	3' GATCAATCTGTTTTAT 87887	CA
		ATAAAACAGAT ATC	
		TATTTTGTCTA TAG	
		AC	
GAM1459	LOC221296	3' GTTTAATTGATTGTCT 91969	T _
		AGA CAATCA TTGAGC	
		TCT GTTAGT AATTTG	
		_ T	
GAM1459	LOC253250	3' GGCTCAATAATATTGCATTGT 94703	AT C__
		ACAG CAAT ATTGAGCC	

	TGTT GTTA TAACTCGG	
	AC TAA	
GAM1459 LOC253296 3'	GGCTGCAGCTGATCTGTTT 94492	ATCA _
	AAACAGATCA TTG AGCC	
	TTTGTCTAGT GAC TCGG	
	C__ G	
GAM1459 LOC253298 5'	GGCTGCAGCTGATCTGTTT 97216	ATCA _
	AAACAGATCA TTG AGCC	
	TTTGTCTAGT GAC TCGG	
	C__ G	
GAM1459 LOC253980 3'	GCTCAGCGTTATCAGTCTGTTT 95074	CA CA__
	AAACAGAT AT TTGAGC	
	TTTGTCTG TA GACTCG	
	AC TTGC	
GAM1459 LOC257570 3'	GGCTGCAGCTGATCTGTTT 97835	ATCA _
	AAACAGATCA TTG AGCC	
	TTTGTCTAGT GAC TCGG	
	C__ G	
GAM1459 LOC257571 5'	GGCTGCAGCTGATCTGTTT 97946	ATCA _
	AAACAGATCA TTG AGCC	
	TTTGTCTAGT GAC TCGG	
	C__ G	
GAM1459 LOC90785 3'	TGATTGGTCCATTTTA 64020	CA
	TAAAA GATCAATCA	
	ATTTT CTGGTTAGT	
	AC	
GAM1459 LOC90785 3'	TGATTGGTCCGTTTTA 64021	A
	TAAAAC GATCAATCA	
	ATTTTG CTGGTTAGT	
	C	
GAM1459 LOC91948 3'	TGATTGGTCCATTTTA 67620	CA
	TAAAA GATCAATCA	
	ATTTT CTGGTTAGT	
	AC	
GAM1460 ANGPT2 3'	GATGAACCCGAGGCTGA 6705	G CA_
	TCAG CC GGTTCATT	
	AGTC GG CCAAGTAG	
	_ AGC	
GAM1460 BARX1 3'	AACGAGGAAGGACACAGACCC 41202	CCCAG_ A
	GG GTTC TTCCTCGTT	

			CC CAGG AAGGAGCAA		
			CAGACA _		
GAM1460	PCDHA11	5'	AACGAGATTTTAACTGAAAC 49031	GCC	CATTC_
		TGA	TCAG CAGGTT CTCGTT		
			AGTC GTCCAA GAGCAA		
			AAA TTTTTA		
GAM1460	PCDHA11	5'	AACGAGATTTTAACTGAAAC 38195	GCC	CATTC_
		TGA	TCAG CAGGTT CTCGTT		
			AGTC GTCCAA GAGCAA		
			AAA TTTTTA		
GAM1460	STK38	3'	AACGAGGAGAGCCCAGGCCT 23440	CA	AT
			AGGCC GGTTC TCCTCGTT		
			TCCGG CCGAG AGGAGCAA		
			AC _		
GAM1460	FLJ13491	5'	AACGAGGAGGCCGCCGTCC 44882	C A	TCA
			GG CC GGT TTCCTCGTT		
			CC GG CCG GAGGAGCAA		
			T _ CCG		
GAM1460	KIAA1553	3'	AACGAGGACTCCAAGCCATGA 91911	_	CCA TTCAT
			TCA GGC GG TCCTCGTT		
			AGT CCG CC AGGAGCAA		
			A AA_ TC__		
GAM1460	KIAA1966	5'	ACGAGAAGGCTGGGCCT 55890	G	CATTC
			AGGCCCAG TT CTCGT		
			TCCGGGTC GA GAGCA		
			G A__		
GAM1461	BTEB1	3'	ATTCAGAATCAGTGTG 6839	AA	
			CATAT ATTCTGAAT		
			GTGTG TAAGACTTA		
			AC		
GAM1461	CDC7L1	3'	CGGAAATTACATGGTGCTG 13028	A A	
			CAGCACCAT TAA TTCTG		
			GTCGTGGTA ATT AAGGC		
			C A		
GAM1461	FMNL	5'	GA CTCAGAATTGGGC 19703	A	TATAA A
			GC CCA ATTCTGA TC		
			CG GGT TAAGACT AG		
			_ _ _ _ C		
GAM1461	GABRE	3'	AATTTGTATGGCACTG 41770	CA	
			CAG CCATATAAATT		



			GTC GGTATGTTTAA			
			AC			
GAM1461	GABRE	3'	AATTTGTATGGCACTG	41779	CA	
			CAG CCATATAAAATT			
			GTC GGTATGTTTAA			
			AC			
GAM1461	GABRE	3'	AATTTGTATGGCACTG	41799	CA	
			CAG CCATATAAAATT			
			GTC GGTATGTTTAA			
			AC			
GAM1461	GABRE	3'	AATTTGTATGGCACTG	17107	CA	
			CAG CCATATAAAATT			
			GTC GGTATGTTTAA			
			AC			
GAM1461	MTRR	3'	TGATTTATTTTATATGATGT	10136	C	TTC
			GCA CATATAAA TGAATCA			
			TGT GTATATTT ATTTAGT			
			A TT_			
GAM1461	MTRR	3'	TGATTTATTTTATATGATGT	43773	C	TTC
			GCA CATATAAA TGAATCA			
			TGT GTATATTT ATTTAGT			
			A TT_			
GAM1461	PKD1	3'	CAGTAATTTATATGGTGTT	4309		_
			AGCACCATATAAAATT CTG			
			TTGTGGTATATTAA GAC			
			T			
GAM1461	PROS1	3'	TGATTCAGAAGGCGTGATACTG	87425	CAC	ATAAA
			CAG CAT TTCTGAATCA			
			GTC GTG AAGACTTAGT			
			ATA CGG_			
GAM1461	PSMB2	3'	ATTCAGAATAAAGGTGACT	10948	_	ATATAA
			AG CACC ATTCTGAAT			
			TC GTGG TAAGACTTA			
			A AAA_			
GAM1461	SUPT6H	5'	GATTCAGAAGATGATGTTG	60396	C	ATAAA
			CAGCA CAT TTCTGAATC			
			GTTGT GTA AAGACTTAG			
			A G_			
GAM1461	TDG	3'	GAGTTTTCCATGGTGCT	12192	AT_	
			AGCACCAT AAATTC			

TCGTGGTA TTTGAG  
CCT

GAM1461 BM-002 3' GATTCAGAATCAGTGCT 33523 CATATAA  
AGCAC ATTCTGAATC  
||||| |||||  
TCGTG TAAGACTTAG  
AC\_\_\_\_

GAM1461 DKFZP434A043 3' CAGGCACTATACATGGTGCTG 31188 \_\_ AAT  
CAGCACCA TATA TCTG  
||||| ||| |||  
GTCGTGGT ATAT GGAC  
AC CAC

GAM1461 FLJ21551 3' ATTCAGAATCAATATGTCACTG 45626 CAC AA  
CAG CATAT ATTCTGAAT  
||| ||||| |||||  
GTC GTATA TAAGACTTA  
ACT AC

GAM1461 FLJ21916 3' TGGAATCTATTGGTGCTG 43647 T A  
CAGCACCA ATA ATTCTG  
||||| ||| |||||  
GTCGTGGT TAT TAAGGT  
\_ C

GAM1461 FYCO1 3' TGATTCAGAACAAATCATGCT 44498 CCATATAAA  
AGCA TTCTGAATCA  
||||| |||||  
TCGT AAGACTTAGT  
ACTAAAC\_\_

GAM1461 KIAA1332 3' GACTCAGGCTCTGGTGCTG 71168 TATAAAT A  
CAGCACCA TCTGA TC  
||||| ||||| |||  
GTCGTGGT GGACT AG  
CTC\_\_\_\_ C

GAM1461 KIAA1500 3' AGTTTATGTGGCACTG 64115 CA  
CAG CCATATAAATT  
||| |||||  
GTC GGTGTATTTGA  
AC

GAM1461 MGC12981 5' TGACCCAGAGGCCTTGGTGCTG 50386 TATAAA AA  
CAGCACCA TTCTG TCA  
||||| ||||| |||  
GTCGTGGT GAGAC AGT  
TCCG\_\_ CC

GAM1461 MGC13007 5' GAGTCTACATGGTGCT 50305 A A  
AGCACCAT TA ATTC  
||||| ||| |||  
TCGTGGTA AT TGAG  
C C

GAM1461 MGC2705 3' TGACCTCATCTTTCTCATGGTG 51118 ATAAATTC A\_  
CT AGCACCAT TGA TCA  
||||| ||| |||

		TCGTGGTA	ACT AGT		
		CTCTTTCT	CC		
GAM1461	RAB39	3'	TGATTCAGAGCATGATGCT	76634	C ATAAA
			AGCA CAT TTCTGAATCA		
			TCGT GTA GAGACTTAGT		
			A C____		
GAM1461	SFRS5	3'	ATTCAGAATTAGTTTAATGC	22643	CCAT A
			GCA AT AATTCTGAAT		
			CGT TG TTAAGACTTA		
			AATT A		
GAM1461	STRIN	3'	ATTACCTGTTTATATGGTGCT	32765	TCTG
			AGCACCATATAAAT AAT		
			TCGTGGTATATTTG TTA		
			TCCA		
GAM1461	TAF2	3'	TGATTTCTTTATATGGTGGTG	12087	G TTCT
			CA CACCATATAAA GAATCA		
			GT GTGGTATATTT TTTAGT		
			G C____		
GAM1461	WDR9	3'	GAATTTATAAAGTGCTG	53351	CA
			CAGCAC TATAAATTC		
			GTCGTG ATATTTAAG		
			AA		
GAM1461	ZIN	3'	CGGGATTTTCATGGCGC	25488	A AT
			GC CCAT AAATTCTG		
			CG GGTA TTTAGGGC		
			C CT		
GAM1461	LOC144848	3'	TGACCCAGGGCCATGGTGCT	73579	ATAAA AA
			AGCACCAT TTCTG TCA		
			TCGTGGTA GGGAC AGT		
			CC____ CC		
GAM1461	LOC158629	5'	CAGAACTTATATGGCCCTG	86874	CA A
			CAG CCATATAA TTCTG		
			GTC GGTATATT AAGAC		
			CC C		
GAM1461	LOC169270	3'	CAGAATTCACATGGTGT	82735	ATA
			GCACCAT AATTCTG		
			TGTGGTA TTAAGAC		
			CAC		
GAM1461	LOC90393	5'	ATTCAGAAATTATGGGGCT	62619	A A A
			AGC CC TATAA TTCTGAAT		

		TCG GG GTATT AAGACTTA	
		— — A	
GAM1462	B4GALT2	3' CTAGAGGCGCTGAAGGA 47581	A_ C
		TCCTTCAG CCTC AG	
		AGGAAGTC GGAG TC	
		GC A	
GAM1462	CCND3	3' CACATCTAAGCCTGAAGGG 8303	AC CC _
		TCCTTCAG CT AGA GTG	
		GGGAAGTC GA TCT CAC	
		C_ A_ A	
GAM1462	CYP4F3	3' TCACTCTGTGAGTGGAAG 6123	AGAC _
		CTTC CTC CAGAGTGA	
		GAAG GAG GTCTCACT	
		GT__ T	
GAM1462	DIAPH2	3' TCACTTTGGTGGTCTGAAG 22070	T
		CTTCAGACC CCAGAGTGA	
		GAAGTCTGG GGTTCCT	
		T	
GAM1462	FACL5	5' CACCCTGTCTCTGGAGGA 64185	CCTC A
		TCCTTCAGA CAG GTG	
		AGGAGGTCT GTC CAC	
		CT__ C	
GAM1462	FUS2	5' CACTGTGGTCTGAAG 24116	TCC G
		CTTCAGACC A AGTG	
		GAAGTCTGG T TCAC	
		__G	
GAM1462	GABRP	5' CTGTAGGCCTGAAGGA 26399	A C
		TCCTTCAG CCT CAG	
		AGGAAGTC GGA GTC	
		C T	
GAM1462	GAC1	3' CTGGGCAAGGGCTGAAGGA 20942	A ____
		TCCTTCAG CCT CCAG	
		AGGAAGTC GGA GGTC	
		G ACG	
GAM1462	GCK	5' CACTGAATCTGTCTGAAGGA 3866	CTCCAG
		TCCTTCAGAC AGTG	
		AGGAAGTCTG TCAC	
		TCTAAG	
GAM1462	GCS1	3' CACTCTGGCTCTGAAGGA 20868	CCT
		TCCTTCAGA CCAGAGTG	

			AGGAAGTCT GGTCTCAC	
			C__	
GAM1462	GNB3	5'	CACCCTGAGCTGAGG 9074	AC C A
			CTTCAG CTC AG GTG	
			GGAGTC GAG TC CAC	
			__ _ C	
GAM1462	GPD2	5'	CACCCTGGCTGGAGGA 4646	ACCT A
			TCCTTCAG CCAG GTG	
			AGGAGGTC GGTC CAC	
			_____ C	
GAM1462	HMGCR	5'	TCTAGTGAGATCTGGAGGA 5974	C C__
			TCCTTCAGA CTC AGA	
			AGGAGGTCT GAG TCT	
			A TGA	
GAM1462	HSD17B1	5'	CACTCTGGAATGAGGA 4683	T GACC
			TCCT CA TCCAGAGTG	
			AGGA GT AGGTCTCAC	
			_ A__	
GAM1462	IL13RA1	3'	TCAGGAGACCTGGAGGA 7779	AC A
			TCCTTCAG CTCC GA	
			AGGAGGTC GAGG CT	
			CA A	
GAM1462	INPP4A	3'	TCAGGAGACTGAAGGA 14438	AC A
			TCCTTCAG CTCC GA	
			AGGAAGTC GAGG CT	
			A_ A	
GAM1462	INSR	3'	CATCCAGGCTGAAGGA 70979	A CCA G
			TCCTTCAG CCT GA TG	
			AGGAAGTC GGA CT AC	
			_ C__ _	
GAM1462	ITPA	3'	TCACCGGCCTGTCTGGAGGA 53092	CT_ AGA
			TCCTTCAGAC CC GTGA	
			AGGAGGTCTG GG CACT	
			TCC C__	
GAM1462	KCNAB1	3'	TCACTCTGAGGTTTACAG 60928	TC C
			CT AGACCTC AGAGTGA	
			GA TTTGGAG TCTCACT	
			CA _	
GAM1462	KRT16	5'	TGGAAGGCCTGAAGGA 95201	A _
			TCCTTCAG CCT CCA	

		AGGAAGTC GGA GGT	
		C A	
GAM1462 LRAT	3'	TCACTCTGAGAGGTAAATGGA 60106	TTCAG _
		TCC ACCTC CAGAGTGA	
		AGG TGGAG GTCTCACT	
		TAAA_ A	
GAM1462 LZTR1	3'	CACAGGGGCTGAAGGA 22231	A CAGA
		TCCTTCAG CCTC GTG	
		AGGAAGTC GGGG CAC	
		_ A__	
GAM1462 MAGEA8	3'	TCACTCTGTGTTTGAAGAGA 18107	_ CTC
		TC CTTCAGAC CAGAGTGA	
		AG GAAGTTTG GTCTCACT	
		A T__	
GAM1462 MAGEB4	3'	TCACTTTGTGGTTGAAAG 9890	CA TC
		CTT GACC CAGAGTGA	
		GAA TTGG GTTTCACCT	
		AG T_	
GAM1462 MEN1	5'	TCACGTGGAATCTGGAGGA 93379	CC GA
		TCCTTCAGA TCCA GTGA	
		AGGAGGTCT AGGT CACT	
		A_ G_	
GAM1462 MUC4	3'	TCACTCTGGAGATTCT 56330	C_
		AGA CTCCAGAGTGA	
		TCT GAGGTCTCACT	
		TA	
GAM1462 MYH11	3'	TCTAGAAGGTCTGGAGGA 43136	_ C
		TCCTTCAGACCT C AGA	
		AGGAGGTCTGGA G TCT	
		A A	
GAM1462 NEO1	3'	TCACTCTGAGGGGGAGGA 10205	AGA TC
		TCCTTC CC CAGAGTGA	
		AGGAGG GG GTCTCACT	
		_ GA	
GAM1462 NNMT	5'	TCACTCCCTGGCTTCTGGAGGA 20505	CCT _
		TCCTTCAGA CCA GAGTGA	
		AGGAGGTCT GGT CTCACCT	
		TC_ CC	
GAM1462 PAFAH1B1	3'	TCACTCTGAAGATGTTAGAG 4731	A C _
		TTC GAC TC CAGAGTGA	

		GAG TTG AG GTCTCACT	
		A T AA	
GAM1462 PBP	3'	TCACTCTGGTCCCTTTAAAG 10384	C CCT_
		CTT AGA CCAGAGTGA	
		GAA TTT GGTCTCACT	
		A CCCT	
GAM1462 PCSK2	3'	CTGAGGCCTGAAGGA 10466	A C
		TCCTTCAG CCTC AG	
		AGGAAGTC GGAG TC	
		C _	
GAM1462 PIP5K1A	3'	TCTTAAGGCTGAAGGA 13058	A CC
		TCCTTCAG CCT AGA	
		AGGAAGTC GGA TCT	
		_ AT	
GAM1462 PKIA	5'	TCTGATAGAAATCTGAAGG 22386	CC ____
		CCTTCAGA TC CAGA	
		GGAAGTCT AG GTCT	
		AA ATA	
GAM1462 PNUTL2	3'	CACATGCAGGACCTGAAGGA 54418	A_ C GA
		TCCTTCAG CCT CA GTG	
		AGGAAGTC GGA GT CAC	
		CA C A_	
GAM1462 PNUTL2	3'	CACATGCAGGACCTGAAGGA 54420	A_ C GA
		TCCTTCAG CCT CA GTG	
		AGGAAGTC GGA GT CAC	
		CA C A_	
GAM1462 PVR	5'	CACCCCAGGCACTGGAGGA 21474	A_ CCAGA
		TCCTTCAG CCT GTG	
		AGGAGGTC GGA CAC	
		AC CCC_	
GAM1462 PYGM	5'	CATGTGCAAGGCCTGGAGGA 18821	A CCAGA
		TCCTTCAG CCT GTG	
		AGGAGGTC GGA TAC	
		C ACGTG	
GAM1462 RAB13	3'	CACCCCGGAAGCTGAACCTGAG 11202	ACC_____ AGA
GGA		TCCTTCAG TCC GTG	
		AGGGAGTC AGG CAC	
		CAAGTCGA CCC	
GAM1462 SH3BP4	3'	TCGAGGGAGAGGCCTGAAGGG 27235	A CAGAG
		TCCTTCAG CCTC TGA	

GGGAAGTC GGAG GCT  
C AGGGA  
GAM1462 SH3GL2 3' TCACCCCAGGGGCCATCTGAAG 11628 \_\_\_\_ CAGA  
G CCTTCAGA CCTC GTGA  
||||||| ||| |||  
GGAAGTCT GGGG CACT  
ACC ACCC  
GAM1462 SIGLEC9 3' CACCCTGATTGAGGGA 62400 ACCTC A  
TCCTTCAG CAG GTG  
||||||| ||| |||  
AGGGAGTT GTC CAC  
A\_\_\_\_ C  
GAM1462 SLC17A2 3' CACTCCAGAGATTCTGAATGA 19544 C C\_ CA  
TC TTCAGA CTC GAGTG  
|| ||||| ||| |||||  
AG AAGTCT GAG CTCAC  
T TA AC  
GAM1462 SNX6 3' TCACTCTGGAAAATGTGGA 41161 TT GACC  
TCC CA TCCAGAGTGA  
||| || |||||  
AGG GT AGGTCTCACT  
T\_ AAA\_  
GAM1462 SOD3 3' CACTCAGTAGGTCTGAAGG 11861 CCA  
CCTTCAGACCT GAGTG  
||||||| |||||  
GGAAGTCTGGA CTCAC  
TGA  
GAM1462 SOX4 3' TCTAGAGACTTGAAGGA 11880 AC C  
TCCTTCAG CTC AGA  
||||||| ||| |||  
AGGAAGTT GAG TCT  
CA A  
GAM1462 TBXAS1 5' CACTCTGGGGTCTCAGAGGA 6508 C\_ T  
TCCTT AGACC CCAGAGTG  
||||| ||||| |||||  
AGGAG TCTGG GGTCTCAC  
AC \_  
GAM1462 TBXAS1 5' CACTCTGGGGTCTCAGAGGA 48292 C\_ T  
TCCTT AGACC CCAGAGTG  
||||| ||||| |||||  
AGGAG TCTGG GGTCTCAC  
AC \_  
GAM1462 TEC 3' TCACTCTGACCCTGGAG 12222 ACCTC  
CTTCAG CAGAGTGA  
||||| |||||  
GAGGTC GTCTCACT  
CCA\_  
GAM1462 TSNAX 3' TCACAGTAGGTCTGATAGA 20003 CT CCAGA  
TC TCAGACCT GTGA  
|| ||||| |||



		AG AGTCTGGA	CACT	
		AT	TGA__	
GAM1462	TXNRD2	5'	CACCCTAGGTCTGAAGG	21235 CC A
			CCTTCAGACCT AG GTG	
			GGAAGTCTGGA TC CAC	
			__ C	
GAM1462	VPS41	3'	CACCTGATGCTGAAGGA	26924 ACCTC A
			TCCTTCAG CAG GTG	
			AGGAAGTC GTC CAC	
			GTA__ _	
GAM1462	WNT2	3'	TCACTTAGAATCTGAAGGG	12658 CC CA
			TCCTTCAGA TC GAGTGA	
			GGGAAGTCT AG TTCACT	
			A_ A_	
GAM1462	WNT3A	3'	CTGGGGAAAGCCTGAAGGG	52431 AC__
			TCCTTCAG CTCCAG	
			GGGAAGTC GGGGTC	
			CGAAA	
GAM1462	WNT8B	3'	CACCTAGGTCTGAG	59595 CC A
			TTCAGACCT AG GTG	
			GAGTCTGGA TC CAC	
			__ _	
GAM1462	ABCC13	3'	CACAGTTCTGAAGGA	56991 C CCAGA
			TCCTTCAGA CT GTG	
			AGGAAGTCT GA CAC	
			T ____	
GAM1462	BAGE	3'	TCATTAATAATCTGAGGGA	6809 CCTCCAG
			TCCTTCAGA AGTGA	
			AGGGAGTCT TTACT	
			AAAA__	
GAM1462	BCKDK	5'	CACCGGGTCTGAAAGG	59792 _ CCAGA
			CCTT CAGACCT GTG	
			GGAA GTCTGGG CAC	
			A C__	
GAM1462	BRAG	5'	CATGGGAAAAACCTGAAGGG	29474 ACC__ AGA
			TCCTTCAG TCC GTG	
			GGGAAGTC AGG TAC	
			CAAAA G__	
GAM1462	C13orf1	3'	TCACTCTGAAGTTTAGA	39975 _ CTC
			TC AGAC CAGAGTGA	

			AG TTTG GTCTCACT		
			A AA_		
GAM1462	C5orf6	5'	TCACAAGTGAGGTCTGGAAGA 33487	C	CAGA
			TC TTCAGACCTC GTGA		
			AG AGGTCTGGAG CACT		
			A TGAA		
GAM1462	CARD9	3'	TCACTCCCCCAGGACCTGGAGG 42291	A_	CCA_
	A		TCCTTCAG CCT GAGTGA		
			AGGAGGTC GGA CTCACT		
			CA CCCC		
GAM1462	CLUL1	5'	CACCCTGGAGGTTGCTGA 26968	__	A
			TCAG ACCTCCAG GTG		
			AGTC TGGAGGTC CAC		
			GT C		
GAM1462	COLEC12	3'	TCACTCTGGAGATAGATGGG 47873	T	AGAC
			TCC TC CTCCAGAGTGA		
			GGG AG GAGGTCTCACT		
			T ATA_		
GAM1462	CXYorf1	5'	TCAGGAGAAGCTGAAGGA 82052	AC_	A
			TCCTTCAG CTCC GA		
			AGGAAGTC GAGG CT		
			GAA A		
GAM1462	DDX34	3'	TCAGAGCTAAGGCCTGAAGGA 27989	A	CC AG_
			TCCTTCAG CCT AG TGA		
			AGGAAGTC GGA TC ACT		
			C A_ GAG		
GAM1462	DEFCAP	5'	CACTCTGGGTTCTGAA 29949	C	T
			TTCAGA C CCAGAGTG		
			AAGTCT G GGTCTCAC		
			T _		
GAM1462	DEFCAP	5'	CTGGAGAGGTCTGAAG 29951	__	
			CTTCAGACC TCCAG		
			GAAGTCTGG AGGTC		
			AG		
GAM1462	DEFCAP	5'	CACTCTGGGTTCTGAA 52229	C	T
			TTCAGA C CCAGAGTG		
			AAGTCT G GGTCTCAC		
			T _		
GAM1462	DEFCAP	5'	CTGGAGAGGTCTGAAG 52231	__	
			CTTCAGACC TCCAG		

			GAAGTCTGG AGGTC		
			AG		
GAM1462	DEPP	3'	TCTGGAGTCTGAAGGA 22825	C	
			TCCTTCAGAC TCCAGA		
			AGGAAGTCTG AGGTCT		
			—		
GAM1462	DKFZP434F0318	3'	TCACTTTGGGGTCTGTAAG 48014	—	T
			CTT CAGACC CCAGAGTGA		
			GAA GTCTGG GGTTTCACT		
			T —		
GAM1462	DKFZP434O047	5'	CACCCTGGAGACTTGGAGGA 31505	AC	A
			TCCTTCAG CTCCAG GTG		
			AGGAGGTT GAGGTC CAC		
			CA C		
GAM1462	DKFZP586F1524	3'	CACAGGCCTGGAGGA 31488	A	CCAGA
			TCCTTCAG CCT GTG		
			AGGAGGTC GGA CAC		
			C —		
GAM1462	DKFZp586I021	3'	CACTCTGGCCGGAGGAAGGA 50087	AGA	T_
			TCCTTC CC CCAGAGTG		
			AGGAAG GG GGTCTCAC		
			GA_ CC		
GAM1462	DOCK3	3'	TCACTCCAGGTCTGAA 66507	CCA	
			TTCAGACCT GAGTGA		
			AAGTCTGGA CTCACT		
			C_		
GAM1462	DONSON	3'	TCTTGAAGTTGAAGGA 34307	A C	C
			TCCTTCAG C TC AGA		
			AGGAAGTT G AG TCT		
			_ A T		
GAM1462	FBXO27	3'	CACTCTGGTTTCTCTGAA 74505	CCT_	
			TTCAGA CCAGAGTG		
			AAGTCT GGTCTCAC		
			CTTT		
GAM1462	FLJ00024	3'	CACTCTGGAGGCTGGG 63751	A	
			TTCAG CCTCCAGAGTG		
			GGGTC GGAGGTCTCAC		
			—		
GAM1462	FLJ10193	3'	CATAGGCTAGGTCTGAA 35882	—	AGA
			TTCAGACCT CC GTG		

	AAGTCTGGA GG TAC	
	TC A__	
GAM1462 FLJ10718 3'	CACTTTGGGTCTGAGG 36490	TC
	CTTCAGACC CAGAGTG	
	GGAGTCTGG GTTTCAC	
	—	
GAM1462 FLJ11722 3'	TCACTCTGCCAATGAGGGA 46399	GACCTC
	TCCTTCA CAGAGTGA	
	AGGGAGT GTCTCACT	
	AACC__	
GAM1462 FLJ12517 3'	TCACCTGGGCCTGAGGGA 43438	ACC A
	TCCTTCAG TCCAG GTGA	
	AGGGAGTC GGGTC CACT	
	C__ _	
GAM1462 FLJ12691 3'	CTCTGGAGGCCAGAAAGA 44702	C AGA
	TC TTC CCTCCAGAG	
	AG AAG GGAGGTCTC	
	A ACC	
GAM1462 FLJ13072 5'	TCACTCTGGCCAAAGAGAGA 89825	C AGACCT
	TC TTC CCAGAGTGA	
	AG GAG GGTCTCACT	
	A AAACC_	
GAM1462 FLJ20085 5'	CACGGTGGCCTTGAAGGA 34513	ACCT GA
	TCCTTCAG CCA GTG	
	AGGAAGTT GGT CAC	
	CC__ GG	
GAM1462 FLJ20232 3'	TCAGGACAAGGCCTTGAAGGA 38676	A_ __ A
	TCCTTCAG CC TCC GA	
	AGGAAGTT GG AGG CT	
	CC AAC A	
GAM1462 FLJ20477 5'	TCTGGGAGGCCTGAGGGA 35243	A _
	TCCTTCAG CCTCC AGA	
	AGGGAGTC GGAGG TCT	
	C G	
GAM1462 FLJ20514 3'	CACTTGAGGTCTGCAGGA 35337	T G
	TCCT CAGACCTCCA AGTG	
	AGGA GTCTGGAGGT TCAC	
	C _	
GAM1462 FLJ20695 5'	TCACTCCGACGTCTGAGG 35561	C CA
	CTTCAGAC TC GAGTGA	

			GGAGTCTG AG CTC	ACT	
			C C_		
GAM1462	FLJ23186	3'	TC	ACTCTGTTTTGCAG	60406 T CCTC
				CT CAGA CAGAGTGA	
				GA GTTT GTCTCACT	
				C T__	
GAM1462	FTSJ3	3'	TC	CAGCTGTCTGAAG	34457 CTCC A_
				CTTCAGAC AG GTGA	
				GAAGTCTG TC CACT	
				__ GA	
GAM1462	GPS2	5'	CAC	GGGCCTGAAGGG	87152 A CCAGA
				TCCTTCAG CCT GTG	
				GGGAAGTC GGG CAC	
				C ____	
GAM1462	H2AV	3'	TC	ACTCTGATCTCTGAATGA	56859 C CCTC
				TC TTCAGA CAGAGTGA	
				AG AAGTCT GTCTCACT	
				T CTA_	
GAM1462	HCGIX	3'	TCT	GGAAGCTGAAGGA	19574 ACC
				TCCTTCAG TCCAGA	
				AGGAAGTC AGGTCT	
				GA_	
GAM1462	HRIHFB2122	3'	CACA	AGGAGGTCTGCAGGA	56835 T AGA
				TCCT CAGACCTCC GTG	
				AGGA GTCTGGAGG CAC	
				C AA_	
GAM1462	HSZFP36	3'	CA	CTCTGGAGAGAAG	63481 AGAC
				CTTC CTCCAGAGTG	
				GAAG GAGGTCTCAC	
				A__	
GAM1462	IL-17RE	3'	CAT	GTCAGTTCTGAAGGA	58290 C CCAGA
				TCCTTCAGA CT GTG	
				AGGAAGTCT GA TAC	
				T CTG__	
GAM1462	KIAA0089	3'	CACC	CTGGACTTCTGAAGGG	69964 CC A
				TCCTTCAGA TCCAG GTG	
				GGGAAGTCT AGGTC CAC	
				TC C	
GAM1462	KIAA0296	3'	TC	CCTGAAAGCTGAAGGA	28118 ACCTC A
				TCCTTCAG CAG GTGA	

			AGGAAGTC	GTC CACT	
			GAAA_ _		
GAM1462	KIAA0350	3'	CACTGAGCACTGAAGGA	61167	AC CAG
			TCCTTCAG CTC AGTG		
			AGGAAGTC GAG TCAC		
			AC _		
GAM1462	KIAA0446	5'	CACTCTGGGGCAGAAG	68856	AGAC
			CTTC CTCCAGAGTG		
			GAAG GGGGTCTCAC		
			AC_		
GAM1462	KIAA0565	3'	TCACTCTGGAAAGGCGGGA	66898	TCAGA _
			TCCT CC TCCAGAGTGA		
			AGGG GG AGGTCTCACT		
			C_ AA		
GAM1462	KIAA1164	3'	TCACTCTGTTGGCTGAAGGA	69509	A TC
			TCCTTCAG CC CAGAGTGA		
			AGGAAGTC GG GTCTCACT		
			_ TT		
GAM1462	KIAA1237	3'	CACTGAAGTCTGAAG	80465	C CAG
			CTTCAGAC TC AGTG		
			GAAGTCTG AG TCAC		
			A _		
GAM1462	KIAA1266	3'	TCAGGCCAGGTCTGAAG	66128	_ A
			CTTCAGACCT CC GA		
			GAAGTCTGGA GG CT		
			CC A		
GAM1462	KIAA1319	3'	CACTCTGGAGCAGGG	40404	TCAGAC
			TCCT CTCCAGAGTG		
			GGA GAGGTCTCAC		
			C_		
GAM1462	KIAA1466	3'	TCACTCTGGAGGCTGG	71918	A
			TCAG CCTCCAGAGTGA		
			GGTC GGAGGTCTCACT		
			_		
GAM1462	KIAA1786	3'	TCACATGGAGGTTGAAGGA	66039	A GA
			TCCTTCAG CCTCCA GTGA		
			AGGAAGTT GGAGGT CACT		
			_ A_		
GAM1462	KIAA1786	3'	TCACTCTCTCACTCTGATGGA	66040	T CCTCC
			TCC TCAGA AGAGTGA		

		AGG AGTCT TCTCACT		
		T CACTC		
GAM1462	LANCL2	3' TCATTTTAAAATCTGAAGGA	38002	CCTCC
		TCCTTCAGA AGAGTGA		
		AGGAAGTCT TTTTACT		
		AAAA_		
GAM1462	MEP50	3' TCACTCTGAGGAAGAAG	44083	AGA C
		CTTC CCTC AGAGTGA		
		GAAG GGAG TCTCACT		
		AA_ _		
GAM1462	MGC10715	3' TCACTCACCTCTGAGGGA	44251	CCTCCA
		TCCTTCAGA GAGTGA		
		AGGGAGTCT CTCACT		
		CCA__		
GAM1462	MGC10960	3' TCACTCTGGTGTCTCTGGA	51011	TTCA CT
		TCC GAC CCAGAGTGA		
		AGG CTG GGTCTCACT		
		TC__ T_		
GAM1462	MGC14161	5' CAAGCTGAAATTTGAAGGA	51838	CCTC AG
		TCCTTCAGA CAG TG		
		AGGAAGTTT GTC AC		
		AAA_ GA		
GAM1462	MGC16025	3' TCTGAGAAAAGTTTGAAG	51925	C__ _
		CTTCAGAC TC CAGA		
		GAAGTTTG AG GTCT		
		AAA A		
GAM1462	MGC20781	3' TCACCAGAGGCTTGAAGGA	53624	GA CAGA
		TCCTTCA CCTC GTGA		
		AGGAAGT GGAG CACT		
		TC AC__		
GAM1462	MGC2628	3' CTAGAGGCTGAAGGA	43971	A C
		TCCTTCAG CCTC AG		
		AGGAAGTC GGAG TC		
		_ A		
GAM1462	MGC2663	3' TCACTCTGGAGAGAAGAAG	44096	AGAC
		CTTC CTCCAGAGTGA		
		GAAG GAGGTCTCACT		
		AAGA		
GAM1462	MGC26766	3' CATGAAGAGCTGAAGGA	58819	AC CAGA
		TCCTTCAG CTC GTG		

			AGGAAGTC GAG TAC		
			__ AAG__		
GAM1462	MGC2963	5'	CACTGCCCGTCTGAGGGA 48509	CTCCAG	
			TCCTTCAGAC AGTG		
			AGGGAGTCTG TCAC		
			CCCG__		
GAM1462	MGC3146	3'	CACTCTGTCTCTGAGGGA 48439	CCTC	
			TCCTTCAGA CAGAGTG		
			AGGGAGTCT GTCTCAC		
			CT__		
GAM1462	MGC4368	5'	CTTGGGGAGACCTGGAGGA 44460	AC A_	
			TCCTTCAG CTCC GAG		
			AGGAGGTC GAGG TTC		
			CA GG		
GAM1462	NPC1L1	3'	CACCCAGGAGTCTGAAGG 25411	C AGA	
			CCTTCAGAC TCC GTG		
			GGAAGTCTG AGG CAC		
			_ ACC		
GAM1462	PGR1	3'	TCTGGAGGTGCTGAAGGA 52757	_	
			TCCTTCAG ACCTCCAGA		
			AGGAAGTC TGGAGGTCT		
			G		
GAM1462	PILR(ALPHA)	5'	TCACCCTGGAGGTGCACTGG 25550	___ A	
			TCAG ACCTCCAG GTGA		
			GGTC TGGAGGTC CACT		
			ACG C		
GAM1462	PILR(BETA)	5'	TCACCCTGGAGGTGTACTGG 25555	___ A	
			TCAG ACCTCCAG GTGA		
			GGTC TGGAGGTC CACT		
			ATG C		
GAM1462	PIP5K2B	3'	CATAGGTAGGTCTGAA 13065	_ AGA	
			TTCAGACCT CC GTG		
			AAGTCTGGA GG TAC		
			T A__		
GAM1462	PIP5K2B	3'	CATAGGTAGGTCTGAA 13066	_ AGA	
			TTCAGACCT CC GTG		
			AAGTCTGGA GG TAC		
			T A__		
GAM1462	PLPL	3'	TCACTCTGTGGTCCAAAAGG 39434	CA_ TC	
			CCTT GACC CAGAGTGA		



			GGAA CTGG GTCTCACT		
			AAC T_		
GAM1462 PNMA3	3'	CACATGGGACCTGGAGGA	25343	ACT GA	
		TCCTTCAG C CCA GTG			
		AGGAGGTC G GGT CAC			
		CA_ A_			
GAM1462 PNMA5	3'	CACGTGGGACCTGGAGGA	73592	ACC AGA	
		TCCTTCAG TCC GTG			
		AGGAGGTC AGG CAC			
		C_ GTG			
GAM1462 PRO0082	3'	TCACTCTGATTTGAG	37737	CCTC	
		TTCAGA CAGAGTGA			
		GAGTTT GTCTCACT			
		A_			
GAM1462 PTK9	3'	TCACTCTGAACTTTAAGGG	11027	C CCTC	
		TCCTT AGA CAGAGTGA			
		GGGAA TTT GTCTCACT			
		_ CAAA			
GAM1462 RoXaN	3'	CTGAGGCCTGGAGGA	46642	A C	
		TCCTTCAG CCTC AG			
		AGGAGGTC GGAG TC			
		C _			
GAM1462 STK3	3'	CACTAGGAATTGAAGGA	73718	ACC AG	
		TCCTTCAG TCC AGTG			
		AGGAAGTT AGG TCAC			
		A_ A_			
GAM1462 TBX4	3'	TCTGAGGTCTGAGGGA	37496	C	
		TCCTTCAGACCTC AGA			
		AGGGAGTCTGGAG TCT			
		-			
GAM1462 TRIAD3	3'	TCACTCTGGCCATTGACAGA	94508	CT ACCT	
		TC TCAG CCAGAGTGA			
		AG AGTT GGTCTCACT			
		AC ACCC			
GAM1462 UQCR	3'	CACTTCGTCTGAGGA	22408	T CTCCA	
		TCCT CAGAC GAGTG			
		AGGA GTCTG TTCAC			
		- C_			
GAM1462 LOC115219	3'	TCACCCTGGTCTGAAGG	73319	TCC A	
		CCTTCAGACC AG GTGA			

		GGAAGTCTGG TC CACT	
		___ C	
GAM1462	LOC124602 3'	TCACCCGGCTCCTGAAGGA 74309	ACCT AGA
		TCCTTCAG CC GTGA	
		AGGAAGTC GG CACT	
		CTC_ CC_	
GAM1462	LOC138389 3'	CACCAGGGAGTCTGAGG 76218	C AGA
		CTTCAGAC TCC GTG	
		GGAGTCTG AGG CAC	
		_ GAC	
GAM1462	LOC144305 3'	TCTGAAAAATCTGAAGG 83038	CC__
		CCTTCAGA TCCAGA	
		GGAAGTCT AGGTCT	
		AAAA	
GAM1462	LOC144308 3'	CACCTCGTGGTCTGAAG 83043	TCC A
		CTTCAGACC AG GTG	
		GAAGTCTGG TC CAC	
		TGC _	
GAM1462	LOC145317 5'	CACTCTGTGACTGAAGGG 83320	ACC _
		TCCTTCAG TC CAGAGTG	
		GGGAAGTC AG GTCTCAC	
		___ T	
GAM1462	LOC147837 3'	CACTCTGGAGAGAAG 78513	AGAC
		CTTC CTCCAGAGTG	
		GAAG GAGGTCTCAC	
		A__	
GAM1462	LOC147949 5'	CACAGAGGAGCTGAAGGA 78580	AC AGA
		TCCTTCAG CTCC GTG	
		AGGAAGTC GAGG CAC	
		_ AGA	
GAM1462	LOC148789 5'	CACCCGCGGTCTGAGGGA 78992	TCCAGA
		TCCTTCAGACC GTG	
		AGGGAGTCTGG CAC	
		CGCC__	
GAM1462	LOC149606 3'	TCACTCTGGAGGCAGG 79456	TCAGA
		CCT CCTCCAGAGTGA	
		GGA GGAGGTCTCACT	
		C__	
GAM1462	LOC149837 3'	CACTCTGGGAGAGGGA 84729	AGACC
		TCCTTC TCCAGAGTG	

	AGGGAG GGGTCTCAC	
	A_____	
GAM1462 LOC150248 5'	CTGGAGGAGGACCTGAAGGA 84944	A_____
	TCCTTCAG CCTCCAG	
	AGGAAGTC GGAGGTC	
	CAGGA	
GAM1462 LOC151475 5'	CTCCCAGAATCTGAAGGA 85401	CC CA_
	TCCTTCAGA TC GAG	
	AGGAAGTCT AG CTC	
	A_ ACC	
GAM1462 LOC152674 3'	TCAGACTGAAGTTGAAGGA 85840	AC C AG
	TCCTTCAG CT CAG TGA	
	AGGAAGTT GA GTC ACT	
	__ A AG	
GAM1462 LOC153222 5'	TCTGTAGAAGACCTGAAGGA 80790	AC___ C
	TCCTTCAG CT CAGA	
	AGGAAGTC GA GTCT	
	CAGAA T	
GAM1462 LOC153328 3'	TCACTCCTCTGTCTGAGG 80809	CTCCA
	CTTCAGAC GAGTGA	
	GGAGTCTG CTCACT	
	TCTC_	
GAM1462 LOC157273 3'	CTGGATGAGTCTGAAGGA 86429	C__
	TCCTTCAGAC TCCAG	
	AGGAAGTCTG AGGTC	
	AGT	
GAM1462 LOC157556 3'	CACCCTGGGCTTGAAGGG 86480	ACC A
	TCCTTCAG TCCAG GTG	
	GGGAAGTT GGGTC CAC	
	C__ C	
GAM1462 LOC157739 3'	CACCCTGGAGGTCATGGAGG 81581	_ A
	CCTTCA GACCTCCAG GTG	
	GGAGGT CTGGAGGTC CAC	
	A C	
GAM1462 LOC158401 5'	TCACTCTCAGAACTGAAGGA 81921	AC CC
	TCCTTCAG CT AGAGTGA	
	AGGAAGTC GA TCTCACT	
	AA C_	
GAM1462 LOC162048 5'	TCACTCTGGGGTGAAG 82329	GAC
	CTTCA CTCCAGAGTGA	

GAAGT GGGGTCTCACT

GAM1462 LOC162083 3' CACTAGGTACCAGAAGGA 82335 AG\_\_ CCAG  
TCCTTC ACCT AGTG  
||||| ||| |||  
AGGAAG TGGA TCAC  
ACCA \_\_\_\_

GAM1462 LOC164295 3' TCAAGGCGGGAGGACTGAAGGA 82511 A AGAG\_  
TCCTTCAG CCTCC TGA  
||||||| ||||| |||  
AGGAAGTC GGAGG ACT  
A GCGGA

GAM1462 LOC167040 5' TGGAGGAACCCTGAAGGA 87269 A\_\_\_\_  
TCCTTCAG CCTCCA  
||||||| |||||  
AGGAAGTC GGAGGT  
CCAA

GAM1462 LOC200058 3' TCTGCGAGACCTGAAGGA 88559 AC \_  
TCCTTCAG CTC CAGA  
||||||| ||| |||  
AGGAAGTC GAG GTCT  
CA C

GAM1462 LOC200093 5' TCAGGAGAAGCTGAAGGA 63100 AC\_ A  
TCCTTCAG CTCC GA  
||||||| ||| ||  
AGGAAGTC GAGG CT  
GAA A

GAM1462 LOC200728 3' TCACTCTGAAATTCCAAGG 90118 CA CCTC  
CCTT GA CAGAGTGA  
||| || |||||  
GGAA CT GTCTCACT  
C\_ TAAA

GAM1462 LOC200982 3' CACTCCTGGCTGAGGGA 90215 A TCCA  
TCCTTCAG CC GAGTG  
||||||| || |||||  
AGGGAGTC GG CTCAC  
\_ TC\_\_

GAM1462 LOC201477 5' TCAACTGAGGTCTGTAAG 89785 \_ C AG  
CTT CAGACCTC AG TGA  
||| ||||| || |||  
GAA GTCTGGAG TC ACT  
T \_ A\_

GAM1462 LOC201707 5' CTGAGGTTCTGAAGGA 89035 \_ C  
TCCTTCAGA CCTC AG  
||||||| ||||| |||  
AGGAAGTCT GGAG TC  
T \_

GAM1462 LOC203397 3' TCACCCGGCTCCTGAAGGA 89353 ACCT AGA  
TCCTTCAG CC GTGA  
||||||| || |||

	AGGAAGTC GG CACT		
	CTC_ CC_		
GAM1462 LOC203557 5'	TCTGAAAGGCCTGAGGGA 89514	A C_	
	TCCTTCAG CCT CAGA		
	AGGGAGTC GGA GTCT		
	C AA		
GAM1462 LOC206426 3'	TCTTAAGGCTGAAGGA 89538	A CC	
	TCCTTCAG CCT AGA		
	AGGAAGTC GGA TCT		
	_ AT		
GAM1462 LOC206480 5'	CACTCTGGAGAGAGCAGAAG 90717	AGAC__	
	CTTC CTCCAGAGTG		
	GAAG GAGGTCTCAC		
	ACGAGA		
GAM1462 LOC219287 3'	TCTAGAGGCCTGAAGGA 93572	A C	
	TCCTTCAG CCTC AGA		
	AGGAAGTC GGAG TCT		
	C A		
GAM1462 LOC219700 5'	CGCTACGGTCTGAGAGA 93062	C TCCAG	
	TC TTCAGACC AGTG		
	AG GAGTCTGG TCGC		
	A CA__		
GAM1462 LOC219940 3'	TCACCTGGTGGTCTGAGG 93358	T A	
	CTTCAGACC CCAG GTGA		
	GGAGTCTGG GGTC CACT		
	T _		
GAM1462 LOC221218 5'	CTGGAAGACCTGGAGGA 91761	AC _	
	TCCTTCAG CT CCAG		
	AGGAGGTC GA GGTC		
	CA A		
GAM1462 LOC253250 3'	TCACTTTGCAAATCTGAA 94705	CCTC	
	TTCAGA CAGAGTGA		
	AAGTCT GTTTCACT		
	AAAC		
GAM1462 LOC253805 3'	CTAGGGAGGTCTGAAGGA 96428	AG	
	TCCTTCAGACCTCC AG		
	AGGAAGTCTGGAGG TC		
	GA		
GAM1462 LOC254173 3'	CAACTGCGAGGTCCTGAAGGA 96840	_ _ AG	
	TCCTTCAG ACCTC CAG TG		

	AGGAAGTC TGGAG GTC AC	
	C C A_	
GAM1462 LOC254746 3'	TCACCCTGGAGGTGGAG 95142	AG A
	CTTC ACCTCCAG GTGA	
	GAGG TGGAGGTC CACT	
	_ C	
GAM1462 LOC256207 3'	TCACTCTGGAAAGGCGGGA 95177	TCAGA _
	TCCT CC TCCAGAGTGA	
	AGGG GG AGGTCTCACT	
	C_ AA	
GAM1462 LOC257127 3'	TGGAGGCTCTGAAGGA 96674	_
	TCCTTCAGA CCTCCA	
	AGGAAGTCT GGAGGT	
	C	
GAM1462 LOC54550 5'	TCACTCTGTCCTGAAGG 77691	ACCTC
	CCTTCAG CAGAGTGA	
	GGAAGTC GTCTCACT	
	CT_	
GAM1462 LOC90297 3'	CTGGAGGCCTGGAGGA 62158	A
	TCCTTCAG CCTCCAG	
	AGGAGGTC GGAGGTC	
	C	
GAM1462 LOC90835 5'	CACTTCCCAGCCTGGAGGA 64125	AC CCA
	TCCTTCAG CT GAGTG	
	AGGAGGTC GA TTCAC	
	C_ CCC	
GAM1462 LOC90936 5'	CATGGACTGGACCTGAAGGA 64432	ACC A_
	TCCTTCAG TCCAG GTG	
	AGGAAGTC AGGTC TAC	
	C_ AGG	
GAM1462 LOC91250 5'	TCACTCTTTGCTATTGAAGGA 65327	ACCTCC
	TCCTTCAG AGAGTGA	
	AGGAAGTT TCTCACT	
	ATCGTT	
GAM1462 LOC91974 5'	TCACTCTGAAAGCTGGTTGAAG 67760	A TC_
GA	TCCTTCAG CC CAGAGTGA	
	AGGAAGTT GG GTCTCACT	
	_ TCGAAA	
GAM1462 LOC92078 3'	CTGAAGGCTGAAGGA 67981	A C
	TCCTTCAG CCT CAG	

			AGGAAGTC GGA GTC		
			— A		
GAM1462	LOC92391	3'	TCACTCTTCATTCTTTGAAGGA 69160		CCTCC_
			TCCTTCAGA AGAGTGA		
			AGGAAGTTT TCTCACT		
			CTTACT		
GAM1463	ABCC1	3'	CACCCCGACTCCAGGC 39131	ACC	AA
			GCCTGGAG TC GGTG		
			CGGACCTC AG CCAC		
			— CC		
GAM1463	ABCC1	3'	CACCCCGACTCCAGGC 17178	ACC	AA
			GCCTGGAG TC GGTG		
			CGGACCTC AG CCAC		
			— CC		
GAM1463	ABCC1	3'	CACCCCGACTCCAGGC 39123	ACC	AA
			GCCTGGAG TC GGTG		
			CGGACCTC AG CCAC		
			— CC		
GAM1463	BCL7B	3'	CATCTGTGACCTCCAGGCA 8130	ACC	_
			TGCCTGGAG TCA AGGTG		
			ACGGACCTC AGT TCTAC		
			C_ G		
GAM1463	DNASE1	5'	CCTTGGGGCCCCCAGACA 17824	C	AGA
			TG CTGG CCTCAAGG		
			AC GACC GGGGTTCC		
			A CCC		
GAM1463	FOXD2	3'	TATTTATGAAGTCTCCAG 15569	C	AGG
			CTGGAGAC TCA TGAATA		
			GACCTCTG AGT ATTTAT		
			A _		
GAM1463	GABRA3	3'	TACCCCGTGAAGCATCCAGGCA 5868	GACC	A_
			TGCCTGGA TCA GGTG		
			ACGGACCT AGT CCAT		
			ACGA GCC		
GAM1463	HOXA3	3'	CACCCAGGTCTCCAGCA 47686	C	CAA
			TGC TGGAGACCT GGTG		
			ACG ACCTCTGGA CCAC		
			_ C_		
GAM1463	KLHL3	3'	TCTTGACATCCCCAGGCA 87468	A	CC
			TGCCTGG GA TCAAGG		

		ACGGACC CT AGTTCT		
		C AC		
GAM1463 LENG4	5'	CACCTTCCTACCCTACAGGCA 44161	G	ACCTC_
		TGCCTG AG AAGGTG		
		ACGGAC TC TTCCAC		
		A CCATCC		
GAM1463 NFYA	3'	TATTCAGAGATGGCTTCCAGGC 41354	GA	_ AAGG
A		TGCCTGGA CC TC TGAATA		
		ACGGACCT GG AG ACTTAT		
		TC T AG__		
GAM1463 NFYA	3'	TATTCAGAGATGGCTTCCAGGC 10219	GA	_ AAGG
A		TGCCTGGA CC TC TGAATA		
		ACGGACCT GG AG ACTTAT		
		TC T AG__		
GAM1463 NOS1	5'	CATTGTGAGGTCTTCAGACA 5245	C	AG
		TG CTGGAGACCTCA GTG		
		AC GACTTCTGGAGT TAC		
		A GT		
GAM1463 NT5C3	5'	TATTCACCTTGAAGAGG 33236	___	
		CCTC AAGGTGAATA		
		GGAG TTCCAATTAT		
		AAG		
GAM1463 PCSK1	3'	TTACAAAGTCTCCAGTCA 4779	C	CTCAAG
		TG CTGGAGAC GTGA		
		AC GACCTCTG CATT		
		T AAA__		
GAM1463 PDE6D	5'	GCCCGAGGTCTCCAAGC 10492	C	AA
		GC TGGAGACCTC GGT		
		CG ACCTCTGGAG CCG		
		A C_		
GAM1463 PLA2G2A	5'	ATTCACCTGCCCTGTCTCCA 4318	CTCA	_
		TGGAGAC AGGTGAAT		
		ACCTCTG TCCACTTA		
		TCCCG		
GAM1463 RBBP2	3'	ATTCACAAGTATTCCAGACA 17319	C	AC CAAG
		TG CTGGAG CT GTGAAT		
		AC GACCTT GA CACTTA		
		A AT A__		
GAM1463 SIRPB2	5'	GCTTCTGAGGTCTCCA 37665	_	
		TGGAGACCTCA AGGT		



			ACCTCTGGAGT TTCG		
			C		
GAM1463	SIRPB2	5'	GCTTCTGAGGTCTCCA	55029	—
			TGGAGACCTCA AGGT		
			ACCTCTGGAGT TTCG		
			C		
GAM1463	ZNF26	5'	TGCCAAAATTTCCAGGCA	72984	CCTCAA
			TGCCTGGAGA GGTG		
			ACGGACCTTT CCGT		
			AAAA_		
GAM1463	AFAP	3'	CACTGGAGGTCTCCAGGCA	41300	AA
			TGCCTGGAGACCTC GGTG		
			ACGGACCTCTGGAG TCAC		
			G_		
GAM1463	APPD	3'	CCCAGGTCTCCAGACA	44214	C CAA
			TG CTGGAGACCT GG		
			AC GACCTCTGGA CC		
			A C_		
GAM1463	C22orf20	3'	ATTCACCTCAGCCCCCAGGCA	47426	AGAC CA
			TGCCTGG CT AGGTGAAT		
			ACGGACC GA TCCACTTA		
			CCCC C_		
GAM1463	DKFZp547H236	3'	CACCGGCAAGGCCTCCAGGC	78539	A CAA_
			GCCTGGAG CCT GGTG		
			CGGACCTC GGA CCAC		
			C ACGG		
GAM1463	DKFZP586C1619	3'	TATTCACCAAAAGCCCCAGGCA	61937	AGAC CAA
			TGCCTGG CT GGTGAATA		
			ACGGACC GA CCACTTAT		
			CC_ AAA		
GAM1463	FLJ12517	3'	CACCAGGGCCTCCAGGCA	43436	A CAA
			TGCCTGGAG CCT GGTG		
			ACGGACCTC GGG CCAC		
			C A_		
GAM1463	FLJ21324	5'	CATCTTGAGATCACCAGGCA	91194	A C
			TGCCTGG GA CTCAAGGTG		
			ACGGACC CT GAGTTCTAC		
			A A		
GAM1463	FLJ21865	3'	CACCGGGAAGACCTCCAGGC	42806	AC _ AA
			GCCTGGAG CT C GGTG		

		CGGACCTC GA G CCAC	
		CA A GG	
GAM1463	FLJ31528	3' GCTGCTACAGTCTCCAGGCA 58376	CTCAA_
		TGCCTGGAGAC GGT	
		ACGGACCTCTG TCG	
		ACATCG	
GAM1463	GGA2	3' CACTCGCGGAAATTCTCCAGGC 56872	CC_ AA_
	A	TGCCTGGAGA TC GGTG	
		ACGGACCTCT AG TCAC	
		TAA GCGC	
GAM1463	H2AV	3' TGAGGATCTCCAGGCA 56860	_
		TGCCTGGAGA CCTCA	
		ACGGACCTCT GGAGT	
		A	
GAM1463	HRI	3' CACCCCAGATGATCTCCAGGCA 26978	CC_ AA_
		TGCCTGGAGA TC GGTG	
		ACGGACCTCT AG CCAC	
		AGT ACC	
GAM1463	KIAA0316	3' CAGCTTAAAGTGTCCAGGCA 69670	G CTC G
		TGCCTGGA AC AAG TG	
		ACGGACCT TG TTC AC	
		G AAA G	
GAM1463	MEIS3	3' CACCGGCAAGGCCTCCAGGC 78276	A CAA_
		GCCTGGAG CCT GGTG	
		CGGACCTC GGA CCAC	
		C ACGG	
GAM1463	MGC4251	3' TCACCTTGAGAGTAGAGCA 50461	_ GGAG _
		TGC CT AC CTCAAGGTGA	
		ACG GA TG GAGTTCCACT	
		A _ _ A	
GAM1463	NFASC	3' GCCTTGAAGCCTCCAGCA 70345	C ACC
		TGC TGGAG TCAAGGT	
		ACG ACCTC AGTTCCG	
		_ CGA	
GAM1463	NPC1L1	3' TCTTGAGGTATCCAGGCA 25416	G
		TGCCTGGA ACCTCAAGG	
		ACGGACCT TGGAGTTCT	
		A	
GAM1463	POLM	3' CACTGAATGTCTCCAGGCA 91087	CTCAA
		TGCCTGGAGAC GGTG	

			ACGGACCTCTG	TCAC	
			TAAG_		
GAM1463	REC14	3'	CATCAAAGTCTCCAGGC	47448	CTCAA
			GCCTGGAGAC	GGTG	
			CGGACCTCTG	CTAC	
			AAA_		
GAM1463	RRN3	3'	CACTGAAGATCTCCAGG	37353	C CAA
			CCTGGAGA CT	GGTG	
			GGACCTCT GA	TCAC	
			A AG_		
GAM1463	STMN4	3'	TTGAGCCTCCAGGCA	47929	AC
			TGCCTGGAG	CTCAA	
			ACGGACCTC	GAGTT	
			C_		
GAM1463	ULK2	3'	TATTCACCCCTCATCCAGGCA	28008	GACCTCAA
			TGCCTGGA	GGTGAATA	
			ACGGACCT	CCACTTAT	
			ACTCC_		
GAM1463	LOC115708	3'	CCTTGAGCCTCCAGGCA	73548	AC
			TGCCTGGAG	CTCAAGG	
			ACGGACCTC	GAGTTCC	
			C_		
GAM1463	LOC118491	5'	TTCATGAGGCCTCCAAACA	73918	CC A AGG
			TG TGGAG CCTCA	TGAA	
			AC ACCTC GGAGT	ACTT	
			AA C _		
GAM1463	LOC133993	5'	CAGCTAAGGTCTCCAGGC	75929	CA G
			GCCTGGAGACCT	AG TG	
			CGGACCTCTGGA	TC AC	
			A_ G		
GAM1463	LOC134266	3'	TGCAATGAAGTCTCCAGCA	75170	C C AG
			TGC TGGAGAC TCA	GTG	
			ACG ACCTCTG AGT	CGT	
			_ A AA		
GAM1463	LOC155376	5'	ATTCACCCAGGATCTCCAGG	81334	_ CAA
			CCTGGAGA CCT	GGTGAAT	
			GGACCTCT GGA	CCACTTA	
			A C_		
GAM1463	LOC165904	3'	CACTGTGAGGTCTCCAG	82607	A
			CTGGAGACCTCA	GGTG	

	GACCTCTGGAGT TCAC		
	G		
GAM1463 LOC197414 3'	CACCCAGGTGTCCAGGCA 88062	G	CAA
	TGCCTGGA ACCT GGTG		
	ACGGACCT TGGA CCAC		
	G C__		
GAM1463 LOC204200 5'	CACCTCTGAAAAGGTCTCCAAG 90661	C	__ _
C	GC TGGAGACCT CA AGGTG		
	CG ACCTCTGGA GT TCCAC		
	A AAG C		
GAM1463 LOC222233 5'	ATTCACCCAGGATCTCCAGG 94251	_	CAA
	CCTGGAGA CCT GGTGAAT		
	GGACCTCT GGA CCACTTA		
	A C__		
GAM1463 LOC253532 5'	ATTCACCCAGGATCTCCAGG 96026	_	CAA
	CCTGGAGA CCT GGTGAAT		
	GGACCTCT GGA CCACTTA		
	A C__		
GAM1463 LOC254028 3'	ATTCACCTCATTTTCCCAG 96538	A	CCTCA
	CTGG GA AGGTGAAT		
	GACC CT TCCACTTA		
	_ TTTAC		
GAM1463 LOC254428 3'	TACCCAGACCTCCAGGC 95463	AC	CAA
	GCCTGGAG CT GGTG		
	CGGACCTC GA CCAT		
	CA C__		
GAM1463 LOC254875 5'	ATTCACCCAGGATCTCCAGG 96056	_	CAA
	CCTGGAGA CCT GGTGAAT		
	GGACCTCT GGA CCACTTA		
	A C__		
GAM1463 LOC256306 5'	GCCCAAGGTCTCCAGCA 96690	C	CAA
	TGC TGGAGACCT GGT		
	ACG ACCTCTGGA CCG		
	_ AC__		
GAM1463 LOC257468 3'	CACCGGCAAGGCCTCCAGGC 95183	A	CAA_
	GCCTGGAG CCT GGTG		
	CGGACCTC GGA CCAC		
	C ACGG		
GAM1463 LOC51226 3'	CCTAAGGTCTCCAGCCA 33151	C	CA
	TG CTGGAGACCT AGG		

AC GACCTCTGGA TCC  
 C A\_  
 GAM1464 AQP3 3' TTCACGATCCACCCTTTC 59593 T\_ \_  
 GAAA GTGG TCGTGAA  
 |||| ||| |||||  
 CTTT CACC AGCACTT  
 CC T  
 GAM1464 ARSB 3' TCACGACTCTTGTC 3502 AATGTG  
 GACAAGA GTCGTGA  
 ||||| |||||  
 CTGTTCT CAGCACT  
  
 GAM1464 B4GALT5 3' TTTTCACAAAAATAGTCCTTTG 16519 AAA\_ GGTC  
 TCA TGACAAG TGT GTGAAAA  
 ||||| || |||||  
 ACTGTTT ATA CACTTTT  
 CCTG AAAA  
 GAM1464 CHRNA3 3' TCGTTACCCATTTCTT 5610 T CG  
 AAGAAATG GGT TGA  
 ||||| || |||  
 TTCTTTAC CCA GCT  
 \_ TT  
 GAM1464 DRD1 3' TTACAACCACATTTCTGGCCA 5840 ACA C  
 TG AGAAATGTGGT GTGA  
 || ||||| |||||  
 AC TCTTTACACCA CATT  
 CGG A  
 GAM1464 FUT1 3' TCTGATCACATCCCCTGTC 3798 AGAA T  
 GACA ATGTGGTCTG GA  
 ||| ||||| ||  
 CTGT TACACTAGT CT  
 CCCC \_  
 GAM1464 IRF1 3' GCCACATTTCTGATCA 64345 CA  
 TGA AGAAATGTGGT  
 ||| ||||| |||||  
 ACT TCTTTACACCG  
 AG  
 GAM1464 MAP3K8 5' TCACGACCACCTCATG 17791 A AAT  
 CA GA GTGGTCTGTA  
 || || ||||| |||||  
 GT CT CACCAGCACT  
 A C\_  
 GAM1464 NGFR 3' TTCTGACCACACTTCCTGTC 10231 A A T  
 GACA GAA TGTGGTCTG GAA  
 |||| ||| ||||| |||  
 CTGT CTT ACACCAGT CTT  
 C C \_  
 GAM1464 OLR1 3' TTCACAACAGTTCTTGTTA 10341 ATGTG C  
 TGACAAGAA GT GTGAA  
 ||||| || |||||

		ATTGTTCTT CA CACTT		
		GA__ A		
GAM1464	POU4F1	3' CACTGAAAACATTTTGTCA	20660	A GG _
		TGACAAGAA TGT TC GTG		
		ACTGTTTTT ACA AG CAC		
		_ AA T		
GAM1464	SMP1	3' TTTCACATGAATAATTTTGTG	26705	A GGTC
	A	TGACAAGAA TGT GTGAAA		
		ACTGTTTTT ATA CACTTT		
		A AGTA		
GAM1464	ZNF264	3' TTCTATTAACATTTCTTTTCA	12769	C GGTCGT
		TGA AAGAAATGT GAA		
		ACT TTCTTTACA CTT		
		T ATTAT_		
GAM1464	C20orf175	3' CGAGCTCCACGTTTCCTGCCA	55063	A A _
		TG CA GAAATGTGG TCG		
		AC GT CTTTGCACC AGC		
		C C TCG		
GAM1464	CAPNS2	3' TTTCACAACCCTACATTTTCT	50323	CA _ C
	GATCA	TGA AGAAATGT GGT GTGAAA		
		ACT TCTTTATA CCA CACTTT		
		AG CATC A		
GAM1464	CLDN6	3' TTTACACTCACATTTTATCA	41041	CA _ C
		TGA AGAAATGTG GT GTGAA		
		ACT TTTTACAC CA CATT		
		A_ T _		
GAM1464	DKFZP564L0864	3' GCACCAATTTCTTGCCA	72555	A G C
		TG CAAGAAAT TGGT GT		
		AC GTTCTTTA ACCA CG		
		C _ _		
GAM1464	DKFZP566B183	3' TTTCCATAAACATTTCTTTTCA	31330	C GGTCGT
		TGA AAGAAATGT GAAA		
		ACT TTCTTTACA CTTT		
		T AATAC_		
GAM1464	GTF2E1	3' TACAGACCTCTTGTCA	18616	AATGT _
		TGACAAGA GGTC GTG		
		ACTGTTCT CCAG CAT		
		_ A		
GAM1464	KIAA0089	3' TTTTAATTCACATTTCTT	69967	TCG
		AAGAAATGTGG TGAAA		

		TTCTTTACACT ATTTT		
		TA_		
GAM1464 KIAA0373	5'	TTTTCAAAGTAACATTTCTT 28015	GGTCG	
		AAGAAATGT TGAAAA		
		TTCTTTACA ACTTTT		
		ATGAA		
GAM1464 KIAA1813	3'	TTTTCACACTGTAAATTTCTTG 70314	__TG C	
	T	ACAAGAAAT G GT GTGAAAA		
		TGTTCTTTA T CA CACTTTT		
		AA GT _		
GAM1464 KIAA1951	3'	TTCCAGGCTTCTCTTGTC 73766	AATGT GT	
		TGACAAGA GGTC GAA		
		ACTGTTCT TCGG CTT		
		CT__ AC		
GAM1464 MGC4170	3'	TTCACCATTTCTTGTC 44227	TGGTC	
		GACAAGAAATG GTGAA		
		CTGTTCTTTAC CACTT		
GAM1464 NRN1	3'	CACTGCACATTTCTCCTCA 33432	CA GTC	
		TGA AGAAATGTG GTG		
		ACT TCTTTACAC CAC		
		CC GT_		
GAM1464 PLA2G12	3'	TTTTCACAACCACATTT 48028	C	
		AAATGTGGT GTGAAAA		
		TTTACACCA CACTTTT		
		A		
GAM1464 PPY2	3'	CACTCCACATTCCTGGCCA 40819	ACA A TC	
		TG AG AATGTGG GTG		
		AC TC TTACACC CAC		
		CGG C T_		
GAM1464 ZNF31	3'	TTTGTAGACCACATTTCTGTT 64992	A _TG	
	A	TGACA GAAATGTGGTC G AA		
		ATTGT CTTTACACCAG T TT		
		C A GT		
GAM1464 LOC115219	3'	CACGACAACGGGTCCTCA 73295	CAA AA G	
		TGA GA TGT GTCGTG		
		ACT CT GCA CAGCAC		
		C__ GG A		
GAM1464 LOC120376	5'	TTCAGAGCATTTCTTTCA 75986	C GG G	
		TGA AAGAAATGT TC TGAA		

ACT TTCTTTACG AG ACTT

GAM1464 LOC133418 3' TTTTCATATACATTTTTTGCCA 75094 A GTC  
TG CAAGAAATGTG GTGAAA  
|| ||||| |||||  
AC GTTTTTTACAT TACTTT  
C A\_\_

GAM1464 LOC151199 3' TTAAAACCACAGCTCTTGCCA 80174 A AA CG  
TG CAAGA TGTGGT TGA  
|| |||| ||||| |||  
AC GTTCT ACACCA ATT  
C CG AA

GAM1464 LOC152317 5' TCACACTGACTTTTGTCA 85649 AATG C  
TGACAAGA TGGT GTGA  
||||| |||||  
ACTGTTTT GTCA CACT  
CA\_\_ \_

GAM1464 LOC152674 3' TTCAACCCACCCTCTTGTC A 85841 AAT TCG  
TGACAAGA GTGG TGAA  
||||| |||||  
ACTGTTCT CACC ACTT  
CC\_ CA\_

GAM1464 LOC152845 5' CATGACCACATTTTTCA 60330 CAA  
TGA GAAATGTGGTCGTG  
||| |||||  
ACT TTTTACACCAGTAC

GAM1464 LOC154743 3' TTTAGTCCACATTGTCTTGTC A 81118 \_ TCG  
TGACAAGA AATGTGG TGAA  
||||| ||||| |||||  
ACTGTTCT TTACACC ATTT  
G TG\_

GAM1464 LOC165476 5' TTCACGGCACCTTCT 87201 AT G  
AGAA GTG TCGTGAA  
|||| |||||  
TCTT CAC GGCACCT  
C\_ \_

GAM1464 LOC254266 5' TTTTCGGTCACACATCTTATCA 97356 C AA GT T  
TGA AAGA TGTG CG GAA  
||| |||| ||||| |||||  
ACT TTCT ACAC GC TTT  
A AC TG T

GAM1464 LOC255919 3' TTTTCATTCTTACATTTCTAATC 95043 CA TC  
A TGA AGAAATGTGG GTGAAA  
||| ||||| |||||  
ACT TCTTTACATT TACTTT  
AA CT

GAM1464 LOC51754 5' CACGGCCACATCTCTGTCA 71027 A A  
TGACA GA ATGTGGTCGTG  
||||| |||||



ACTGT CT TACACCGGCAC  
 \_ C  
 GAM1464 LOC55862 3' ACCTCATTCTTGCCA 37485 A T  
 TG CAAGAAATG GGT  
 || ||||| ||  
 AC GTTCTTTAC CCA  
 C T  
 GAM1464 LOC55954 3' CACGTGGTCACTTTTCTCATCA 38877 CA T GT \_  
 TGA AGAAA GTG C GTG  
 || |||| | ||  
 ACT TCTTT CAC G CAC  
 AC T TG TG  
 GAM1465 ADH1B 3' CTTAGACATAAAGTAAAAT 72644 C CAC  
 ATTT ACTTT TGTCTGAG  
 ||| |||| |||||  
 TAAA TGAAA ACAGATTC  
 A T \_  
 GAM1465 AHR 3' ATCTCAGATGTTAAATAAATG 7875 CAC C T  
 CATTT TTT AC GTCTGAGAT  
 |||| || |||||  
 GTAAA AAA TG TAGACTCTA  
 TA\_ T \_  
 GAM1465 FDFT1 3' TAGGAAAGTGAAATG 15518 A  
 CATTTCACTTTC CTG  
 ||||| ||  
 GTAAAGTGAAAG GAT  
 \_  
 GAM1465 JTB 3' ATCTCAGACAGTGAAAGTGAAA 21959  
 TG CATTTCACTTTCACTGTCTGAGAT  
 ||||| ||||| |||||  
 GTAAAGTGAAAGTGACAGACTCTA  
 GAM1465 KLF4 3' TCCCAGACAGTGGATATG 14891 CT A  
 CA TTCAGTGTCTG GA  
 || ||||| ||  
 GT AGGTGACAGAC CT  
 AT C  
 GAM1465 PHYH 3' ACAGTAAAAGTGAAAT 20608 C  
 ATTTCACTTT ACTGT  
 ||||| ||||  
 TAAAGTGAAA TGACA  
 A  
 GAM1465 PKD2 3' TCCAGGTTGAAAGTGAAA 60096 CTG A  
 TTTCAGTTTCA TCTG GA  
 ||||| |||| ||  
 AAAGTGAAAGT GGAC CT  
 T\_ \_  
 GAM1465 WRN 3' GGGCAGTGAAAATGAAA 5098 C  
 TTTCA TTTCAGTGTCT  
 |||| |||||

AAAGT AAAGTGACGGG  
 A  
 GAM1465 ZNF216 3' ATCTGCACAGCAAAGTGAAA 20017 CA CTG  
 TTTCAC TTT CTGT AGAT  
 ||||| ||| |||  
 AAAGTGAAA GACA TCTA  
 C\_ CG\_  
 GAM1465 CG012 5' CTCAC TCTGAAAAGTGAA 83218 CT CT  
 TTCAC TTTCA GT GAG  
 ||||| || |||  
 AAGTGAAAGT CA CTC  
 CT \_  
 GAM1465 EIF2C2 3' ATCTTCTGAGAGTGAAAG 71946 G T\_  
 CTTTCACT TC GAGAT  
 ||||| || |||  
 GAAAGTGA AG TTCTA  
 G TC  
 GAM1465 FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802 ACTTTCACT  
 G CATTTC GTCTGAGAT  
 |||| | |||||  
 GTAAAG CAGACTCTA  
 AAACATTT\_  
 GAM1465 FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281 CTT  
 CATTTCA TCACTGTCTGAGAT  
 |||| | |||||  
 GTAAAGT AGTGACAGACTCTA  
 C\_  
 GAM1465 KIAA0984 3' TTTGTCCAGTGAAAATGAA 65534 C TC  
 TTCA TTTCAC TGAG  
 ||| ||||| |||  
 AAGT AAAGTGAC GTTT  
 A CT  
 GAM1465 KLHL6 3' ATCTCAGAGCAGGAAA 55299 A \_  
 TTTC CTG TCTGAGAT  
 ||| ||| |||||  
 AAAG GAC AGACTCTA  
 \_ G  
 GAM1465 NIR3 3' GCAGTGAAAAGTGCAAT 66242 T  
 ATT CACTTTCACTGT  
 || |||||  
 TAA GTGAAAAGTGACG  
 C  
 GAM1465 PORIMIN 3' ATCTCAGAGGGCCAAAGTGAA 53598 CA G  
 TTCACTTT CT TCTGAGAT  
 ||||| || |||||  
 AAGTGAAA GG AGACTCTA  
 CC G  
 GAM1465 PP35 3' ATCTCAGACTGAAA 22814 CT  
 TTTC A GTCTGAGAT  
 |||| | |||||

AAAGT CAGACTCTA

GAM1465 PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148 TCAC C\_  
CATTTCACCTT TGT TGAG  
||||||| ||| |||  
GTAAAGTGAA ACG ACTC  
TA\_\_ TT

GAM1465 SEP15 3' TCCTACAGTAAGAGTGAAA 14934 C CT  
TTTCACTTT ACTGT GA  
||||||| ||||| ||  
AAAGTGAGA TGACA CT  
A TC

GAM1465 SFXN2 3' CTCAGGGGAAAAAAGTGAAA 73941 CACTG  
TTTCACTTT TCTGAG  
||||||| |||||  
AAAGTGAAA GGA CTC  
AAAGG

GAM1465 LOC149703 3' ATCTCAGACAGCCGTTTGAAA 84647 ACTTTCA  
TTTC CTGTCTGAGAT  
||| |||||  
AAAG GACAGACTCTA  
GTTTGCC

GAM1465 LOC154007 3' ATCTCAAACCCTTTAGTGAAA 81015 TTCACT C  
TTTCACT GT TGAGAT  
||||| || |||||  
AAAGTGA CA ACTCTA  
TTTCC\_ A

GAM1465 LOC155004 3' TCATTTAAGTGAAAGGAAA 81226 A GTC\_  
TTTC CTTTCACT TGA  
||| ||||| |||  
AAAG GAAAGTGA ACT  
\_ ATTT

GAM1465 LOC222134 5' ACAGTGAAGTGAAATG 94136 T  
CATTTCACCTT CACTGT  
||||||| |||||  
GTAAAGTGAA GTGACA

GAM1466 CEACAM5 3' ATGAACTAACTGACAGCTTCA 15156 C CAC\_  
TGAAGCTG CA TCAT  
||||||| || |||  
ACTTCGAC GT AGTA  
A CAATCA

GAM1466 HDAC4 3' TGGGCGTGGCAGCCTCA 20120 A A  
TGA GCTGCCAC CTCA  
||| ||||| |||  
ACT CGACGGTG GGGT  
C C

GAM1466 MHC2TA 3' TGGAAGCACAGCTTCA 4196 CCACA CA  
TGAAGCTG CT TCCA  
||||||| || |||

			ACTTCGAC	GA AGGT		
			AC___			
GAM1466	NEF3	3'	AATGCATGTGATTGGCAGCTTC	18194	CACT	C
	A		TGAAGCTGCCA	CAT CATT		
			ACTTCGACGGT	GTA GTAA		
			TAGT	C		
GAM1466	PER2	3'	ATGGAGATAGCAGCCTC	43027	A	CACAC A
			GA GCTGC	TC TCCAT		
			CT CGACG	AG AGGTA		
			C	AT___		
GAM1466	PTPRA	5'	ATGGATGATGCAGTTCA	55081	G	CACAC
			TGAA CTGC	TCATCCAT		
			ACTT GACG	AGTAGGTA		
			-	T___		
GAM1466	PTPRA	5'	ATGGATGATGCAGTTCA	11090	G	CACAC
			TGAA CTGC	TCATCCAT		
			ACTT GACG	AGTAGGTA		
			-	T___		
GAM1466	PTPRA	5'	ATGGATGATGCAGTTCA	55089	G	CACAC
			TGAA CTGC	TCATCCAT		
			ACTT GACG	AGTAGGTA		
			-	T___		
GAM1466	TMP21	3'	AATGGTGTGATGGATGTGACACCT	22400	A C C	CT ___
	CA		TGA G TG CACA	CAT CCATT		
			ACT C AC GTGT	GTA GGTA		
			-	C A AG GT		
GAM1466	UBL1	3'	AATGGACATTGTCTGTACCAGC	12528	CC	CT ___
	TTCA		TGAAGCTG ACA CA	TCCATT		
			ACTTCGAC TGT GT	AGGTAA		
			CA	CT TAC		
GAM1466	CDC14B	3'	ATGACAGTGTGACAGCTTCA	52845	C	___
			TGAAGCTG CACAC	TCAT		
			ACTTCGAC GTGTG	AGTA		
			A	AC		
GAM1466	FAM3C	3'	GGCTGGAGGTGGCAGCTTCA	29685	A	AT_
			TGAAGCTGCCAC	CTC CC		
			ACTTCGACGGTG	GAG GG		
			-	GTC		
GAM1466	FLJ13110	3'	TGAGTGTGCAGCCTCA	43309	A	C
			TGA GCTGC	ACACTCA		

ACT CGACG TGTGAGT  
 C \_  
 GAM1466 FLJ20086 3' AATGGATGTAATGCAAATTCA 34521 GC CACACT  
 TGAA TGC CATCCATT  
 |||| ||| |||||  
 ACTT ACG GTAGGTAA  
 AA TAAT\_  
 GAM1466 FLJ22794 5' AATGGTCCCCAGTGCAGCAGCT 91598 CA CAT\_  
 TC GAAGCTGC CACT CCATT  
 ||||| ||| ||||  
 CTTGACG GTGA GGTA  
 AC CCCCT  
 GAM1466 KIAA0057 3' AATGGACACGGATTGTGACAGT 24413 C C A\_  
 TTCA TGAAGCTG CACA TC TCCATT  
 ||||| ||| |||  
 ACTTTGAC GTGT AG AGGTAA  
 A T GCAC  
 GAM1466 KIAA1877 3' AGTAAGTGGCAGCTCA 66162 A \_  
 TGA GCTGCCAC ACT  
 ||| ||||| |||  
 ACT CGACGGTG TGA  
 \_ AA  
 GAM1466 MAL2 3' AATGAATGAGTGTGGTTATGTT 53550 GCT\_ C  
 C GAA GCCACACTCAT CATT  
 ||| ||||| |||  
 CTT TGGTGTGAGTA GTAA  
 GTAT A  
 GAM1466 PEG10 3' ATGGATGAAAAGCCTCA 30519 A GCCACAC  
 TGA GCT TCATCCAT  
 ||| ||| |||||  
 ACT CGA AGTAGGTA  
 C AA\_  
 GAM1466 PKNOX2 3' ATGGACGTGCAGTTTCA 90874 C ACTCA  
 TGAAGCTGC AC TCCAT  
 ||||| ||| ||||  
 ACTTTGACG TG AGGTA  
 \_ C\_  
 GAM1466 TPD52 3' AATGGTTTTTGTGGCAGATTCA 17419 G CTCAT  
 TGAA CTGCCACA CCATT  
 ||| ||||| ||||  
 ACTT GACGGTGT GGTA  
 A TTTT\_  
 GAM1466 LOC126917 3' AATGGATGATTTCAGGCTCA 74578 A GCCACAC  
 TGA GCT TCATCCATT  
 ||| ||| |||||  
 ACT CGG AGTAGGTAA  
 \_ ACCTTT\_  
 GAM1466 LOC132321 3' ATGACTGCTCATAGCAGCTTTA 75057 CA\_ C  
 TGAAGCTGC CA TCAT  
 ||||| ||| |||

	ATTCGACG	GT AGTA		
	ATACTC	C		
GAM1466 LOC139422 3'	GATGGTTAAAGTAGCTTCA	75840	CAC_	T
	TGAAGCTGC	AC CATC		
	ACTTCGATG	TG GTAG		
	AAAT	_		
GAM1466 LOC149076 3'	GGGTGCGGCAGCTTCA	79154	A	
	TGAAGCTGCC	CACTC		
	ACTTCGACGG	GTGGG		
	C			
GAM1466 LOC150372 5'	ATGAGGATGGCAGCTCA	79785	A	CA
	TGA GCTGCCA	CTCAT		
	ACT CGACGGT	GAGTA		
	_	AG		
GAM1466 LOC153914 5'	GAGTTTGGCAGCTCCA	80990	A	C
	TG AGCTGCCA	ACTC		
	AC TCGACGGT	TGAG		
	C	T		
GAM1466 LOC155372 5'	ATGATTGAGGACAGCTTCA	81340	_	A C_
	TGAAGCTG	CC CA TCAT		
	ACTTCGAC	GG GT AGTA		
	A	A TT		
GAM1466 LOC196283 3'	AATGGCATTTCATGCCAGCTTCA	87618	C	CACTCAT
	TGAAGCTG	CA CCATT		
	ACTTCGAC	GT GGTA		
	C	ACTTAC_		
GAM1466 LOC201194 3'	GGTAGTGGCAGCTCCA	89779	A	_
	TG AGCTGCCAC	ACT		
	AC TCGACGGTG	TGG		
	C	A		
GAM1466 LOC221547 3'	GTGAATGTGGCAGTTCA	91008	G	C
	TGAA CTGCCACA	TCAT		
	ACTT GACGGTGT	AGTG		
	_	A		
GAM1466 LOC253912 3'	AATGGAGCGTGGGTGGCAGCT	97357	ACTCA_	
	AGCTGCCAC	TCCATT		
	TCGACGGTG	AGGTAA		
	GGTGCG			
GAM1466 LOC257577 3'	GTGAATGTGGCAGTTCA	97839	G	C
	TGAA CTGCCACA	TCAT		

			ACTT GACGGTGT AGTG		
			— A		
GAM1466	LOC90981	3'	AATGGTGATGGATGTGACACTT 64533	C C	CT —
		CA	TGAAG TG CACA CAT CCATT		
			ACTTC AC GTGT GTA GGTA		
			— A AG GT		
GAM1467	ABCB10	3'	ATGAACTGCTAGGTATTATT 23886	AG	A
			AATAATAC GGTA GTTCAT		
			TTATTATG TCGT CAAGTA		
			GA —		
GAM1467	BPAG1	3'	GCACCTGTATCATTGAA 31429	A	—
			TTCAAT ATACAGG GT		
			AAGTTA TATGTCC CG		
			C A		
GAM1467	EML1	3'	ACCATGTATTATTGAA 59728	G	
			TTCAATAATACA GGT		
			AAGTTATTATGT CCA		
			A		
GAM1467	HEM1	5'	ATGAACTTCTCAACACCATTGA 18049	AATACA	T
			TCAAT GGG AAGTTCAT		
			AGTTA CTC TTCAAGTA		
			CCACAA —		
GAM1467	TTC3	5'	ATCCTTATTATTGAA 12416	C	
			TTCAATAATA AGGGT		
			AAGTTATTAT TCCTA		
			—		
GAM1467	FLJ10468	3'	ATGTTTATCCCTGTTTACTGAA 36144	A T	TAAGTT
			TTCA TAA ACAGGG CAT		
			AAGT ATT TGTCCC GTA		
			C — TATTT—		
GAM1467	KIAA1280	5'	AACTTACCCAGATTGAG 69707	AATACA	
			TTCAAT GGGTAAGTT		
			GAGTTA CCCATTCAA		
			GA—		
GAM1467	NEUROD6	5'	TGAAAACCTGATTATTGAA 42688	A	GGTAAG
			TTCAATAAT CAG TTCA		
			AAGTTATTA GTC AAGT		
			— AA—		
GAM1467	LOC144202	5'	TGAACTGCACATTGTTGAA 76710	ACAGG	A
			TTCAATAAT GTA GTTCA		

			AAGTTGTTA CGT CAAGT		
			CA__ _		
GAM1467	LOC221552	3'	AACTTACCTATCATTTGAA 93804	TAATACA	
			TTCAA GGGTAAGTT		
			AAGTT TCCATTCAA		
			TACTA__		
GAM1467	LOC257493	3'	AACTTACCTATCATTTGAA 97799	TAATACA	
			TTCAA GGGTAAGTT		
			AAGTT TCCATTCAA		
			TACTA__		
GAM1467	LOC257609	3'	AACTTACCTATCATTTGAA 97939	TAATACA	
			TTCAA GGGTAAGTT		
			AAGTT TCCATTCAA		
			TACTA__		
GAM1467	LOC90768	5'	ATGAACTTACTGCGCCATTTGA 63951	TAATACAG	
	A		TTCAA GGTAAGTTCAT		
			AAGTT TCATTCAAGTA		
			TACCGCG_		
GAM1468	ABCC2	3'	CCATGAACCTACTACCCA 4616	A A A	
			TG GGTA TA GTTTATGG		
			AC CCAT AT CAAGTACC		
			_ C C		
GAM1468	ACTA1	3'	CATTAACCTTATTACCTCA 59356	T	
			TGAGGTAATAAGTT ATG		
			ACTCCATTATTCAA TAC		
			T		
GAM1468	CACNA1D	3'	TCGTGTCGTTACCTCA 5565	AAGTTTAT GT	
			TGAGGTAAT G ACGA		
			ACTCCATTG C TGCT		
			_____TG		
GAM1468	MYCBP	3'	CCATCTAACTCATTACCTTA 24694	A T_	
			TGAGGTAAT AGTT ATGG		
			ATTCCATTA TCAA TACC		
			C TC		
GAM1468	TNXB	5'	CTATAAACTTCCCACCTCA 50639	AAT	
			TGAGGT AAGTTTATGG		
			ACTCCA TTCAAATATC		
			CCC		
GAM1468	ATIP1	3'	CCAAAACCTTATTACCTC 40391	A	
			GAGGTAATAAGTTT TGG		



CTCCATTATTCAAA ACC

GAM1468 KIAA1508 5' ACCATAAACCTGTCCT 61871 TA A  
AGG ATA GTTTATGGT  
||| ||| |||||  
TCC TGT CAAATACCA  
\_ C

GAM1468 MGC15435 3' TACCAAAGACTTATCACACCA 50419 AG A A  
TG GT ATAAGTTT TGGTA  
|| || ||||| ||||  
AC CA TATTCAGA ACCAT  
CA C A

GAM1468 LOC151194 3' CCAAAACCTATTATCTCA 59214 A A  
TGAGGTAATA GTTT TGG  
||||||| ||| |||  
ACTCTATTAT CAAA ACC  
C \_

GAM1468 LOC151248 5' ATTATAAACTCATTACTCCA 80184 AG A  
TG GTAAT AGTTTATGGT  
|| |||| |||||  
AC CATTA TCAAATATTA  
CT C

GAM1468 LOC220766 5' CCATAGAACTTATTCCCCA 90794 A T \_  
TG GG AATAAGTTT ATGG  
|| || ||||| |||  
AC CC TTATTCAAG TACC  
\_ C A

GAM1469 AHCY 3' CAGAAAAACATGAATGCAGGCA 5474 G \_ TACTCTC\_  
GA TCTG CCTGTGT C CTG  
|||| ||||| | |||  
AGAC GGACGTA G GAC  
\_ A TACAAAAA

GAM1469 BCL2L2 3' CAGGAGAGCAGGAACAGAACAG 14464 GC GT A  
A TCTG CTGT CT CTCTCCTG  
|||| ||| || |||||  
AGAC GACA GA GAGAGGAC  
AA AG C

GAM1469 BRAF 3' CAGGAGAGTAGCAACA 15084 GT  
TGT CTACTCTCCTG  
||| |||||  
ACA GATGAGAGGAC  
AC

GAM1469 CASQ1 5' CAGGAGAGCCAACCCAGA 6928 CC T TCTA  
TCTGG TG G CTCTCCTG  
|||| ||| |||||  
AGACC AC C GAGAGGAC  
CA \_ \_ \_ \_

GAM1469 CD5 3' CAGAACATGGACAGAGGCCAGA 26389 G CTCTC  
TCTGGCCT TGTCTA CTG  
|||||| ||||| |||

			AGACCGGA ACAGGT	GAC		
			G ACAA_			
GAM1469	CELSR1	3'	TCAGGAACGCCGGGCACAGACC	26487	C	ACTC_
	A		TGG CTGTGTCT TCCTGA			
			ACC GACACGGG AGGACT			
			A CCGCA			
GAM1469	CEP2	3'	CAGGAGCACACAGACAGA	23226	GC	CTACT
			TCTG CTGTGT CTCCTG			
			AGAC GACACA GAGGAC			
			A_ C_			
GAM1469	FMOD	3'	CAGAAGAGGAAAGGCCAGA	8929		GTGTCTA C
			TCTGGCCT CTCT CTG			
			AGACCGGA GAGA GAC			
			AAG_ A			
GAM1469	MTNR1B	3'	CAGGAGATGCTCACAGGCCA	19894		TC C
			TGGCCTGTG TA TCTCCTG			
			ACCGGACAC GT AGAGGAC			
			TC _			
GAM1469	MUC12	3'	TCAGGAGAGCTGCAAACACAG	94241		CTA_
			CTGTGT CTCTCCTGA			
			GACACA GAGAGGACT			
			AACGTC			
GAM1469	P53AIP1	3'	GGAAGCAGACACAGGCCAGG	42082		A C
			TCTGGCCTGTGTCT CT TCC			
			GGACCGGACACAGA GA AGG			
			C _			
GAM1469	PKIG	3'	AGATAAACCAGGCCAGA	22958		_
			TCTGGCCTG TGTCT			
			AGACCGGAC ATAGA			
			CAA			
GAM1469	SYNGR1	3'	CAGGATGACACAGGCAAGA	16312	G	TACTC
			TCT GCCTGTGTC TCCTG			
			AGA CGGACACAG AGGAC			
			A T_			
GAM1469	VIPR2	3'	CAAGAGAATAGGGGAGCCA	12604	_	GTG C C
			TGGC CT TCTA TCTC TG			
			ACCG GG GGAT AGAG AC			
			A _ A A			
GAM1469	DDX17	5'	CAGGGAACCTAAAACAGGCCAG	48039		GTCTAC_ T
	A		TCTGGCCTGT TC CCTG			

		AGACCGGACA	AG GGAC		
		AAATCCA _			
GAM1469	DKFZp762P2111	3'	CAGGAGCTTCACAAACCAGA	86354	CC TCTACT
			TCTGG TGTG CTCCTG		
			AGACC ACAC GAGGAC		
			AA TTC__		
GAM1469	FLJ11286	3'	CAGGTGCAGATACAAACCAGA	37217	CC ACTCT
			TCTGG TGTGTCT CCTG		
			AGACC ACATAGA GGAC		
			AA CGT__		
GAM1469	FLJ12505	3'	CAGGAGAGCAGACGGCCG	45385	TGT A
			TGGCC GTCT CTCTCCTG		
			GCCGG CAGA GAGAGGAC		
			__ C		
GAM1469	HUMGT198A	3'	TCAGGAGACAAGCATAAACCAG	33333	CC T AC
	A		TCTGG TGTG CT TCTCCTGA		
			AGACC ATAC GA AGAGGACT		
			AA _ AC		
GAM1469	HUMGT198A	3'	TCAGGAGACAAGCATAAACCAG	25237	CC T AC
	A		TCTGG TGTG CT TCTCCTGA		
			AGACC ATAC GA AGAGGACT		
			AA _ AC		
GAM1469	KIAA1677	3'	CAAGAAAGAGCCATCAGGCCAG	67063	_ T A C C
	G		TCTGGCCTG TG CT CT TC TG		
			GGACCGGAC AC GA GA AG AC		
			T C _ A A		
GAM1469	KIAA1727	3'	TCAAAAAAGTTTTTTTCAGGCC	64064	TGTCT_ CTCC
	AG		CTGGCCTG ACT TGA		
			GACCGGAC TGA ACT		
			TTTTTT AAAA		
GAM1469	moblak	5'	CAGGAGAGCAGGCGTCACCA	55489	CC _ A
			TGG TG TGTCT CTCTCCTG		
			ACC AC GCGGA GAGAGGAC		
			_ T C		
GAM1469	PDZD2	5'	TCAGGAGAGCAAAGAGGCCA	80880	GTGTCTA
			TGGCCT CTCTCCTGA		
			ACCGGA GAGAGGACT		
			GAAAC__		
GAM1469	RALGPS1A	3'	CAGAAGAGCCAGGCACAG	27598	A_ C
			CTGTGTCT CTCT CTG		

			GACACGGA GAGA GAC			
			CC A			
GAM1469	WNT8A	3'	CAGGAGAATAGAAGCA	49190	G C	
			TGT TCTA TCTCCTG			
			ACG AGAT AGAGGAC			
			A A			
GAM1469	WNT8A	3'	CAGGAGAATAGAAGCA	54281	G C	
			TGT TCTA TCTCCTG			
			ACG AGAT AGAGGAC			
			A A			
GAM1469	LOC135763	3'	CAGGAGAGCAGCCACA	56788	T A	
			TGTG CT CTCTCCTG			
			ACAC GA GAGAGGAC			
			C C			
GAM1469	LOC146315	5'	CAGGAGAGTGTGGAATCCAGA	60886	CCTGTG _	
			TCTGG TC TACTCTCCTG			
			AGACC GG GTGAGAGGAC			
			TAA__ T			
GAM1469	LOC146713	3'	TCAGAAGTGGGCACTGACCAGA	83733	CCT CTC	
			TCTGG GTGTCTACT CTGA			
			AGACC CACGGGTGA GACT			
			AGT A__			
GAM1469	LOC150378	3'	GAGCAGACACAGCCAGA	79746	C A	
			TCTGGC TGTGTCT CTC			
			AGACCG ACACAGA GAG			
			_ C			
GAM1469	LOC150481	3'	TCAAGAGACACTGGACACAACC	79897	CC C__ C	
	CA		TGG TGTGTCTA TCTC TGA			
			ACC ACACAGGT AGAG ACT			
			CA CAC A			
GAM1469	LOC150793	3'	CAAGAGATTTACAGACCAGG	80013	C TCTAC C	
			TCTGG CTGTG TCTC TG			
			GGACC GACAT AGAG AC			
			A TT__ A			
GAM1469	LOC158191	3'	TCAAGAGACACTGGACACAACC	81783	CC C__ C	
	CA		TGG TGTGTCTA TCTC TGA			
			ACC ACACAGGT AGAG ACT			
			CA CAC A			
GAM1469	LOC163682	5'	CAGGAGAGCCCCAGAGCCA	87024	_ TGTCTA	
			TGGC CTG CTCTCCTG			

ACCG GAC GAGAGGAC  
 A CCCC\_\_  
 GAM1469 LOC51001 5' TCAGGAGAATAATTCTGCC 31953 CTGT C C  
 GGC GT TA TCTCCTGA  
 ||| ||| |||||  
 CCG TA AT AGAGGACT  
 TCT\_ \_ A  
 GAM1470 ALDH3B2 3' TCCCAACTGCACCAGCACTGCC 5510 AGCTTA TG  
 GGCAGTGT G GTTGGGA  
 ||||| | |||||  
 CCGTCACG C CAACCCT  
 ACCA\_\_GT  
 GAM1470 M6PR 3' CCCAAACCAAAGCTACACAGCC 9862 A AG \_  
 GGC GTGTAGCTT TGGTT GGG  
 ||| ||||| |||||  
 CCG CACATCGAA ACCAA CCC  
 A \_ A  
 GAM1470 MAFF 3' CCCAACACTGTCCACACTGCC 24645 AGCT G  
 GGCAGTGT TAGTG TTGGG  
 ||||| ||||| |||||  
 CCGTCACA GTCAC AACCC  
 CCT\_ \_  
 GAM1470 OA1 3' CCAACACTGCACTGCC 4253 CTTAGTG  
 GGCAGTGTAG GTTGG  
 ||||| |||||  
 CCGTCACGTC CAACC  
 A\_\_\_\_\_  
 GAM1470 SIX3 3' CCCAACCACCATCTACCACT 18274 \_ CTTA  
 AGTG TAG GTGGTTGGG  
 ||||| |||||  
 TCAC ATC CACCAACCC  
 C TAC\_  
 GAM1470 SLC6A12 5' CCCAACCCACCACACAGCC 11732 A AGCTTA \_  
 GGC GTGT GTGG TTGGG  
 ||| ||||| |||||  
 CCG CACA CACC AACCC  
 A C\_\_\_\_\_ C  
 GAM1470 C22orf20 3' CCCAAGAACGACACTGCC 47429 AGCTTA GG  
 GGCAGTGT GT TTGGG  
 ||||| || |||||  
 CCGTCACA CA AACCC  
 G\_\_\_\_\_ AG  
 GAM1470 DKFZP566G1424 5' CCCATCCAGCCACACCACC 84782 CA A TAGT T  
 GG GTGT GCT GG TGGG  
 || ||||| || |||||  
 CC CACA CGA CC ACCC  
 AC C \_\_\_\_\_ T  
 GAM1470 KIAA0285 5' TCCTAGGCCAGGCCACACTGCC 29023 A TAG \_  
 GGCAGTGT GCT TGGT TGGGA  
 ||||| ||| |||||

CCGTCACA CGG ACCG ATCCT  
 C \_ G  
 GAM1470 KIAA1434 3' TCCCATGTTCTCAAACCTACGCT 69620 C \_ TGGT  
 GCC GGCAGTGTAG TT AG TGGGA  
 ||||| || || ||||  
 CCGTCGCATC AA TC ACCCT  
 A C TTGT  
 GAM1470 MGC12992 3' TCCCTCCACACAGCCACACTGC 50347 A TA TT  
 C GGCAGTGT GCT GTGG GGGA  
 ||||| || || || ||||  
 CCGTCACA CGA CACC CCCT  
 C CA T\_  
 GAM1470 LOC150372 5' CCCAACCACCAAGGCTTTCC 79794 CAGTGT A\_  
 GG AGCTT GTGGTTGGG  
 || |||| |||||  
 CC TCGGA CACCAACCC  
 TT \_ AC  
 GAM1470 LOC153196 5' TCCTCTTCCAATGCCACACTGC 85979 A TTAG TT\_  
 C GGCAGTGT GC TGG GGGA  
 ||||| || || ||||  
 CCGTCACA CG ACC TCCT  
 C TA \_ TTC  
 GAM1470 LOC201617 5' TCCAGCCAAACTCCACTGCC 90236 T CTTAG  
 GGCAGTG AG TGGTTGGG  
 ||||| || |||||  
 CCGTCAC TC ACCGACCT  
 C AA\_  
 GAM1471 ANXA5 3' AGTGGTGCTTCTTTCTG 6713 GACA A  
 CAGAAAGA AGCA CTA CT  
 ||||| || |||||  
 GTCTTTCT TCGT GGTGA  
 \_ \_  
 GAM1471 APLP2 3' AAAGTAGTCCAGGCTGTCCCT 90892 A A A\_  
 AG GACA GC ACTACTTT  
 || |||| || |||||  
 TC CTGT CG TGATGAAA  
 C \_ GACC  
 GAM1471 BPAG1 3' AAGTTTTGCCTTTTTCTG 8170 ACAA CT  
 CAGAAAGAG GCAA ACTT  
 ||||| || || ||||  
 GTCTTTTTTC CGTT TGAA  
 \_ T\_  
 GAM1471 CALCR 3' AAAGTAGTTTAAAGTCTCCTTT 8214 A AAGC  
 GAA GAGAC AACTACTTT  
 || |||| |||||  
 TTT CTCTG TTGATGAAA  
 C AAT\_  
 GAM1471 CSNK1G2 3' AAAGTCCAGCTTGTCTCCCTC 7167 AA AACT  
 GA GAGACAAGC ACTTT  
 || ||||| ||||

			CT CTCTGTTCTG	TGAAA		
			CC	ACC_		
GAM1471	FGF18	3'	GGTGCTTGTCTCTCTCT	13913	A	A
			AGA AGAGACAAGCA	CT		
			TCT TCTCTGTTTCGT	GG		
			C	_		
GAM1471	FGF18	3'	GGTGCTTGTCTCTCTCT	53348	A	A
			AGA AGAGACAAGCA	CT		
			TCT TCTCTGTTTCGT	GG		
			C	_		
GAM1471	GNAQ	3'	AAAGATAAGACTTGTCTTTCTTT	9061		CAACTA
	TG		CAGAAAGAGACAAG	CTTT		
			GTCTTTCTTTGTTC	GAAA		
			AGAATA			
GAM1471	HRH1	3'	TAGTTGCTGTCCCCTTC	5987	AGA	A
			GAA GACA GCAACTA			
			CTT CTGT CGTTGAT			
			CCC	_		
GAM1471	HS3ST3B1	3'	GCTTCCCTGTCTCTTCCTG	20150	A	_____
			CAG AAGAGACA	AGC		
			GTC TTCTCTGT	TCG		
			C	CCCT		
GAM1471	IRTA2	3'	AAAGTAGCTGCCACTATCTTT	48400	GACAA	A
			AAAGA GCA CTACTTT			
			TTTCT CGT GATGAAA			
			ATCAC	C		
GAM1471	KRT6B	3'	GGTTGCTTGTCTCTCCCTG	18697	AA_	A
			CAG AG GACAAGCAACT			
			GTC TC CTGTTTCGTTGG			
			CCC	_		
GAM1471	MSL3L1	3'	AGTGCTATCTTTTCTG	54363	CA	A
			CAGAAAGAGA	AGCA CT		
			GTCTTTTCT	TCGT GA		
			A_	_		
GAM1471	PPM1D	3'	AAAGTAGTTACTCCCTTCTC	13249	CA__	C
			GAGA AG AACTACTTT			
			CTCT TC TTGATGAAA			
			TCCC	A		
GAM1471	PRX	3'	AGTTGTTTCTCTCCCTG	40519	AA	CA
			CAG AGAGA	AGCAACT		

GTC TCTCT TTGTTGA  
 CC \_  
 GAM1471 RUNX3 3' TAGTTGCTGACTCCCTG 15117 AAA ACA  
 CAG GAG AGCAACTA  
 ||| ||| |||||  
 GTC CTC TCGTTGAT  
 C\_ AG\_  
 GAM1471 SOCS4 3' AAAGTAATTGTGGGGTTTTTCT 55112 AA AA\_ C  
 G CAGA GAGAC GCAA TACTTT  
 |||| |||| ||| |||||  
 GTCT TTTTG TGTT ATGAAA  
 \_ GGG A  
 GAM1471 APBA2BP 3' AAAGACCAGGGCTTGTCTCCTC 48350 AAA AACTA\_  
 CTG CAG GAGACAAGC CTTT  
 ||| ||||| |||  
 GTC CTCTGTTCTG GAAA  
 CTC GGACCA  
 GAM1471 CBARA1 3' AAAGTAGTTGCTTCATGGCTCT 20289 AC\_  
 AGAG AAGCAACTACTTT  
 ||| |||||  
 TCTC TTCGTTGATGAAA  
 GGTAC  
 GAM1471 CECR2 3' AAGTGGTGTCCCTTCCTG 48606 A A AAGCA  
 CAG AAG GAC ACTACTT  
 ||| ||| |||||  
 GTC TTC CTG TGGTGAA  
 C C \_  
 GAM1471 CYLC2 3' AAAGAAGCACACTTGTCTCGCT 7194 AA CAA\_ A  
 CTG CAGA GAGACAAG CT CTTT  
 |||| ||||| |||||  
 GTCT CTCTGTTC GA GAAA  
 CG ACAC A  
 GAM1471 E46L 3' AAAGTAACTGAGTGTTCTCTT 25083 \_ AG AC  
 AAGAGA CA CA TACTTT  
 ||||| || || |||||  
 TTCTCT GT GT ATGAAA  
 T GA CA  
 GAM1471 FLJ10607 3' AAAGTACCACTTGTCTTTTCTG 77102 A CAAC  
 CAGAA GAGACAAG TACTTT  
 |||| ||||| |||||  
 GTCTT TTCTGTTC ATGAAA  
 \_ ACC\_  
 GAM1471 FLJ11715 3' AAAGTACAGCCGTCTCTTTCT 44664 AA AAC  
 AGAAAGAGAC GC TACTTT  
 ||||| || |||||  
 TCTTTCTCTG CG ATGAAA  
 C\_ AC\_  
 GAM1471 FLJ21596 3' TTGCTTGTTTCTCCCT 45709 AA  
 AG AGAGACAAGCAA  
 || |||||



			TC TCTTTGTTGTT		
			CC		
GAM1471	FLJ22624	5'	TTGCTGTCTCTTCCTG	45654	A A
			CAG AAGAGACA GCAA		
			GTC TTCTCTGT CGTT		
			C _		
GAM1471	FLJ31101	3'	AAGTAAAGGTCTCTTTT	35702	AAGCAAC
			GAAAGAGAC TACTT		
			TTTTCTCTG ATGAA		
			GAA _		
GAM1471	GRP3	3'	TGCTTGTCCCTTCTG	31124	A A
			CAGAA G GACAAGCA		
			GTCTT C CTGTTCGT		
			_ C		
GAM1471	KIAA0546	3'	AAAGTTTTTCTGTCTCTTTT	71302	A C CT
			GAAAGAGACA G AA ACTTT		
			TTTTCTCTGT C TT TGAAA		
			_ _ TT		
GAM1471	KIAA0923	3'	TTGTTTCCCATCTCTTTCT	25841	C _
			AGAAAGAGA AAGCAA		
			TCTTTCTCT TTTGTT		
			ACCC		
GAM1471	KIAA1203	3'	AAGTAGTTACTTGATTC	71631	A C
			GAG CAAG AACTACTT		
			CTT GTTC TTGATGAA		
			A A		
GAM1471	KIAA1257	3'	AGTGCCTACTCTTTCTG	62727	ACAA A
			CAGAAAGAG GCA CT		
			GTCTTTCTC CGT GA		
			ATC _ _		
GAM1471	KIAA1391	3'	TAGTTGCTGAGGTTTTTT	67265	A _
			AAGAGAC AGCAACTA		
			TTTTTTG TCGTTGAT		
			GAG		
GAM1471	KIAA1904	3'	TGGCCACTTCCCTCTTTCTG	73498	AC CAA
			CAGAAAGAG AAG CTA		
			GTCTTTCTC TTC GGT		
			CC ACC		
GAM1471	MGC4604	3'	TGCCTGCCTTCTTTCTG	48982	A _ A
			CAGAAAGAG CA GCA		

		GTCTTTCTT GT CGT		
		CC C		
GAM1471	MRPL43	3' AAGAGCTGCCTGTTTCTTTC 49504	A A A	
		GAAAGAGACA GCA CT CTT		
		CTTTCTTTGT CGT GA GAA		
		C C _		
GAM1471	NEDD5	5' AGTGGGCACTTGTCTCCTTCT 15309	A	CAA
		AGAA GAGACAAG CTACT		
		TCTT CTCTGTTT GGTGA		
		C ACG		
GAM1471	LOC145719	3' AAAGGGTCTGTTTGTCTCCCTC 83443	AA	_ A
		GA GAGACAAGCA ACT CTTT		
		CT CTCTGTTTGT TGG GAAA		
		CC C _		
GAM1471	LOC145720	3' AAAGGGTCTGTTTGTCTCCCTC 83424	AA	_ A
		GA GAGACAAGCA ACT CTTT		
		CT CTCTGTTTGT TGG GAAA		
		CC C _		
GAM1471	LOC146520	5' AGAGGCTTGTCTCTCTCT 77949	A	AA
		AGA AGAGACAAGC CT		
		TCT TCTCTGTTTG GA		
		C GA		
GAM1471	LOC148898	5' GGCTGCCTGCCTCCTTCTG 84253	A A A A	
		CAGAA GAG CA GCA CT		
		GTCTT CTC GT CGT GG		
		C C C C		
GAM1471	LOC150311	5' TGCTTGTCTGTTTCCTG 79759	A G	
		CAG AA AGACAAGCA		
		GTC TT TCTGTTTCGT		
		C G		
GAM1471	LOC154761	3' GGTCTTGTGTCTTTCTG 81125	G	CA
		CAGAAAGA ACAAG ACT		
		GTCTTTCT TGTTT TGG		
		G _		
GAM1471	LOC154881	3' TTGTACCTGTCTCTTCCTG 81173	A	A__
		CAG AAGAGACA GCAA		
		GTC TTCTCTGT TGTT		
		C CCA		
GAM1471	LOC197114	3' AAAGGGTCTGTTTGTCTCCCTC 89696	AA	_ A
		GA GAGACAAGCA ACT CTTT		

	CT CTCTGTTTGT TGG GAAA		
	CC C _		
GAM1471 LOC197117 3'	AAAGGGTCTGTTTGTCTCCCTC 89711	AA	_ A
	GA GAGACAAGCA ACT CTTT		
	CT CTCTGTTTGT TGG GAAA		
	CC C _		
GAM1471 LOC200081 3'	AGTAGTCCTTGCCTCTTCCTG 88560	A A	CA
	CAG AAGAG CAAG ACTACT		
	GTC TTCTC GTTC TGATGA		
	C C C_		
GAM1471 LOC200830 3'	AGTAGCTTGACTTTTTCTG 90146	A A	
	CAGAAAGAG CAAGC ACT		
	GTCTTTTTC GTTCG TGA		
	A A		
GAM1471 LOC205989 5'	TGGTGCCTGCTCTTTCTG 90710	A A A	
	CAGAAAGAG CA GCA CTA		
	GTCTTTCTC GT CGT GGT		
	_ C _		
GAM1471 LOC221454 5'	AAAGTGCTCCTTGTCTCT 92300	CAAC	
	AGAGACAAG TACTTT		
	TCTCTGTTC GTGAAA		
	CTC_		
GAM1471 LOC221663 5'	GTTAATTATCTCTTTCT 93821	C GC	
	AGAAAGAGA AA AAC		
	TCTTTCTCT TT TTG		
	A AA		
GAM1471 LOC255320 3'	AGTAGCCCTCTTTCTG 95003	ACAA A	
	CAGAAAGAG GC ACT		
	GTCTTTCTC CG TGA		
	C_ A		
GAM1471 LOC256642 3'	GTTGTTGCTCTTTCTG 96307	A G	
	CAGAAAGAG CAA CAAC		
	GTCTTTCTC GTT GTTG		
	- -		
GAM1471 LOC90979 3'	AAAGTAGTTGAGATCCTT 64522	A CAAG	
	AAG GA CAACTACTTT		
	TTC CT GTTGATGAAA		
	_ AGA_		
GAM1471 LOC92391 3'	AAGTAGTTGTGCCTTTGTG 69153	G AGACAA	
	CA AAAG GCAACTACTT		

			GT TTTC	TGTTGATGAA		
			G	CG_____		
GAM1472	CASQ1	3'	GGCCTCAATAAAGACATCT	6932	GA	AA
			AGA TCTTTATTGA	CC		
			TCT AGAAATAACT	GG		
			AC	CC		
GAM1472	S100A4	3'	TTCAATAAAGATTCT	11425	A	
			AGAG TCTTTATTGAA			
			TCTT AGAAATAACTT			
			—			
GAM1472	S100A4	3'	TTCAATAAAGATTCT	38954	A	
			AGAG TCTTTATTGAA			
			TCTT AGAAATAACTT			
			—			
GAM1472	CROC4	3'	TTCAATAAAGACTCT	21021	A	
			AGAG TCTTTATTGAA			
			TCTC AGAAATAACTT			
			—			
GAM1472	CYLC2	3'	TTCAATGAATGATCTCT	7195	—	
			AGAGATC TTTATTGAA			
			TCTCTAG AAGTAACTT			
			T			
GAM1472	DDX17	5'	GATTCTACAGCCAATAAAGATC	48040	A	AAACC_
	CT		AG GATCTTTATTG	GAATC		
			TC CTAGAAATAAC	CTTAG		
			CGACAT			
			—			
GAM1472	DKFZp761H2121	3'	GATTCTGTCCAATAAAGCCTC	56371	AT	AA C
			GAG CTTTATTG	AC GAATC		
			CTC GAAATAAC	TG CTTAG		
			C_	C_ T		
GAM1472	FKBP3	5'	TTCAGAATCGAAGATCTCT	8897	A_	
			AGAGATCTTT	TTGAA		
			TCTCTAGAAG	GACTT		
			CTAA			
GAM1472	KIAA0893	3'	TTTCAATAAAGACCTCT	30362	A	
			AGAG TCTTTATTGAAA			
			TCTC AGAAATAACTTT			
			C			
GAM1472	KIAA1579	3'	ATTCGGCTCAGTAAAAATC	36602	C	AA
			GAT TTTATTGA	CCGAAT		

CTA AAATGACT GGCTTA  
 A C\_  
 GAM1472 MGC14480 3' TTCAAACAAGATCTCT 58751 TA  
 AGAGATCTT TTGAA  
 ||||| ||||  
 TCTCTAGAA AACTT  
 CA  
 GAM1472 SCAND2 3' GATTCAGTCAGTAAAGACGTCT 41889 GA AACC  
 AGA TCTTTATTGA GAATC  
 || ||||| ||||  
 TCT AGAAATGACT CTTAG  
 GC GA\_  
 GAM1472 LOC145660 5' GGTGTTCAATAAACATCTCT 77323 C \_  
 AGAGAT TTTATTGAA ACC  
 |||| ||||| ||||  
 TCTCTA AAATAACTT TGG  
 C G  
 GAM1472 LOC147077 5' ATTCGGTTCCTGTCTC 78247 CTTTATT A  
 GAGAT GAA CCGAAT  
 |||| || |||||  
 CTCTG CTT GGCTTA  
 TCC\_\_\_\_ \_  
 GAM1472 LOC255272 3' TTCAATAAAGATTCT 94602 A  
 AGAG TCTTTATTGAA  
 |||| |||||  
 TCTT AGAAATAACTT  
 \_  
 GAM1472 LOC51175 3' GATGTGTCTTCAATAAAAATCT 32747 C AC A  
 T GAGAT TTTATTGAA CG ATC  
 |||| ||||| || ||||  
 TTCTA AAATAACTT GT TAG  
 A CT G  
 GAM1472 LOC90979 3' ATTCAGTTTCCCCCAAGGATCT 64523 ATT\_ C  
 CT AGAGATCTTT GAAAC GAAT  
 ||||| |||| ||||  
 TCTCTAGGAA CTTTG CTTA  
 CCCC A  
 GAM1473 ADRA1A 3' GCACAAATCCAACATG 52784 AAGCC A  
 CATGT TG ATTTGTGC  
 |||| || |||||  
 GTACA AC TAAACACG  
 \_\_\_\_ C  
 GAM1473 AEGL1 5' GCACAAATACACTACAT 6679 AGCC A  
 ATGTA TG ATTTGTGC  
 |||| || |||||  
 TACAT AC TAAACACG  
 C\_\_ A  
 GAM1473 CDH2 3' GCACAAATGTTTTACAT 8377 CCTGA  
 ATGTAAG ATTTGTGC  
 ||||| |||||

TACATTT TAAACACG  
 TG\_\_\_\_  
 GAM1473 CHRNE 3' GCCCTCAGGCCACAGGT 3586 A AA ATTTGT  
 ACC TGT GCCTGA GC  
 ||| ||| ||||| ||  
 TGG ACA CGGACT CG  
 \_ CC CC\_\_\_\_  
 GAM1473 COL4A3 3' GGCCATGGCTCACATGGT 3622 A TGAATT T  
 ACCATGT AGCC TG GCC  
 ||||| ||| || |||  
 TGGTACA TCGG AC CGG  
 C T\_\_\_\_\_  
 GAM1473 COL4A3 3' GGCCATGGCTCACATGGT 48568 A TGAATT T  
 ACCATGT AGCC TG GCC  
 ||||| ||| || |||  
 TGGTACA TCGG AC CGG  
 C T\_\_\_\_\_  
 GAM1473 COL4A3 3' GGCCATGGCTCACATGGT 48557 A TGAATT T  
 ACCATGT AGCC TG GCC  
 ||||| ||| || |||  
 TGGTACA TCGG AC CGG  
 C T\_\_\_\_\_  
 GAM1473 CYP3A4 3' ACAAGCCTGGCCTACATGGT 33923 A TGAA  
 ACCATGTA GCC TTTGT  
 ||||| ||| |||||  
 TGGTACAT CGG GAACA  
 C TCC\_  
 GAM1473 HIVEP3 5' GGCACAAACCCAGCAGCCTCA 44439 TAA \_\_ AA  
 TG GC CTG TTTGTGCC  
 || || ||| |||||  
 AC CG GAC AAACACGG  
 TC\_ AC CC  
 GAM1473 RECK 3' GCAACAGGCTCACTGGT 40869 T A AAT  
 ACCA GT AGCCTG TTGT  
 ||| || ||||| |||  
 TGGT CA TCGGAC AACG  
 \_ C \_\_\_\_  
 GAM1473 TNFSF8 3' GCACAAATTTAATACA 6966 AGCC  
 TGTA TGAATTTGTGC  
 ||| |||||  
 ACAT ATTTAAACACG  
 A\_\_\_\_  
 GAM1473 ADAR3 3' CACAAATTCAGAACGTG 38018 AAGC  
 CATGT CTGAATTTGTG  
 ||| |||||  
 GTGCA GACTTAAACAC  
 A\_\_\_\_  
 GAM1473 BIVM 3' CACAAATTCACCTTA 34667 CC  
 TAAG TGAATTTGTG  
 ||| |||||

ATTC ACTTAAACAC

GAM1473 C20orf160 3' GCAGTTACAGGATTACATGGT 54648 G AAT  
ACCATGTAA CCTG TTGT  
||||||| ||| |||  
TGGTACATT GGAC GACG  
A ATT

GAM1473 EPHA7 3' CACAAATTTGCTGCACA 15433 A\_ CT  
TGT AGC GAATTTGTG  
||| ||| |||||  
ACA TCG TTAAACAC  
CG \_

GAM1473 FLJ12783 3' AGTTCAGGCTCACTG 48675 T A  
CA GT AGCCTGAATT  
|| || |||||  
GT CA TCGGACTTGA  
\_ C

GAM1473 HSC3 3' CACAGGTTTCAGACTACA 59067 A C  
TGTA G CTGAATTTGTG  
|||| | |||||  
ACAT C GACTTGGACAC  
\_ A

GAM1473 KIAA0316 3' GCACAAATGCTCTTCACAGTGG 69674 \_ \_ CCTGA  
T ACCA TGT AAG ATTTGTGC  
|||| ||| |||||  
TGGT ACA TTC TAAACACG  
G C TCG\_

GAM1473 KIAA0453 3' GCACAAGTAGCTACATAGT 69047 C A CTGA  
AC ATGTA GC ATTTGTGC  
|| |||| || |||||  
TG TACAT CG TGAACACG  
A \_ A\_

GAM1473 KIAA1423 3' AATTCAAGTTTACATG 61719 C  
CATGTAAGC TGAATT  
||||||| |||||  
GTACATTTG ACTTAA  
A

GAM1473 KIAA1691 3' GCACAAATGCTGTCCATGG 92556 TA\_ CTGA  
CCATG AGC ATTTGTGC  
|||| ||| |||||  
GGTAC TCG TAAACACG  
CTG \_

GAM1473 PPP1R3B 3' GCCAGGTTTCAGATTACA 44820 GC T  
TGTA CTGAATTTG GC  
|||| ||||| |||  
ACATT GACTTGGAC CG  
A\_ \_

GAM1473 SFXN2 3' GCAGCAGAGTTACATGGT 73946 GC AATTG  
ACCATGTAA CTG TGC  
||||||| ||| |||

		TGGTACATT GAC ACG	
		GA G_____	
GAM1473	TBC1D2	5' TAAATTCAGACCTACTGGT 37321	T AGC
		ACCA GTA CTGAATTTG	
		TGGT CAT GACTTAAAT	
		_ CCA	
GAM1473	ZNF347	3' GGCTTTATTCAGGCCTCACA 50848	AA_ TTGT
		TGT GCCTGAAT GCC	
		ACA CGGACTTA CGG	
		CTC TTT_	
GAM1473	LOC134147	3' CACAAATTCAGTAGGACGT 57158	AAGC
		ATGT CTGAATTTGTG	
		TGCA GACTTAAACAC	
		GGAT	
GAM1473	LOC151195	5' GCACAAATTTATTTACA 80169	CC
		TGTAAG TGAATTTGTGC	
		ACATTT ATTTAAACACG	
		—	
GAM1473	LOC152860	3' AATTCCAGCTTACATGG 80695	CT
		CCATGTAAGC GAATT	
		GGTACATTCTG CTTAA	
		AC	
GAM1473	LOC200382	3' ACAGGGGCCAGACTTACATG 88801	C AA_
		CATGTAAG CTG TTTGT	
		GTACATTC GAC GGACA	
		A CGG	
GAM1473	LOC93622	3' ACAGTCATTCCAGGCTTAGATG 56929	G _ _
		CAT TAAGCCTG AAT TTGT	
		GTA ATTCGGAC TTA GACA	
		G C CT	
GAM1474	FCMD	3' AATGGCACATAGATAGGCA 22085	CCTG A
		TGCCTGTTT AT TGCCATT	
		ACGGATAGA TA ACGGTAA	
		— C	
GAM1474	GIPR	3' AATGGTGAAGGAAACAG 3895	GATAT
		CTGTTTCCT GCCATT	
		GACAAAGGA TGGTAA	
		AG_	
GAM1474	MPP3	3' GGCATATCAGAAAACA 8637	C
		TGTTT CTGATATGCC	



ACAA GACTATACGG  
 A  
 GAM1474 SOS2 5' GAATGGCATATCAGCAAAC 68536 C  
 GTTT CTGATATGCCATTC  
 |||| |||||  
 CAAA GACTATACGGTAAG  
 C  
 GAM1474 SPAG6 3' GAATGAACAAAGAAGCAGGCA 24905 CTGATATGC  
 TGCCTGTTTC CATT  
 ||||| ||||  
 ACGGACGAAG GTAAG  
 AAACAA\_\_  
 GAM1474 TTC3 5' AATGGCATATTTACAG 12411 TTCCT  
 CTGT GATATGCCATT  
 ||| |||||  
 GACA TTATACGGTAA  
 CT\_\_  
 GAM1474 ZNF144 3' AATGCCACAGGAAACA 23076 ATA C  
 TGTTTCCTG TG CATT  
 ||||| ||||  
 ACAAAGGAC AC GTAA  
 \_\_ C  
 GAM1474 DRCTNNB1A 3' GCCAATCTGAAAACAGGCA 50840 CCT AT  
 TGCCTGTTT GAT GC  
 ||||| ||| ||  
 ACGGACAAA CTA CG  
 AGT AC  
 GAM1474 FLJ12888 3' AATGGCATATTGAAAACA 46314 CC  
 TGTTT TGATATGCCATT  
 |||| |||||  
 ACAA GTTATACGGTAA  
 A\_  
 GAM1474 FLJ20695 3' AATGGAGAGGAAACAGGC 35553 GATATG  
 GCCTGTTTCCT CCATT  
 ||||| ||||  
 CGGACAAAGGA GGTA  
 GA\_\_  
 GAM1474 FLJ33069 5' TATACCAGGAAACAGACA 58321 C A  
 TG CTGTTTCCTG TATG  
 || ||||| ||||  
 AC GACAAAGGAC ATAT  
 A C  
 GAM1474 FPGT 3' AATGCAGACATCAAGAAGCAGG 13844 C A\_\_ C  
 CA TGCCTGTTTC TGAT TGC ATT  
 ||||| ||| |||  
 ACGGACGAAG ACTA ACG TAA  
 A CAG \_  
 GAM1474 OR51E2 3' GAATAACATATCAAATGAAACA 47793 C\_\_ CC  
 GG CCTGTTTC TGATATG ATTC  
 ||||| ||||| |||

GGACAAAG ACTATAC TAAG  
TAA AA  
GAM1474 PTBP2 3' AATGGCATATGTAAAGGCA 41028 GTTTCCTG  
TGCCT ATATGCCATT  
||||| |||||  
ACGGA TATACGGTAA  
AATG\_\_\_\_  
GAM1474 LOC144571 3' AATGAACAGGAAACAGG 83153 ATATGC  
CCTGTTTCCTG CATT  
||||||| |||  
GGACAAAGGAC GTAA  
AA\_\_\_\_  
GAM1474 LOC148562 3' GAATGGCATTTAAGAAAACAAG 78915 C C GAT  
C GC TGTTC CT ATGCCATT  
|| ||| || |||||  
CG ACAA GA TACGGTAAG  
A A ATT  
GAM1474 LOC157867 3' GAATGAAAGGAAGAAATAGGCA 86557 CTGATATGC  
TGCCTGTTTC CATT  
||||||| |||  
ACGATAAAG GTAAG  
AAGGAAA\_\_\_\_  
GAM1474 LOC169966 3' AATGGCAAACAGGAAA 82555 ATA  
TTTCCTG TGCCATT  
||||| |||||  
AAAGGAC ACGGTAA  
AA\_  
GAM1474 LOC197125 3' GAATGAGGATGTAGGAAGCAGG 87899 ATATGC  
CA TGCCTGTTTCCTG CATT  
||||||| |||  
ACGGACGAAGGAT GTAAG  
GTAGGA  
GAM1474 LOC199837 5' ATATCAGGACACAAGCA 88404 C T  
TGC TGT TCCTGATAT  
||| ||| |||||  
ACG ACA AGGACTATA  
A C  
GAM1474 LOC200317 3' GCACCAGGAAACAGCA 88795 C ATA  
TGC TGTTCCTG TGC  
||| ||||| |||  
ACG ACAAAGGAC ACG  
\_ C\_  
GAM1474 LOC200471 5' AACAGCAGGGAAACAGGC 90047 GATA CA  
GCCTGTTTCCT TGC TT  
||||||| ||| |||  
CGGACAAAGGG ACG AA  
\_\_\_\_ AC  
GAM1474 LOC220021 3' ATGGCAAAGACAGGCA 93391 CCTGATA  
TGCCTGTTT TGCCAT  
||||||| |||||

ACGGACAGA ACGGTA  
 A\_\_\_\_\_  
 GAM1474 LOC253981 3' AATAGCAATACAACAGGCA 95827 TCCTG A C  
 TGCCTGTT AT TGC ATT  
 ||||| || ||| |||  
 ACGGACAA TA ACG TAA  
 CA\_\_\_\_ A  
 GAM1475 ARHGEF6 3' CAAACTTGAAGCCAGGC 68197 ACCA  
 GCCTGG CAAGTTTG  
 ||||| |||||  
 CGGACC GTTCAAAC  
 GAA\_  
 GAM1475 CNTN2 3' GTCACAACCCAGGTGA 17411 ACCACAA \_  
 TCGCCTGG GTT TGAC  
 ||||| || ||| |||  
 AGTGGACC CAA ACTG  
 \_\_\_\_\_ C  
 GAM1475 CORO2A 3' AAAGTGTGGTCCAGAGA 12642 GC A  
 TC CTGGACCACA GTTT  
 || ||||| ||||| |||  
 AG GACCTGGTGT CAAA  
 A\_ \_  
 GAM1475 CORO2A 3' AAAGTGTGGTCCAGAGA 53398 GC A  
 TC CTGGACCACA GTTT  
 || ||||| ||||| |||  
 AG GACCTGGTGT CAAA  
 A\_ \_  
 GAM1475 GRLF1 3' AGGTCAGAAAGTGGCCCAGG 78551 A AAG  
 CCTGG CCAC TTTGACCT  
 ||||| ||| |||||  
 GGACC GGTG AGACTGGA  
 C AA\_  
 GAM1475 LAPTM5 3' AGGCTTGTGGTCAAGC 22199 CTG  
 GC GACCACAAGTTT  
 || ||||| |||||  
 CG CTGGTGTTCGGA  
 AA\_  
 GAM1475 POU2AF1 3' AGATTTACAGTCCAGGC 20647 CAC  
 GCCTGGAC AAGTTT  
 ||||| |||||  
 CGGACCTG TTTAGA  
 ACA  
 GAM1475 PTGS1 3' GTCTCCTGTCTTATGGTCCAG 54574 C TTT\_\_\_\_  
 CTGGACCA AAG GAC  
 ||||| || |||  
 GACCTGGT TTC CTG  
 A TGTCT  
 GAM1475 PTGS1 3' GTCTCCTGTCTTATGGTCCAG 6355 C TTT\_\_\_\_  
 CTGGACCA AAG GAC  
 ||||| || |||

			GACCTGGT TTC	CTG		
			A TGCCT			
GAM1475	TRIM34	5'	AGGTCAAGTTGAGCCCAG	55224	ACCA	G
			CTGG CAA TTTGACCT			
			GACC GTT GAACTGGA			
			CGA_ _			
GAM1475	TRIM9	5'	AGGCCAGGCAAGTCCAGGC	30749	CACAA	A
			GCCTGGAC GTTTG CCT			
			CGGACCTG CGGAC GGA			
			AA_ _ C			
GAM1475	ABLM	5'	GATATGTAACCCAGGCGG	22030	ACC	A
			TCGCCTGG ACA GTT			
			GGCGGACC TGT TAG			
			CAA A			
GAM1475	AMOT	3'	AGGCATCTTCATGGTCCAGGGA	55716	G	C_ TT A
			TC CCTGGACCA AAG TG CCT			
			AG GGACCTGGT TTC AC GGA			
			_ AC T_ _			
GAM1475	DKFZp434D177	5'	TTAGACCCAGGCGA	50056	ACCACAA	
			TCGCCTGG GTTTGA			
			AGCGGACC CAGATT			
			_____			
GAM1475	DKFZp434D177	5'	TTAGACCCAGGCGA	79443	ACCACAA	
			TCGCCTGG GTTTGA			
			AGCGGACC CAGATT			
			_____			
GAM1475	FLJ23420	3'	CAAGTGGGTCCAGGC	46845	A	AG
			GCCTGGACC CA TTTG			
			CGGACCTGG GT GAAC			
			_____			
GAM1475	HSA249128	5'	GGCGCGGTCCAGGCGG	34152	ACAA	
			TCGCCTGGACC GTT			
			GGCGGACCTGG CGG			
			CG_			
GAM1475	MGC15668	5'	AGACCCGGTGGTCCAGACG	51277	C	AA_
			CG CTGGACCAC GTTT			
			GC GACCTGGTG CAGA			
			A GCC			
GAM1475	MGC22014	3'	AGGTCCCGAGTGTAACCCAGGT	64486	ACC	AGTTT
			GA TCGCCTGG ACA GACCT			

		AGTGGACC TGT CTGGA		
		CAA GAGCC		
GAM1475	SDCCAG10 5'	AGAGTTGTGGTCCAAAGA	19641	GCC G
		TC TGGACCACAA TTT		
		AG ACCTGGTGTGTT AGA		
		AA_ G		
GAM1475	LOC115442 3'	AGGTCAGGGATGGTCCAG	72676	CAAG
		CTGGACCA TTTGACCT		
		GACCTGGT GGA CTGGA		
		AG_		
GAM1475	LOC129011 5'	AGACCTGCGGTCCAGGC	74862	A A
		GCCTGGACC CA GTTT		
		CGGACCTGG GT CAGA		
		C C		
GAM1475	LOC130536 5'	GCAAAGTCCAGGCG	75746	CACAAG A
		CGCCTGGAC TTTG C		
		GCGGACCTG AAAC G		
		_____ C		
GAM1475	LOC149108 3'	AGACTTCACTGTGGTCCA	84357	_____
		TGGACCACA AGTTT		
		ACCTGGTGT TCAGA		
		CACT		
GAM1475	LOC221688 5'	AGACTCGGGCCCAGACGA	93674	C A ACA
		TCG CTGG CC AGTTT		
		AGC GACC GG TCAGA		
		A C GC_		
GAM1475	LOC256228 5'	AGACTTGTGGTCAAAGC	96233	CTG
		GC GACCACAAGTTT		
		CG CTGGTGTT CAGA		
		AAA		
GAM1475	LOC257441 5'	TTAGACCCAGGCGA	95566	ACCACAA
		TCGCCTGG GTTTGA		
		AGCGGACC CAGATT		
		_____		
GAM1475	LOC91960 3'	AGGTGCCTCTCGTGGTCCAAGC	67657	C A TTTG
		GC TGGACCAC AG ACCT		
		CG ACCTGGTG TC TGGA		
		A C TCCG		
GAM1475	LOC92840 3'	GTCCCTCGGGTCCAGGC	56435	ACA TTT
		GCCTGGACC AG GAC		

CGGACCTGG TC CTG  
GC\_ C\_\_

GAM1476 CASP8 3' TTCATCTGCTGTATCCTCTCCC 52956 AA C \_  
A TG AGAG ATACAGTAG TGAG  
|| ||| ||||| |||  
AC TCTC TATGTCGTC ACTT  
CC C T

GAM1476 CCND1 3' CTGTGTATCTCTTTCA 53887 C G  
TGAAAGAG ATACA TAG  
||||| ||| |||  
ACTTTCTC TATGT GTC

GAM1476 CHRN2 3' CTCATCTCCATGCTCTTTCA 5623 AC TA  
TGAAAGAGCAT AG GTGAG  
||||||| || |||  
ACTTTCTCGTA TC TACTC  
CC \_

GAM1476 CR2 3' TTCACTGCCATATACTCTTCA 8535 A C CA  
TGAA GAG ATA GTAGTGAG  
||| ||| ||| |||||  
ACTT CTC TAT CGTCACTT  
\_ A AC

GAM1476 EPB49 3' CTCACACACTATGCTCTCTCA 8785 A CA A  
TGA AGAGCATA GT GTGAG  
|| ||||| || |||  
ACT TCTCGTAT CA CACTC  
C CA \_

GAM1476 G6PC 3' CTCAGCACAGACTCTTTCA 3823 CATACA AG  
TGAAAGAG GT TGAG  
||||| || |||  
ACTTTCTC CA ACTC  
AGA\_\_ CG

GAM1476 GYG2 3' CTCACTACCTCAGTTCTCA 14048 A ATACA  
A AGAGC GTAGTGAG  
| ||| |||||  
A TCTTG CATCACTC  
C ACTC\_

GAM1476 LIMD1 3' TCTCACTGATGTTATTC 26466 CAT G  
GAG ACA TAGTGAGA  
|| || |||||  
CTT TGT GTCACCTCT  
AT\_ A

GAM1476 PSMC1 3' TTCCCAATAAAGCGTGCTCTTT 10968 ACAG G A  
CA TGAAAGAGCAT TA TG GAA  
||||||| || |||  
ACTTTCTCGTG AT AC CTT  
CGAA A C

GAM1476 SOX12 3' CTCACTACCTGTATCTC 22696 C \_  
GAG ATACAG TAGTGAG  
|| ||||| |||||

CTC TATGTC ATCACTC  
 \_ C  
 GAM1476 TOX 3' CTCAAGCTGCATGCTTTTCA 28290 A A AG  
 TGAA GAGCAT CAGT TGAG  
 ||| ||||| ||| ||||  
 ACTT TTCGTA GTCG ACTC  
 \_ C A\_  
 GAM1476 ZNF6 3' CTCACTAACTGTCTC 41817 CAT \_  
 GAG ACAGT AGTGAG  
 || ||||| |||||  
 CTC TGTCA TCACTC  
 \_ A  
 GAM1476 APACD 5' ACTGCTGCTCTTTCA 19354 TACA  
 TGAAAGAGCA GTAGT  
 ||||| ||||  
 ACTTTCTCGT CGTCA  
 \_  
 GAM1476 DKFZP434E2135 3' CTCTGCATGCTCTTTC 47954 A T  
 GAAAGAGCAT CAG AG  
 ||||| ||| ||  
 CTTTCTCGTA GTC TC  
 C \_  
 GAM1476 FLJ20006 3' TTCTCACTACTGCACTTGACT 34327 \_ TA\_  
 AG CA CAGTAGTGAGAA  
 || || ||||| |||||  
 TC GT GTCATCACTCTT  
 A TCAC  
 GAM1476 FLJ21870 3' TCCACACCACACCCTCTTTCA 43465 CATACA A A  
 TGAAAGAG GT GTG GA  
 ||||| || ||| ||  
 ACTTTCTC CA CAC CT  
 CCACAC \_ \_  
 GAM1476 HIF1AN 3' TTCTCAAGTGTAGCTCTTTCA 61982 A GTAG  
 TGAAAGAGC TACA TGAGAA  
 ||||| ||| |||||  
 ACTTTCTCG ATGT ACTCTT  
 \_ GA\_  
 GAM1476 KIAA0255 3' CTCAGTCCCCACATTCTCCCA 28467 AA CATACA  
 TG AGAG GTAGTGAG  
 || ||| |||||  
 AC TCTT CGTCACTC  
 CC ACACCC  
 GAM1476 KIAA0373 3' TTCTCACTACCTTGTACCTTT 28014 CA \_  
 AGAG TACA GTAGTGAGAA  
 ||| ||| ||||| |||||  
 TTTC ATGT CATCACTCTT  
 C\_ TC  
 GAM1476 KIAA0408 3' TCTCATAATATGCTTT 28138 CAGTA  
 AGAGCATA GTGAGA  
 ||||| |||||

		TTTCGTAT	TACTCT		
		AA__			
GAM1476 KIAA0449	3'	TTCTCTGCCC	ACTCTTTCA	34203	CATACA T
		TGAAAGAG	G TAG GAG		
		ACTTTCTC	CGTC CTT		
		ACC__	T		
GAM1476 KIAA1328	3'	TCTCACTACTACATTTCT		61657	C AC
		AGAG AT	AGTAGTGAGA		
		TCTT TA	TCATCACTCT		
		_ CA			
GAM1476 MacGAP	3'	CTGTAATATATGCTCTCTCA		53182	A ____
		TGA AGAGCA	TACAG		
		ACT TCTCGT	ATGTC		
		C	ATATA		
GAM1476 MGC4643	3'	TTCTCACTAAAATTTACTTTC		51160	AGCATACAG
		GAAAG	TAGTGAGAA		
		CTTTC	ATCACTCTT		
		ATTTAAA__			
GAM1476 MRPL48	3'	CTACTGTAGACCCTTTCA		32134	AGCA
		TGAAAG	TACAGTAG		
		ACTTTC	ATGTCATC		
		CCAG			
GAM1476 OCT11	3'	CTCACTGCATGCTCTGCCA		26818	AA ACA
		TG AGAGCAT	G TAGTGAG		
		AC TCTCGTA	CGTCACTC		
		CG	__		
GAM1476 PRO0038	5'	TTCTCACTTTTATACTACTTCTT		26094	AG CATACAGT
	CA	TGAA AG	AGTGAGAA		
		ACTT TC	TCACTCTT		
		CT ATCATATT			
GAM1476 SEMA4G	5'	TCCCAGAACAAATGCTCTTCCA		94685	A ACA AG A
		TG AAGAGCAT	GT TG GA		
		AC TTCTCGTA	CA AC CT		
		C	AA_ AG C		
GAM1476 SKIP	5'	CTCTTGCCCTGCTCTTTCA		55369	TACA T
		TGAAAGAGCA	G TAG GAG		
		ACTTTCTCGT	CGTT CTC		
		C__ _			
GAM1476 LOC127703	3'	TTCACTGCATGGCCCTTCA		74684	A A ATACA
		TGAA G GC	G TAGTGAG		



	ACTT C CG CGTCACTT	
	_ C GTA__	
GAM1476 LOC144231 5'	TCTCATCTATGCTCTTTC 83020	CAGTA
	GAAAGAGCATA GTGAGA	
	CTTTCTCGTAT TACTCT	
	C__	
GAM1476 LOC145980 5'	CACTAGGCTGCTGCTCTTTC 83600	TA _
	GAAAGAGCA CAGT AGTG	
	CTTTCTCGT GTCG TCAC	
	C_ GA	
GAM1476 LOC147093 5'	TTCTCACTACCCCCAGCTT 83946	ATACA
	GAGC GTAGTGAGAA	
	TTCG CATCACTCTT	
	ACCCC	
GAM1476 LOC149535 3'	TCCTCTAGTAATGCTCTTTCA 79421	_ _ T T
	TGAAAGAGCAT AC AG AG GA	
	ACTTTCTCGTA TG TC TC CT	
	A A _ _	
GAM1476 LOC155036 5'	TTCTCACTTCTCATTCTCTTCC 86347	A CATAC T
A	TG AAGAG AG AGTGAGAA	
	AC TTCTC TC TCACTCTT	
	C TTAC_ T	
GAM1476 LOC158435 3'	CTCACTGCTACACTCCCATCA 56717	AA_ CATAC
	TGA GAG AGTAGTGAG	
	ACT CTC TCGTCACTC	
	ACC ACA__	
GAM1476 LOC158471 3'	TTCTCAAGATGAATGCTCTTTC 57183	A GTAG
A	TGAAAGAGCAT CA TGAGAA	
	ACTTTCTCGTA GT ACTCTT	
	A AGA_	
GAM1476 LOC196463 3'	TCCTACTGCTGCTCTCTCA 87715	A TA T
	TGA AGAGCA CAGTAG GA	
	ACT TCTCGT GTCATC CT	
	C C_ _	
GAM1476 LOC200169 5'	TTTTACTGCACCTCTTCCA 89961	A CATACA
	TG AAGAG GTAGTGAGA	
	AC TTCTC CGTCATTTT	
	C CA__	
GAM1476 LOC201562 3'	TTCATTTGAGCATGCTCTTTCA 88977	ACAGT
	TGAAAGAGCAT AGTGAG	

		ACTTTCTCGTA	TTACTT		
		CGACT			
GAM1476	LOC202754	3'	TCCTTAGATGCTCTTTCA	82710	ACAGT T
			TGAAAGAGCAT	AG GA	
			ACTTTCTCGTA	TC CT	
			GAT__		
GAM1476	LOC219988	3'	TTCTCACTTACTCCTCTCCCA	91628	AA CATAC _
			TG AGAG	AGTA GTGAGAA	
			AC TCTC	TCAT CACTCTT	
			CC C__	T	
GAM1476	LOC51619	3'	TTCTCACTACCGCCCGCTC	32020	ATACA
			GAGC	GTAGTGAGAA	
			CTCG	CATCACTCTT	
			CCCGC		
GAM1476	LOC90564	3'	CTCACTACCGCCCTCTCA	63244	A A ATACA
			TGA AG GC	GTAGTGAG	
			ACT TC CG	CATCACTC	
			C C CC__		
GAM1476	LOC93496	3'	TCTCTGATACATCACTCTTTCA	72440	CATACA GT_
			TGAAAGAG	GTA GAGA	
			ACTTTCTC	CAT CTCT	
			ACTA__	AGT	
GAM1477	ARSD	3'	TCACAGTCTTAAAAGTCTGCA	23796	CTCTCTT A
			TGCAGACTTTT	CT TGA	
			ACGTCTGAAAA	GA ACT	
			TTCT__	C	
GAM1477	CUL4B	3'	TCATAGAAGAGAAAAATC	13142	C C
			GA TTTT	TCTCTTCTATGA	
			CT AAAA	AGAGAAGATACT	
			- -		
GAM1477	OTOR	3'	AGAAAAAAAAAAGTCTGTA	39345	CTCTC
			TGCAGACTTTT	TTCT	
			ATGTCTGAAAA	AAGA	
			AAAA_		
GAM1477	PHGDH	3'	ATAGGGAGAGAAAATCCACA	64260	CA C T
			TG GA TTTTCTCTCT	CTAT	
			AC CT AAAAGAGAGG	GATA	
			AC _		
GAM1477	PLAG1	3'	TCATAGAAAAGAAGATCATGCA	10610	_ C CTC
			TGCA GA TTTTCT	TTCTATGA	

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          ACGT CT AGAAGA AAGATACT
          A _ A__
GAM1477 POU4F1 3' CATAGAAGAGAAAAAGAGCA 20662 AGA C
          TGC CTTTT TCTCTTCTATG
          ||| |||| ||||||||
          ACG GAAAA AGAGAAGATAC
          A__ A
GAM1477 DKFZP434C171 5' GAAAGAGAAAAATCTG 31555 C C
          CAGA TTTTCTCT TTC
          |||| |||||| |||
          GTCT AAAAGAGA AAG
          A _
GAM1477 DKFZP564I052 3' TGGGAGAGAGAAAAACCTG 66721 AC
          CAG TTTTCTCTCTTCTA
          ||| |||||||||
          GTC AAAAGAGAGAGGGT
          CA
GAM1477 DKFZP586N0721 3' TCATAGAAAAGAACTTGC 31206 ACT CTC
          GCAG TTTCT TTCTATGA
          |||| |||| ||||||
          CGTT AAAGA AAGATACT
          C__ A__
GAM1477 DNAJC6 3' CATAGAAACAAAGTCTCA 28845 C TCTCTC
          TG AGACTTT TTCTATG
          || ||||| |||||
          AC TCTGAAA AAGATAC
          _ CA__
GAM1477 FLJ10081 3' TCATAGAAGACCTGGAA 35802 TC_
          TTTC TCTTCTATGA
          |||| |||||||
          AAGG AGAAGATACT
          TCC
GAM1477 FLJ11753 3' AGAGAGAAAAGAAAATCTGCA 45077 ____
          TGCAGA CTTTTCTCTCT
          ||||| |||||||
          ACGTCT GAAAAGAGAGA
          AAAA
GAM1477 FLJ12770 3' CAAGGGAAGAGAAAAGTCTGC 49738 C A
          GCAGACTTTTCTCT TTCT TG
          ||||||||| ||| ||
          CGTCTGAAAAGAGA AGGG AC
          _ A
GAM1477 FLJ21302 5' AAGAAAAAAGGTCTGCA 43206 CTC
          TGCAGACTTTT TCTT
          ||||||| |||
          ACGTCTGGAAA AGAA
          AAA
GAM1477 FXC1 3' CACAGAAGAGAGATGAAACCTG 69033 AC _ A
          TA TGCAG TTT TCTCTCTTCT TG
          |||| ||| ||||||| ||

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		ATGTC AAG AGAGAGAAGA AC		
		CA T C		
GAM1477	HSPC251	3' AGCTAGAAAACAGTCTGCA	33247	___ CT
		TGCAGACT TTTCT CT		
		ACGTCTGA AAAGA GA		
		CA TC		
GAM1477	KIAA0063	3' AGGAAAAAAAAAGTCTGC	29616	CTC
		GCAGACTTTT TCTT		
		CGTCTGAAAA AGGA		
		AAA		
GAM1477	KIAA0265	3' AGGCAGAGAAAACCTGCA	69875	AC _
		TGCAG TTTTCTCT CTT		
		ACGTC AAAAGAGA GGA		
		C_ C		
GAM1477	KIAA0326	3' CACAGGTCCCTGAAGAGTCCGC	64319	A TCTCT A
	A	TGC GACTTTTC TCT TG		
		ACG CTGAGAAG GGA AC		
		C TCCCT C		
GAM1477	KIAA1573	3' TGGAAGAGAGAAAAATCTGC	62692	C
		GCAGA TTTTCTCTCTTCTA		
		CGTCT AAAAGAGAGAAGGT		
		A		
GAM1477	SH2D3A	3' TCACAGAAGAGGTGGGGACCGC	18508	AGAC TT _ A
	A	TGC TT C TCTCTTCT TGA		
		ACG AG G GGAGAAGA ACT		
		CC_ GG T C		
GAM1477	SLC37A1	3' AGTGAGAAAAGTCTGCA	38562	T
		TGCAGACTTTTCTC CT		
		ACGTCTGAAAAGAG GA		
		T		
GAM1477	Spir-1	5' GAAAAGAGAAAAATCTCA	64700	C C C
		TG AGA TTTTCTCT TTC		
		AC TCT AAAAGAGA AAG		
		_ A A		
GAM1477	TAGAP	3' CATAGAAGAAAGAAACAGACTG	54029	A _ C
	C	GCAG CT TTTCT TCTTCTATG		
		CGTC GA AAAGA AGAAGATAC		
		A C A		
GAM1477	TUSP	3' CATAGCAAAAAGTCTGCA	39628	CTCTCTT
		TGCAGACTTTT CTATG		

			ACGTCTGAAAA	GATAC		
			AC_____			
GAM1477	UBE2E1	3'	AAGAAGAGAGCTGC	12482	ACTTTT	A
			GCAG CTCTCTTCT T			
			CGTC GAGAGAAGA A			
			_____ C			
GAM1477	ZFD25	3'	TCATACTGGAGAGAAAGCCTAC	32584	C A T	TC
	A		TG AG CTTT CTCTCT TATGA			
			AC TC GAAA GAGAGG ATACT			
			A C _ TC			
GAM1477	LOC145748	3'	AGAGAAAGAAGCCTGCA	83460	A C	
			TGCAG CTTTT TCTCT			
			ACGTC GAAGA AGAGA			
			C A			
GAM1477	LOC150630	5'	CATAGAAGCTTGAAGTT	85101	TCTCT	
			GACTTT CTTCTATG			
			TTGAAG GAAGATAC			
			TTC_			
GAM1477	LOC158327	3'	TCATAGAAGAAAGTTGGATCTC	81882	C _ TTT	C
	A		TG AGA CT CT TCTTCTATGA			
			AC TCT GG GA AGAAGATACT			
			_ A TT_ A			
GAM1477	LOC254945	5'	TAGAAAAAAGAAAAGCCTGTA	96895	A	CTC
			TGCAG CTTTTCT TTCTA			
			ATGTC GAAAAGA AAGAT			
			C AAA			
GAM1477	LOC51279	3'	CATAAAAGAGAGAAGAG	33309	C	
			CTTTTCTCTCTT TATG			
			GAGAAGAGAGAA ATAC			
			A			
GAM1477	LOC90594	5'	TCACAGAAGAGAAAAGTC	63471	TTC	A
			GACTT TCTCTTCT TGA			
			CTGAA AGAGAAGA ACT			
			_____ C			
GAM1477	LOC91548	5'	CATAGAAGAAATGGTTTCCA	66411	C	TTTCTC
			TG AGACT TCTTCTATG			
			AC TTTGG AGAAGATAC			
			C TAA_____			
GAM1478	ACADSB	3'	CAGCTCACTGCAGCCTTGACCT	7843	CAA	
			AGG GAGGTTGCAGTGAGCTG			

TCC TTCCGACGTCACCTCGAC  
 AG\_  
 GAM1478 ADAMTS4 3' CAGCTCACTGCAACCTTCGCC 17503 AA  
 GGC GAGGTTGCAGTGAGCTG  
 ||| |||||  
 CCG TTCCAACGTCACCTCGAC  
 C\_  
 GAM1478 ADRB3 3' CAGCCTTTCCACAACCTCTACC 3431 CA CAGT \_  
 T AGG AGAGGTTG GAG CTG  
 ||| ||||| ||| |||  
 TCC TCTCCAAC TTC GAC  
 A\_ ACCT C  
 GAM1478 AHR 3' CACTGCAACCTCTACCT 7876 CA  
 AGG AGAGGTTGCAGTG  
 ||| |||||  
 TCC TCTCCAACGTCAC  
 A\_  
 GAM1478 AK2 3' CTGCAACCTCTTGACC 25500 \_  
 GG CAAGAGGTTGCAG  
 || |||||  
 CC GTTCTCCAACGTC  
 A  
 GAM1478 ALDH1B1 3' CACTGCAACCTCCGCCT 5490 AA  
 AGGC GAGGTTGCAGTG  
 |||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 AP3B2 5' CGCCGCAACCTCCTCCT 16186 CAA A  
 AGG GAGGTTGC GTG  
 ||| ||||| |||  
 TCC CTCCAACG CGC  
 TC\_ C  
 GAM1478 APM1 3' CTTACTGCAACCTTTGCCT 16591 A  
 AGGCA GAGGTTGCAGTGAG  
 |||| |||||  
 TCCGT TTCCAACGTCATTG  
 \_  
 GAM1478 APOL1 3' CAGCTCACTGCAAGCTCTGCCT 13343 A G  
 AGGCA GAG TTGCAGTGAGCTG  
 |||| ||| |||||  
 TCCGT CTC AACGTCACCTCGAC  
 \_ G  
 GAM1478 APPBP2 3' CACTGCAACCTCCGCCT 21073 AA  
 AGGC GAGGTTGCAGTG  
 |||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 AQP6 3' CACTGCAACCTCTACCT 53911 CA  
 AGG AGAGGTTGCAGTG  
 ||| |||||

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TCC TCTCCAACGTCAC
A_
GAM1478 AQP6 3' CACTGCAACCTCTACCT 7940 CA
AGG AGAGGTTGCAGTG
||| |||||
TCC TCTCCAACGTCAC
A_
GAM1478 ARCN1 3' CAGCTCACTGCAACCTCCGCCT 7973 AA
AGGC GAGGTTGCAGTGAGCTG
||| |||||
TCCG CTCCAACGTCACCTCGAC
C_
GAM1478 ATP1B2 3' CAGCTCACTGCAACTTCCGC 8045 AA
GC GAGGTTGCAGTGAGCTG
|| |||||
CG CTTCAACGTCACCTCGAC
C_
GAM1478 ATP7A 3' CACTGCAACCTCTGCCT 3520 A
AGGCA GAGGTTGCAGTG
||| |||||
TCCGT CTCCAACGTCAC
-
GAM1478 ATP8B2 3' CAGCTCACTGCAACCTCCACCT 65214 CAA
AGG GAGGTTGCAGTGAGCTG
||| |||||
TCC CTCCAACGTCACCTCGAC
AC_
GAM1478 AXL 3' CACTGCAACCTTCACCT 8094 CAA
AGG GAGGTTGCAGTG
||| |||||
TCC TTCCAACGTCAC
AC_
GAM1478 AXL 3' CACTGCAACCTTCACCT 41591 CAA
AGG GAGGTTGCAGTG
||| |||||
TCC TTCCAACGTCAC
AC_
GAM1478 BMP1 3' CAGCTCACTAGGCCGATCCTGC 20417 A _ GC
T GGCA GA GGTT AGTGAGCTG
||| || ||| |||||
TCGT CT CCGG TCACTCGAC
C AG A_
GAM1478 BRIP1 3' CACTGCAACCTTCACCT 49396 CAA
AGG GAGGTTGCAGTG
||| |||||
TCC TTCCAACGTCAC
AC_
GAM1478 C7 3' CTGCAACCTCCGCCT 5160 AA
AGGC GAGGTTGCAG
||| |||||

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TCCG CTCCAACGTC  
 C\_  
 GAM1478 CAMLG 3' CACCGCAACCTCCACCT 8232 CAA A  
 AGG GAGGTTGC GTG  
 ||| ||||| |||  
 TCC CTCCAACG CAC  
 AC\_ C  
 GAM1478 CASP2 3' CAGCTCACTGCAAGCTC 6895 G  
 GAG TTGCAGTGAGCTG  
 ||| |||||  
 CTC AACGTCACTCGAC  
 G  
 GAM1478 CASP2 3' CAGCTCACTGCAAGCTC 52137 G  
 GAG TTGCAGTGAGCTG  
 ||| |||||  
 CTC AACGTCACTCGAC  
 G  
 GAM1478 CASP2 3' CAGCTCACTGCAAGCTC 52150 G  
 GAG TTGCAGTGAGCTG  
 ||| |||||  
 CTC AACGTCACTCGAC  
 G  
 GAM1478 CASP2 3' CAGCTCACTGCAAGCTC 52165 G  
 GAG TTGCAGTGAGCTG  
 ||| |||||  
 CTC AACGTCACTCGAC  
 G  
 GAM1478 CBFA2T3 3' ACTCCAACCTCTCGGCC 17755 A\_ C  
 GGC AGAGGTTG AGT  
 ||| ||||| |||  
 CCG TCTCCAAC TCA  
 GC C  
 GAM1478 CCNF 3' CTCAGTGTAACTCCGCCT 8317 AA  
 AGGC GAGGTTGCAGTGAG  
 ||| |||||  
 TCCG CTCCAATGTCACTC  
 C\_  
 GAM1478 CD5L 5' AGCTCATCACCTTCACCT 19708 CAA TGCA  
 AGG GAGGT GTGAGCT  
 ||| ||| |||||  
 TCC TTCCA TACTCGA  
 AC\_ C\_\_  
 GAM1478 CD81 3' CAGCTCACCTTGTTCCCTC 15132 TT \_  
 GAGG GCA GTGAGCTG  
 ||| ||| |||||  
 CTCC TGT CACTCGAC  
 CT TC  
 GAM1478 CDH1 3' CAGCTCACTGCAGCCTTGTCTCCT 15142 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||



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TCC TTCCGACGTCACTCGAC
TG_
GAM1478 CDH17 3' CAGCTCACTGCAACCTCCGCCT 14502 AA
AGGC GAGGTTGCAGTGAGCTG
|||||
TCCG CTCCAACGTCACTCGAC
C_
GAM1478 CDK10 3' AGCTCATCCCCTTGGCT 13399 G A TTGCA
AG CAAG GG GTGAGCT
|| ||| || |||||
TC GTTC CC TACTCGA
G C _____
GAM1478 CDK10 3' AGCTCATCCCCTTGGCT 53766 G A TTGCA
AG CAAG GG GTGAGCT
|| ||| || |||||
TC GTTC CC TACTCGA
G C _____
GAM1478 CDK10 3' AGCTCATCCCCTTGGCT 53774 G A TTGCA
AG CAAG GG GTGAGCT
|| ||| || |||||
TC GTTC CC TACTCGA
G C _____
GAM1478 CHST1 3' CAGCTCACCCCACTCCCTTCTG 13333 AG T__ CA
CC GGCA AGG TG GTGAGCTG
||||| ||| || |||||
CCGT TCC AC CACTCGAC
CT CTC CC
GAM1478 CLECSF12 3' CACCGCAACCTCCGCC 76684 AA A
GGC GAGGTTGC GTG
||| ||||| |||
CCG CTCCAACG CAC
C_ C
GAM1478 CRTAP 3' CAGCTCACTGCAACCTCCGCCT 21031 AA
AGGC GAGGTTGCAGTGAGCTG
|||||
TCCG CTCCAACGTCACTCGAC
C_
GAM1478 CSNK2A2 5' CAGCTCACTGCAACCTCCACCT 8560 CAA
AGG GAGGTTGCAGTGAGCTG
||| |||||
TCC CTCCAACGTCACTCGAC
AC_
GAM1478 CYP1A2 3' CAGCTCACTACAACCTCCGCCT 5681 AA C
AGGC GAGGTTG AGTGAGCTG
||||| |||||
TCCG CTCCAAC TCACTCGAC
C_ A
GAM1478 CYP1A2 3' CAGCTCACTGCAACCTCCACCT 5682 CAA
AGG GAGGTTGCAGTGAGCTG
||| |||||

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			TCC CTCCAACGTC	ACTCGAC		
			AC_			
GAM1478	CYP1A2	3'	CAGCTCACTGCAACCTCTGCCT	5684	AA	A
			AGGCA GAGGTTGCAGTGAGCTG			
			TCCGT CTCCAACGTC	ACTCGAC		
			—			
GAM1478	CYP1A2	3'	CAGCTCACTACAACCTCCGCCT	69100	AA	C
			AGGC GAGGTTG AGTGAGCTG			
			TCCG CTCCAAC	TCACTCGAC		
			C_	A		
GAM1478	CYP1A2	3'	CAGCTCACTGCAACCTCCACCT	69101	CAA	
			AGG GAGGTTGCAGTGAGCTG			
			TCC CTCCAACGTC	ACTCGAC		
			AC_			
GAM1478	CYP1A2	3'	CAGCTCACTGCAACCTCTGCCT	69103	A	
			AGGCA GAGGTTGCAGTGAGCTG			
			TCCGT CTCCAACGTC	ACTCGAC		
			—			
GAM1478	CYP2B6	3'	CACTGCAACCTCCACC	5724	CAA	
			GG GAGGTTGCAGTG			
			CC CTCCAACGTC	AC		
			AC_			
GAM1478	CYP2B6	3'	CACTGCAACCTCTGCCT	5725	A	
			AGGCA GAGGTTGCAGTG			
			TCCGT CTCCAACGTC	AC		
			—			
GAM1478	CYP4F3	3'	CATTGCAACCTCCGCCT	6111	AA	
			AGGC GAGGTTGCAGTG			
			TCCG CTCCAACGTT	AC		
			C_			
GAM1478	CYP51	3'	CAGCTCACTGCATCCTCTGCCT	5781	A	T
			AGGCA GAGG TGCAGTGAGCTG			
			TCCGT CTCC	ACGTC	ACTCGAC	
			—			
			T			
GAM1478	CYP8B1	3'	CACTACAACCTCTGCCT	15257	A	C
			AGGCA GAGGTTG AGTG			
			TCCGT CTCCAAC	TCAC		
			—			
			A			
GAM1478	CYP8B1	3'	CACTGCAACCTCTGCCT	15259	A	
			AGGCA GAGGTTGCAGTG			

TCCGT CTCCAACGTCAC

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      -
GAM1478 DFFB  3' CACTGCAACCTCCGCCT  87377  AA
                AGGC GAGGTTGCAGTG
                |||| |||||
                TCCG CTCCAACGTCAC
                C_
GAM1478 DHFR  3' CTTACTGCAACCTCCGCCT  5804  AA
                AGGC GAGGTTGCAGTGAG
                |||| |||||
                TCCG CTCCAACGTCATTC
                C_
GAM1478 DISC1 3' CACTGCAACCTCTACCT  37872  CA
                AGG AGAGGTTGCAGTG
                ||| |||||
                TCC TCTCCAACGTCAC
                A_
GAM1478 DSCR3 3' CAGCTCACTGCAACCTCCACCT 20173 CAA
                AGG GAGGTTGCAGTGAGCTG
                ||| |||||
                TCC CTCCAACGTCACTCGAC
                AC_
GAM1478 EFNB2 3' CAGCTCACTGCTGCTGCCT  14570  AGAG T
                AGGCA GT GCAGTGAGCTG
                |||| |||||
                TCCGT CG CGTCACTCGAC
                ____ T
GAM1478 EHD2  3' CAGCTCACTGCAACCTCCACCT 27489 CAA
                AGG GAGGTTGCAGTGAGCTG
                ||| |||||
                TCC CTCCAACGTCACTCGAC
                AC_
GAM1478 EIF2S3 3' GTGATCTGCAACCTCTGCC  7419  A    TGA
                GGCA GAGGTTGCAG GC
                |||| ||||| ||
                CCGT CTCCAACGTC TG
                ____ TAG
GAM1478 EPB72 3' CACTGCAACCTCCGCCT  14599  AA
                AGGC GAGGTTGCAGTG
                |||| |||||
                TCCG CTCCAACGTCAC
                C_
GAM1478 F2RL2 3' CATTGCAACCTCTGCCT  14619  A
                AGGCA GAGGTTGCAGTG
                |||| |||||
                TCCGT CTCCAACGTTAC
                -
GAM1478 FANCF 3' CAGTGCAACCTCTGCCT  42670  A    G
                AGGCA GAGGTTGCA TG
                |||| ||||| ||
```

			TCCGT CTCCAACGT AC	
			— G	
GAM1478 FCAR	3'	CACTGCAACCTTCGCCT	55791	AA
		AGGC GAGGTTGCAGTG		
		TCCG TTCCAACGTCAC		
		C_		
GAM1478 FCAR	3'	CACTGCAACCTTCGCCT	55810	AA
		AGGC GAGGTTGCAGTG		
		TCCG TTCCAACGTCAC		
		C_		
GAM1478 FEZ1	3'	CACTGCAACCTCCACCT	42566	CAA
		AGG GAGGTTGCAGTG		
		TCC CTCCAACGTCAC		
		AC_		
GAM1478 FGFR1	3'	CAGCTCACCTCTCCCTCCACCT	43628	CAA TTGCA
		AGG GAGG GTGAGCTG		
		TCC CTCC CACTCGAC		
		AC_ CTCTC		
GAM1478 FGFR1	3'	CAGCTCACCTCTCCCTCCACCT	31795	CAA TTGCA
		AGG GAGG GTGAGCTG		
		TCC CTCC CACTCGAC		
		AC_ CTCTC		
GAM1478 FGFR1	3'	CAGCTCACCTCTCCCTCCACCT	5202	CAA TTGCA
		AGG GAGG GTGAGCTG		
		TCC CTCC CACTCGAC		
		AC_ CTCTC		
GAM1478 FHL2	5'	CAGCTCACTGCAAGCTCTACCT	7561	CA G
		AGG AGAG TTGCAGTGAGCTG		
		TCC TCTC AACGTCACTCGAC		
		A_ G		
GAM1478 FUT1	3'	CAGCTCACTGCAAGCTCTGCCT	3786	A G
		AGGCA GAG TTGCAGTGAGCTG		
		TCCGT CTC AACGTCACTCGAC		
		_ G		
GAM1478 FZD4	3'	CACTGCAACCTCTGCCT	24128	A
		AGGCA GAGGTTGCAGTG		
		TCCGT CTCCAACGTCAC		
		—		
GAM1478 G6PC	3'	GGCTCACTGCAACCTCTTCCT	3831	C
		AGG AAGAGGTTGCAGTGAGCT		

TCC TTCTCCAACGTCACTCGG

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      -
GAM1478 GM2A  3' CACTGCAACCTCCGCCT  67773  AA
               AGGC GAGGTTGCAGTG
               |||| ||||||||
               TCCG CTCCAACGTCAC
               C_
GAM1478 GNE   3' CAATGCAACCTCTGCC  18476  A   G
               GGCA GAGGTTGCA TG
               |||| |||||||| ||
               CCGT CTCCAACGT AC
               -   A
GAM1478 GPR81 3' CACTGCAACCTCTGCCT  50753  A
               AGGCA GAGGTTGCAGTG
               |||| ||||||||
               TCCGT CTCCAACGTCAC
               -
GAM1478 GRAF  3' CACTGCAACCTCCGCCT  30550  AA
               AGGC GAGGTTGCAGTG
               |||| ||||||||
               TCCG CTCCAACGTCAC
               C_
GAM1478 HCS   3' CACCGCAACCTCCGCCT  38459  AA   A
               AGGC GAGGTTGC GTG
               |||| |||||||| ||
               TCCG CTCCAACG CAC
               C_   C
GAM1478 HCS   3' CACTGCAACCTCCGCCT  38460  AA
               AGGC GAGGTTGCAGTG
               |||| ||||||||
               TCCG CTCCAACGTCAC
               C_
GAM1478 HLCS  5' CACCACAACCTCTGCCT  4661   A   CA
               AGGCA GAGGTTG GTG
               |||| |||||||| ||
               TCCGT CTCCAAC CAC
               -   AC
GAM1478 HOXC5 3' AGTGAGCTGCTCCACAACCTCT 38492 C   G_____ TGAG
      TCCC      AAGAGGTT      CAG CT
               |||||||| ||| ||
               TTCTCAA      GTC GA
               C   CACCTC||| GAGT
GAM1478 HTR1D 3' CAGCTCACTGCAACCTCCGC  5993  AA
               GC GAGGTTGCAGTGAGCTG
               || ||||||||||||
               CG CTCCAACGTCACTCGAC
               C_
GAM1478 HTR1E 5' CATTGCAACCTCCGCCT  6011  AA
               AGGC GAGGTTGCAGTG
               |||| ||||||||
```

			TCCG CTCCAACGTTAC		
			C_		
GAM1478	ITGAM	3'	CACTGCAACCTCCGCCT	71835	AA
			AGGC GAGGTTGCAGTG		
			TCCG CTCCAACGTCAC		
			C_		
GAM1478	JRK	3'	CAGCTCACTGCAGCCTCGACCT	86523	CAA
			AGG GAGGTTGCAGTGAGCTG		
			TCC CTCCGACGTCACTCGAC		
			AG_		
GAM1478	KMO	3'	CACTGCAACCTCTGCCT	13446	A
			AGGCA GAGGTTGCAGTG		
			TCCGT CTCCAACGTCAC		
			-		
GAM1478	LANCL1	3'	CTCACTGCATGACCCT	20212	A _
			AG GGT TGCAGTGAG		
			TC CCA ACGTCACTC		
			_ GT		
GAM1478	LILRA3	3'	CACTGCAACCTCCGCCT	95307	AA
			AGGC GAGGTTGCAGTG		
			TCCG CTCCAACGTCAC		
			C_		
GAM1478	LNK	3'	CACTGCAACCTCCACCT	18458	CAA
			AGG GAGGTTGCAGTG		
			TCC CTCCAACGTCAC		
			AC_		
GAM1478	LYZ	3'	CACTGCAACCTCCACCT	4096	CAA
			AGG GAGGTTGCAGTG		
			TCC CTCCAACGTCAC		
			AC_		
GAM1478	MAK	3'	CTTACTGCAACCTCCACCT	19759	CAA
			AGG GAGGTTGCAGTGAG		
			TCC CTCCAACGTCATTC		
			AC_		
GAM1478	MEF2A	5'	CACTGCAACCTCCGCCT	18780	AA
			AGGC GAGGTTGCAGTG		
			TCCG CTCCAACGTCAC		
			C_		
GAM1478	MEFV	3'	CACTGCAACCTCCGCCT	4127	AA
			AGGC GAGGTTGCAGTG		

TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 MEFV 3' CAGCTCACTGCAACCTCCACCT 4129 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC CTCCAACGTCACCTCGAC  
 AC\_  
 GAM1478 MGST2 5' CAGCCCCAGACCTGCCTGCCT 10032 AG\_ GCAGTGA  
 AGGCA AGGTT GCTG  
 |||| |||| ||||  
 TCCGT TCCAG CGAC  
 CCG ACCC\_  
 GAM1478 MHC2TA 3' CACTGCAACCTCCGCCT 4165 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 MICB 3' CAGCTCACTGCAACCTCTGCCT 19823 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| |||||  
 TCCGT CTCCAACGTCACCTCGAC  
 -  
 GAM1478 MPL 3' CACTGCAACCTCTGCCT 18132 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||  
 TCCGT CTCCAACGTCAC  
 -  
 GAM1478 MPL 3' CAGCTCACTGCAACCTCCACCT 18134 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC CTCCAACGTCACCTCGAC  
 AC\_  
 GAM1478 MYCL2 3' CACTGCAACCTCTGCCT 18176 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||  
 TCCGT CTCCAACGTCAC  
 -  
 GAM1478 MYO1C 3' CACCTGCAATCTCCACCT 61201 CAA \_  
 AGG GAGGTTGCAG TG  
 ||| ||||| ||  
 TCC CTCTAACGTC AC  
 ACC C  
 GAM1478 NCOA6IP 3' CAGCTCACTGCAGGTTTCAGCCT 45735 AA G  
 AGGC GAG TTGCAGTGAGCTG  
 |||| ||| |||||  
 TCCG CTT GACGTCACCTCGAC  
 A\_ G  
 GAM1478 NDRG3 3' CACTGCAACCTCTGCC 49293 A  
 GGCA GAGGTTGCAGTG  
 |||| |||||

CCGT CTCCAACGTCAC

GAM1478 NQO1 3' CACTGCAACCTCTGCCT 6153 A  
AGGCA GAGGTTGCAGTG  
||||| |||||||||  
TCCGT CTCCAACGTCAC

GAM1478 OAS3 3' CAGCTCACACACTCCCCTGCCT 20538 A A TTGCA  
AGGCA G GG GTGAGCTG  
||||| || |||||  
TCCGT C CC CACTCGAC  
\_C TCACA

GAM1478 OVOL1 3' GCAGCCCACCCTCCTGCAACCT 15858 \_\_\_\_\_ A III  
CTCACC AGAGGTTGCA GTG GCTG C  
||||||| ||| ||| |  
TCTCCAACGT CAC CGAC G  
CCTCC C III

GAM1478 PCDHB11 3' CAGCTCACTGCAACCTCTGCCT 38412 A  
AGGCA GAGGTTGCAGTGAGCTG  
||||| |||||||||  
TCCGT CTCCAACGTCAGTCACTCGAC

GAM1478 PCDHB11 3' CAGCTCACTGCACCCTCCGCCT 38413 AA T  
AGGC GAGG TGCAGTGAGCTG  
||| ||| |||||||||  
TCCG CTCC ACGTCACTCGAC  
C\_ C

GAM1478 PCDHB16 3' CACTGCAACCTCTGCCT 40550 A  
AGGCA GAGGTTGCAGTG  
||||| |||||||||  
TCCGT CTCCAACGTCAC

GAM1478 PCDHB9 3' CAGCTCACTGCAACCTCCGCCT 38937 AA  
AGGC GAGGTTGCAGTGAGCTG  
||| |||||||||  
TCCG CTCCAACGTCAGTCACTCGAC  
C\_

GAM1478 PDCL 3' CACTGCAACCTCCACCT 18210 CAA  
AGG GAGGTTGCAGTG  
||| |||||||||  
TCC CTCCAACGTCAC  
AC\_

GAM1478 PDE6B 3' CAGCTCACTGCAACCTCCACCT 4274 CAA  
AGG GAGGTTGCAGTGAGCTG  
||| |||||||||  
TCC CTCCAACGTCAGTCACTCGAC  
AC\_

GAM1478 PER2 3' CACTGCAACCTCTGCCT 43028 A  
AGGCA GAGGTTGCAGTG  
||||| |||||||||



TCCGT CTCCAACGTCAC

GAM1478 PIGR 3' CACTGCAACCTCCGCCT 72591 AA  
AGGC GAGGTTGCAGTG  
|||||  
TCCG CTCCAACGTCAC

C\_  
GAM1478 PIM2 3' CAGATTCTTGCAACCTCCTCCT 59989 CAA T \_  
AGG GAGGTTGCAG GAG CTG  
||| ||||| ||| |||  
TCC CTCCAACGTT CTT GAC

TC\_ \_ A  
GAM1478 PLA2G4C 5' AGCCCGCGACCTCCTCC 73412 CAA AGT A  
GG GAGGTTGC G GCT  
|| ||||| | |||  
CC CTCCAGCG C CGA  
TC\_ \_ C

GAM1478 PRKCM 3' CAGCTGCTCAGCAACCTTTTCAC 10812 CA \_ G  
CT AGG AGAGGTTGC AGT AGCTG  
||| ||||| ||| |||||  
TCC TTTCCAACG TCG TCGAC  
AC AC \_

GAM1478 PRKWNK3 3' TGCTGCAACCTCCCCCT 61557 CAA  
AGG GAGGTTGCAGTG  
||| |||||  
TCC CTCCAACGTCGT  
CC\_

GAM1478 PSMB2 3' CACTGCAACCTCCGCCT 10949 AA  
AGGC GAGGTTGCAGTG  
|||||  
TCCG CTCCAACGTCAC  
C\_

GAM1478 PSMD9 3' CAGCCCACTGCTAGTTTGACT 10981 G AGGTT A  
AG CAAG GCAGTG GCTG  
|| ||| ||||| |||  
TC GTTT CGTCAC CGAC  
A GAT\_ C

GAM1478 PTGIS 3' CAGCTCACCACAACCTCCACCT 6325 CAA CA  
AGG GAGGTTG GTGAGCTG  
||| ||||| |||||  
TCC CTCCAAC CACTCGAC  
AC\_ AC

GAM1478 RAB36 3' CAGTGCAACCTCTGCCT 16950 A G  
AGGCA GAGGTTGCA TG  
||||| ||||| ||  
TCCGT CTCCAACGT AC  
\_ G

GAM1478 RALBP1 3' CAGCTCACTTTGTACCCCTC 22293 T\_ \_  
GAGG TGCA GTGAGCTG  
|||| ||| |||||

			CTCC ATGT CACTCGAC		
			CC TT		
GAM1478	RBBP9	3'	CAGCTCACTCTAACCTGCACCT 70130	CAAG	C
			AGG AGGTTG AGTGAGCTG		
			TCC TCCAAT TCACTCGAC		
			ACG_ C		
GAM1478	RHD	3'	CACTGCAACCTCCGCCT 32297	AA	
			AGGC GAGGTTGCAGTG		
			TCCG CTCCAACGTCAC		
			C_		
GAM1478	RHD	3'	CACTGCAACCTCTACCT 32299	CA	
			AGG AGAGGTTGCAGTG		
			TCC TCTCCAACGTCAC		
			A_		
GAM1478	RHD	3'	CACTGCAACCTCCGCCT 32606	AA	
			AGGC GAGGTTGCAGTG		
			TCCG CTCCAACGTCAC		
			C_		
GAM1478	RHD	3'	CACTGCAACCTCTACCT 32608	CA	
			AGG AGAGGTTGCAGTG		
			TCC TCTCCAACGTCAC		
			A_		
GAM1478	RPH3AL	3'	CACTGCAACCTCCACCT 22741	CAA	
			AGG GAGGTTGCAGTG		
			TCC CTCCAACGTCAC		
			AC_		
GAM1478	RPP30	3'	CAGCTCACTGCAACCTCAATCC 21162	CAA	
	T		AGG GAGGTTGCAGTGAGCTG		
			TCC CTCCAACGTCAC TCGAC		
			TAA		
GAM1478	SAS	3'	CACCGCAACCTCTGCCT 19949	A	A
			AGGCA GAGGTTGC GTG		
			TCCGT CTCCAACG CAC		
			_ C		
GAM1478	SDPR	5'	CACCGCAACTTCTCACC 16223	CA	A
			GG AGAGGTTGC GTG		
			CC TCTTCAACG CAC		
			AC C		
GAM1478	SEDL	3'	CACTGCAACCTCCACCT 27323	CAA	
			AGG GAGGTTGCAGTG		

			TCC CTCCAACGTCAC		
			AC_		
GAM1478	SEDL	3'	CACTGCAACCTCCACCT	27324	CAA
			AGG GAGGTTGCAGTG		
			TCC CTCCAACGTCAC		
			AC_		
GAM1478	SEDL	3'	CACTGCAACCTCCGCCT	27327	AA
			AGGC GAGGTTGCAGTG		
			TCCG CTCCAACGTCAC		
			C_		
GAM1478	SEPN1	3'	CACTGCAACCTCCACCT	66362	CAA
			AGG GAGGTTGCAGTG		
			TCC CTCCAACGTCAC		
			AC_		
GAM1478	SERPINB9	3'	GGCTCACTGCAACCTCCTCCT	14759	CAA
			AGG GAGGTTGCAGTGAGCT		
			TCC CTCCAACGTCAC		
			TC_		
GAM1478	SFRP4	3'	CTCACTGCAGTGCTCT	11576	_
			AGAG GTTGCAGTGAG		
			TCTC TGACGTCACTC		
			G		
GAM1478	SHOX	3'	CAGCTCACCGCCACCTCCGCC	4832	AA T A
			GGC GAGGT GC GTGAGCTG		
			CCG CTCCA CG CACTCGAC		
			C_ C C		
GAM1478	SHOX	3'	CACTGCAACCTCCGCCT	22530	AA
			AGGC GAGGTTGCAGTG		
			TCCG CTCCAACGTCAC		
			C_		
GAM1478	SIL	3'	CACTGCAACCTCTGCCT	11685	A
			AGGCA GAGGTTGCAGTG		
			TCCGT CTCCAACGTCAC		
			-		
GAM1478	SLA2	3'	CAGCTCACTGCAACCTC	49893	
			GAGGTTGCAGTGAGCTG		
			CTCCAACGTCAC		
GAM1478	SLC14A2	5'	CACTGCAACCTCCACCT	23129	CAA
			AGG GAGGTTGCAGTG		

TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 SLC15A1 3' CAGCTCACTGCAACCTCCGCCT 17399 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCG CTCCAACGTCACCTCGAC  
 C\_  
 GAM1478 SMAC 5' CACTGCAACCTCTGCCT 57203 A  
 AGGCA GAGGTTGCAGTG  
 ||| |||||  
 TCCGT CTCCAACGTCAC  
 -  
 GAM1478 SMAC 5' CAGCTCACTGCAACCTGTGCCT 57206 AG  
 AGGCA AGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCGT TCCAACGTCACCTCGAC  
 G\_  
 GAM1478 SMP1 3' ACTGAGCACAACCTCTTTCC 26695 C \_\_\_\_  
 GG AAGAGGTTG CAGT  
 || ||||| |||  
 CC TTCTCCAAC GTCA  
 T ACGA  
 GAM1478 SNAP23 3' CACTGCAACCTCCGCCT 13805 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 SNAP23 3' CACTGCAACCTCCGCCT 55458 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 SNX15 3' CACTGCAACCTCCACCT 73734 CAA  
 AGG GAGGTTGCAGTG  
 || |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 SOST 3' GGAGCTGCAGACAACCTCTTAC 47470 C G\_\_\_\_\_ TGAG  
 TT GG AAGAGGTT CAG C  
 || ||||| ||| |  
 TC TTCTCCAA GTC G  
 A CAGAC||| GAGT  
 GAM1478 SPG3A 5' AGCTCACCGCCACCAGCT 31914 AAGA T A  
 GGC GGT GC GTGAGCT  
 || ||| || |||||  
 TCG CCA CG CACTCGA  
 A\_\_\_ C C  
 GAM1478 SPN 3' CACTGCAACCTCTGCCT 11916 A  
 AGGCA GAGGTTGCAGTG  
 ||| |||||

TCCGT CTCCAACGTCAC

GAM1478 SS18 3' CAGCTCACTGCAACCTCCGCCT 18884 AA  
AGGC GAGGTTGCAGTGAGCTG  
|||||  
TCCG CTCCAACGTCACCTCGAC  
C\_

GAM1478 STAU 5' CACTGCAACCTCCACCT 15996 CAA  
AGG GAGGTTGCAGTG  
|||  
TCC CTCCAACGTCAC  
AC\_

GAM1478 SULT2B1 5' CACTGCAACCTCCGCCT 16022 AA  
AGGC GAGGTTGCAGTG  
|||||  
TCCG CTCCAACGTCAC  
C\_

GAM1478 TAGLN 3' AGCCCAACTTCTTACC 59632 C CAGTGA  
GG AAGAGGTTG GCT  
|||  
CC TTCTTCAAC CGA  
A C\_

GAM1478 TAPBP 3' CTTACTGCAACCTCCGCCT 12124 AA  
AGGC GAGGTTGCAGTGAG  
|||||  
TCCG CTCCAACGTCATTC  
C\_

GAM1478 TAT 3' CACTGCAACCTCCACCT 4462 CAA  
AGG GAGGTTGCAGTG  
|||  
TCC CTCCAACGTCAC  
AC\_

GAM1478 TBXA2R 3' CACTGCAACCTCCGCCT 6482 AA  
AGGC GAGGTTGCAGTG  
|||||  
TCCG CTCCAACGTCAC  
C\_

GAM1478 TBXA2R 3' CAGCTCACTGCAACCTCCACCT 6484 CAA  
AGG GAGGTTGCAGTGAGCTG  
|||  
TCC CTCCAACGTCACCTCGAC  
AC\_

GAM1478 TCF2 3' AGTGTAGCAGCCTCCTGCCT 21372 A AGTGA  
AGGCA GAGGTTGC GCT  
|||||  
TCCGT CTCCGACG TGA  
C ATG\_

GAM1478 TJP1 5' CAGCTCACTGCAGCCTTGACCT 12297 CAA  
AGG GAGGTTGCAGTGAGCTG  
|||

			TCC TTCCGACGTC	ACTCGAC		
			AG_			
GAM1478	TMC1	5'	CTGCAACCTCCGCCT	56901	AA	
			AGGC GAGGTTGCAG			
			TCCG CTCCAACGTC			
			C_			
GAM1478	TNFRSF10B	3'	CAGTGCAACCTCCGCCT	13866	AA	G
			AGGC GAGGTTGCA TG			
			TCCG CTCCAACGT AC			
			C_ G			
GAM1478	TPMT	3'	CACTGCAACCTCTGCCT	4533	A	
			AGGCA GAGGTTGCAGTG			
			TCCGT CTCCAACGTCAC			
			—			
GAM1478	TRAF5	3'	CAGCTCACTGCAAACTCTGCCT	16075	A	G
			AGGCA GAG TTGCAGTGAGCTG			
			TCCGT CTC AACGTC			
			— A			
GAM1478	TRIM9	5'	CACTGCAACCTCCGCCT	30754	AA	
			AGGC GAGGTTGCAGTG			
			TCCG CTCCAACGTCAC			
			C_			
GAM1478	TRPM6	3'	CACTGCAACCTCTGCCT	34534	A	
			AGGCA GAGGTTGCAGTG			
			TCCGT CTCCAACGTCAC			
			—			
GAM1478	TRPV1	3'	CACTGCAACCTCTGCCT	38072	A	
			AGGCA GAGGTTGCAGTG			
			TCCGT CTCCAACGTCAC			
			—			
GAM1478	TRPV1	3'	CTGCAACCTCCGCCT	38079	AA	
			AGGC GAGGTTGCAG			
			TCCG CTCCAACGTC			
			C_			
GAM1478	TRPV1	3'	CACTGCAACCTCTGCCT	54791	A	
			AGGCA GAGGTTGCAGTG			
			TCCGT CTCCAACGTCAC			
			—			
GAM1478	TRPV1	3'	CTGCAACCTCCGCCT	54800	AA	
			AGGC GAGGTTGCAG			

			TCCG CTCCAACGTC		
			C_		
GAM1478	TRPV1	3'	CACTGCAACCTCTGCCT	54826	A
			AGGCA GAGGTTGCAGTG		
			TCCGT CTCCAACGTCAC		
			-		
GAM1478	TRPV1	3'	CTGCAACCTCCGCCT	54833	AA
			AGGC GAGGTTGCAG		
			TCCG CTCCAACGTC		
			C_		
GAM1478	TRPV1	3'	CACTGCAACCTCTGCCT	54858	A
			AGGCA GAGGTTGCAGTG		
			TCCGT CTCCAACGTCAC		
			-		
GAM1478	TRPV1	3'	CTGCAACCTCCGCCT	54865	AA
			AGGC GAGGTTGCAG		
			TCCG CTCCAACGTC		
			C_		
GAM1478	TUFT1	3'	CAGCTCACTGCAACCTCTGCCT	39254	A
			AGGCA GAGGTTGCAGTGAGCTG		
			TCCGT CTCCAACGTCACTCGAC		
			-		
GAM1478	VENTX2	3'	CACTGCAACCTCCGCCT	27107	AA
			AGGC GAGGTTGCAGTG		
			TCCG CTCCAACGTCAC		
			C_		
GAM1478	VHL	3'	CACTGCAACCTCTGCCT	5063	A
			AGGCA GAGGTTGCAGTG		
			TCCGT CTCCAACGTCAC		
			-		
GAM1478	ZNF133	5'	CTCACTGCAACCTCCACCC	12836	CAA
			GG GAGGTTGCAGTGAG		
			CC CTCCAACGTCACTC		
			CAC		
			-		
GAM1478	ZNF157	3'	CAGCTCATTTCAACCTTCGCCT	12876	AA C
			AGGC GAGGTTG AGTGAGCTG		
			TCCG TTCCAAC TTA		
			CTCGAC		
			C_ T		
GAM1478	ZNF264	3'	CACTGCAACCTCCGCCT	12745	AA
			AGGC GAGGTTGCAGTG		

TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 ZNF264 3' CTGCAACCTCTGCCT 12752 A  
 AGGCA GAGGTTGCAG  
 |||| |||||  
 TCCGT CTCCAACGTC

—  
 GAM1478 20D7-FC4 5' CAGCTCACTGCAGCCTCCACCT 60897 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 || |||||  
 TCC CTCCGACGTCACCTCGAC  
 AC\_

GAM1478 APCL 5' CAGCCCGACTCCATCCTCCCAC 19665 CAA T C \_ A  
 CT AGG GAGG TG AGT G GCTG  
 || ||| || |||  
 TCC CTCC AC TCA C CGAC  
 ACC T C G C

GAM1478 ARPP-19 3' CACTGCAACCTCTGCCT 21790 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||  
 TCCGT CTCCAACGTCAC

—  
 GAM1478 ARPP-19 3' CAGCTCACTGCAACCTTACTCC 21792 CAA  
 T AGG GAGGTTGCAGTGAGCTG  
 || |||||  
 TCC TTCCAACGTCACCTCGAC  
 TCA

GAM1478 ASB16 5' CACTGCAACCTCCGCCT 69931 AA  
 AGGC GAGGTTGCAGTG  
 |||| |||||  
 TCCG CTCCAACGTCAC  
 C\_

GAM1478 ASE-1 3' CACTGCAACCTCCGCCT 23945 AA  
 AGGC GAGGTTGCAGTG  
 |||| |||||  
 TCCG CTCCAACGTCAC  
 C\_

GAM1478 ATP1B4 3' CACTGCAACCTCCACCT 23813 CAA  
 AGG GAGGTTGCAGTG  
 || |||||  
 TCC CTCCAACGTCAC  
 AC\_

GAM1478 BA108L7.2 3' CACTGCAACCTCTGCCT 48258 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||  
 TCCGT CTCCAACGTCAC

—  
 GAM1478 BAG5 3' CAGCTCACTGCAACCTCCACCT 16839 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 || |||||



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TCC CTCCAACGTCAC TCGAC
AC_
GAM1478 BNIP-S 3' CACTGCAACCTCCGCCT 56256 AA
AGGC GAGGTTGCAGTG
|||||
TCCG CTCCAACGTCAC
C_
GAM1478 BTN3A1 3' CAGCTCCCTGCAACCTCCACCT 22915 CAA T
AGG GAGGTTGCAG GAGCTG
||| |||||
TCC CTCCAACGTC CTCGAC
AC_ C
GAM1478 C14orf4 5' CAGCTCACCGTGCCCCCAACC 67333 CAAGA TT A
T
AGG GG GC GTGAGCTG
||| || |||||
TCC CC TG CACTCGAC
AACCC CG C
GAM1478 C1orf24 3' CACTGCAACCTCCGCCT 53709 AA
AGGC GAGGTTGCAGTG
|||||
TCCG CTCCAACGTCAC
C_
GAM1478 C1QTNF6 3' CACTGCAACCTCTGCCT 49138 A
AGGCA GAGGTTGCAGTG
|||||
TCCGT CTCCAACGTCAC
-
GAM1478 C21orf25 3' CAGCTTACTGCAACCTCCACCT 63543 CAA
AGG GAGGTTGCAGTGAGCTG
||| |||||
TCC CTCCAACGTCATTCGAC
AC_
GAM1478 C3F 3' CAGCTCACCGCAACCTCCACCT 19286 CAA A
AGG GAGGTTGC GTGAGCTG
||| |||||
TCC CTCCAACG CACTCGAC
AC_ C
GAM1478 C6orf5 3' CAGCTCACTGCAGCTTTGACCT 31343 CAA
AGG GAGGTTGCAGTGAGCTG
||| |||||
TCC TTTCGACGTCAC TCGAC
AG_
GAM1478 C9orf9 3' CACTGCAACCTCCACCT 38503 CAA
AGG GAGGTTGCAGTG
||| |||||
TCC CTCCAACGTCAC
AC_
GAM1478 C9orf9 3' CACTGCAACCTCCGCCT 38505 AA
AGGC GAGGTTGCAGTG
|||||

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TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 CEACAM8 3' CTCAGTCAAGCTCCGCCT 8422 AA G  
 AGGC GAG TTGCAGTGAG  
 |||| ||| |||||  
 TCCG CTC AACGTCCTC  
 C\_ G  
 GAM1478 CENPH 3' CACTGCAACCTCTGCCT 43270 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||  
 TCCGT CTCCAACGTCAC  
  
 —  
 GAM1478 CHRAC1 3' CAGCTCACTGCAACCTCCGCCT 33868 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 |||| |||||  
 TCCG CTCCAACGTCCTCGAC  
 C\_  
 GAM1478 CL24751 5' CAGCTCACCTGACCCCTC 64685 TTG\_ \_  
 GAGG CAG TGAGCTG  
 |||| ||| |||||  
 CTCC GTC ACTCGAC  
 CCCA C  
 GAM1478 CPSF2 3' CACCGCAACCTCTGCCT 61573 A A  
 AGGCA GAGGTTGC GTG  
 |||| ||||| |||  
 TCCGT CTCCAACG CAC  
 — C  
 GAM1478 DBR1 3' CACCGCAACCTCCGCCT 32527 AA A  
 AGGC GAGGTTGC GTG  
 |||| ||||| |||  
 TCCG CTCCAACG CAC  
 C\_ C  
 GAM1478 DKFZP434C212 3' CACTGCAACCTCCACCT 68905 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 DKFZp434E2220 5' CACTGCAACCTCCGCCT 34293 AA  
 AGGC GAGGTTGCAGTG  
 |||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 DKFZp434F1719 3' CAGCTCACTGCAGGCTCTGCCT 49997 A G  
 AGGCA GAG TTGCAGTGAGCTG  
 |||| ||| |||||  
 TCCGT CTC GACGTCCTCGAC  
 — G  
 GAM1478 DKFZP434J037 3' CAGCTCACCTCAACCTCCGCCT 48207 AA CA  
 AGGC GAGGTTG GTGAGCTG  
 |||| ||||| |||||

TCCG CTCCAAC CACTCGAC  
 C\_ TC  
 GAM1478 DKFZp547H025 3' CAGCTCACTGCAACCTCCACCT 39352 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC CTCCAACGTCACCTCGAC  
 AC\_  
 GAM1478 DKFZP564G092 5' CAGCTCACTGGAGCCTCTGCCT 31534 A G  
 AGGCA GAGGTT CAGTGAGCTG  
 |||| |||||  
 TCCGT CTCCGA GTCACCTCGAC  
 \_ G  
 GAM1478 DKFZP564O0523 3' CACTGCAACCTCCACCT 49511 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 DKFZp761J139 5' CAGCTCACTGCAACGTCCACCT 50105 CAA G  
 AGG GA GTTGCAGTGAGCTG  
 ||| || |||||  
 TCC CTCAACGTCACTCGAC  
 AC\_ G  
 GAM1478 DKFZp761N1114 3' CACTGCAACCTCCGCCT 79014 AA  
 AGGC GAGGTTGCAGTG  
 |||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 DKFZp762L0311 3' CACTGCAACCTTTGCCT 38054 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||  
 TCCGT TTCCAACGTCAC  
 \_  
 GAM1478 DKFZp762P2111 3' CACTGCAACCTCCGCCT 86352 AA  
 AGGC GAGGTTGCAGTG  
 |||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 DRIM 3' CAGCTCACTGCAGCCTCAACCT 27176 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC CTCCGACGTCACTCGAC  
 AA\_  
 GAM1478 FBP17 3' CACTACAACCTCCACCT 72782 CAA C  
 AGG GAGGTTG AGTG  
 ||| |||||  
 TCC CTCCAAC TCAC  
 AC\_ A  
 GAM1478 FBXO4 3' CAGCCCACCTTGTCTGCCT 24097 AGA TTGCA A  
 AGGCA GG GTG GCTG  
 |||| || ||||

			TCCGT CC CAC CGAC		
			___ TGTC C		
GAM1478	FER1L4	3'	CTGACTGCAACCTCCACCT 47341	CAA	G
			AGG GAGGTTGCAGT AG		
			TCC CTCCAACGTCA TC		
			AC_ G		
GAM1478	FER1L4	3'	CTGACTGCAACCTCCACCT 47342	CAA	G
			AGG GAGGTTGCAGT AG		
			TCC CTCCAACGTCA TC		
			AC_ G		
GAM1478	FKBP9	3'	CAGCTCATCACACCCCGCC 94062	AAGA T CA	
			GGC GG TG GTGAGCTG		
			CCG CC AC TACTCGAC		
			C___ C AC		
GAM1478	FLJ00024	5'	CACTGCAACCTCTGCCT 63752	A	
			AGGCA GAGGTTGCAGTG		
			TCCGT CTCCAACGTCAC		
			—		
GAM1478	FLJ10232	3'	CACTGCAACCTCCGCCT 35921	AA	
			AGGC GAGGTTGCAGTG		
			TCCG CTCCAACGTCAC		
			C_		
GAM1478	FLJ10297	3'	CAGCTCACTGTGACCTTGACCT 35978	CAA TG	
			AGG GAGGT CAGTGAGCTG		
			TCC TTCCA GTCACGAC		
			AG_ GT		
GAM1478	FLJ10535	3'	CACTGCAACCTCTGCCT 36234	A	
			AGGCA GAGGTTGCAGTG		
			TCCGT CTCCAACGTCAC		
			—		
GAM1478	FLJ10916	3'	AGCTCACCACCTTCACGC 36857	AA_ TGCA	
			GC GAGGT GTGAGCT		
			CG TTCCA CACTCGA		
			CAC C___		
GAM1478	FLJ10922	3'	CACTGCAACCTCCGCCT 36870	AA	
			AGGC GAGGTTGCAGTG		
			TCCG CTCCAACGTCAC		
			C_		
GAM1478	FLJ11004	5'	CACTGCAACCTCTACCT 36966	CA	
			AGG AGAGGTTGCAGTG		

TCC TCTCCAACGTCAC  
 A\_  
 GAM1478 FLJ11151 3' CAGCTGCACACAACCTCTTGCT 67872 CA \_  
 GGCAAGAGGTTG GTG AGCTG  
 ||||| ||| |||||  
 TCGTTCTCCAAC CAC TCGAC  
 A\_ G  
 GAM1478 FLJ11467 3' CAGCTCACTGCAGCCTTGACCT 46375 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC TTCCGACGTCACCTCGAC  
 AG\_  
 GAM1478 FLJ12190 3' AGCTCATCTCCTTGCCCT 46870 AG TTGCA  
 AGGCAAG G GTGAGCT  
 ||||| | |||||  
 TCCGTTC C TACTCGA  
 CT \_\_\_\_\_  
 GAM1478 FLJ12363 3' CAGCTCACTGCAACCTCCACCT 49674 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC CTCCAACGTCACCTCGAC  
 AC\_  
 GAM1478 FLJ12409 3' CACTGCAACCTCCGCCT 47043 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 FLJ12572 5' CACTGCAACCTCTGCCT 43246 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||  
 TCCGT CTCCAACGTCAC  
 -  
 GAM1478 FLJ12649 3' CACTGCAACCTCCGCCT 44776 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 FLJ12687 3' CACTGCAACCTCCGCCT 46187 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 FLJ12747 3' CACTGCAACCTCTGCCT 49711 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||  
 TCCGT CTCCAACGTCAC  
 -  
 GAM1478 FLJ12787 3' CACTGCAACCTCTGCC 49746 A  
 GGCA GAGGTTGCAGTG  
 |||| |||||

CCGT CTCCAACGTCAC

—  
GAM1478 FLJ12973 3' CACCGCAACCTCCGCCT 46102 AA A  
AGGC GAGGTTGC GTG  
||||| ||||| |||  
TCCG CTCCAACG CAC  
C\_ C

GAM1478 FLJ12975 3' CGGCTCACCACAACCTCCTCCT 69580 CAA CA  
AGG GAGGTTG GTGAGCTG  
||| ||||| |||||  
TCC CTCCAAC CACTCGGC  
TC\_ AC

GAM1478 FLJ13072 5' CACTGCAACCTCTGCCT 89803 A  
AGGCA GAGGTTGCAGTG  
||||| |||||  
TCCGT CTCCAACGTCAC

—  
GAM1478 FLJ13089 5' CTCACTGCAGGCACTGACT 70861 GCA AG \_  
AG AG GT TGCAGTGAG  
|| || || |||||  
TC TC CG ACGTCACTC  
AG\_ A\_ G

GAM1478 FLJ13105 3' ACTAAAAATCTCCTGCCT 46542 A GC\_  
AGGCA GAGGTT AGT  
||||| ||||| |||  
TCCGT CTCTAA TCA  
C AAA

GAM1478 FLJ13162 3' GCTGCGACCCCTGCCT 46558 AGA  
AGGCA GGTTCAGT  
||||| |||||  
TCCGT CCAGCGTCG  
CCC

GAM1478 FLJ13197 3' CACTGCAACCTCTACCT 44848 CA  
AGG AGAGGTTGCAGTG  
||| |||||  
TCC TCTCCAACGTCAC  
A\_

GAM1478 FLJ14442 3' CAGCTCACTGCAACTTCTGCCT 51362 A  
AGGCA GAGGTTGCAGTGAGCTG  
||||| |||||  
TCCGT CTTCAACGTCAGT

—  
GAM1478 FLJ14810 3' CAGCTCACTGATCTCTTGCCT 51624 TG  
AGGCAAGAGGT CAGTGAGCTG  
||||| |||||  
TCCGTTCTCTA GTCAGT

—  
GAM1478 FLJ14871 3' CAGCTCACTGGATTCCATC 51665 \_ TTG\_  
GA GG CAGTGAGCTG  
|| || |||||

			CT CC	GTC	ACTCGAC		
			A	TTAG			
GAM1478	FLJ14950	3'	CACTGCAACCTCCACCT	51713	CAA		
			AGG	GAGGTTGCAGTG			
			TCC	CTCCAACGTCAC			
			AC_				
GAM1478	FLJ14957	3'	CACTGCAACCTCTGCCT	51741	A		
			AGGCA	GAGGTTGCAGTG			
			TCCGT	CTCCAACGTCAC			
			—				
GAM1478	FLJ20004	3'	CATTGCAACCTCCGCCT	95290	AA		
			AGGC	GAGGTTGCAGTG			
			TCCG	CTCCAACGTTAC			
			C_				
GAM1478	FLJ20034	5'	CAGCTCACCTGACCTGC	34360	AGA	GCA	
			GCA	GGTT GTGAGCTG			
			CGT	CCAG CACTCGAC			
			—	TC_			
GAM1478	FLJ20034	3'	CAGCTCACTGCAACCTCTGCCT	34361	A		
			AGGCA	GAGGTTGCAGTGAGCTG			
			TCCGT	CTCCAACGTC	ACTCGAC		
			—				
GAM1478	FLJ20045	3'	CACTGCAACCTCTGCCT	34415	A		
			AGGCA	GAGGTTGCAGTG			
			TCCGT	CTCCAACGTCAC			
			—				
GAM1478	FLJ20079	3'	CACCGCAACCTCCACCT	34487	CAA	A	
			AGG	GAGGTTGC GTG			
			TCC	CTCCAACG CAC			
			AC_	C			
GAM1478	FLJ20342	3'	CACTGCAACCTCTGCCT	34986	A		
			AGGCA	GAGGTTGCAGTG			
			TCCGT	CTCCAACGTCAC			
			—				
GAM1478	FLJ20344	3'	CACTGCAACCTCCGCCT	35005	AA		
			AGGC	GAGGTTGCAGTG			
			TCCG	CTCCAACGTCAC			
			C_				
GAM1478	FLJ20507	3'	CAGCTCACTGCAACCTCTGCCT	35277	A		
			AGGCA	GAGGTTGCAGTGAGCTG			

TCCGT CTCCAACGTCACTCGAC

—  
GAM1478 FLJ20507 3' CAGCTCACTGCAACCTCTGCCT 60212 A  
AGGCA GAGGTTGCAGTGAGCTG  
||||| |||||||||  
TCCGT CTCCAACGTCACTCGAC

—  
GAM1478 FLJ21302 3' CACTGCAACCTCCGCCT 43211 AA  
AGGC GAGGTTGCAGTG  
||| |||||||  
TCCG CTCCAACGTCAC

C\_  
GAM1478 FLJ21432 3' CAGCTCACTACCAACAGCCT 44631 AAGA TGC  
AGGC GGT AGTGAGCTG  
||| || |||||||  
TCCG CCA TCACTCGAC  
ACAA —

GAM1478 FLJ22002 3' CAGCTCACTGCAACCTCCGCCT 45769 AA  
AGGC GAGGTTGCAGTGAGCTG  
||| |||||||||  
TCCG CTCCAACGTCACTCGAC  
C\_

GAM1478 FLJ22167 5' CAGCTCACTGCCACCTCTGCCT 44566 A T  
AGGCA GAGGT GCAGTGAGCTG  
||||| ||| |||||||  
TCCGT CTCCA CGTCACTCGAC  
— C

GAM1478 FLJ22531 5' CACTGCAACCTCCACCT 45027 CAA  
AGG GAGGTTGCAGTG  
||| |||||||||  
TCC CTCCAACGTCAC  
AC\_

GAM1478 FLJ22684 3' CTGCAACCTCTGCCT 46793 A  
AGGCA GAGGTTGCAG  
||||| |||||||  
TCCGT CTCCAACGTC

—  
GAM1478 FLJ22794 3' CAGCTCACTGCAACTTCCACCT 91604 CAA  
AGG GAGGTTGCAGTGAGCTG  
||| |||||||||  
TCC CTTCAACGTCACTCGAC  
AC\_

GAM1478 FLJ22965 3' CACTGCAACCTCCGCCT 42048 AA  
AGGC GAGGTTGCAGTG  
||| |||||||||  
TCCG CTCCAACGTCAC

C\_  
GAM1478 FLJ22969 3' CACTGCAACCTCTGCCT 68645 A  
AGGCA GAGGTTGCAGTG  
||||| |||||||||



TCCGT CTCCAACGTCAC

GAM1478 FLJ23024 3' CAGCTCACTGCAACCTCTGCCT 46267 A  
AGGCA GAGGTTGCAGTGAGCTG  
||||| |||||||||  
TCCGT CTCCAACGTCACCTCGAC

GAM1478 FLJ23042 3' AGTGAGCTGCAACCCACCTCTT 47169 TG\_\_\_\_\_ TGAG  
GCCT GCAAGAGGT CAG CT  
||||| ||| ||  
CGTTCTCCA GTC GA  
CCCAACIII GAGT

GAM1478 FLJ23392 3' CAGCTCACTGCAACCTCTGCCT 45528 A  
AGGCA GAGGTTGCAGTGAGCTG  
||||| |||||||||  
TCCGT CTCCAACGTCACCTCGAC

GAM1478 FLJ23563 3' CACTGCAACCTCTGCCT 67591 A  
AGGCA GAGGTTGCAGTG  
||||| |||||||||  
TCCGT CTCCAACGTCAC

GAM1478 FLJ31101 3' CAGCTCACTGCAACCTCTGCCT 35707 A  
AGGCA GAGGTTGCAGTGAGCTG  
||||| |||||||||  
TCCGT CTCCAACGTCACCTCGAC

GAM1478 FLJ32332 3' CAGCCCACCAGGTCCTGCCT 58300 A A GT GCA A  
AGGCA G G T GTG GCTG  
||||| | | ||| |||  
TCCGT C C G CAC CGAC  
\_\_ TG AC\_ C

GAM1478 FLJ32356 5' CACCCCGCAACCTCGCGCCT 58359 AA A\_\_  
AGGC GAGGTTGC GTG  
||| ||||| |||  
TCCG CTCCAACG CAC  
CG CCC

GAM1478 FLJ32865 3' CAGCTCACTGCAACCTCTGCCT 58170 A  
AGGCA GAGGTTGCAGTGAGCTG  
||||| |||||||||  
TCCGT CTCCAACGTCACCTCGAC

GAM1478 FOXD4 5' CAGCATCCGCCACAACCTCTCG 82744 A CA A\_\_  
CT GGC AGAGGTTG GTG GCTG  
||| ||||| ||| |||  
TCG TCTCCAAC CGC CGAC  
C AC CTA

GAM1478 FXYD5 3' CAGCTCACCGTGCCCAGCCT 26341 AAGA TT A  
AGGC GG GC GTGAGCTG  
||| || || |||||

			TCCG	CC	TG	CACTCGAC		
			A		CG	C		
GAM1478	GAL3ST-4	3'	CACTGCAACCTCTGCCT	44933		A		
			AGGCA GAGGTTGCAGTG					
			TCCGT CTCCAACGTCAC					
GAM1478	GBA2	3'	AGCCCAGCCTCCAGCCT	71022	AA	CAGTGA		
			AGGC GAGGTTG	GCT				
			TCCG CTCCGAC	CGA				
			AC	C				
GAM1478	GMPPB	5'	CACTGCAACCTCCACCT	95724	CAA			
			AGG GAGGTTGCAGTG					
			TCC CTCCAACGTCAC					
			AC					
GAM1478	GNG4	3'	CAGCTCACTGCGACCTCCACCT	15610	CAA			
			AGG GAGGTTGCAGTGAGCTG					
			TCC CTCCAGCGTCACTCGAC					
			AC					
GAM1478	GREB1	3'	CACTGCAACCTCTGCCT	27864	A			
			AGGCA GAGGTTGCAGTG					
			TCCGT CTCCAACGTCAC					
GAM1478	GRWD	3'	CACTGCAACCTCCGCCT	48962	AA			
			AGGC GAGGTTGCAGTG					
			TCCG CTCCAACGTCAC					
			C					
GAM1478	GTF2E1	3'	CACTGCAACCTCTGCCT	18610	A			
			AGGCA GAGGTTGCAGTG					
			TCCGT CTCCAACGTCAC					
GAM1478	GTPBG3	3'	CTTACTGCAACCTCCACCT	50899	CAA			
			AGG GAGGTTGCAGTGAG					
			TCC CTCCAACGTCATTC					
			AC					
GAM1478	H-plk	5'	CACTGCAACCTCCACCT	31804	CAA			
			AGG GAGGTTGCAGTG					
			TCC CTCCAACGTCAC					
			AC					
GAM1478	HPRP3P	3'	TACTGCAAGCCCTTGCCT	16284	A			
			AGGCAAG GGTG GCAGTG					

TCCGTTC CCGA CGTCAT  
 — A  
 GAM1478 HRH4 3' CACTGCAACCTCTGCCT 41247 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||  
 TCCGT CTCCAACGTCAC  
  
 —  
 GAM1478 HRH4 3' CAGCTCACTGCAGCCCTGACT 41249 GCA A  
 AG AG GGTTCAGTGAGCTG  
 || || |||||  
 TC TC CCGACGTCAGTCGAC  
 AG\_ \_  
 GAM1478 HRIHFB2436 5' CAGCTCACCGCCGCTTCCGCC 26791 AA T A  
 GGC GAGGT GC GTGAGCTG  
 ||| |||| || |||||  
 CCG TTCCG CG CACTCGAC  
 CC C C  
 GAM1478 HSPC065 3' CACTGCAACCTCCACCT 26289 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 HSPC065 3' CGCTGCAACCTCCTCCT 26292 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||  
 TCC CTCCAACGTCGC  
 TC\_  
 GAM1478 ICK 3' CTGCAACCTCTGCCT 29926 A  
 AGGCA GAGGTTGCAG  
 |||| |||||  
 TCCGT CTCCAACGTC  
  
 —  
 GAM1478 JAM1 5' CGGCTCACTGCAACCTCCTCCT 57922 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC CTCCAACGTCAGTCGGC  
 TC\_  
 GAM1478 JM11 3' CAGCTCACTGCAACCTCTGCCT 53253 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| |||||  
 TCCGT CTCCAACGTCAGTCGAC  
  
 —  
 GAM1478 KIAA0063 3' CACTGCAACCTCCACCT 29619 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 KIAA0205 3' CAGCTCACTGCAGTCTCTGCCT 29577 A GT  
 AGGCA GAG TGCAGTGAGCTG  
 |||| || |||||

TCCGT CTC ACGTCACTCGAC  
 \_ TG  
 GAM1478 KIAA0210 5' CAGCTCACCGCAATCTCCGCCT 28471 AA A  
 AGGC GAGGTTGC GTGAGCTG  
 ||| ||||| |||||  
 TCCG CTCTAACG CACTCGAC  
 C\_ C  
 GAM1478 KIAA0247 3' CAGCCTTTTACCCTCTTGCCT 28391 TTGCA \_  
 AGGCAAGAGG GTGA GCTG  
 ||||| ||| |||  
 TCCGTTCTCC CATT CGAC  
 \_ TTC  
 GAM1478 KIAA0391 3' CACTGCAACCTCTGCCT 27908 A  
 AGGCA GAGGTTGCAGTG  
 ||| |||||  
 TCCGT CTCCAACGTCAC  
 \_  
 GAM1478 KIAA0426 3' CACTGCAACCTCCGCCT 28254 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 KIAA0459 3' CACTGCAACCTCCACCT 60985 CAA  
 AGG GAGGTTGCAGTG  
 || |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 KIAA0472 5' CAGCTCACTGCAACCTCCTCCT 71860 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 || |||||  
 TCC CTCCAACGTCACACTCGAC  
 TC\_  
 GAM1478 KIAA0513 3' CACTGCAACCTCCACCT 28342 CAA  
 AGG GAGGTTGCAGTG  
 || |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 KIAA0527 3' CACTGCAACCTCTGCCT 95794 A  
 AGGCA GAGGTTGCAGTG  
 ||| |||||  
 TCCGT CTCCAACGTCAC  
 \_  
 GAM1478 KIAA0537 5' CAGCTCACGGCGGCCCGGCC 29243 AAGA A  
 GGC GGTTCG GTGAGCTG  
 || |||||  
 CCG CCGGCG CACTCGAC  
 GCC\_ G  
 GAM1478 KIAA0544 3' CACTGCAACCTCCGCCT 70895 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||

TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 KIAA0561 3' CAGCTCACTGCAACCTCCGCCT 65876 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCG CTCCAACGTCAGTCTGAC  
 C\_  
 GAM1478 KIAA0562 3' CTGCAACCTCCGCCT 28151 AA  
 AGGC GAGGTTGCAG  
 ||| |||||  
 TCCG CTCCAACGTC  
 C\_  
 GAM1478 KIAA0563 5' CACTGCAACCTCTGCCT 29183 A  
 AGGCA GAGGTTGCAGTG  
 ||| |||||  
 TCCGT CTCCAACGTCAC  
 -  
 GAM1478 KIAA0594 3' CTTACTGCAACCTCCGCCT 64896 AA  
 AGGC GAGGTTGCAGTGAG  
 ||| |||||  
 TCCG CTCCAACGTCATTC  
 C\_  
 GAM1478 KIAA0599 3' CACTGCAACCTCCGCCT 77168 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 KIAA0599 3' CTTACTGCAACCTCCGCCT 77176 AA  
 AGGC GAGGTTGCAGTGAG  
 ||| |||||  
 TCCG CTCCAACGTCATTC  
 C\_  
 GAM1478 KIAA0682 3' CAGCCTGAGACGCAGCCTCCCG 32473 AA AG\_\_ GA  
 CCT AGGC GAGGTTGC T GCTG  
 ||| ||||| | |||  
 TCCG CTCCGACG G CGAC  
 CC CAGA TC  
 GAM1478 KIAA0720 3' CACTGCAACCTCTGCCT 62317 A  
 AGGCA GAGGTTGCAGTG  
 ||| |||||  
 TCCGT CTCCAACGTCAC  
 -  
 GAM1478 KIAA0737 3' CAGCTCACTGAAACCTCTGCCT 29132 A G  
 AGGCA GAGGTT CAGTGAGCTG  
 ||| ||||| |||||  
 TCCGT CTCCAA GTCAGTCTGAC  
 - A  
 GAM1478 KIAA0828 3' GGAGCTGCCTCCAACCTCTTAC 81197 C G\_\_\_\_\_ TGAG  
 CT GG AAGAGGTT CAG C  
 || ||||| || |

CC TTCTCCAA GTC G  
 A CCTCCIII GAGT  
 GAM1478 KIAA0841 3' CAGCTCACTGCAACCTCCGCCT 71378 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 |||| ||||||||  
 TCCG CTCCAACGTCACTCGAC  
 C\_

GAM1478 KIAA0841 3' CAGCTCACTGCAACCTCTGCCT 71379 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| ||||||||  
 TCCGT CTCCAACGTCACTCGAC

—  
 GAM1478 KIAA1026 3' CAGCTCACTGCAACCAACACCT 71188 CAAGA  
 AGG GGTTCAGTGAGCTG  
 ||| ||||||||  
 TCC CCAACGTCACTCGAC  
 ACAA\_

GAM1478 KIAA1041 3' CACTGCAACCTCCGCCT 30127 AA  
 AGGC GAGGTTGCAGTG  
 |||| ||||||||  
 TCCG CTCCAACGTCAC  
 C\_

GAM1478 KIAA1054 3' CACTGCAACCTCCGCCT 68428 AA  
 AGGC GAGGTTGCAGTG  
 |||| ||||||||  
 TCCG CTCCAACGTCAC  
 C\_

GAM1478 KIAA1143 3' CAGCTCACTGCAAGCTCCGCCT 68673 AA G  
 AGGC GAG TTGCAGTGAGCTG  
 |||| ||| ||||||||  
 TCCG CTC AACGTCACTCGAC  
 C\_ G

GAM1478 KIAA1161 5' CAGCTCACTGCAACCCCTCCT 81738 CA A  
 AGG AG GGTTCAGTGAGCTG  
 ||| || ||||||||  
 TCC TC CCAACGTCACTCGAC  
 \_ C

GAM1478 KIAA1170 3' CACTGCAACCTCCGCCT 69845 AA  
 AGGC GAGGTTGCAGTG  
 |||| ||||||||  
 TCCG CTCCAACGTCAC  
 C\_

GAM1478 KIAA1193 3' CACTGCAACCTCCGCCT 67631 AA  
 AGGC GAGGTTGCAGTG  
 |||| ||||||||  
 TCCG CTCCAACGTCAC  
 C\_

GAM1478 KIAA1198 3' CACCGCAACCTCCGCCT 63290 AA A  
 AGGC GAGGTTGC GTG  
 |||| ||||| ||

			TCCG CTCCAACG CAC		
			C_ C		
GAM1478	KIAA1198	3'	CAGCTCACTGCAAGCTCCGCCT 63295	AA	G
			AGGC GAG TTGCAGTGAGCTG		
			TCCG CTC AACGTCACCTCGAC		
			C_ G		
GAM1478	KIAA1254	3'	CAGCTCACTGCAACCTCTGTCT 70016	A	
			AGGCA GAGGTTGCAGTGAGCTG		
			TCTGT CTCCAACGTCACCTCGAC		
			—		
GAM1478	KIAA1257	3'	CAGCTCACCGCAACCTCCGCCT 62732	AA	A
			AGGC GAGGTTGC GTGAGCTG		
			TCCG CTCCAACG CACTCGAC		
			C_ C		
GAM1478	KIAA1320	5'	CACTGCAACCTCTGCCT 69296	A	
			AGGCA GAGGTTGCAGTG		
			TCCGT CTCCAACGTCAC		
			—		
GAM1478	KIAA1320	5'	CAGCTCACTGTAGCCTTGACT 69298	GCAA	
			AG GAGGTTGCAGTGAGCTG		
			TC TTCCGATGTCACTCGAC		
			AG__		
GAM1478	KIAA1373	3'	CAGCTCACTGCAACCTCCACCT 70931	CAA	
			AGG GAGGTTGCAGTGAGCTG		
			TCC CTCCAACGTCACCTCGAC		
			AC_		
GAM1478	KIAA1443	3'	CAGCTCACTGCAAGCTCCGCCT 63826	AA	G
			AGGC GAG TTGCAGTGAGCTG		
			TCCG CTC AACGTCACCTCGAC		
			C_ G		
GAM1478	KIAA1467	3'	CACTGCAACCTTCGCCT 71603	AA	
			AGGC GAGGTTGCAGTG		
			TCCG TTCCAACGTCAC		
			C_		
GAM1478	KIAA1473	3'	CAGCTCACTGCAACCTCCGTCT 70664	AA	
			AGGC GAGGTTGCAGTGAGCTG		
			TCTG CTCCAACGTCACCTCGAC		
			C_		
GAM1478	KIAA1493	3'	CAGCTCACTACAAGCTCCCCT 64156	CAA	G C
			AGG GAG TTG AGTGAGCTG		

TCC CTC AAC TCACTCGAC  
 C\_ G A  
 GAM1478 KIAA1497 5' CACTGCAACCTCTGCCT 67504 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||  
 TCCGT CTCCAACGTCAC  
  
 —  
 GAM1478 KIAA1508 3' CAGCTCACTGCAACCTCCGCCT 61880 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCG CTCCAACGTCAGTCACTCGAC  
 C\_  
 GAM1478 KIAA1571 3' CACCGCAACCTCCACCT 60951 CAA A  
 AGG GAGGTTGC GTG  
 || |||||  
 TCC CTCCAACG CAC  
 AC\_ C  
 GAM1478 KIAA1615 3' CACTGCAACCTCCACCT 68701 CAA  
 AGG GAGGTTGCAGTG  
 || |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 KIAA1617 3' CAGCTCACTGCAACCTCTCTCT 91424 CA  
 GG AGAGGTTGCAGTGAGCTG  
 || |||||  
 TC TCTCCAACGTCAGTCACTCGAC  
 TC  
 GAM1478 KIAA1649 3' CAGCTCACTGCAACCTCCGC 50246 AA  
 GC GAGGTTGCAGTGAGCTG  
 || |||||  
 CG CTCCAACGTCAGTCACTCGAC  
 C\_  
 GAM1478 KIAA1655 3' CAGCTCACTGTAACTCCACCT 66599 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC CTCCAATGTCACTCGAC  
 AC\_  
 GAM1478 KIAA1655 3' CATTGCAACCTCCGCCT 66600 AA  
 AGGC GAGGTTGCAGTG  
 |||| |||||  
 TCCG CTCCAACGTTAC  
 C\_  
 GAM1478 KIAA1668 3' CAGCTCACTGCAAGCTCCGCCT 66469 AA G  
 AGGC GAG TTGCAGTGAGCTG  
 |||| || |||||  
 TCCG CTC AACGTCACTCGAC  
 C\_ G  
 GAM1478 KIAA1712 3' CACCGCAACCTCTGCCT 67533 A A  
 AGGCA GAGGTTGC GTG  
 |||| ||||| ||



TCCGT CTCCAACG CAC  
 \_ C  
 GAM1478 KIAA1737 3' CACTGCAACCTCCGCCT 67350 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 KIAA1751 3' CAGCTCACTGCAGCCTCGACCT 71690 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC CTCCGACGTCACTCGAC  
 AG\_  
 GAM1478 KIAA1784 3' CACTGCAACCTCCGCCT 65144 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 KIAA1855 3' GGAGCTGCAGAAACCTCTTGCC 92344 GC\_\_\_\_\_ TGAG  
 T AGGCAAGAGGTT AG C  
 ||||| || |  
 TCCGTTCTCAA TC G  
 AGACIIIG GAGT  
 GAM1478 KIAA1922 5' CAGCTCACTGCAACCTCCGCCT 73618 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCG CTCCAACGTCACTCGAC  
 C\_  
 GAM1478 KIAA1956 3' CAGCTCACTGCAGCCTCCACCT 78432 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC CTCCGACGTCACTCGAC  
 AC\_  
 GAM1478 KIAA1971 3' CTTACTGCAACCTCCACCT 74217 CAA  
 AGG GAGGTTGCAGTGAG  
 ||| |||||  
 TCC CTCCAACGTCATTC  
 AC\_  
 GAM1478 KLK7 3' CACTGCAACCTCCGCCT 17288 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 KLK7 3' CACTGCAACCTCCGCCT 57728 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 LMOD1 5' CAGCTCACCCCGCGCCCTTTCC 24041 C A T A\_  
 T AGG AAG GGT GC GTGAGCTG  
 ||| ||| || |||||

TCC TTC CCG CG CACTCGAC  
 T \_ \_ CCC  
 GAM1478 LRRN3 5' GCTGCAGCCTCCTGCCT 69438 A  
 AGGCA GAGGTTGCAGT  
 |||| |||||  
 TCCGT CTCCGACGTCG  
 C  
 GAM1478 MCLC 3' CACTGCAACCTCCACCT 30678 CAA  
 AGG GAGGTTGCAGTG  
 || |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 MEF-2 3' CACTGCAACCTCCGCCT 64378 AA  
 AGGC GAGGTTGCAGTG  
 |||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 MGC12518 3' TACTGCAACCTCTGCC 64083 A  
 GGCA GAGGTTGCAGTG  
 |||| |||||  
 CCGT CTCCAACGTCAT  
 -  
 GAM1478 MGC13138 3' CAGCTCACTGCAACCTCTGCCT 53015 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| |||||  
 TCCGT CTCCAACGTCACTCGAC  
 -  
 GAM1478 MGC13198 5' CAGCTCACTGCAACCTCCGTCT 51094 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 |||| |||||  
 TCTG CTCCAACGTCACTCGAC  
 C\_  
 GAM1478 MGC14836 3' CACTGCAACCTCCGCCT 53036 AA  
 AGGC GAGGTTGCAGTG  
 |||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 MGC15873 5' CAGCTCACTGCAGCCTTGACCT 51901 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 || |||||  
 TCC TTCCGACGTCACTCGAC  
 AG\_  
 GAM1478 MGC16025 3' CAGCCCACTGTGGGCCCTTCCC 51915 C A \_ TG A  
 GG AAG GG T CAGTG GCTG  
 || ||| |||||  
 CC TTC CC G GTCAC CGAC  
 C \_ G GT C  
 GAM1478 MGC1842 3' CTTACTACAACCTCCGCCT 65647 AA C  
 AGGC GAGGTTG AGTGAG  
 |||| |||||

TCCG CTCCAAC TCATTC  
 C\_ A  
 GAM1478 MGC21675 3' CAGCTCACTGCAATCTCTGCC 53480 A  
 GGCA GAGGTTGCAGTGAGCTG  
 |||| ||||||||||||  
 CCGT CTCTAACGTCACTCGAC  
  
 —  
 GAM1478 MGC27171 3' GCTGCAGCCTCTTGCCT 58086  
 AGGCAAGAGGTTGCAGT  
 ||||||||||||  
 TCCGTTCTCCGACGTCG  
  
 GAM1478 MGC29891 3' CACTGCAACCTCCGCCT 58201 AA  
 AGGC GAGGTTGCAGTG  
 |||| ||||||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 MGC3113 3' CAGCTCACTGCAGCCTCCACCT 43841 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 || ||||||||||||  
 TCC CTCCGACGTCACTCGAC  
 AC\_  
 GAM1478 MGC3329 3' CACTGCAACCCCCGCCT 44014 AAGA  
 AGGC GGTGAGTGAGTG  
 |||| ||||||||  
 TCCG CCAACGTCAC  
 CCC\_  
 GAM1478 MGC5149 3' CAGCTCACTGCAACCTCTGCCT 72287 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| ||||||||||||  
 TCCGT CTCCAACGTCACTCGAC  
  
 —  
 GAM1478 MGC5508 3' CAGCCCTCCTGCCAGCCCCCTG 44033 AGA \_ T \_  
 CC GGCA GGTG CAG GA GCTG  
 |||| |||| || || ||||  
 CCGT CCGAC GTC CT CGAC  
 CCC C \_ CC  
 GAM1478 MGC9912 3' CACTGCAACCTCCACCT 54714 CAA  
 AGG GAGGTTGCAGTG  
 || ||||||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 MLZE 5' CAGCTCACTGCAACCTCTGCCT 48616 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| ||||||||||||  
 TCCGT CTCCAACGTCACTCGAC  
  
 —  
 GAM1478 MOCS3 3' CAGCTCACTGCAACCTCCGCCT 27150 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 |||| ||||||||||||

TCCG CTCCAACGTCACCTCGAC  
 C\_  
 GAM1478 MRPL44 3' CACTGCAACCTCCACCT 43314 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 MtFMT 3' CAGCTCACTGCAACCTCCGCCT 57650 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCG CTCCAACGTCACCTCGAC  
 C\_  
 GAM1478 N4BP3 3' CAGCTCACCAGTCTCTTCCCT 66254 C GT CA  
 AGG AAGAG TG GTGAGCTG  
 ||| ||| || |||||  
 TCC TTCTC AC CACTCGAC  
 C TG \_  
 GAM1478 NDUFB1 5' CAGCTCACTGCAACCTCTGCCT 15816 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| |||||  
 TCCGT CTCCAACGTCACCTCGAC  
 \_  
 GAM1478 NDUFC2 3' CACTGCAACCTCCACCT 15827 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 Nup43 3' CACTGCAACCTCCACCT 44995 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 OSBPL2 3' CACCGCAACCTCCGCCT 57855 AA A  
 AGGC GAGGTTGC GTG  
 |||| ||||| |||  
 TCCG CTCCAACG CAC  
 C\_ C  
 GAM1478 OSBPL2 3' CACCGCAACCTCCGCCT 29204 AA A  
 AGGC GAGGTTGC GTG  
 |||| ||||| |||  
 TCCG CTCCAACG CAC  
 C\_ C  
 GAM1478 PASK 5' CACTGCAACCTCTGCCT 30712 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||  
 TCCGT CTCCAACGTCAC  
 \_  
 GAM1478 PELI1 5' CACTGCAACCTCTGCCT 40256 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||

TCCGT CTCCAACGTCAC

GAM1478 PELI1 5' CGGCTCACTGCAACCTCCTCCT 40260 CAA  
AGG GAGGTTGCAGTGAGCTG  
||| |||||  
TCC CTCCAACGTCACCTCGGC  
TC\_

GAM1478 PIP3-E 3' CACTGCAACCTCTGCCT 66800 A  
AGGCA GAGGTTGCAGTG  
|||||  
TCCGT CTCCAACGTCAC

GAM1478 PPP1R10 3' CAGCTCACTCCCTGCTCCCACC 10729 CAA GTTGC  
T AGG GAG AGTGAGCTG  
||| ||| |||||  
TCC CTC TCACTCGAC  
ACC GTCCC

GAM1478 PRO0365 5' CAGCTCACTGCAACCTCCACCT 26152 CAA  
AGG GAGGTTGCAGTGAGCTG  
||| |||||  
TCC CTCCAACGTCACCTCGAC  
AC\_

GAM1478 PRO1048 3' CAGCTCACTGAAGTCTCGACCT 37513 CAA GT G  
AGG GAG T CAGTGAGCTG  
||| ||| | |||||  
TCC CTC A GTCACCTCGAC  
AG\_ TG A

GAM1478 PRO1992 5' CACTGCAACCTCTGCCT 26053 A  
AGGCA GAGGTTGCAGTG  
|||||  
TCCGT CTCCAACGTCAC

GAM1478 PRO2955 3' CAGCTCACTGCAACCTCTGCCT 37633 A  
AGGCA GAGGTTGCAGTGAGCTG  
|||||  
TCCGT CTCCAACGTCACCTCGAC

GAM1478 PSTPIP2 3' CAGCTCACTGCAACCTCTGCCT 44385 A  
AGGCA GAGGTTGCAGTGAGCTG  
|||||  
TCCGT CTCCAACGTCACCTCGAC

GAM1478 RAB33B 3' CACTGCAACCTCCGCCT 48488 AA  
AGGC GAGGTTGCAGTG  
||| |||||  
TCCG CTCCAACGTCAC

GAM1478 RAI 5' CACTGCAACCTCCGCCT 21873 AA  
AGGC GAGGTTGCAGTG  
||| |||||

TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 RASSF2 3' CAGCTCACTGCAACATCCGCCT 28430 AA G  
 AGGC GA GTTGCAGTGAGCTG  
 |||| || ||||||||  
 TCCG CT CAACGTCACCTCGAC  
 C\_ A  
 GAM1478 RNF8 3' CAGCTCACTGCAACCTCCACCT 14217 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 || ||||||||  
 TCC CTCCAACGTCACCTCGAC  
 AC\_  
 GAM1478 RNO2 5' CAGCTCACTGCAACCTCCACCT 52765 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 || ||||||||  
 TCC CTCCAACGTCACCTCGAC  
 AC\_  
 GAM1478 SARM 3' AGCTCAGGGCTCCTGCC 30594 AGA TT AG  
 GGCA GG GC TGAGCT  
 |||| || || ||||  
 CCGT CC CG ACTCGA  
 \_\_\_\_ T\_ GG  
 GAM1478 SC4MOL 3' CAGCTCACTGCAACCTCTGCCT 22152 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| ||||||||  
 TCCGT CTCCAACGTCACCTCGAC  
 -  
 GAM1478 SCAMP-4 3' CACTGCAACCTCTGCCT 54390 A  
 AGGCA GAGGTTGCAGTG  
 |||| ||||||||  
 TCCGT CTCCAACGTCAC  
 -  
 GAM1478 SDC3 3' CACTGCAACCTCTTGCT 27741  
 GGCAAGAGGTTGCAGTG  
 ||||||||  
 TCGTTCTCCAACGTCAC  
 -  
 GAM1478 SERF1B 3' CACTGCAACCTCCGCCT 43409 AA  
 AGGC GAGGTTGCAGTG  
 |||| ||||||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 SERF1B 3' CAGCTCCATGCAACCTCTGCCT 43411 A GT  
 AGGCA GAGGTTGCA GAGCTG  
 |||| ||||| ||||  
 TCCGT CTCCAACGT CTCGAC  
 - AC  
 GAM1478 SHANK3 5' CAGCTCACCCCTGGCCCTTGCC 65490 A CA\_  
 GGCAAG GGTG GTGAGCTG  
 |||| |||| |||||

CCGTTC CCGGT CACTCGAC  
 \_ CCC  
 GAM1478 SIRPB1 3' CACTGCAACCCCCGCCT 20243 AAGA  
 AGGC GGTTGCAGTG  
 ||| |||||  
 TCCG CCAACGTCAC  
 CCC\_  
 GAM1478 SLC11A1 3' CATTGCAACCTCCACCT 59452 CAA  
 AGG GAGGTTGCAGTG  
 || |||||  
 TCC CTCCAACGTTAC  
 AC\_  
 GAM1478 SLC6A14 3' CAGCTCACTGCAACCTCTGCCT 23348 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCGT CTCCAACGTCACTCGAC  
 \_  
 GAM1478 SQV7L 5' CAGCTCACTGCAACCACTGCCT 70569 A A  
 AGGCA G GGTTGCAGTGAGCTG  
 ||| | |||||  
 TCCGT C CCAACGTCACTCGAC  
 \_A  
 GAM1478 STAF65(gamma) 3' CACTGCAACCTCTGCCT 29427 A  
 AGGCA GAGGTTGCAGTG  
 ||| |||||  
 TCCGT CTCCAACGTCAC  
 \_  
 GAM1478 SULT1C2 5' GCTCACTTTCTCCCT 21677 CAA TTGC  
 AGG GAGG AGTGAGC  
 || ||| |||||  
 TCC CTCT TCACTCG  
 \_ T \_  
 GAM1478 SYT13 3' CACTGCAACCTCCGCCT 93450 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 TGIF2 3' CAGCTCACTGTACTCCAGCC 41448 AA GT  
 GGC GAG TGCAGTGAGCTG  
 || || |||||  
 CCG CTC ATGTCACTCGAC  
 AC \_  
 GAM1478 THEA 3' CAGCTCACTGCAACCTCGGCCT 66277 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCG CTCCAACGTCACTCGAC  
 G\_  
 GAM1478 TLN1 3' CAGCCCACTCCACCCTGCC 20816 A A T C A  
 GGCA G GGT G AGTG GCTG  
 ||| | ||| |||

CCGT C CCA C TCAC CGAC  
 \_ \_ \_ C C  
 GAM1478 TM4SF11 3' GGAGCTGCAACCAACCTCTCCC 32037 CA G\_\_\_\_\_ TGAG  
 T GG AGAGGTT CAG C  
 || ||||| ||| |  
 CC TCTCAA GTC G  
 C\_ CCAACIII GAGT  
 GAM1478 TNRC4 3' CAGCTCACCTCACCCAGCCT 23220 AAGA TGCA  
 AGGC GGT GTGAGCTG  
 ||| ||| |||||  
 TCCG CCA CACTCGAC  
 ACC\_ CTCC  
 GAM1478 TOR1B 3' CTCACTGCAACCTCCGCT 27198 AA  
 GGC GAGGTTGCAGTGAG  
 ||| |||||  
 TCG CTCCAACGTCCTC  
 C\_  
 GAM1478 TPRA40 5' CAGCTCACTGGGCGGCTCTC 33038 \_ \_  
 GAG GTTGC AGTGAGCTG  
 ||| ||| |||||  
 CTC CGGCG TCACTCGAC  
 T GG  
 GAM1478 TRAF3 3' AGCTCACTGCAAGGGC 59732 AAGAGG  
 GC TTGCAGTGAGCT  
 || |||||  
 CG AACGTCCTCGA  
 GG\_\_\_\_  
 GAM1478 TRIM5 3' CACTGCAACCTCCACCT 52294 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 TRIM6 3' CACTGCAACCTCTGCCT 54134 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||  
 TCCGT CTCCAACGTCAC  
 \_  
 GAM1478 TU12B1-TY 3' AGCCCACCCCTCCAGCCT 33368 AA TTGCA A  
 AGGC GAGG GTG GCT  
 ||| ||| ||| |||  
 TCCG CTCC CAC CGA  
 AC C\_\_\_\_ C  
 GAM1478 TU12B1-TY 3' CAGCTCACTGCAACCTCTGCCT 33372 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| |||||  
 TCCGT CTCCAACGTCCTCGAC  
 \_  
 GAM1478 TU12B1-TY 3' CGGCTCACTGCAACCTCTTGCC 33376  
 T AGGCAAGAGGTTGCAGTGAGCTG  
 ||||| |||||



TCCGTTCTCCAACGTCACCTCGGC

GAM1478 TUCAN 3' CAGCTCACTGCAACCTCTGCCT 30272 A  
AGGCA GAGGTTGCAGTGAGCTG  
||||| |||||||||  
TCCGT CTCCAACGTCACCTCGAC

—  
GAM1478 UBF-fl 3' CACTGCAACCTCTGCCT 51554 A  
AGGCA GAGGTTGCAGTG  
||||| |||||||||  
TCCGT CTCCAACGTCAC

—  
GAM1478 USP22 3' CACTGCAACCTCCACCT 68006 CAA  
AGG GAGGTTGCAGTG  
||| |||||||||  
TCC CTCCAACGTCAC  
AC\_

GAM1478 VDU1 3' CAGCTCACTGCAGCCTCCACCT 30415 CAA  
AGG GAGGTTGCAGTGAGCTG  
||| |||||||||  
TCC CTCCGACGTCACCTCGAC  
AC\_

GAM1478 VPS33A 3' CACTGCAACCTCCACCT 43335 CAA  
AGG GAGGTTGCAGTG  
||| |||||||||  
TCC CTCCAACGTCAC  
AC\_

GAM1478 WBSCR20A 5' CACCGCAACCTCTGCCT 49649 A A  
AGGCA GAGGTTGC GTG  
||||| ||||||| |||  
TCCGT CTCCAACG CAC  
C

—  
GAM1478 YWHAQ 3' CACTTACACCTCCTGCCT 22394 A TGC  
AGGCA GAGGT AGTG  
||||| ||||| |||||  
TCCGT CTCCA TCAC  
C CAT

GAM1478 ZIC4 5' CAGCTCACCGCCGCTCCAGCC 49616 AA T A  
GGC GAGGT GC GTGAGCTG  
||| ||||| || |||||||  
CCG CTCCG CG CACTCGAC  
AC C C

GAM1478 ZTL1 3' CACTGCAACCTCTGCCT 43910 A  
AGGCA GAGGTTGCAGTG  
||||| |||||||||  
TCCGT CTCCAACGTCAC

—  
GAM1478 LOC112724 5' CACTGCAACCTCCACCT 56492 CAA  
AGG GAGGTTGCAGTG  
||| |||||||||

TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC113675 5' CACTGCAACCTCCGCCT 56569 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 LOC115219 5' CACTGCAACCTCCGCCT 73297 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 LOC115648 3' CAGCTCATCAAAACCTTTGCCT 59295 A GCA  
 AGGCA GAGGT GTGAGCTG  
 ||| ||| |||||  
 TCCGT TTCAA TACTCGAC  
 \_ AAC  
 GAM1478 LOC116349 5' CTCAGGCCCTCTCGCT 73829 A TT AG  
 GGC AGAGG GC TGAG  
 || ||| || |||  
 TCG TCTCC CG ACTC  
 C \_ G\_  
 GAM1478 LOC116411 5' CGCTACAACCTCCACCT 73859 CAA C  
 AGG GAGGTTG AGTG  
 || ||||| |||  
 TCC CTCCAAC TCGC  
 AC\_ A  
 GAM1478 LOC116411 5' CGGCTCACTGCAACCTCCCTGC 73861 A\_  
 CT AGGCA GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCGT CTCCAACGTCAGTCCGGC  
 CC  
 GAM1478 LOC119392 3' CACTGCAACCTCTGCCT 59131 A  
 AGGCA GAGGTTGCAGTG  
 ||| |||||  
 TCCGT CTCCAACGTCAC  
 \_  
 GAM1478 LOC120114 3' CAGCTCACTGCAATCTCCACCT 75520 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 || |||||  
 TCC CTCTAACGTCAGTCTCGAC  
 AC\_  
 GAM1478 LOC120939 3' CAGCTCACTGTAACCTCCACCT 76249 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 || |||||  
 TCC CTCCAATGTCACTCGAC  
 AC\_  
 GAM1478 LOC126364 3' CAGCTCACTGCAACCTCCGCCT 75685 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 ||| |||||

		TCCG CTCCAACGTCACTCGAC		
		C_		
GAM1478	LOC126661 3'	CAGCTCACTGCAACCTCCGCCT 74546	AA	
		AGGC GAGGTTGCAGTGAGCTG		
		TCCG CTCCAACGTCACTCGAC		
		C_		
GAM1478	LOC127534 3'	CAGCTCACCCAGACCTGCC 75437	AGA	GCA
		GGCA GGTT GTGAGCTG		
		CCGT CCAG CACTCGAC		
		ACC		
GAM1478	LOC128077 3'	CACTGCAACCTCCGCCT 74706	AA	
		AGGC GAGGTTGCAGTG		
		TCCG CTCCAACGTCAC		
		C_		
GAM1478	LOC128077 3'	CACTGCAACCTCTGCCT 74708	A	
		AGGCA GAGGTTGCAGTG		
		TCCGT CTCCAACGTCAC		
		-		
GAM1478	LOC128989 3'	CACTGCAACCTCCGCCT 74805	AA	
		AGGC GAGGTTGCAGTG		
		TCCG CTCCAACGTCAC		
		C_		
GAM1478	LOC130813 3'	CACCGCAACCTCCGCCT 75763	AA	A
		AGGC GAGGTTGC GTG		
		TCCG CTCCAACG CAC		
		C_ C		
GAM1478	LOC132625 3'	CACTGCAACCTCCACCT 75899	CAA	
		AGG GAGGTTGCAGTG		
		TCC CTCCAACGTCAC		
		AC_		
GAM1478	LOC135154 3'	CTCACTGCAACTTCCGCC 75214	AA	
		GGC GAGGTTGCAGTGAG		
		CCG CTTCAACGTCACTC		
		C_		
GAM1478	LOC135293 3'	CACTGCAACCTCTGCCT 76174	A	
		AGGCA GAGGTTGCAGTG		
		TCCGT CTCCAACGTCAC		
		-		
GAM1478	LOC135763 3'	CACTGCAACCTCCGCCT 56786	AA	
		AGGC GAGGTTGCAGTG		

TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 LOC135818 3' CAGCTCACCACAACCTCCGCCT 75232 AA CA  
 AGGC GAGGTTG GTGAGCTG  
 ||| ||||| |||||  
 TCCG CTCCAAC CACTCGAC  
 C\_ AC  
 GAM1478 LOC143187 3' CACTGCAACCTCCACCT 59095 CAA  
 AGG GAGGTTGCAGTG  
 || |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC143241 5' CAGCTCACTGCAACCTCTGCCT 57175 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCGT CTCCAACGTCACTCGAC  
 -  
 GAM1478 LOC144248 5' CACTGCAACCTCCACCT 76735 CAA  
 AGG GAGGTTGCAGTG  
 || |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC144317 5' CTCCTGCAACCTCTTCCT 76787 C  
 AGG AAGAGGTTGCAGTGAG  
 || |||||  
 TCC TTCTCCAACGTCACTC  
 -  
 GAM1478 LOC144524 5' CAGCTCACTGCAACCTCCACCT 83122 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 || |||||  
 TCC CTCCAACGTCACTCGAC  
 AC\_  
 GAM1478 LOC144742 5' CTGCAACCTTCGCCT 76943 AA  
 AGGC GAGGTTGCAG  
 ||| |||||  
 TCCG TTCCAACGTC  
 C\_  
 GAM1478 LOC145009 3' CAGCTCACTGCATCCTCCGCCT 60346 AA T  
 AGGC GAGG TGCAGTGAGCTG  
 ||| ||| |||||  
 TCCG CTCC ACGTCACTCGAC  
 C\_ T  
 GAM1478 LOC145268 5' CACTGCAACCTCCACC 77054 CAA  
 GG GAGGTTGCAGTG  
 || |||||  
 CC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC145757 5' CACTACAACCTCTGCCT 77456 A C  
 AGGCA GAGGTTG AGTG  
 ||| ||||| |||

TCCGT CTCCAAC TCAC  
 — A  
 GAM1478 LOC146050 3' CAGCTCACTGCAACCTCTGCCT 77632 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| ||||||||||||  
 TCCGT CTCCAACGTCACCTCGAC  
 —  
 GAM1478 LOC146050 3' CAGCTCACTGCAACCTCTGCTT 77633 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| ||||||||||||  
 TCCGT CTCCAACGTCACCTCGAC  
 —  
 GAM1478 LOC146229 3' CACTGCAACCTCCACCT 77733 CAA  
 AGG GAGGTTGCAGTG  
 || |||||||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC146733 3' CAGCTCACTCCTCCCTCTGGCC 83756 A TTGC  
 GGC AGAGG AGTGAGCTG  
 || |||| |||||||  
 CCG TCTCC TCACTCGAC  
 G CTCC  
 GAM1478 LOC146784 5' CACTGCAACCTCCACCT 78104 CAA  
 AGG GAGGTTGCAGTG  
 || |||||||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC146839 3' CACCACAACCTCCGCCT 83807 AA CA  
 AGGC GAGGTTG GTG  
 |||| ||||| ||  
 TCCG CTCCAAC CAC  
 C\_ AC  
 GAM1478 LOC146901 3' CATTGCAACCTCCACCT 83834 CAA  
 AGG GAGGTTGCAGTG  
 || |||||||||  
 TCC CTCCAACGTTAC  
 AC\_  
 GAM1478 LOC146909 3' CACTGCAACCTCCGCCT 78167 AA  
 AGGC GAGGTTGCAGTG  
 |||| |||||||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 LOC146952 5' CAGCTCACTGCAACCTCCACCT 83861 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 || |||||||||||||  
 TCC CTCCAACGTCACCTCGAC  
 AC\_  
 GAM1478 LOC147071 5' CACTGCAACCTCTGCCT 72994 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||||||

TCCGT CTCCAACGTCAC

GAM1478 LOC147276 3' CAGCTCACTGCAACGTCTGCCT 78331 A G  
AGGCA GA GTTGCAGTGAGCTG  
||||| || |||||  
TCCGT CT CAACGTCACTCGAC

— G  
GAM1478 LOC147407 3' CACTGCAACCTCCGCCT 76323 AA  
AGGC GAGGTTGCAGTG  
||| |||||  
TCCG CTCCAACGTCAC

C—  
GAM1478 LOC147463 3' CAGCTCAGGGACCCTCTTGCC 78369 TTGCAG  
GGCAAGAGG TGAGCTG  
||||| |||||  
CCGTTCTCC ACTCGAC  
CAGGG—

GAM1478 LOC147817 3' CACTGCAACCTCCACCT 78490 CAA  
AGG GAGGTTGCAGTG  
||| |||||  
TCC CTCCAACGTCAC  
AC—

GAM1478 LOC147841 3' CAGCTCACAGCAACCTCTGCCT 78525 A A  
AGGCA GAGGTTGC GTGAGCTG  
||||| |||||  
TCCGT CTCCAACG CACTCGAC  
— A

GAM1478 LOC147895 5' CAGCTCACTGCAGCCTC 84077  
GAGGTTGCAGTGAGCTG  
|||||  
CTCCGACGTCACTCGAC

GAM1478 LOC147990 3' CACTACAACCTCTGCCT 84089 A C  
AGGCA GAGGTTG AGTG  
||||| |||||  
TCCGT CTCCAAC TCAC

— A  
GAM1478 LOC148147 3' CAGCTCACTGCAATCTCTGCCT 78672 A  
AGGCA GAGGTTGCAGTGAGCTG  
||||| |||||  
TCCGT CTCTAACGTCACTCGAC

—  
GAM1478 LOC148189 5' CACTGCAACCTCCACCT 78705 CAA  
AGG GAGGTTGCAGTG  
||| |||||  
TCC CTCCAACGTCAC  
AC—

GAM1478 LOC148198 3' CAGCTCACTGCAACCTC 70677  
GAGGTTGCAGTGAGCTG  
|||||

## CTCCAACGTCACTCGAC

GAM1478 LOC148293 3' CAGCTCACTGGACCCCAGCCT 78778 AAGA G  
 AGGC GGTTCAGTGAGCTG  
 |||| ||| |||||  
 TCCG CCAG GTCACCTCGAC  
 ACC\_ \_

GAM1478 LOC148438 3' CAGCACCTAAAAACCTCTTGCC 84156 GCAGTGA  
 T AGGCAAGAGGTT GCTG  
 ||||| |||  
 TCCGTTCTCCAA CGAC  
 AAATCCA

GAM1478 LOC148709 3' CACTACAACCTCCGCCT 78934 AA C  
 AGGC GAGGTTG AGTG  
 ||| ||||| |||  
 TCCG CTCCAAC TCAC  
 C\_ A

GAM1478 LOC148887 5' CAGCCCACCCTGCAGCCCTGCT 84230 A A \_ A  
 GGCA G GGTTCGA GTG GCTG  
 |||| | ||||| || |||  
 TCGT C CCGACGT CAC CGAC  
 \_ \_ CC C

GAM1478 LOC149506 3' CAGCTCACTGCAACCTCTGCCT 84455 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| |||||  
 TCCGT CTCCAACGTCACTCGAC

GAM1478 LOC149703 5' CAGCTTAATGCAACCTCTACCT 84649 CA G  
 AGG AGAGTTGCA TGAGCTG  
 ||| ||||| |||||  
 TCC TCTCCAACGT ATTCGAC  
 A\_ A

GAM1478 LOC149832 5' AGCTCACCTCCTCTGCC 84695 A TTGCA  
 GGCA GAGG GTGAGCT  
 |||| ||| |||||  
 CCGT CTCC CACTCGA  
 \_ TC\_

GAM1478 LOC150054 5' CACTGCAACCTTCGCCT 84826 AA  
 AGGC GAGGTTGCAGTG  
 |||| |||||  
 TCCG TTCCAACGTCAC  
 C\_

GAM1478 LOC150095 5' CATCTGCAACCTGCTGCC 84856 AG \_  
 GGCA AGGTTGCAG TG  
 |||| ||||| ||  
 CCGT TCCAACGTC AC  
 CG T

GAM1478 LOC150397 3' CATTGCAACCTCCGCCT 79842 AA  
 AGGC GAGGTTGCAGTG  
 |||| |||||

TCCG CTCCAACGTTAC  
 C\_  
 GAM1478 LOC150407 3' CAGCTCACTGCAACCTC 79817  
 GAGGTTGCAGTGAGCTG  
 |||||  
 CTCCAACGTCACTCGAC

GAM1478 LOC150960 3' CGCTGCAACCTCCGCCT 80057 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCGC  
 C\_  
 GAM1478 LOC151005 3' AGCTCATACCCCTGCC 80095 A A TGCA  
 GGCA G GGT GTGAGCT  
 ||| ||| |||||  
 CCGT C CCA TACTCGA  
 \_ C \_  
 GAM1478 LOC151057 3' CACTGCAACCTCTGCCT 85207 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||  
 TCCGT CTCCAACGTCAC

-  
 GAM1478 LOC151103 3' CAGCTCACTACAAATTGT 85223 GAG TGC  
 GCAA GT AGTGAGCTG  
 ||| || |||||  
 TGTT CA TCACTCGAC  
 AAA \_  
 GAM1478 LOC151201 3' CAGCTCACTGCAACCTCCACCT 85273 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 || |||||  
 TCC CTCCAACGTCACTCGAC  
 AC\_  
 GAM1478 LOC151475 5' CACTGCAACCTCCACCT 85392 CAA  
 AGG GAGGTTGCAGTG  
 || |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC151475 5' CAGCTCACTGCAACCTCTGCCT 85395 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| |||||  
 TCCGT CTCCAACGTCACTCGAC

-  
 GAM1478 LOC151826 3' CAGCTCACTGCAACCTCCGCCT 80355 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCG CTCCAACGTCACTCGAC  
 C\_  
 GAM1478 LOC152220 3' CAGCTCACTGCAACCTCCGCTT 85579 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 ||| |||||



		TTCG CTCCAACGTC	ACTCGAC		
		C_			
GAM1478	LOC152245 3'	CACTGCAACCTCCGCCT	85597	AA	
		AGGC GAGGTTGCAGTG			
		TCCG CTCCAACGTCAC			
		C_			
GAM1478	LOC152300 3'	CAGCTCACTGCAAGCTCTGCCT	80542	A	G
		AGGCA GAG TTGCAGTGAGCTG			
		TCCGT CTC AACGTC			
		ACTCGAC			
		_ G			
GAM1478	LOC152343 3'	CAGTGCAACCTCCGCCT	80557	AA	G
		AGGC GAGGTTGCA TG			
		TCCG CTCCAACGT AC			
		C_ G			
GAM1478	LOC152445 3'	CACTGCAACCTCTGCCT	85748	A	
		AGGCA GAGGTTGCAGTG			
		TCCGT CTCCAACGTCAC			
		-			
GAM1478	LOC152582 5'	CACCGCAACCTCTGCCT	85788	A	A
		AGGCA GAGGTTGC GTG			
		TCCGT CTCCAACG CAC			
		- C			
GAM1478	LOC152620 3'	CAGCTCACTACAACCTCTGCCT	60079	A	C
		AGGCA GAGGTTG AGTGAGCTG			
		TCCGT CTCCAAC TCACTCGAC			
		- A			
GAM1478	LOC152719 5'	CACTGCAACCTCTGCCT	85847	A	
		AGGCA GAGGTTGCAGTG			
		TCCGT CTCCAACGTCAC			
		-			
GAM1478	LOC152794 5'	CACTGCAACCTCTACCT	80672	CA	
		AGG AGAGGTTGCAGTG			
		TCC TCTCCAACGTCAC			
		A_			
GAM1478	LOC152851 3'	CGCTGCAACCTCCACC	80707	CAA	
		GG GAGGTTGCAGTG			
		CC CTCCAACGTCGC			
		AC_			
GAM1478	LOC153077 3'	CACTGCAACCTCCGCCT	85906	AA	
		AGGC GAGGTTGCAGTG			

TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 LOC153688 3' CACTGCAACCTCCACCT 86096 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC153883 5' CACTGCAACCTCCACC 80979 CAA  
 GG GAGGTTGCAGTG  
 || |||||  
 CC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC154075 3' CAGCTCACTGCAACCTCCGCCT 81045 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCG CTCCAACGTCACCTCGAC  
 C\_  
 GAM1478 LOC154282 5' CACTGCAACCTCCACCT 86193 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC154726 5' CAGCTCACCACAACCTCCGCCT 81103 AA CA  
 AGGC GAGGTTG GTGAGCTG  
 ||| ||||| |||||  
 TCCG CTCCAAC CACTCGAC  
 C\_ AC  
 GAM1478 LOC154877 3' CAGCTCACTGCAACCTCTACCT 86283 CA  
 AGG AGAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC TCTCCAACGTCACCTCGAC  
 A\_  
 GAM1478 LOC154877 3' CATTGCAACCTCCGCCT 86285 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTTAC  
 C\_  
 GAM1478 LOC157247 5' CAGCTCACTGCAACCTCCACCC 81360 CAA  
 GG GAGGTTGCAGTGAGCTG  
 || |||||  
 CC CTCCAACGTCACCTCGAC  
 CAC  
 GAM1478 LOC157798 5' CACTGCAACCTCCGCCT 86547 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 LOC157858 5' CACTGCAACCTCTGCCT 86583 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||

TCCGT CTCCAACGTCAC

GAM1478 LOC158310 5' CAGCTCACTGCAACCTTGGCCT 86750 AA  
AGGC GAGGTTGCAGTGAGCTG  
||||| |||||||||  
TCCG TTCCAACGTCAGTCTCGAC  
G\_

GAM1478 LOC158402 5' CAGCTCACTGTAACCTCTGCCT 86801 A  
AGGCA GAGGTTGCAGTGAGCTG  
||||| |||||||||  
TCCGT CTCCAATGTCACTCGAC

GAM1478 LOC158476 3' CAGCTCACTGCAACCTCCGCC 86839 AA  
GGC GAGGTTGCAGTGAGCTG  
||| |||||||||  
CCG CTCCAACGTCAGTCTCGAC  
C\_

GAM1478 LOC158668 3' CAGCTCACTGCAACCTCTGCCT 69366 A  
AGGCA GAGGTTGCAGTGAGCTG  
||||| |||||||||  
TCCGT CTCCAACGTCAGTCTCGAC

GAM1478 LOC158828 3' CTGCAACCTCTGACCT 82028 CA  
AGG AGAGGTTGCAG  
||| |||||||  
TCC TCTCCAACGTC  
AG

GAM1478 LOC158865 5' CACTGCAACCTCTGCCT 86932 A  
AGGCA GAGGTTGCAGTG  
||||| |||||||||  
TCCGT CTCCAACGTCAC

GAM1478 LOC161829 3' CACTGCAACCTCCGCCT 82311 AA  
AGGC GAGGTTGCAGTG  
||||| |||||||||  
TCCG CTCCAACGTCAC  
C\_

GAM1478 LOC169611 3' CAGCTCACTGCAATCTCCGCCT 82758 AA  
AGGC GAGGTTGCAGTGAGCTG  
||||| |||||||||  
TCCG CTCTAACGTCAGTCTCGAC  
C\_

GAM1478 LOC196047 5' CACTGCAACCTCCGCCT 89593 AA  
AGGC GAGGTTGCAGTG  
||||| |||||||||  
TCCG CTCCAACGTCAC  
C\_

GAM1478 LOC196264 3' CACTGCAACCTCTGCCT 87602 A  
AGGCA GAGGTTGCAGTG  
||||| |||||||||

TCCGT CTCCAACGTCAC

GAM1478 LOC196411 3' CACTGCAACCTCCGCCT 87667 AA  
AGGC GAGGTTGCAGTG  
|||| |||||||||  
TCCG CTCCAACGTCAC  
C\_

GAM1478 LOC196529 3' CACTGCAACCTCCACCT 87769 CAA  
AGG GAGGTTGCAGTG  
||| |||||||||  
TCC CTCCAACGTCAC  
AC\_

GAM1478 LOC196529 3' CAGCTTACCACAACCTCCACCT 87770 CAA CA  
AGG GAGGTTG GTGAGCTG  
||| ||||| |||||||  
TCC CTCCAAC CATTGAC  
AC\_ AC

GAM1478 LOC197358 3' CAGCTCACTGTAGGCTCTACCT 88025 CA G  
AGG AGAG TTGCAGTGAGCTG  
||| ||| |||||||||  
TCC TCTC GATGTCACTCGAC  
A\_ G

GAM1478 LOC197358 3' CAGCTCCCTGCAACCTCCGCCT 88026 AA T  
AGGC GAGGTTGCAG GAGCTG  
|||| ||||||| |||||  
TCCG CTCCAACGTC CTCGAC  
C\_ C

GAM1478 LOC199699 3' CAGCTCACTGCAAGCTCCACCT 88299 CAA G  
AGG GAG TTGCAGTGAGCTG  
||| ||| |||||||||  
TCC CTC AACGTCACTCGAC  
AC\_ G

GAM1478 LOC199725 5' CTTACTGCAACCTTCGCCT 89837 AA  
AGGC GAGGTTGCAGTGAG  
|||| |||||||||  
TCCG TTCCAACGTCATTC  
C\_

GAM1478 LOC199786 3' CACTGCAACCTCCGCCT 88369 AA  
AGGC GAGGTTGCAGTG  
|||| |||||||||  
TCCG CTCCAACGTCAC  
C\_

GAM1478 LOC199906 3' CTTACTGCAACCTCCGCCT 88483 AA  
AGGC GAGGTTGCAGTGAG  
|||| |||||||||  
TCCG CTCCAACGTCATTC  
C\_

GAM1478 LOC200014 3' CAGCTCGCTGCAACCCCCACCT 88519 CAAGA  
AGG GGTTGCAGTGAGCTG  
||| |||||||||

		TCC CCAACGTCGCTCGAC			
		ACCC_			
GAM1478	LOC200169 5'	CACTGCAACCTCTGCCT	89944	A	
		AGGCA GAGGTTGCAGTG			
		TCCGT CTCCAACGTCAC			
		—			
GAM1478	LOC200268 3'	CACTGCAACCTCTGCCT	88677	A	
		AGGCA GAGGTTGCAGTG			
		TCCGT CTCCAACGTCAC			
		—			
GAM1478	LOC200310 3'	CACTACAACCTCTGCCT	65728	A	C
		AGGCA GAGGTTG AGTG			
		TCCGT CTCCAAC TCAC			
		— A			
GAM1478	LOC200314 3'	CACTGCAACCTCCACCT	90002	CAA	
		AGG GAGGTTGCAGTG			
		TCC CTCCAACGTCAC			
		AC_			
GAM1478	LOC200316 3'	CAGCTCACTGCAAACCTCTGCTT	88765	A	G
		AGGCA GAG TTGCAGTGAGCTG			
		TTCGT CTC AACGTCAGTCTCGAC			
		— A			
GAM1478	LOC200339 3'	CACTGCAACCTCTGCCT	90032	A	
		AGGCA GAGGTTGCAGTG			
		TCCGT CTCCAACGTCAC			
		—			
GAM1478	LOC200471 5'	CAGCTCACCAGCCCCACGCT	90051	AAGA	CA
		GGC GGTTG GTGAGCTG			
		TCG CCGAC CACTCGAC			
		CACC _			
GAM1478	LOC200845 5'	CACTGCAACCTCCGCCT	88895	AA	
		AGGC GAGGTTGCAGTG			
		TCCG CTCCAACGTCAC			
		C_			
GAM1478	LOC200860 3'	CACTGCAACCTCCACCT	90159	CAA	
		AGG GAGGTTGCAGTG			
		TCC CTCCAACGTCAC			
		AC_			
GAM1478	LOC201173 5'	CACTGCAACCTCTGCCT	87324	A	
		AGGCA GAGGTTGCAGTG			

TCCGT CTCCAACGTCAC

GAM1478 LOC201220 5' CACTGCAACCTCTGCCT 87344 A  
AGGCA GAGGTTGCAGTG  
||||| |||||||||  
TCCGT CTCCAACGTCAC

GAM1478 LOC201294 3' CACTGCAACCTCCGCCT 88202 AA  
AGGC GAGGTTGCAGTG  
||| |||||||||  
TCCG CTCCAACGTCAC

C\_  
GAM1478 LOC201294 3' CAGCTCACTGCAACCTCCGCCT 88205 AA  
AGGC GAGGTTGCAGTGAGCTG  
||| |||||||||  
TCCG CTCCAACGTCACCTCGAC

C\_  
GAM1478 LOC201411 3' CAGCTCACTGCAACCTCTGCCT 62953 A  
AGGCA GAGGTTGCAGTGAGCTG  
||||| |||||||||  
TCCGT CTCCAACGTCACCTCGAC

GAM1478 LOC201626 3' CACTGCAACCTCCGCC 88988 AA  
GGC GAGGTTGCAGTG  
||| |||||||||  
CCG CTCCAACGTCAC  
C\_

GAM1478 LOC201627 3' CTGACTGCAACCTCCACCT 89011 CAA G  
AGG GAGGTTGCAGT AG  
||| ||||||||| ||  
TCC CTCCAACGTCA TC  
AC\_ G

GAM1478 LOC201696 3' CAGCTCACTGCAGCCACTGCCT 63130 A A  
AGGCA G GGTTGCAGTGAGCTG  
||||| | |||||||||  
TCCGT C CCGACGTCACCTCGAC  
\_A

GAM1478 LOC201702 5' CAGCTCACTGCAACCTCTGACT 89030 CA  
GG AGAGGTTGCAGTGAGCTG  
|| |||||||||  
TC TCTCCAACGTCACCTCGAC  
AG

GAM1478 LOC202025 3' CACTGCAACCTCCGCCT 90283 AA  
AGGC GAGGTTGCAGTG  
||| |||||||||  
TCCG CTCCAACGTCAC  
C\_

GAM1478 LOC202934 3' CAGCTCACTACAACCTCTGCCT 90406 A C  
AGGCA GAGGTTG AGTGAGCTG  
||||| ||||| |||||||

TCCGT CTCCAAC TCACTCGAC  
 \_ A  
 GAM1478 LOC203297 5' CACTGCAACCTCTGCCT 75348 A  
 AGGCA GAGGTTGCAGTG  
 |||| |||||  
 TCCGT CTCCAACGTCAC  
  
 \_  
 GAM1478 LOC203350 3' CTGACTGCAACCTCCGCCT 90566 AA G  
 AGGC GAGGTTGCAGT AG  
 ||| ||||| ||  
 TCCG CTCCAACGTCA TC  
 C\_ G  
 GAM1478 LOC219690 3' CAGCTATAAGCCTCTTGCCT 93070 GCAGTG  
 AGGCAAGAGGTT AGCTG  
 ||||| ||||  
 TCCGTTCTCCGA TCGAC  
 ATA\_  
 GAM1478 LOC219920 3' CAGCTGAATAAACCTCTTCCT 93304 C GCAGTG  
 AGG AAGAGGTT AGCTG  
 ||| ||||| ||||  
 TCC TTCTCCAA TCGAC  
 \_ ATAAG\_  
 GAM1478 LOC220074 3' CAGCTCACTGCAACCTCCGCCT 59266 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCG CTCCAACGTCACTCGAC  
 C\_  
 GAM1478 LOC220662 3' CACTGCAACCTCCACCT 91165 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC220846 3' CAGCCTTTCCACAACCTCTACC 90812 CA CAGT \_  
 T AGG AGAGGTTG GAG CTG  
 ||| ||||| |||  
 TCC TCTCCAAC TTC GAC  
 A\_ ACCT C  
 GAM1478 LOC221035 3' CACTACAACCTCTGCCT 93161 A C  
 AGGCA GAGGTTG AGTG  
 |||| ||||| ||||  
 TCCGT CTCCAAC TCAC  
 \_ A  
 GAM1478 LOC221174 5' CAGCTCACTGCGACCTCCACCT 93500 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC CTCCAGCGTCACTCGAC  
 AC\_  
 GAM1478 LOC221271 3' CAGCTCACTGCAACCTCTGCCT 91851 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| |||||

TCCGT CTCCAACGTCAC

GAM1478 LOC221296 3' CACTGCAACCTCCACCT 91958 CAA  
AGG GAGGTTGCAGTG  
||| |||||  
TCC CTCCAACGTCAC  
AC\_

GAM1478 LOC221362 5' CAGCCCTCCCAAACCTCTTGCCT 93758 G CAGTGA  
AGGCAAGAG TTG GCTG  
||||| ||| |||  
TCCGTTCTC AAC CGAC  
A CCTCC\_

GAM1478 LOC221663 5' CACTGCAACCTCCACCT 93810 CAA  
AGG GAGGTTGCAGTG  
||| |||||  
TCC CTCCAACGTCAC  
AC\_

GAM1478 LOC221773 3' CAGCTCACTGTGACCTCCGCCT 91039 AA TG  
AGGC GAGGT CAGTGAGCTG  
||| ||| |||||  
TCCG CTCCA GTCACGAC  
C\_ GT

GAM1478 LOC222070 5' CACTGCAACCTCTGCCT 94151 A  
AGGCA GAGGTTGCAGTG  
|||| |||||  
TCCGT CTCCAACGTCAC

GAM1478 LOC253612 5' CACTGCAACCTCCGCCT 96741 AA  
AGGC GAGGTTGCAGTG  
||| |||||  
TCCG CTCCAACGTCAC  
C\_

GAM1478 LOC253664 3' CATTGCAACCTCTGCCT 94808 A  
AGGCA GAGGTTGCAGTG  
|||| |||||  
TCCGT CTCCAACGTTAC

GAM1478 LOC253666 5' CAGCTCACTGCAACCTCCGCCT 95061 AA  
AGGC GAGGTTGCAGTGAGCTG  
||| |||||  
TCCG CTCCAACGTCACGAC  
C\_

GAM1478 LOC253779 3' CACTGCAACCTCCGCCT 97143 AA  
AGGC GAGGTTGCAGTG  
||| |||||  
TCCG CTCCAACGTCAC  
C\_

GAM1478 LOC254268 3' CAGCTCACTGCAACCTTTGTCT 95403 A  
AGGCA GAGGTTGCAGTGAGCTG  
|||| |||||



TCTGT TTCCAACGTCACTCGAC

—  
GAM1478 LOC254655 3' CACTGCAACCTCTGCCT 95469 A  
AGGCA GAGGTTGCAGTG  
||||| |||||||||  
TCCGT CTCCAACGTAC

—  
GAM1478 LOC255177 3' CAGCTCACCGCATCCTCCACCT 96603 CAA T A  
AGG GAGG TGC GTGAGCTG  
||| ||||| ||| |||||||  
TCC CTCC ACG CACTCGAC  
AC\_ T C

GAM1478 LOC255465 3' CAGCTCACTGTATCCTCTGCCT 97283 A T  
AGGCA GAGG TGCAGTGAGCTG  
||||| ||||| |||||||||  
TCCGT CTCC ATGTCACCTCGAC

— T  
GAM1478 LOC255497 3' CACTGCAACCTCCGCCT 97187 AA  
AGGC GAGGTTGCAGTG  
||||| |||||||||  
TCCG CTCCAACGTAC

C\_  
GAM1478 LOC255919 3' CTTTCTGCAACCTCTGCCT 95034 A T  
AGGCA GAGGTTGCAG GAG  
||||| ||||||||| |||  
TCCGT CTCCAACGTC TTC

— T  
GAM1478 LOC256267 3' CAGCTCACTGCAACCTCCGCCT 96799 AA  
AGGC GAGGTTGCAGTGAGCTG  
||||| ||||||||| |||||||  
TCCG CTCCAACGTCACTCGAC

C\_  
GAM1478 LOC256273 5' CAGTGAAACAACCTCCTCCCT 96404 CAA CAGTGA  
AGG GAGGTTG GCTG  
||| ||||||| |||  
TCC CTCCAAC TGAC  
CTC AAAG\_

GAM1478 LOC256306 3' CAGCTCACTGCAACCTCCACCT 96682 CAA  
AGG GAGGTTGCAGTGAGCTG  
||| ||||||||| |||||||  
TCC CTCCAACGTCACTCGAC  
AC\_

GAM1478 LOC257054 5' CAGCTCACTGCAGCCTCGACCT 95656 CAA  
AGG GAGGTTGCAGTGAGCTG  
||| ||||||||| |||||||  
TCC CTCCGACGTCACTCGAC  
AG\_

GAM1478 LOC257334 3' CACTGCAACCTCCGCCT 97275 AA  
AGGC GAGGTTGCAGTG  
||||| |||||||||

TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 LOC51200 3' CACCACAACCTCTGCCT 32990 A CA  
 AGGCA GAGGTTG GTG  
 |||| ||||| ||  
 TCCGT CTCCAAC CAC  
 \_ AC  
 GAM1478 LOC51219 5' CACCGCAACCTCCGCCT 33111 AA A  
 AGGC GAGGTTGC GTG  
 ||| ||||| ||  
 TCCG CTCCAACG CAC  
 C\_ C  
 GAM1478 LOC51696 3' CAGCTCACTGCAACCTCTGCCT 32544 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 |||| |||||||||  
 TCCGT CTCCAACGTCACCTCGAC  
 \_  
 GAM1478 LOC57107 3' CACTGCAACCTCCGCCT 39830 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 LOC81034 3' CAGCTCACTGCAACCTCCACCT 47845 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||||||  
 TCC CTCCAACGTCACCTCGAC  
 AC\_  
 GAM1478 LOC89932 3' CACTGCAACCTCCACCT 60790 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC89932 3' CAGCTCACTGCAACCTCCGTCT 60792 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 |||| |||||||||  
 TCTG CTCCAACGTCACCTCGAC  
 C\_  
 GAM1478 LOC90139 3' CAAGGCAGCCTCCTGCCT 55400 A AG  
 AGGCA GAGGTTGC TG  
 |||| ||||| ||  
 TCCGT CTCCGACG AC  
 C GA  
 GAM1478 LOC90288 3' CACTGCAACCTCCACCT 62084 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC90333 3' CAGCTCACTGCAACCTCCTCCT 62286 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||||||

TCC CTCCAACGTCAC TCGAC  
 TC\_  
 GAM1478 LOC90371 5' CACTGCAACCTCCACCT 62493 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC90408 5' CACTGCAACCTCTACCT 62657 CA  
 AGG AGAGGTTGCAGTG  
 ||| |||||  
 TCC TCTCCAACGTCAC  
 A\_  
 GAM1478 LOC90459 3' CACTGCAACCTCCGCCT 62882 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 LOC90485 3' CACTGCAACCTCCGCCT 63007 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 LOC90591 3' CAGCTCACTGCAAGCTCCACCT 63417 CAA G  
 AGG GAG TTGCAGTGAGCTG  
 ||| ||| |||||  
 TCC CTC AACGTCAC TCGAC  
 AC\_ G  
 GAM1478 LOC91115 3' CACTGCAACCTCCACCT 64925 CAA  
 AGG GAGGTTGCAGTG  
 ||| |||||  
 TCC CTCCAACGTCAC  
 AC\_  
 GAM1478 LOC91115 3' CACTGCAACCTCCGCCT 64926 AA  
 AGGC GAGGTTGCAGTG  
 ||| |||||  
 TCCG CTCCAACGTCAC  
 C\_  
 GAM1478 LOC91115 3' CAGCTCACTGCAACTTCTGCCT 64928 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 ||||| |||||  
 TCCGT CTTCAACGTCAC TCGAC  
 -  
 GAM1478 LOC91291 5' CAGCTCACTGCAACCTCGACCT 65477 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC CTCCAACGTCAC TCGAC  
 AG\_  
 GAM1478 LOC91547 3' CAGCTCACTGCAGCCTC 66400  
 GAGGTTGCAGTGAGCTG  
 |||||

## CTCCGACGTCACTCGAC

GAM1478 LOC91561 5' CAGCTCACTGCAAGCTCCGCCT 66447 AA G  
 AGGC GAG TTGCAGTGAGCTG  
 |||| ||| |||||  
 TCCG CTC AACGTCACTCGAC  
 C\_ G

GAM1478 LOC91813 5' CAGCTCACTGAGCTCTCTGCC 67245 A \_ G  
 GGCA GAG GTT CAGTGAGCTG  
 |||| ||| ||| |||||  
 CCGT CTC CGA GTCACCTCGAC  
 \_ T \_

GAM1478 LOC91893 3' CAGCTCACTATAAGCTCCACCT 67459 CAA G C  
 AGG GAG TTG AGTGAGCTG  
 ||| ||| ||| |||||  
 TCC CTC AAT TCACTCGAC  
 AC\_ G A

GAM1478 LOC92267 3' CAGCTCACTGCAACCTCCACCT 68606 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC CTCCAACGTCACTCGAC  
 AC\_

GAM1478 LOC92303 3' CTCAGTCAACCTCTGCC 68823 A  
 GGCA GAGGTTGCAGTGAG  
 |||| |||||  
 CCGT CTCCAACGTCACTC

GAM1478 LOC92466 3' CAGCTCACTGCAACCTCCGCCT 69424 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 |||| |||||  
 TCCG CTCCAACGTCACTCGAC  
 C\_

GAM1478 LOC92689 3' CACTGCAACCTCCGCCT 70218 AA  
 AGGC GAGGTTGCAGTG  
 |||| |||||  
 TCCG CTCCAACGTAC

GAM1478 LOC92697 5' CACCGCAACCTCCGCCT 70261 AA A  
 AGGC GAGGTTGC GTG  
 |||| ||||| |||  
 TCCG CTCCAACG CAC  
 C\_ C

GAM1478 LOC92697 5' CGCTACAACCTCCACCT 70263 CAA C  
 AGG GAGGTTG AGTG  
 ||| ||||| |||  
 TCC CTCCAAC TCGC  
 AC\_ A

GAM1478 LOC92841 3' GGCTCACCGCAACCTCCTCCT 70716 CAA A  
 AGG GAGGTTGC GTGAGCT  
 ||| ||||| |||||

TCC CTCCAACG CACTCGG  
 TC\_ C  
 GAM1478 LOC93129 3' CAGCTCACTGTAGCCTCGACCT 71462 CAA  
 AGG GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCC CTCCGATGTCACTCGAC  
 AG\_  
 GAM1478 LOC93132 5' CAGCTCACTGCAACCTCCGCCT 71486 AA  
 AGGC GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCG CTCCAACGTCACTCGAC  
 C\_  
 GAM1478 LOC93349 3' CAGCTCACTGCAACCTCTGCCT 56454 A  
 AGGCA GAGGTTGCAGTGAGCTG  
 ||| |||||  
 TCCGT CTCCAACGTCACTCGAC  
 -  
 GAM1478 LOC93408 5' CACTGCAACCTCTGCCT 56474 A  
 AGGCA GAGGTTGCAGTG  
 ||| |||||  
 TCCGT CTCCAACGTCACTCGAC  
 -  
 GAM1479 B3GAT1 3' CCAGCCAAGCTGGTGCTC 53973 CTG  
 GAGCACT AGCTTGGCTGG  
 ||||| |||||  
 CTCGTGG TCGAACCGACC  
 -  
 GAM1479 B3GAT1 3' CCAGCCAAGCTGGTGCTC 37828 CTG  
 GAGCACT AGCTTGGCTGG  
 ||||| |||||  
 CTCGTGG TCGAACCGACC  
 -  
 GAM1479 COL4A2 3' GCCAGCCGTGGCCAGAGGCTCG 8468 A A \_  
 A TCGAGC CTCTG GCT TGGCTGGC  
 ||||| ||||| |||||  
 AGCTCG GAGAC CGG GCCGACCG  
 - - T  
 GAM1479 EVPL 5' CCAGCCAAGCCCAGCCTG 8804 CT A  
 CA CTG GCTTGGCTGG  
 || |||||  
 GT GAC CGAACCGACC  
 CC C  
 GAM1479 OCLN 5' GCCAGGTCCAGAGCGCCGA 10316 A A AG  
 TCG GC CTCTG CTTGGC  
 ||| |||||  
 AGC CG GAGAC GGACCG  
 \_ C CT  
 GAM1479 TBX1 3' CCAGTGCCAAAGCGCCCGG 54671 A A C A TTG  
 TCG GC CT TG GC GCTGG  
 ||| |||||

GGC CG GA AC CG TGACC  
C C A \_ \_  
GAM1479 TRIM14 3' GCCAAGGAAACCCAGAGTGC 28856 AG\_\_\_\_  
GCACTCTG CTTGGC  
||||| |||||  
CGTGAGAC GAACCG  
CCAAAG  
GAM1479 USH3A 3' GCCAGCAGACATCAGAACACAC 53784 AGCAC\_ GCTTG  
CGA TCG TCTGA GCTGGC  
||| ||||| |||||  
AGC AGACT CGACCG  
CACACA ACAGA  
GAM1479 Apg4B 3' GCCCAGCTCAGAGTGCCCG 25285 A T  
CG GCACTCTGAGCT GGC  
|| ||||| |||||  
GC CGTGAGACTCGA CCG  
C C  
GAM1479 APPD 3' CCAGCCAAGCCCTGCCGA 44213 A CTCTGA  
TCG GCA GCTTGGCTGG  
||| ||| |||||  
AGC CGT CGAACCGACC  
\_ CC\_\_\_\_  
GAM1479 ARFGAP1 3' GCCAGCCATGCATGCGCCCGA 36592 A ACTCTGA T  
TCG GC GC TGGCTGGC  
||| || || |||||  
AGC CG CG ACCGACCG  
C CGTA\_\_ T  
GAM1479 dJ383J4.3 3' GCCATTCTCAAAATGCTGA 66944 G CTC CT  
TC AGCA TGAG TGGC  
|| ||| ||| |||  
AG TCGT ACTC ACCG  
\_ AAA TT  
GAM1479 FLJ12387 3' GCCAGTCACCAGAGCGC 43067 A AGCT  
GC CTCTG TGGCTGGC  
|| ||| |||||  
CG GAGAC ACTGACCG  
C C\_\_\_\_  
GAM1479 KIAA1453 3' CCAGCCCAGAGCACTCGG 46972 CA AGCTT  
TCGAG CTCTG GGCTGG  
||||| ||||| |||||  
GGCTC GAGAC CCGACC  
AC \_\_\_\_\_  
GAM1479 KIAA1854 3' CAAGCTCAAAGTGCTC 71738 C  
GAGCACT TGAGCTTG  
||||| |||||  
CTCGTGA ACTCGAAC  
A  
GAM1479 KIAA1948 5' GCCAGCCATGCAAAGAG 82402 GA T  
CTCT GC TGGCTGGC  
||| || |||||

		GAGA CG ACCGACCG		
		AA T		
GAM1479	MGC13114	3' GCCAGCCAACAACAAATGCCTG 50415	A CTC AGC	
	A	TCG GCA TG TTGGCTGGC		
		AGT CGT AC AACCGACCG		
		C AA_ AAC		
GAM1479	MYO3B	3' GCCAAATCAAAGTACTTGA 57307	C C GC	
		TCGAG ACT TGA TTGGC		
		AGTTC TGA ACT AACCG		
		A A A_		
GAM1479	PGLYRPlalpha	3' CCAGCCAAGCTGGCTC 53579	ACTCTG	
		GAGC AGCTTGGCTGG		
		CTCG TCGAACCGACC		
		G_____		
GAM1479	THEA	3' GCCAGGAACCAGAGTGCTT 66285	AG_	
		GAGCACTCTG CTTGGC		
		TTCGTGAGAC GGACCG		
		CAA		
GAM1479	LOC128259	5' CCAACCAGCGGGTGCTC 74726	TGA T C	
		GAGCACTC GCT GG TGG		
		CTCGTGGG CGA CC ACC		
		____ _ A		
GAM1479	LOC144308	3' GCCAGCCAGAGTGC 83047	A T	
		GCACTCTG GCT GGC		
		CGTGAGAC CGA CCG		
		____ _		
GAM1479	LOC148029	3' GCTCGAGCTCAGAAGCCCGA 78620	A AC	_____
		TCG GC TCTGAGCTTG GC		
		AGC CG AGACTCGAGC CG		
		C A_ T		
GAM1479	LOC151568	5' GCCAACCTGCAGAGCACTCG 56695	CA _ C	
		CGAG CTCTG AG TTGGC		
		GCTC GAGAC TC AACCG		
		AC G C		
GAM1479	LOC155036	5' CCAACCAAGCCAGTCAGC 86338	ACT A C	
		GC CTG GCTTGG TGG		
		CG GAC CGAACC ACC		
		ACT C A		
GAM1479	LOC200933	5' CCCATTGCTCAGAGCACTGA 90194	G CA T_ CT	
		TC AG CTCTGAGC TGG GG		

AG TC GAGACTCG ACC CC  
 \_ AC TT \_  
 GAM1479 LOC203601 3' GCCGTGGTCACTCAAAGTGCTT 90645 C CT \_  
 GA TCGAGCACT TGAG TGGCT GGC  
 ||||| ||| ||| |||  
 AGTTCGTGA ACTC ACTGG CCG  
 A \_ TG  
 GAM1480 RELN 3' CTACATCTGATATCAGGA 94304 CA G A  
 TCC ATAT CAGATG AG  
 || ||| ||||| ||  
 AGG TATA GTCTAC TC  
 AC \_ A  
 GAM1480 UBE3A 3' AATGCTTTCCATATTGTGA 4863 C CAGAT  
 TC CAATATG GAAGCATT  
 || ||||| |||||  
 AG GTTATAC TTTCGTAA  
 T C\_\_\_\_  
 GAM1480 UBE3A 3' AATGCTTTCCATATTGTGA 55575 C CAGAT  
 TC CAATATG GAAGCATT  
 || ||||| |||||  
 AG GTTATAC TTTCGTAA  
 T C\_\_\_\_  
 GAM1480 UBE3A 3' AATGCTTTCCATATTGTGA 55585 C CAGAT  
 TC CAATATG GAAGCATT  
 || ||||| |||||  
 AG GTTATAC TTTCGTAA  
 T C\_\_\_\_  
 GAM1480 C20orf50 5' CAATATTTATCACACATATTGG 70073 CA\_ GC  
 CCAATATG GATGAA ATTG  
 ||||| ||||| |||  
 GGTATAC CTATTT TAAC  
 ACA A\_  
 GAM1480 CYB5-M 3' CAATACTTTGATTGCATATT 94563 A C  
 AATATGCAG TGAAG ATTG  
 ||||| ||||| |||  
 TTATACGTT GTTTC TAAC  
 A A  
 GAM1480 CYB5-M 3' CAATACTTTGATTGCATATT 47566 A C  
 AATATGCAG TGAAG ATTG  
 ||||| ||||| |||  
 TTATACGTT GTTTC TAAC  
 A A  
 GAM1480 DKFZp761D221 3' TATCTGCACTTGGA 50164 TA  
 TCCCAA TGCAGATG  
 ||||| |||||  
 AGGGTT ACGTCTAT  
 C\_  
 GAM1480 FLJ10613 3' TGAAGCATCTGCATATTG 38827 AAG  
 CAATATGCAGATG CA  
 ||||| |||



	GTTATACGTCTAC GT	
	GAA	
GAM1480 FLJ12595 3'	TGAAGCATCTGCATATT 46508	AAG
	AATATGCAGATG CA	
	TTATACGTCTAC GT	
	GAA	
GAM1480 KIAA0319 3'	CAATGCTTTTTTAACACATGGG 29031	ATA CA T
A	TCCCA TG GA GAAGCATTG	
	AGGGT AC TT TTTCGTAAC	
	AC_ AA T	
GAM1480 KIAA0563 5'	CAATGCATGACTGCATAT 29182	ATGAA
	ATATGCAG GCATTG	
	TATACGTC CGTAAC	
	AGTA_	
GAM1480 TU12B1-TY 3'	TTTCATCTGCTCATTGG 33412	AT
	CCAAT GCAGATGAAG	
	GGTTA CGTCTACTTT	
	CT	
GAM1480 LOC143310 3'	AATACTTTTCATATTGGGA 76524	CAGAT C
	TCCCAATATG GAAG ATT	
	AGGGTTATAC TTTC TAA	
	_____ A	
GAM1480 LOC147071 5'	CAATGCATGACTGCATAT 72993	ATGAA
	ATATGCAG GCATTG	
	TATACGTC CGTAAC	
	AGTA_	
GAM1480 LOC153441 5'	ATGCCTGCATATCAGGG 80828	A_ ATGAA
	CCC ATATGCAG GCAT	
	GGG TATACGTC CGTA	
	AC _____	
GAM1480 LOC201173 5'	CAATGCATGACTGCATAT 87323	ATGAA
	ATATGCAG GCATTG	
	TATACGTC CGTAAC	
	AGTA_	
GAM1480 LOC201220 5'	CAATGCATGACTGCATAT 87343	ATGAA
	ATATGCAG GCATTG	
	TATACGTC CGTAAC	
	AGTA_	
GAM1480 LOC257068 3'	CATCATACATATTGGGA 95816	CA_
	TCCCAATATG GATG	

		AGGGTTATAC CTAC	
		ATA	
GAM1481 ADH7	5'	GGCACAAGCTGCTGTTATA 5420	CAC ACA
		TATAACAGC CTTG GTC	
		ATATTGTCG GAAC CGG	
		TC_ A__	
GAM1481 BACH2	3'	ACTAGTTTGGTAACTGTTA 41481	CC TT _
		TAACAG ACC GAC AGT	
		ATTGTC TGG TTG TCA	
		AA T_ A	
GAM1481 G6PT1	3'	AAGGTGACTTGTTATA 7596	_C
		TATAACA G CACCTT	
		ATATTGT C GTGGAA	
		T A	
GAM1481 H3F3B	3'	GACTTGTTGGGTAGCTATTA 18021	C C T _
		TAA AGC ACCT GACA GTC	
		ATT TCG TGGG TTGT CAG	
		A A _ T	
GAM1481 MNT	3'	ACTGTATTCTAGTGGCTGTTCA 39701	T CTTG__
		A AACAGCCAC ACAGT	
		A TTGTCGGTG TGTC A	
		C ATCTTA	
GAM1481 PHEMX	3'	GACCATTTCAGGCTGTTG 19120	ACCT CA_
		TAACAGCC TGA GTC	
		GTTGTCGG ACT CAG	
		____ TAC	
GAM1481 PHEMX	3'	GACCATTTCAGGCTGTTG 57360	ACCT CA_
		TAACAGCC TGA GTC	
		GTTGTCGG ACT CAG	
		____ TAC	
GAM1481 PHEMX	3'	GACCATTTCAGGCTGTTG 57365	ACCT CA_
		TAACAGCC TGA GTC	
		GTTGTCGG ACT CAG	
		____ TAC	
GAM1481 PHEMX	3'	GACCATTTCAGGCTGTTG 57369	ACCT CA_
		TAACAGCC TGA GTC	
		GTTGTCGG ACT CAG	
		____ TAC	
GAM1481 RFXAP	3'	GACTTAATCATGGCTGTT 5014	CCT C__
		AACAGCCA TGA AGTC	

TTGTCGGT ACT TCAG  
 \_\_\_\_ AAT  
 GAM1481 SMN1 3' ACTGGTGGACATGGCTGTTCA 43153 T \_\_\_\_ TTGA  
 A AACAGCCA CC CAGT  
 ||||| || |||  
 A TTGTCGGT GG GTCA  
 C ACA TG\_\_  
 GAM1481 SMN1 3' ACTGGTGGACATGGCTGTTCA 4429 T \_\_\_\_ TTGA  
 A AACAGCCA CC CAGT  
 ||||| || |||  
 A TTGTCGGT GG GTCA  
 C ACA TG\_\_  
 GAM1481 SMT3H1 3' GACTGTCACTTGCTGTTA 59959 CACCT  
 TAACAGC TGACAGTC  
 ||||| |||||  
 ATTGTCG ACTGTCAG  
 TTC\_\_  
 GAM1481 SNAI1 3' GACTGTGAGTAATGGCTGT 19969 CC\_ G  
 ACAGCCA TT ACAGTC  
 ||||| || |||||  
 TGTCGGT GA TGTCAG  
 AAT G  
 GAM1481 SS18 3' ACTGTGTTTCAAATGGACTGTT 18881 \_ CC \_\_\_\_  
 A TAACAG CCA TTGA CAGT  
 ||||| || ||| |||  
 ATTGTC GGT AACT GTCA  
 A A\_ TTGT  
 GAM1481 UPK1B 3' CAAGGTGCCTGTTATA 22716 C  
 TATAACAG CACCTTG  
 ||||| |||||  
 ATATTGTC GTGGAAC  
 C  
 GAM1481 DKFZP434A0225 3' ACTGTTGGAATGGCTGTT 93904 CC TG  
 AACAGCCA T ACAGT  
 ||||| | |||||  
 TTGTCGGT G TGTCAG  
 AA GT  
 GAM1481 FLJ10462 3' ACTGTCAAATGTACACCTGTTAT 36138 CC\_ C\_  
 G TATAACAG AC TTGACAGT  
 ||||| || |||||  
 GTATTGTC TG AACTGTCA  
 CAC TA  
 GAM1481 FLJ11175 3' GACCAATGTTATGGCTGTT 37134 CCT \_\_\_\_  
 AACAGCCA TGACA GTC  
 ||||| |||| |||  
 TTGTCGGT ATTGT CAG  
 \_\_\_\_ AAC  
 GAM1481 FLJ13491 5' GACTTCCAGCAGCTGTTA 44885 CAC T C  
 TAACAGC CT GA AGTC  
 ||||| || || |||

ATTGTCG GA CT TCAG  
 AC\_ C \_  
 GAM1481 FLJ20079 3' GTTAAGATGGCTGATATA 34498 A C  
 TATA CAGCCA CTTGAC  
 |||| |||| ||||  
 ATAT GTCGGT GAATTG  
 A A  
 GAM1481 FLJ23518 3' CGACTGTCAAGTGAATGAGCTG 45306 \_ C\_\_\_ III  
 TTG AACAGC CA CTTGACAGTC G  
 ||||| || ||||| ||  
 TTGTCG GT GAACTGTCAG C  
 A AAGT III  
 GAM1481 FLJ32334 3' ACTGCCCTCAGGGTGGCTGTTA 57980 \_\_\_\_  
 TAACAGCCACCTTGA CAGT  
 ||||| ||||  
 ATTGTCGGTGGGACT GTCA  
 CCC  
 GAM1481 KIAA0418 5' GACCACAGTGTGGCTGT 27556 C ACA  
 ACAGCCAC TTG GTC  
 ||||| || ||  
 TGTCCGGTG GAC CAG  
 T AC\_  
 GAM1481 KIAA0438 3' TTAAGATAGCTGTTGTA 29075 CAC  
 TATAACAGC CTTGA  
 ||||| ||||  
 ATGTTGTCG GAATT  
 ATA  
 GAM1481 KIAA0459 3' GACTGTTGTCAGCAGCTGTTA 60996 CACCT\_  
 TAACAGC TGACAGTC  
 ||||| |||||  
 ATTGTCG GTTGTGTCAG  
 ACGACT  
 GAM1481 KIAA1280 5' GACTGTCCGTGGTGGCTGT 69716 TT\_  
 ACAGCCACC GACAGTC  
 ||||| |||||  
 TGTCCGGTGG CTGTCAG  
 TGC  
 GAM1481 KIAA1376 3' GACTGTCAAGATTGT 63622 CCAC  
 ACAG CTTGACAGTC  
 ||| |||||  
 TGTT GAACTGTCAG  
 A\_  
 GAM1481 KIAA1962 3' ACAGTTAAAAGCTGTTATA 81915 CACC A  
 TATAACAGC TTGAC GT  
 ||||| |||| ||  
 ATATTGTCG AATTG CA  
 AA\_ A  
 GAM1481 MGC19606 3' TCAGGATGGGGCTGTCATA 53042 A AC\_  
 TATACAGCC CTTGA  
 ||| |||| ||||

ATA TGTCGG GGACT  
 C GGTA  
 GAM1481 MGC3178 3' ACTGTCAAGAGTCTTGT 47981 CC \_  
 ACAG AC CTTGACAGT  
 |||| || |||||  
 TGTT TG GAACTGTCA  
 C\_ A  
 GAM1481 MPPE1 5' AAGCATGGCTGTTATA 43559 C\_  
 TATAACAGCCA CTT  
 ||||| ||  
 ATATTGTCGGT GAA  
 AC  
 GAM1481 NMP200 3' GACGTGGTGGTGGCTGTT 27174 TTGA \_  
 AACAGCCACC CA GTC  
 ||||| || ||  
 TTGTCGGTGG GT CAG  
 TG\_ G  
 GAM1481 NUDT13 3' ACTGCCAAAATGTGCCTGTTGT 63212 C C\_ A  
 A TATAACAG CAC TTG CAGT  
 ||||| || || ||  
 ATGTTGTC GTG AAC GTCA  
 C TAA C  
 GAM1481 NYD-SP25 5' ACTGTCAAGGTGTCCATTGTA 53183 CAGC  
 TATAA CACCTTGACAGT  
 |||| |||||  
 ATGTT GTGGAAGTGTCA  
 ACCT  
 GAM1481 PC4 3' ACTGTCAAAATGTTAT 22011 GCCACC  
 ATAACA TTGACAGT  
 |||| |||||  
 TATTGT AACTGTCA  
 AA\_\_\_\_  
 GAM1481 PDE1C 3' GACTGTCAATGCCGTTA 17220 A CACC  
 TAAC GC TTGACAGTC  
 |||| || |||||  
 ATTG CG AACTGTCAG  
 C T\_\_\_\_  
 GAM1481 PEPP3 3' GACTGCCTGGGAGATGGCTGTT 30040 \_\_\_\_ TGA  
 A TAACAGCCA CCT CAGTC  
 ||||| || ||||  
 ATTGTCGGT GGG GTCAG  
 AGA TCC  
 GAM1481 PRO1992 5' TAAGGTGGCTAGTATA 26060 AC  
 TATA AGCCACCTTG  
 |||| |||||  
 ATAT TCGGTGGAAT  
 GA  
 GAM1481 PTGES2 3' GACCCTCAGTGGCTGT 46881 CT CA  
 ACAGCCAC TGA GTC  
 ||||| || ||

			TGTCGGTG ACT CAG		
			__ CC		
GAM1481	SRP9	3'	GACTGTCACAACTGTTATG 79192		CCACCT
			TATAACAG TGACAGTC		
			GTATTGTC ACTGTCAG		
			AAC__		
GAM1481	SYNE-1	5'	GACCATCAAGGTGCTG 30968	C	CA
			CAGC ACCTTGA GTC		
			GTCG TGGA ACT CAG		
			_ AC		
GAM1481	ZNF185	3'	ACTCAGAGAGGTGGCTATTG 23105	C	GAC_
			TAA AGCCACCTT AGT		
			GTT TCGGTGGAG TCA		
			A AGAC		
GAM1481	LOC130507	3'	GACTTCCATGGCTTGTATA 74951	_	CCT AC
			TATAACA GCCA TG AGTC		
			ATATTGT CGGT AC TCAG		
			T __ CT		
GAM1481	LOC134359	5'	ACTGTCAGGTTGCCGT 75182	A C	T
			AC GC ACCT GACAGT		
			TG CG TGGA CTGTCA		
			C T _		
GAM1481	LOC143914	5'	GACTGTCAAAGTG GTTGT 76612		C
			ACAGCCAC TTGACAGTC		
			TGTTGGTG AACTGTCAG		
			A		
GAM1481	LOC144465	5'	ACTATCAAGTGAACCACTGTTA 76851	C__	C C
			TG TATAACAG CAC TTGA AGT		
			GTATTGTC GTG AACT TCA		
			ACCAA _ A		
GAM1481	LOC148078	3'	GACCCGTAAGTGGCTGT 84112	C	ACA
			ACAGCCAC TTG GTC		
			TGTCGGTG AAT CAG		
			_ GCC		
GAM1481	LOC150378	5'	GACTGATGTGAGGTGGCT 79745		A__
			AGCCACCTTG CAGTC		
			TCGGTGGAGT GTCAG		
			GTA		
GAM1481	LOC153727	5'	GACTGTCAAACTTGTT 86152		CCACC
			AACAG TTGACAGTC		

TTGTT AACTGTCAG  
 CAA\_\_  
 GAM1481 LOC163231 5' TCAGCAGGTGGCTGTTA 82443 \_\_  
 TAACAGCCACCT TGA  
 ||||| |||  
 ATTGTCGGTGGA ACT  
 CG  
 GAM1481 LOC201931 3' ACTTCTGTGGCTGTTTA 89108 T CTT C  
 A AACAGCCAC GA AGT  
 | ||||| || |||  
 A TTGTCGGTG CT TCA  
 T T\_\_ \_  
 GAM1481 LOC253698 3' ACTGTCAAGAGCCGTGTTA 94887 \_\_ CAC  
 TAACA GC CTTGACAGT  
 |||| || |||||  
 ATTGT CG GAACTGTCA  
 GC A\_\_  
 GAM1481 LOC256158 5' GACAGGCGAGGTGGCCGTCATG 97665 A A ACA  
 TAT AC GCCACCTTG GTC  
 ||| || ||||| |||  
 GTA TG CGGTGGAGC CAG  
 C C GGA  
 GAM1481 LOC90906 3' CAAGGTGGCTGTTATA 64293  
 TATAACAGCCACCTTG  
 |||||  
 ATATTGTCGGTGGAAC  
  
 GAM1481 LOC91012 3' TAAGGTGGTTGCTATA 64643 A  
 TATA CAGCCACCTTG  
 |||| |||||  
 ATAT GTTGGTGGAAT  
 C  
 GAM1482 AARS 3' TTGCTGCAGAGAATAAAAG 7833 CAG TATT  
 CTTT TCTT TGCAGCAA  
 |||| ||| |||||  
 GAAA AGAG ACGTCGTT  
 ATA \_\_\_\_  
 GAM1482 ADRA2B 3' TTGCTGCAGGGAGATGAAAG 5466 G AT  
 CTTTCA TCTTT TTGCAGCAA  
 |||| |||| |||||  
 GAAAGT AGAGG GACGTCGTT  
  
 GAM1482 AGRN 3' CTGTGAAATAAAGTCTGAAA 78836 T \_  
 TTTCAG CTTTATTT GCAG  
 |||| ||||| |||  
 AAAGTC GAAATAAA TGTC  
 T G  
 GAM1482 BECN1 3' TTTGCTGCAGTCTGAAAAGTGA 13650 C T\_  
 AA  
 TTTCAGT TTTA TTGCAGCAAA  
 ||||| ||| |||||

AAAGTCA AAGT GACGTCGTTT  
 A CT  
 GAM1482 CLASP1 3' CTGCAACTGCTAGGACTGAAAG 65302 TAT\_\_  
 CTTTCAGTCTT TTGCAG  
 ||||| ||||  
 GAAAGTCAGGA AACGTC  
 TCGTC  
 GAM1482 DNMT3L 5' CTGCAAACCGGCACTGAAGG 25358 \_ TTA  
 CTTTCAGT CT TTTGCAG  
 ||||| || |||||  
 GGAAGTCA GG AAACGTC  
 C CC\_  
 GAM1482 ENC1 3' TTTGCTGCACAAACATGAAA 13287 GTCTTTATT  
 TTTCA TGCAGCAAA  
 |||| |||||  
 AAAGT ACGTCGTTT  
 ACAAAC\_\_  
 GAM1482 FLRT3 3' CTGCAAAACACTGGAA 25216 CTTTA  
 TTTTCAGT TTTGCAG  
 ||||| |||||  
 AAGGTCA AAACGTC  
 CA\_\_  
 GAM1482 FSTL3 3' AAATAAAGACTCAAAG 19605 C  
 CTTT AGTCTTTATTT  
 ||| |||||  
 GAAA TCAGAAATAAA  
 C  
 GAM1482 KCNK10 3' CTGTGCCATAAACAACACTGAAAG 40969 C\_ TT\_  
 CTTTCAGT TTTAT GCAG  
 ||||| |||| |||  
 GAAAGTCA AAATA TGTC  
 AC CCG  
 GAM1482 KCNK10 3' CTGTGCCATAAACAACACTGAAAG 56338 C\_ TT\_  
 CTTTCAGT TTTAT GCAG  
 ||||| |||| |||  
 GAAAGTCA AAATA TGTC  
 AC CCG  
 GAM1482 KCNK10 3' CTGTGCCATAAACAACACTGAAAG 56343 C\_ TT\_  
 CTTTCAGT TTTAT GCAG  
 ||||| |||| |||  
 GAAAGTCA AAATA TGTC  
 AC CCG  
 GAM1482 RP2 3' TTTGATAAAACTAAGACTGAAA 22622 TA GCAG  
 TTTTCAGTCTT TTT CAAA  
 ||||| || |||  
 AAAGTCAGAA AAA GTTT  
 TC ATA\_  
 GAM1482 SCA1 5' TGCTGCAAGGAACACTGATAG 4401 T CTTTA  
 CT TCAGT TTTGCAGCA  
 || |||| |||||



			GA AGTCA	GAACGTCGT		
			T	AG__		
GAM1482	VSX1	3'	CTGTCAAAGGCTGAAA	27466	ATTT	
			TTTCAGTCTTT	GCAG		
			AAAGTCGGA	TGTC		
			C__			
GAM1482	DKFZP586C1324	3'	CTGCATTGGGTGAAGACTAAAA	69797	C	__
			TTT AGTCTTTATT	TGCAG		
			AAA TCAGAAAGTGG	ACGTC		
			A	GTT		
GAM1482	DNAH7	3'	TGAAATAAATAAAGACTAAAG	38159	C	CAG
			CTTT AGTCTTTATTTG	CA		
			GAAA TCAGAAATAAAT	GT		
			-	AAA		
GAM1482	EDR1	3'	TGCTGCAGGGACTAAAAG	15385	C	TTAT
			CTTT AGTCT	TTGCAGCA		
			GAAA TCAGG	GACGTCGT		
			A	__		
GAM1482	FLJ10305	5'	CTGCAGCCAGCACTGAAAG	68359	_	TTAT
			CTTTCAGT CT	TTGCAG		
			GAAAGTCA GA	GACGTC		
			C	CC__		
GAM1482	FLJ10460	3'	TTTGCTGCTGGTAATACTGAAA	36135	CT	TT
	G		CTTTCAGT	TTAT GCAGCAAA		
			GAAAGTCA AATG	CGTCGTTT		
			T_	GT		
GAM1482	FLJ20340	3'	TTTGCTACAAAGGGGCTGCAAA	34981	_	TA C
	G		CTTT CAGTCTT	TTTG AGCAAA		
			GAAA GTCGGGG	AAAC TCGTTT		
			C	_ A		
GAM1482	FLJ22557	3'	TGTTGAAAAGACTGAAAG	45256	ATTG	
			CTTTCAGTCTTT	CAGCA		
			GAAAGTCAGAAA	GTTGT		
			A__			
GAM1482	FLJ22940	5'	TGCTGCAGACCAGAAAG	44698	A_	TTATTT
			CTTTC GTCT	GCAGCA		
			GAAAG CAGA	CGTCGT		
			AC	_____		
GAM1482	GBTS1	3'	TTGCTGTTGCAAGACTGAAGG	59066	TATTT	
			CTTTCAGTCTT	GCAGCAA		

GGAAGTCAGAA TGTCGTT  
 CGT\_\_  
 GAM1482 GT650 3' CTGCTATTCAAAAAGTCTGAGAG 53455 C ATTT\_  
 CTTTCAGT TTT GCAG  
 ||||| || |||  
 GAGAGTCA AAA CGTC  
 A CTTAT  
 GAM1482 KIAA0537 3' GCTGTGACAACAGACTGAAA 29250 TTAT TG  
 TTTTCAGTCT T CAGC  
 ||||| | |||  
 AAAGTCAGA A GTCG  
 CAAC GT  
 GAM1482 KIAA1165 3' CTGCCTTAAAGATTGAAA 67406 TTT  
 TTTTCAGTCTTTA GCAG  
 ||||| |||  
 AAAGTTAGAAAT CGTC  
 TC\_  
 GAM1482 KIAA1464 3' TTGCTACAAATAAGGA 68278 C  
 TCTTTATTTG AGCAA  
 ||||| |||  
 AGGAATAAAC TCGTT  
 A  
 GAM1482 MAP2K4 3' TGCCACAAACCACCAGGACTGA 11553 TA\_\_ CA  
 AAG CTTTCAGTCTT TTTG GCA  
 ||||| ||| |||  
 GAAAGTCAGGA AAAC CGT  
 CCACC AC  
 GAM1482 NYD-SP15 3' GAATAAATACTGAAAG 48110 C  
 CTTTCAGT TTTATTT  
 ||||| |||||  
 GAAAGTCA AAATAAG  
 T  
 GAM1482 PEX11A 3' TTTGCTGAATGAATAAAAATTG 13890 C G\_  
 AAAG CTTTCAGT TTTATTT CAGCAAA  
 ||||| ||||| |||||  
 GAAAGTTA AAATAAG GTCGTTT  
 A TAA  
 GAM1482 PIGM 5' TGCTGCAAAGAACCGAAGG 59047 A CTTTA  
 CTTTC GT TTTGCAGCA  
 |||| || |||||  
 GGAAG CA AAACGTCGT  
 C AG\_\_  
 GAM1482 PPIL3 5' GCTGTAAGACTGAGA 50645 TTATT  
 TTTTCAGTCT TGCAGC  
 ||||| |||||  
 AGAGTCAGA ATGTCG  
 \_\_\_\_\_  
 GAM1482 PPIL3 5' GCTGTAAGACTGAGA 55656 TTATT  
 TTTTCAGTCT TGCAGC  
 ||||| |||||

AGAGTCAGA ATGTCG

GAM1482 PPIL3 5' GCTGTAAGACTGAGA 55658 TTATT  
TTTCAGTCT TGCAGC  
||||||| |||||  
AGAGTCAGA ATGTCG

GAM1482 SLC17A6 3' TTGCTGTAAAAATGAAA 39749 GTCTTTA  
TTTCA TTTGCAGCAA  
||||| |||||  
AAAGT AAATGTCGTT  
AA\_\_\_\_\_

GAM1482 TBLR1 3' CTGCCAATTAAAGACTAGAAG 45101 TC T \_  
CTT AGTCTTTA TTG CAG  
||| ||||| ||| |||  
GAA TCAGAAAT AAC GTC  
GA T C

GAM1482 ZNF304 3' TTGCTAGGAAAGACTGAAA 40319 ATTT  
TTTCAGTCTTT GCAG  
||||||| |||  
AAAGTCAGAAA CGTT  
GGAT

GAM1482 LOC113115 5' TGCTGTAAGACAGAAAG 56547 A TTATT  
CTTTC GTCT TGCAGCA  
||||| ||| |||||  
GAAAG CAGA ATGTCGT  
A \_\_\_\_\_

GAM1482 LOC115004 3' TGCTGCTCAGACTGAA 73176 TTATTT  
TTCAGTCT GCAGCA  
||||||| |||||  
AAGTCAGA CGTCGT  
CT\_\_\_\_\_

GAM1482 LOC145845 3' CAGATAAAGACTAAAA 83552 C  
TTT AGTCTTTATTTG  
||| |||||  
AAA TCAGAAATAGAC  
A

GAM1482 LOC160897 3' GCAGTACCAAGACTGAAA 82246 TAT\_  
TTTCAGTCTT TTGC  
||||||| |||  
AAAGTCAGAA GACG  
CCAT

GAM1482 LOC162333 5' CTCAGATAAAGACTGAA 87129 C  
TTCAGTCTTTATTTG AG  
||||||| |||  
AAGTCAGAAATAGAC TC

GAM1482 LOC223073 5' TTGCCTGAAGACTGAAA 94381 TTT  
TTTCAGTCTTTA GCAG  
||||||| |||

		AAAGTCAGAAAGT CGTT	
		C__	
GAM1482	LOC255177 3'	CTGGGATTACAGAGACTGAAA 96604	AT__ G
		TTTCAGTCTTT TT CAG	
		AAAGTCAGAGA AG GTC	
		CATT G	
GAM1482	LOC256730 3'	TTGCAGCAAGACTGAAA 95236	TTATT A
		TTTCAGTCT TGC GCAA	
		AAAGTCAGA ACG CGTT	
		_____ A	
GAM1482	LOC257469 3'	CTGCTGGTGAAGACTG 95714	TT
		CAGTCTTTAT GCAG	
		GTCAGAAGTG CGTC	
		GT	
GAM1482	LOC90529 3'	TGCCGCAGACTGAAGG 63165	TTATTT A
		CTTTCAGTCT GC GCA	
		GGAAGTCAGA CG CGT	
		_____ C	
GAM1483	DLG5 5'	CAACAAGGACAAGAAGCAGG 82911	G C A_
		CC TGTT CT TCCTTGTTG	
		GG ACGA GA AGGAACAAC	
		_ A AC	
GAM1483	FLNB 3'	CAACAAGGACGGCACGG 62174	CCTA
		CCGTGTT TCCTTGTTG	
		GGCACGG AGGAACAAC	
		C__	
GAM1483	MBP 3'	CAAGGCACAGAGACACGGG 89780	TC AT_
		CCCGTGT CT CCTTG	
		GGGCACA GA GGAAC	
		GA CAC	
GAM1483	PSCD4 5'	CAAGCGACAGGAGCACGGGT 25401	A _
		ACCCGTGTTCT TC CTTG	
		TGGGCACGAGGA AG GAAC	
		C C	
GAM1483	SH3BP2 3'	CAAGGACAGGAACACTGGT 11592	C A
		ACC GTGTTCT TCCTTG	
		TGG CACAAGGA AGGAAC	
		T C	
GAM1483	SORCS1 3'	CAACAGGGTATAACACAGG 53582	C CCTAT
		CC GTGTT CCTTGTTG	

GG CACAA GGGACAAC  
A TAT\_\_  
GAM1483 ANAPC11 3' CAACAAGGTGGAACAAGGG 33210 G C T  
CCC TGTT CTA CCTTGTTG  
||| ||| ||| |||||  
GGG ACAA GGT GGAACAAC  
A A \_  
GAM1483 C20orf142 3' AAGGAGCAGAAACACAGGT 74763 C C A\_  
ACC GTGTT CT TCCTT  
||| ||||| || |||||  
TGG CACAA GA AGGAA  
A A CG  
GAM1483 CFLAR 5' AACAAAGGACCACGGG 13926 TTCCTA  
CCCGTG TCCTTGTT  
||||| |||||  
GGGCAC AGGAACAA  
C\_\_\_\_\_  
GAM1483 CLSTN2 3' CAACAAGGACAACAAGG 42121 G CCTA  
CC TGTT TCCTTGTTG  
|| ||| |||||  
GG ACAA AGGAACAAC  
A C\_\_\_\_  
GAM1483 CLSTN2 3' CAACAAGGACACAACAC 42122 CCTA  
GTGTT TCCTTGTTG  
||||| |||||  
CACAA AGGAACAAC  
CAC\_  
GAM1483 CLSTN2 3' CAACAAGGACAGTCACAAC 42123 \_ TC A  
GT GT CT TCCTTGTTG  
|| || || |||||  
CA CA GA AGGAACAAC  
A CT C  
GAM1483 CLSTN2 3' CAACAAGGACAGTCACAACAAG 42124 CG\_\_ TC A  
G CC TGT CT TCCTTGTTG  
|| ||| || |||||  
GG ACA GA AGGAACAAC  
AACA CT C  
GAM1483 ERp44 3' CAACAAGGTAGCACACAGG 81691 C TC T  
CC GTGT CTA CCTTGTTG  
|| ||| ||| |||||  
GG CACA GAT GGAACAAC  
A C\_ \_  
GAM1483 FLJ10101 5' CGGGGAGACAGGAACACGGG 45264 A\_\_  
CCCGTGTTTCCT TCCTTG  
||||||| |||||  
GGGCACAAGGA AGGGGC  
CAG  
GAM1483 FLJ23306 5' AACAAAGCCACACGGGT 44555 TC ATCC  
ACCCGTGT CT TTGTT  
||||||| || |||||

			TGGGCACA GA AACAA		
			CC ____		
GAM1483	KIAA0391	3'	CAAGAGACAGGAACAC	27906	A _
			GTGTTTCCT TC CTTG		
			CACAAGGA AG GAAC		
			C A		
GAM1483	MGC13251	3'	GATGGAGACAGGGACACGGG	51148	A C TG
			CCCGTGTTTCCT TC T TT		
			GGGCACAGGGA AG G AG		
			C A GT		
GAM1483	SEMA3E	3'	CAACTTGGAGAAACAGGG	24879	G CCTA TT
			CCC TGTT TCC GTTG		
			GGG ACAA AGG CAAC		
			_ AG_ TT		
GAM1483	SLC26A9	3'	CAACACAGGGAAAAACGG	53617	G ATCCT
			CCGT TTCCT TGTTG		
			GGCA AAGGG ACAAC		
			A AC_		
GAM1483	SLC26A9	3'	CAACACAGGGAAAAACGG	56178	G ATCCT
			CCGT TTCCT TGTTG		
			GGCA AAGGG ACAAC		
			A AC_		
GAM1483	LOC147639	3'	CAATAACAGGGACAC	78377	ATCC
			GTGTTTCCT TTGTTG		
			CACAGGGA AATAAC		
			C_		
GAM1483	LOC148809	3'	CAAGGGTAAGAGCACGGG	79001	C
			CCCGTGTTT TATCCTTG		
			GGGCACGAG ATGGGAAC		
			A		
GAM1483	LOC150287	3'	CAACCTCTCAGGAACAGGG	79781	G ATCCTT
			CCC TGTTTCCT GTTG		
			GGG ACAAGGA CAAC		
			_ CTCTC_		
GAM1483	LOC157869	5'	CAACAAGGAGAGAACACG	81625	CTA
			CGTGTTT TCCTTGTTG		
			GCACAAG AGGAACAAC		
			AG_		
GAM1483	LOC219743	3'	AGGGACAGAAACAGGAGT	93125	_ G C A
			AC CC TGTT CT TCCTT		

TG GG ACAA GA AGGGA  
 A \_ A C  
 GAM1483 LOC221495 3' CAACAAGGCCAGGAAAC 93855 G AT\_  
 GT TTCCT CCTTGTTG  
 || |||| |||||  
 CA AAGGA GGAACAAC  
 \_ CCC  
 GAM1483 LOC221760 3' CAACAAGGATACCAC 93782 TTCC  
 GTG TATCCTTGTTG  
 ||| |||||  
 CAC ATAGGAACAAC  
 C\_\_  
 GAM1483 LOC253289 5' CAAGCAGGAACAGGGGT 96049 G ATC  
 ACCC TGTTCT CTTG  
 ||| ||||| |||  
 TGGG ACAAGGA GAAC  
 G C\_\_  
 GAM1483 LOC255652 3' GGGATGGAACACAGG 96721 C T  
 CC GTGTTCC ATCCT  
 || ||||| ||||  
 GG CACAAGG TAGGG  
 A \_  
 GAM1483 LOC257206 5' CAACGGCAGAAGCACGGG 97095 C AT C  
 CCGTGTT CT C TTG  
 ||||| || |||  
 GGGCACGA GA G AAC  
 A CG C  
 GAM1483 LOC90342 5' CAACAAGGACAAGGGCATCGCG 62353 T\_\_ A\_  
 CGTG TCCT TCCTTGTTG  
 ||| ||| |||||  
 GCGC GGGA AGGAACAAC  
 TAC AC  
 GAM1484 DACH 3' TGAGAATGTTTGTAATGTACA 54974 CATCC CT  
 TGTACA ACA CATTCTCA  
 |||| || |||||  
 ACATGT TGT GTAAGAGT  
 AAA\_\_ TT  
 GAM1484 IL11RA 3' GGAACGTGTGTAATGTGTACA 15712 C\_ TCA  
 TGTACACAT CACAC TTCT  
 ||||| |||| |||  
 ACATGTGTA GTGTG AAGG  
 AT C\_\_  
 GAM1484 LYPLA1 3' AGAATGAGGTGGTATTACA 20922 CACAT A  
 TGTA CCAC CTCATTCT  
 ||| ||| |||||  
 ACAT GGTG GAGTAAGA  
 TAT\_\_ \_  
 GAM1484 NAPB 3' GAGAATGAATGTATGT 70183 CC C  
 ACAT ACA TCATTCTC  
 ||| || |||||

			TGTA TGT AGTAAGAG		
			— A		
GAM1484	NRF1	3'	GAATATATGTATATGTGTACA 60120	CC	CTC
			TGTACACAT ACA ATTC		
			ACATGTGTA TGT TAAG		
			TA ATA		
GAM1484	PRKAB1	3'	AGAGGGAATGGACTGTACA 20734	CA	CA AT
			TGTACA TCCA CTC TCT		
			ACATGT AGGT GGG AGA		
			C_ AA _		
GAM1484	PTGFR	3'	TGAGAGAGATGTGTACA 6319	CACA	
			TGTACACATC CTCA		
			ACATGTGTAG GAGT		
			AGA_		
GAM1484	RBBP5	3'	AGATTGGATAGATGTGTACA 17327	CACAC	T
			TGTACACATC TCA TCT		
			ACATGTGTAG GGT AGA		
			ATA__ T		
GAM1484	SAT	3'	TGAGTCATTTAAATGTGTACA 11436	CCAC__	
			TGTACACAT ACTCA		
			ACATGTGTA TGAGT		
			AATTTAC		
GAM1484	TMP21	3'	AATGGTGTATGGATGTGACA 22399	A	_ T
			TGT CACATCCA CAC CATT		
			ACA GTGTAGGT GTG GTAA		
			_ A _		
GAM1484	UBE2V1	3'	TGAAATGTGGATGCATAC 41797	CA	C_
			GTA CATCCACA TCA		
			CAT GTAGGTGT AGT		
			AC AA		
GAM1484	UBE2V1	3'	TGAAATGTGGATGCATAC 42374	CA	C_
			GTA CATCCACA TCA		
			CAT GTAGGTGT AGT		
			AC AA		
GAM1484	UBE2V1	3'	TGAAATGTGGATGCATAC 12522	CA	C_
			GTA CATCCACA TCA		
			CAT GTAGGTGT AGT		
			AC AA		
GAM1484	ZIC1	3'	AGAATGTTCTAGTAAATGTGTA 12720	CC	ACT__
	C		GTACACAT AC CATTCT		



			CATGTGTA TG	GTAAGA		
			AA ATCTT			
GAM1484	AF038169	5'	TGAAAATGAGTGCTGTAGATG	25255	__ _	C
			CATC CA CACTCATT TCA			
			GTAG GT GTGAGTAA AGT			
			AT C A			
GAM1484	CDC14A	3'	AGAAGTGGATGTATATA	13391	C	ACTCA
			TGTA ACATCCAC TTCT			
			ATAT TGTAGGTG AAGA			
			A			
GAM1484	DKFZP564I052	3'	GATGATCATGTGATGTGTACA	66710	C C__	
			TGTACACATC ACA TCATT			
			ACATGTGTAG TGT AGTAG			
			_ ACT			
GAM1484	DKFZP761F241	3'	TGAGAATGAGTGAGGTTTCGTA	48800	ACAT A	
			CA TGTAC CC CACTCATTCTCA			
			ACATG GG GTGAGTAAGAGT			
			CTTT A			
GAM1484	FLJ11101	3'	AGAAGTGTGAGTGTGTACA	37049	TC _	CAT
			TGTACACA CA CACT TCT			
			ACATGTGT GT GTGA AGA			
			GA T			
GAM1484	FLJ14642	3'	AGTATGGGTGTGTACA	51492	C	
			TGTACACATCCA ACT			
			ACATGTGTGGGT TGA			
			A			
GAM1484	FLJ20399	3'	GGTGGCTGTGGATGCCACA	35125	ACA	CT
			TGT CATCCACA CATT			
			ACA GTAGGTGT GTGG			
			CC_ CG			
GAM1484	GFPT1	3'	GAAGATGGGATGTGTACA	9022	A C A	
			TGTACACATCC CA TC TTC			
			ACATGTGTAGG GT AG AAG			
			- - -			
GAM1484	KIAA0450	3'	GAGGGCAGTGTGGATG	27640	CA	
			CATCCACACT TTCTC			
			GTAGGTGTGA GGGAG			
			C_			
GAM1484	KIAA0530	3'	GATGGTATGAAAATGTGTACA	70867	C__ C T	
			TGTACACAT CA AC CATT			

		ACATGTGTA GT TG GTAG		
		AAA A _		
GAM1484	KIAA0753	3' GGGGAGTTAAATGTGTACA 28999	CCAC	ATT
		TGTACACAT ACTC CTC		
		ACATGTGTA TGAG GGG		
		AAT_ _		
GAM1484	KIAA0788	3' TGAATTAGGAATGTGTACA 71339	_ ACAC	
		TGTACACAT CC TCA		
		ACATGTGTA GG AGT		
		A ATTA		
GAM1484	KIAA0855	3' AGAATGAGCAGTGTAC 30400	ATCCACA	
		GTACAC CTCATTCT		
		CATGTG GAGTAAGA		
		AC_		
GAM1484	KIAA0865	5' GAGCAAGTGGAATGTGTACA 61250	_ A_	
		TGTACACAT CCAC CTC		
		ACATGTGTA GGTG GAG		
		A AAC		
GAM1484	KIAA0992	3' GGAAGTGTGGAGCACACA 32207	ACACA	CAT
		TGT TCCACACT TCT		
		ACA AGGTGTGA AGG		
		CACG_ _		
GAM1484	MGC16037	5' TGAGGTGTAGATATGTATA 51822	C C _	
		TGTACA ATC ACAC TCA		
		ATATGT TAG TGTG AGT		
		A A G		
GAM1484	OSRF	3' TGAAAATGCACACAAATGTGTA 59525	CCACACT	C
	CA	TGTACACAT CATT TCA		
		ACATGTGTA GTAA AGT		
		AACACAC A		
GAM1484	RAB3-GAP150	3' TGAGAATCAGAGATGTGTA 24839	CACA	C
		TACACATC CT ATTCTCA		
		ATGTGTAG GA TAAGAGT		
		A_ C		
GAM1484	RAP140	3' GATGGGTAAATGTGTACA 30844	CCAC	
		TGTACACAT ACTCATT		
		ACATGTGTA TGGGTAG		
		AA_		
GAM1484	TACTILE	5' GAGTGCATGTGTACA 19471	CCA	
		TGTACACAT CACTC		

ACATGTGTA GTGAG  
 C\_\_  
 GAM1484 LOC131873 3' GATGTATGCATATGTGTACA 75880 CCA CT  
 TGTACACAT CA CATT  
 ||||| || |||  
 ACATGTGTA GT GTAG  
 TAC AT  
 GAM1484 LOC134145 3' AGCTGTATATGTGTACA 75144 CC \_  
 TGTACACAT ACA CT  
 ||||| ||| ||  
 ACATGTGTA TGT GA  
 TA C  
 GAM1484 LOC145482 3' AATGGTATGATGTGTACA 77226 CAC T  
 TGTACACATC AC CATT  
 ||||| || |||  
 ACATGTGTAG TG GTAA  
 TA\_ \_  
 GAM1484 LOC148195 3' GAAAAGGTGGATGTGTCA 84129 T A CA  
 TG ACACATCCAC CT TTC  
 || ||||| || |||  
 AC TGTGTAGGTG GA AAG  
 \_ \_ A\_  
 GAM1484 LOC152633 5' TGAGCTGTACATGTAGAGTGTA 85826 A C CT\_\_ TT  
 CA TGTACAC TC ACA CA CTCA  
 ||||| || ||| || |||  
 ACATGTG AG TGT GT GAGT  
 \_ A ACAT C\_  
 GAM1484 LOC153630 5' AATGAGTGTGCGTAC 86079 ACATC  
 GTAC CACACTCATT  
 ||| |||||  
 CATG GTGTGAGTAA  
 C\_\_  
 GAM1484 LOC221662 3' AGAATGAGGGGAATGGGCA 92399 TA CA ACA  
 TG CA TCC CTCATTCT  
 || || ||| |||||  
 AC GT AGG GAGTAAGA  
 GG A\_ G\_  
 GAM1484 LOC254659 5' GAGAATGGAGATGCTACA 95113 CA CACAC  
 TGTA CATC TCATTCTC  
 ||| ||| |||||  
 ACAT GTAG GGTAAGAG  
 C\_ A\_\_  
 GAM1484 LOC83693 3' AGGGTGTGTGGATGGCACA 48830 ACA TC  
 TGT CATCCACAC ATTCT  
 || ||||| |||||  
 ACA GTAGGTGTG TGGGA  
 CG\_ \_  
 GAM1484 LOC90981 3' AATGGTGTGATGGATGTGACA 64532 A \_ T  
 TGT CACATCCA CAC CATT  
 || ||||| || |||

			ACA GTGTAGGT GTG GTAA	
			— A —	
GAM1485	FZD1	5'	GCCACCCGGGTTCTCC 13035	CA
			GGAGAACCCGGG GT	
			CCTCTTGGGCCC CG	
			AC	
GAM1485	GA	5'	GCCACCCGGGTTCTCC 25176	CA
			GGAGAACCCGGG GT	
			CCTCTTGGGCCC CG	
			AC	
GAM1485	OTOF	3'	CTCCCCAGGTTTTCCA 16642	C C
			TGGAGAACC GGG AG	
			ACCTTTTGG CCC TC	
			A C	
GAM1485	PCDHGA1	3'	ACTGCCCAGGTCCCCA 38280	A A C
			TGG GA CC GGGCAGT	
			ACC CT GG CCCGTCA	
			C _ A	
GAM1485	PCDHGA10	3'	ACTGCCCAGGTCCCCA 38287	A A C
			TGG GA CC GGGCAGT	
			ACC CT GG CCCGTCA	
			C _ A	
GAM1485	PCDHGA11	3'	ACTGCCCAGGTCCCCA 38294	A A C
			TGG GA CC GGGCAGT	
			ACC CT GG CCCGTCA	
			C _ A	
GAM1485	PCDHGA11	3'	ACTGCCCAGGTCCCCA 49458	A A C
			TGG GA CC GGGCAGT	
			ACC CT GG CCCGTCA	
			C _ A	
GAM1485	PCDHGA12	3'	ACTGCCCAGGTCCCCA 13590	A A C
			TGG GA CC GGGCAGT	
			ACC CT GG CCCGTCA	
			C _ A	
GAM1485	PCDHGA2	3'	ACTGCCCAGGTCCCCA 38301	A A C
			TGG GA CC GGGCAGT	
			ACC CT GG CCCGTCA	
			C _ A	
GAM1485	PCDHGA3	3'	ACTGCCCAGGTCCCCA 38311	A A C
			TGG GA CC GGGCAGT	

			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGA4	3'	ACTGCCCAGGTCCCCA	38318	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGA5	3'	ACTGCCCAGGTCCCCA	38325	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGA6	3'	ACTGCCCAGGTCCCCA	38332	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGA7	3'	ACTGCCCAGGTCCCCA	38339	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGA8	3'	ACTGCCCAGGTCCCCA	49450	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGA9	3'	ACTGCCCAGGTCCCCA	38346	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGB1	3'	ACTGCCCAGGTCCCCA	38353	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGB2	3'	ACTGCCCAGGTCCCCA	38360	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGB3	3'	ACTGCCCAGGTCCCCA	38367	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGB4	3'	ACTGCCCAGGTCCCCA	13597	A A C
			TGG GA CC GGGCAGT		

			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGB5	3'	ACTGCCCAGGTCCCCA	38374	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGB6	3'	ACTGCCCAGGTCCCCA	38381	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGB7	3'	ACTGCCCAGGTCCCCA	38388	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGC3	3'	ACTGCCCAGGTCCCCA	10451	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGC3	3'	ACTGCCCAGGTCCCCA	50514	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGC4	3'	ACTGCCCAGGTCCCCA	38395	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PCDHGC5	3'	ACTGCCCAGGTCCCCA	38402	A A C
			TGG GA CC GGGCAGT		
			ACC CT GG CCCGTCA		
			C _ A		
GAM1485	PPP2R5D	3'	ACTGCCCTGGCCCTCCA	20715	AA C
			TGGAG CC GGGCAGT		
			ACCTC GG CCCGTCA		
			CC T		
GAM1485	caspr5	3'	AAATGCACTGTTTCAGTTTTCCA	55379	CC
			TGGAGAAC GGGCAGTGCAATTT		
			ACCTTTTG CTTGTCACGTAAA		
			A_		
GAM1485	CDC14B	3'	ACGTGCACCGGGTTCCCCA	52842	A _ _
			TGG GAACCCGG GCA GT		

		ACC CTTGGGGCC CGT CA	
		C A G	
GAM1485 CPLX1	3'	AATGCATCAAGTCTCCA 21834	ACCCG GCA
		TGGAGA G GTGCATT	
		ACCTCT C TACGTAA	
		GAA__	
GAM1485 FLJ12747	3'	ACCACCTGGGTTCTCCA 49704	CA
		TGGAGAACCCGGG GT	
		ACCTCTTGGGTCC CA	
		AC	
GAM1485 FLJ13491	3'	GCTGCCCCGGGTTCCCA 44886	A
		TGG GAACCCGGGCAGT	
		ACC CTTGGGCCCCGTCG	
		-	
GAM1485 FLJ14225	5'	AATGCATATGTTCTCCA 45900	CCGGGCA
		TGGAGAAC GTGCATT	
		ACCTCTTG TACGTAA	
		TA__	
GAM1485 FLJ20580	3'	AAATACACCTGAGTTAGTTTTTC 35422	CCGGG _ C
	CA	TGGAGAAC CAG TG ATTT	
		ACCTTTTG GTC AC TAAA	
		ATTGA C A	
GAM1485 HPIP	3'	AAATGCATGCAAATACTCCA 40045	AACCCGG G
		TGGAG GCA TGCATTT	
		ACCTC CGT ACGTAAA	
		ATAAA__	
GAM1485 KIAA0416	5'	AAATGCACTCATGCTGCTCCA 31460	AACC GGC
		TGGAG CG AGTGCATTT	
		ACCTC GT TCACGTAAA	
		GTC_ AC_	
GAM1485 KIAA1655	5'	GCTGCCCCGAATCTCCA 66618	ACC
		TGGAGA CGGGCAGT	
		ACCTCT GCCCGTCG	
		AA_	
GAM1485 KSR	5'	GCTGCTGCCCAGCTTCCCCA 64044	A CCC _
		TGG GAA GGGCAGT GC	
		ACC CTT CCCGTCG CG	
		C CGA T	
GAM1485 MIG-6	3'	AATGCACTGATTTCTGCA 38485	G CCCGGG
		TG AGAA CAGTGCATT	

AC TCTT GTCACGTAA  
 G TA\_\_\_\_  
 GAM1485 NAGK 3' AAATGCACTTTATCCACTCC 62246 AACCC C\_\_\_\_  
 GGAG GGG AGTGCAATTT  
 |||| ||| |||||  
 CCTC CCT TCACGTAAA  
 A\_\_\_\_ ATT  
 GAM1485 PRDM10 3' CACAGGTTTCGGGTTCCC 39577 A A\_  
 GG GAACCCGGGC GTG  
 || ||||| |||  
 CC CTTGGGCTTG CAC  
 \_ GA  
 GAM1485 TRIM26 3' GTTCTGACCGGTTCCCCA 12894 A G T  
 TGG GAACCCGG CAG GC  
 ||| ||||| ||| ||  
 ACC CTTGGGCC GTC TG  
 C A T  
 GAM1485 TRIM38 3' TATTGCCCATGTTCCCCA 20990 A CC  
 TGG GAAC GGGCAGTG  
 ||| ||| |||||  
 ACC CTTG CCCGTTAT  
 C TA  
 GAM1485 LOC116437 3' AAATGCACCCATGTGGCTCCCCA 73889 A A \_ \_ CA  
 TGG GA CC CG GG GTGCATTT  
 ||| || ||| ||| |||||  
 ACC CT GG GT CC CACGTAAA  
 \_ C T A \_  
 GAM1485 LOC123264 5' GCTGCCGCAGGCTCTCCA 74205 A CG\_  
 TGGAGA CC GGCAGT  
 ||||| || |||||  
 ACCTCT GG CCGTCG  
 C ACG  
 GAM1485 LOC145783 5' CGCTGCCCAGGTCCCCG 77479 A A C  
 TGG GA CC GGGCAGTG  
 ||| || |||||  
 GCC CT GG CCCGTCGC  
 C \_ A  
 GAM1485 LOC152829 5' AAATGCACCACTGCACTCCA 80691 AACC GCA  
 TGGAG CGG GTGCATTT  
 |||| ||| |||||  
 ACCTC GTC CACGTAAA  
 AC\_\_ AC\_  
 GAM1485 LOC220021 3' TGCTGCCAAGTTCCCCA 93399 A CCG  
 TGG GAAC GGCAGTG  
 ||| ||| |||||  
 ACC CTTG CCGTCGT  
 C AA\_  
 GAM1485 LOC255852 5' ACTTGCCAGGTTCTCCA 97571 C G \_  
 TGGAGAACC GG CA GT  
 ||||| || |||



		ACCTCTTGG CC GT CA	
		A G T	
GAM1485	LOC257494 3'	GTTCTGACCGGGTTCCCCA 97798	A G T
		TGG GAACCCGG CAG GC	
		ACC CTTGGGGCC GTC TG	
		C A T	
GAM1485	LOC90233 3'	TGTTGCCCAGGTCCTGCA 56388	G A C GT
		TG AG ACC GGGCA GCA	
		AC TC TGG CCCGT TGT	
		G C A _	
GAM1486	ARHGEF7 3'	GTTGATGCTACACTGTTGTAA 14011	CA _ C
		TTACAACAG TA CA TCAGC	
		AATGTTGTC AT GT AGTTG	
		AC C _	
GAM1486	COL8A1 5'	CTGAAAGAAGCTGTTGTGA 8483	ATACAC
		TTACAACAGC TCAG	
		AGTGTTGTCG AGTC	
		AAGAA_	
GAM1486	GALC 3'	TAGCCAATGCTGTTGTAG 3849	ACACTCA
		TTACAACAGCAT GCTA	
		GATGTTGTCGTA CGAT	
		AC_____	
GAM1486	PRAME 3'	GTGTAGACTGTTGTAA 20372	CA
		TTACAACAG TACAC	
		AATGTTGTC ATGTG	
		AG	
GAM1486	SAR1 3'	ATAGCTGAAAGAAGCTGCTGTG 39322	A ATACAC
	A	TTACA CAGC TCAGCTAT	
		AGTGT GTCG AGTCGATA	
		C AAGAA_	
GAM1486	SRGAP1 5'	ATAGCTGAGGTAGAGTGCTGTT 72258	___ A
	G	CAACAGCAT AC CTCAGCTAT	
		GTTGTCGTG TG GAGTCGATA	
		AGA _	
GAM1486	C21orf6 3'	ATAGCTGAAATGCATCTGTT 33743	C A C_
		AACAG AT CA TCAGCTAT	
		TTGTC TA GT AGTCGATA	
		_ C AA	
GAM1486	FHR-3 3'	ATAGCTTCTGATATTGTTGTAA 40705	C A CTC
		TTACAACAG AT CA AGCTAT	

			AATGTTGTT TA GT TCGATA		
			A _ CT_		
GAM1486	FHR-4	3'	ATAGCTTCTGATATTGTTGTAA 21932	C A CTC	
			TTACAACAG AT CA AGCTAT		
			AATGTTGTT TA GT TCGATA		
			A _ CT_		
GAM1486	GIT2	3'	ATAGCTTGACCATATGCTGTCA 28753	CA CAC _	
	TGA		TTA ACAGCATA TCA GCTAT		
			AGT TGTCGTAT AGT CGATA		
			AC ACC T		
GAM1486	GIT2	3'	ATAGCTTGACCATATGCTGTCA 54075	CA CAC _	
	TGA		TTA ACAGCATA TCA GCTAT		
			AGT TGTCGTAT AGT CGATA		
			AC ACC T		
GAM1486	GIT2	3'	ATAGCTTGACCATATGCTGTCA 54088	CA CAC _	
	TGA		TTA ACAGCATA TCA GCTAT		
			AGT TGTCGTAT AGT CGATA		
			AC ACC T		
GAM1486	HSA243666	3'	TGTACTTGCTGTTGTAA 34148	___	
			TTACAACAGCA TACA		
			AATGTTGTCGT ATGT		
			TC		
GAM1486	KIAA0555	5'	ATAGCTGAATTGAATGC 60112	A C_	
			GCAT CA TCAGCTAT		
			CGTA GT AGTCGATA		
			A TA		
GAM1486	LOC120196	3'	GAGTGTTTCATATGCTGTT 75547	_____	
			AACAGCAT ACACTC		
			TTGTCGTA TGTGAG		
			TACT		
GAM1486	LOC149013	3'	CTAGTGTCTGCTGTTG 79131	T C	
			CAACAGCA ACACT AG		
			GTTGTCGT TGTGA TC		
			C _		
GAM1486	LOC149317	3'	CTAGTGTCTGCTGTTG 79288	T C	
			CAACAGCA ACACT AG		
			GTTGTCGT TGTGA TC		
			C _		
GAM1486	LOC151273	5'	AGGTATCTGTTGTAA 67014	C A	
			TTACAACAG ATAC CT		

AATGTTGTC TATG GA

GAM1486 LOC153139 5' TAGCTGAGTGTTTCATGT 85928 —  
GCAT ACACTCAGCTA  
||||| |||||  
TGTA TGTGAGTCGAT  
CT

GAM1486 LOC154184 5' TAGCTGAGTGTTTCATGT 86183 —  
GCAT ACACTCAGCTA  
||||| |||||  
TGTA TGTGAGTCGAT  
CT

GAM1486 LOC221601 5' TAGCTGAGTGTTTCATGT 93651 —  
GCAT ACACTCAGCTA  
||||| |||||  
TGTA TGTGAGTCGAT  
CT

GAM1486 LOC93622 3' TTGATATGTTGTTGTAA 56933 CAC  
TTACAACAGCATA TCAG  
||||| |||||  
AATGTTGTTGTAT AGTT

GAM1487 CAPNS1 3' GCCAAGCTCCAGACCG 8253 A CGTA  
CGG TC GAGCTTGGC  
||| || |||||  
GCC AG CTCGAACCG  
\_ AC\_

GAM1487 CDKN2C 5' CCAAGCTCTACTCC 54357 TCC  
GGA GTAGAGCTTGG  
||| |||||  
CCT CATCTCGAACC

GAM1487 CTNS 3' CCAAGCTTGCAGCCGA 17038 ATCC G  
TCGG GTA AGCTTGG  
|||| ||| |||||  
AGCC CGT TCGAACC  
GA\_ \_

GAM1487 CYP4A11 3' CCAAGCTCTGTGCTGA 5753 ATC  
TCGG CGTAGAGCTTGG  
|||| |||||  
AGTC GTGTCTCGAACC

GAM1487 DDX11 3' GCCAAGCTGCCGGCCTGGATCC 47655 \_ AG\_  
GAG CTCGGATCC GT AGCTTGGC  
||||| || |||||  
GAGCCTAGG CG TCGAACCG  
TC GCCG

GAM1487 DHCR24 3' GCCAAAGCCAGGTCCGAG 28628 T GTAGA \_  
CTCGGA CC GCTT GGC  
||||| || |||||

		GAGCCT GG CGAA CCG	
		_ AC_ A	
GAM1487 EXT2	5'	CCAAGCTCGGGGCCGAG 4632	AT GTA
		CTCGG CC GAGCTTGG	
		GAGCC GG CTCGAACC	
		GG _	
GAM1487 FUT7	3'	GCCAAACCTGGGACCCCGAG 15584	A_ G AGC
		CTCGG TCC TAG TTGGC	
		GAGCC AGG GTC AACCG	
		CC _ CA_	
GAM1487 GPC1	5'	CCCGGCCAGGATCCGAG 9100	GTAGA T
		CTCGGATCC GCT GG	
		GAGCCTAGG CGG CC	
		AC_ C	
GAM1487 MVK	3'	GCCAAGCTCTGCAGTCC 60650	CC
		GGAT GTAGAGCTTGGC	
		CCTG CGTCTCGAACCG	
		A_	
GAM1487 TNFRSF6B	5'	CCCCTCACGGTCCGAG 51964	T A CTT
		CTCGGA CCGT GAG GG	
		GAGCCT GGCA CTC CC	
		_ _ C_	
GAM1487 TP53BP2	5'	CCAAGATCTCAGGATCC 18300	GT G
		GGATCC AGA CTTGG	
		CCTAGG TCT GAACC	
		AC A	
GAM1487 VDR	3'	GCCCTCCTTCCACGGATCC 4569	A CTT_
		GGATCCGT GAG GGC	
		CCTAGGCA CTT CCG	
		C CTC	
GAM1487 CIDEB	5'	GCCAAGCTCCACACCA CGA 27044	GATCC A
		TCG GT GAGCTTGGC	
		AGC CA CTCGAACCG	
		ACCA_ C	
GAM1487 CTAG2	3'	GCTGAGCTACGATTCCGA 40650	TC AG TG
		TCGGA CGT AGCT GC	
		AGCCT GCA TCGA CG	
		TA _ GT	
GAM1487 DDX12	3'	GCCAAGCTGCCGGCCTGGATCC 59698	_ AG_
GAG		CTCGGATCC GT AGCTTGGC	

GAGCCTAGG CG TCGAACCG  
 TC GCCG  
 GAM1487 DKFZP434F0318 3' CCAAGCTGGGTTAGGAGCCGA 48006 A GTAG\_\_  
 TCGG TCC AGCTTGG  
 |||| ||| |||||  
 AGCC AGG TCGAACC  
 G ATTGGG  
 GAM1487 FLJ10120 3' GCCAAGCTCATCTCC 35833 TCC A  
 GGA GT GAGCTTGGC  
 ||| || |||||  
 CCT TA CTCGAACCG  
 C\_\_ \_  
 GAM1487 FLJ20420 3' GCCAGAAAACATAGATCCGAG 35141 CG AGAGC  
 CTCGGATC T TTGGC  
 ||||| | ||||  
 GAGCCTAG A GACCG  
 AT CAAAA  
 GAM1487 FLJ22625 5' GCCAAGCTCTGACTTCCGAG 45258 TCCG  
 CTCGGA TAGAGCTTGGC  
 ||||| |||||  
 GAGCCT GTCTCGAACCG  
 TCA\_  
 GAM1487 GBTS1 3' CCAGCAGGATCCGAG 59052 GTAGA T  
 CTCGGATCC GCT GG  
 ||||| ||| ||  
 GAGCCTAGG CGA CC  
 A\_\_ \_  
 GAM1487 KIAA0682 3' GCCAAGCTCCCTGGCTGAG 32476 AT TA  
 CTCGG CCG GAGCTTGGC  
 |||| ||| |||||  
 GAGTC GGT CTCGAACCG  
 \_ CC  
 GAM1487 KIAA1061 3' GCCAAGCTGCACACCGAG 71177 ATCC AG  
 CTCGG GT AGCTTGGC  
 |||| || |||||  
 GAGCC CA TCGAACCG  
 A\_\_ CG  
 GAM1487 KIAA1978 3' GCCAGAGCCACAGATGCC 74423 \_ C AGA \_  
 GG ATC GT GCT TGGC  
 || ||| || ||||  
 CC TAG CA CGA ACCG  
 G A C\_\_ G  
 GAM1487 MAFB 3' GCCAAGCTCCGCACCCAGAG 18413 \_ ATCC TA  
 CTC GG G GAGCTTGGC  
 ||| || | |||||  
 GAG CC C CTCGAACCG  
 A CCA\_ GC  
 GAM1487 MGC2217 3' CCAAGCTCAGGTTTCTAAG 44176 CG T\_ GTA  
 CT GA CC GAGCTTGG  
 || || || |||||

		GA CT GG CTCGAACC		
		AT TT A__		
GAM1487	MGC26847	3' GCCAAGCTGACATCCAAG	58763	C CC AG
		CT GGAT GT AGCTTGGC		
		GA CCTA CA TCGAACCG		
		A __ G_		
GAM1487	MRPL20	3' GCCAAGCTCTGCCCACCCGG	35734	ATCC
		TCGG GTAGAGCTTGGC		
		GGCC CGTCTCGAACCG		
		CACC		
GAM1487	PADI3	3' GCCAAGCTCCTGCCC	32660	ATCC _
		GG GTAG AGCTTGGC		
		CC CGTC TCGAACCG		
		____ C		
GAM1487	PLA2G6	3' GCCAAGCTGCCTGCCCGAG	66490	ATCC ____
		CTCGG GTAG AGCTTGGC		
		GAGCC CGTC TCGAACCG		
		____ CG		
GAM1487	TEX27	3' GCCAAGCTCTGGTCCCGA	41663	AT GT
		TCGG CC AGAGCTTGGC		
		AGCC GG TCTCGAACCG		
		CT ____		
GAM1487	TIGD5	5' GCCAGATCTACGGGCCCGAG	51702	AT GC
		CTCGG CCGTAGA TTGGC		
		GAGCC GGCATCT GACCG		
		CG A_		
GAM1487	LOC112885	3' GCCAAGCTGGAAGATCCG	56526	CGTAG
		CGGATC AGCTTGGC		
		GCCTAG TCGAACCG		
		AAGG_		
GAM1487	LOC115219	3' CCAAGCTCAGCAATCTGA	73301	CC A
		TCGGAT GT GAGCTTGG		
		AGTCTA CG CTCGAACC		
		A_ A		
GAM1487	LOC116113	3' CCAAGCTCTCCCTGAG	92212	ATCCGT
		CTCGG AGAGCTTGG		
		GAGTC TCTCGAACC		
		CC____		
GAM1487	LOC144508	5' GCCAAGCTCAGATCC	87069	CGTA
		GGATC GAGCTTGGC		

CCTAG CTCGAACCG  
 A\_\_\_\_  
 GAM1487 LOC150370 3' GCCAAGCTGCCATCC 84941 CC AG  
 GGAT GT AGCTTGGC  
 |||| || |||||  
 CCTA CG TCGAACCG  
 C\_ \_  
 GAM1487 LOC155435 3' CCAAGCTTAACTCGAG 81348 ATCC A  
 CTCGG GT GAGCTTGG  
 |||| || |||||  
 GAGCT CA TTCGAACC  
 \_\_\_\_ A  
 GAM1487 LOC196993 3' GCATCACCCGGATCCGAG 89669 TA\_ \_  
 CTCGGATCCG GA GC  
 ||||| || ||  
 GAGCCTAGGC CT CG  
 CCA A  
 GAM1487 LOC197322 5' GCCAGTACTGGATCCGAG 89739 GT A T  
 CTCGGATCC AG GCT GGC  
 ||||| || || ||  
 GAGCCTAGG TC TGA CCG  
 \_\_\_\_ A \_  
 GAM1487 LOC199221 5' GCCAAGCTAAAGTGGACCC 80350 A TAG\_  
 GG TCCG AGCTTGGC  
 || ||| |||||  
 CC AGGT TCGAACCG  
 C GAAA  
 GAM1487 LOC201522 3' CCAAGCTCACGTGCGAG 88255 G TC A  
 CTCG A CGT GAGCTTGG  
 |||| | || |||||  
 GAGC T GCA CTCGAACC  
 G\_ \_  
 GAM1487 LOC219300 5' CCAAGCTCTGTCTCAG 94311 C CCGT  
 CT GGAT AGAGCTTGG  
 || ||| |||||  
 GA TCTG TCTCGAACC  
 C \_\_\_\_  
 GAM1487 LOC221535 5' GCCAAGCTCACTCTGACCCG 93801 A C\_ A  
 CGG TC GT GAGCTTGGC  
 ||| || || |||||  
 GCC AG CA CTCGAACCG  
 C TCT \_  
 GAM1487 LOC222057 3' GCCAAGCTCATGCCCC 92777 ATC A  
 GG CGT GAGCTTGGC  
 || ||| |||||  
 CC GTA CTCGAACCG  
 CC\_ \_  
 GAM1487 LOC223009 5' GCCAAGCTCATGCCTC 94378 TC A  
 GA CGT GAGCTTGGC  
 || ||| |||||

CT GTA CTCGAACCG  
 CC \_  
 GAM1487 LOC253018 5' GCCAAGCTCACTCTGACCCG 96007 A C\_\_ A  
 CGG TC GT GAGCTTGGC  
 ||| || || |||||  
 GCC AG CA CTCGAACCG  
 C TCT \_  
 GAM1487 LOC255096 5' GCCAAGCTCTACAACCCAGAG 97623 \_ ATCC  
 CTC GG GTAGAGCTTGGC  
 ||| || |||||  
 GAG CC CATCTCGAACCG  
 A CAA\_  
 GAM1487 LOC255975 5' GCCAAGCTCATGCTTC 95893 TC A  
 GA CGT GAGCTTGGC  
 || |||||  
 CT GTA CTCGAACCG  
 TC \_  
 GAM1487 LOC257101 3' GCCAAGCTCTGCCTTCCCAG 96907 C TCC  
 CT GGA GTAGAGCTTGGC  
 || |||||  
 GA CCT CGTCTCGAACCG  
 C TC\_  
 GAM1487 LOC257548 5' GCCAAGCTCACTCTGACCCG 97741 A C\_\_ A  
 CGG TC GT GAGCTTGGC  
 ||| || || |||||  
 GCC AG CA CTCGAACCG  
 C TCT \_  
 GAM1487 LOC257549 5' GCCAAGCTCACTCTGACCCG 97748 A C\_\_ A  
 CGG TC GT GAGCTTGGC  
 ||| || || |||||  
 GCC AG CA CTCGAACCG  
 C TCT \_  
 GAM1487 LOC257610 5' GCCAAGCTCACTCTGACCCG 97857 A C\_\_ A  
 CGG TC GT GAGCTTGGC  
 ||| || || |||||  
 GCC AG CA CTCGAACCG  
 C TCT \_  
 GAM1487 LOC257611 5' GCCAAGCTCACTCTGACCCG 97870 A C\_\_ A  
 CGG TC GT GAGCTTGGC  
 ||| || || |||||  
 GCC AG CA CTCGAACCG  
 C TCT \_  
 GAM1487 LOC90326 3' GCCAAGCTCCCCGGCGAG 62273 GAT TA  
 CTCG CCG GAGCTTGGC  
 |||| || |||||  
 GAGC GGC CTCGAACCG  
 \_ CC  
 GAM1487 LOC96652 3' GCCAAGCTGTGGGGCTCCGAG 65469 T G G  
 CTCGGA CC TA AGCTTGGC  
 ||||| || || |||||



GAGCCT GG GT TCGAACCG  
 C G G  
 GAM1488 ARHGEF7 3' CGGCACTGCCGCATCCACC 14003 CA T TA  
 GG GATGC GGCA GCTG  
 || ||||| ||||  
 CC CTACG CCGT CGGC  
 AC \_ CA  
 GAM1488 DPEP1 3' TGCAAGGACCAGCATCTCC 15334 C CATAGC  
 GG AGATGCTGG TGCA  
 || ||||| ||||  
 CC TCTACGACC ACGT  
 \_ AGGA\_  
 GAM1488 KLK8 3' GTCTATACCAACATCTGCC 57963 C C \_  
 GGCAGATG TGG ATAG C  
 ||||| || ||||  
 CCGTCTAC ACC TATC G  
 A A T  
 GAM1488 LOXL1 5' CGTGCAGCCCTGGGCACCGCC 60189 AGA GG TA  
 GGC TGCT CA GCTGCACG  
 ||| |||| || |||||  
 CCG ACGG GT CGACGTGC  
 CC\_ \_ CC  
 GAM1488 MUC4 3' TGGAGGCCAGTGCCAGCACCTG 56331 A A\_ G\_  
 CC GGCAG TGCTGGCAT GCT CA  
 |||| ||||| ||| ||  
 CCGTC ACGACCGTG CGG GT  
 C AC AG  
 GAM1488 RRP22 3' TTATGCCACACCTACC 21360 C A C  
 GG AG TG TGGCATAG  
 || || |||||  
 CC TC AC ACCGTATT  
 A C \_  
 GAM1488 TCF20 3' CGTGCAGCCACACCCTGCCCTG 66956 AT T CATA\_  
 CC GGCAG GC GG GCTGCACG  
 |||| || |||||  
 CCGTC CG CC CGACGTGC  
 C\_ T CACAC  
 GAM1488 C20orf150 3' CAGCTGCCAGCACCC 65390 CAGA TA  
 GG TGCTGGCA GCTG  
 || ||||| ||||  
 CC ACGACCGT CGAC  
 C\_ \_  
 GAM1488 CCR1 3' CAGTAGCCAGCATCTGCC 7107 ATA  
 GGCAGATGCTGGC GCTG  
 ||||| ||||  
 CCGTCTACGACCG TGAC  
 A\_  
 GAM1488 EIF2C2 3' GTGTTCTGCCAGCACCGCC 71947 AGA TAGCT  
 GGC TGCTGGCA GCAC  
 || ||||| ||||

CCG ACGACCGT TGTG  
 CC\_ CT\_\_\_\_  
 GAM1488 EPSIN 5' CGGTGACCTGCCAGCACCTGCC 25297 A TA\_\_\_\_  
 GGCAG TGCTGGCA GCTG  
 ||||| ||||| ||||  
 CCGTC ACGACCGT TGGC  
 C CCAG  
 GAM1488 FLJ14566 5' CAGACCGCATCTGCC 51445 T CATAG  
 GGCAGATGC GG CTG  
 ||||| || |||  
 CCGTCTACG CC GAC  
 \_ A\_\_\_\_  
 GAM1488 FLJ20152 3' GGACCATGCCAGCAACTACC 38646 C A AG\_\_\_\_  
 GG AG TGCTGGCAT CT  
 || || ||||| ||  
 CC TC ACGACCGTA GG  
 A A CCA  
 GAM1488 HT002 3' GCAGCCACAGGGTTTCACC 25942 C\_ G GCATA  
 GG AGAT CTG GCTGC  
 || ||| || |||||  
 CC TTTG GAC CGACG  
 AC G AC\_\_\_\_  
 GAM1488 KIAA1323 5' CAGCTATGCAAGCTGCT 63040 GAT G  
 GGCA GCT GCATAGCTG  
 ||| || |||||  
 TCGT CGA CGTATCGAC  
 \_ A  
 GAM1488 OSBPL8 3' CTATGCCATCATCCACC 40456 CA C  
 GG GATG TGGCATAG  
 || ||| |||||  
 CC CTAC ACCGTATC  
 AC T  
 GAM1488 TJP4 5' CAGCTGTTAGCAGCATCTGCC 54609 GC\_\_\_\_  
 GGCAGATGCTG ATAGCTG  
 ||||| |||||  
 CCGTCTACGAC TGTCGAC  
 GAT  
 GAM1488 LOC113146 3' TGGCCTGCCAGCATCCGCC 72973 A TA  
 GGC GATGCTGGCA GCTG  
 || ||||| |||  
 CCG CTACGACCGT CGGT  
 C C\_\_\_\_  
 GAM1488 LOC123855 3' TGCAGAGCGCAGCATCTGGC 75630 G \_ ATAG  
 G CAGATGCTG GC CTGCA  
 | ||||| || |||||  
 C GTCTACGAC CG GACGT  
 G G A\_\_\_\_  
 GAM1488 LOC126302 3' CAGTCACCAGCATCCC 74492 CA CATA  
 GG GATGCTGG GCTG  
 || ||||| |||

		CC CTACGACC TGAC		
		___ AC___		
GAM1488	LOC146272 3'	TGCAACCACAAGGTGTCTGCC 77796		GGCATAGC
		GGCAGATGCT TGCA		
		CCGTCTGTGG ACGT		
		AACACCA_		
GAM1488	LOC151996 5'	CGTGCAGCCACACCCTCTTCCC 85532		ATGCT_ CATA_
		TGCC GGCAG GG GCTGCACG		
		CCGTC CC CGACGTGC		
		CCTTCT CACAC		
GAM1488	LOC200305 5'	CGCACAGCCAAGCCCACATGCC 89979		GA CT ATA CA
		GGCA TG GGC GCTG CG		
		CCGT AC CCG CGAC GC		
		AC ___ AAC AC		
GAM1488	LOC219942 3'	GTCAGACACCACATCTGCC 93348		C CATAG C
		GGCAGATG TGG CTG AC		
		CCGTCTAC ACC GAC TG		
		_ ACA_ _		
GAM1488	LOC220992 5'	CGTGCAGCTCCGCAGCCCTGCC 91468		AT G AT
		GGCAG GCTG C AGCTGCACG		
		CCGTC CGAC G TCGACGTGC		
		C_ _CC		
GAM1488	LOC253974 3'	CGTACTCAGCACCAGCATCGCC 97423		A CATA C_
		GGC GATGCTGG GCTG ACG		
		CCG CTACGACC CGAC TGC		
		_ A_ TCA		
GAM1488	LOC51720 3'	CAGCACCACCAGCACCTACC 32819		C A CATA
		GG AG TGCTGG GCTG		
		CC TC ACGACC CGAC		
		A C ACCA		
GAM1488	LOC92305 3'	CAGACACAGCGTCTGCC 56413		GCATAG
		GGCAGATGCTG CTG		
		CCGTCTGCGAC GAC		
		ACA_		
GAM1489	AICDA 5'	GCCTGAGACTTGCAGGGAGGCA 40329		C ATTTGC_
		AGAA TTC TGCTCCCT CAGGC		
		AAG ACGGAGGGA GTCCG		
		A CGTTCAGA		
GAM1489	ANK1 3'	GCCTCCGGCCCAGGGAGGCCAG 3473		CT ATTT _
		AA TTC GCCTCCCT GCC AGGC		

			AAG CGGAGGGA CGG TCCG		
			AC CC_ CC		
GAM1489	ANK1	3'	GCCTCCGGCCCAGGGAGGCCAG 40027	CT	ATTT _
	AA		TTC GCCTCCCT GCC AGGC		
			AAG CGGAGGGA CGG TCCG		
			AC CC_ CC		
GAM1489	EIF2C1	3'	CCCAAATCCAGAGGAAGCAAGG 24170	_ C _ _	CCA
	A		TCCT GC TCC CT ATTTG GG		
			AGGA CG AGG GA TAAAC CC		
			A A A CC _		
GAM1489	IKBKG	3'	CCCGGCACTGGGGAAGTCAAGA 13311	C _ C	TT A
	A		TTC TG C TCCCTA TGCC GG		
			AAG AC G AGGGGT ACGG CC		
			A T A C_ C		
GAM1489	IKBKG	3'	CCCGGCACTGGGGAAGTCAAGA 94663	C _ C	TT A
	A		TTC TG C TCCCTA TGCC GG		
			AAG AC G AGGGGT ACGG CC		
			A T A C_ C		
GAM1489	LY9	3'	AAATAAAAGGCAGGAA 71680	CCC	
			TTCCTGCCT TATTT		
			AAGGACGGA ATAAA		
			AA_		
GAM1489	MAFF	3'	TGGCAAATAGGGAGACAAGGA 24655	GC_	
			TCCT CTCCCTATTTGCCA		
			AGGA GAGGGATAAACGGT		
			ACA		
GAM1489	MC1R	5'	GCCCAGATGGAAGGAGGCAGG 9954	_	CCA
			CCTGCCTCC CTATTTG GGC		
			GGACGGAGG GGTAGAC CCG		
			AA _		
GAM1489	MYO15A	3'	GCCTGAGGGAGGAGGCAGGAG 32671	_	ATTTGC
			TTCCTGCCTCC CT CAGGC		
			GAGGACGGAGG GG GTCCG		
			A GA_		
GAM1489	NRG1	3'	GCAAATAGAAAACAGGAA 25659	CCTCC	
			TTCCTG CTATTTGC		
			AAGGAC GATAAACG		
			AAAA_		
GAM1489	NRG1	3'	GCAAATAGAAAACAGGAA 25646	CCTCC	
			TTCCTG CTATTTGC		

AAGGAC GATAAACG  
 AAAA\_  
 GAM1489 SEPN1 3' GCCTGGCAGAGGAAGAAGGAA 66369 GC C AT  
 TTCCT CT CCT TTGCCAGGC  
 |||| |||| ||||  
 AAGGA GA GGA GACGGTCCG  
 A\_ A \_  
 GAM1489 SMURF1 3' GCCTAACCCGCGGGAGGCGGAA 92453 T TATTTGCC  
 TTCC GCCTCCC AGGC  
 |||| |||| ||||  
 AAGG CGGAGGG TCCG  
 \_ CGCCCA\_  
 GAM1489 STAT6 3' GCCTAGGACGGATAGGCAGGAA 12021 CCCT \_ \_  
 TTCCTGCCT ATTTG CC AGGC  
 |||| |||| ||||  
 AAGGACGGA TAGGC GG TCCG  
 \_ A A  
 GAM1489 TFF3 3' GCCCAGGCCTCAAGGGCAGGAA 63566 CCCTATTT A\_  
 TTCCTGCCT GCC GGC  
 |||| |||| ||||  
 AAGGACGGG CGG CCG  
 AACTC\_ AC  
 GAM1489 TOP3B 5' GCCCGGCGGCTCAGAAAGGCGG 14129 CC AT\_ A  
 GAA TTCCTGCCT CT TTGCC GGC  
 |||| |||| ||||  
 AAGGGCGGA GA GGCGG CCG  
 AA CTC C  
 GAM1489 VAV1 3' GCCTTGGCAGAGAGACGAG 18305 C\_ A \_  
 CTC CT TTTGCCA GGC  
 |||| |||| ||||  
 GAG GA AGACGGT CCG  
 CA G T  
 GAM1489 YWHAB 5' GCTGTGGATAGAGAAGCAGGAA 12692 C C TG CA  
 TTCCTGC TC CTATT C GGC  
 |||| |||| ||||  
 AAGGACG AG GATAG G TCG  
 A A GT\_  
 GAM1489 AF020591 3' GCCTGGCAAACATGGCA 27141 TCCCTA  
 TGCC TTTGCCAGGC  
 |||| ||||  
 ACGG AAACGGTCCG  
 TAC\_  
 GAM1489 BCL2L1 3' CCTCAGGCAGGAAGGGCAGGAA 56804 CC ATT \_  
 TTCCTGCCT CT TGCC AGG  
 |||| |||| ||||  
 AAGGACGGG GG ACGG TCC  
 AA \_ AC  
 GAM1489 BNIP-S 5' TAAAGAAGGAGGCAGGAA 56263 CTA  
 TTCCTGCCTCC TTTG  
 |||| ||||

AAGGACGGAGG AAAT  
 AAG  
 GAM1489 BTBD3 5' GCAAATAAGAGAAACAGGAA 30311 C\_\_ CC  
 TTCCTG CTC TATTTGC  
 ||||| ||| |||||  
 AAGGAC GAG ATAAACG  
 AAA A\_  
 GAM1489 C20orf28 3' GCCTGAGACGGGAGGCAGGAA 31224 TAT GC  
 TTCCTGCCTCCC TT CAGGC  
 ||||| || |||||  
 AAGGACGGAGGG AG GTCCG  
 C\_\_ A\_  
 GAM1489 CHODL 5' CCCGGCAGGGAGGCAGGGA 46310 ATTT A  
 TTCCTGCCTCCCT GCC GG  
 ||||| ||| ||  
 AGGGACGGAGGGA CGG CC  
 \_\_\_\_ C  
 GAM1489 D2S448 3' CCTGAAGGGAAGCAGG 73519 C ATTTGC  
 CCTGC TCCCT CAGG  
 ||||| ||| |||  
 GGACG AGGGA GTCC  
 A A\_\_\_\_  
 GAM1489 DKFZP434K1772 3' GCCTTACTCAGGAAGGCAGGAG 67714 C ATTTGCC  
 TTCCTGCCT CCT AGGC  
 ||||| ||| |||  
 GAGGACGGA GGA TCCG  
 A CTCAT\_\_  
 GAM1489 DKFZp547I094 3' CCTGGCAACCTGAGGGAGG 49637 AT\_\_  
 CCTCCCT TTGCCAGG  
 ||||| |||||  
 GGAGGGA AACGGTCC  
 GTCC  
 GAM1489 DKFZP547L112 3' CCTGGATATAGCAAGGCAGGAA 66529 CC TTG  
 TTCCTGCCT CTAT CCAGG  
 ||||| ||| |||||  
 AAGGACGGA GATA GGTCC  
 AC TA\_  
 GAM1489 FABP7 5' CAAATAAGAAGGCAGGAG 7542 CCC  
 TTCCTGCCT TATTTG  
 ||||| |||||  
 GAGGACGGA ATAAAC  
 AGA  
 GAM1489 FLJ14957 3' CCCAAAGTGGGAGGCAGGGA 51744 TA CCA  
 TTCCTGCCTCCC TTTG GG  
 ||||| ||| ||  
 AGGGACGGAGGG AAAC CC  
 TG \_\_\_\_  
 GAM1489 FLJ20343 3' CCTGGCAAAGTACCAG 34998 CC CCTA  
 CTG TC TTTGCCAGG  
 ||| || |||||

GAC AG AAACGGTCC  
 C\_ TC\_\_  
 GAM1489 FLJ23185 3' CCTGGCAGGATGAGGCAGAGA 46830 \_ CCTA  
 TC CTGCCTC TTTGCCAGG  
 || ||||| |||||  
 AG GACGGAG GGACGGTCC  
 A TA\_\_  
 GAM1489 GGA2 3' GCCTGATGGGTGGGAGAAGGAA 56882 GC T GC  
 TTCCT CTCCC ATTT CAGGC  
 |||| |||| |||| ||||  
 AAGGA GAGGG TGGG GTCCG  
 A\_ \_ TA  
 GAM1489 GGA2 3' GCCTGATGGGTGGGAGAAGGAA 30468 GC T GC  
 TTCCT CTCCC ATTT CAGGC  
 |||| |||| |||| ||||  
 AAGGA GAGGG TGGG GTCCG  
 A\_ \_ TA  
 GAM1489 HDAC11 3' GCCCATAGGTCCAGGGAGGCAG 45718 ATTT A\_\_  
 G CCTGCCTCCCT GCC GGC  
 ||||| ||| |||  
 GGACGGAGGGA TGG CCG  
 CC\_\_ ATAC  
 GAM1489 IKKE 5' CACAAGGAGGCAGGGA 25746 CTAT CCA  
 TTCCTGCCTCC TTG G  
 ||||| ||| |  
 AGGGACGGAGG AAC C  
 \_\_\_\_ A\_  
 GAM1489 IL1F10 3' CAAGAAGGAGGCAGGAA 50771 CTA  
 TTCCTGCCTCC TTTG  
 ||||| ||||  
 AAGGACGGAGG GAAC  
 AA\_  
 GAM1489 KIAA0370 5' GCCCAGCAAATAGGAGCCTGGA 73209 T\_ CTC CA  
 G TTCC GC CCTATTTGC GGC  
 |||| || ||||| |||  
 GAGG CG GGATAAACG CCG  
 TC A\_\_ AC  
 GAM1489 KIAA0551 3' GCCTGGTTGAGAAGGAGAG 66839 \_ A\_ T  
 CTC CCT TT GCCAGGC  
 ||| ||| || |||||  
 GAG GGA AG TGGTCCG  
 A AG T  
 GAM1489 KIAA1183 3' CCCGGATGGGAGGAGGAA 62530 G TATTTG A  
 TTCCT CCTCCC CC GG  
 |||| |||| || ||  
 AAGGA GGAGGG GG CC  
 \_ TA\_\_ C  
 GAM1489 KIAA1464 3' CCTGACCCATGGAGGCAGGAG 68264 CTATTTGC  
 TTCCTGCCTCC CAGG  
 ||||| |||

GAGGACGGAGG GTCC  
 TACCCA\_\_  
 GAM1489 MAPK8IP3 3' GCCTGGTAGATGAAGCAG 52987 C CCT  
 CTGC TC ATTTGCCAGGC  
 |||| || |||||  
 GACG AG TAGATGGTCCG  
 A \_\_\_\_  
 GAM1489 MGC2306 3' GCCTGGCAGGGGGTGAAGGCAG 50963 \_\_\_\_ AT  
 GAG TTCCTGCCT CCCT TTGCCAGGC  
 ||||| ||| |||||  
 GAGGACGGA GGGG GACGGTCCG  
 AGT \_\_\_\_  
 GAM1489 MGC2865 5' GCCTGGCAAACCGAAGCAAGAA 50451 C C C CTA  
 TTC TGC TC TTTGCCAGGC  
 ||| ||| ||| |||||  
 AAG ACG AG AAACGGTCCG  
 A A CC\_\_  
 GAM1489 MGC9753 3' GCCTGATTTTGGGGAGGAGGAA 53049 G TTTGC  
 TTCCT CCTCCCTA CAGGC  
 |||| ||||| ||||  
 AAGGA GGAGGGGT GTCCG  
 \_ TTTA\_  
 GAM1489 PALM 3' GCCTGGTAGGAGAGAGACAGGA 10414 C C A  
 TCCTG CTC CT TTTGCCAGGC  
 |||| ||| ||| |||||  
 AGGAC GAG GA GGATGGTCCG  
 A A \_  
 GAM1489 PDZD2 5' CCTGGCACGGAAGGAGGAA 80866 G C TATT  
 TTCCT CCT CC TGCCAGG  
 |||| ||| ||| |||||  
 AAGGA GGA GG ACGGTCC  
 \_ A C\_\_  
 GAM1489 PLPL 3' CCTGGAGGGGGAGGCAGGAG 39431 ATTTG  
 TTCCTGCCTCCCT CCAGG  
 ||||| ||||| ||||  
 GAGGACGGAGGGG GTCC  
 GA\_\_  
 GAM1489 RABEX5 3' GCCTGGAATGGAAGGCGGGAA 27186 C TATTTG  
 TTCCTGCCT CC CCAGGC  
 ||||| || |||||  
 AAGGGCGGA GG GGTCCG  
 A TAA\_\_  
 GAM1489 SHANK3 5' GCCTGCTCGCAGGGAGGCAGAG 65500 \_ ATTT C  
 A TC CTGCCTCCCT GC AGGC  
 || ||||| || ||||  
 AG GACGGAGGGA CG TCCG  
 A CGCT \_  
 GAM1489 SRF 5' CCGGGCCACAGGGGCAGGAA 11944 CCTATTT A  
 TTCCTGCCTC GCC GG  
 ||||| ||| ||



		AAGGACGGGG	CGG CC		
		ACAC__	G		
GAM1489	TREX1	5'	CCCAGCAGAGGGAGGCAG	53280	AT CA
			CTGCCTCCCT TTGC GG		
			GACGGAGGGA GACG CC		
			__ AC		
GAM1489	TREX1	5'	CCCAGCAGAGGGAGGCAG	53290	AT CA
			CTGCCTCCCT TTGC GG		
			GACGGAGGGA GACG CC		
			__ AC		
GAM1489	URG4	3'	GCCCCCAGGGTAGGGAGACA	35506	C GCCA
			TG CTCCCTATTT GGC		
			AC GAGGGATGGG CCG		
			A ACCC		
GAM1489	LOC124222	3'	CCTGACAAACAGGCAGGGA	74271	CCCTA C
			TTCCTGCCT TTTG CAGG		
			AGGGACGGA AAAC GTCC		
			C__ A		
GAM1489	LOC131873	5'	CCCGGAGGAGAGGCAGGGA	75877	_ ATTTG A
			TTCCTGCCTC CCT CC GG		
			AGGGACGGAG GGA GG CC		
			A ____ C		
GAM1489	LOC144348	5'	CCTTCCGTAGAAAGACAGGCA	76806	CC A C__
			TGCCT CT TTTGC AGG		
			ACGGA GA AGATG TCC		
			CA A CCT		
GAM1489	LOC146316	5'	CTTCGAGAGGCAGGAA	60872	CCTAT CC
			TTCCTGCCTC TTG AG		
			AAGGACGGAG AGC TC		
			____ T_		
GAM1489	LOC148529	5'	CCTGGCAGACAGGAAGACA	84167	C C A
			TG CT CCT TTTGCCAGG		
			AC GA GGA AGACGGTCC		
			A A C		
GAM1489	LOC149606	3'	GCCCGCGGAGCAGGGAG	79454	A_ CA
			CTCCCT TTTGC GGC		
			GAGGGA AGGCG CCG		
			CG C_		
GAM1489	LOC151057	3'	CCAGGAAAGAAGGCAGGAA	85209	CCCTA G A
			TTCCTGCCT TTT CC GG		

		AAGGACGGA	AAA GG CC	
		AG___ _ A		
GAM1489	LOC153346 5'	CCCAGATGGAAGGCA	86022 CC CCA	
		TGCCT CTATTTG GG		
		ACGGA GGTAGAC CC		
		A_ ____		
GAM1489	LOC196418 5'	CCTTCCGTAGAAAGACAGGCA	87696 CC A C__	
		TGCCT CT TTTGC AGG		
		ACGGA GA AGATG TCC		
		CA A CCT		
GAM1489	LOC199786 3'	GCCTGGCAGCTGAGGCAGAGA	88386 _ CCTAT	
		TC CTGCCTC TTGCCAGGC		
		AG GACGGAG GACGGTCCG		
		A TC__		
GAM1489	LOC200058 3'	CCTGAAGGATGGGAAGCCAGGA	88556 C C GC	
	A	TTCCTG CT CCTATTT CAGG		
		AAGGAC GA GGGTAGG GTCC		
		C A AA		
GAM1489	LOC204579 5'	CCCGGCTATGAGGCAGGAA	89465 CCTATTT A	
		TTCCTGCCTC GCC GG		
		AAGGACGGAG CGG CC		
		TAT__ C		
GAM1489	LOC219700 5'	GCCTGGCAGTCCAAAGACCAAG	93064 C CCTCCCTAT	
	AA	TTC TG TTGCCAGGC		
		AAG AC GACGGTCCG		
		A CAGAAACCT		
GAM1489	LOC253181 5'	GCCTGGCAAACAGCACAGGA	97558 CCTCC A	
		TCCTG CT TTTGCCAGGC		
		AGGAC GA AAACGGTCCG		
		AC__ C		
GAM1489	LOC253296 3'	GCCTGGGGCCACAGGAAAGGCA	94490 C_ ATTTG_	
	GGAA	TTCCTGCCT CCT CCAGGC		
		AAGGACGGA GGA GGTCCG		
		AA CACCGG		
GAM1489	LOC253298 5'	GCCTGGGGCCACAGGAAAGGCA	97215 C_ ATTTG_	
	GGAA	TTCCTGCCT CCT CCAGGC		
		AAGGACGGA GGA GGTCCG		
		AA CACCGG		
GAM1489	LOC254107 5'	CCCAGAGGGCAGGAA	94384 CCCTA CCA	
		TTCCTGCCT TTTG G		

			AAGGACGGG	AGAC	C	
			_____	C_		
GAM1489	LOC255189	5'	CTGACCAAGGCAGGAA	96589	CCCTATT	C_
			TTCCTGCCT	TG	CAG	
			AAGGACGGA	AC	GTC	
			_____	CA		
GAM1489	LOC257160	3'	CCTGACTGGGGAGGAAG	94846	G	TTTGC
			CTCCTCCCTA	CAGG		
			GA	GGAGGGGT	GTCC	
			A	CA_		
GAM1489	LOC257570	3'	GCCTGGGGCCACAGGAAAGGCA	97833	C_	ATTTG_
			GGAA	TTCCTGCCT	CCT	CCAGGC
			AAGGACGGA	GGA	GGTCCG	
			AA	CACCGG		
GAM1489	LOC257571	5'	GCCTGGGGCCACAGGAAAGGCA	97945	C_	ATTTG_
			GGAA	TTCCTGCCT	CCT	CCAGGC
			AAGGACGGA	GGA	GGTCCG	
			AA	CACCGG		
GAM1490	ABCC3	3'	TACCGGCCCGGGCCTAGACCTGG	39161	AA_	_A_
			TG	CACCAGGTCTA	CTG	C
			GTGGTCCAGAT	GGC	G	CAT
			CCG	C	GC	
GAM1490	ABCC3	3'	TACCGGCCCGGGCCTAGACCTGG	39142	AA_	_A_
			TG	CACCAGGTCTA	CTG	C
			GTGGTCCAGAT	GGC	G	CAT
			CCG	C	GC	
GAM1490	ANGPT1	3'	CAGTTTCAAACCTGGTGA	6702	CT_	
			TCACCAGGT	AAACTG		
			AGTGGTTCA	TTTGAC		
			AAC			
GAM1490	BLNK	3'	TATTGCCTGACCTGATGA	25257	C	TAAACT
			TCA	CAGGTC	GCAGTA	
			AGT	GTCCAG	CGTTAT	
			A	TC_		
GAM1490	CELSR1	3'	CTGTCAGACCTGGTGA	26483	AAACT	
			TCACCAGGTCT	GCAG		
			AGTGGTCCAGA	TGTC		
			C_			
GAM1490	DGCR2	3'	TACTGCAGCTCAGTGCCCAGTG	17630	CA	_ AAA
			CAC	GGTCT	CTGCAGTA	

			GTG CCG GA GACGTCAT		
			AC T CTC		
GAM1490	FGF2	3'	ACTGCAGTCCAGCCTAGG 8865	_ T AA	
			CC AGG CT ACTGCAGT		
			GG TCC GA TGACGTCA		
			A _ CC		
GAM1490	GRIN2B	3'	TACTG GGGGCAACCCTGGTGA 5906	TCTAAA G	
			TCACCAGG CT CAGTA		
			AGTGGTCC GG GTCAT		
			CAACG_ G		
GAM1490	GTF2H1	3'	TTACTGCAGTTGCTCAGG 18009	A_ CTA	
			CC GGT AACTGCAGTAA		
			GG TCG TTGACGTCATT		
			AC _		
GAM1490	HOXD4	3'	ACTGCAGTCCCTAGGCT 27518	A_	
			GGTCTA ACTGCAGT		
			TCGGAT TGACGTCA		
			CCC		
GAM1490	IFNAR1	3'	ACTGCACTCCAGCCTGGTGA 5280	CTAAAC	
			TCACCAGGT TGCAGT		
			AGTGGTCCG ACGTCA		
			ACCTC_		
GAM1490	IFNGR2	5'	ACTGCACTCCAGCCTGGTGA 18648	CTAAAC	
			TCACCAGGT TGCAGT		
			AGTGGTCCG ACGTCA		
			ACCTC_		
GAM1490	KPNB1	5'	TACCCAGACAGAGCCGGTGA 9626	A _ AAA CA	
			TCACC GG TCT CTG GTA		
			AGTGG CC AGA GAC CAT		
			_ G CA_ C_		
GAM1490	LPHH1	3'	TACTGCAGCAGTCTGTGA 24539	C T AAA	
			TCAC AGG CT CTGCAGTA		
			AGTG TCT GA GACGTCAT		
			_ _ C_		
GAM1490	MAPT	3'	TTGCAGACCTGGGA 33693	A AACT	
			TC CCAGGTCT GCAG		
			AG GGTCCAGA CGTT		
			_ _ _		
GAM1490	MAPT	3'	TTGCAGACCTGGGA 19782	A AACT	
			TC CCAGGTCT GCAG		

			AG GGTCCAGA	CGTT		
GAM1490	MAPT	3'	TTGCAGACCTGGGA	33702	A	AAACT
			TC CCAGGTCT	GCAG		
			AG GGTCCAGA	CGTT		
GAM1490	MAPT	3'	TTGCAGACCTGGGA	33712	A	AAACT
			TC CCAGGTCT	GCAG		
			AG GGTCCAGA	CGTT		
GAM1490	MSL3L1	3'	ACTGCAGTCGAGCCTGG	54360	T	AA
			CCAGG CT	ACTGCAGT		
			GGTCC GA	TGACGTCA		
			_ GC			
GAM1490	MYO1E	3'	TTATTGTATTTAAACCTGGTGA	17192	C	C
			TCACCAGGT TAAA	TGCAGTAA		
			AGTGGTCCA ATTT	ATGTTATT		
			A _			
GAM1490	NR3C1	3'	TACTGCAGCTTTACAT	3925	C	_
			GT TAAA	CTGCAGTA		
			TA ATTT	GACGTCAT		
			C C			
GAM1490	PXN	3'	TGCCCTAGGCCTGGCGA	11164	A	AACT
			TC CCAGGTCTA	GCA		
			AG GGTCCGGAT	CGT		
			C CC_			
GAM1490	RGS6	3'	ACCGCAGTCCAGGGCCTGG	15026	AA_	A
			CCAGGTCT	ACTGC GT		
			GGTCCGGG	TGACG CA		
			ACC C			
GAM1490	UBE2G2	3'	TTACTGCAGTTTTAC	64865	CT	
			GT AA	ACTGCAGTAA		
			CA TTTGACGTCATT			
			T_			
GAM1490	UBE3A	3'	TTACTGTAGATCAACCTGATGA	4871	C	CTAAA
			TCA CAGGT	CTGCAGTAA		
			AGT GTCCA	GATGTCATT		
			A ACTA_			
GAM1490	UBE3A	3'	TTACTGTAGATCAACCTGATGA	55583	C	CTAAA
			TCA CAGGT	CTGCAGTAA		

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AGT GTCCA GATGTCATT
A ACTA_
GAM1490 UBE3A 3' TTACTGTAGATCAACCTGATGA 55596 C CTAAA
TCA CAGGT CTGCAGTAA
||| |||| |||||
AGT GTCCA GATGTCATT
A ACTA_
GAM1490 WNT5A 3' ACTGCAGTCCAGTTGGGA 12660 A GT AA
TC CCAG CT ACTGCAGT
|| ||| || |||||
AG GGTT GA TGACGTCA
_ _ CC
GAM1490 ZNF215 5' TTACTGCAATCTAGTAAGGCGG 25120 A AGGT AAC
TC CC CTA TGCAGTAA
|| || || |||||
GG GG GAT ACGTCATT
C AAT_ CTA
GAM1490 AAMP 3' TTGCCCAGACCTGGTGG 6561 AA ACT
TCACCAGGTCT GCAG
||||||| |||
GGTGGTCCAGA CGTT
CC_
GAM1490 ADMP 5' TACTGCAGCTTGAAGG 58869 AGG T A
CC TC AA CTGCAGTA
|| ||| |||||
GG AG TT GACGTCAT
A_ _ C
GAM1490 AKR1D1 3' ACTGCAGTCCGGCCTGGGTGA 19971 _ TAA
TCACC AGGTC ACTGCAGT
|||| |||| |||||
AGTGG TCCGG TGACGTCA
G CC_
GAM1490 AP1GBP1 3' ACTGCAGTGTGCAGTGA 23388 CAG CTAA
TCAC GT ACTGCAGT
||| || |||||
AGTG CG TGACGTCA
A_ TG_
GAM1490 AP1GBP1 3' ACTGCAGTGTGCAGTGA 54514 CAG CTAA
TCAC GT ACTGCAGT
||| || |||||
AGTG CG TGACGTCA
A_ TG_
GAM1490 C20orf121 5' ACTGACAGAAGACCTGGT 44275 AAA _
ACCAGGTCT CTG CAGT
|||||| ||| |||
TGGTCCAGA GAC GTCA
A_ A
GAM1490 CPR2 3' ACTGCAGTCCAGCCTGG 48087 T AA
CCAGG CT ACTGCAGT
|||| || |||||

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GGTCC GA TGACGTCA  
\_ CC  
GAM1490 DIS3 3' ACTGCAGTTCAGCCTGGATGA 30225 \_ T A  
TCA CCAGG CT AACTGCAGT  
||| ||||| || |||||  
AGT GGTCC GA TTGACGTCA  
A \_ C  
GAM1490 DNAJB5 3' ACTGCAGTGGCTGGAGA 24352 A G TAA  
TC CCAG TC ACTGCAGT  
|| ||||| || |||||  
AG GGTC GG TGACGTCA  
A \_ \_  
GAM1490 ELF4 5' TTACTGCAGCTCAGGGGGT 7440 AGG AAA  
ACC TCT CTGCAGTAA  
||| ||| |||||  
TGG GGA GACGTCATT  
G\_ CTC  
GAM1490 FIGN 5' TGGTCTCGACCTGGTGA 95646 TAA  
TCACCAGGTC ACTG  
||||||| |||  
AGTGGTCCAG TGGT  
CTC  
GAM1490 FLJ10597 3' ACTGCATCACACAGACTGGTGA 36313 G AAAC\_  
TCACCAG TCT TGCAGT  
||||||| ||| |||||  
AGTGGTC AGA ACGTCA  
\_ CACACT  
GAM1490 FLJ12750 3' ACTGCAGCCCTGGTGA 45120 TCTAAA  
TCACCAGG CTGCAGT  
||||||| |||||  
AGTGGTCC GACGTCA  
C\_  
GAM1490 FLJ14117 3' ACTGCACTCCAGCCTGGTGA 42897 CTAAAC  
TCACCAGGT TGCAGT  
||||||| |||||  
AGTGGTCCG ACGTCA  
ACCTC\_  
GAM1490 FLJ14457 3' TACTAGCTGGAAACTCTGGTGA 51388 \_ AACT \_  
TCACCAGG TCTA GC AGTA  
||||||| ||| || |||||  
AGTGGTCT AGGT CG TCAT  
CAA \_ A  
GAM1490 FLJ20340 3' ACTGTACTCCAGCCTGGTGA 34971 CTAAAC  
TCACCAGGT TGCAGT  
||||||| |||||  
AGTGGTCCG ATGTCA  
ACCTC\_  
GAM1490 FLJ20825 3' ACTGCAGTCCAGCCTGG 35692 T AA  
CCAGG CT ACTGCAGT  
||||| || |||||

		GGTCC GA TGACGTCA		
		_ CC		
GAM1490	H-L(3)MBT	3' TTACTGCAAGGATCCT	31310	_ AAAC
		AGG TCT TGCAGTAA		
		TCC AGG ACGTCATT		
		T A__		
GAM1490	HEYL	3' ACCACAGCCAAGGCCTGGAGA	27388	A AAA CA
		TC CCAGGTCT CTG GT		
		AG GGTCCGGA GAC CA		
		A ACC AC		
GAM1490	HNRPA3	3' TTACTGCAGCTTAAACAGG	19263	AG C A
		CC GT TAA CTGCAGTAA		
		GG CA ATT GACGTCATT		
		A_ A C		
GAM1490	HSA250303	3' TACTGCAGTCCAGCCTGG	37412	T AA
		CCAGG CT ACTGCAGTA		
		GGTCC GA TGACGTCAT		
		_ CC		
GAM1490	HSGP25L2G	3' CAGCCTAGACCTGCTGA	62166	C AA
		TCA CAGGTCTA CTG		
		AGT GTCCAGAT GAC		
		C CC		
GAM1490	HSH2	3' ACTGCAGTCCAGCCTGGATGA	51670	_ T AA
		TCA CCAGG CT ACTGCAGT		
		AGT GGTCC GA TGACGTCA		
		A _ CC		
GAM1490	KIAA1909	5' CTGCATTTAGGCCTG	73839	C
		CAGGTCTAAA TGCAG		
		GTCCGGATTT ACGTC		
		-		
GAM1490	LIM	3' ACTGCACTCCAGCCTGGTGA	21300	CTAAAC
		TCACCAGGT TGCAGT		
		AGTGGTCCG ACGTCA		
		ACCTC_		
GAM1490	LIMK2	3' TTGTACATAGACCTGATGA	33631	C AAC
		TCA CAGGTCTA TGCAG		
		AGT GTCCAGAT ATGTT		
		A AC_		
GAM1490	LIMK2	3' TTGTACATAGACCTGATGA	18731	C AAC
		TCA CAGGTCTA TGCAG		



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AGT GTCCAGAT ATGTT
A AC_
GAM1490 LSM5 3' TACTGCAGTAGCCAGTGG 24639 CA T AA
TCAC GG CT ACTGCAGTA
|||| ||| |||||
GGTG CC GA TGACGTCAT
A_ _ _
GAM1490 MACMARCKS 3' ACTGCCTGGACCTGGTG 43447 AACT
CACCAGGTCTA GCAGT
||||||| |||
GTGGTCCAGGT CGTCA
C_
GAM1490 MGC17998 3' ACTCCAGCCTGGTGA 58740 TCTAAA C
TCACCAGG CTG AGT
||||| ||| |||
AGTGGTCC GAC TCA
_ C
GAM1490 MGC23280 5' ACTACAACCTGGTGA 58391 CTAAAC C
TCACCAGGT TG AGT
||||| ||| |||
AGTGGTCCA AC TCA
_ A
GAM1490 MGC2474 3' ACTGCAGCCTAGACCTGCTGG 43712 C AA
TCA CAGGTCTA CTGCAGT
||| ||||| |||||
GGT GTCCAGAT GACGTCA
C CC
GAM1490 MGC4663 3' ACTGCCAACTTGGTGA 44503 CTAAACT
TCACCAGGT GCAGT
||||| |||
AGTGGTTCA CGTCA
AC_
GAM1490 NFAT5 5' GCGCGGACCTAGACCTGG 56944 AA_ A
CCAGGTCTA CTGC GT
||||| ||| |||
GGTCCAGAT GGCG CG
CCA _
GAM1490 PTK9L 3' ACTGCAGTTTGGGATGGTTGA 23466 _ GG
TCA CCA TCTAAACTGCAGT
||| ||| |||||
AGT GGT GGGTTTGACGTCA
T A_
GAM1490 PTR4 3' TTA CTGCAGCGTGTCTCCTGG 74057 TC_ AA
CCAGG TA CTGCAGTAA
|||| ||| |||||
GGTCC GT GACGTCATT
TCT GC
GAM1490 RAB35 3' GCGCCTGGACCTGGCGA 22480 A AAC
TC CCAGGTCTA TGC
|| ||||| |||

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			AG GGTCCAGGT GCG		
			C CC_		
GAM1490	SCN12A	3'	ACTGCACTCCAGCCTGGTGA 26221	CTAAAC	
			TCACCAGGT TGCAGT		
			AGTGGTCCG ACGTCA		
			ACCTC_		
GAM1490	SULT1C2	3'	CAGCCTAGACCTGCTGA 21675 C AA		
			TCA CAGGTCTA CTG		
			AGT GTCCAGAT GAC		
			C CC		
GAM1490	TOMM34	3'	ACTGCAGTTCATCTG 22332 CTA		
			CAGGT AACTGCAGT		
			GTCTA TTGACGTCA		
			C_		
GAM1490	VEZATIN	3'	TTACTGCAGCTTAGGGATGG 34229 GG A		
			CCA TCTAA CTGCAGTAA		
			GGT GGATT GACGTCATT		
			AG C		
GAM1490	ZFP106	3'	ACTGCACTCCAGCCTGGTGA 42460 CTAAAC		
			TCACCAGGT TGCAGT		
			AGTGGTCCG ACGTCA		
			ACCTC_		
GAM1490	LOC120227	5'	ACTGCCAACTTGGTGA 74006 CTAAACT		
			TCACCAGGT GCAGT		
			AGTGGTTCA CGTCA		
			AC_____		
GAM1490	LOC124411	3'	ACTTCAGAAAAGCCTGGTGA 74282 T AAA C		
			TCACCAGG CT CTG AGT		
			AGTGGTCC GA GAC TCA		
			_ AAA T		
GAM1490	LOC126282	3'	ACTGCACTTCAGCCTGGTGA 74468 T A C		
			TCACCAGG CT AA TGCAGT		
			AGTGGTCC GA TT ACGTCA		
			_ C C		
GAM1490	LOC127281	3'	TAGTCCAGACCTGGGGA 74650 A AA		
			TC CCAGGTCT ACTG		
			AG GGTCCAGA TGAT		
			G CC		
GAM1490	LOC142779	3'	ACTGCATTGCAGCCTGGTGA 76390 CTA C		
			TCACCAGGT AA TGCAGT		

	AGTGGTCCG TT ACGTCA	
	ACG _	
GAM1490 LOC145078 3'	TTACTGCAGCTTAAACAGG 60294	AG C A
	CC GT TAA CTGCAGTAA	
	GG CA ATT GACGTCATT	
	A_ A C	
GAM1490 LOC148137 3'	CTGTAACCTAGACCTGG 58427	AAC
	CCAGGTCTA TGCAG	
	GGTCCAGAT ATGTC	
	CCA	
GAM1490 LOC148981 3'	TTACTGCAGCTTAAACAGG 84319	AG C A
	CC GT TAA CTGCAGTAA	
	GG CA ATT GACGTCATT	
	A_ A C	
GAM1490 LOC149332 5'	TTACTGCATTTAACATGATGA 84399	C G C C
	TCA CA GT TAAA TGCAGTAA	
	AGT GT CA ATTT ACGTCATT	
	A A _ _	
GAM1490 LOC150481 3'	ACTGCATTCCAGCCTGGTGA 79880	CTAAAC
	TCACCAGGT TGCAGT	
	AGTGGTCCG ACGTCA	
	ACCTT_	
GAM1490 LOC150935 3'	GGTTCTAGTACCTGGTGA 80037	_ _
	TCACCAGGT CTA AACT	
	AGTGGTCCA GAT TTGG	
	T C	
GAM1490 LOC151248 3'	ACTGCACTCCAGCCTGGTGA 80182	CTAAAC
	TCACCAGGT TGCAGT	
	AGTGGTCCG ACGTCA	
	ACCTC_	
GAM1490 LOC151258 5'	TTACTGCAGAAATGATGACCTG 80197	TAAA__
GT	ACCAGGTC CTGCAGTAA	
	TGGTCCAG GACGTCATT	
	TAGTAAA	
GAM1490 LOC153883 5'	TACTGCAGTTTTTAGTG 80985	CAGGTCT
	CAC AAACCTGCAGTA	
	GTG TTTGACGTCAT	
	ATT__	
GAM1490 LOC158450 3'	TACTGAACAGCCTGGTGA 81932	CTAAACTG
	TCACCAGGT CAGTA	

		AGTGGTCCG	GTCAT		
		ACAA_____			
GAM1490	LOC158504	3'	TACTGAACAGCCTGGTGA	81940	CTAAACTG
			TCACCAGGT CAGTA		
			AGTGGTCCG GTCAT		
			ACAA_____		
GAM1490	LOC166979	5'	CTGACTTAGACCTGGGA	82669	A ACTG
			TC CCAGGTCTAA CAG		
			AG GGTCCAGATT GTC		
			_ CA_		
GAM1490	LOC202404	5'	TTGTGTTTCAGCCTGGTGA	89169	T A T
			TCACCAGG CT AAC GCAG		
			AGTGGTCC GA TTG TGTT		
			_ C _		
GAM1490	LOC202934	3'	TACTGCAGCACCACCTAGTGG	90426	C CTAA
			TCAC AGGT CTGCAGTA		
			GGTG TCCA GACGTCAT		
			A CCAC_		
GAM1490	LOC220988	3'	TTACTGCAGCTTAAACAGG	90849	AG C A
			CC GT TAA CTGCAGTAA		
			GG CA ATT GACGTCATT		
			A_ A C		
GAM1490	LOC253981	3'	TTACTTTTCCCTTTAGGCCTGG	95835	CTGC_
			CCAGGTCTAAA AGTAA		
			GGTCCGGATTT TCATT		
			CCCTTT		
GAM1490	LOC255190	3'	TTACTGCAGCTTAAACAGG	97690	AG C A
			CC GT TAA CTGCAGTAA		
			GG CA ATT GACGTCATT		
			A_ A C		
GAM1490	LOC255465	3'	TACTGCAGCGCCACCTAGTGG	97300	C CTAA
			TCAC AGGT CTGCAGTA		
			GGTG TCCA GACGTCAT		
			A CCGC_		
GAM1490	LOC256433	5'	ACTGTAGTAAAACCCAGTGA	97475	CA CTAA
			TCAC GGT ACTGCAGT		
			AGTG CCA TGATGTCA		
			AC AAA_		
GAM1490	LOC57149	3'	ACTGCAGTCACCTTTGG	39935	_ CTAA
			CCA GGT ACTGCAGT		

GGT CCA TGACGTCA  
TT C\_\_\_\_  
GAM1490 LOC92521 3' TACTGCAGCTTTTCCTGG 69598 TCT A  
CCAGG AA CTGCAGTA  
||||| || |||||  
GGTCC TT GACGTCAT  
TT\_ C  
GAM1490 LOC92979 3' ACCACGGTGACTTGGTGA 56436 TAA CA  
TCACCAGGTC ACTG GT  
||||||| ||| ||  
AGTGGTTCAG TGGC CA  
\_\_\_\_ AC  
GAM1491 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
GTA GGAT GGGTTGTTT  
||| ||| |||||  
CGT CCTA CCCAACAAA  
C CGTG\_  
GAM1491 LCT 3' AACCGTAAAAATCCTT 9697 G  
AAGGATTTTTTA GGTT  
||||||| |||  
TTCCTAAAAAT CCAA  
G  
GAM1491 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
GTAAGGATTTTTAGGGTTGTTT  
|||||||  
CATTCCTAAAAATCCCAACAAA  
GAM1491 FBXO30 3' AACTAAAAAAATCCTGAC 49573 A AG  
GT AGGATTTTT GGTT  
|| ||||| |||  
CA TCCTAAAAA TCAA  
G AA  
GAM1491 KIAA0494 3' AACAACCCTTACTTAC 28736 GATTTT  
GTAAG AGGGTTGTT  
||||| |||||  
CATTC TCCCAACAA  
AT\_\_\_\_  
GAM1491 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
TAAG TTTT GGGTTGTTT  
||| ||| |||||  
GTTC AAAA CCCAACAAA  
\_\_\_\_ C  
GAM1491 SMT3H2 3' AACAACATAAAAAATCCTTGC 22670 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_  
GAM1491 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_  
GTAAGGATTTTT GGGTT  
||||||| |||||

		CGTTCCTAAAAA	TCCAA		
		GTA			
GAM1491	LOC129831 3'	AAACAACCCCAATGTCC	74889	TT	A
		GGAT TT GGGTTGTTT			
		CCTG AA CCCAACAAA			
		T_ C			
GAM1491	LOC133088 5'	AAACAAAATAGAAAAATCCCTG	75075	A	AGGG_
	C	GTA GGATTTTT TTGTTT			
		CGT CCTAAAAA AACAAA			
		C GATAA			
GAM1491	LOC148089 3'	GGCCCTAAAAATTCCTAC	78637	A	
		GTA GGATTTTTTAGGGTT			
		CAT CTTAAAAATCCCGG			
		C			
GAM1491	LOC154547 3'	AACAACATAAAAAATCCTTGC	76050		GG
		GTAAGGATTTTTTA GTTGTT			
		CGTTCCTAAAAAT CAACAA			
		A_			
GAM1491	LOC158104 3'	ACAGCCAAAAATCCTTA	60313	AG	
		TAAGGATTTTT GTTGT			
		ATTCCTAAAAA CCGACA			
		—			
GAM1491	LOC205880 5'	AAACAACCATCATCCTGAC	90709	A	TTTTAG
		GT AGGAT GGTGTTT			
		CA TCCTA CCAACAAA			
		G CTA_			
GAM1491	LOC221561 3'	AACAACATAAAAAATCCTTGC	92130		GG
		GTAAGGATTTTTTA GTTGTT			
		CGTTCCTAAAAAT CAACAA			
		A_			
GAM1491	LOC257591 3'	AACAACATAAAAAATCCTTGC	97840		GG
		GTAAGGATTTTTTA GTTGTT			
		CGTTCCTAAAAAT CAACAA			
		A_			
GAM1491	LOC51145 3'	AGCTAAAATCCTTAC	32393	TAG	
		GTAAGGATTTT GTT			
		CATTCCTAAAA TCGA			
		—			
GAM1492	CETN1 3'	ATAAAATCTAATACTGGCCCA	95258	A _	TT
		TG GGC AGTATTA ATTTTAT			

			AC CCG TCATAAT TAAAATA		
			_ G _ C _		
GAM1492	MYC	3'	ATAATGTAAACTGCCTCA 10157	AT_	
			TGAGGCAGT TATTAT		
			ACTCCGTCA GTAATA		
			AAT		
GAM1492	MYF5	3'	AAAATATAATACTGCCT 18789	T	
			AGGCAGTATTAT ATTTT		
			TCCGTCATAATA TAAAA		
			-		
GAM1492	PSMD5	3'	ATAAAATAAAAACTGCC 17301	TA A	
			GGCAG TT TTATTTTAT		
			CCGTC AA AATAAAATA		
			CA _		
GAM1492	SLC25A12	3'	ATAAAATAATCATTTGCCCA 13520	A T T	
			TG GGCAG AT ATTATTTTAT		
			AC CCGTT TA TAATAAAATA		
			- _ C		
GAM1492	UBE4A	3'	ATAAAATAAGCTTCTGCCT 16559	TATTA	
			AGGCAG TTATTTTAT		
			TCCGTC AATAAAATA		
			TTCG_		
GAM1492	CG018	3'	ATAAAATAAGCCTGCCTT 53390	TATTA	
			GAGGCAG TTATTTTAT		
			TTCCGTC AATAAAATA		
			CG__		
GAM1492	dJ383J4.3	3'	AAAGTGAGACTCTGCCTCA 66942	TATTA	
			TGAGGCAG TTATTTT		
			ACTCCGTC AGTGAAA		
			TCAG_		
GAM1492	KIAA0527	3'	ATAAAATAACCTCTGTCTCA 95792	TATTA	
			TGAGGCAG TTATTTTAT		
			ACTCTGTC AATAAAATA		
			TCC__		
GAM1492	KIAA0934	3'	ATAAAATAAGTTAACTTCCTCA 64217	C ATTA	
			TGAGG AGT TTATTTTAT		
			ACTCC TCA AATAAAATA		
			T ATTG		
GAM1492	KIAA1915	3'	TATAAAATAAGCAGTCAATGCT 73283	A_____	
			GCCTCA GCAGTATT TTATTTTAT A		

			CGTCGTAA	AATAAAATA	T	
			CTGACG	III		
GAM1492	KIAA1918	3'	TAAAATATCCTGCCTTA	73165		TATTAT
			TGAGGCAG	TATTTTA		
			ATTCCGTC	ATAAAAT		
			CT____			
GAM1492	PLA2G3	3'	AATAATACATGCCTCA	31682		_
			TGAGGCA	GTATTATT		
			ACTCCGT	CATAATAA		
			A			
GAM1492	TP53TG3	3'	TGATAGACACTGCCTCA	31108		A_
			TGAGGCAGT	TTATTA		
			ACTCCGTCA	GATAGT		
			CA			
GAM1492	LOC158629	5'	ATAAAATAATAAATTGCC	86873		A
			GGCAGT	TTATTATTTTAT		
			CCGTTA	AATAATAAAATA		
			-			
GAM1492	LOC221143	3'	ATAAAATAGCTCTGCCTC	93563		TATTA
			GAGGCAG	TTATTTTAT		
			CTCCGTC	GATAAAATA		
			TC____			
GAM1492	LOC51241	3'	AAAATGTGAATACTGCTCCA	33206	AG	AT
			TG	GCAGTATT TATTTT		
			AC	CGTCATAA GTAAAA		
			CT	GT		
GAM1493	ACP1	3'	GCTCCCCAGTGCTACCTCT	15033	AG	CA
			AGAGGTAGTA	TGG GAGC		
			TCTCCATCGT	ACC CTCG		
			G_	C_		
GAM1493	ACP1	3'	GCTCCCCAGTGCTACCTCT	23021	AG	CA
			AGAGGTAGTA	TGG GAGC		
			TCTCCATCGT	ACC CTCG		
			G_	C_		
GAM1493	ACPT	3'	CTCCGCCCACCTGCCCT	54982	A	TAA _A
			AG	GGTAG GTGG C GAG		
			TC	CCGTC CACC G CTC		
			C	__ C C		
GAM1493	ACPT	3'	CTCCGCCCACCTGCCCT	54988	A	TAA _A
			AG	GGTAG GTGG C GAG		



			TC CCGTC CACC G CTC		
			C ____ C C		
GAM1493	ADD2	3'	CTCTGTCCTCCTTACTACC 33929	T__	
			GGTAGTAAG GGCAGAG		
			CCATCATTG CTGTCTC		
			CTC		
GAM1493	ADD2	3'	CTCTGTCCTCCTTACTACC 33940	T__	
			GGTAGTAAG GGCAGAG		
			CCATCATTG CTGTCTC		
			CTC		
GAM1493	ADD2	3'	CTCTGTCCTCCTTACTACC 33957	T__	
			GGTAGTAAG GGCAGAG		
			CCATCATTG CTGTCTC		
			CTC		
GAM1493	AKAP2	5'	GCTCTGCCCGCCGCCCT 23262	A TA AAGT	
			AG GG GT GGCAGAGC		
			TC CC CG CCGTCTCG		
			C GC C__		
GAM1493	ANXA3	3'	CTCCACCTTACTTCT 17635	TAA C	
			AGAGGTAG GTGG AG		
			TCTTCATT CACC TC		
			C__ _		
GAM1493	APM1	3'	GCTCACTGCTACCTCT 16595	A _	
			AGAGGTAGTA GTG GC		
			TCTCCATCGT CAC CG		
			_ T		
GAM1493	ARHGAP6	3'	GCTCTGCCACTTTCAACCT 25517	AGT	
			AGGT AAGTGGCAGAGC		
			TCCA TTCACCGTCTCG		
			ACT		
GAM1493	ARHGAP6	3'	GCTCTGCCACTTTCAACCT 20408	AGT	
			AGGT AAGTGGCAGAGC		
			TCCA TTCACCGTCTCG		
			ACT		
GAM1493	B4GALT1	3'	GCTCTGCTAGCCCACTC 7672	_ A AAG	
			GAG GT GT TGGCAGAGC		
			CTC CA CG ATCGTCTCG		
			A C ____		
GAM1493	C2	3'	GCCCCTCCATCTTCTACCTCT 3558	T _ C A_	
			AGAGGTAG AAG TGG AG GC		

			TCTCCATC TTC ACC TC CG		
			_ T _ CC		
GAM1493	CA7	3'	GCCCTCTCGGCATTACCTCT 60199	A__ T_	
			AGAGGTAGT AG GGC		
			TCTCCATTA TC CCG		
			CGGC TC		
GAM1493	CA7	3'	GCTCTGCCATGCACGCACCTC 60200	A_ AA	
			GAGGT GT GTGGCAGAGC		
			CTCCA CA TACCGTCTCG		
			CG CG		
GAM1493	CAPS	3'	GCCTGTCACTCCCCACCCCT 14480	A AGTA A	
			AG GGT AGTGGCAG GC		
			TC CCA TCACTGTC CG		
			C CCCC _		
GAM1493	CASP2	3'	CTCTGTAACACCTCT 6898	AGTAA G	
			AGAGGT GT GCAGAG		
			TCTCCA CA TGTCTC		
			C__ A		
GAM1493	CASP2	3'	CTCTGTAACACCTCT 52140	AGTAA G	
			AGAGGT GT GCAGAG		
			TCTCCA CA TGTCTC		
			C__ A		
GAM1493	CASP2	3'	CTCTGTAACACCTCT 52153	AGTAA G	
			AGAGGT GT GCAGAG		
			TCTCCA CA TGTCTC		
			C__ A		
GAM1493	CASP2	3'	CTCTGTAACACCTCT 52168	AGTAA G	
			AGAGGT GT GCAGAG		
			TCTCCA CA TGTCTC		
			C__ A		
GAM1493	CASP3	5'	CCTGCACCTGCCTCT 15099	TAA G A	
			AGAGGTAG GTG CAG G		
			TCTCCGTC CAC GTC C		
			_ _ C		
GAM1493	CCND2	5'	GCTCTGCTCGCCCACCACC 8293	A AA _	
			GGT GT GTG GCAGAGC		
			CCA CA CGC CGTCTCG		
			C CC T		
GAM1493	CD80	3'	CTGTTTTACCCACTACCTC 17767	AA _	
			GAGGTAGT GTG GCAG		

			CTCCATCA CAT TGTC		
			CC TT		
GAM1493	CDC7L1	5'	CTGCTTTGCTCCCCCT 13029	A T	GT
			AG GG AGTAA GGCAG		
			TC CC TCGTT TCGTC		
			C C _		
GAM1493	CHST5	3'	CTCTTGCCCCTACCTCT 24024	TAAGT	_
			AGAGGTAG GGCA GAG		
			TCTCCATC CCGT CTC		
			C _ _ T		
GAM1493	CKAP1	5'	GCTCTTGCCACTCCTACCTC 73539	TA	_
			GAGGTAG AGTGGCA GAGC		
			CTCCATC TCACCGT CTCG		
			C _ T		
GAM1493	CLASP1	3'	CTCTGCCAAGACCCTC 65301	TA AAG	
			GAGG GT TGGCAGAG		
			CTCC CA ACCGTCTC		
			_ GA _		
GAM1493	CLASP2	3'	GCTCAAATTCTCTACCTCT 64594	TA GGCA	
			AGAGGTAG AGT GAGC		
			TCTCCATC TTA CTCG		
			TC AA _		
GAM1493	CPLX2	3'	CTCCACCTGTTACTACTTCT 21833	GT CA	
			AGAGGTAGTAA GG GAG		
			TCTTCATCATT CC CTC		
			GT AC		
GAM1493	CREBL2	3'	CTCCATTTACTACCT 7144	C	
			AGGTAGTAAGTGG AG		
			TCCATCATTTACC TC		
			-		
GAM1493	CTSD	3'	GCTCTGCCACCCTACCT 8584	TAA	
			AGGTAG GTGGCAGAGC		
			TCCATC CACCGTCTCG		
			C _		
GAM1493	DLST	3'	GCCTCTTCTACCTCT 8645	T T	
			AGAGGTAG AAG GGC		
			TCTCCATC TTC CCG		
			- T		
GAM1493	EZH1	3'	GTCACCTTACTACCTC 8825	-	
			GAGGTAGTAAG TGGC		

			CTCCATCATTC ACTG		
			C		
GAM1493	FABP3	3'	CTCTGCCAATCGGCTACC 71423	AAG_	
			GGTAGT TGGCAGAG		
			CCATCG ACCGTCTC		
			GCTA		
GAM1493	FACL4	5'	CTCTGCCACACCACC 43398	A AA	
			GGT GT GTGGCAGAG		
			CCA CA CACCGTCTC		
			C _		
GAM1493	FACL4	5'	CTCTGCCACACCACC 15508	A AA	
			GGT GT GTGGCAGAG		
			CCA CA CACCGTCTC		
			C _		
GAM1493	FCN3	3'	CTTTGCCAACCACCTCT 13367	A AAG	
			AGAGGT GT TGGCAGAG		
			TCTCCA CA ACCGTTTC		
			C _		
GAM1493	FGD1	3'	GCTCTGCCACTGACCCT 15525	TA A	
			AGG GT AGTGGCAGAGC		
			TCC CA TCACCGTCTCG		
			_ G		
GAM1493	FSTL3	3'	CTCCAGCTTCCCCACTGCCTCT 19607	AAGT_ A_	
			AGAGGTAGT GGC GAG		
			TCTCCGTCA TCG CTC		
			CCCCT AC		
GAM1493	GAB2	3'	CTCCACCCACTACCTC 24493	AA C	
			GAGGTAGT GTGG AG		
			CTCCATCA CACC TC		
			CC _		
GAM1493	GAB2	3'	CTCCACCCACTACCTC 54450	AA C	
			GAGGTAGT GTGG AG		
			CTCCATCA CACC TC		
			CC _		
GAM1493	GABRE	5'	CTTTGTCACTGCCTC 41776	AGTA	
			GAGGT AGTGGCAGAG		
			CTCCG TCACTGTTTC		
			_____		
GAM1493	GABRE	5'	CTTTGTCACTGCCTC 41785	AGTA	
			GAGGT AGTGGCAGAG		

CTCCG TCACTGTTTC

GAM1493 GABRE 5' CTTTGTCACTGCCTC 41808 AGTA  
GAGGT AGTGGCAGAG  
||||| |||||  
CTCCG TCACTGTTTC

GAM1493 GALNT2 3' CTCCGCCACGCTTCT 15598 AGTAA A  
AGAGGT GTGGC GAG  
||||| |||||  
TCTTCG CACCG CTC  
C

GAM1493 GCGR 5' GCTCTGCCACTCAGCTGCCCT 3856 A A\_  
AG GGTAGT AGTGGCAGAGC  
|| ||||| |||||  
TC CCGTCG TCACCGTCTCG  
AC

GAM1493 GCK 5' CTCTGCCAGACTCTCCTCT 53179 T TAAG  
AGAGG AG TGGCAGAG  
||||| || |||||  
TCTCC TC ACCGTCTC  
TCAG

GAM1493 GGCX 3' CTGCCACTTGTAATTTT 5879 AG  
GAGGT TAAGTGGCAG  
||||| |||||  
TTTTA GTTCACCGTC  
AT

GAM1493 GPRK6 3' GCTCAGGCTGCTACCTCT 9113 AAGT A\_  
AGAGGTAGT GGC GAGC  
||||||| ||| |||||  
TCTCCATCG TCG CTCG  
GA

GAM1493 GPT 5' GCCTTCACCCACTGCCTCT 17964 AA C A  
AGAGGTAGT GTGG AG GC  
||||||| ||||| ||  
TCTCCGTCA CACT TC CG  
CC \_ \_

GAM1493 HOXC13 3' CTTTGCCCCACTGCCTC 59685 AAGT  
GAGGTAGT GGCAGAG  
||||||| |||||  
CTCCGTCA CCGTTTC  
CC\_

GAM1493 HYAL3 3' GCCCCTGCCACTGCCTCT 13052 AGTA A\_  
AGAGGT AGTGGCAG GC  
||||| ||||| ||  
TCTCCG TCACCGTC CG  
CC

GAM1493 ICOS 3' CTATCATACTACCTCT 23905 AA GC  
AGAGGTAGT GTG AG  
||||||| ||| ||

TCTCCATCA TAC TC  
 — TA  
 GAM1493 IGF2 5' CTCTGTCTCTCCCACTATCTCT 5219 A\_\_ T  
 AGAGGTAGT AG GGCAGAG  
 ||||| || |||||  
 TCTCTATCA TC CTGTCTC  
 CCC T  
 GAM1493 IL22RA2 3' GCCCCTCCTGCTCACTGCCTCT 53692 A TG C A\_  
 AGAGGTAGT AG G AG GC  
 ||||| || | ||  
 TCTCCGTCA TC C TC CG  
 C GT C CC  
 GAM1493 IL2RB 3' GCTCCCTCACACCCCTCT 6074 TA AA CA  
 AGAGG GT GTGG GAGC  
 |||| || ||| |||  
 TCTCC CA CACT CTCG  
 CC \_\_ CC  
 GAM1493 ITPKB 3' CTCTGCCATGCTGAGCTC 9430 G\_ AA  
 GAG TAGT GTGGCAGAG  
 ||| ||| |||||  
 CTC GTCG TACCGTCTC  
 GA \_\_  
 GAM1493 ITPR3 3' CTCTGCCAGACACCCT 9455 A A AAG  
 AG GGT GT TGGCAGAG  
 || ||| || |||||  
 TC CCA CA ACCGTCTC  
 \_ \_ G\_  
 GAM1493 KCNAB1 3' GCCCTGCCACTATTGGCTACT 60927 A\_\_ A  
 GGTAGT AGTGGCAG GC  
 ||||| ||||| ||  
 TCATCG TCACCGTC CG  
 GTTA C  
 GAM1493 KCNK4 5' CTCTGCCACCCACCTC 52806 AGTAA  
 GAGGT GTGGCAGAG  
 |||| |||||  
 CTCCA CACCGTCTC  
 CC\_\_  
 GAM1493 KIF3C 3' CTCTCCCACTGACCTCT 9601 AGTA C  
 AGAGGT AGTGG AGAG  
 ||||| ||||| |||  
 TCTCCA TCACC TCTC  
 G\_\_ C  
 GAM1493 KIF5C 3' CTCTCCTCACTACTTC 15734 AAGT C  
 GAGGTAGT GG AGAG  
 ||||| || |||  
 CTTTCATCA CC TCTC  
 CT\_\_ \_  
 GAM1493 KLK2 3' GCCCCTGTCCACCCCTACCTC 18690 TAA \_\_ A\_  
 T AGAGGTAG GTGG CAG GC  
 ||||| ||| ||| ||

			TCTCCATC CACC GTC CG		
			CC_ CT CC		
GAM1493	LARS2	3'	GCTCTGCCTTAGGCACTTCT 31057	A	AAGT
			AGAGGT GT GGCAGAGC		
			TCTTCA CG CCGTCTCG		
			_ GATT		
GAM1493	LASS2	3'	CCCTTACCCTACCTCT 67684	_	T
			AGAGGTA GTAAG GG		
			TCTCCAT CATTG CC		
			CC _		
GAM1493	LIM2	5'	GCTCTGCCACTCAGATC 47667	AGTA	
			GGT AGTGGCAGAGC		
			CTA TCACCGTCTCG		
			GAC_		
GAM1493	LRP1	5'	GCTCGGAACTCTACCTCT 9805	TA	GGCA
			AGAGGTAG AGT GAGC		
			TCTCCATC TCA CTCG		
			_ AGG_		
GAM1493	LTBP2	3'	GCCCTGTCCACCACCTTT 4723	AGTAA	_ A
			AGAGGT GTGG CAG GC		
			TTTCCA CACC GTC CG		
			C_ T C		
GAM1493	LTBP2	3'	TTTTGCCACACCTC 4725	AGTAA	
			GAGGT GTGGCAGAG		
			CTCCA CACCGTTTT		
			_____		
GAM1493	MDFI	3'	GCCGTAGCTCTCTACCTCT 18772	TA	_____
			AGAGGTAG AGT GGC		
			TCTCCATC TCG CCG		
			TC ATG		
GAM1493	METTL1	3'	GCTCAATTACCACTTCT 18124	A	G _
			AGAGGT GTAA TG GC		
			TCTTCA CATT AC CG		
			C A T		
GAM1493	METTL1	3'	GCTCAATTACCACTTCT 43509	A	G _
			AGAGGT GTAA TG GC		
			TCTTCA CATT AC CG		
			C A T		
GAM1493	METTL1	3'	GCTCAATTACCACTTCT 43515	A	G _
			AGAGGT GTAA TG GC		

			TCTTCA CATT AC CG		
			C A T		
GAM1493 MFNG	5'	GCCTCAGTCCTACCTCT	10005	TA	___
		AGAGGTAG AGT GGC			
		TCTCCATC TCG CCG			
		C_ ACT			
GAM1493 MIA	3'	GCCCTGCCGTTTCCCCTC	21526	TAGT	A
		GAGG AAGTGGCAG GC			
		CTCC TTTGCCGTC CG			
		CC_ C			
GAM1493 MN1	5'	CTCTGCCACGGA CTCC	10091	T	AA
		GG AGT GTGGCAGAG			
		CC TCA CACCGTCTC			
		_ GG			
GAM1493 MTCP1	5'	CTCCCAGCTACCTCT	26431	AAG	C
		AGAGGTAGT TGG AG			
		TCTCCATCG ACC TC			
		_ C			
GAM1493 NPAS1	3'	CTCTGCCCGTAGCCCT	59880	A	AG AGT
		AG GGT TA GGCAGAG			
		TC CCG AT CCGTCTC			
		_ _ GC_			
GAM1493 NRXN2	5'	GCTCTGCTACCCACCCTC	57014	TA	AA
		GAGG GT GTGGCAGAGC			
		CTCC CA CATCGTCTCG			
		_ CC			
GAM1493 NRXN2	5'	GCTCTGCTACCCACCCTC	30628	TA	AA
		GAGG GT GTGGCAGAGC			
		CTCC CA CATCGTCTCG			
		_ CC			
GAM1493 NXF5	3'	CTTCATCACTACCTCT	52509	AA	C
		AGAGGTAGT GTGG AG			
		TCTCCATCA TACT TC			
		C_ _			
GAM1493 NXF5	3'	CTTCATCACTACCTCT	52514	AA	C
		AGAGGTAGT GTGG AG			
		TCTCCATCA TACT TC			
		C_ _			
GAM1493 NXF5	3'	CTTCATCACTACCTCT	52518	AA	C
		AGAGGTAGT GTGG AG			



			TCTCCATCA TACT TC		
			C_ _		
GAM1493	NXF5	3'	CTTCATCACTACCTCT 52522	AA	C
			AGAGGTAGT GTGG AG		
			TCTCCATCA TACT TC		
			C_ _		
GAM1493	OLR1	3'	CTCTACCACTTACGGAC 10335	A_	C
			GT GTAAGTGG AGAG		
			CA CATTACAC TCTC		
			GG A		
GAM1493	P3	5'	GCTCTGCTAGCCACC 39066	A	AAG
			GGT GT TGGCAGAGC		
			CCA CG ATCGTCTCG		
			C _		
GAM1493	PBX3	3'	GCTCACTTACTACCTCT 20565		-
			AGAGGTAGTAAGTG GC		
			TCTCCATCATTAC CG		
			T		
GAM1493	PEX14	3'	GCTAGCGTCCCTACTGCCTC 63644	A T	AG_
			GAGGTAGTA G GGC AGC		
			CTCCGTCAT C CTG TCG		
			_C CGA		
GAM1493	PIG3	5'	GCTCTGCCGCATCCAGCCCT 16877	A	AGTAA
			AG GGT GTGGCAGAGC		
			TC CCG CGCCGTCTCG		
			_ ACCTA		
GAM1493	PIG8	3'	GCTCTGCCAAGGGCCCCTCT 16871	TA	AAG
			AGAGG GT TGGCAGAGC		
			TCTCC CG ACCGTCTCG		
			C_ GGA		
GAM1493	PIP5K1A	3'	GCTCTGCCAGAAGCAGCT 13056	A	AAG
			GGT GT TGGCAGAGC		
			TCG CG ACCGTCTCG		
			A AAG		
GAM1493	PKD1	3'	GCCCCTAAGTTATTACCTCT 4311		___ T
			AGAGGTAGTA AG GGC		
			TCTCCATTAT TC CCG		
			TGAA C		
GAM1493	PLAGL1	3'	GCTTAAACCTACTACCTC 10613	A	GGCA
			GAGGTAGTA GT GAGC		

CTCCATCAT CA TTCG  
C AA\_\_

GAM1493 PRPF31 3' GCCCTGCCACTGGCCCC 31571 TA A A  
GG GT AGTGGCAG GC  
|| || ||||| ||  
CC CG TCACCGTC CG  
C\_ G C

GAM1493 PTK7 3' CTCTGCCACTCATCTGCC 11016 TA\_  
GGTAG AGTGGCAGAG  
|||| |||||  
CCGTC TCACCGTCTC  
TAC

GAM1493 PTMS 3' CTCTGCCATTGTTCCACCTC 11034 AGTA\_  
GAGGT AGTGGCAGAG  
|||| |||||  
CTCCA TTACCGTCTC  
CCTTG

GAM1493 PXMP3 3' GCTCCTTCATTTTACTACTTCT 4348 \_ CA  
AGAGGTAGTAAG TGG GAGC  
||||||| || |||  
TCTTCATCATTT ACT CTCG  
T TC

GAM1493 RASGRP1 3' GCTCCTTCTTCACTACCTC 19207 \_ T CA  
GAGGTAGT AAG GG GAGC  
||||| || || |||  
CTCCATCA TTC TC CTCG  
C T \_

GAM1493 RORB 5' GCTCTGCCATCCACACC 22608 A AA  
GGT GT GTGGCAGAGC  
||| || |||||  
CCA CA TACCGTCTCG  
\_ CC

GAM1493 RTN3 3' CTCTGCCACTATCCCC 73901 TA A  
GG GTA GTGGCAGAG  
|| || |||||  
CC TAT CACCGTCTC  
CC \_

GAM1493 SDC1 3' CGCCCTGCCACTCACTAGGCC 11471 \_ A A III  
GGT AGT AGTGGCAG GC G  
||| || ||||| || |  
CCG TCA TCACCGTC CG C  
GA C C III

GAM1493 SEPN1 3' CCTGTCACTCCTCT 66366 TAGTA A  
AGAGG AGTGGCAG G  
|||| ||||| |  
TCTCC TCACTGTC C  
\_\_\_\_ C

GAM1493 SEPN1 3' GCTCTTCTACCTCT 66373 T T  
AGAGGTAG AAG GGC  
||||| || |||

TCTCCATC TTC TCG

GAM1493 SLC35A2 3' CTCCACACTATCTCT 18977 AA C  
AGAGGTAGT GTGG AG  
||||||| ||| ||  
TCTCTATCA CACC TC

GAM1493 SLC8A2 3' GCCCTCCACTACCTCT 66332 A\_ T  
AGAGGTAGT AG GGC  
||||||| || |||  
TCTCCATCA TC CCG

CC \_  
GAM1493 SLC9A1 3' GCTCTGCCTCTAACTCCCTC 70409 T A T  
GAGG AGT AG GGCAGAGC  
||| ||| || |||||  
CTCC TCA TC CCGTCTCG  
C A T

GAM1493 SMARCD1 3' CTCCACCCTGCCTCT 57433 TAA C  
AGAGGTAG GTGG AG  
||||||| ||| ||  
TCTCCGTC CACC TC  
C\_ \_

GAM1493 SMARCD1 3' CTCCACCCTGCCTCT 11815 TAA C  
AGAGGTAG GTGG AG  
||||||| ||| ||  
TCTCCGTC CACC TC  
C\_ \_

GAM1493 SMARCD3 3' GCTCCAGCATCACTCCTCT 11830 T AAGTG A\_  
AGAGG AGT GC GAGC  
||||| ||| || |||||  
TCTCC TCA CG CTCG  
\_ CTA\_ AC

GAM1493 STARD4 3' CTGCCCACACTATCTCT 57512 AAGT  
AGAGGTAGT GGCAG  
||||||| |||||  
TCTCTATCA CCGTC  
C\_

GAM1493 TAF4B 3' TTTGTTACTACCTGCC 87171 TA  
GGTAG AGTGGCAGA  
||||| |||||  
CCGTC TCATTGTTT  
CA

GAM1493 TAL1 5' GCCCTGCCTCTTTCTCTCC 12106 T\_ T T A  
GG AG AAG GGCAG GC  
|| || ||| ||||| ||  
CC TC TTC CCGTC CG  
TC T T C

GAM1493 TK1 3' GCCCTTCCTACCTCT 12304 T T  
AGAGGTAG AAG GGC  
||||||| ||| |||

TCTCCATC TTC CCG  
 C \_  
 GAM1493 TMPRSS2 3' CTCTACCATGGTTCTGCCTC 18965 TAA\_ C  
 GAGGTAG GTGG AGAG  
 ||||| ||| ||||  
 CTCCGTC TACC TCTC  
 TTGG A  
 GAM1493 TMPRSS3 5' CTGTGGCCTACTATCTCT 50535 A G  
 AGAGGTAGTA GT GCAG  
 ||||| || ||||  
 TCTCTATCAT CG TGTC  
 C G  
 GAM1493 TMPRSS3 5' CTGTGGCCTACTATCTCT 43794 A G  
 AGAGGTAGTA GT GCAG  
 ||||| || ||||  
 TCTCTATCAT CG TGTC  
 C G  
 GAM1493 TNFRSF1B 3' GCCCTGCCACTTTGGTAC 6524 G \_ A  
 GTA TAA GTGGCAG GC  
 ||| ||| ||||| ||  
 CAT GTT CACCGTC CG  
 G T C  
 GAM1493 TRPM2 3' GCCCTGCCACTCTCCC 12403 T TA A  
 GG AG AGTGGCAG GC  
 || || ||||| ||  
 CC TC TCACCGTC CG  
 C \_ C  
 GAM1493 UBE2V1 3' GCCCTGCCACCCTCTGCT 12519 TAA A  
 GGTAG GTGGCAG GC  
 |||| ||||| ||  
 TCGTC CACCGTC CG  
 TCC C  
 GAM1493 UBE2V1 3' GCCCTGCCACCCTCTGCT 42371 TAA A  
 GGTAG GTGGCAG GC  
 |||| ||||| ||  
 TCGTC CACCGTC CG  
 TCC C  
 GAM1493 UBE2V1 3' GCCCTGCCACCCTCTGCT 41794 TAA A  
 GGTAG GTGGCAG GC  
 |||| ||||| ||  
 TCGTC CACCGTC CG  
 TCC C  
 GAM1493 VAT1 3' GCTCTGCCCTCCCTCCC 21046 T TA T  
 GG AG AG GGCAGAGC  
 || || || |||||  
 CC TC TC CCGTCTCG  
 C CC \_  
 GAM1493 VIPR1 3' GCTTCCTACCCACACCTCT 16115 A AA CA  
 AGAGGT GT GTGG GAGC  
 ||||| || ||| ||||

TCTCCA CA CATC TTCG  
 \_ CC C\_  
 GAM1493 WBSCR14 3' GCTCTGCCACTGTGCTCC 51970 T \_  
 GG AGTA AGTGGCAGAGC  
 || ||| |||||  
 CC TCGT TCACCGTCTCG  
 \_ G  
 GAM1493 WBSCR14 3' GCTCTGCCACTGTGCTCC 51975 T \_  
 GG AGTA AGTGGCAGAGC  
 || ||| |||||  
 CC TCGT TCACCGTCTCG  
 \_ G  
 GAM1493 XPC 3' GCCCTCACTGCCTCT 16136 A T  
 AGAGGTAGT AG GGC  
 ||||| |||  
 TCTCCGTCA TC CCG  
 C \_  
 GAM1493 APXL2 5' CTGGTCCTACTTCCTCT 75188 T A T AG  
 AGAGG AGTA G GGC AG  
 |||| ||| ||| ||  
 TCTCC TCAT C CTG TC  
 T \_ \_ G\_  
 GAM1493 AQP10 3' CTCTCTTGTTACTGCC 54432 GT C  
 GGTAGTAA GG AGAG  
 ||||| || |||  
 CCGTCATT TC TCTC  
 GT \_  
 GAM1493 ARHGEF4 3' CTCTGCCCTGGGCACC 52212 A A\_ T  
 GGT GT AG GGCAGAG  
 ||| || || |||||  
 CCA CG TC CCGTCTC  
 \_ GG \_  
 GAM1493 B3GNT5 3' GCTATAATACACACTACCTC 49427 AA GCAG  
 GAGGTAGT GTG AGC  
 ||||| ||| |||  
 CTCCATCA CAT TCG  
 CA AATA  
 GAM1493 BBX 3' CTTTACCTACTACCCT 39588 A AGT C  
 AG GGTAGTA GG AGAG  
 || ||||| || |||  
 TC CCATCAT CC TTTC  
 \_ \_ A  
 GAM1493 BG1 5' CTCCCAATACTACCT 87310 AG CA  
 AGGTAGTA TGG GAG  
 ||||| ||| |||  
 TCCATCAT ACC CTC  
 A\_ \_  
 GAM1493 BRD3 3' CTCTGCCGTACCCCTCT 23757 TA AG  
 AGAGG GTA TGGCAGAG  
 |||| ||| |||||

TCTCC CAT GCCGTCTC  
 C\_ \_  
 GAM1493 C1orf2 3' GCTCTGCCACCTCTAGCT 21682 G TAA  
 AG TAG GTGGCAGAGC  
 || ||| |||||  
 TC ATC CACCGTCTCG  
 G TC\_  
 GAM1493 C1orf2 3' GCTCTGCCACCTCTAGCT 94623 G TAA  
 AG TAG GTGGCAGAGC  
 || ||| |||||  
 TC ATC CACCGTCTCG  
 G TC\_  
 GAM1493 C20orf122 3' GCTGGGTCCTTTCTACCTCT 55117 T T AG  
 AGAGGTAG AAG GGC AGC  
 ||||| ||| |||  
 TCTCCATC TTC CTG TCG  
 T \_ GG  
 GAM1493 C20orf139 3' CTCTTTGTACTATCTCT 84756 AGTGGC  
 AGAGGTAGTA AGAG  
 ||||| |||  
 TCTCTATCAT TCTC  
 GTT\_  
 GAM1493 C20orf150 3' GCTCTACCCTCTGCCTCT 65399 TA T C  
 AGAGGTAG AG GG AGAGC  
 ||||| || || ||||  
 TCTCCGTC TC CC TCTCG  
 \_ \_ A  
 GAM1493 C2F 5' GCTCTGCCACCCAAGCGGCC 20930 A AA\_  
 GGT GT GTGGCAGAGC  
 ||| || |||||  
 CCG CG CACCGTCTCG  
 G AACC  
 GAM1493 C4.4A 3' CTCTAAGCACTGCCTC 26944 AA GGC  
 GAGGTAGT GT AGAG  
 ||||| || |||  
 CTCCGTCA CG TCTC  
 \_ AA\_  
 GAM1493 C6orf28 3' GCCTTTCTCACTACTTCT 40994 A T\_  
 AGAGGTAGT AG GGC  
 ||||| || |||  
 TCTTCATCA TC CCG  
 C TTT  
 GAM1493 C9orf7 3' CTCTGCCCGCCCTCT 34170 TA AAGT  
 AGAGG GT GGCAGAG  
 |||| || |||||  
 TCTCC CG CCGTCTC  
 \_ C\_  
 GAM1493 C9orf9 3' CTGCCACTTACTAACC 38513 \_  
 GGT AGTAAGTGGCAG  
 ||| |||||

CCA TCATTCACCGTC  
 A  
 GAM1493 CASKIN1 3' GCTCTGCCGGGGGCTCCTC 40399 T AAG  
 GAGG AGT TGGCAGAGC  
 ||||| ||| |||||  
 CTCC TCG GCCGTCTCG  
 \_ GGG  
 GAM1493 CLDN1 3' CTTAATCTTTCTACCTCT 40849 T TGGCA  
 AGAGGTAG AAG GAG  
 ||||| ||| |||  
 TCTCCATC TTC TTC  
 T TAA\_\_  
 GAM1493 CLIC5 3' GCTTCAGTCTCACTACTTCT 33719 AAGT A\_  
 AGAGGTAGT GGC GAGC  
 ||||| ||| |||  
 TCTTCATCA CTG TTCG  
 CT\_\_ AC  
 GAM1493 CNNM4 3' CTCTGCCGACAGCCTCT 39480 A AAG  
 AGAGGT GT TGGCAGAG  
 ||||| || |||||  
 TCTCCG CA GCCGTCTC  
 A \_\_\_\_  
 GAM1493 CRNKL1 3' GCTCTGCCACTCATGATT 33600 A A  
 GGT GT AGTGGCAGAGC  
 ||| || |||||  
 TTA TA TCACCGTCTCG  
 G C  
 GAM1493 CYP4F8 3' GCCCAAGATACTCACTGCCTCT 23411 A \_\_\_\_  
 AGAGGTAGT AGT GGC  
 ||||| ||| |||  
 TCTCCGTCA TCA CCG  
 C TAGAAC  
 GAM1493 DKFZp434D0917 3' GCTCAAGTTCACCTCT 91255 AAGT A\_  
 AGAGGTAGT GGC GAGC  
 ||||| ||| |||  
 TCTCCATCA TTG CTCG  
 C\_\_ AA  
 GAM1493 DKFZp434G118 3' CTCAGCCACTGCCTC 50058 AGTA A  
 GAGGT AGTGGC GAG  
 |||| ||||| |||  
 CTCCG TCACCG CTC  
 \_\_\_\_ A  
 GAM1493 DKFZp547M072 3' GCTTTGCTTCCTACCTC 61082 TAAGT  
 GAGGTAG GGCAGAGC  
 ||||| |||||  
 CTCCATC TCGTTTCG  
 CT\_\_  
 GAM1493 DKFZP564O0423 3' CTCTGCCACCACCTT 91686 AGTAA  
 GAGGT GTGGCAGAG  
 |||| |||||

TTCCA CACCGTCTC  
 C\_\_\_\_  
 GAM1493 DKFZP566N034 3' GCCCTGCCACTCCTGGTTC 80140 G TA A  
 GAG TAG AGTGGCAG GC  
 ||| ||| ||||| ||  
 CTT GTC TCACCGTC CG  
 G C\_ C  
 GAM1493 DKK3 3' CTCAGCTCCTACCTCT 25130 TAAGT A  
 AGAGGTAG GGC GAG  
 ||||| ||| |||  
 TCTCCATC TCG CTC  
 C\_\_\_\_ A  
 GAM1493 ENAH 3' CTCTGCCTGCCACTCT 36614 GTA AGT  
 AGAG GTA GGCAGAG  
 ||| ||| |||||  
 TCTC CGT CCGTCTC  
 AC\_ \_  
 GAM1493 EPN3 5' CTGCCGCTGCCCCTCT 35660 TA A  
 AGAGG GTA GTGGCAG  
 |||| ||| |||||  
 TCTCC CGT CGCCGTC  
 C\_ \_  
 GAM1493 FLJ10103 3' GCTCCCGACTACTAGCTCT 35817 G AG CA  
 AGAG TAGTA TGG GAGC  
 ||| |||| ||| |||  
 TCTC ATCAT GCC CTCG  
 G CA \_  
 GAM1493 FLJ10314 5' GCCAGCTTACTGCCTC 36013 \_  
 GAGGTAGTAAG TGGC  
 ||||| ||||| |||||  
 CTCCGTCATTC ACCG  
 G  
 GAM1493 FLJ10357 3' GCCCTGCCACCACTATCTCT 36064 AA A  
 AGAGGTAGT GTGGCAG GC  
 ||||| ||||| ||  
 TCTCTATCA CACCGTC CG  
 C\_ C  
 GAM1493 FLJ10376 3' GCTCGCCTCCCTACCTCT 36076 TAAGT A  
 AGAGGTAG GGC GAGC  
 ||||| ||| |||  
 TCTCCATC CCG CTCG  
 CCT\_ \_  
 GAM1493 FLJ10415 3' CTCCCTTTCACTACCTC 36096 A T CA  
 GAGGTAGT AG GG GAG  
 ||||| || ||| |||  
 CTCCATCA TT CC CTC  
 C T \_  
 GAM1493 FLJ10829 3' GCTCTGCCCAGAGCCATCCCT 36710 A A AAGT  
 AG GGT GT GGCAGAGC  
 || ||| || |||||



			TC CTA CG CCGTCTCG		
			C C AGAC		
GAM1493	FLJ10901	3'	CTTTGACAGCTACCTCT 36824	AAG	G
			AGAGGTAGT TG CAGAG		
			TCTCCATCG AC GTTTC		
			___ A		
GAM1493	FLJ11078	3'	GCCCTGCCACTCCCTGGCCT 37032	_ TA	A
			AGGT AG AGTGGCAG GC		
			TCCG TC TCACCGTC CG		
			G CC C		
GAM1493	FLJ11099	3'	CTCTGCCACATCACTTC 37046	A	AA
			GAGGT GT GTGGCAGAG		
			CTTCA TA CACCGTCTC		
			C _		
GAM1493	FLJ12409	5'	GCTCTGCCAGAACACC 47049	A	AAG
			GGT GT TGGCAGAGC		
			CCA CA ACCGTCTCG		
			_ AG_		
GAM1493	FLJ14775	3'	CTGCCATACTACCTCT 51601	AA	
			AGAGGTAGT GTGGCAG		
			TCTCCATCA TACCGTC		
			___		
GAM1493	FLJ20371	3'	GCTCTGCCGGGGTCATCTC 35061	AG	AAG
			GAGGT T TGGCAGAGC		
			CTCTA G GCCGTCTCG		
			CT GG_		
GAM1493	FLJ20825	3'	GCTGGTTACTTGCCACCTCT 35698	A	AG
			AGAGGT GTAAGTGGC AGC		
			TCTCCA CGTTCATTG TCG		
			C G_		
GAM1493	FLJ21324	5'	CTCCAGCCGCACACCTC 91200	A	AA A_
			GAGGT GT GTGGC GAG		
			CTCCA CA CGCCG CTC		
			_ _ AC		
GAM1493	FLJ21596	3'	TTCTGCCACTCCTC 45707	TAGTA	
			GAGG AGTGGCAGAG		
			CTCC TCACCGTCTT		
			___		
GAM1493	FLJ21977	3'	GCTCCCTAGCCTACCTCT 49885	TAAGT	CA
			AGAGGTAG GG GAGC		

TCTCCATC CC CTCG  
 CGAT\_ \_  
 GAM1493 FLJ22167 5' CTCTGCTCTCACCTCT 44570 \_ TAAGT  
 AGAGGT AG GGCAGAG  
 ||||| || |||||  
 TCTCCA TC TCGTCTC  
 C \_  
 GAM1493 FLJ22167 3' CTCTTGCCCCTACCTCT 44571 TAAGT \_  
 AGAGGTAG GGCA GAG  
 ||||| ||| |||  
 TCTCCATC CCGT CTC  
 C \_ T  
 GAM1493 FLJ22169 5' CTCTGCCAGACGCCT 44002 A AAG  
 AGGT GT TGGCAGAG  
 ||| || |||||  
 TCCG CA ACCGTCTC  
 \_ G\_  
 GAM1493 FLJ22944 3' GCCCTGCCACTGTGGACTGCC 47125 A \_ A  
 GG TAGT AGTGGCAG GC  
 ||||| ||||| ||  
 CCGTCA TCACCGTC CG  
 GGTG C  
 GAM1493 FLJ23071 5' GCCCTTGTA TACTACTACCTC 47265 \_ T  
 GAGGTAGTA AG GGC  
 ||||| || |||  
 CTCCATCAT TC CCG  
 CATGT \_  
 GAM1493 FLJ23519 3' GCTCTGGCCCAGCACCTC 49968 A AAGT \_  
 GAGGT GT GGC AGAGC  
 ||||| || ||| |||||  
 CTCCA CG CCG TCTCG  
 \_ AC \_ G  
 GAM1493 FLJ30092 3' TTCAGACCACACCACCTCT 58692 A AA CA\_  
 AGAGGT GT GTGG GAG  
 ||||| || ||| |||  
 TCTCCA CA CACC CTT  
 C \_ AGA  
 GAM1493 FLJ31101 3' GCTCTGCCACTGTGCC 35714 GTA  
 GGTA AGTGGCAGAGC  
 ||| |||||  
 CCGT TCACCGTCTCG  
 G\_  
 GAM1493 FLJ32468 5' CTTTGCCACCACCCT 59042 A AGTAA  
 AG GGT GTGGCAGAG  
 || ||| |||||  
 TC CCA CACCGTTTC  
 \_ C\_  
 GAM1493 FLJ32783 3' GCTCTGCCACTTACTAGCT 58646 G  
 AG TAGTAAGTGGCAGAGC  
 || |||||

			TC ATCATTACCGTCTCG		
			G		
GAM1493	GGA2	3'	GCCCAGCTCCTACCTCT 56881	TA	___
			AGAGGTAG AGT GGC		
			TCTCCATC TCG CCG		
			C_ AC		
GAM1493	GGA2	3'	GCCCAGCTCCTACCTCT 30467	TA	___
			AGAGGTAG AGT GGC		
			TCTCCATC TCG CCG		
			C_ AC		
GAM1493	GP5	3'	CTCTGCCACCTCATTTTC 15644	_ TAA	
			GAGGT AG GTGGCAGAG		
			CTTTA TC CACCGTCTC		
			C ___		
GAM1493	GP5	3'	GCTCTACCACTTACTAACT 15651	G	C
			AG TAGTAAGTGG AGAGC		
			TC ATCATTACAC TCTCG		
			A A		
GAM1493	GRIN3A	3'	CTCTGCCACCATGCTCT 55970	G	GTAA
			AGAG TA GTGGCAGAG		
			TCTC GT CACCGTCTC		
			_ AC__		
GAM1493	H326	3'	GCTCTGCCTCAGATCTCCTACC 31707	TAAGT	_____
	TCT		AGAGGTAG GGCAGAGC		
			TCTCCATC CCGTCTCG		
			CTCTAGACT		
GAM1493	HARS2	3'	GCTCTGCCACAGTGTCTT 55035	TAGTAA	
			GAGG GTGGCAGAGC		
			TTCC CACCGTCTCG		
			TGTGA_		
GAM1493	HRMT1L3	3'	GCTCTGCCCTGGTAGCCCT 39075	A	AGTA T
			AG GGT AG GGCAGAGC		
			TC CCG TC CCGTCTCG		
			_ ATGG _		
GAM1493	HSJ1	3'	CTCTGCCACCTGTGTTGCT 22129	A	___
			GGTAGTA GTGGCAGAG		
			TCGTTGT CACCGTCTC		
			GTC		
GAM1493	HSN44A4A	5'	GCCACTTACTAGCTCT 31113	G	
			AGAG TAGTAAGTGGC		

		TCTC ATCATTACCG		
		G		
GAM1493 IL14	5'	GCTCTGCCTAGGGACACCTTT	95433	A AAGT_
		AGAGGT GT GGCAGAGC		
		TTTCCA CA CCGTCTCG		
		_ GGGAT		
GAM1493 ITPK1	3'	GCTCTGCCGTCTGACCCCT	26410	TAG AG
		AGG TA TGGCAGAGC		
		TCC GT GCCGTCTCG		
		CCA CT		
GAM1493 KIAA0057	3'	GCCAAACTTACTACCTT	24429	__
		GAGGTAGTAAGT GGC		
		TTCCATCATTCA CCG		
		AA		
GAM1493 KIAA0057	3'	GCTCTGCCAGACACCTC	24433	A AAG
		GAGGT GT TGGCAGAGC		
		CTCCA CA ACCGTCTCG		
		_ G__		
GAM1493 KIAA0082	3'	CTCCCTTACTACCCT	92165	A T C
		AG GGTAGTAAG GG AG		
		TC CCATCATTC CC TC		
		- - -		
GAM1493 KIAA0237	3'	GCTCTTTGTCAATTCCACCTC	28527	AGTA __
		GAGGT AGTGGCA GAGC		
		CTCCA TTA CTGT CTCG		
		CC__ TT		
GAM1493 KIAA0342	3'	GCCCTGCCACTGGCCACC	70618	A A A
		GGT GT AGTGGCAG GC		
		CCA CG TCACCGTC CG		
		C G C		
GAM1493 KIAA0441	3'	GCTCTATAACAGTCTACCTCT	28957	TAA GGC
		AGAGGTAG GT AGAGC		
		TCTCCATC CA TCTCG		
		TGA ATA		
GAM1493 KIAA0451	3'	GCTCCCTGCCACTCACCTC	29109	AGTA __
		GAGGT AGTGGCA GAGC		
		CTCCA TCACCGT CTCG		
		C__ CC		
GAM1493 KIAA0628	3'	GCTCCACGTGGCTTCCTACCTC	28873	T G A__
T		AGAGGTAG AAGT GC GAGC		

TCTCCATC TTCG TG CTCG  
 C G CAC  
 GAM1493 KIAA0783 3' CTCTGCCACAGCTCATC 27799 \_ AA  
 GGT AGT GTGGCAGAG  
 ||| ||| |||||  
 CTA TCG CACCGTCTC  
 C A\_

GAM1493 KIAA0937 3' GCCCTGTGCATCTACTACCTT 91587 AG \_ A  
 GAGGTAGTA TG GCAG GC  
 ||||| || ||| ||  
 TTCCATCAT AC TGTC CG  
 CT G C

GAM1493 KIAA1084 5' GCTCTGCCACTTAACAGCC 29837 AG\_  
 GGT TAAGTGGCAGAGC  
 || |||||  
 CCG ATTCACCGTCTCG  
 ACA

GAM1493 KIAA1143 3' CTCCCATTCCTACCTCT 68678 TA CA  
 AGAGGTAG AGTGG GAG  
 ||||| ||| ||  
 TCTCCATC TTACC CTC  
 C\_ \_

GAM1493 KIAA1202 3' CTCTACCCTTACCTTT 72017 GTA T C  
 AGAGGTA AG GG AGAG  
 ||||| || |||  
 TTTCCAT TC CC TCTC  
 \_ \_ A

GAM1493 KIAA1202 3' CTCTGCCACAGCATCCCT 72018 A TA AA  
 AG GG GT GTGGCAGAG  
 || || || |||||  
 TC CC CG CACCGTCTC  
 \_ TA A\_

GAM1493 KIAA1218 5' CTCTGCCAGCAGCACCTC 94305 A AAG  
 GAGGT GT TGGCAGAG  
 |||| || |||||  
 CTCCA CG ACCGTCTC  
 \_ ACG

GAM1493 KIAA1266 3' GCTCTGCAGGCTATCTC 66123 AAGTG  
 GAGGTAGT GCAGAGC  
 ||||| |||||  
 CTCTATCG CGTCTCG  
 GA\_

GAM1493 KIAA1297 3' GCTCTGCCACGGACATCT 72181 A AA  
 AGGT GT GTGGCAGAGC  
 ||| || |||||  
 TCTA CA CACCGTCTCG  
 \_ GG

GAM1493 KIAA1465 3' CTTACCTACTCCTC 60829 T A C  
 GAGG AGTA GTGG AG  
 ||| ||| ||| ||

			CTCC TCAT CACT TC		
			— C —		
GAM1493	KIAA1602	3'	GCTCTGCTTCCTGCCTCT 64633	TAAGT	
			AGAGGTAG GGCAGAGC		
			TCTCCGTC TCGTCTCG		
			CT___		
GAM1493	KIAA1671	3'	GCTCTGCCATGACCTCT 65680	AGTAA	
			AGAGGT GTGGCAGAGC		
			TCTCCA TACCGTCTCG		
			G___		
GAM1493	KIAA1691	3'	GCTCTGCCCTGGCCTTCCTCT 92557	TA_ A T	
			AGAGG GT AG GGCAGAGC		
			TCTCC CG TC CCGTCTCG		
			TTC G _		
GAM1493	KIAA1753	3'	GCTCTGCCCTTCTACC 64883	T T	
			GGTAG AAG GGCAGAGC		
			CCATC TTC CCGTCTCG		
			— —		
GAM1493	KIAA1775	3'	GCCGTGACTCACACACCTCT 52382	A_ A _	
			AGAGGT GT AGT GGC		
			TCTCCA CA TCA CCG		
			CA C GTG		
GAM1493	KIAA1813	3'	GCTCTTGTTACTACC 70303	AGTG _	
			GGTAGTA GCA GAGC		
			CCATCAT TGT CTCG		
			___ T		
GAM1493	KIAA1838	3'	GCCCTGCCAGCGCCCTCCTCT 64733	T TAA_ A	
			AGAGG AG G TGGCAG GC		
			TCTCC TC C ACCGTC CG		
			_ CCG G C		
GAM1493	KIAA1870	3'	GCCCACGTTTGCTACCTC 49661	— —	
			GAGGTAGTAA GTGG C		
			CTCCATCGTT CACC G		
			TG C		
GAM1493	KPNA6	3'	CTTGGCCTGCTACCTC 24606	AGT A	
			GAGGTAGTA GGC GAG		
			CTCCATCGT CCG TTC		
			___ G		
GAM1493	KRTHB5	5'	CTCTGCCGCCCGCACC 9653	A AA	
			GGT GT GTGGCAGAG		

		CCA CG CGCCGTCTC		
		_ CC		
GAM1493	LHPP	3' CTATGCCCACTGCCTC	42100	AAGT G
		GAGGTAGT GGCA AG		
		CTCCGTCA CCGT TC		
		C__ A		
GAM1493	LIMK2	3' GCCATTCCTATTACCTC	18727	__
		GAGGTAGTA AGTGGC		
		CTCCATTAT TTACCG		
		CC		
GAM1493	LIMK2	3' GCCATTCCTATTACCTC	33625	__
		GAGGTAGTA AGTGGC		
		CTCCATTAT TTACCG		
		CC		
GAM1493	MAPK8IP3	3' CGCCCTGCCACCTGGGCCACC	52979	A_ AA__ A III
	TC	GAGGT GT GTGGCAG GC G		
		CTCCA CG CACCGTC CG C		
		CC GGTC C III		
GAM1493	MGC10818	3' CTCAGCCACCTGCTACCTCT	47540	A A
		AGAGGTAGTA GTGGC GAG		
		TCTCCATCGT CACCG CTC		
		C A		
GAM1493	MGC11266	3' GCTCTGCCACCCTCCTGCT	44240	TAA_
		GGTAG GTGGCAGAGC		
		TCGTC CACCGTCTCG		
		CTCC		
GAM1493	MGC15854	5' TTCCCCCACTACCTCT	58853	AGTA CA
		AGAGGT AGTGG GAG		
		TCTCCA TCACC CTT		
		__ CC		
GAM1493	MGC15875	3' GCTCTGCCTAAGTGTACTCC	51910	T AGT__
		GG AGTA GGCAGAGC		
		CC TCAT CCGTCTCG		
		_ GTGAAT		
GAM1493	MGC20702	3' CTCTGAACATACTACCTT	53641	A GG
		GAGGTAGTA GT CAGAG		
		TTCCATCAT CA GTCTC		
		A A_		
GAM1493	MGC26954	3' CTCTGCCACCTATTAGCTTT	58836	G A
		AGAG TAGTA GTGGCAGAG		

		TTTC ATTAT CACCGTCTC		
		G C		
GAM1493	MGC3035	5' CTCTGCCCGGCACCCT	44150	A A AAGT
		AG GGT GT GGCAGAG		
		TC CCA CG CCGTCTC		
		_ _ GC_		
GAM1493	MGC32043	3' GCCCTACTTTCCTCCCTCT	58050	T T_ _
		AGAGG AG AAGT GGC		
		TCTCC TC TTCA CCG		
		C CT TC		
GAM1493	MGC32104	3' CTCAAGCCTTACTACC	58407	GT A_
		GGTAGTAA GGC GAG		
		CCATCATT CCG CTC		
		_ AA		
GAM1493	MGC3329	3' CTCTGGACTGCCTCT	44016	AAGTGG
		AGAGGTAGT CAGAG		
		TCTCCGTCA GTCTC		
		G_		
GAM1493	MGC4266	3' GCTCTGCCCCACTCCTCT	51059	T AAGT
		AGAGG AGT GGCAGAGC		
		TCTCC TCA CCGTCTCG		
		_ CC_		
GAM1493	MGC4604	3' GCTCTGCCCCATACCCCT	48981	A GTAAGT
		AG GGTA GGCAGAGC		
		TC CCAT CCGTCTCG		
		C ACC_		
GAM1493	MGC4796	3' GCCCAGCACTTACTCCCCCT	61490	A T _
		AG GG AGTAAGT GGC		
		TC CC TCATTCA CCG		
		C C CGAC		
GAM1493	MGC9753	3' GCTCTGCCCCTGACCCCT	53050	TA A T
		AGG GT AG GGCAGAGC		
		TCC CA TC CCGTCTCG		
		C_ G C		
GAM1493	MYH10	3' GCTCTGCCGGCGCCCTC	69141	TA AAG
		GAGG GT TGGCAGAGC		
		CTCC CG GCCGTCTCG		
		CG _		
GAM1493	NDRG4	3' CTCTGCCACCTCCTGGCCCT	43288	A _ TAA
		AG GGT AG GTGGCAGAG		



		TC CCG TC CACCGTCTC		
		_ G CTC		
GAM1493	NDRG4	3' CTCTGCCACCTCCTGGCCCT 39985	A _ TAA	
		AG GGT AG GTGGCAGAG		
		TC CCG TC CACCGTCTC		
		_ G CTC		
GAM1493	NEIL1	5' CTCTGCCACCCTCCCTC 44828	T TAA	
		GAGG AG GTGGCAGAG		
		CTCC TC CACCGTCTC		
		C C_		
GAM1493	nexilin	3' CTCCAACCTTTCTTACTACATC 58008	G T_ CA_	
		GA GTAGTAAG GG GAG		
		CT CATCATTC TC CTC		
		A TT AAC		
GAM1493	NKX2B	3' CTCTGCCCATGCCTCT 10234	GTAAGT	
		AGAGGTA GGCAGAG		
		TCTCCGT CCGTCTC		
		AC_		
GAM1493	NR6A1	3' GCCCGGCTGCTACCTCT 7647	A _	
		AGAGGTAGTA GT GGC		
		TCTCCATCGT CG CCG		
		_ GC		
GAM1493	NR6A1	3' GCCCGGCTGCTACCTCT 52872	A _	
		AGAGGTAGTA GT GGC		
		TCTCCATCGT CG CCG		
		_ GC		
GAM1493	NR6A1	3' GCCCGGCTGCTACCTCT 52884	A _	
		AGAGGTAGTA GT GGC		
		TCTCCATCGT CG CCG		
		_ GC		
GAM1493	NS1-BP	3' CTCTGCCACTTTATTTCTCT 72544	TAGT	
		AGAGG AAGTGGCAGAG		
		TCTCT TTCACCGTCTC		
		TTAT		
GAM1493	OCT11	3' GCTCTGCCACTTGGGTTC 26819	TAG	
		GG TAAGTGGCAGAGC		
		CT GTTCACCGTCTCG		
		TGG		
GAM1493	ODC-p	5' GCAACTGCCACTCCTC 53797	TAGTA A_	
		GAGG AGTGGCAG GC		

		CTCC TCACCGTC CG	
		AA	
GAM1493	ORF1-FL49 3'	GCTCTGCTGCCACCTCT 50551	AGTAA TG
		AGAGGT G GCAGAGC	
		TCTCCA C CGTCTCG	
		C___ GT	
GAM1493	PAK7 5'	GCTCTGCCTCTCACCCCCTC 69648	TA A T
		GAGG GT AG GGCAGAGC	
		CTCC CA TC CCGTCTCG	
		CC C T	
GAM1493	PDE2A 3'	CTGGACAAGTACTACCTT 10471	AG G_
		GAGGTAGTA TG CAG	
		TTCCATCAT AC GTC	
		GA AG	
GAM1493	PFDN1 3'	GCTTTGCCTGCCACCTCT 10512	A AGT
		AGAGGT GTA GGCAGAGC	
		TCTCCA CGT CCGTTTCG	
		C _	
GAM1493	PMF1 3'	GCTCTGCCCTCCGCCCCC 23327	TA A_ T
		GG GT AG GGCAGAGC	
		CC CG TC CCGTCTCG	
		CC CC C	
GAM1493	POLD3 3'	CTCCACCAGAAATTACCTC 91644	AAG CA
		GAGGTAGT TGG GAG	
		CTCCATTA ACC CTC	
		AAG AC	
GAM1493	PPP1R1B 3'	GCTCTGCCCTTTCCCCT 49827	TAGT T
		AGG AAG GGCAGAGC	
		TCC TTC CCGTCTCG	
		CCT_ C	
GAM1493	PRDM7 3'	GCCCCTGTCACCTACC 53789	TAA A_
		GGTAG GTGGCAG GC	
		CCATC CACTGTC CG	
		___ CC	
GAM1493	PRO0082 3'	CTGTTGCTTACACCCT 37734	A A TG
		AG GGT GTAAG GCAG	
		TC CCA CATTG TGTC	
		C _ GT	
GAM1493	PRSS22 3'	GCTCATCTACCTCTACCTCT 42091	TAA CA
		AGAGGTAG GTGG GAGC	

TCTCCATC CATC CTCG  
 TC\_ TA  
 GAM1493 PTGES2 3' CCTGCCACTGCCCT 46879 A AGTA A  
 AG GGT AGTGGCAG G  
 || ||| ||||| |  
 TC CCG TCACCGTC C  
 \_ \_ \_ C  
 GAM1493 PTGES2 3' CTCTGCCGCCCTCT 46880 TAGTAA  
 AGAGG GTGGCAGAG  
 |||| |  
 TCTCC CGCCGTCTC  
 C \_ \_  
 GAM1493 PTPRU 3' GCTCTGCCCAAACACACTC 19117 \_ A AAGT  
 GAG GT GT GGCAGAGC  
 ||| || |||||  
 CTC CA CA CCGTCTCG  
 A \_ AAC\_  
 GAM1493 PTPRU 3' GCTCTGCCCAAACACACTC 55690 \_ A AAGT  
 GAG GT GT GGCAGAGC  
 ||| || |||||  
 CTC CA CA CCGTCTCG  
 A \_ AAC\_  
 GAM1493 PTPRU 3' GCTCTGCCCAAACACACTC 55696 \_ A AAGT  
 GAG GT GT GGCAGAGC  
 ||| || |||||  
 CTC CA CA CCGTCTCG  
 A \_ AAC\_  
 GAM1493 QPRT 3' GCTCTGCCACCTGCTGCTCCT 59790 AG A  
 AG GTAGTA GTGGCAGAGC  
 || ||||| |||||  
 TC CGTCGT CACCGTCTCG  
 CT C  
 GAM1493 RAB1B 3' CTCTGCTAGCACCTC 48288 A AAG  
 GAGGT GT TGGCAGAG  
 |||| |  
 CTCCA CG ATCGTCTC  
 \_ \_  
 GAM1493 RAI16 3' CTCCTGTCCACACCTCT 42755 AGTAA \_ \_  
 AGAGGT GTGG CAG AG  
 |||| |  
 TCTCCA CACC GTC TC  
 \_ \_ T C  
 GAM1493 RDH-E2 3' GCTCTGGATTCTACC 57271 T GG  
 GG TAG AAGT CAGAGC  
 |||| |  
 CCATC TTTA GTCTCG  
 \_ G\_  
 GAM1493 RLUCL 3' GCTCTGCCACGTCACCGCCT 54220 TA AA\_  
 AGG GT GTGGCAGAGC  
 || | |||||

			TCC CA CACCGTCTCG		
			GC CTG		
GAM1493	RNF8	3'	GCTCACTCTACCTCT 14228	TA	_
			AGAGGTAG AGTG GC		
			TCTCCATC TCAC CG		
			_ T		
GAM1493	RODH-4	3'	GCCCATGCCATTACCTC 13534	GTAA	GA_
			GAGGTA GTGGCA GC		
			CTCCAT TACCGT CG		
			_____ ACC		
GAM1493	SDS3	3'	GCTCTGCTGTGGCTGCCTCT 69231	AA	TG
			AGAGGTAGT G GCAGAGC		
			TCTCCGTCG T CGTCTCG		
			G_ GT		
GAM1493	SEC6	3'	GCTCTGCCGCACAGCCTCT 71596	A	AA
			AGAGGT GT GTGGCAGAGC		
			TCTCCG CA CGCCGTCTCG		
			A _		
GAM1493	SLC16A5	3'	CTCCGCCACTATCTGCC 16277	TA	A
			GGTAG AGTGGC GAG		
			CCGTC TCACCG CTC		
			TA C		
GAM1493	SLC38A5	5'	GCTCTGTCCCCCACCTCT 53191	AGTA	AGT
			AGAGGT GGCAGAGC		
			TCTCCA CTGTCTCG		
			CCCC_		
GAM1493	SSB-4	3'	GCCCCAGACAGCACTGCCTCT 55101	AA_	_____
			AGAGGTAGT GT GGC		
			TCTCCGTCA CA CCG		
			CGA GACC		
GAM1493	SSI-1	3'	CTCGCACCTCCTACCTCT 13628	TA	TG A
			AGAGGTAG AG GC GAG		
			TCTCCATC TC CG CTC		
			C_ CA _		
GAM1493	SUPT4H1	3'	GCCCTTCTACTCCCTCT 12064	T	_ T
			AGAGG AGTA AG GGC		
			TCTCC TCAT TC CCG		
			C CT _		
GAM1493	TLOC1	5'	GCTCTGCCATCTACCACCT 12312	A	AG
			AGGT GTA TGGCAGAGC		

			TCCA CAT ACCGTCTCG		
			C CT		
GAM1493	TNRC4	3'	GCCCTAAAACTCACTGCCTC 23222	A	_____
			GAGGTAGT AGT GGC		
			CTCCGTCA TCA CCG		
			C AAATC		
GAM1493	TOM1	3'	GCTGGGCCCCACTGCCCT 18507	A	AAGT AG
			AG GGTAGT GGC AGC		
			TC CCGTCA CCG TCG		
			C CC_ GG		
GAM1493	TTY7	3'	CTCTTTTCCTCCTACCTCT 49180	TA	TG C
			AGAGGTAG AG G AGAG		
			TCTCCATC TC T TCTC		
			C_ CT T		
GAM1493	TUBB5	3'	GCCCCAGCTCCTACCTCT 20303	TA	_____
			AGAGGTAG AGT GGC		
			TCTCCATC TCG CCG		
			C_ ACC		
GAM1493	USP19	3'	GCCCTGCCCAAGCTACTTC 88958	AAGT	A
			GAGGTAGT GGCAG GC		
			CTTCATCG CCGTC CG		
			AAC_ C		
GAM1493	VRP	5'	GCTGGTCACCTACTACTCCT 22946	AG	A AG
			AG GTAGTA GTGGC AGC		
			TC CATCAT CACTG TCG		
			CT C G_		
GAM1493	ZF5128	3'	GCTCTGTCAGCCGCCACCTCT 26806	A	AAG
			AGAGGT GT TGGCAGAGC		
			TCTCCA CG ACTGTCTCG		
			C CCG		
GAM1493	ZIC4	5'	CCTGCTGCTACTTCT 49618	AAGT	A
			AGAGGTAGT GGCAG G		
			TCTTCATCG TCGTC C		
			_____ C		
GAM1493	ZIC4	5'	CTCTGCCGCTACCATCCCT 49619	A	A A
			AG GGT GTA GTGGCAGAG		
			TC CTA CAT CGCCGTCTC		
			C C _		
GAM1493	ZNF237	3'	GCTCTACCACCTGCCTTT 26474	TAA	C
			AGAGGTAG GTGG AGAGC		

	TTTCCGTC CACC TCTCG	
	____ A	
GAM1493 ZNF340	3' GCTCTGCCGTCCTGCCTCT 84560	TAAG
	AGAGGTAG TGGCAGAGC	
	TCTCCGTC GCCGTCTCG	
	CT__	
GAM1493 LOC112609	3' GCCCTGCCACTACTATGCTCT 72840	_ A A
	AGAG GTAGTA GTGGCAG GC	
	TCTC TATCAT CACCGTC CG	
	G _ C	
GAM1493 LOC114971	3' GCCCCTGACACAGCCACCTCT 73148	A AA G A_
	AGAGGT GT GTG CAG GC	
	TCTCCA CG CAC GTC CG	
	C A_ A CC	
GAM1493 LOC123346	5' CTCCACAGAAGGCTTACCTCT 75607	_ AA__ C
	AGAGGTA GT GTGG AG	
	TCTCCAT CG CACC TC	
	T GAAGA _	
GAM1493 LOC124446	5' GCTCTGCCACTTACTG 74290	
	TAGTAAGTGGCAGAGC	
	GTCATTACCGTCTCG	
GAM1493 LOC124801	3' CTCTGCCCTTTACTTCT 74338	GT T
	AGAGGTA AAG GGCAGAG	
	TCTTCAT TTC CCGTCTC	
	__ _	
GAM1493 LOC126526	3' CCACTTTTCTACCTCT 74534	T_
	AGAGGTAG AAGTGG	
	TCTCCATC TTCACC	
	TT	
GAM1493 LOC126661	3' CTCTGCCCCACTACCTT 74550	AAGT
	GAGGTAGT GGCAGAG	
	TTCCATCA CCGTCTC	
	C__	
GAM1493 LOC129303	5' CTTCCCCATCTACCTCT 74871	TAA CA
	AGAGGTAG GTGG GAG	
	TCTCCATC TACC TTC	
	__ CC	
GAM1493 LOC130612	3' CTCTGCAGTCACCAGCTCT 74958	T AA __
	GG AGT GTG GCAGAG	

TC TCG CAC CGTCTC  
 \_ AC TGA  
 GAM1493 LOC132166 3' GCCCTTCCTTTCTACCTCT 75038 T T\_\_\_\_  
 AGAGGTAG AAG GGC  
 ||||| ||| |||  
 TCTCCATC TTC CCG  
 T CTTC  
 GAM1493 LOC138835 5' CTCTCTGCTTACCACATC 75955 G A TG C  
 GA GT GTAAG G AGAG  
 || ||||| | |||  
 CT CA CATT C TCTC  
 A C GT\_  
 GAM1493 LOC144501 3' GCTCTGCCAAGGCCCTCT 83110 TA AAG  
 AGAGG GT TGGCAGAGC  
 |||| | |||||  
 TCTCC CG ACCGTCTCG  
 C\_ GA\_  
 GAM1493 LOC144698 5' CTCTGCCACCAGCTCC 76908 T AA  
 GG AGT GTGGCAGAG  
 || ||| |||||  
 CC TCG CACCGTCTC  
 \_ AC  
 GAM1493 LOC144866 5' CTCTGCGTGGGCCACCTGCT 83205 \_ A AAGTG  
 AG AGGT GT GCAGAG  
 || |||| | |||||  
 TC TCCA CG CGTCTC  
 G C GGTG\_  
 GAM1493 LOC145622 5' GCTCTGCCACCCAGGACATC 77304 G AGTAA  
 GA GT GTGGCAGAGC  
 || || |||||  
 CT CA CACCGTCTCG  
 A GGACC  
 GAM1493 LOC145945 3' GCTCTGCCACTTACTTAATT 83576 GGT  
 GA AGTAAGTGGCAGAGC  
 || |||||  
 TT TCATTACCGTCTCG  
 AAT  
 GAM1493 LOC147299 5' GCCCTGGGCGCACTACCTT 78347 AA GG A  
 GAGGTAGT GT CAG GC  
 ||||| || |||  
 TTCCATCA CG GTC CG  
 CG G\_ C  
 GAM1493 LOC148758 3' CTCTGCCGCCACCCTC 78968 TA AA  
 GAGG GT GTGGCAGAG  
 ||| || |||||  
 CTCC CA CGCCGTCTC  
 \_ CC  
 GAM1493 LOC149271 5' GCTCAAATACCATTACCTCT 79244 AA GCA  
 AGAGGTAGT GTG GAGC  
 ||||| ||| |||

TCTCCATTA CAT CTCG  
 C\_ AAA  
 GAM1493 LOC149606 3' CTCTGCCATCCCACCACC 79450 A AA\_  
 GGT GT GTGGCAGAG  
 ||| || |||||  
 CCA CA TACCGTCTC  
 C CCC  
 GAM1493 LOC149670 5' GCCCTGCCACTCCTTCCTC 79492 T TA A  
 GAGG AG AGTGGCAG GC  
 ||| || ||||| ||  
 CTCC TC TCACCGTC CG  
 T C\_ C  
 GAM1493 LOC149912 5' GCTCTGCCACTTACCAGCT 84716 A\_  
 GGT GTAAGTGGCAGAGC  
 || |||||  
 TCG CATTACCGTCTCG  
 AC  
 GAM1493 LOC150319 3' GCTCTGCCACCCTTACCCCT 79657 A TAA \_  
 AG GGTAG GTGG CAGAGC  
 || ||| ||| |||||  
 TC CCATT CACC GTCTCG  
 C CC\_ C  
 GAM1493 LOC150343 5' GCTCCGCACTGGACACCCCT 79673 A A A\_ G A  
 AG GGT GT AGTG C GAGC  
 || ||| || ||| |||||  
 TC CCA CA TCAC G CTCG  
 C \_ GG \_ C  
 GAM1493 LOC150378 5' GCCATTTCCCCTACCTCT 79748 T\_\_  
 AGAGGTAG AAGTGGC  
 ||||| |||||  
 TCTCCATC TTTACCG  
 CCC  
 GAM1493 LOC150776 5' GCCCTGCCACTCTCCTC 63223 T TA A  
 GAGG AG AGTGGCAG GC  
 ||| || ||||| ||  
 CTCC TC TCACCGTC CG  
 \_ \_ C  
 GAM1493 LOC150933 5' CTTGATCCTTGCTACCCCT 85162 A T CA  
 AG GGTAGTAAG GG GAG  
 || ||||| || |||  
 TC CCATCGTTC CT TTC  
 C \_ AG  
 GAM1493 LOC150935 3' GCTCTGCCAACCACC 80034 A AAG  
 GGT GT TGGCAGAGC  
 ||| || |||||  
 CCA CA ACCGTCTCG  
 C \_  
 GAM1493 LOC151196 3' GCCCAGAGATTAGCTACCTCT 85267 A \_  
 AGAGGTAGT AGT GGC  
 ||||| || |||



TCTCCATCG TTA CCG  
 A GAGAC  
 GAM1493 LOC151568 5' GCTCTGCCAGAAACCACCT 56699 A AAG  
 AGGT GT TGGCAGAGC  
 |||| || |||||  
 TCCA CA ACCGTCTCG  
 C AAG  
 GAM1493 LOC151760 5' GCCCTGCCACCCGTTGTTGCC 85495 \_\_\_\_ A  
 GGTAGTAA GTGGCAG GC  
 ||||| ||||| ||  
 CCGTTGTT CACCGTC CG  
 GCC C  
 GAM1493 LOC152274 5' CTCCAACCTTCCTACCTCT 80506 T \_ C  
 AGAGGTAG AAGT GG AG  
 ||||| ||| || ||  
 TCTCCATC TTCA CC TC  
 C A \_  
 GAM1493 LOC152905 3' CTCTGCCACTATCCCC 60477 TA A  
 GG GTA GTGGCAGAG  
 || ||| |||||  
 CC TAT CACCGTCTC  
 CC \_  
 GAM1493 LOC153711 3' CTCTGCTAGTACCACGCCT 86134 A\_\_ AG  
 AGGT GTA TGGCAGAG  
 ||| ||| |||||  
 TCCG CAT ATCGTCTC  
 CAC G\_  
 GAM1493 LOC153937 5' CTGCTACTACTCCTCT 81006 T A  
 AGAGG AGTA GTGGCAG  
 |||| ||| |||||  
 TCTCC TCAT CATCGTC  
 \_ \_  
 GAM1493 LOC154089 3' GCTCTGCCACCTACC 81039 TAA  
 GG TAG GTGGCAGAGC  
 |||| |||||  
 CCATC CACCGTCTCG  
 \_  
 GAM1493 LOC154449 5' CTCTGCCGTTACCTCT 81086 TAAG  
 AGAGGTAG TGGCAGAG  
 ||||| |||||  
 TCTCCATT GCCGTCTC  
 \_  
 GAM1493 LOC154877 3' CTCTGGTCCCCACCACTTC 86294 AGTAA \_\_\_\_  
 GAGGT GTGG CAGAG  
 |||| ||| ||||  
 CTTCA CACC GTCTC  
 C\_\_\_\_ CCTG  
 GAM1493 LOC155066 3' GCTCTGCCACCATCCTGCT 81281 TAA\_  
 GG TAG GTGGCAGAGC  
 |||| |||||

	TCGTC CACCGTCTCG		
	CTAC		
GAM1493 LOC158668 3'	CTCTGCTCACTACCTT 69368	AAGT	
	GAGGTAGT GGCAGAG		
	TTCCATCA TCGTCTC		
	C__		
GAM1493 LOC159090 5'	CTTCCACCACTACCTCT 82088	AA C	
	AGAGGTAGT GTGG AG		
	TCTCCATCA CACC TC		
	C_ T		
GAM1493 LOC196812 3'	GTCACCTACCATCTCT 89574	A	
	AGAGGT GTAAGTGGC		
	TCTCTA CATTCACTG		
	C		
GAM1493 LOC197135 5'	GCTCTGCTTAGCTCCCCT 87893	A T AAGT	
	AG GG AGT GGCAGAGC		
	TC CC TCG TCGTCTCG		
	_ C AT__		
GAM1493 LOC197342 3'	GCCCTGCCACTCCAGCCT 88004	AGTA A	
	AGGT AGTGGCAG GC		
	TCCG TCACCGTC CG		
	ACC_ C		
GAM1493 LOC199729 3'	CTGTTCTCACTACTTCT 73032	A T	
	AGAGGTAGT AG GGCAG		
	TCTTCATCA TC TTGTC		
	C _		
GAM1493 LOC199990 3'	GCTCTGCCACACCTGACACCT 88513	A AA__	
	AGGT GT GTGGCAGAGC		
	TCCA CA CACCGTCTCG		
	_ GTCCA		
GAM1493 LOC200081 3'	CTCACACTTCAGCTACCTCT 88563	__ GCA	
	AGAGGTAGT AAGTG GAG		
	TCTCCATCG TTCAC CTC		
	AC A__		
GAM1493 LOC203052 3'	CTCCTGAGCCTACCTCT 90453	TAA GG _	
	AGAGGTAG GT CAG AG		
	TCTCCATC CG GTC TC		
	__ A_ C		
GAM1493 LOC203339 3'	CTCTGATCACTACTCT 90543	T A _	
	GG AGTA GTGG CAGAG		

TC TCAT CACT GTCTC  
 \_ \_ A  
 GAM1493 LOC203378 5' TTCTGTTACCACTCCT 90620 T AA  
 AGG AGT GTGGCAGAG  
 ||| ||| |||||  
 TCC TCA CATTGTCTT  
 \_ C\_  
 GAM1493 LOC203557 5' GCCCCTGCTGTTCAACACCTTT 89513 A A TG A\_  
 AGAGGT GT AG GCAG GC  
 ||||| || ||| ||  
 TTTCCA CA TT CGTC CG  
 C C GT CC  
 GAM1493 LOC206426 3' GCTCTGCCAGAAGCAGCT 89533 A AAG  
 GGT GT TGGCAGAGC  
 ||| || |||||  
 TCG CG ACCGTCTCG  
 A AAG  
 GAM1493 LOC220895 3' GCTCTGCCTTAGCACTCCCT 90823 T AAGT\_  
 AGG AGT GGCAGAGC  
 ||| ||| |||||  
 TCC TCA CCGTCTCG  
 C CGATT  
 GAM1493 LOC220929 3' GCTCTGCCGCCACCTT 91403 AGTAA  
 GAGGT GTGGCAGAGC  
 |||| |||||  
 TTCCA CGCCGTCTCG  
 C\_\_\_\_  
 GAM1493 LOC221466 5' GCTCCTTCCACCCCTACCTCT 93689 TAA CA\_  
 AGAGGTAG GTGG GAGC  
 ||||| ||| |||  
 TCTCCATC CACC CTCG  
 CC\_ TTC  
 GAM1493 LOC221692 3' CTGGCCACTTAACACCCCT 92240 A AG AG  
 AG GGT TAAGTGGC AG  
 || ||| ||||| ||  
 TC CCA ATTCACCG TC  
 C CA G\_  
 GAM1493 LOC221773 3' GCTGGGGCCACTACCTC 91050 AGTA AG\_  
 GAGGT AGTGGC AGC  
 |||| ||||| ||  
 CTCCA TCACCG TCG  
 \_\_\_\_\_ GGG  
 GAM1493 LOC221935 3' GCTCTGCCCAAAGCCACTTCT 92623 A AAGT  
 AGAGGT GT GGCAGAGC  
 ||||| || |||||  
 TCTTCA CG CCGTCTCG  
 C AAAC  
 GAM1493 LOC245771 5' CTTTGACAGCTACCTCT 92891 AAG G  
 AGAGGTAGT TG CAGAG  
 ||||| || |||

TCTCCATCG AC GTTTC  
 \_\_\_\_ A  
 GAM1493 LOC254755 5' CTCCTGTCCACACCTCT 97368 AGTAA \_ \_  
 AGAGGT GTGG CAG AG  
 ||||| ||| ||| ||  
 TCTCCA CACC GTC TC  
 \_\_\_\_ T C  
 GAM1493 LOC255096 5' GCCTGGGCTCCTACCTCT 97624 TA \_\_\_\_  
 AGAGGTAG AGT GGC  
 ||||| ||| |||  
 TCTCCATC TCG CCG  
 C\_ GGT  
 GAM1493 LOC256055 3' GCTCTGCCTGGCCAGCCCT 95932 A A\_ AAGT  
 AG GGT GT GGCAGAGC  
 || ||| || |||||  
 TC CCG CG CCGTCTCG  
 \_ AC GT\_\_  
 GAM1493 LOC256267 5' CTGTCTTACTACTCT 96801 G TG  
 AGAG TAGTAAG GCAG  
 ||| ||||| |||  
 TCTC ATCATTC TGTC  
 \_ \_  
 GAM1493 LOC256995 3' GTCACCTACTAGCCCT 97590 A \_  
 AG GGT AGTAAGTGGC  
 || ||| |||||  
 TC CCG TCATTCACTG  
 \_ A  
 GAM1493 LOC257109 3' GCCCTTCACTATCTCT 95572 \_ T  
 AGAGGTAGT AAG GGC  
 ||||| ||| |||  
 TCTCTATCA TTC CCG  
 C \_  
 GAM1493 LOC257479 5' GCTCTGCCCCGCGCCTC 96245 A AAGT  
 GAGGT GT GGCAGAGC  
 ||||| || |||||  
 CTCCG CG CCGTCTCG  
 \_ CC\_\_  
 GAM1493 LOC51112 5' CTCCTTTACTACCTC 32088 T C  
 GAGGTAGTAAG GG AG  
 ||||| ||| |||  
 CTCCATCATTT CC TC  
 \_ \_  
 GAM1493 LOC51145 3' CTCTGCTTACTTACCTC 32394 \_ AGT  
 GAGGTA GTA GGCAGAG  
 ||||| ||| |||||  
 CTCCAT CAT TCGTCTC  
 T \_\_\_\_  
 GAM1493 LOC57795 3' GCTCCCCTCCCTTACTCCTC 69323 T T CA\_\_  
 GAGG AGTAAG GG GAGC  
 ||| ||||| || |||

		CTCC TCATTCC CC	CTCG	
		_ _ TCCC		
GAM1493	LOC58512	3'	GCTTTGTCCCCACCTCCTC	64658 TA AAGT
			GAGG GT GGCAGAGC	
			CTCC CA CTGTTTCG	
			TC CCC_	
GAM1493	LOC83468	5'	GCTCTGCCTTGCAGCTCT	48518 GTA GT
			AGAG GTAA GGCAGAGC	
			TCTC CGTT CCGTCTCG	
			GA_ _	
GAM1493	LOC88745	3'	CTCTGCCACTGCCCC	92265 TA A
			GG GTA GTGGCAGAG	
			CC CGT CACCGTCTC	
			C_ _	
GAM1493	LOC90167	3'	CTCTTCCATTACCTCT	61703 GTAA C
			AGAGGTA GTGG AGAG	
			TCTCCAT TACC TCTC	
			_ _ T	
GAM1493	LOC90271	5'	GCTCTGCTCTCCTACCTC	61984 TA T
			GAGGTAG AG GGCAGAGC	
			CTCCATC TC TCGTCTCG	
			C_ _	
GAM1493	LOC90346	3'	GCCTTCTCACTATCTCT	56389 A T_
			AGAGGTAGT AG GGC	
			TCTCTATCA TC CCG	
			C TT	
GAM1493	LOC90415	3'	GCTCATACTTGCTACCTC	62710 GCA
			GAGGTAGTAAGTG GAGC	
			CTCCATCGTTCAT CTCG	
			A_	
GAM1493	LOC90826	5'	GCCTATGCCCACTACCTC	64094 AAGT GA_
			GAGGTAGT GGCA GC	
			CTCCATCA CCGT CG	
			C_ _ ATC	
GAM1493	LOC91208	5'	CTCTGCCACGCTCCCT	65247 T AA
			AGG AGT GTGGCAGAG	
			TCC TCG CACCGTCTC	
			C _	
GAM1493	LOC91250	5'	GCTCCAAATTCTCACTACTTCT	65325 A TGGCA_
			AGAGGTAGT AG GAGC	

TCTTCATCA TC CTOG  
 C TTAAAC  
 GAM1493 LOC91409 3' CTCTGCCCCTAGCTCC 65956 T A T  
 GG AGT AG GGCAGAG  
 || ||| || |||||  
 CC TCG TC CCGTCTC  
 \_ A C  
 GAM1493 LOC91695 5' GCTTCTCACTACCTCT 66970 A T  
 AGAGGTAGT AG GGC  
 ||||| || |||  
 TCTCCATCA TC TCG  
 C T  
 GAM1493 LOC92466 5' CTGTCTTACTACTCT 69426 G TG  
 AGAG TAGTAAG GCAG  
 ||| ||||| |||  
 TCTC ATCATTG TGTC  
  
 GAM1494 MMP20 3' TCCAAATCAACACAATGCAC 16484 CAGGA  
 GTGCATTGTGTTG TTGGG  
 ||||| |||||  
 CACGTAACACAAC AACCT  
 TA\_\_  
 GAM1494 PIM2 3' TCCCAATCCTACAAAGGAGC 59991 A GTG C  
 GC TT TTG AGGATTGGGA  
 || || ||| |||||  
 CG AG AAC TCCTAACCCT  
 \_ GA\_ A  
 GAM1494 RXRA 3' CCCAATCCTTAGCAATGC 11405 GTTGC  
 GCATTGT AGGATTGGG  
 ||||| |||||  
 CGTAACG TCCTAACCC  
 AT\_\_  
 GAM1494 BRAG 3' TCCCAATTCCAAAACACAATGC 29477 GCA  
 AC GTGCATTGTGTT GGATTGGGA  
 ||||| |||||  
 CACGTAACACAA CTTAACCCT  
 AAC  
 GAM1494 DKFZp547O146 5' CCCAATCCCCCAACAC 39564 CA  
 GTGTTG GGATTGGG  
 ||||| |||||  
 CACAAC CCTAACCC  
 CC  
 GAM1494 KIAA1762 3' TCCCAATCCCCACAGACACACA 63792 CAT GCA\_\_  
 C GTG TGTGTT GGATTGGGA  
 || |||| |||||  
 CAC ACACAG CCTAACCCT  
 \_ ACACC  
 GAM1494 LOC145820 3' CCCAATCCTTAAGCAATCAC 77512 C GTTGC  
 GTG ATTGT AGGATTGGG  
 || |||| |||||

CAC TAACG TCCTAACCC  
\_ AAT\_  
GAM1494 LOC253980 3' TCCCAACCCCATTGCTAACAA 95076 GTT \_ A  
TTGT GCA GG TTGGGA  
||||| ||| || |||||  
AACA CGT CC AACCCCT  
AT\_ TAC C  
GAM1495 ABCB11 5' TCTGGCTTCCTCAAATTC 13618 A ATGA  
GAATTTGA GAAG AGA  
||||||| ||| |||  
CTTAAACT CTTC TCT  
C GG\_  
GAM1495 APC 3' CTTTCATCTTCTTGTGCA 3477 G TTG  
TG AAT AAGAAGATGAAG  
|| ||| |||||  
AC TTG TTCTTCTACTTC  
G \_  
GAM1495 ATP1B2 3' CTTCCCAGAATATCCTTCAAGT 8049 AA AA\_  
TCCA GGAATTTGAAG GATG GAAG  
||||||| ||| |||  
CCTTGAAGCTTC CTAT CTTC  
\_ AAGACC  
GAM1495 CA4 3' TCAGCTCTCCAAGTTCCA 5552 A AGA  
TGGAATTTG AGA TGA  
||||||| ||| |||  
ACCTTGAAC TCT ACT  
C CG\_  
GAM1495 CEP1 5' CTTCCGTTTCGTTCTTCAAAACC 22816 AA \_ T\_  
CA TGG TTTGAAGAA GA GAAG  
||| ||||| || |||  
ACC AAATTCTT CT CTTC  
CA G TGC  
GAM1495 CEP2 3' CTTTCATCTTCTCCTTCAA 23227 \_  
TTGA AGAAGATGAAG  
||||| |||||  
AACT TCTTCTACTTC  
TCC  
GAM1495 FBLN5 3' CTTCTTCACCTCTTCCACTCC 20916 ATTT A A  
GGA GAAGA G TGAAGAAG  
||| ||||| |||||  
CCT CTTCT C ACTTCTTC  
CAC\_ \_ C  
GAM1495 GAC1 3' TCCCCATCTTCTCTCTGCCCA 20945 AATTT \_ AA  
TGG GA AGAAGATG GA  
||| || ||||| ||  
ACC CT TCTTCTAC CT  
CGT\_ C CC  
GAM1495 GATA4 3' CTTCCCTCCTCAAATTCC 9005 A AGAT  
GGAATTTGA GA GAAG  
||||||| || |||

			CCTTAAACT CT CTTC		
			C CC__		
GAM1495 MGA	3'	TTCTTTATCCCAAATCCCA	62812	A	AAGAA
		TGG ATTTG GATGAAGAA			
		ACC TAAAC CTATTTCTT			
		C C__			
GAM1495 PIK3R3	3'	TCGTTTCCTTACAAATTCCA	61064	_	A
		TGGAATTTG AAG AGATGA			
		ACCTTAAAC TTC TTTGCT			
		A C			
GAM1495 POU2F2	3'	TCTTCATCCTCATCCTCC	10692	ATTT	A A
		GGA GA GA GATGAAGA			
		CCT CT CT CTACTTCT			
		C__ A C			
GAM1495 PTPRS	3'	TCCTTTCCTTCCAATTCCA	11141	T	A T
		TGGAATT GAAG AGA GA			
		ACCTTAA CTTC TTT CT			
		C C C			
GAM1495 PTPRS	3'	TCCTTTCCTTCCAATTCCA	55645	T	A T
		TGGAATT GAAG AGA GA			
		ACCTTAA CTTC TTT CT			
		C C C			
GAM1495 PTPRS	3'	TCCTTTCCTTCCAATTCCA	55648	T	A T
		TGGAATT GAAG AGA GA			
		ACCTTAA CTTC TTT CT			
		C C C			
GAM1495 PTPRS	3'	TCCTTTCCTTCCAATTCCA	55651	T	A T
		TGGAATT GAAG AGA GA			
		ACCTTAA CTTC TTT CT			
		C C C			
GAM1495 SELL	3'	TCCCCACCTTCTTCAGCCACC	5393	AAT	A AA
		GG TTGAAGAAG TG GA			
		CC GACTTCTTC AC CT			
		ACC C CC			
GAM1495 TEM7	3'	CTTTTTCTTCCTCAAATTC	39885	A	T
		GAATTTGA GAAGA GAAG			
		CTTAAACT CTTCT TTTC			
		C T			
GAM1495 WT1	3'	TTCTTCATCCAACCTTCCA	44357	T	AAGAA
		TGGAA TTG GATGAAGAA			



ACCTT AAC CTACTTCTT  
 C \_\_\_\_\_  
 GAM1495 WT1 3' TTCTTCATCCAACCTTCCA 44367 T AAGAA  
 TGGAA TTG GATGAAGAA  
 ||||| ||| |||||  
 ACCTT AAC CTACTTCTT  
 C \_\_\_\_\_  
 GAM1495 WT1 3' TTCTTCATCCAACCTTCCA 44377 T AAGAA  
 TGGAA TTG GATGAAGAA  
 ||||| ||| |||||  
 ACCTT AAC CTACTTCTT  
 C \_\_\_\_\_  
 GAM1495 WT1 3' TTCTTCATCCAACCTTCCA 4592 T AAGAA  
 TGGAA TTG GATGAAGAA  
 ||||| ||| |||||  
 ACCTT AAC CTACTTCTT  
 C \_\_\_\_\_  
 GAM1495 AD-003 5' CTTCCCATCTTCTTC 25931 AA  
 GAAGAAGATG GAAG  
 ||||| |||  
 CTTCTTCTAC CTTC  
 CC  
 GAM1495 CEACAM7 3' CTTCTAGCTCCTTCAATCCCA 22557 AAT A AT\_  
 TGG TTGAAG AG GAAG  
 ||| ||||| || |||||  
 ACC AACTTC TC CTTC  
 CT\_ C GAT  
 GAM1495 CSMD1 3' CTTCTTTGTCCTCAATTTCCA 73120 T AGAA TG  
 TGGAA TTGA GA AAGAAG  
 ||||| ||||| || |||||  
 ACCTT AACT CT TTCTTC  
 T C\_\_ GT  
 GAM1495 DDX34 3' CATGTCTCCAGATTCCA 27979 A AG  
 TGAATTTG AGA ATG  
 ||||| ||| |||  
 ACCTTAGAC TCT TAC  
 C G\_  
 GAM1495 DKFZP434B205 3' CTTCTTCATCTTCTGACGTC 75320 ATTTGAA  
 GA GAAGATGAAGAAG  
 || |||||  
 CT CTTCTACTTCTTC  
 GCAGGTC  
 GAM1495 FENS-1 3' CTTCCCTTTCCCCCAAATTCC 40439 AA\_ AT  
 GGAATTTG GAAG GAAG  
 ||||| ||| |||  
 CCTTAAAC CTTT CTTC  
 CCC CC  
 GAM1495 FLJ13262 3' ATCCTCTCCAAATTCC 46155 A A  
 GGAATTTG AGA GAT  
 ||||| ||| |||

CCTTAAAC TCT CTA  
 C C  
 GAM1495 FLJ20170 3' TCACCTTCTTCAACTCCA 34672 AT A  
 TGGG TTGAAGAAG TGA  
 |||| ||||| ||  
 ACCT AACTTCTTC ACT  
 C\_ C  
 GAM1495 FLJ20375 3' CTTCTCCCTGCTAAATTCCA 35085 A\_ AA T  
 TGGGATTTG AG GA GAAG  
 ||||| || ||||  
 ACCTTAAAT TC CT CTTC  
 CG C\_ \_  
 GAM1495 FLJ20802 3' CTTCTTCACCTTTGCATCC 35669 ATT AA A  
 GGA TG GAAG TGAAGAAG  
 || || |||| |||||  
 CCT AC TTTC ACTTCTTC  
 \_ G\_ C  
 GAM1495 FLJ22055 3' CTTTCATCTTCTGCTCCA 45496 ATTTGA  
 TGGG AGAAGATGAAG  
 |||| |||||  
 ACCT TCTTCTACTTC  
 CG\_  
 GAM1495 HUMAGCGB 5' CTATGCCTTCCTCAAGTTCCA 25231 A AT A  
 TGGGATTTGA GAAG G AG  
 ||||| ||| ||  
 ACCTTGAAGT CTTC T TC  
 C CG A  
 GAM1495 INA 3' CACCTCCTTCAATTCCA 51187 T A A  
 TGGGATT GAAG AG TG  
 ||||| ||| ||  
 ACCTTAA CTTC TC AC  
 \_ C C  
 GAM1495 KIAA0451 5' TCATAATTCTCAAATTCCA 29114 AG AG  
 TGGGATTTGA A ATGA  
 ||||| || |||  
 ACCTTAAAGT T TACT  
 CT AA  
 GAM1495 KIAA0972 5' CTTCTTCATCCCCTTGCCCA 30010 AATTTG AA  
 TGG AAG GATGAAGAAG  
 || || |||||  
 ACC TTC CTACTTCTTC  
 CG\_ CC  
 GAM1495 MGC15854 5' TTCCCCATCTTCTCCTCTA 58852 ATTT A AA  
 TGGG GA GAAGATG GAA  
 |||| || ||||| ||  
 ATCT CT CTTCTAC CTT  
 C\_ \_ CC  
 GAM1495 MGC17998 3' TTCCTCATCTTCTGGTCC 58746 ATTTGA A  
 GGA AGAAGATGA GAA  
 || ||||| |||

			CCT	TCTTCTACT	CTT		
			GG		C		
GAM1495	MIL1	3'	TCTTCACCCCCAGGTTCC	31097		AAGAAGA	
			GGAATTTG		TGAAGA		
			CCTTGGAC		ACTTCT		
			CCCC				
GAM1495	NYD-SP21	3'	CTTCAGCTTCCTCAAATTC	50873		A	A
			GAATTTGA		GAAG TGAAG		
			CTTAAACT		CTTC ACTTC		
			C		G		
GAM1495	PCDH19	3'	TTCTTCATCCAAAATTGCA	63713		G	GAAGAA
			TG AATTT		GATGAAGAA		
			AC TTAAA		CTACTTCTT		
			G		AC		
GAM1495	PEG10	3'	CTTCACCGTCTTCAAACCTCCA	30525		A	AGA
			TGGA TTTGAAGA		TGAAG		
			ACCT AAACCTTCT		ACTTC		
			C		GCC		
GAM1495	TRIM16	3'	TCATCTTCTAGTGCCA	21343		A	TGA
			TGG ATT		AGAAGATGA		
			ACC TGA		TCTTCTACT		
			G				
GAM1495	LOC124245	3'	CTCCATCTTCTTCCCTGGCC	58152		AATTT	A
			GG		GAAGAAGATG AG		
			CC		CTTCTTCTAC TC		
			GGTCC		C		
GAM1495	LOC144231	5'	ATCTTCCTCAAACCTTCA	83011		A	A
			TGGA TTTGA		GAAGAT		
			ACTT AAACCT		CTTCTA		
			C		C		
GAM1495	LOC145739	3'	TCATTCTTCAAAGCCCA	77443		AA	AG
			TGG TTTGAAGA		ATGA		
			ACC AAACCTTCT		TACT		
			CG				
GAM1495	LOC146856	3'	CTTCCTTTTTTCTTCTTCAACC	82802		AT	T_ _
			TCCA		TGGA TTGAAGAAGA		GAAG AAG
			ACCT AACTTCTTCT		TTTC TTC		
			CC		TT C		
GAM1495	LOC147166	3'	TCATCTTCTAGTGCCA	78290		A	TGA
			TGG ATT		AGAAGATGA		

	ACC TGA TCTTCTACT	
	G ____	
GAM1495 LOC151124 5'	TCTGTTCTTCCCCAAATTCC 85234	AA TGA
	GGAATTTG GAAGA AGA	
	CCTTAAAC CTTCT TCT	
	CC TG_	
GAM1495 LOC151405 5'	CTTCTTCATGACACCAAATCCA 85337	A AAGAAG
	TGGA TTTG ATGAAGAAG	
	ACCT AAAC TACTTCTTC	
	_ CACAG_	
GAM1495 LOC151438 5'	CTTCTGGGACCAAATCCA 85365	A_____
	TGGAATTTG AGAAG	
	ACCTTAAAC TCTTC	
	CAGGG	
GAM1495 LOC153469 3'	CTTCATCTTCTCCTCA 80841	__
	TGA AGAAGATGAAG	
	ACT TCTTCTACTTC	
	CC	
GAM1495 LOC157909 5'	CTTCTCAGACTTAAAATTCCA 81627	G AAGA A
	TGGAATTT AAG TGA GAAG	
	ACCTTAAA TTC ACT CTTC	
	A AG__ _	
GAM1495 LOC165140 5'	TCTTCATCTTCTGCATCCA 82467	ATT A
	TGGA TG AGAAGATGAAGA	
	ACCT AC TCTTCTACTTCT	
	__ G	
GAM1495 LOC169831 5'	CTTCTTCATCTTCCCTTC 82783	__
	GAA GAAGATGAAGAAG	
	CTT CTCTACTTCTTC	
	CC	
GAM1495 LOC197414 3'	CTTGGCTTCTTCAAACGCCA 88066	AA ATG
	TGG TTTGAAGAAG AAG	
	ACC AAATTCTTC TTC	
	GC GG_	
GAM1495 LOC219894 3'	CTTCCCAACTTCTTCAAATTC 93281	A AA
	GAATTTGAAGAAG TG GAAG	
	CTTAAACTTCTTC AC CTTC	
	A C_	
GAM1495 LOC255040 3'	CTTCCTTTTGCTCCAAATTC 96382	A _ T
	GGAATTTG AG AAGA GAAG	

CCTTAAAC TC TTTT CTTC  
 C G C  
 GAM1495 LOC255041 3' CTTCTTTTGCTCCAAATTCC 96388 A \_ T  
 GGAATTTG AG AAGA GAAG  
 ||||| || ||| |||  
 CCTTAAAC TC TTTT CTTC  
 C G C  
 GAM1495 LOC90371 5' TCTTCATCCTCCTCTACC 62504 AATT A A  
 GG GA GA GATGAAGA  
 || || || |||||  
 CC CT CT CTACTTCT  
 AT\_\_ C C  
 GAM1495 LOC92539 5' TCCTCTCTTCAAGTCCCA 69643 A A T  
 TGG ATTTGAAGA GA GA  
 || ||||| || ||  
 ACC TGAACCTTCT CT CT  
 C \_ C  
 GAM1496 CYP4A11 5' CTGGCACACAGTAAATGCTCA 5755 TA C A  
 TG CA TTACT TGTGCCAG  
 || || || |||||  
 AC GT AATGA ACACGGTC  
 TC A C  
 GAM1496 D10S170 3' GTATAAGCAAGTGTACAA 18366 A A  
 TTGTACACTT CT TGTGC  
 ||||| || |||  
 AACATGTGAA GA ATATG  
 C \_  
 GAM1496 DLEU1 3' CTGGCACACAGTAAGCACTCAA 19695 TACA A  
 TA TATTG CTTACT TGTGCCAG  
 |||| ||||| |||||  
 ATAAC GAATGA ACACGGTC  
 TCAC C  
 GAM1496 DVL3 3' GCTGGCACACAGTAGAGTAGGT 15370 A A\_\_\_\_\_ |||  
 GCTCAATA CACTTACT TGTGCCAG C  
 ||||| ||||| |  
 GTGGATGA ACACGGTC G  
 C GATGAC |||  
 GAM1496 GJB3 5' CTGGTACATAGTAAATGCTCAA 43767 TA C  
 TA TATTG CA TTACTATGTGCCAG  
 |||| || ||||| |||||  
 ATAAC GT AATGATACATGGTC  
 TC A  
 GAM1496 IRTA1 3' ATGGAAGTGTACAATA 48417 A  
 TATTGTACACTT CTAT  
 ||||| |||||  
 ATAACATGTGAA GGTA  
 \_  
 GAM1496 JJAZ1 3' CTGGCACATTAACAAGCACCAA 31079 TACA ACT\_  
 TA TATTG CTT ATGTGCCAG  
 |||| || |||||

			ATAAC GAA TACACGGTC		
			CAC_ CAAT		
GAM1496	MEF2D	3'	CTGGCACATAGTAGGCACTCAA 96912	TACA	
	TA		TATTG CTTACTATGTGCCAG		
			ATAAC GGATGATACACGGTC		
			TCAC		
GAM1496	PLS3	3'	GTATGCTAAGTGTACAATA 17273	CTA	
			TATTGTACACTTA TGTGC		
			ATAACATGTGAAT GTATG		
			C_		
GAM1496	S100A6	3'	TGGTGGGTAATTGTACAATA 27546	C ATG	
			TATTGTACA TTACT TGCCA		
			ATAACATGT AATGG GTGGT		
			T _		
GAM1496	SULT1C1	3'	CTGGCACACAGCAAGTG 6466	A A	
			CACTT CT TGTGCCAG		
			GTGAA GA ACACGGTC		
			C C		
GAM1496	TRIM14	3'	CTGACACATAGTAGGCACACAG 28855	ACA C	
	TA		TATTGT CTTACTATGTG CAG		
			ATGACA GGATGATACAC GTC		
			CAC A		
GAM1496	ZNF10	3'	CTGGCACATAGTAGGTG 31179		
			CACTTACTATGTGCCAG		
			GTGGATGATACACGGTC		
GAM1496	C4.4A	3'	CTGGCACATAAATGCCTCAATA 26945	TACACTTAC	
			TATTG TATGTGCCAG		
			ATAAC ATACACGGTC		
			TCCGTAA_		
GAM1496	CDH22	3'	CTGGCACATAGTAGGTGTTCAA 41156	T	
	TA		TATTG ACACTTACTATGTGCCAG		
			ATAAC TGTGGATGATACACGGTC		
			T		
GAM1496	CRTAC1	3'	CTGGCACATAGTAAAGGCTCAA 36025	TACAC	
	TA		TATTG TTACTATGTGCCAG		
			ATAAC AATGATACACGGTC		
			TCGGA		
GAM1496	DKFZP434J193	3'	CTGGCACACTCAGGTAACAA 71005	AC ACTA	
			TTGT ACTT TGTGCCAG		

		AACA TGGA ACACGGTC		
		A_ CTC_		
GAM1496	DKFZp761P1010	3' CTGGCACATATGCGCTCAATA	37338	TACACTTAC
		TATTG TATGTGCCAG		
		ATAAC ATACACGGTC		
		TCGCGT__		
GAM1496	FLJ12598	3' CTGGCACATAGTACATGCAATA	45396	CACT
		TATTGTA TACTATGTGCCAG		
		ATAACGT ATGATACACGGTC		
		AC__		
GAM1496	FLJ20320	3' CTGGCACACAGTAAGTGCCTGG	34941	TA A
	TA	TATTG CACTTACT TGTGCCAG		
		ATGGT GTGAATGA ACACGGTC		
		CC C		
GAM1496	HSPC065	3' CTGGCACACAGCAAACACTCAA	26298	TACACTTA A
	TA	TATTG CT TGTGCCAG		
		ATAAC GA ACACGGTC		
		TCACAAAC C		
GAM1496	KIAA0227	3' GCACATAGAATGTGTTCAA	60697	T TTA
		TTG ACAC CTATGTGC		
		AAC TGTG GATACACG		
		T TAA		
GAM1496	KIAA0970	3' CATATAACAAGTGTACA	29955	AC
		TGTACACTT TATGTG		
		ACATGTGAA ATATAC		
		CA		
GAM1496	KIAA1130	3' GCACATAGTAGATGTTCAATA	62422	T C
		TATTG ACA TTA CTATGTGC		
		ATAAC TGT GATGATACACG		
		T A		
GAM1496	PRO1787	3' CTGGCATGCAGGAAGCATACAA	37768	CA A AT
	TA	TATTGTA CTT CT GTGCCAG		
		ATAACAT GAA GA TACGGTC		
		AC G CG		
GAM1496	VELI1	3' GCACATAGTAAAAGACAA	16236	ACAC
		TTGT TTA CTATGTGC		
		AACA AATGATACACG		
		GAA_		
GAM1496	LOC113523	3' CTGATACATAGTAAACTCACAA	73045	ACAC C
	TA	TATTGT TTA CTATGTG CAG		

	ATAACA AATGATACAT GTC	
	CTCA A	
GAM1496 LOC143903 3'	CTGGCACATAGTAGAGTCTCAA 76618	TAC _
TA	TATTG ACTT ACTATGTGCCAG	
	ATAAC TGAG TGATACACGGTC	
	TC_ A	
GAM1496 LOC150481 3'	GCTCAGAGTAAGTGCTCAATA 79889	TA A T
	TATTG CACTTACT TG GC	
	ATAAC GTGAATGA AC CG	
	TC G T	
GAM1496 LOC150622 3'	GCATTTTGAAATGTACAATG 79960	C ACTAT
	TATTGTACA TT GTGC	
	GTAACATGT AA TACG	
	A GTTT_	
GAM1496 LOC154562 3'	CTGGCACATAGTAGGCACTCAA 81091	TACA
TA	TATTG CTTACTATGTGCCAG	
	ATAAC GGATGATACACGGTC	
	TCAC	
GAM1496 LOC158191 3'	CTGGCTCAGAGTAAGTGCTCAA 81774	TA A T
TA	TATTG CACTTACT TG GCCAG	
	ATAAC GTGAATGA AC CGGTC	
	TC G T	
GAM1496 LOC197358 3'	CTGGCACACTGGTTATCAATA 88034	TACACTT _
	TATTG ACTA TGTGCCAG	
	ATAAC TGGT ACACGGTC	
	TAT___ C	
GAM1496 LOC203068 3'	CTGGCACATAGTAGGCGCTCAA 89255	TACA
TA	TATTG CTTACTATGTGCCAG	
	ATAAC GGATGATACACGGTC	
	TCGC	
GAM1496 LOC205327 3'	TGTCCACAAGTGTTACAATA 89504	TACTA C_
	TATTGTACACT TGTG CA	
	ATAACATGTGA ACAC GT	
	___ CT	
GAM1496 LOC219942 3'	CTGGCACATTGTCAATGTTCAA 93345	T CTT T
TA	TATTG ACA AC ATGTGCCAG	
	ATAAC TGT TG TACACGGTC	
	T AAC T	
GAM1496 LOC221354 3'	CTGGCACTTAGTAGGTGCACAA 92410	A T
	TTGT CACTTACTA GTGCCAG	



			AACA GTGGATGAT CACGGTC		
			C T		
GAM1496	LOC255269	3'	TGGTGGGTAATTGTACAATA	94603	C ATG
			TATTGTACA TTACT TGCCA		
			ATAACATGT AATGG GTGGT		
			T _		
GAM1496	LOC255919	3'	ACAAGAAGTGTGCAATA	95030	A A
			TATTGTACACTT CT TGT		
			ATAACGTGTGAA GA ACA		
			- -		
GAM1496	LOC91628	3'	TAGTAAGTGCTCAATA	66762	TA
			TATTG CACTTACTA		
			ATAAC GTGAATGAT		
			TC		
GAM1496	LOC92755	3'	CTGGCACATAGTAGGCACTCAA	70501	TACA
		TA	TATTG CTTACTATGTGCCAG		
			ATAAC GGATGATACACGGTC		
			TCAC		
GAM1497	ADH1B	3'	CTTAGACATAAAGTAAAAT	72644	C CAC
			ATTT ACTTT TGTCTGAG		
			TAAA TGAAA ACAGATTC		
			A T_		
GAM1497	AHR	3'	ATCTCAGATGTTAAAATAAATG	7875	CAC C T
			CATTT TTT AC GTCTGAGAT		
			GTAAA AAA TG TAGACTCTA		
			TA_ T _		
GAM1497	FDFT1	3'	TAGGAAAGTGAAATG	15518	A
			CATTTCACTTTC CTG		
			GTAAAGTGAAAG GAT		
			-		
GAM1497	JTB	3'	ATCTCAGACAGTGAAAGTGAAA	21959	
	TG		CATTTCACTTTCACTGTCTGAGAT		
			GTAAAGTGAAAGTGACAGACTCTA		
GAM1497	KLF4	3'	TCCCAGACAGTGGATATG	14891	CT A
			CA TTCACTGTCTG GA		
			GT AGGTGACAGAC CT		
			AT C		
GAM1497	PHYH	3'	ACAGTAAAAGTGAAAT	20608	C
			ATTTCACTTT ACTGT		

			TAAAGTGAAA TGACA		
			A		
GAM1497	PKD2	3'	TCCAGGTTGAAAAGTGAAA 60096	CTG	A
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T__ _		
GAM1497	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1497	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA	CTG
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1497	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT	CT
			TTCAC TTTCA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1497	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G	T_
			CTTTCACT TC GAGAT		
			GAAAGTGA AG TTCTA		
			G TC		
GAM1497	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT 45802	ACTTTCACT	
	G		CATTTT GTCTGAGAT		
			GTAAAG CAGACTCTA		
			AAACATTT_		
GAM1497	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281	CTT	
			CATTTCA TCACTGTCTGAGAT		
			GTAAAGT AGTGACAGACTCTA		
			C_		
GAM1497	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C	TC
			TTCA TTTCACTG TGAG		
			AAGT AAAGTGAC GTTT		
			A CT		
GAM1497	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A	_
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1497	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T	
			ATT CACTTTCACTGT		

		TAA GTGAAAGTGACG	
		C	
GAM1497	PORIMIN	3' ATCTCAGAGGGCCAAAGTGAA 53598	CA G
		TTCACTTT CT TCTGAGAT	
		AAGTGAAA GG AGACTCTA	
		CC G	
GAM1497	PP35	3' ATCTCAGACTGAAA 22814 CT	
		TTTCA GTCTGAGAT	
		AAAGT CAGACTCTA	
		—	
GAM1497	PRTD-NY3	3' CTCATTGCAATAAGTGAAATG 48148	TCAC C_
		CATTTCACTT TGT TGAG	
		GTAAAGTGAA ACG ACTC	
		TA__ TT	
GAM1497	SEP15	3' TCCTACAGTAAGAGTGAAA 14934	C CT
		TTTCACTTT ACTGT GA	
		AAAGTGAGA TGACA CT	
		A TC	
GAM1497	SFXN2	3' CTCAGGGGAAAAAAGTGAAA 73941	CACTG
		TTTCACTTT TCTGAG	
		AAAGTGAAA GGA CTC	
		AAAGG	
GAM1497	LOC149703	3' ATCTCAGACAGCCGTTTGAAAA 84647	ACTTTCA
		TTTC CTGTCTGAGAT	
		AAAG GACAGACTCTA	
		GTTTGCC	
GAM1497	LOC154007	3' ATCTCAAACCCTTTAGTGAAA 81015	TTCACT C
		TTTCACT GT TGAGAT	
		AAAGTGA CA ACTCTA	
		TTTCC_ A	
GAM1497	LOC155004	3' TCATTTAAGTGAAAGGAAA 81226	A GTC_
		TTTC CTTTCACT TGA	
		AAAG GAAAGTGA ACT	
		_ ATTT	
GAM1497	LOC222134	5' ACAGTGAAGTGAAATG 94136	T
		CATTTCACTT CACTGT	
		GTAAAGTGAA GTGACA	
		—	
GAM1498	ATP11A	3' CCCCAGGGCTGCTGTGATA 77026	CA_ T
		TATCACAGC TCTGG GG	

			ATAGTGTCTG	GGACC CC		
			TCG _			
GAM1498	CABC1	5'	CAGCCCTGAAGGATGGCTGCCA	39652	CA	GGT_ A
	TA		TAT CAGCCATCT GG GCTG			
			ATA GTCGGTAGG CC CGAC			
			CC AAGT _			
GAM1498	FBXL7	3'	CAGCTCTGTCAATGACTATGA	24544	C C C	TG
			TCA AG CAT TGG GAGCTG			
			AGT TC GTA ACT CTCGAC			
			A A _ GT			
GAM1498	GBE1	3'	CAGCTCCACCAGATGC	3851	C	
			GC ATCTGGTGGAGCTG			
			CG TAGACCACCTCGAC			
			_			
GAM1498	GPR30	5'	CAGCTCCACGCGGGACTGTG	7690	CCA	_
			CACAG TCTG GTGGAGCTG			
			GTGTC GGGC CACCTCGAC			
			A_ G			
GAM1498	STAT6	3'	AGTGGGTCCAAGTGGCTGTGA	12018	TC	TGGA
			TCACAGCCA TGG GCT			
			AGTGTCTGGT ACC TGA			
			GA TGGG			
GAM1498	TNNI1	5'	CAGCTCCACGAGGACTG	12348	CCA	G
			CAG TCT GTGGAGCTG			
			GTC GGA CACCTCGAC			
			A_ G			
GAM1498	CLECSF9	3'	CAGCTCCAAACAGGCTGT	26838	ATCTGG	
			ACAGCC TGGAGCTG			
			TGTCTGG ACCTCGAC			
			ACAA_			
GAM1498	DKFZP434C0826	5'	CAGCTCCACCTTTCTGTGAT	84034	CCATCT	
			ATCACAG GGTGGAGCTG			
			TAGTGTC CCACCTCGAC			
			TTT_			
GAM1498	FBP17	3'	CAGCCTCCCAAATAGCTGTGAT	72783	C C	TG A
			ATCACAGC AT TGG G GCTG			
			TAGTGTCG TA ACC C CGAC			
			A A CT_			
GAM1498	FLJ13993	3'	GCCCCACACTGTGATG	60461	CCATCTG	A
			TATCACAG GTGG GC			

			GTAGTGTC	CACC CG		
			A_____	C		
GAM1498	FLJ14007	3'	CAGCTGTTGATTGGCTGTGA	45210	TC GG GG	
			TCACAGCCA T T AGCTG			
			AGTGTCGGT G G TCGAC			
			TA TT _			
GAM1498	FLJ20371	3'	CAGCCTGTGCTGGCTGCAATA	35058	CA TCTG TG A	
			TAT CAGCCA G G GCTG			
			ATA GTCGGT T C CGAC			
			AC CG__GT_			
GAM1498	FLJ23548	5'	ACTAGATGGCTATGATA	44745	C	
			TATCA AGCCATCTGGT			
			ATAGT TCGGTAGATCA			
			A			
GAM1498	GMFB	3'	AGCAAAGAGCTGTGATA	14662	CA GGTGGA	
			TATCACAGC TCT GCT			
			ATAGTGTCG AGA CGA			
			_ AA_____			
GAM1498	KIAA0252	3'	CAGCTTTGTGGTAGCTGTGA	62788	C TG TG	
			TCACAGC ATC G GAGCTG			
			AGTGTCG TGG T TTCGAC			
			A _GT			
GAM1498	KIAA0319	3'	CAGTCAGATGGCTGTG	29033	_	
			CACAGCCATCTGG TG			
			GTGTCGGTAGACT AC			
			G			
GAM1498	KIAA1257	3'	CAGCCTGTGCAGATGGCTGTG	62731	_TG A	
			CACAGCCATCTG G G GCTG			
			GTGTCGGTAGAC T C CGAC			
			G GT _			
GAM1498	MGC2474	3'	CAGCCTCTCAGATGGCTGTGA	43716	GT A	
			TCACAGCCATCTG GG GCTG			
			AGTGTCGGTAGAC TC CGAC			
			TC _			
GAM1498	MGC33177	3'	AGCACAGATGGCCATGA	58009	CA GTGGA	
			TCA GCCATCTG GCT			
			AGT CGGTAGAC CGA			
			AC A_____			
GAM1498	NLI-IF	3'	AGCCCCACCAGGCGGTGT	41045	G AT A	
			ACA CC CTGGTGG GCT			

			TGT GG GACCACC CGA		
			_ CG C		
GAM1498	LOC130902	3'	CACCAATGGCTATGA	74991	C C
			TCA AGCCAT TGGTG		
			AGT TCGGTA ACCAC		
			A _		
GAM1498	LOC149194	3'	AGTACAGATGGCTGT	79222	GTGGA
			ACAGCCATCTG GCT		
			TGTCGGTAGAC TGA		
			A _		
GAM1498	LOC151473	5'	CAGCTCCACCAAACGCT	80255	CATC
			AGC TGGTGGAGCTG		
			TCG ACCACCTCGAC		
			CAA_		
GAM1498	LOC90784	5'	CAGCTCCACCTGGGGCT	63999	A T
			AGCC TC GGTGGAGCTG		
			TCGG GG CCACCTCGAC		
			_ T		
GAM1499	BTRC	3'	AGCACAACTGACTGCTTCA	14139	ATA
			TGAGGCAGTCAGTT TGTT		
			ACTTCGTCAGTCAA ACGA		
			C_		
GAM1499	BTRC	3'	AGCACAACTGACTGCTTCA	53310	ATA
			TGAGGCAGTCAGTT TGTT		
			ACTTCGTCAGTCAA ACGA		
			C_		
GAM1499	VHL	3'	CCAAACATAAGCCACCAGCCTC	5066	AGTCA A
	A		TGAGGC GTT TATGTTTG		
			ACTCCG CGA ATACAAACC		
			ACCAC _		
GAM1499	FLJ20557	3'	CCACCTAGTAACTGGCTGCCTC	61896	ATGTT
	A		TGAGGCAGTCAGTTAT TGG		
			ACTCCGTCGGTCAATG ACC		
			ATCC_		
GAM1499	PRO0611	5'	CAGACAACCAACTGACTCA	26009	C ATA
			G AGTCAGTT TGTTTG		
			A TCAGTCAA ACAGAC		
			C CCA		
GAM1499	SES2	3'	CAAACCTCTGACTGCC	48805	TTATAT
			GGCAGTCAG GTTTG		

		CCGTCAGTC CAAAC		
		TC____		
GAM1499	LOC115399 3'	CCATGGTAACTGACTTGCCTCA 73429	_	ATGTT
		TGAGGCA GTCAGTTAT TGG		
		ACTCCGT CAGTCAATG ACC		
		T GT____		
GAM1499	LOC221087 3'	AAACACACCGACTGCCTCA 93238	A	TATA
		TGAGGCAGTC GT TGTTT		
		ACTCCGTCAG CA ACAA		
		C C____		
GAM1499	LOC255975 5'	CAGGCACAACTGCTGCCTCA 95885	T	ATA
		TGAGGCAG CAGTT TGTTTG		
		ACTCCGTC GTCAA ACGGAC		
		- C____		
GAM1499	LOC256477 5'	CCAGGACGCAACTGACTGCC 97439		ATATG
		GGCAGTCAGTT TTTGG		
		CCGTCAGTCAA GGACC		
		CGCA_		
GAM1500	ACAA1 3'	CATTGGAATGTGAA 7837		CT
		TTCACATTTTCTA TG		
		AAGTGTAAGGT AC		
		TT		
GAM1500	CD69 3'	TGGAATATGTGCAATA 8356	T	
		TATT CACATTTTCTA		
		ATAA GTGTAAAGGT		
		C		
GAM1500	CLK2 3'	GTGAATATGTGAAATA 14339	T	T
		TATTTACAT TTC AC		
		ATAAAGTGTA AAG TG		
		T _		
GAM1500	CLK2 3'	GTGAATATGTGAAATA 7097	T	T
		TATTTACAT TTC AC		
		ATAAAGTGTA AAG TG		
		T _		
GAM1500	CLK2 3'	GTGAATATGTGAAATA 60382	T	T
		TATTTACAT TTC AC		
		ATAAAGTGTA AAG TG		
		T _		
GAM1500	CNN2 3'	TCCGTGAGATAATGTGAAATA 15179	T	ACTT
		TATTTACATT TCT GA		

		ATAAAGTGTAAGAGACT			
		TGTGC			
GAM1500	DSCR5	3' TGTTC AAGTATTGTTAATG 33154	TTC__		
		CATT TACTTGAACA			
		GTAA ATGAACTTGT			
		TTGTT			
GAM1500	FKBP1B	3' TCTTTGAGAAAATGTAAAATA 54012	C	ACTT	
		TATTTACATTTTCTGA			
		ATAAA TGTAAGA CT			
		A GTTT			
GAM1500	FKBP1B	3' TCTTTGAGAAAATGTAAAATA 14651	C	ACTT	
		TATTTACATTTTCTGA			
		ATAAA TGTAAGA CT			
		A GTTT			
GAM1500	GPLD1	3' AGAAATATGTGAAATA 92016	_		
		TATTTACATTTTCT			
		ATAAAGTGTA AAAGA			
		T			
GAM1500	MRC1	3' TAGATAATGTGAAATA 10115	T		
		TATTTACATT TCTA			
		ATAAAGTGTAAGAT			
		T			
GAM1500	NRXN1	3' TTCAAAAATGTGAAATA 57033	CTACT		
		TATTTACATTTT TGAA			
		ATAAAGTGTA AAAA ACTT			
GAM1500	NRXN1	3' TTCAAAAATGTGAAATA 16637	CTACT		
		TATTTACATTTT TGAA			
		ATAAAGTGTA AAAA ACTT			
GAM1500	OTC	5' AGGTAGAAAAGTGAAATA 5000	A		
		TATTTCAC TTTTCTACTT			
		ATAAAGTG AAAAGATGGA			
GAM1500	PPIF	3' TGTTCACCTTAAATGTGAAA 19172	TCTACT		
		TTTCACATTT TGAACA			
		AAAGTGTA AAA ACTTGT			
		TTCC__			
GAM1500	SLA2	3' TTCAAGTATGTGAAA 49912	TTTTC		
		TTTCACA TACTTGAA			



AAAGTGT ATGAACTT

GAM1500 TMOD2 3' TCAGGAGAAAAATGTGAA 27253 \_ A  
TTCACATTTT CT CTTGA  
||||||| || |||||  
AAGTGTAAAA GA GGA CT

A \_

GAM1500 ABCA8 3' TAGGTAGAAAATGTGAAATA 23151  
TATTTACATTTTCTACTTG  
|||||||  
ATAAAGTGTAAAAGATGGAT

GAM1500 BNIP2 3' GTTCACTAATGTGAAATA 66767 TTCTACT  
TATTTACATT TGAAC  
||||||| |||||  
ATAAAGTGTAA ACTTG

TC\_\_\_\_\_

GAM1500 C8orf13 3' TAGAAAAAGTGAAATA 81577 A  
TATTTAC TTTTCTA  
||||||| |||||  
ATAAAGTG AAAAGAT

A

GAM1500 DCLRE1A 3' TAGAAATGTGAAATA 69168 T  
TATTTACATTT CTA  
||||||| |||  
ATAAAGTGATAA GAT

GAM1500 ELF2 3' TTCAAGTAGGTTTTCTGAAATA 22502 CATTT  
TATTTCA TCTACTTGAA  
||||||| |||||  
ATAAAGT GGATGAACTT

CTTTT

GAM1500 HEY1 3' TGTTCAAGACATTAAATTGAAA 91253 C TCTA\_  
TA TATTTCA ATTT CTTGAACA  
||||||| ||| |||||  
ATAAAGT TAAA GAACTTGT

\_ TTACA

GAM1500 KIAA1028 3' TCAAGTAGAAGCCTGAAA 91948 CAT  
TTTCA TTTCTACTTGA  
||||| |||||  
AAAGT GAAGATGAACT

CC\_

GAM1500 MGC12966 3' TGTTTGGGGAAAATGAAAAATA 51129 CA TA TG  
TATTT CATTTTCT CT AACA  
||||| ||||| || |||||  
ATAAA GTAAAAG GG TTGT

AA \_ GT

GAM1500 PABPC5 3' TGTTTTTTCAAAAAATGTGAAA 55073 CTACTT  
TG TATTTACATTTT GAACA  
||||||| |||||

			GTAAAGTGTA AAA TTTGT		
			AACTTT		
GAM1500	PTD002	3'	TAGGAAGGAAATGTAAATA 32348	C	A
			TATTT ACATTTTCT CTTG		
			ATAAA TGTAAAGGA GGAT		
			A A		
GAM1500	SEC3	3'	AGTAATAAATGTGAAATA 36810	TC	
			TATTTACATTT TACT		
			ATAAAGTGTA AAA ATGA		
			TA		
GAM1500	SENP7	3'	TGTCAGGGTAAAATTTGAAA 40304	C	CTA
			TTTCA ATTTT CTTGAACA		
			AAAGT TAAAA GGA CTTGT		
			T TG_		
GAM1500	SERPINB7	3'	GGTAAAAAATGTGAAAT 13688	C	
			ATTTACATTTT TACT		
			TAAAGTGTA AAA ATGG		
			A		
GAM1500	SLC25A21	3'	CAAGTAGGAAACATGAAATA 47616	CA	
			TATTTCA TTTTCTACTTG		
			ATAAAGT AAAGGATGAAC		
			AC		
GAM1500	SLC6A14	3'	TGTTCTTTATAAAAAGTGAAAT 23361	A	C CTT
	A		TATTTAC TTTT TA GAACA		
			ATAAAGTG AAAA AT CTTGT		
			A T TT_		
GAM1500	LOC120856	3'	TCAAGTAGAAAATGGAAA 74030	A	
			TTTC CATTTTCTACTTGA		
			AAAG GTAAAAGATGAACT		
			—		
GAM1500	LOC153442	3'	AGAAGTAAATGTGAAATA 86040	T	A
			TATTTACATTT CT CT		
			ATAAAGTGTA AAA GA GA		
			T A		
GAM1500	LOC199920	3'	GTTCAAGAGAATGTGAAA 88493	ACT	
			TTTCACATTTTCT TGAAC		
			AAAGTGTAAGAGA ACTTG		
			—		
GAM1501	EPHA8	3'	ATGCCCAGCCCTGACAC 40053	CATT	A
			GTG TCAG GCTGGGCAT		

			CAC	AGTC CGACCCGTA		
			_____ C			
GAM1501	PDE6B	3'	CTCTGAAATCACTGA	4278	C	
			TCAGTG ATTTCAGAG			
			AGTCAC TAAAGTCTC			
			_____			
GAM1501	PPP2R2B	3'	CCCCTAGGAAAGGCACT	15906	A	AG CT
			AGTGC TTTC AG GGG			
			TCACG AAAG TC CCC			
			G GA _____			
GAM1501	DKFZp434F142	3'	CCCAGCTCTTGCCTCACTG	50021		CATTTC
			CAGTG AGAGCTGGG			
			GTCAC TCTCGACCC			
			TCCGT_____			
GAM1501	DKFZP566D193	3'	CTCTGAAAACACTGA	85568	CA	
			TCAGTG TTTCAGAG			
			AGTCAC AAAGTCTC			
			A_____			
GAM1501	FLJ13657	3'	CAGAGATCTGAAATGACTGA	45720	G	G_____
			TCAGT CATTTCAGA CTG			
			AGTCA GTAAAGTCT GAC			
			_____ AGA			
GAM1501	FLJ22362	3'	CCCAGAAGAGAGATGCACT	43074		AGAG
			AGTGCATTTT CTGGG			
			TCACGTAGAG GACCC			
			AGAA			
GAM1501	KIAA0417	3'	ATGCCCAGCCCTGATTTCTGA	71242	TGCATT	A
			TCAG TCAG GCTGGGCAT			
			AGTC AGTC CGACCCGTA			
			TTT_____ C			
GAM1501	KIAA0830	3'	CCACCTGAAATGCACTGG	69696		AGC
			TCAGTGCATTTTCA TGG			
			GGTCACGTAAAGTC ACC			
			C_____			
GAM1501	KIAA0982	3'	TGACCCTGAAATGACTGA	25851	G	GAGCT _
			TCAGT CATTTC GGG CA			
			AGTCA GTAAAGT CCC GT			
			_____ A			
GAM1501	KIAA1493	3'	ATGCCCAGCCCTGACCCCTGC	64153	TT_____	A
			GCA TCAG GCTGGGCAT			

		CGT AGTC CGACCCGTA	
		CCCC C	
GAM1501 KIAA1906	3'	TCATGAAATGCACTGA 73199	—
		TCAGTGCATTTCA GA	
		AGTCACGTAAAGT CT	
		A	
GAM1501 MGC4604	3'	AGATACTGAAATGCACT 48975	AG_
		AGTGCATTTCAAG CT	
		TCACGTAAAGTC GA	
		ATA	
GAM1501 MOST2	5'	CCCAGCTCAGAGCCT 39679	T ATT A
		AG GC TC GAGCTGGG	
		TC CG AG CTCGACCC	
		— — A	
GAM1501 OSBPL11	3'	TGCTGCGAAATGCACTGA 42894	AGA TG
		TCAGTGCATTTTC GC GGCA	
		AGTCACGTAAAG CG TCGT	
		— —	
GAM1501 POFUT1	3'	ATGCCCAGCTCCAAATCACCTT 70464	— C CA
		GA TCA GTG ATTT GAGCTGGGCAT	
		AGT CAC TAAA CTCGACCCGTA	
		TC _ C_	
GAM1501 SDFR1	3'	AGCTCTAAAATGCACTG 33912	C
		CAGTGCATTT AGAGCT	
		GTCACGTAAA TCTCGA	
		A	
GAM1501 SDFR1	3'	AGCTCTAAAATGCACTG 24862	C
		CAGTGCATTT AGAGCT	
		GTCACGTAAA TCTCGA	
		A	
GAM1501 ZNF213	3'	GCCCAGCTCCACCGTACTGG 65101	ATTCA
		TCAGTGC GAGCTGGGC	
		GGTCATG CTCGACCCG	
		GCCAC_	
GAM1501 LOC125268	3'	ATGCCCAGCCCAAGTGC 76069	CAGA
		GCATTT GCTGGGCAT	
		CGTGAA CGACCCGTA	
		CC_	
GAM1501 LOC144438	3'	CCCAGCTTTTAACTGA 76833	GCATTTC
		TCAGT AGAGCTGGG	

AGTCA TTTCGACCC  
 AT\_\_\_\_  
 GAM1501 LOC152719 3' CACCTATAATGCACTGA 85846 TCAG C  
 TCAGTGCATT AG TG  
 ||||| ||  
 AGTCACGTAA TC AC  
 TA\_\_ C  
 GAM1501 LOC157858 3' ATGCCCAGCTCTGAGTCAAACG 86581 A GCAT  
 GA TC GT TTCAGAGCTGGGCAT  
 || || |||||  
 AG CA GAGTCTCGACCCGTA  
 G AACT  
 GAM1501 LOC164714 3' GCCCCAGCTCTGCCTGA 87232 T TTTCA \_  
 TCAG GCA GAGCTGGG C  
 ||| || ||||| |  
 AGTC CGT CTCGACCC G  
 \_ \_ \_ C  
 GAM1501 LOC221596 3' CCAGTAAATGCACTGA 91977 CAGA  
 TCAGTGCATTT GCTGG  
 ||||| ||||  
 AGTCACGTAAA TGACC  
 \_ \_ \_  
 GAM1501 LOC222057 3' CCCAGCTCTTGCCTCTGA 92771 T\_ TTTC  
 TCAG GCA AGAGCTGGG  
 ||| || |||||  
 AGTC CGT TCTCGACCC  
 TC \_\_\_\_  
 GAM1502 BCL2 3' ATCCCAACACATGTCTAGCTTT 5298 C CCA\_ A  
 CA TGAAAGCTA ACA TTG GAT  
 ||||| || |||  
 ACTTTCGAT TGT AAC CTA  
 C ACAC C  
 GAM1502 GAGED2 3' ATCTCAATAAAGTTTTGCAGCT 39906 A C\_ C\_  
 TTCA TGAAAGCT CA AC ATTGAGAT  
 ||||| || |||||  
 ACTTTCGA GT TG TAACTCTA  
 C TT AAA  
 GAM1502 GAGED2 3' ATCTCAATAAAGTTTTGCAGCT 55927 A C\_ C\_  
 TTCA TGAAAGCT CA AC ATTGAGAT  
 ||||| || |||||  
 ACTTTCGA GT TG TAACTCTA  
 C TT AAA  
 GAM1502 GAGED2 3' ATCTCAATAAAGTTTTGCAGCT 55931 A C\_ C\_  
 TTCA TGAAAGCT CA AC ATTGAGAT  
 ||||| || |||||  
 ACTTTCGA GT TG TAACTCTA  
 C TT AAA  
 GAM1502 HOXC10 3' ATCTTTTGCATGTAGCTT 61267 CAC TT  
 AAGCTACA CA GAGAT  
 ||||| || ||||

			TTCGATGT GT TTCTA		
			AC_ T_		
GAM1502	ITK	3'	CTCAACCTGACAGCTTTCA 18681	ACA CCA	
			TGAAAGCT CA TTGAG		
			ACTTTCGA GT AACTC		
			CA_ CC_		
GAM1502	MAPK4	3'	CTCAATGGTGCGTGC 10826 T A		
			GC AC CACCATTGAG		
			CG TG GTGGTAACTC		
			_ C		
GAM1502	NR2E1	3'	CGGGGAATGTGTAGCCTTCA 12324 A _ A		
			TGAA GCTACACA CC TTG		
			ACTT CGATGTGT GG GGC		
			C AA _		
GAM1502	SMARCA1	3'	CTGAAATGTGTAGCTTT 57389 CCA G		
			AAAGCTACACA TT AG		
			TTTCGATGTGT AA TC		
			A_ G		
GAM1502	SMARCA1	3'	CTGAAATGTGTAGCTTT 11779 CCA G		
			AAAGCTACACA TT AG		
			TTTCGATGTGT AA TC		
			A_ G		
GAM1502	TLL1	3'	ATCTCAATGGTGTCTA 24947 C		
			TA ACACCATTGAGAT		
			AT TGTGGTAACTCTA		
			C		
GAM1502	YWHAZ	3'	TGCTGTAGCTTTCAT 12708 C C		
			ATGAAAGCTA ACA CA		
			TACTTTCGAT TGT GT		
			_ C		
GAM1502	ADAMTSL1	3'	TGGTTGTAGCTTTCAT 53503 C		
			ATGAAAGCTACA ACCA		
			TACTTTCGATGT TGGT		
			-		
GAM1502	AKAP8	3'	ATGGTGTGTGACTTTCA 19601 C		
			TGAAAG TACACACCAT		
			ACTTTC GTGTGTGGTA		
			A		
GAM1502	CGGBP1	3'	ATTTCGAACCATAGCTTTCAT 13361 CACACCA		
			ATGAAAGCTA TTGAGAT		

			TACTTTTCGAT	AGCTTTTA		
			ACCA__			
GAM1502	DDR1	3'	TCTCTAGTGTAGCTGCCA	8726	AA	ACCATT
			TG AGCTACAC	GAGA		
			AC TCGATGTG	CTCT		
			CG AT__			
GAM1502	DDR1	3'	TCTCTAGTGTAGCTGCCA	25699	AA	ACCATT
			TG AGCTACAC	GAGA		
			AC TCGATGTG	CTCT		
			CG AT__			
GAM1502	DDR1	3'	TCTCTAGTGTAGCTGCCA	25708	AA	ACCATT
			TG AGCTACAC	GAGA		
			AC TCGATGTG	CTCT		
			CG AT__			
GAM1502	FLJ10314	3'	ATCTCAATGGCAAGTGAGCCCT	36010	AA	A A A__
	CA		TGA GCT CAC CCATTGAGAT			
			ACT CGA GTG GGTA ACTCTA			
			CC _ AAC			
GAM1502	FLJ11838	3'	GTCTCGACACACAGCTTTTAT	45094		ACACACCA
			ATGAAAGCT TTGAGAT			
			TATTTTCGA AGCTCTG			
			CACAC__			
GAM1502	KDEL R2	3'	TTCAGTGTGTAGCTTCA	22455	A	CAT
			TGAA GCTACACAC TGAG			
			ACTT CGATGTGTG ACTT			
			— —			
GAM1502	KIAA0408	5'	ATCTCAGTAATATCTAGCCCTC	28132	AA	CACACC
	A		TGA GCTA ATTGAGAT			
			ACT CGAT TGA CTCTA			
			CC CTATAA			
GAM1502	MAIL	3'	ATCTCAATGGTAACATTGCCTT	48649	A	TACAC_
	CA		TGAA GC ACCATTGAGAT			
			ACTT CG TGGTA ACTCTA			
			C TTACAA			
GAM1502	PCDH20	3'	ATGGTTTGCAGCTTTCAT	43128	A	C
			ATGAAAGCT CA ACCAT			
			TACTTTTCGA GT TGGTA			
			C T			
GAM1502	PP1044	5'	TTCATGTAGCTTTCG	41367		CACCAT
			TGAAAGCTACA TGAG			

GCTTTCGATGT ACTT

GAM1502 LOC148293 5' TCAAGTTATGTGTAGCTTCA 78783 A CCA\_  
TGAA GCTACACA TTGA  
||||| ||||  
ACTT CGATGTGT AACT  
\_ ATTG

GAM1502 LOC151124 5' CTGCAGTGGTGCCAGCTCCCA 85228 AA ACA \_  
TG AGCT CACCATTG AG  
|| ||| ||||| ||  
AC TCGA GTGGTGAC TC  
CC CC\_ G

GAM1502 LOC202908 5' TTTAATGGTAGCTTCCA 89247 A ACAC  
TG AAGCT ACCATTGAG  
|| ||| |||||  
AC TTCGA TGGTAATTT  
C \_

GAM1502 LOC219920 5' ATCTCCTGCAGTGTAGCTTCAT 93302 A AC TT  
ATGAA GCTACAC CA GAGAT  
||||| || ||||  
TACTT CGATGTG GT CTCTA  
\_ AC C\_

GAM1502 LOC51031 3' TCTGAATCGTGTAGCTTTTAT 32198 ACC G  
ATGAAAGCTACAC ATT AGA  
||||||| ||| |||  
TATTTTCGATGTG TAA TCT  
C\_ G

GAM1502 LOC90049 3' TCAAGTTATGTGTAGCTTCA 61214 A CCA\_  
TGAA GCTACACA TTGA  
||||| ||||  
ACTT CGATGTGT AACT  
\_ ATTG

GAM1502 LOC93380 5' CTTTTTCCGTGTAGCTTTC 72200 ACCATT  
GAAAGCTACAC GAG  
||||||| |||  
CTTTCGATGTG TTC  
CCTTT\_

GAM1503 ADCY2 3' AGGTATCACACACTTTCTGACT 65014 ACA\_ GC  
AGTCAGAAG GTGA ACCT  
||||| ||| |||  
TCAGTCTTT CACT TGGA  
CACA A\_

GAM1503 BAZ2A 3' GAGGTCCCTGTCTTCTG 25603 T GCA  
CAGAAGACAG GA CCTC  
||||||| || |||  
GTCTTCTGTC CT GGAG  
C \_

GAM1503 CCNF 3' GGAGATGCTCACTGAGCTGCTG 8322 T A A\_ C  
CT AG CAG AG CAGTGAGCA CTCC  
|| ||| || ||||| |||



		TC GTC TC GTC	ACTCGT GAGG	
		_ G GA	A	
GAM1503	DRP2	3'	GGAGGCATGATTCTTCTGAC 8663	CA_ AGCA
			GTCAGAAGA GTG CCTCC	
			CAGTCTTCT TAC GGAGG	
			TAG ____	
GAM1503	EHD3	3'	GCAAACCGTGCCTTCTGGCT 27479	__ A GA
			AGTCAGAAG AC GT GC	
			TCGGTCTTC TG CA CG	
			CG C AA	
GAM1503	ELAC2	3'	AGGCTGTGTGTCTTCTGC 36228 T	GTGA _
			G CAGAAGACA GCA CCT	
			C GTCTTCTGT TGT GGA	
			_ G__ C	
GAM1503	EMP1	3'	GGAAGCCATCCTGCCCTTCTGA 7445	A_ T GCACC
	C		GTCAGAAG CAG GA TCC	
			CAGTCTTC GTC CT AGG	
			CC _ ACCGA	
GAM1503	FIGF	5'	GACATGTCCACCTTCTGATT 15556	ACA AG CC
			AGTCAGAAG GTG CA TC	
			TTAGTCTTC CAC GT AG	
			__ CT AC	
GAM1503	FNTB	3'	GGAGGTGCCTCTGCCTCTCGAC 8955	_ A A TGA
	T		AGTC AGA G CAG GCACCTCC	
			TCAG TCT C GTC CGTGGAGG	
			C _C TC_	
GAM1503	IL11RA	3'	AGGTGCTTGACCTCTGATT 15711	A ACA TG
			AGTCAGA G G AGCACCT	
			TTAGTCT C T TCGTGGA	
			_CA_ GT	
GAM1503	IL17	3'	GAGACATTGTCTTCAGACT 9331 A	AGCAC
			AGTC GAAGACAGTG CTC	
			TCAG CTTCTGTTAC GAG	
			A A__	
GAM1503	KPNA1	3'	GTATCTGCCTTCTGGCT 80322	A TGA
			AGTCAGAAG CAG GC	
			TCGGTCTTC GTC TG	
			C TA_	
GAM1503	MGAT1	3'	GCTCACTGCCTCCTGC 10008 T A A	
			G CAG AG CAGTGAGC	

			C GTC TC GTC	ACTCG			
			_ C C				
GAM1503	PLP2	3'	GGAGACTTTTGTCTTCCAGC	10653	CA	T	CAC
			GT GAAGACAG GAG	CTCC			
			CG CTTCTGTT TTC	GAGG			
			AC _ A_				
GAM1503	POMZP3	3'	GGAGGTGTCGCACTGCCTCCCA	24243	CA A A	A_	
	C		GT GA G CAGTG	GCACCTCC			
			CA CT C GTCAC	TGTGGAGG			
			CC _ C	GC			
GAM1503	PVT1	3'	GCCCACTGTTTTCTAACT	65572	C	A	
			AGT AGAAGACAGTG	GC			
			TCA TCTTTTGTAC	CG			
			A	C			
GAM1503	SDC4	3'	GAGACATTGTCTTCTACT	11478	C	AGCAC	
			AGT AGAAGACAGTG	CTC			
			TCA TCTTCTGTTAC	GAG			
			_ A_				
GAM1503	SIRT2	3'	GCCCCACTGTCTCTAAC	47592	C A	A_	
			GT AGA GACAGTG	GC			
			CA TCT CTGTCAC	CG			
			A _ CC				
GAM1503	SIRT2	3'	GCCCCACTGTCTCTAAC	24262	C A	A_	
			GT AGA GACAGTG	GC			
			CA TCT CTGTCAC	CG			
			A _ CC				
GAM1503	SIRT3	3'	AGCACCTCCAAAAGCTTTCTTC	24267	C T	_____	CAC
	TGACT		CAGAAGA AG	GAG	CT		
			GTCTTCT TC	CTC	GA		
			T GAAAIIIC	CAC			
GAM1503	SLC6A3	3'	CTCCTCTCTTCTGACT	6448	C T		
			AGTCAGAAGA AG	GAG			
			TCAGTCTTCT TC	CTC			
			C _				
GAM1503	TCF2	3'	GCCAAACACTGTTTCTAACT	21381	C A	A_	
			AGT AGA GACAGTG	GC			
			TCA TCT TTGTCAC	CG			
			A _ AAAC				
GAM1503	TFEB	3'	GGAGATTCCCTGTCTTCTGA	92127	T	CAC	
			TCAGAAGACAG GAG	CTCC			

		AGTCTTCTGTC CTT GAGG	
		C A__	
GAM1503 TLL2	3'	AGGTGCCAGGCTGTCTTCTG 24961	GA_
		CAGAAGACAGT GCACCT	
		GTCTTCTGTCG CGTGGA	
		GAC	
GAM1503 UBQLN2	3'	GTGTGTCTTTTGA CT 25567	AGTGA
		AGTCAGAAGAC GCAC	
		TCAGTTTCTG TGTG	
		_____	
GAM1503 ZP3A	3'	GGAGGTGTCGCACTGCCTCCCA 23121	CA A A A_
C		GT GA G CAGTG GCACCTCC	
		CA CT C GTCAC TGTGGAGG	
		CC _ C GC	
GAM1503 AP1GBP1	3'	AGGTGCTTTTGTCTCCAGACT 54528	A_ AG T
		AGTC GA ACAG GAGCACCT	
		TCAG CT TGTT TTCGTGGA	
		AC CT _	
GAM1503 ATP10D	3'	AGATGCTTTTGGTCTTCTGGCT 73139	AGT C
		AGTCAGAAGAC GAGCA CT	
		TCGGTCTTCTG TTCGT GA	
		GTT A	
GAM1503 C22orf23	3'	GCTTCCCACCACTTCTGAC 50784	ACA ____
		GTCAGAAG GTG AGC	
		CAGTCTTC CAC TCG	
		AC_ CCT	
GAM1503 CDCA4	3'	GCTTCTTGTCTTCTGAC 35656	T
		GTCAGAAGACAG GAGC	
		CAGTCTTCTGTT TTCG	
		C	
GAM1503 DKFZP434O047	5'	AGGTGCTCTCCCTGAC 31502	AA CAGT
		GTCAG GA GAGCACCT	
		CAGTC CT CTCGTGGA	
		C_ ____	
GAM1503 FLJ11800	3'	GAGGTGTGTGCATTTCTGACT 46426	ACA A
		AGTCAGAAG GTG GCACCTC	
		TCAGTCTTT CGT TGTGGAG	
		A_ G	
GAM1503 FLJ12057	3'	GAGATGCCCACTTTCTGACT 45439	GAC A C
		AGTCAGAA AGTG GCA CTC	

TCAGTCTT TCAC CGT GAG  
 \_\_\_\_ C A  
 GAM1503 FLJ13231 3' GGAGATCTTCTGTCTTCTGC 43552 T T CAC  
 G CAGAAGACAG GAG CTCC  
 I ||||| ||| ||||  
 C GTCTTCTGTC TTC GAGG  
 \_ \_ TA\_  
 GAM1503 FLJ13710 3' AGGTGCTGCTTCATTTCTGAC 45679 AC\_ G  
 GTCAGAAG AGT AGCACCT  
 ||||| || |||||  
 CAGTCTTT TCG TCGTGGA  
 ACT \_  
 GAM1503 FLJ20445 3' TCACTGCCTTGCTAACT 35180 C \_ A  
 AGT AG AAG CAGTGA  
 ||| || |||||  
 TCA TC TTC GTCACT  
 A G C  
 GAM1503 FLJ22729 5' GAGGTGGAGATGCTTTCTGAC 45189 GA GTGAG  
 GTCAGAA CA CACCTC  
 ||||| || |||||  
 CAGTCTT GT GTGGAG  
 TC AGAG\_  
 GAM1503 FLJ23878 3' GGAGGTGCCTCAGTCTCCTCAC 58710 C A AG \_  
 GT AG AGAC TGAG CACCTCC  
 || |||| |||| |||||  
 CA TC TCTG ACTC GTGGAGG  
 C C \_ C  
 GAM1503 HTCD37 3' GAGGCCATTGTCTTCTG 67676 A AC  
 CAGAAGACAGTG GC CTC  
 ||||| || |||  
 GTCTTCTGTTAC CG GAG  
 \_ \_  
 GAM1503 KIAA0298 3' GAAGTGAGTCTTCTGAC 76578 AGTGAG C  
 GTCAGAAGAC CAC TC  
 ||||| ||| ||  
 CAGTCTTCTG GTG AG  
 A \_ A  
 GAM1503 KIAA0494 3' CTCACCCTTCTGACT 28741 ACA  
 AGTCAGAAG GTGAG  
 ||||| ||||  
 TCAGTCTTC CACTC  
 C\_  
 GAM1503 KIAA0940 3' AGGTCACTATTCTGACT 29863 AC GCA  
 AGTCAGAAG AGTGA CCT  
 ||||| |||| ||  
 TCAGTCTTT TCACT GGA  
 A\_ \_  
 GAM1503 KIAA1191 3' GAGGTGCTCACTGACTCGCT 39955 C AAGA  
 AGT AG CAGTGAGCACCTC  
 ||| || ||||| |||||

		TCG TC	GTC	ACT	CGT	G	G	A	
		C	A	_____					
GAM1503	KIAA1655	3'	GCC	ACT	GT	C	C	T	G
			666	12		A		A	
			TC	A	G	A	C	A	G
			T	C	A	G	A	G	T
			A	G	T	C	T	G	T
			C	_____					
GAM1503	KIAA1674	3'	G	A	T	G	G	G	C
			687	81					
			CT						
			A	G	T	C	A	G	A
			A	G	A	C	A	G	T
			T	C	G	G	T	C	T
			C	_____	T				
GAM1503	MGC5601	5'	G	A	G	G	T	G	C
			475	07					
			AA			TG			
			A	G	T	C	A	G	A
			A	G	C	A	C	C	T
			T	C	A	G	T	T	C
			C	_____	G	T			
GAM1503	NPTXR	3'	G	G	A	C	T	T	G
			541	84					
			AC	A		AC	_____		
			G	A	C	T	T	C	T
			G	T	C	A	G	A	A
			T	G	G	C			
			CT	C	C				
			C	A	G	T	C	T	T
			A	C	C	G			
			G	A	G	G			
			C	G	_____	C			
GAM1503	NPTXR	3'	G	G	A	C	T	T	G
			266	48					
			AC	A		AC	_____		
			G	A	C	T	T	C	T
			G	T	C	A	G	A	A
			T	G	G	C			
			CT	C	C				
			C	A	G	T	C	T	T
			A	C	C	G			
			G	A	G	G			
			C	G	_____	C			
GAM1503	PDZD2	3'	G	C	T	A	A	C	T
			808	75					
			A			G	_____		
			G	T	C	A	G	A	A
			T	G	A	C			
			C	A	G	T	T	C	T
			T	C	A				
			AA						
GAM1503	PEL1	3'	G	T	A	T	C	A	G
			402	77					
			AG			GC			
			T	C	A	G	A	A	G
			A	C					
			A	G	T	C	T	T	C
			A	C	T				
			_____	A	_____				
GAM1503	PIP5K2B	3'	A	G	C	A	C	T	C
			130	63					
			CA			T	_____		
			C	A					
			C	A	G	C			
			G	A	A	G	A	C	A
			G	A	G				
			CT						
			C	T	T	C	T	G	T
			C	T	C				
			G	A					
			AC			G	A	A	G
			I	I	I	C			
			C	A	C				
GAM1503	PP1628	5'	G	A	G	G	C	A	C
			472	97					
			ACA			AG	C	A	
			G	T	C	A	G	A	A
			G	T					
			C	C	T				
			C	G	G	T	C	T	T
			T	A					
			G	G	A	G			
			CC	_____	C	A	C	_____	
GAM1503	PTPNS1	3'	G	A	G	A	C	A	C
			549	99					
			ACA			AG	C	A	C
			A	G	T	C	A	G	A
			A	G					
			CT						

			TCGGTCTTC CAC GAG		
			CGA A____		
GAM1503 REA	5'	GGCGGGCCGGCACCCCCTTCTG 23446		ACA A__ A T	
	AC	GTCAGAAG GTG GC CC CC			
		CAGTCTTC CAC CG GG GG			
		CCC GGC _ C			
GAM1503 SERP1	3'	CTTGATCGTTTTCTGACT 27060		AG_	
		AGTCAGAAGAC TGAG			
		TCAGTCTTTTG GTTC			
		CTA			
GAM1503 SFXN2	3'	GCCAATGTCTTCTAGCT 73948	TC	G A	
		AG AGAAGACA TG GC			
		TC TCTTCTGT AC CG			
		GA A _			
GAM1503 TBX4	3'	GGAGAGCATCCATCTTCTGAC 37494		CAGT _ AC	
		GTCAGAAGA GA GC CTCC			
		CAGTCTTCT CT CG GAGG			
		AC_ A A_			
GAM1503 TMPRSS5	5'	GGAGACCTCATCTTCCAAC 47785	CA	CAG CAC	
		GT GAAGA TGAG CTCC			
		CA CTTCT ACTC GAGG			
		AC _ CA_			
GAM1503 TRIM17	3'	AGGTGTGGGCCTTCTGCT 32254	T	ACA GA	
		AG CAGAAG GT GCACCT			
		TC GTCTTC CG TGTGGA			
		_ _ GG			
GAM1503 ULK2	3'	GGGCAGCTGTCTTCTGCCT 28004	T	GA A	
		AG CAGAAGACAGT GC CC			
		TC GTCTTCTGTCTG CG GG			
		C A_ _			
GAM1503 ZF	5'	TGTTGCTGCCCCTCTGAC 41092	AGA		
		GTCAGA CAGTGAGCA			
		CAGTCT GTCGCTTGT			
		CCC			
GAM1503 ZNF340	3'	GCTTACTGCTTCCAAC 84561	CA	A	
		AGT GAAG CAGTGAGC			
		TCA CTTC GTCATTCTG			
		AC _			
GAM1503 LOC124753	5'	GGCCTTCCCCCTGTCTTCCAAC 74323	CA	T_ CA	
		GT GAAGACAG GAG CC			

	CA CTTCTGTC CTT GG	
	AC CCC CC	
GAM1503 LOC133584 3'	GTTCAGTGTGTTCTGACT 75100	G
	AGTCAGAA ACAGTGAGC	
	TCAGTCTT TGTCAC TTG	
	G	
GAM1503 LOC143680 3'	AGGAGCTATTTCTGACT 82985	GACAGTG A
	AGTCAGAA AGC CCT	
	TCAGTCTT TCG GGA	
	TA _____ A	
GAM1503 LOC146819 3'	GAGGTGTTGAAGTCTCCA ACT 78151	CA A AGTG
	AGT GA GAC AGCACCTC	
	TCA CT CTG TTGTGGAG	
	AC _ AAG_	
GAM1503 LOC146821 3'	GAGGTGTTGAAGTCTCCA ACT 78143	CA A AGTG
	AGT GA GAC AGCACCTC	
	TCA CT CTG TTGTGGAG	
	AC _ AAG_	
GAM1503 LOC149113 3'	AGATGCTGCACTTCTGGC 79160	AGAC _ C
	GTCAGA AGTG AGCA CT	
	CGGTCT TCAC TCGT GA	
	_____ G A	
GAM1503 LOC150005 3'	AGGTGTCCTGTCTTCCCACT 84815	CA T G
	AGT GAAGACAG GA CACCT	
	TCA CTTCTGTC CT GTGGA	
	CC _ _	
GAM1503 LOC151190 5'	AGCACCTCCGAAAGCTGTCTTC 80164	T_____ CAC
TGA	CAGAAGACAG GAG CT	
	GTCTTCTGTC CTC GA	
	GAAAGIIIC CAC	
GAM1503 LOC151723 5'	CTCACCATCTTCTGGC 82605	CA
	GTCAGAAGA GTGAG	
	CGGTCTTCT CACTC	
	AC	
GAM1503 LOC152317 3'	AGGCCGCCACCTTCTGCT 85636	T ACA A A_
	AG CAGAAG GTG GC CCT	
	TC GTCTTC CAC CG GGA	
	_ _ _ CC	
GAM1503 LOC154403 3'	AGATGCTGCACTTCTGGC 81068	AGAC _ C
	GTCAGA AGTG AGCA CT	

		CGGTCT TCAC TCGT GA		
		_____ G A		
GAM1503	LOC154992 3'	AGATGCTGCACTTCTGGC 81210	AGAC	_ C
		GTCAGA AGTG AGCA CT		
		CGGTCT TCAC TCGT GA		
		_____ G A		
GAM1503	LOC166983 5'	GGCCTTCACTGTCCCCGAC 87265	AGAA	CA
		GTC GACAGTGAG CC		
		CAG CTGTCACTT GG		
		CCCC CC		
GAM1503	LOC196485 3'	GCCACTGTCTCCTGCT 87732	T A	A
		AG CAG AGACAGTG GC		
		TC GTC TCTGTCAC CG		
		_ C _		
GAM1503	LOC200854 3'	GTGGTTCTTCTGACT 87423	CAGTG G	
		AGTCAGAAGA A CAC		
		TCAGTCTTCT T GTG		
		_____ G		
GAM1503	LOC201868 3'	AGATGCTGCACTTCTGGC 89073	AGAC	_ C
		GTCAGA AGTG AGCA CT		
		CGGTCT TCAC TCGT GA		
		_____ G A		
GAM1503	LOC202986 3'	GCCACTGTCTCCTGCT 90443	T A	A
		AG CAG AGACAGTG GC		
		TC GTC TCTGTCAC CG		
		_ C _		
GAM1503	LOC220575 3'	GAGGTGTGTGCATTTCTGACT 76310	ACA	A
		AGTCAGAAG GTG GCACCTC		
		TCAGTCTTT CGT TGTGGAG		
		A_ G		
GAM1503	LOC221354 3'	GCCACTGTCTCCTGCCT 92414	T A	A
		AG CAG AGACAGTG GC		
		TC GTC TCTGTCAC CG		
		C C _		
GAM1503	LOC56959 5'	AGCACCTCCAGAAGCAGTTTTTC 81923	A T_____	CAC
	TGAC	CAGAAGAC G GAG CT		
		GTCTTTTG C CTC GA		
		A GAAGAIIC CAC		
GAM1503	LOC90148 3'	GGAAACAGAGCACCTGTTTTCT 61663	_ AGCACC_	
	GACT	AGTCAGAAGACAG TG TCC		



TCAGTCTTTTGTC AC AGG  
 C GAGACAA  
 GAM1503 LOC90333 3' TGGTCTCTATCTTCTGACT 62306 C T G  
 AGTCAGAAGA AG GA CA  
 ||||| || ||  
 TCAGTCTTCT TC CT GT  
 A T G  
 GAM1503 LOC90639 5' GGAAGTGAGAACCTTCTGGCT 63659 ACA GAG C  
 AGTCAGAAG GT CAC TCC  
 ||||| || ||||  
 TCGGTCTTC CA GTG AGG  
 \_\_\_\_ AGA A  
 GAM1503 LOC92521 3' GGAAGCGCCTGATTACTGTCCA 69596 AA \_\_\_\_ ACC  
 CTGAC GTCAG GACAGTGA GC TCC  
 |||| ||||| || ||  
 CAGTC CTGTCATT CG AGG  
 AC AGTC CGA  
 GAM1503 LOC93624 3' GGAAGTCTTTTGTCTTCCAGCT 72727 CA T C C  
 AGT GAAGACAG GAG AC TCC  
 || ||||| || ||||  
 TCG CTTCTGTT TTC TG AGG  
 AC \_ \_ A  
 GAM1504 ADAM20 5' GCACTGCAGCTCTGA 13767 A AT  
 TCA AGCTGCAG TGC  
 || ||||| ||  
 AGT TCGACGTC ACG  
 C \_\_\_\_  
 GAM1504 ANXA9 5' CACAGGCAATCTACCAGGC 13102 GC\_\_\_\_  
 GCT AGATTGCCTGTG  
 || ||||| |||||  
 CGG TCTAACGGACAC  
 ACCA  
 GAM1504 E2F1 3' CAATCTGCACTTTGA 84795 C  
 TCAAAG TGCAGATTG  
 |||| |||||  
 AGTTTC ACGTCTAAC  
 \_\_\_\_  
 GAM1504 E2F1 3' CACCTTGTCTCTGCAGCCCTGG 84796 AA TTGCCT  
 TCA GCTGCAGA GTG  
 || ||||| ||  
 GGT CGACGTCT CAC  
 CC CTGTTC  
 GAM1504 FPRL1 5' CACTGCATTTGCAGCCTTGA 7590 A T CT  
 TCAA GCTGCAGAT GC GTG  
 |||| ||||| || ||  
 AGTT CGACGTTTA CG CAC  
 C \_ T\_  
 GAM1504 FSHPRH1 5' CACGGCTCTCTGCAGC 22114 TT T  
 GCTGCAGA GCC GTG  
 ||||| || |||

			CGACGTCT CGG CAC		
			CT _		
GAM1504 IL10RA	3'	CACAGGCATGGAAGCTGTGA	59641	A	GCAGAT
		TCA AGCT TGCCTGTG			
		AGT TCGA ACGGACAC			
		G AGGT__			
GAM1504 ITGA6	3'	CACAGGTGCAACAGACTTGA	3983	AG	CAGATT
		TCAA CTG GCCTGTG			
		AGTT GAC TGGACAC			
		CA AACG__			
GAM1504 ITPKA	3'	CATGTGGACCTGCAGCTTTG	9415	ATTG	_
		CAAAGCTGCAG CC TGTG			
		GTTTCGACGTC GG GTAC			
		CA__ T			
GAM1504 LILRB4	3'	CAGGACCTGCAGCTTTG	22431	ATTG	
		CAAAGCTGCAG CCTG			
		GTTTCGACGTC GGAC			
		CA__			
GAM1504 MBD3	3'	CACAGGCACCCAGCTTTGG	14093	CAGAT	
		TCAAAGCTG TGCCTGTG			
		GGTTTCGAC ACGGACAC			
		CC__			
GAM1504 MPP3	3'	CACAGGCAAGCTGACCCT	8635	CTG	A
		AG CAG TTGCCTGTG			
		TC GTC AACGGACAC			
		CCA G			
GAM1504 NR1I2	3'	CAAAGTGCAGCTGTGA	13963	A	A
		TCA AGCTGCAG TTG			
		AGT TCGACGTC AAC			
		G A			
GAM1504 NR1I2	3'	CAAAGTGCAGCTGTGA	41826	A	A
		TCA AGCTGCAG TTG			
		AGT TCGACGTC AAC			
		G A			
GAM1504 OCM	3'	CACAGGCAATGCCTCT	20546	CT	GA
		AG GCA TTGCCTGTG			
		TC CGT AACGGACAC			
		TC _			
GAM1504 OGDH	3'	CACAGAAAGGGCAGCTT	91105	AGA	GC
		AAGCTGC TT CTGTG			

			TTCGACG AA GACAC		
			GG_ A_		
GAM1504	PACE4	3'	GGAATCCACAGCTCTGG 56348	A CA G	
			TCA AGCTG GATT CC		
			GGT TCGAC CTAA GG		
			C AC G		
GAM1504	PACE4	3'	GGAATCCACAGCTCTGG 10403	A CA G	
			TCA AGCTG GATT CC		
			GGT TCGAC CTAA GG		
			C AC G		
GAM1504	PIGK	3'	GGAATCCTGCAGCTTT 66701	_ G	
			AAAGCTGCAG ATT CC		
			TTTCGACGTC TAA GG		
			C _		
GAM1504	STARD4	3'	CACAGCTCACTGCAGCTTTGA 57510	ATT C	
			TCAAAGCTGCAG GC TGTG		
			AGTTTCGACGTC CG ACAC		
			ACT _		
GAM1504	UBE4A	3'	CACAAGCAAGTGTGTAGCTT 16561	G _ C	
			AAGCTGCA ATT GC TGTG		
			TTCGATGT TGA CG ACAC		
			G A A		
GAM1504	BIRC8	5'	CAGGTTTATCCGCAGCTTT 52904	A T_	
			AAAGCTGC GAT GCCTG		
			TTTCGACG CTA TGGAC		
			C TT		
GAM1504	C11orf9	3'	CACTCATTCTCAGCTTTGA 25207	C T CCT	
			TCAAAGCTG AGA TG GTG		
			AGTTTCGAC TCT AC CAC		
			_ T T_		
GAM1504	C20orf98	3'	CACAGGCAATTACTAGC 71512	CA	
			GCTG GATTGCCTGTG		
			CGAT TTAACGGACAC		
			CA		
GAM1504	C6orf5	3'	GCTCACTGCAGCTTTGA 31354	ATT	
			TCAAAGCTGCAG GC		
			AGTTTCGACGTC CG		
			ACT		
GAM1504	CHST3	3'	ACAGACAATCTGCCGT 14963	T C	
			GC GCAGATTG CTGT		

		TG CGTCTAAC GACA		
		C     A		
GAM1504	DKFZP434B103	3' CACAGGCAGAGGGCAGCT	31588	AGA
		AGCTGC TTGCCTGTG		
		TCGACG GACGGACAC		
		GGA		
GAM1504	FLJ10813	3' TAATCTGCCACTTTGA	36686	CT
		TCAAAG GCAGATTG		
		AGTTTC CGTCTAAT		
		AC		
GAM1504	FLJ12168	3' CACAGGCACTTTAGC	45184	C AT
		GCTG AG TGCCTGTG		
		CGAT TC ACGGACAC		
		T ____		
GAM1504	FLJ12331	3' CAATCAGTGCAGTTTGA	46475	G ____
		TCAAA CTGCA GATTG		
		AGTTT GACGT CTAAC		
		____ GA		
GAM1504	FLJ12650	3' CACAGGCATGGAGCT	44524	G GAT
		AGCT CA TGCCTGTG		
		TCGA GT ACGGACAC		
		G ____		
GAM1504	FLJ14082	5' CACATGGAGAGCTGCAGCT	46670	ATTG ____
		AGCTGCAG CC TGTG		
		TCGACGTC GG ACAC		
		GAGA T		
GAM1504	FLJ14326	5' CATCCTGCCCCAGCTTTGA	49804	____ AT
		TCAAAGCT GCAG TG		
		AGTTTCGA CGTC AC		
		CCC CT		
GAM1504	FLJ20249	3' CACAGTCCTTTCTGCAGCTT	79424	TTGC_
		AAGCTGCAGA CTGTG		
		TTCGACGTCT GACAC		
		TTCCT		
GAM1504	FLJ20436	3' CACAGGCAACCCAGACT	35167	_ CAGA
		AG CTG TTGCCTGTG		
		TC GAC AACGGACAC		
		A CC__		
GAM1504	FLJ21945	3' ACAGGCAATGTCTGCA	47313	____
		TGCAGAT TGCCTGT		

ACGTCTG ACGGACA  
 TA  
 GAM1504 FLJ22037 5' CACAAGTTCCTGCAGCT 93913 ATT C  
 AGCTGCAG GC TGTG  
 ||||| |||||  
 TCGACGTC TG ACAC  
 CT\_ A  
 GAM1504 FLJ23185 3' CACAGGCCACCGGCTCCAGCTT 46828 C ATT\_\_\_\_  
 TGA TCAAAGCTG AG GCCTGTG  
 ||||| || |||||  
 AGTTTCGAC TC CGGACAC  
 C GGCCAC  
 GAM1504 FLJ23563 5' CACGGTCACCCACAGCTTTGA 67590 CAGAT C  
 TCAAAGCTG TG CTGTG  
 ||||| |||||  
 AGTTTCGAC AC GGCAC  
 ACCC\_ T  
 GAM1504 KIAA0544 3' CACAAGCTGCGTGCAGCTCTGG 70888 A GATT C  
 TCA AGCTGCA GC TGTG  
 ||||| |||||  
 GGT TCGACGT CG ACAC  
 C GCGT A  
 GAM1504 KIAA0557 3' CAGACATCTGTAGCCCTGA 77991 AA T C  
 TCA GCTGCAGAT G CTG  
 || ||||| |||||  
 AGT CGATGTCTA C GAC  
 CC \_ A  
 GAM1504 KIAA0844 3' CACAGGCAAGCACCT 30198 C AGA  
 AG TGC TTGCCTGTG  
 || |||||  
 TC ACG AACGGACAC  
 C \_\_\_\_  
 GAM1504 KIAA1348 3' CACAAAAATCTGCAAATTTGA 68574 GC GCC  
 TCAAA TGCAGATT TGTG  
 |||| ||||| |||||  
 AGTTT ACGTCTAA ACAC  
 AA AA\_  
 GAM1504 KIAA1579 3' CACAAATTGCTGCAGTCTGA 36604 AA ATTGCC  
 TCA GCTGCAG TGTG  
 || ||||| |||||  
 AGT TGACGTC ACAC  
 C\_ GTTAA\_  
 GAM1504 KIAA1712 5' CACAGAGAAGCTCCCAGCTTTG 67532 C\_ A GC  
 A TCAAAGCTG AG TT CTGTG  
 ||||| || |||||  
 AGTTTCGAC TC AA GACAC  
 CC G GA  
 GAM1504 MGC20258 5' CAGGAATCTGCAGCCTGGA 58150 AAA G  
 TC GCTGCAGATT CCTG  
 || ||||| |||||

			AG CGACGTCTAA GGAC		
			GTC _		
GAM1504	MGC5528	3'	CACAGGCAATGCTCACT 44043	C C _	
			AG TG AG ATTGCCTGTG		
			TC AC TC TAACGGACAC		
			_ _ G		
GAM1504	MIC2L1	3'	CACTGGAATCTGCAGC 48820	G T	
			GCTGCAGATT CC GTG		
			CGACGTCTAA GG CAC		
			_ T		
GAM1504	MYO5C	3'	ACAGGTGACAGCTGTGA 38104	A CAGA TG	
			TCA AGCTG T CCTGT		
			AGT TCGAC A GGACA		
			G _ _ _ GT		
GAM1504	OSR2	3'	CAGCCGCACCTGCAGCT 53805	AT _	
			AGCTGCAG TGC CTG		
			TCGACGTC ACG GAC		
			C_ CC		
GAM1504	PLSCR3	3'	CACAGGCATATCAGCTTT 90759	CAGAT	
			AAAGCTG TGCCTGTG		
			TTTCGAC ACGGACAC		
			TAT_		
GAM1504	PLSCR3	3'	CACAGGCATATCAGCTTT 39792	CAGAT	
			AAAGCTG TGCCTGTG		
			TTTCGAC ACGGACAC		
			TAT_		
GAM1504	STATI2	3'	CACAGGCCTCACTGCAATTTGA 13920	GC ATT_	
			TCAA TGCAG GCCTGTG		
			AGTTT ACGTC CGGACAC		
			A_ ACTC		
GAM1504	STATI2	3'	CACAGGCCTCACTGCAATTTGA 94550	GC ATT_	
			TCAA TGCAG GCCTGTG		
			AGTTT ACGTC CGGACAC		
			A_ ACTC		
GAM1504	TRIM11	3'	CACAGTTCCTGCAGCTTTG 72830	ATTGC	
			CAAAGCTGCAG CTGTG		
			GTTTCGACGTC GACAC		
			CTT_		
GAM1504	LOC115574	3'	CACAGGTCATGTCTGCAGC 73464	_ _	
			GCTGCAGAT TG CCTGTG		

		CGACGTCTG AC GGACAC		
		T T		
GAM1504	LOC124976 3'	CGATCTGCAGCTTTGA	74378	
		TCAAAGCTGCAGATTG		
		AGTTTCGACGTCTAGC		
GAM1504	LOC130471 3'	GCACTGCAGCTCTGA	74941	A AT
		TCA AGCTGCAG TGC		
		AGT TCGACGTC ACG		
		C _		
GAM1504	LOC145501 3'	CACAGGAGGCTATCTGTAGC	77251	TG__
		GCTGCAGAT CCTGTG		
		CGATGTCTA GGACAC		
		TCGGA		
GAM1504	LOC146819 3'	CACATTATTTTGCAGCTCTGA	78150	A TTGCC
		TCA AGCTGCAGA TGTG		
		AGT TCGACGTTT ACAC		
		C TATT_		
GAM1504	LOC146821 3'	CACATTATTTTGCAGCTCTGA	78142	A TTGCC
		TCA AGCTGCAGA TGTG		
		AGT TCGACGTTT ACAC		
		C TATT_		
GAM1504	LOC150005 5'	CACAGGCACCAGCTCTGA	84817	A CAGAT
		TCA AGCTG TGCCTGTG		
		AGT TCGAC ACGGACAC		
		C C__		
GAM1504	LOC150005 3'	CACAGGCAGGGGTAGC	84818	AGA
		GCTGC TTGCCTGTG		
		CGATG GACGGACAC		
		GG_		
GAM1504	LOC151318 3'	CACAGGCAATCTACCTTCTGA	80225	_ CTGC
		TCA AAG AGATTGCCTGTG		
		AGT TTC TCTAACGGACAC		
		C CA__		
GAM1504	LOC151907 3'	CAGTTATCTAAGCTTTGA	80397	GC TGC
		TCAAAGCT AGAT CTG		
		AGTTTCGA TCTA GAC		
		A_ TT_		
GAM1504	LOC163724 5'	CACACCAGCTGCAGCTT	82152	A CC
		AAGCTGCAG TTG TGTG		

TTCGACGTC GAC ACAC  
 \_ C\_  
 GAM1504 LOC168667 3' CACCCTCGTATCTGCAGCCTGA 92756 AA \_ CCT  
 TCA GCTGCAGAT TG GTG  
 ||| ||||| || |||  
 AGT CGACGTCTA GC CAC  
 C\_ T TCC  
 GAM1504 LOC201324 3' CACATCAGCTGCAGCT 68561 A CC  
 AGCTGCAG TTG TGTG  
 ||||| ||| ||||  
 TCGACGTC GAC ACAC  
 \_ T\_  
 GAM1504 LOC219818 3' CAGTCTTATTACAGCTTTGA 90887 C\_\_\_\_  
 TCAAAGCTG AGATTG  
 ||||| |||||  
 AGTTTCGAC TCTGAC  
 ATTAT  
 GAM1504 LOC220980 3' ACATACTGCAGTTTGA 93141 G ATTGCC  
 TCAA CTGCAG TGT  
 |||| ||||| |||  
 AGTTT GACGTC ACA  
 \_ AT\_\_\_\_  
 GAM1504 LOC221576 3' AATCTGCAAGCTTTGA 93700 \_  
 TCAAAGCT GCAGATT  
 ||||| |||||  
 AGTTTCGA CGTCTAA  
 A  
 GAM1504 LOC254962 3' CACAGGCAATCTTGCTTCT 96614 CT \_  
 AG GCA GATTGCCTGTG  
 || ||| |||||  
 TC CGT CTAACGGACAC  
 TT T  
 GAM1504 LOC255299 5' CAACCTGGAGCTTTGA 97464 G A  
 TCAAAGCT CAG TTG  
 ||||| ||| |||  
 AGTTTCGA GTC AAC  
 G C  
 GAM1504 LOC255545 3' CAGTTATCTAAGCTTTGA 95706 GC TGC  
 TCAAAGCT AGAT CTG  
 ||||| ||| |||  
 AGTTTCGA TCTA GAC  
 A\_ TT\_  
 GAM1504 LOC256940 3' CACAGGTTTTCTGCAGT 96492 TT  
 GCTGCAGA GCCTGTG  
 ||||| |||||  
 TGACGTCT TGGACAC  
 TT  
 GAM1504 LOC257319 3' ACATGCTGCAGCTTGA 95771 A ATTGCC  
 TCAA GCTGCAG TGT  
 ||| ||||| |||



		AGTT CGACGTC	ACA		
		— GT—			
GAM1504	LOC257515	3' AATCTGCAAGCTTTGA	97780	—	
		TCAAAGCT GCAGATT			
		AGTTTCGA CGTCTAA			
		A			
GAM1504	LOC257572	3' AATCTGCAAGCTTTGA	97909	—	
		TCAAAGCT GCAGATT			
		AGTTTCGA CGTCTAA			
		A			
GAM1504	LOC51075	3' CACAAGCCTGAGGTGCAGCTTT	31989	GA _ C	
		AAAGCTGCA TT GC TGTG			
		TTTCGACGT AG CG ACAC			
		GG TC A			
GAM1504	LOC56267	3' CACAGATTTTACAGCTTTGG	39010	C TTGC	
		TCAAAGCTG AGA CTGTG			
		GGTTTCGAC TTT GACAC			
		A TA_			
GAM1504	LOC90139	3' CACAGGCGTGACAGTTCTGA	55401	A _ GAT	
		TCA AGCTG CA TGCCTGTG			
		AGT TTGAC GT GCGGACAC			
		C A _			
GAM1505	AQP6	3' GCTGAGGAGACCAGGCC	53932	G T	
		GGCCTGG TCTCCTTA GC			
		CCGGACC AGAGGAGT CG			
		— —			
GAM1505	BCAS1	5' CAGCACGCACTGGAGACCCAGG	13339	TTA CA_	
		CCTGGGTCTCC TGC CTG			
		GGACCCAGAGG ACG GAC			
		TC_ CAC			
GAM1505	CACNB1	3' AGTGGGTGAGATCCAGACC	5568	C CTTATG	
		GG CTGGGTCTC CCACT			
		CC GACCTAGAG GGTGA			
		A TG_			
GAM1505	FUT6	5' AGTGGTGAAGACCCAGCC	3806	C CCTTA	
		GGC TGGGTCT TGCCACT			
		CCG ACCCAGA GTGGTGA			
		— A_			
GAM1505	LDHB	5' CAGTGGCATGCCCAAACCCA	9704	CTCCT	
		TGGGT TATGCCACTG			

		ACCCA GTACGGTGAC	
		AACCC	
GAM1505 LDHB	5'	CAGTGGCATGCCCAAACCCA 9705	CTCCT
		TGGGT TATGCCACTG	
		ACCCA GTACGGTGAC	
		AACCC	
GAM1505 LFG	3'	GCTCCAGGGACCCAGGCC 76723	T TAT
		GGCCTGGGTC CCT GC	
		CCGGACCCAG GGA CG	
		_ CCT	
GAM1505 PREB C	3'	CAGCGGTATCTGAAGCCCAGGC 25410	TC CTT A
		GGCCTGGG TC ATGCC CTG	
		CCGGACCC AG TATGG GAC	
		GA TC_ C	
GAM1505 RENT1	5'	CAGCGGCAGCGACCCGAGGCC 11286	_ TCCTTA A
		GGCCT GGGTC TGCC CTG	
		CCGGA CCCAG ACGG GAC	
		G CG_____ C	
GAM1505 SCG3	3'	AGTGACATAAAAAGGATCC 25094	CC_ C
		GGGTCT TTATG CACT	
		CCTAGG AATAC GTGA	
		AAA A	
GAM1505 SKI	3'	GCGACAAGGACCCAGGTC 11703	CCTTA
		GGCCTGGGTCT TGC	
		CTGGACCCAGG GCG	
		AACA_	
GAM1505 TBL2	3'	CAGCAGCAGCTGACCCAGGCC 52179	TCCTTA CA
		GGCCTGGGTC TGC CTG	
		CCGGACCCAG ACG GAC	
		TCG_____ AC	
GAM1505 TOP3A	3'	ATAAAGAACCCAGGCC 16070	C C
		GGCCTGGGT TC TTAT	
		CCGGACCCA AG AATA	
		_ A	
GAM1505 CREB-H	3'	GCCTGAAAGAGACCCAG 50884	C_ T
		CTGGGTCTC TTA GC	
		GACCCAGAG AGT CG	
		AA C	
GAM1505 CRTAM	3'	CAGCAACATGAGGACCAAACC 38978	CC GTC CCA
		GG TGG TCCTTATG CTG	

CC ACC AGGAGTAC GAC  
 AA \_\_\_\_ AAC  
 GAM1505 DKFZP586G1122 3' GTAGCAACCCAGGCC 61287 CTCCTTA C  
 GGCCTGGGT TGC AC  
 ||||| |||  
 CCGGACCCA ACG TG  
 \_\_\_\_ A  
 GAM1505 KIAA0040 5' CAGTGGCATGCCCAAACCCA 27779 CTCCT  
 TGGGT TATGCCACTG  
 |||| |||||  
 ACCCA GTACGGTGAC  
 AACCC  
 GAM1505 KIAA0057 3' CAGGGGGCAAGGAGCCCAGGCC 24418 T TA A\_  
 GGCCTGGG CTCCT TGCC CTG  
 ||||| |||| ||| |||  
 CCGGACCC GAGGA ACGG GAC  
 \_\_\_\_ GG  
 GAM1505 KIAA0574 3' AGCAGCAAGAGCCCAGGCC 69279 T CTTA CA  
 GGCCTGGG CTC TGC CT  
 ||||| ||| ||| |||  
 CCGGACCC GAG ACG GA  
 \_\_\_\_ A \_\_\_\_ AC  
 GAM1505 KIAA1946 3' GCATAGAGACCCAAACC 82472 CC CT  
 GG TGGGTCTC TATGC  
 || ||||| ||||  
 CC ACCCAGAG ATACG  
 AA \_\_\_\_  
 GAM1505 MATR3 3' ATAAAAAGAAAACCCTAGGCC 38115 \_\_\_\_ CC  
 GGCCTGGG TCT TTAT  
 ||||| ||| |||  
 CCGGATCC AGA AATA  
 CAAA AA  
 GAM1505 MGC29667 5' CAGTGACAGCCCGGACCCGGCC 58332 T CCTTA C  
 GGCC GGGTCT TG CACTG  
 ||| ||||| || |||||  
 CCGG CCCAGG AC GTGAC  
 \_\_\_\_ CCCG\_ A  
 GAM1505 PRPF8 3' GCAACTATGAGACCCAGACT 61191 C CTTA\_  
 GG CTGGGTCTC TGC  
 || ||||| |||  
 TC GACCCAGAG ACG  
 A TATCA  
 GAM1505 PSR 3' CAGTGGCAGTGACCCAGC 65178 C TCCTTA  
 GC TGGGTC TGCCACTG  
 || ||||| |||||  
 CG ACCCAG ACGGTGAC  
 \_\_\_\_ TG\_\_\_\_  
 GAM1505 LOC115708 3' GCGCTAGGAGACCAGGCC 73552 G TA  
 GGCCTGG TCTCCT TGC  
 ||||| ||||| |||

CCGGACC AGAGGA GCG  
 \_ TC  
 GAM1505 LOC124739 5' AGCGGCGAAACCCAGGTC 74325 C CTTAT A  
 GGCCTGGGT TC GCC CT  
 ||||| || ||  
 CTGGACCCA AG CGG GA  
 A \_ C  
 GAM1505 LOC128823 5' GCAAGGAGACACAGACC 75786 C G TA  
 GG CTG GTCTCCT TGC  
 || || ||||| ||  
 CC GAC CAGAGGA ACG  
 A A \_  
 GAM1505 LOC144278 5' GCATCCGGAACCCAGGTC 76769 C TT  
 GGCCTGGGT TCC ATGC  
 ||||| || ||  
 CTGGACCCA AGG TACG  
 A CC  
 GAM1505 LOC151429 3' GCACTTTGGGAGGCCAGGCC 85354 TA\_  
 GGCCTGGGTCTCCT TGC  
 ||||| ||  
 CCGGACCCGGAGGG ACG  
 TTTC  
 GAM1505 LOC152447 5' CAGTGGCACCTGGAGCCAGACC 80587 C GT TTA  
 GG CTGG CTCC TGCCACTG  
 || || || |||||  
 CC GACC GAGG ACGGTGAC  
 A \_ TCC  
 GAM1505 LOC157285 5' GCAGAAGAAGAGCCAGGCC 86436 G C A  
 GGCCTGG TCT CTT TGC  
 ||||| || || ||  
 CCGGACC AGA GAA ACG  
 G A G  
 GAM1505 LOC200982 3' GTGAGAGCCCCAGGCC 90226 T CTTATGC  
 GGCCTGGG CTC CAC  
 ||||| || ||  
 CCGGACCC GAG GTG  
 C A\_  
 GAM1505 LOC220021 5' GCAGAAGAGGAGACCAGACC 93396 C G A\_  
 GG CTGG TCTCCTT TGC  
 || || ||||| ||  
 CC GACC AGAGGAG ACG  
 A \_ AAG  
 GAM1505 LOC256015 5' GCAGAGACAGAGACCCATGCC 97612 C \_ A  
 GGC TGGGTCTC CTT TGC  
 || ||||| || ||  
 CCG ACCCAGAG GAG ACG  
 T ACA \_  
 GAM1505 LOC91695 3' GCAGTCCTGGAGACCCAGGC 66968 TTA\_  
 GCCTGGGTCTCC TGC  
 ||||| ||

CGGACCCAGAGG ACG  
 TCCTG  
 GAM1506 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
 GTA GGAT GGGTTGTTT  
 ||| ||| |||||  
 CGT CCTA CCCAACAAA  
 C CGTG\_  
 GAM1506 LCT 3' AACCGTAAAAATCCTT 9697 G  
 AAGGATTTTTTA GGTT  
 ||||| |||  
 TTCCTAAAAAT CCAA  
 G  
 GAM1506 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
 GTAAGGATTTTTAGGGTTGTTT  
 |||||  
 CATTCTAAAAATCCCAACAAA  
  
 GAM1506 FBXO30 3' AACTAAAAAATCCTGAC 49573 A AG  
 GT AGGATTTTT GGTT  
 || ||||| |||  
 CA TCCTAAAAA TCAA  
 G AA  
 GAM1506 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTTT  
 GTAAG AGGGTTGTT  
 ||| |||||  
 CATTCT TCCCAACAA  
 AT\_\_\_\_  
 GAM1506 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
 TAAG TTTT GGGTTGTTT  
 ||| ||| |||||  
 GTTC AAAA CCCAACAAA  
 \_\_\_\_ C  
 GAM1506 SMT3H2 3' AACCAACATAAAAAATCCTTGC 22670 GG  
 GTAAGGATTTTTTA GTTGTT  
 ||||| |||||  
 CGTTCCTAAAAAT CAACAA  
 A\_  
 GAM1506 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
 GTAAGGATTTTTT GGGTT  
 ||||| |||||  
 CGTTCCTAAAAA TCCAA  
 GTA  
 GAM1506 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
 GGAT TT GGGTTGTTT  
 ||| || |||||  
 CCTG AA CCCAACAAA  
 T\_ C  
 GAM1506 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
 C GTA GGATTTTT TTGTTT  
 ||| ||||| |||||

		CGT CCTAAAAA AACAAA		
		C GATAA		
GAM1506	LOC148089 3'	GGCCCTAAAAATTCCTAC	78637	A
		GTA GGATTTTTAGGGTT		
		CAT CTTAAAAATCCCGG		
		C		
GAM1506	LOC154547 3'	AACAACATAAAAAATCCTTGC	76050	GG
		GTAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1506	LOC158104 3'	ACAGCCAAAAATCCTTA	60313	AG
		TAAGGATTTTT GTTGT		
		ATTCCTAAAAA CCGACA		
		—		
GAM1506	LOC205880 5'	AAACAACCATCATCCTGAC	90709	A TTTTAG
		GT AGGAT GGTGTTT		
		CA TCCTA CCAACAAA		
		G CTA_		
GAM1506	LOC221561 3'	AACAACATAAAAAATCCTTGC	92130	GG
		GTAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1506	LOC257591 3'	AACAACATAAAAAATCCTTGC	97840	GG
		GTAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1506	LOC51145 3'	AGCTAAAATCCTTAC	32393	TAG
		GTAAGGATTTT GTT		
		CATTCCTAAAA TCGA		
		—		
GAM1507	CCNK 3'	ACCAGCTTTCAGAGTAGCCTC	77282	ACC_ G A
		GAG CTC TGAAAGCT GT		
		CTC GAG ACTTTCGA CA		
		CGAT _ C		
GAM1507	DPYSL2 3'	GCAGCCCCCAGCGAGGGTCTC	7300	GAAA_ A
		GAGACCCTCGT GCT GT		
		CTCTGGGAGCG CGA CG		
		ACCCC _		
GAM1507	LARS2 3'	AGCTACCACGAGGGCCTC	31051	A AA
		GAG CCCTCGTG AGCT		

		CTC GGGAGCAC TCGA	
		C CA	
GAM1507	MAP3K9	3' GGCCAATTTCAGAGGGTCTC 60708	G A__
		GAGACCCTC TGAA GCT	
		CTCTGGGAG ACTT CGG	
		_ CAC	
GAM1507	MBD1	3' ATGAATCCGCTCCCAAGGGTCT 31772	CG AA TAG_
	C	GAGACCCT TG AGC TCAT	
		CTCTGGGA AC TCG AGTA	
		_ CC CCTA	
GAM1507	MBD1	3' ATGAATCCGCTCCCAAGGGTCT 31780	CG AA TAG_
	C	GAGACCCT TG AGC TCAT	
		CTCTGGGA AC TCG AGTA	
		_ CC CCTA	
GAM1507	MBD1	3' ATGAATCCGCTCCCAAGGGTCT 31787	CG AA TAG_
	C	GAGACCCT TG AGC TCAT	
		CTCTGGGA AC TCG AGTA	
		_ CC CCTA	
GAM1507	MBD1	3' ATGAATCCGCTCCCAAGGGTCT 9946	CG AA TAG_
	C	GAGACCCT TG AGC TCAT	
		CTCTGGGA AC TCG AGTA	
		_ CC CCTA	
GAM1507	acmsd	5' AGTTTTACAAAGGTCTC 56353	CTC
		GAGACC GTGAAAGCT	
		CTCTGG CACTTTTGA	
		AAA	
GAM1507	B3GNT7	3' ATGACCCTTTCACGTGG 71124	T CTA
		CC CGTGAAAG GTCAT	
		GG GCACTTTC CAGTA	
		T C__	
GAM1507	DKFZP434F0318	3' AGCTTTCACGAAGTCTC 48004	CC
		GAGAC TCGTGAAAGCT	
		CTCTG AGCACTTTCGA	
		A_	
GAM1507	DKFZP547E1010	5' ATGACTTTCCAGAAGGGTCTC 66933	CG AAAGCT
		GAGACCCT TG AGTCAT	
		CTCTGGGA AC TCAGTA	
		AG CTT__	
GAM1507	DKFZP547E1010	5' ATGACTTTCCAGAAGGGTCTC 31540	CG AAAGCT
		GAGACCCT TG AGTCAT	

CTCTGGGA AC TCAGTA  
 AG CTT\_\_\_\_  
 GAM1507 FLJ20313 3' GACTAAGCAGGGTCTC 34932 CGTGAAA \_  
 GAGACCCT GCT AGTC  
 ||||| ||| |||  
 CTCTGGGA CGA TCAG  
 \_\_\_\_\_ A  
 GAM1507 FLJ31978 3' ACTAGCTTGGATCTC 58346 C TCGTGA  
 GAGA CC AAGCTAGT  
 ||| || |||||  
 CTCT GG TTCGATCA  
 A \_\_\_\_\_  
 GAM1507 KIAA0210 3' ATGACTAGCTCTTTGAG 28469 TGAA  
 CTCG AGCTAGTCAT  
 ||| |||||  
 GAGT TCGATCAGTA  
 TTC\_  
 GAM1507 ORF1-FL49 3' ATGACTAGCTTTGCAC 50550 \_  
 GTG AAAGCTAGTCAT  
 ||| |||||  
 CAC TTTCGATCAGTA  
 G  
 GAM1507 PRO2012 3' ACTAAAAACACAAGAGGGTCTC 37777 \_ AAAGC  
 GAGACCCTC GTG TAGT  
 ||||| ||| |||  
 CTCTGGGAG CAC ATCA  
 AA AAAA\_  
 GAM1507 LOC144667 3' GTGTTGCTTCCAGAGGGTCTC 83172 G A TAGT  
 GAGACCCTC TG AAGC CAT  
 ||||| || ||| |||  
 CTCTGGGAG AC TTCG GTG  
 \_ C TT\_  
 GAM1507 LOC150372 5' GCTACTTTTCATGAAGATCTC 79802 CCC C  
 GAGA TCGTGAAAG TAGT  
 ||| ||||| |||  
 CTCT AGTACTTTC ATCG  
 AGA \_  
 GAM1507 LOC220776 3' AGTTTCCACGAGGGTCTC 68383 A  
 GACCCTCGTG AAGCT  
 ||||| |||  
 CTGGGAGCAC TTTGA  
 C  
 GAM1508 ABCC3 3' GCCCGAGCCCTGCTCCGCA 39141 GA T T  
 TG GAGCAGGGCTC G GC  
 || ||||| |||  
 AC CTCGTCCCGAG C CG  
 GC \_C  
 GAM1508 ABCC3 3' GCCCGAGCCCTGCTCCGCA 39155 GA T T  
 TG GAGCAGGGCTC G GC  
 || ||||| |||



			AC CTCGTCCCGAG C CG		
			GC _ C		
GAM1508	ARRB1	3'	ACGGGCCGGCCCTGCCTCCA 39695	A	___
			TGGAG GCAGGGCT CTGT		
			ACCTC CGTCCCGG GGCA		
			_ CCG		
GAM1508	ARRB1	3'	ACGGGCCGGCCCTGCCTCCA 14459	A	___
			TGGAG GCAGGGCT CTGT		
			ACCTC CGTCCCGG GGCA		
			_ CCG		
GAM1508	ARVCF	3'	ACAGGTGCCCCACCTCCCCA 8025	A CA_ _	
			TGG GAG GGGC TCTGT		
			ACC CTC CCCG GGACA		
			C CAC T		
GAM1508	B4GALT5	3'	CACACATCTCTGGCTCTCCA 16494	_ CTC	
			TGGAGAGC AGGG TGTG		
			ACCTCTCG TCTC ACAC		
			G TAC		
GAM1508	BCL11A	3'	CACACCGCTCTTCA 43159	A GCTC	
			TGGAGAGC GG TGTG		
			ACTTCTCG CC ACAC		
			_ _		
GAM1508	C11orf8	5'	GCACCATGCCTGCTTCCA 7817	G G TCT	
			TGGA AGCAGG C GTGC		
			ACCT TCGTCC G CACG		
			_ _ TAC		
GAM1508	CACNA1S	3'	ACAGGCCCTGCCCTC 3562	A_ T	
			GAG GCAGGGC CTGT		
			CTC CGTCCCG GACA		
			CC _		
GAM1508	CACNG7	3'	GTGCAAGCGCCCAGCTCCCCA 49097	A A T G	
			TGG GAGC GGGC CT TGCAC		
			ACC CTCG CCCG GA ACGTG		
			C A C _		
GAM1508	CCNF	3'	CACACCCTGCTGCCA 8315	AG CTC	
			TGG AGCAGGG TGTG		
			ACC TCGTCCC ACAC		
			G_ _		
GAM1508	CD4	3'	GCATTTGTGCCCACTCTCCA 5225	CA TCT_	
			TGGAGAG GGGC GTGC		

			ACCTCTC CCCG TACG			
			A_ TGTT			
GAM1508	CD74	3'	GCAAGGCCCTGCTGCCCA 15130	AG	T	G
			TGG AGCAGGGC CT TGC			
			ACC TCGTCCCG GA ACG			
			CG _ _			
GAM1508	CDK10	3'	GCTGGATCCCTGCTCCCCA 13404	A	C	T
			TGG GAGCAGGG TCTG GC			
			ACC CTCGTCCC AGGT CG			
			C T _			
GAM1508	CDK10	3'	GCTGGATCCCTGCTCCCCA 53771	A	C	T
			TGG GAGCAGGG TCTG GC			
			ACC CTCGTCCC AGGT CG			
			C T _			
GAM1508	CDK10	3'	GCTGGATCCCTGCTCCCCA 53780	A	C	T
			TGG GAGCAGGG TCTG GC			
			ACC CTCGTCCC AGGT CG			
			C T _			
GAM1508	CHAD	3'	TGCACAGAGCTGCCTACA 7012	G	A	GG
			TG AG GCA GCTCTGTGCA			
			AC TC CGT CGAGACACGT			
			A _ _			
GAM1508	CLCN7	3'	GCGCAGGCCAGCCTCCA 7089	A	A	T
			TGGAG GC GGGC CTGTGC			
			ACCTC CG CCCG GACGCG			
			_ A _			
GAM1508	CLECSF11	5'	ACAGTCACCCTGCTCCCCA 55272	A	CT	_
			TGG GAGCAGGG CTGT			
			ACC CTCGTCCC GACA			
			_ ACT			
GAM1508	CYP4A11	3'	AGAACCTGCTCTCCA 5751	GC		
			TGGAGAGCAGG TCT			
			ACCTCTCGTCC AGA			
			A_			
GAM1508	DPEP1	3'	TGCCAGGAGCCCTGCTGCCCA 15335	AG		GT
			TGG AGCAGGGCTCT GCA			
			ACC TCGTCCCGAGG CGT			
			CG AC			
GAM1508	DUSP3	3'	CACACTGTACCCTGCTCCCCA 14562	A	_	TC
			TGG GAGCAGGG C TGTG			

			ACC CTCGTCCC G ACAC		
			— AT TC		
GAM1508	EGFL4	5'	GCCAGCTCTGCTCCCCA 61811 A	CT T	
			TGG GAGCAGGGCT G GC		
			ACC CTCGTCTCGA C CG		
			C —		
GAM1508	EGR1	3'	AGAGCCCTGCCCTGCA 8737 G A		
			TG AG GCAGGGCTCT		
			AC TC CGTCCCGAGA		
			G C		
GAM1508	EPHA1	3'	AGAACCCTGCTCTGCA 17857 G C		
			TG AGAGCAGGG TCT		
			AC TCTCGTCCC AGA		
			G A		
GAM1508	F13A1	5'	GCACAGAGCAAGCCCA 91059 AGA AGG		
			TGG GC GCTCTGTGC		
			ACC CG CGAGACACG		
			— AA—		
GAM1508	F2RL3	3'	GCACCCCCAACTCTGCTCCCCA 14182 A	CTCT—	
			TGG GAGCAGGG GTGC		
			ACC CTCGTCTC CACG		
			C AACCC		
GAM1508	FGF4	5'	GCGCAGCTCTGCCCCCCA 8881 AGA	CT	
			TGG GCAGGGCT GTGC		
			ACC CGTCTCGA CGCG		
			CCC —		
GAM1508	FGFR3	3'	TGCACAGCCACTCCCC 3777 A CAG	CT	
			GG GAG GGCT GTGCA		
			CC CTC CCGA CACGT		
			C A— —		
GAM1508	FMO4	3'	GTGCATCCCTCCTCTGCTCTCC 8927	CTCT—	
	A		TGGAGAGCAGGG GTGCAC		
			ACCTCTCGTCTC TACGTG		
			CTCCC		
GAM1508	FXD2	5'	GCACCTCCCTGCTCTCC 41211	CTCT	
			GGAGAGCAGGG GTGC		
			CCTCTCGTCCC CACG		
			TC—		
GAM1508	GALE	3'	GCAGCTGCCTGCTCTCCA 63158	G T—	
			TGGAGAGCAGG C CTGT		

			ACCTCTCGTCC G GACG		
			_ TC		
GAM1508	GMPR	3'	CATCAGAGCCCTGCTGCCCA 91002	AG	_
			TGG AGCAGGGCTCTG TG		
			ACC TCGTCCCGAGAC AC		
			CG T		
GAM1508	GNA11	5'	ATGGGGCCCCGCCCTGCA 76094	G A A	
			TG AG GC GGGCTCTGT		
			AC TC CG CCCGGGGTA		
			G C C		
GAM1508	GNB5	5'	GCGCATTCCCGCTCTCC 21664	A CTC	
			GGAGAGC GGG TGTGC		
			CCTCTCG CCC ACGCG		
			_ TT_		
GAM1508	GPR17	3'	GCACAAGCCTGCAACCC 17955	AGA G C	
			GG GCAGG CT TGTGC		
			CC CGTCC GA ACACG		
			CAA _ _		
GAM1508	GTF2F1	3'	TACATGGCTCTGCCCCCA 9155	AGA C	
			TGG GCAGGGCT TGTG		
			ACC CGTCTCGG ACAT		
			CCC T		
GAM1508	GTF2F1	3'	TACATGGCTCTGCCCTCCA 9156	A C	
			TGGAG GCAGGGCT TGTG		
			ACCTC CGTCTCGG ACAT		
			C T		
GAM1508	HOXC10	3'	CACAGCATTCTGTTCTCCA 61268	CT	
			TGGAGAGCAGGG CTGTG		
			ACCTCTTGTCTT GACAC		
			AC		
GAM1508	HYAL1	5'	TGCGTCTCCCCTGCCCTCC 23609	A CTCTG	
			GGAG GCAGGG TGCA		
			CCTC CGTCCC GCGT		
			C CTCT_		
GAM1508	ID3	3'	GCGCCTGGGCCCTGCCCTCC 79046	A T_	
			GGAG GCAGGGCTC GTGC		
			CCTC CGTCCCGGG CGCG		
			C TC		
GAM1508	IFNA4	5'	TGCACAGAGCAAAGTCTTCA 40770	G AGG	
			TGGAGA C GCTCTGTGCA		

		ACTTCT G CGAGACACGT		
		_ AAA		
GAM1508	IKBKG	3' TGCACACGGGTGCTCTCC 13316	AGG	_
		GGAGAGC GCTC TGTGCA		
		CCTCTCG TGGG ACACGT		
		_ C		
GAM1508	IKBKG	3' TGCACACGGGTGCTCTCC 94665	AGG	_
		GGAGAGC GCTC TGTGCA		
		CCTCTCG TGGG ACACGT		
		_ C		
GAM1508	IL21R	3' GCGGAGCCCAGCCCTCCA 41429	A A	
		TGGAG GC GGGCTCTGT		
		ACCTC CG CCCGAGGCG		
		C A		
GAM1508	INMT	3' GTGCACAGGCACACACCTCCA 22276	AGCAGG	T
		TGGAG GC CTGTGCAC		
		ACCTC CG GACACGTG		
		CACACA _		
GAM1508	IRS1	5' GCGAGGAGCCTCCGCCCCCA 18664	AGA A_	G
		TGG GC GGGCTCT TGC		
		ACC CG TCCGAGG GCG		
		CCC CC A		
GAM1508	ITGA5	3' CACAGGCCCTCCCTGTTCCCCA 61278	A	C_
		TGG GAGCAGGG TCTGTG		
		ACC CTTGTCCC GGACAC		
		C TCCC		
GAM1508	JPH2	3' GCAGGCCCTGCCCTCCA 94447	A	T
		TGGAG GCAGGGC CTGT		
		ACCTC CGTCCCG GACG		
		C _		
GAM1508	JUN	5' AGAGCCCTGCTGCCCA 9475	AG	
		TGG AGCAGGGCTCT		
		ACC TCGTCCCGAGA		
		CG		
GAM1508	KCNA6	3' GTGCATTTGACCTGCTCTC 9517	GCTCT	
		GAGAGCAGG GTGCAC		
		CTCTCGTCC TACGTG		
		AGTT_		
GAM1508	KCNJ6	5' GCGCCCAGCCCTGCTCTCC 9530	CT	
		GGAGAGCAGGGCT GTGC		

			CCTCTCGTCCCGA CGCG		
			CC		
GAM1508	LAMC2	3'	GCACCACTGCTCTCCA	38148	GGCTCT
			TGGAGAGCAG GTGC		
			ACCTCTCGTC CACG		
			AC_____		
GAM1508	LAMP1	5'	GCACGCGACCCCGCTCTCC	18703	A C _
			GGAGAGC GGG TC TGTGC		
			CCTCTCG CCC AG GCACG		
			C _ C		
GAM1508	LANGERIN	3'	GTGCCGAGCCCTGCCTTCCA	31691	A T TG
			TGGAG GCAGGGCTC G C		
			ACCTT CGTCCCGAG C G		
			C C GT		
GAM1508	LILRB1	3'	CGCAGACCCACACTCCA	21900	AGCA C
			TGGAG GGG TCTGTG		
			ACCTC CCC AGACGC		
			ACA_ C		
GAM1508	LILRB1	3'	GCACCACTGCTCTCCA	21902	GGCTCT
			TGGAGAGCAG GTGC		
			ACCTCTCGTC CACG		
			AC_____		
GAM1508	LOXL1	3'	GCAGGCCCTGCTCCCC	60190	A T
			GG GAGCAGGGC CTGT		
			CC CTCGTCCCG GACG		
			C _		
GAM1508	MBP	3'	GTGCACAGACGTCCCTCCA	9952	AGCA _
			TGGAG GGGC TCTGTGCAC		
			ACCTC CCTG AGACACGTG		
			_____ C		
GAM1508	MHC2TA	3'	GTACTTCTCCACCCTGCTCTCC	4183	CTCT_____
			GGAGAGCAGGG GTGC		
			CCTCTCGTCCC CATG		
			ACCTCTT		
GAM1508	MKPX	5'	GCACAGAAAGCCCTGCCCTCCA	39486	A _
			TGGAG GCAGGGC TCTGTGC		
			ACCTC CGTCCCG AGACACG		
			C AA		
GAM1508	MOG	5'	GCAGCACTGCCCTCCA	10103	A G CTGT
			TGGAG GCAG GCT GC		

ACCTC CGTC CGA CG  
 C A \_\_\_\_  
 GAM1508 MPP2 3' ACAGGTCAGCCCTGCTCCCCA 59815 A \_\_\_\_  
 TGG GAGCAGGGCT CTGT  
 ||| ||||| |||  
 ACC CTCGTCCCGA GACA  
 C CTG  
 GAM1508 OTX1 3' GCACAGAGCCGCATCCC 27307 A \_ AG  
 GG GA GC GGCTCTGTGC  
 || ||| |||||  
 CC CT CG CCGAGACACG  
 \_ A \_  
 GAM1508 PCK1 3' ATGAAGCCCTGCTCCCCA 52260 A CT  
 TGG GAGCAGGGCT GT  
 ||| ||||| ||  
 ACC CTCGTCCCGA TA  
 \_ AG  
 GAM1508 PCK1 3' ATGAAGCCCTGCTCCCCA 52265 A CT  
 TGG GAGCAGGGCT GT  
 ||| ||||| ||  
 ACC CTCGTCCCGA TA  
 \_ AG  
 GAM1508 PCK1 3' ATGAAGCCCTGCTCCCCA 20576 A CT  
 TGG GAGCAGGGCT GT  
 ||| ||||| ||  
 ACC CTCGTCCCGA TA  
 \_ AG  
 GAM1508 PML 3' TGCATGTTCTGCTTCCA 52659 G CTC  
 TGGA AGCAGGG TGTGCA  
 |||| ||||| |||||  
 ACCT TCGTCCT GTACGT  
 \_ T \_  
 GAM1508 PMX1 5' GTGCACAACGCTCTGCTCTACA 42661 G TC  
 TG AGAGCAGGGC TGTGCAC  
 || ||||| |||||  
 AC TCTCGTCTCG ACACGTG  
 A CA  
 GAM1508 PMX1 5' GTGCACAACGCTCTGCTCTACA 22594 G TC  
 TG AGAGCAGGGC TGTGCAC  
 || ||||| |||||  
 AC TCTCGTCTCG ACACGTG  
 A CA  
 GAM1508 PPP2R5D 3' AACTGCCCTGGCCCTCCA 20714 A \_ TC  
 TGGAG GC AGGGC TGT  
 |||| || ||||| |||  
 ACCTC CG TCCCG ACA  
 C G TC  
 GAM1508 PYCS 3' GTGCACAGTCTGGCTCCCCA 11168 A A CT  
 TGG GAGC GGGCT GTGCAC  
 ||| |||| ||||| |||||

ACC CTCG TCTGA CACGTG  
 \_ G \_  
 GAM1508 RAD52 3' GTGCACAGACAGCACCTCC 56207 AGCA \_ \_  
 GGAG GG GC TCTGTGCAC  
 ||| || |||||  
 CCTC CC CG AGACACGTG  
 \_ A AC  
 GAM1508 RANBP3 3' GCCAGAGCCCTGCCCCA 13257 AGA T  
 TGG GCAGGGCTCTG GC  
 || ||||| ||  
 ACC CGTCCCGAGAC CG  
 CC \_ \_  
 GAM1508 RARA 3' GCACCAGCCCTGCCCCA 6367 AGA CT  
 TGG GCAGGGCT GTGC  
 || ||||| |||  
 ACC CGTCCCGA CACG  
 CC \_ C \_  
 GAM1508 RET 3' TGCACAACACTCCTCCA 4375 AGCA CTC  
 TGGAG GGG TGTGCA  
 ||| || |||||  
 ACCTC CTC ACACGT  
 \_ ACA  
 GAM1508 RET 3' TGCACAACACTCCTCCA 40184 AGCA CTC  
 TGGAG GGG TGTGCA  
 ||| || |||||  
 ACCTC CTC ACACGT  
 \_ ACA  
 GAM1508 RET 3' TGCACAACACTCCTCCA 40600 AGCA CTC  
 TGGAG GGG TGTGCA  
 ||| || |||||  
 ACCTC CTC ACACGT  
 \_ ACA  
 GAM1508 RHAG 3' CACCATTCCTGCTCTCCA 4377 CTCT  
 TGGAGAGCAGGG GTG  
 ||||| |||  
 ACCTCTCGTCCT CAC  
 TAC \_  
 GAM1508 RNH 5' AGAGCCCTCTCCCA 11361 A C  
 TGG GAG AGGGCTCT  
 || || |||||  
 ACC CTC TCCCGAGA  
 C \_  
 GAM1508 RNH 5' AGAGCCCTCTCCCA 59616 A C  
 TGG GAG AGGGCTCT  
 || || |||||  
 ACC CTC TCCCGAGA  
 C \_  
 GAM1508 SCN2B 3' GTGCTCCTCCCCTGCTCCA 15943 A CTCTGT  
 TGG GAGCAGGG GCAC  
 || ||||| |||



			ACC CTCGTCCC	CGTG	
			— CTCCT—		
GAM1508	SERPIND1	5'	CACAGAGCTTTAGCTCC	3944	AGC
			GGAG AGGGCTCTGTG		
			CCTC TTTCGAGACAC		
			GA—		
GAM1508	SH2D1A	3'	CACCTGGTCCCTGCTCTC	9848	— CT
			GAGAGCAGGG CT GTG		
			CTCTCGTCCC GG CAC		
			T TC		
GAM1508	SH3GL1	3'	GCAGGGCCCTGCCTCC	11625	A
			GGAG GCAGGGCTCTGT		
			CCTC CGTCCCGGGACG		
			—		
GAM1508	TCF1	3'	ACAGCTGTGCCTCGCTCCCCA	5032	A AG T—
			TGG GAGC GGC CTGT		
			ACC CTCG CCG GACA		
			C CT TGTC		
GAM1508	TEM8	5'	GCGGACCCTGCTCTCC	49854	C
			GGAGAGCAGGG TCTGT		
			CCTCTCGTCCC AGGCG		
			—		
GAM1508	TEM8	5'	GCGGACCCTGCTCTCC	53834	C
			GGAGAGCAGGG TCTGT		
			CCTCTCGTCCC AGGCG		
			—		
GAM1508	TEM8	5'	GCGGACCCTGCTCTCC	36329	C
			GGAGAGCAGGG TCTGT		
			CCTCTCGTCCC AGGCG		
			—		
GAM1508	TIC	3'	CACTGTTCCCTGCTCCCA	24936	A CTCT
			TGG GAGCAGGG GTG		
			ACC CTCGTCCC CAC		
			— TTGT		
GAM1508	TNF	3'	GCTGAGCCTCTGCTCCCCA	91058	A — TGT
			TGG GAGCAG GGCTC GC		
			ACC CTCGTC CCGAG CG		
			C T T—		
GAM1508	TULP3	3'	GCAGGGAGCCCTTCTCCCCA	12433	A C G
			TGG GAG AGGGCTCT TGC		

			ACC CTC TCCCGAGG ACG		
			C T G		
GAM1508 VAT1	3'	TACAGAGCCCCCACCCTTCA	21048	AGCA_	
		TGGAG GGGCTCTGTG			
		ACTTC CCCGAGACAT			
		CCACC			
GAM1508 VPS41	3'	TGCACAGAACATATCTTCA	26928	GCAGGGC	
		TGGAGA TCTGTGCA			
		ACTTCT AGACACGT			
		ATACA_			
GAM1508 WDR1	3'	CACAGAGCCCCTGGCC	33982	AG CA	
		GG AG GGGCTCTGTG			
		CC TC CCCGAGACAC			
		GG _			
GAM1508 WDR1	3'	CACAGAGCCCCTGGCC	17582	AG CA	
		GG AG GGGCTCTGTG			
		CC TC CCCGAGACAC			
		GG _			
GAM1508 AF9Q34	3'	GCAGAGGCCCTGCCCCA	50737	AGA T G	
		TGG GCAGGGC CT TGC			
		ACC CGTCCCG GA ACG			
		CC_ _ G			
GAM1508 AKAP6	3'	ACAAAGCCCTGCCCTC	14986	A C	
		GAG GCAGGGCT TGT			
		CTC CGTCCCGA ACA			
		C A			
GAM1508 ALOX15B	5'	GGAGCCCCGCTCTGCA	6690	G A	
		TG AGAGC GGGCTCT			
		AC TCTCG CCCGAGG			
		G C			
GAM1508 C20orf110	3'	GCCAAACCCTGCTCCCA	79546	A CTC T	
		TGG GAGCAGGG TG GC			
		ACC CTCGTCCC AC CG			
		_ AA_ _			
GAM1508 C20orf149	3'	GTGAGAGCCCCGCTCTCTA	44174	A G	
		TGGAGAGC GGGCTCT TGC			
		ATCTCTCG CCCGAGA GTG			
		C _			
GAM1508 C21orf80	3'	TGCACAGAATTCCTCCA	30849	AGCA C	
		TGGAG GGG TCTGTGCA			

ACCTC CTT AGACACGT  
 \_\_\_\_\_ A  
 GAM1508 C9orf7 3' GCCCAAGCCCTGCCCTC 34174 A C T  
 GAG GCAGGGCT TG GC  
 ||| ||||| ||  
 CTC CGTCCCGA AC CG  
 C \_ C  
 GAM1508 CECR7 5' GCCCACCCCGCTTTCCA 79625 A CTC T  
 TGGAGAGC GGG TG GC  
 ||||| || ||  
 ACCTTTCG CCC AC CG  
 C \_ C  
 GAM1508 CNNM4 3' GCTCACCCCTGCTCCCCA 39482 A CTC T  
 TGG GAGCAGGG TG GC  
 ||| ||||| ||  
 ACC CTCGTCCC AC CG  
 C C\_ T  
 GAM1508 CRMP5 3' TGCACAGAGCCCAATGC 39295 \_  
 GCA GGGCTCTGTGCA  
 ||| |||||  
 CGT CCCGAGACACGT  
 AA  
 GAM1508 CYLD 3' GCTAGCCCTGCCTCCA 30886 A CTGT  
 TGGAG GCAGGGCT GC  
 |||| ||||| ||  
 ACCTC CGTCCCGA CG  
 \_ T\_  
 GAM1508 DGKD 3' GTGCGAGCTGCCCCGCCCTCCA 59410 A A TCTG  
 TGGAG GC GGGC TGCAC  
 |||| || ||| ||||  
 ACCTC CG CCCG GCGTG  
 C C TCGA  
 GAM1508 DKFZP434A043 3' TGCAATTTTTCCTGCTCTC 31197 CTCTG  
 GAGAGCAGGG TGCA  
 ||||| |||  
 CTCTCGTCCT ACGT  
 TTTTA  
 GAM1508 DKFZp434C0923 3' ACAGAGCCCACCCTCCA 34209 AGCA  
 TGGAG GGGCTCTGT  
 |||| |||||  
 ACCTC CCCGAGACA  
 CCA\_  
 GAM1508 DKFZp434F142 5' CACACCCAGCTCCTGCCACCCA 50016 AGA \_ C\_  
 TGG GCAGG GCT TGTG  
 || |||| || |||  
 ACC CGTCC CGA ACAC  
 CAC T CCC  
 GAM1508 DKFZp434G179 3' ACAGAGCCCTGATCTCCA 80088 G  
 TGGAGA CAGGGCTCTGT  
 ||||| |||||

ACCTCT GTCCCGAGACA  
 A  
 GAM1508 DKFZP434H132 5' GCGCAAGGCCACCCAGCTCTCC 73607 AG\_\_ TC  
 A TGGAGAGC GGC TGTGC  
 ||||| || ||||  
 ACCTCTCG CCG ACGCG  
 ACCCA GA  
 GAM1508 DKFZP434H132 3' GCACTCCCTGCTCCCA 31319 A CTCT  
 TGG GAGCAGGG GTGC  
 || ||||| ||||  
 ACC CTCGTCCC CACG  
 \_ T\_\_  
 GAM1508 DKFZP434N178 5' GCAGCCGCCCTGCTCCCG 71906 A T\_  
 TGG GAGCAGGGC CTGT  
 || ||||| ||||  
 GCC CTCGTCCCG GACG  
 \_ CC  
 GAM1508 DKFZp586I021 3' ACATGCCCTGCTTCCA 50085 G TC  
 TGGAGAGCAGGGC TGT  
 ||| ||||| |||  
 ACCT TCGTCCCG ACA  
 \_ T\_  
 GAM1508 DKFZP727G051 3' GTGCACAGCTGTCCCTCCA 69476 AGCA T\_  
 TGGAG GGGC CTGTGCAC  
 |||| ||| |||||  
 ACCTC CCTG GACACGTG  
 \_ TC  
 GAM1508 DKFZp761F2014 3' TGCACAGGGCAGCCCCCA 39541 AGA AGG  
 TGG GC GCTCTGTGCA  
 ||| || |||||  
 ACC CG CGGGACACGT  
 CCC A\_  
 GAM1508 DOC2B 3' CACAGGGCCTGCCCTC 13135 A G  
 GAG GCAGG CTCTGTG  
 || |||| |||||  
 CTC CGTCC GGGACAC  
 C \_  
 GAM1508 DRIL2 3' TGCACAGAATTTACCTC 21331 CA C  
 GAG GGG TCTGTGCA  
 ||| || |||||  
 CTC TTT AGACACGT  
 CA A  
 GAM1508 E2F6 3' GTACCTTGCCCTCTCTCCA 8715 C TCT  
 TGGAGAG AGGGC GTGC  
 ||||| |||| ||||  
 ACCTCTC TCCCG CATG  
 \_ TTC  
 GAM1508 FEM-2 3' GCACACAGGGGCCCTCCT 27581 C \_  
 AG AGGGCTCT GTGC  
 || ||||| ||||

			TC TCCCGGGG CACG		
			C ACA		
GAM1508	FLJ10314	5'	GCTAGAGCCCTGTCCCCCA 36014	AGA	T
			TGG GCAGGGCTCTG GC		
			ACC TGTCCCGAGAT CG		
			CCC _		
GAM1508	FLJ12057	5'	CACTGCTGGCCCGGCTCTCCA 45434	A	CT__
			TGGAGAGC GGGCT GTG		
			ACCTCTCG CCCGG CAC		
			G TCGT		
GAM1508	FLJ12572	3'	GCACAGGGCCCTCCCTCCA 43252	AGC	
			TGGAG AGGGCTCTGTGC		
			ACCTC TCCCGGGACACG		
			CCC		
GAM1508	FLJ13710	3'	GCTCTCAGCCCTGCTCCA 45682	A	CTGT
			TGG GAGCAGGGCT GC		
			ACC CTCGTCCGA CG		
			_ CTCT		
GAM1508	FLJ20375	3'	TGCACAGGGTCACTCTGCA 35087	G	CAG
			TG AGAG GGCTCTGTGCA		
			AC TCTC CTGGGACACGT		
			G A__		
GAM1508	FLJ20546	3'	TGCAAGCCCTCCACCTCCA 35372	A	C____ CTG
			TGG GAG AGGGCT TGCA		
			ACC CTC TCCGA ACGT		
			_ CACCC _		
GAM1508	FLJ21736	3'	GCGCCGCCCCCTGCTCCACA 46229	GA	CTCT
			TG GAGCAGGG GTGC		
			AC CTCGTCCC CGCG		
			AC CCGC		
GAM1508	FLJ22419	5'	GCGCTCACTGCTCTCCA 45205		GGCTCT
			TGGAGAGCAG GTGC		
			ACCTCTCGTC CGCG		
			ACT__		
GAM1508	FLJ22501	5'	CACCTGGGCCCAACTCCCCA 45368	A	CA_ T_
			TGG GAG GGGCTC GTG		
			ACC CTC CCCGGG CAC		
			C AAC TC		
GAM1508	FLJ22593	5'	GCCCAAGCCCTGCCCTCCA 45225	A_	C T
			TGGAG GCAGGGCT TG GC		

ACCTC CGTCCCGA AC CG  
 CC \_ C  
 GAM1508 FLJ22709 3' AGGGCCTGCTCTCCA 44717 G  
 TGGAGAGCAGG CTCT  
 ||||| ||||  
 ACCTCTCGTCC GGGA  
  
 GAM1508 FLJ22955 5' CACTTGCCCTGCTCTCCA 95118 TCT  
 TGGAGAGCAGGGC GTG  
 ||||| ||||  
 ACCTCTCGTCCCG CAC  
 TT\_  
 GAM1508 FLJ23519 5' AGAGCCCTCTCCCCA 69199 A C  
 TGG GAG AGGGCTCT  
 ||| ||| |||||  
 ACC CTC TCCCGAGA  
 C \_  
 GAM1508 FLJ32356 3' GCAAGCCCTGCTCTCCA 58362 CTG  
 TGGAGAGCAGGGCT TGC  
 ||||| ||||  
 ACCTCTCGTCCCGA ACG  
  
 GAM1508 FTHFD 3' TGCACAGCACCTCCCA 24113 A GCA GCT  
 TGG GA GG CTGTGCA  
 ||| || |||||  
 ACC CT CC GACACGT  
 \_ \_ AC\_  
 GAM1508 GOLGA3 3' GCAGGGGCCCTGCCCACCA 19717 AGA G  
 TGG GCAGGGCTCT TGC  
 ||| ||||| ||||  
 ACC CGTCCCGGGG ACG  
 ACC \_  
 GAM1508 H6PD 3' GCGTGCCCTGGCTCTCCA 15011 \_ TCTG  
 TGGAGAGC AGGGC TGC  
 ||||| |||| |||  
 ACCTCTCG TCCCG GCG  
 G T\_  
 GAM1508 HML2 5' GCGCCGGCCCTGCCTCCA 20952 A CT  
 TGGAG GCAGGGCT GTGC  
 |||| ||||| ||||  
 ACCTC CGTCCCGG CGCG  
 \_ C\_  
 GAM1508 HPA2 3' CACAGACTTGCTCTCCA 41543 GC  
 TGGAGAGCAGG TCTGTG  
 ||||| ||||  
 ACCTCTCGTTC AGACAC  
  
 GAM1508 HRH3 3' GTGGCCGGCCCTGCCCCCA 23370 AGA CT G  
 TGG GCAGGGCT GT CAC  
 ||| ||||| || |||

ACC CGTCCCGG CG GTG  
 CCC C\_\_  
 GAM1508 HSA250839 3' ACAACCGTCCTGCTCCCA 37258 A TC\_  
 TGG GAGCAGGGC TGT  
 ||| ||||| |||  
 ACC CTCGTCCTG ACA  
 C CCA  
 GAM1508 HT011 5' GTGCACAGGATGGCCCTCCA 37475 A AGGG T  
 TGGAG GC C CTGTGCAC  
 ||||| || | |||||  
 ACCTC CG G GACACGTG  
 C GTA\_\_  
 GAM1508 HYA22 3' TGCACAGGCACTCCCA 19432 A CAGG T  
 TGG GAG GC CTGTGCA  
 ||| ||| || |||||  
 ACC CTC CG GACACGT  
 \_ A\_\_ \_  
 GAM1508 IL-17RE 5' GCAAGGCCCTGCCACCA 58294 AGA T G  
 TGG GCAGGGC CT TGC  
 ||| ||||| |||  
 ACC CGTCCCG GA ACG  
 CAC \_ \_  
 GAM1508 ITGB8 5' GCAGAGCCCTCTCTCCA 9408 C  
 TGGAGAG AGGGCTCTGT  
 ||||| |||||  
 ACCTCTC TCCCGAGACG  
 \_  
 GAM1508 KIAA0125 3' GTGCACAGAGCATCTCTCC 60507 CAGG  
 GGAGAG GCTCTGTGCAC  
 ||||| |||||  
 CCTCTC CGAGACACGTG  
 TA\_\_  
 GAM1508 KIAA0450 3' CACGGAGCCCGCCCA 27619 AGA A  
 TGG GC GGGCTCTGTG  
 ||| || |||||  
 ACC CG CCCGAGGCAC  
 C\_\_ \_  
 GAM1508 KIAA0450 3' TGCACCAGCACCTCCA 27651 AGCA \_ CT  
 TGGAG GG GCT GTGCA  
 ||||| ||| |||  
 ACCTC CC CGA CACGT  
 \_ \_ A C\_  
 GAM1508 KIAA0451 3' GTAAGCCCTGCCCCCA 29113 AGA CTG  
 TGG GCAGGGCT TGC  
 ||| ||||| |||  
 ACC CGTCCCGA ATG  
 CCC \_  
 GAM1508 KIAA0523 5' GCCAGGAGCCCTGCTGCCCA 67737 AG GT  
 TGG AGCAGGGCTCT GC  
 ||| ||||| ||| ||

			ACC TCGTCCCGAGG CG			
			CG AC			
GAM1508	KIAA0590	3'	GCACCTGCCCCCCTGCTCCCCA	28197	A	CTCT__
			TGG GAGCAGGG GTGC			
			ACC CTCGTCCC CACG			
			C CCGTC			
GAM1508	KIAA0628	3'	GCGTCCTGGAGCCCTGCCTCC	28871	A	__
			GGAG GCAGGGCTCTG TGC			
			CCTC CGTCCCGAGGT GCG			
			__ CCT			
GAM1508	KIAA0895	3'	GCCTTAGCCCCTGCTCCCCA	92724	A	CT T_
			TGG GAGCAGGG CTG GC			
			ACC CTCGTCCC GAT CG			
			C C_ TC			
GAM1508	KIAA0984	5'	GCGCTCCCTGCTCCCCA	65530	A	CTCT
			TGG GAGCAGGG GTGC			
			ACC CTCGTCCC CGCG			
			__ T__			
GAM1508	KIAA1001	5'	CACCCCTGCTCCCCA	30290	A	CTCT
			TGG GAGCAGGG GTG			
			ACC CTCGTCCC CAC			
			C __			
GAM1508	KIAA1126	3'	GCGGGCCCTGCCTCC	71931	A	T
			GGAG GCAGGGC CTGT			
			CCTC CGTCCCG GGCG			
			__ __			
GAM1508	KIAA1196	3'	GTGCTCAGGCCCTGCCCCCA	61479	AGA	T T
			TGG GCAGGGC CTG GCAC			
			ACC CGTCCCG GAC CGTG			
			CCC _ T			
GAM1508	KIAA1271	5'	GCCAGAGCCCTCTCTCCA	69547	C	T
			TGGAGAG AGGGCTCTG GC			
			ACCTCTC TCCCGAGAC CG			
			__ __			
GAM1508	KIAA1538	5'	CGCCTCAGCCCTGCCTCCA	71540	A	CT_
			TGGAG GCAGGGCT GTG			
			ACCTC CGTCCCGA CGC			
			__ CTC			
GAM1508	KIAA1602	3'	TGCACAGACGCCCTC	64635	CA	_
			GAG GGGC TCTGTGCA			



			CTC CCG AGACACGT			
			— C			
GAM1508	KIAA1615	5'	TACAGACCCTGCTCTC	68724	C	
			GAGAGCAGGG TCTGTG			
			CTCTCGTCCC AGACAT			
			—			
GAM1508	KIAA1751	3'	GCGGGCCCTGCCCTCC	71697	A	T
			GGAG GCAGGGC CTGT			
			CCTC CGTCCCG GGCG			
			C —			
GAM1508	KIAA1753	3'	GCAGGCCCTGCTCCCC	64881	A	T
			GG GAGCAGGGC CTGT			
			CC CTCGTCCCG GACG			
			C —			
GAM1508	KIAA1856	3'	GTGCCAGGGGCCCTGCCCCA	92668	AGA	GT
			TGG GCAGGGCTCT GCAC			
			ACC CGTCCCGGG CGTG			
			CC_ AC			
GAM1508	KIAA1884	3'	TGCTTCATGCCCTGTTCCCA	73342	A	TCTGT
			TGG GAGCAGGGC GCA			
			ACC CTTGTCCCG CGT			
			C TACTT			
GAM1508	KIAA1904	3'	ACACAGCCCTGCCCA	73476	AGA	C
			TGG GCAGGGCT TGT			
			ACC CGTCCCGA ACA			
			C_ C			
GAM1508	MASA	3'	GCAGACCGCCCTGTTCCCA	64843	A	—
			TGG GAGCAGGGC TCTGT			
			ACC CTTGTCCCG AGACG			
			C CC			
GAM1508	MDS028	3'	GCTTCAGAAGCCCTGCTCCA	37464	A	_ T_
			TGG GAGCAGGGCT CTG GC			
			ACC CTCGTCCCGA GAC CG			
			_ A TT			
GAM1508	MGC12972	3'	GCACAGGGCCCACTCTGCCA	51078	_	CA
			TGG AGAG GGGCTCTGTGC			
			ACC TCTC CCCGGGACACG			
			G A_			
GAM1508	MGC29891	3'	TGCACCACTGCTCTCCA	58218		GGCTCT
			TGGAGAGCAG GTGCA			

			ACCTCTCGTC	CACGT		
			AC			
GAM1508	MGC34923	3'	CACAGAGTCTCTCTCTA	58519	CA	
			TGGAGAG GGGCTCTGTG			
			ATCTCTC TCTGAGACAC			
GAM1508	MLL4	3'	AGGGCCCTGCCTCCA	28285	A	
			TGGAG GCAGGGCTCT			
			ACCTC CGTCCCGGGA			
GAM1508	MRPL4	5'	GCACACCCCGCTTTCCA	31980	A	CTC
			TGGAGAGC GGG TGTGC			
			ACCTTTCG CCC ACACG			
			C			
GAM1508	MYO3B	3'	GTGCACAGAGCCTAGC	57309	A	
			GC GGGCTCTGTGCAC			
			CG TCCGAGACACGTG			
			A			
GAM1508	NIN283	3'	GCACGGTCTCTGCTCCCA	50072	A	CT
			TGG GAGCAGGG CTGTGC			
			ACC CTCGTCTC GGCACG			
			C T			
GAM1508	NIN283	3'	TGCACAGCAGGCTCCCA	50078	A	AGG CT
			TGG GAGC GCT GTGCA			
			ACC CTCG CGA CACGT			
			C GA			
GAM1508	OBSCN	3'	GCCGAGGCCCACTCTCCA	70654	CA	TC T
			TGGAGAG GGGC TG GC			
			ACCTCTC CCG GC CG			
			A GA			
GAM1508	P450RAI-2	3'	CACAGACTGCTCTCCA	39099	GGC	
			TGGAGAGCAG TCTGTG			
			ACCTCTCGTC AGACAC			
GAM1508	PCBP3	3'	GCACACAGCTGCTCTCTA	40071	GG	C
			TGGAGAGCA GCT TGTGC			
			ATCTCTCGT CGA ACACG			
GAM1508	PEPP3	5'	CGGAGCCCCGCTCTGCA	30039	G	A
			TG AGAGC GGGCTCTG			

			AC TCTCG CCCGAGGC		
			G C		
GAM1508	PHYHIP	3'	CACTCCCCCTGCTCTCTA	28606	CTCT
			TGGAGAGCAGGG GTG		
			ATCTCTCGTCCC CAC		
			CCT_		
GAM1508	PI4KII	3'	ATAGGCCCTGCCTCCA	37341	A T
			TGGAG GCAGGGC CTGT		
			ACCTC CGTCCCG GATA		
GAM1508	PPP1R16B	3'	CACAGACCTGCTCCCC	61380	A GC
			GG GAGCAGG TCTGTG		
			CC CTCGTCC AGACAC		
			C		
GAM1508	PPP1R16B	3'	TGCACAGATGCTTCCCA	61390	AG GGGC
			TGG AGCA TCTGTGCA		
			ACC TCGT AGACACGT		
			CT		
GAM1508	PTPRU	3'	GCAGCCCAGCCCCACCTCCA	55689	AGCA CT_
			TGGAG GGGCT G TGC		
			ACCTC CCCGA C ACG		
			CAC_ CC G		
GAM1508	PTPRU	3'	GCAGCCCAGCCCCACCTCCA	55695	AGCA CT_
			TGGAG GGGCT G TGC		
			ACCTC CCCGA C ACG		
			CAC_ CC G		
GAM1508	PTPRU	3'	GCAGCCCAGCCCCACCTCCA	19116	AGCA CT_
			TGGAG GGGCT G TGC		
			ACCTC CCCGA C ACG		
			CAC_ CC G		
GAM1508	RGS11	3'	GTGAGCTGGCCTTGCTCCCCA	13827	A CT G
			TGG GAGCAGGGCT GT CAC		
			ACC CTCGTTCCGG CG GTG		
			C T_ A		
GAM1508	RGS11	3'	GTGCACAGCCTCCCTCCCTCCA	13828	AGC CT_
			TGGAG AGGG CTGTGCAC		
			ACCTC TCCC GACACGTG		
			CC_ TCC		
GAM1508	S100Z	5'	AGACACCCAGCTCTCCA	55376	A C_
			TGGAGAGC GGG TCT		

ACCTCTCG CCC AGA  
 A AC  
 GAM1508 SBI54 3' CACCCCTGCTCCCA 56361 A CTCT  
 TGG GAGCAGGG GTG  
 ||| ||||| |||  
 ACC CTCGTCCC CAC  
 C \_\_\_\_  
 GAM1508 SDC3 3' TGCACAGTCTCACTCCA 27768 AGCA CT  
 TGGAG GGG CTGTGCA  
 |||| | |||||  
 ACCTC CTC GACACGT  
 A\_\_ T\_  
 GAM1508 SDCCAG33 5' GCGCCCCCTGCTCCCC 19364 A CTCT  
 GG GAGCAGGG GTGC  
 || ||||| |||  
 CC CTCGTCCC CGCG  
 C CC\_  
 GAM1508 SERPING1 3' GGCCCTGCCATGCTCTCCA 3557 \_\_\_\_  
 TGGAGAGCA GGGCT  
 ||||| ||||  
 ACCTCTCGT CCCGG  
 ACCGT  
 GAM1508 SNPH 3' GCACCCTCCCTGCTCCCA 28242 A CTCT  
 TGG GAGCAGGG GTGC  
 ||| ||||| |||  
 ACC CTCGTCCC CACG  
 \_ TCC\_  
 GAM1508 Spir-1 3' CAGAGCCCTACACTCCA 64695 AGC  
 TGGAG AGGGCTCTG  
 |||| |||||  
 ACCTC TCCCGAGAC  
 ACA  
 GAM1508 TRAF6 5' GTGGGGGAGCCCTGCCCTCC 16096 A GTG  
 GGAG GCAGGGCTCT CAC  
 |||| ||||| |||  
 CCTC CGTCCCGAGG GTG  
 C GG\_  
 GAM1508 TROAP 5' GTACCTGAGCCCTGCCCTCCA 18498 A T\_  
 TGGAG GCAGGGCTC GTGC  
 |||| ||||| |||  
 ACCTC CGTCCCGAG CATG  
 C TC  
 GAM1508 TSPAN-3 5' GCGCAGCCCCGCTCTCC 19160 A CT  
 GGAGAGC GGGCT GTGC  
 ||||| |||| |||  
 CCTCTCG CCCGA CGCG  
 C \_\_\_\_  
 GAM1508 TTC4 3' GTACTTCCCTGCTCCCA 66307 A CTCT  
 TGG GAGCAGGG GTGC  
 ||| ||||| |||

			ACC CTCGTCCC CATG		
			TT__		
GAM1508	WNT10A	5'	GCGCCCCTGGCTCTCCA 47404	CTCT	
			TGGAGAGC AGGG GTGC		
			ACCTCTCG TCCC CGCG		
			G ____		
GAM1508	ZDHC7	5'	GCACCGCCCCGCTCTCCA 34840	TCT	
			TGGAGAGC GGGC GTGC		
			ACCTCTCG CCCG CACG		
			C C__		
GAM1508	ZDHC8	3'	CAGAGCCCCCTCCCCA 63905	CA	
			TGG GAG GGGCTCTG		
			ACC CTC CCCGAGAC		
			C C_		
GAM1508	ZNF340	3'	GTACCAGTCCCTGCTCTC 84563	CT	
			GAGAGCAGGG CTG TGC		
			CTCTCGTCCC GAC ATG		
			T_ C		
GAM1508	LOC112885	3'	GCTTCCAGGCCCTGCTCTCCA 56527	T T__	
			TGGAGAGCAGGGC CTG GC		
			ACCTCTCGTCCCG GAC CG		
			_ CTT		
GAM1508	LOC116113	3'	GCAGGGCCCTGCCCCCC 92216	AGA	
			GG GCAGGGCTCTGT		
			CC CGTCCCGGGACG		
			CCC		
GAM1508	LOC122416	5'	TGCACACCGGTCTCCA 74121	GCA GCTC	
			TGGAGA GG TGTGCA		
			ACCTCT CC ACACGT		
			GG_ ____		
GAM1508	LOC125268	3'	GCTGGAACCTGCTCTC 76075	C T	
			GAGAGCAGGG TCTG GC		
			CTCTCGTCCC AGGT CG		
			A _		
GAM1508	LOC127703	5'	GCACAGAGCCCCGCGGCTA 74678	AGA A	
			TGG GC GGGCTCTGTGC		
			ATC CG CCCGAGACACG		
			GG_ C		
GAM1508	LOC128344	3'	GTGCACAGTGCTATCTCCA 74737	GCAG T	
			TGGAGA GGC CTGTGCAC		

ACCTCT TCG GACACGTG  
 A\_\_ T  
 GAM1508 LOC128346 3' GTGCACAGAGTATTCACC 74741 A GCAGG  
 GG GA GCTCTGTGCAC  
 || || |||||  
 CC CT TGAGACACGTG  
 A TA\_\_  
 GAM1508 LOC129138 3' GCCCCAGCCCTGCTCCCA 57123 A CTGT  
 TGG GAGCAGGGCT GC  
 ||| ||||| ||  
 ACC CTCGTCCCGA CG  
 \_ CCC\_  
 GAM1508 LOC130813 5' AGAGCCCTGTCCCCA 75762 A G  
 TGG GA CAGGGCTCT  
 ||| |||||  
 ACC CT GTCCCGAGA  
 C \_  
 GAM1508 LOC137964 3' GCGGCCACCCGCTCTCCA 75284 A CT\_  
 TGGAGAGC GGG CTGT  
 ||||| ||| |||  
 ACCTCTCG CCC GGCG  
 \_ ACC  
 GAM1508 LOC143308 5' GTGGAGAGCCCTACCTTCCA 82939 AGC G  
 TGGAG AGGGCTCT TGC  
 |||| ||||| |||  
 ACCTT TCCCGAGA GTG  
 CCA G  
 GAM1508 LOC144481 3' GTACACAAGCCCCATCTCCA 83100 GCA C\_  
 TGGAGA GGGCT TGTGC  
 |||| |||| ||||  
 ACCTCT CCCGA ACATG  
 AC\_ AC  
 GAM1508 LOC144583 3' GTGTCTGCCCTGCTCTCC 76895 TCTGT  
 GGAGAGCAGGGC GCAC  
 ||||| |||  
 CCTCTCGTCCCG TGTG  
 TC\_  
 GAM1508 LOC144699 3' TGCATTTCTCTCCCCA 76917 A C CTCT  
 TGG GAG AGGG GTGCA  
 ||| ||| ||| ||||  
 ACC CTC TCCT TACGT  
 C \_ T\_  
 GAM1508 LOC145601 3' GTGCACAGAGCCTGGGTGC 83371 \_  
 GCA GGGCTCTGTGCAC  
 ||| |||||  
 CGT TCCGAGACACGTG  
 GGG  
 GAM1508 LOC145694 5' GCACACTCGCTCTGCTCCACA 83422 GA TC\_  
 TG GAGCAGGGC TGTGC  
 || ||||| ||||

		AC CTCGTCTCG ACACG			
		AC CTC			
GAM1508	LOC146429 5'	ACAGGAGGCCCTGTCCCCA	83669	A G	___
		TGG GA CAGGGCT CTGT			
		ACC CT GTCCCGG GACA			
		C _ AG			
GAM1508	LOC146745 5'	GCGGGCCTGCCCTCCA	78089	A G T	
		TGGAG GCAGG C CTGT			
		ACCTC CGTCC G GGCG			
		C _ _			
GAM1508	LOC146909 5'	GCCAGCCCTGCACCCCA	78174	AGA	CT T
		TGG GCAGGGCT G GC			
		ACC CGTCCCGA C CG			
		CCA _ _			
GAM1508	LOC147782 3'	CACCAAGCCCTACTCTCTA	78482	C	CT
		TGGAGAG AGGGCT GTG			
		ATCTCTC TCCCGA CAC			
		A AC			
GAM1508	LOC147791 5'	GCCTCAAGCCCTGCCCCCA	84071	AGA	C T _
		TGG GCAGGGCT TG GC			
		ACC CGTCCCGA AC CG			
		CC _ _ TC			
GAM1508	LOC148930 3'	CACATTCTGTCTCCA	79091	G	CTC
		TGGAGA CAGGG TGTG			
		ACCTCT GTCCT ACAC			
		_ T _			
GAM1508	LOC149465 3'	GCAGGGCCCTCTCCCCA	79393	A C	
		TGG GAG AGGGCTCTGT			
		ACC CTC TCCCGGGACG			
		C _			
GAM1508	LOC149478 5'	GCGCTGCTGCCCTGCTCCGCA	79380	GA	_ TCT _
		TG GAGCAGGG C GTGC			
		AC CTCGTCCC G CGCG			
		GC C TCGT			
GAM1508	LOC150372 3'	TGCACAGGGGCCTCCCA	79810	A GCA G	
		TGG GA GG CTCTGTGCA			
		ACC CT CC GGGACACGT			
		_ _ _ G			
GAM1508	LOC152573 3'	GTGGAGCCCTGCTCCCA	80619	A	TG
		TGG GAGCAGGGCTC T			

		ACC CTCGTCCCGAG G		
		— GT		
GAM1508	LOC154807 5'	GCCGGAATCCTGCTCTCCA	86252	GC T
		TGGAGAGCAGG TCTG GC		
		ACCTCTCGTCC AGGC CG		
		TA —		
GAM1508	LOC158056 5'	TGCCCACCTGCTCTCCA	81688	GCTC T
		TGGAGAGCAGG TG GCA		
		ACCTCTCGTCC AC CGT		
		— C		
GAM1508	LOC158292 5'	TGCCATCCCTGCTCCCA	86731	A CTC T
		TGG GAGCAGGG TG GCA		
		ACC CTCGTCCC AC CGT		
		— T —		
GAM1508	LOC159766 5'	CACAAGACCCCTGCCCTCC	82198	A C _
		GGAG GCAGGG TCT GTG		
		CCTC CGTCCC AGA CAC		
		C C A		
GAM1508	LOC163669 5'	CACTTCAGCCCTGCCTCCA	82150	A CT_
		TGGAG GCAGGGCT GTG		
		ACCTC CGTCCCGA CAC		
		— CTT		
GAM1508	LOC163682 3'	GTGAGGCCCTGCTCCCA	87040	A T G
		TGG GAGCAGGGC CT TGC		
		ACC CTCGTCCCG GA GTG		
		— — —		
GAM1508	LOC195977 3'	TGCACAGGCTCCCTGCTGCCCA	87542	AG C_
		TGG AGCAGGG TCTGTGCA		
		ACC TCGTCCC GGACACGT		
		CG TC		
GAM1508	LOC196759 5'	GCAGGAGCCCTGCCCTCC	87517	A G
		GGAG GCAGGGCTCT TGC		
		CCTC CGTCCCGAGG ACG		
		C —		
GAM1508	LOC196955 3'	GCGGAGCCTGCTCCCCA	77381	A G
		TGG GAGCAGG CTCTGT		
		ACC CTCGTCC GAGGCG		
		C —		
GAM1508	LOC199986 5'	GTCAAGCCCTGCCCTCC	89908	A C T
		GGAG GCAGGGCT TG GC		



			CCTC CGTCCCGA AC TG		
			C _ _		
GAM1508	LOC201181 5'	GCCCAGCCCTGCCTTCCA	88138	A	CTGT
		TGGAG GCAGGGCT GC			
		ACCTT CGTCCCGA CG			
		C CC_			
GAM1508	LOC201243 5'	GCGGGCCTGCCCTCCA	88161	A	G T
		TGGAG GCAGG C CTGT			
		ACCTC CGTCC G GGCG			
		C _ _			
GAM1508	LOC203636 3'	TGCAGACCTGCTCTC	89434		GC
		GAGAGCAGG TCTGTG			
		CTCTCGTCC AGACGT			
		—			
GAM1508	LOC203871 3'	GCAGACCTGCTCCCG	89442	A	C
		TGG GAGCAGGG TCTGT			
		GCC CTCGTCCC AGACG			
		— —			
GAM1508	LOC204970 3'	GTTCGAATCCCGCTCTCCA	89417	A	GC TGT
		TGGAGAGC GG TC GC			
		ACCTCTCG CC AG TG			
		C TA CT_			
GAM1508	LOC221297 5'	ACAGTGCCTGCTCTCCA	91838		G T
		TGGAGAGCAGG C CTGT			
		ACCTCTCGTCC G GACA			
		— T			
GAM1508	LOC222066 3'	GTGCACAGGGAACGTTCTCCA	92747		AGGG
		TGGAGAGC CTCTGTGCAC			
		ACCTCTTG GGGACACGTG			
		CAA_			
GAM1508	LOC245812 3'	GCACTCTCCCTGCTCCACA	93954	GA	CTCT
		TG GAGCAGGG GTGC			
		AC CTCGTCCC CACG			
		AC TCT_			
GAM1508	LOC253897 3'	GCGGCCACCCGCTCTCCA	96106	A	CT_
		TGGAGAGC GGG CTGT			
		ACCTCTCG CCC GGCG			
		_ ACC			
GAM1508	LOC254045 3'	GTACACAAGCCCCATCTCCA	96509	GCA	C_
		TGGAGA GGGCT TGTGC			

		ACCTCT CCCGA ACATG		
		AC_ AC		
GAM1508	LOC254946 5'	GTGCACCTGCCGCCACCTTCC 96042	G CA	TCT__
	A	TGGA AG GGGC GTGCAC		
		ACCT TC CCCG CACGTG		
		_ CA CCGTC		
GAM1508	LOC255057 5'	GCGCTGAGGGCCCTCCTCCCCA 95351	A C	_
		TGG GAG AGGGCTCT GTGC		
		ACC CTC TCCCGGGA CGCG		
		C C GT		
GAM1508	LOC255314 5'	GTGCACGGAAGTGTGTCCA 97634	G	GGC
		TGGA AGCAG TCTGTGCAC		
		ACCT TCGTC AGGCACGTG		
		G A__		
GAM1508	LOC255452 3'	GCACACACCCTGCCTTCCA 97537	A	CTC
		TGGAG GCAGGG TGTGC		
		ACCTT CGTCCC ACACG		
		C AC_		
GAM1508	LOC255520 5'	GTGCGAGCCCTGCCCTCC 95863	A	T TG
		GGAG GCAGGGCTC G C		
		CCTC CGTCCCGAG C G		
		C _GT		
GAM1508	LOC256158 5'	ACGGGGCCCTGCTCCCCA 97642	A	
		TGG GAGCAGGGCTCTGT		
		ACC CTCGTCCCGGGGCA		
		C		
GAM1508	LOC256849 5'	GCACCAGGAGCCCTGCGCCCCA 96950	AGA	_
		TGG GCAGGGCTCT GTGC		
		ACC CGTCCCGAGG CACG		
		CCG AC		
GAM1508	LOC257551 3'	GCTGAGCCTCTGCTCCCCA 97711	A	_ TGT
		TGG GAGCAG GGCTC GC		
		ACC CTCGTC CCGAG CG		
		C T T__		
GAM1508	LOC257601 3'	GCTGAGCCTCTGCTCCCCA 97817	A	_ TGT
		TGG GAGCAG GGCTC GC		
		ACC CTCGTC CCGAG CG		
		C T T__		
GAM1508	LOC51049 3'	TGCACAATTGCTTTCCA 31888	GGCTC	
		TGGAGAGCAG TGTGCA		

			ACCTTTCGTT	ACACGT		
			A_____			
GAM1508	LOC90246	5'	GCACAACCTGTCCCCA	61908	A G	GCTC
			TGG GA CAGG TGTGC			
			ACC CT GTCC ACACG			
			C _ A_____			
GAM1508	LOC90630	5'	ACACAGCCCGTCTCCA	63627	G A	C
			TGGAGA C GGGCT TGT			
			ACCTCT G CCCGA ACA			
			__ C			
GAM1508	LOC90631	3'	GCCGAGCCCTGCTGTCCA	63635	G	T T
			TGGA AGCAGGGCTC G GC			
			ACCT TCGTCCCGAG C CG			
			G __			
GAM1508	LOC90639	3'	TGTACCACTGCTCTCCA	63664		GGCTCT
			TGGAGAGCAG GTGCA			
			ACCTCTCGTC CATGT			
			AC_____			
GAM1508	LOC90785	3'	ACAGCCCACCCTGCTCTCC	64009		CT__
			GGAGAGCAGGG CTGT			
			CCTCTCGTCCC GACA			
			ACCC			
GAM1508	LOC91208	5'	ACACAGCCCGTCTCCA	65242	G A	C
			TGGAGA C GGGCT TGT			
			ACCTCT G CCCGA ACA			
			__ C			
GAM1509	DNLC2A	3'	GTCGCTTGGAACCCACTCAC	26363	CAA T	_
			GTGAG GTT CCAGGCG C			
			CACTC CAA GGTTGCG G			
			ACC _ T			
GAM1509	ELMO1	3'	GCCCCAAAACCTTGCCCAC	55282	A	CCA
			GTG GCAAGTTT GGC			
			CAC CGTTCAAA CCG			
			C AAC			
GAM1509	ETV5	3'	GTCCTTTGGAAACCTGGTCAC	15488	G A	__
			GTGA CA GTTTCCA GGC			
			CACT GT CAAAGGT CTG			
			G C TTC			
GAM1509	KRTHB6	3'	CAGCGCCTGTCGCCGTCAC	9656	GCAA	TTC
			GTGA GT CAGGCGCTG			

			CACT CG GTCCGCGAC			
			GC__ CT_			
GAM1509	MAPK9	5'	TCTGAAACTTGCCAC 57420	A	C	
			GTG GCAAGTTTC AGG			
			CAC CGTTCAAAG TCT			
			C _			
GAM1509	MAPK9	5'	TCTGAAACTTGCCAC 10855	A	C	
			GTG GCAAGTTTC AGG			
			CAC CGTTCAAAG TCT			
			C _			
GAM1509	MAPK9	5'	TCTGAAACTTGCCAC 57425	A	C	
			GTG GCAAGTTTC AGG			
			CAC CGTTCAAAG TCT			
			C _			
GAM1509	MAPK9	5'	TCTGAAACTTGCCAC 57415	A	C	
			GTG GCAAGTTTC AGG			
			CAC CGTTCAAAG TCT			
			C _			
GAM1509	MLLT7	3'	GTCAGCGCCTGGCCTAC 19868	TT_		
			GT CCAGGCGCTGAC			
			CA GGTCCGCGACTG			
			TCC			
GAM1509	PAG	3'	CAGCATTAGGAACTTGTTTAC 37400		AG C	
			GTGAGCAAGTTTCC G GCTG			
			CACTTGTTCAAAGG T CGAC			
			AT A			
GAM1509	PCOLCE2	3'	TGATTGAAACCTGCCG 25342	A A	G	
			TG GCA GTTTCAG CG			
			GC CGT CAAAGGTT GT			
			_ C A			
GAM1509	TRPM8	3'	GCCAAGACAGAAACTTGCCCA 43985	A	_____ CA	
			TG GCAAGTT TC GGC			
			AC CGTTCAA AG CCG			
			C AAGAC AA			
GAM1509	AP1GBP1	3'	GCACCAGAAGCTTGCTCAC 54520		CA C	
			GTGAGCAAGTTTC GG GC			
			CACTCGTTCGAAG CC CG			
			A_ A			
GAM1509	AP1GBP1	3'	GCACCAGAAGCTTGCTCAC 23395		CA C	
			GTGAGCAAGTTTC GG GC			

CACTCGTTCGAAG CC CG  
 A\_ A  
 GAM1509 C20orf52 5' CAGCGCCTGGGCCAC 54958 A AAGTTT  
 GTG GC CCAGGCGCTG  
 ||| || |||||  
 CAC CG GGTCCGCGAC  
 C \_\_\_\_  
 GAM1509 ERp44 5' CAGCGCCTGTCCCTGTCAC 81692 G AGTTTC  
 GTGA CA CAGGCGCTG  
 ||| || |||||  
 CACT GT GTCCGCGAC  
 \_ CCCT\_  
 GAM1509 FLJ11200 5' GTCAGCGCCCGTGTACCGCCA 37160 A AAGTTTCCA  
 C GTG GC GGCGCTGAC  
 ||| || |||||  
 CAC CG CCGCGACTG  
 \_ CCACTGTGC  
 GAM1509 KIAA0493 5' GTCAGAAACTTGCCAC 64280 A CCA  
 GTG GCAAGTTT GGC  
 ||| ||||| |||  
 CAC CGTTCAA CTG  
 \_ AGA  
 GAM1509 KIAA1045 3' CAGCGTCTTAACCTTGTCAC 71046 G TCC  
 GTGA CAAGTT AGGCGCTG  
 ||| ||||| |||||  
 CACT GTTCAA TCTGCGAC  
 \_ T\_  
 GAM1509 KIAA1193 3' GTCAGCGCCCGGCACTGCCAC 67647 A A TT A  
 GTG GCA GT CC GGCGCTGAC  
 ||| ||| || |||||  
 CAC CGT CA GG CCGCGACTG  
 \_ \_ C\_ C  
 GAM1509 KIAA1940 3' CAGCGCCTGGTGTATCAC 79976 GCAAGTTT  
 GTGA CCAGGCGCTG  
 ||| |||||  
 CACT GGTCCGCGAC  
 ACTGT\_  
 GAM1509 PRO0529 3' GTCGCTTGGAACCCACTCAC 25999 CAA T \_  
 GTGAG GTT CCAGGCG C  
 |||| ||| ||||| |  
 CACTC CAA GGTTGCG G  
 ACC \_ T  
 GAM1509 TLN2 3' TTAGCTGGAACCGCCCAC 61690 A AA GGC  
 GTG GC GTTTCCA GCTGA  
 ||| || ||||| |||||  
 CAC CG CAAAGGT CGATT  
 C C\_ \_  
 GAM1509 ZDHHC7 3' TCAGACTGAAACTTGCTCAC 34845 C GCG  
 GTGAGCAAGTTTC AG CTGA  
 ||||| ||||| ||| |||

CACTCGTTCAAAG TC GACT  
     — A—  
 GAM1509 LOC123855 3' CTGGAAACTTCTCAC 75628 C  
     GTGAG AAGTTTCCAG  
     ||||| |||||  
     CACTC TTCAAAGGTC  
  
 —  
 GAM1509 LOC138389 5' CAACGCCTGGGTGTCAC 76217 G AGTT C  
     GTGA CA TCCAGGCG TG  
     ||||| || ||||| ||  
     CACT GT GGGTCCGC AC  
  
 — ——— A  
 GAM1509 LOC202181 3' GTGGGACTGGAAACTGCTCAC 89159 A G—  
     GTGAGCA GTTTCCAG CGC  
     ||||| ||||| ||  
     CACTCGT CAAAGGTC GTG  
     — AGG  
 GAM1509 LOC90120 5' CAGCGCCTTCCCTTCGCCCAT 61532 A \_ TTTCC  
     GTG GC AAG AGGCGCTG  
     ||| ||| |||||  
     TAC CG TTC TCCGCGAC  
     C C CCT—  
 GAM1509 LOC90906 5' GTCTTCGGAAGTTGCCAC 64310 A C—  
     GTG GCAAGTTTC AGGC  
     ||| ||||| |||  
     CAC CGTTCAAGG TCTG  
     C CT  
 GAM1509 LOC91151 5' TCAGTTTTTATGGAACTTATC 52618 GC GGC—  
     AC GTGA AAGTTTCCA GCTGA  
     ||||| ||||| |||||  
     CACT TTCAAAGGT TGACT  
     A\_ ATTTT  
 GAM1510 CIT 3' CACGGACACCCCTGTCTCCAG 69743 AA CA—  
     CT AGACAGGGG GTG  
     || ||||| ||  
     GA TCTGTCCCC CAC  
     CC ACAGG  
 GAM1510 HMG20A 5' CTGCCCCTGTCGTCAGCA 36538 AAA  
     TGCT GACAGGGGCAG  
     ||||| |||||  
     ACGA CTGTCCCCGTC  
     CTG  
 GAM1510 MN1 5' CTCCCCTGCCCTTAGCA 10089 AGA C  
     TGCTAA CAGGGG AG  
     ||||| ||||| ||  
     ACGATT GTCCCC TC  
     CCC —  
 GAM1510 NRL 3' ACCTCCCCATTTTAGCA 20513 ACA CA  
     TGCTAAAG GGGG GT  
     ||||| ||| ||

		ACGATTTT CCCC CA			
		A__ TC			
GAM1510	PCDHB13	3' TGCCCCTATCTTTAGC	38428	C	
		GCTAAAGA AGGGGCA			
		CGATTTCT TCCCCGT			
		A			
GAM1510	PRLR	3' CACTTGCCTCTTTCTCCAGCA	6278	AA C	_
		TGCT AGA AGGGGCA GTG			
		ACGA TCT TCTCCGT CAC			
		CC T T			
GAM1510	SCG3	3' AATTTCCCCCTGTTCTTAACA	25093	C AG	CAGT
		TG TAA ACAGGGG GATT			
		AC ATT TGTCCCC TTAA			
		A CT CT__			
GAM1510	SLC7A8	3' CTGCCCCTGCCTCCTGCA	24279	TAA A	
		TGC AG CAGGGGCAG			
		ACG TC GTCCCCGTC			
		TCC C			
GAM1510	SNX13	3' CTGCCCCCATCTCAAGCA	30700	AA CA	
		TGCT AGA GGGGCAG			
		ACGA TCT CCCCGTC			
		AC AC			
GAM1510	XRCC5	3' AGTCACCTCTGTCTTCAGCA	40931	A	CAG
		TGCT AAGACAGGGG TGATT			
		ACGA TTCTGTCTCC ACTGA			
		C			
GAM1510	C20orf39	5' CGCGCCCGCTGCCTCCAGCA	46043	AA A	_ A
		TGCT AG CAG GGGC GTG			
		ACGA TC GTC CCCG CGC			
		CC C G _			
GAM1510	CLSTN1	5' CTGCCGCTGCCTTCAGCA	30106	A A G	
		TGCT AAG CAG GGCAG			
		ACGA TTC GTC CCGTC			
		C C G			
GAM1510	CTAG2	3' GCTCCTGTCTCCAGCA	40649	AA	
		TGCT AGACAGGGGC			
		ACGA TCTGTCCTCG			
		CC			
GAM1510	DKFZP761I2123	3' CAGTGGCCCCTGTGCCCAGCA	48757	AAAG	_ G
		TGCT ACAGGGGC A TG			

		ACGA TGTCCCCG T AC		
		CCCG G G		
GAM1510 DMWD	3'	TCATCCCTGTCCCCAGCA 60881	AAA	GCA
		TGCT GACAGGG GTGA		
		ACGA CTGTCCC TACT		
		CCC _		
GAM1510 ECE2	3'	TGCCCCTGCCTCCAGCA 28070	AA	A
		TGCT AG CAGGGGCA		
		ACGA TC GTCCCCGT		
		CC C		
GAM1510 FLJ10305	3'	TTGCCCCTCCTCCAGCA 68361	AA	AC
		TGCT AG AGGGGCAG		
		ACGA TC TCCCCGTT		
		CC C_		
GAM1510 KIAA1196	3'	CACTGCCTCTGCCCCAGCA 61461	AAAGA	
		TGCT CAGGGGCAGTG		
		ACGA GTCTCCGTCAC		
		CCCC		
GAM1510 MGC2574	3'	CACTGCCTCTGTCCCCAGCA 44050	AAA	
		TGCT GACAGGGGCAGTG		
		ACGA CTGTCTCCGTCAC		
		CCC		
GAM1510 PELI1	3'	TAGTGCCCCCGTTTTTAGCA 40281	A	G
		TGCTAAAGAC GGGGCA TG		
		ACGATTTTGT CCCC GT AT		
		C G		
GAM1510 LOC114987	3'	AATCACTGCTCCTCAGCA 59119	AAAGAC	
		TGCT AGGGGCAGTGATT		
		ACGA TCCTCGTCACTAA		
		C_		
GAM1510 LOC123036	5'	GCGCCCACTGCCTCCAGCA 74193	AA A _	A
		TGCT AG CAG GGGC GT		
		ACGA TC GTC CCCG CG		
		CC C A _		
GAM1510 LOC145371	3'	GCAGCCCCTGTCCCCAGC 77155	AAA	A
		GCT GACAGGGGC GT		
		CGA CTGTCCCCG CG		
		CCC A		
GAM1510 LOC145719	5'	ACTGCCTCACCTCTAGCA 83444	A	ACA
		TGCTA AG GGGGCAGT		



	ACGAT TC CTCCGTCA		
	C CA_		
GAM1510 LOC145720 5'	ACTGCCTCACCTCTAGCA 83425	A	ACA
	TGCTA AG GGGGCAGT		
	ACGAT TC CTCCGTCA		
	C CA_		
GAM1510 LOC150142 5'	AATCACTGCCTGTCTTTGCA 79574	T	GG
	TGC AAAGACA GGCAGTGATT		
	ACG TTTCTGT CCGTCACTAA		
	— —		
GAM1510 LOC158288 5'	GCCCCTGTCTCTACA 86716	C	A
	TG TA AGACAGGGGC		
	AC AT TCTGTCCCCG		
	— C		
GAM1510 LOC196812 3'	CATGCCCCATCTTTACA 89567	C	CA G
	TG TAAAGA GGGGCA TG		
	AC ATTTCT CCCCCG AC		
	— A_ —		
GAM1510 LOC197114 5'	ACTGCCTCGCCTCTAGCA 89697	A	ACA
	TGCTA AG GGGGCAGT		
	ACGAT TC CTCCGTCA		
	C CG_		
GAM1510 LOC197117 3'	ACTGCCTCACCTCTAGCA 89712	A	ACA
	TGCTA AG GGGGCAGT		
	ACGAT TC CTCCGTCA		
	C CA_		
GAM1510 LOC220954 3'	CACTGTCTCTTACAGCA 93139	AAAGAC	
	TGCT AGGGGCAGTG		
	ACGA TCTCTGTCAC		
	CAT_		
GAM1510 LOC221362 3'	ACCATCCCATTTTAGCA 93754	ACA	CA
	TGCTAAAG GGGG GT		
	ACGATTTT CCCT CA		
	A_ AC		
GAM1510 LOC221421 3'	CAAACTCCTGTCCCCAGCA 92275	AAA	CAG
	TGCT GACAGGGG TG		
	ACGA CTGTCCTC AC		
	CCC AAA		
GAM1510 LOC93259 3'	CATACCCCTGTCCTTAGC 71808	A	CA
	GCTAA GACAGGGG GTG		

		CGATT CTGTCCCC TAC	
		C A_	
GAM1510	LOC93426	3' TAATCATACCTGTCTT 55408	GGCA
		AAGACAGG GTGATTA	
		TTCTGTCC TACTAAT	
		A__	
GAM1511	ADH4	3' TAAAAAGATTTTTACTGGA 5409	CGT
		TCCAGTGG TCTTTTTA	
		AGGTCATT AGAAAAAT	
		TTT	
GAM1511	ADRA2B	3' GGGGGAACACACTAGAG 5465	C GC
		CTC AGTG GTTCTTTT	
		GAG TCAC CAAGGGGG	
		A A_	
GAM1511	CTBP1	3' AAAAAAGAAACCTGAAGGAG 67942	AGT_ CG
		CTCC GG TTCTTTTT	
		GAGG CC AAGAAAAA	
		AAGT AA	
GAM1511	EGFL5	5' GTAAAAAGAAAAATATGGGGA 86626	T GTGGCG
		TCC CCA TTCTTTTAC	
		AGG GGT AAGAAAAATG	
		_ ATAAA_	
GAM1511	ENPP3	3' TAAAAAGAACAGCAGAGAG 17227	CAGTG _
		CTC GC GTTCTTTTTA	
		GAG CG CAAGAAAAAT	
		AGA_ A	
GAM1511	F8	3' TAAAAAAATAAGTCAGGAGGA 3733	AG GTTC_
		TCCTCC TGGC TTTTTA	
		AGGAGG ACTG AAAAAT	
		_ AATAA	
GAM1511	ID4	3' AAAAAAGCCACCGGAGGA 7752	A GTTC
		TCCTCC GTGGC TTTT	
		AGGAGG CACCG AAAAA	
		C AA_	
GAM1511	PITX1	3' AAAAAGACGTCGGAG 10596	AGT T
		CTCC GGCGT CTTTTT	
		GAGG CTGCA GAAAAA	
		_ _	
GAM1511	TDG	3' AAAAAGATGCTGGAG 12184	GCGT
		CTCCAGTG TCTTTTT	

GAGGTCGT AGAAAAA

GAM1511 XRCC2 3' AAAAAGAACAAAGCTGGAGG 18314 GGC  
CCTCCAGT GTTCTTTTT  
||||||| |||||||  
GGAGGTCG CAAGAAAAA  
AAA

GAM1511 ABCA10 5' AAAAAGAGACCAGTGGG 54406 G CG  
TCCA TGG TTCTTTTT  
||||| |||||||  
AGGT ACC GAGAAAAA  
G A\_

GAM1511 ABCC13 3' AAAAGTTTTCCACTGGGGA 56988 T CGTT  
TCC CCAGTGG CTTTT  
||| ||||||| |||||  
AGG GGTCACC GAAAA  
\_ TTTT

GAM1511 ARFGAP1 3' GGAACACCCTGGAAGA 36593 C T C  
TC TCCAG GG GTTCT  
|| ||||| || |||||  
AG AGGTC CC CAAGG  
A \_ A

GAM1511 BA526D8.4 5' TAAAAAATTCATACTGGAGGG 70385 GCGTTC  
TCCTCCAGTG TTTTAA  
||||||||| |||||  
GGGAGGTCAT AAAAAT  
ACTTAA

GAM1511 DKFZP727M111 5' AAAAGGAAAAGCCCTGAAG 31402 C T G\_  
CT CAG GGC TTCTTTTT  
|| ||| ||| |||||||  
GA GTC CCG AAGGAAAA  
A \_ AA

GAM1511 DKFZp761H079 3' AAAAAGAGCCAATGGA 58727 G GT  
TCCA TGGC TCTTTTT  
||||| ||||| |||||||  
AGGT ACCG AGAAAAA  
A \_

GAM1511 FLJ10648 3' AAAAAGAACAAAGTCCTGGAGG 36377 T \_  
A TCCTCCAG GGC GTTCTTTTT  
||||||| ||| |||||||  
AGGAGGTC CTG CAAGAAAAA  
\_ AAA

GAM1511 FLJ20151 3' AAAGACCCTGGAGGA 34649 T CGT  
TCCTCCAG GG TCTTT  
||||||| || |||||  
AGGAGGTC CC AGAAA

GAM1511 FLJ20190 5' AAAGGACACCATTTGGAG 34702 C  
CTCCAGTGG GTTCTTT  
||||||||| |||||||

GAGGTTACC CAGGAAA

A

GAM1511 FLJ20435 3' TAAAAAGAGCCATCTGGAGGA 35163 \_ GT

TCCTCCAG TGGC TCTTTTTA

||||||| ||| |||||||

AGGAGGTC ACCG AGAAAAAT

T \_

GAM1511 FLJ22477 5' GACACCATCTGGAGGA 45343 \_ C

TCCTCCAG TGG GTT

||||||| ||| |||

AGGAGGTC ACC CAG

T A

GAM1511 HNRPA3 3' GTAAAAATCTGTACAGAAGGA 19256 CCA TTC

TCCT GTGGCG TTTTAC

||| ||||| |||||||

AGGA CACTGT AAAAATG

AGA CT\_

GAM1511 KIAA1091 3' GTAAAAAGAAAAGTAGAGGA 69685 CAG CG

TCCTC TGG TTCTTTTAC

||||| ||| |||||||||

AGGAG ATC AAGAAAAATG

\_ AA

GAM1511 KIAA1546 3' AAAAAGAAGGTGGGGA 67900 CAGTG G

TCCTC GC TTCTTTTT

||||| || |||||||

AGGGG TG AAGAAAAA

\_ G

GAM1511 KIAA1956 3' GTAAACATAACACTGGAGGA 78439 GC TCT

TCCTCCAGTG GT TTTTAC

||||||||| || |||||

AGGAGGTCAC TA AAAATG

AA C\_

GAM1511 MDS024 3' AAAAAGAATTGCCAAGGA 41523 AG \_

TCC TGGCG TTCTTTTT

||| ||||| |||||||

AGG ACCGT AAGAAAAA

A\_ T

GAM1511 MEGF11 3' AAAAGGAGACTGGGGA 50576 T GGCG

TCC CCAGT TTCTTTTT

||| ||||| |||||||

AGG GGTCA GAGGAAAA

- \_

GAM1511 MGC11082 5' AAAAAAAGGCGGAGGG 51098 AGTG G C

TCCTCC GC TT TTTT

||||| || || |||||

GGGAGG CG AA AAAAA

\_ G A

GAM1511 MGC13105 3' AAAAAGTCACACTAGAGGA 71477 C GCGTT

TCCTC AGTG CTTTTT

||||| ||||| |||||||

AGGAG TCAC GAAAAA  
 A ACT\_\_  
 GAM1511 RPL13 3' AAAAAGAGCCAAGGA 78080 AG GT  
 TCC TGGC TCTTTT  
 ||| ||| |||||  
 AGG ACCG AGAAAAA  
 A\_ \_\_  
 GAM1511 ShrmL 5' AGAGCGCCACTGAAGGA 40464 C  
 TCCT CAGTGGCGTTCT  
 ||| |||||  
 AGGA GTCACCGCGAGA  
 A  
 GAM1511 SIAT8C 5' TAAAAAAGCCCCACAGAGGA 31884 CA C C  
 TCCTC GTGG GTT TTTTAA  
 |||| ||| ||| |||||  
 AGGAG CACC CGA AAAAAT  
 A\_ C \_  
 GAM1511 VEST1 5' AAAAAGATGCACTGGGGA 53679 T G T  
 TCC CCAGTG CGT CTTTTT  
 ||| ||||| ||| |||||  
 AGG GGTCAC GTA GAAAAA  
 - - -  
 GAM1511 ZFD25 5' AAAAAGAGCCCTGGA 32574 T GT  
 TCCAG GGC TCTTTT  
 ||||| ||| |||||  
 AGGTC CCG AGAAAAA  
 - -  
 GAM1511 LOC124626 3' GTAAGACCAAACCACTGGA 74315 CGTTCT  
 TCCAGTGG TTTTAC  
 ||||| |||||  
 AGGTCACC AGAATG  
 AAACC\_  
 GAM1511 LOC126302 3' AAAAAGAAGCAGGAGGA 74486 AGTG G  
 TCCTCC GC TTCTTTT  
 ||||| || |||||  
 AGGAGG CG AAGAAAAA  
 A\_\_ \_  
 GAM1511 LOC132332 5' AAAAAGAAGGCTGGA 76159 GTG G  
 TCCA GC TTCTTTT  
 ||| || |||||  
 AGGT CG AAGAAAAA  
 \_ G  
 GAM1511 LOC144577 3' TAAAAAGAAGCCACAAAGAG 76903 CA\_ G  
 CTC GTGGC TTCTTTTAA  
 ||| ||||| |||||  
 GAG CACCG AAGAAAAAT  
 AAA \_  
 GAM1511 LOC145078 3' GTAAAAATCTGCCACAGAAGGA 60292 CCA TTC  
 TCCT GTGGCG TTTTAC  
 ||| ||||| |||||

	AGGA CACCGT AAAAATG		
	AGA CT_		
GAM1511 LOC145837 5'	AAAAAGAACCAAAGAGGA 83540	CAG CG	
	TCCTC TGG TTCTTTTT		
	AGGAG ACC AAGAAAAA		
	AA_ _		
GAM1511 LOC148753 3'	AAAAGGAGCACCAGGGA 84207	AG C	
	TCC TGG GTTCTTTTT		
	AGG ACC CGAGGAAAA		
	G_ A		
GAM1511 LOC148981 3'	GTAAAAATCTGCCACAGAAGGA 84317	CCA TTC	
	TCCT GTGGCG TTTTAC		
	AGGA CACCGT AAAAATG		
	AGA CT_		
GAM1511 LOC153711 5'	AAAAGCGTCCCGCCAGAGGA 86129	CA C TT	
	TCCTC GTGG G CTTT		
	AGGAG CGCC T GAAAA		
	AC C GC		
GAM1511 LOC154789 5'	GTAAAATCTCAGGCCACTAGAG 81140	C GTTCT_	
	CTC AGTGGC TTTTAC		
	GAG TCACCG AAAATG		
	A GACTCT		
GAM1511 LOC197322 3'	AAAGACTCCACTGGAGGA 89737	C T	
	TCCTCCAGTGG GT CTTT		
	AGGAGGTCACC CA GAAA		
	T _		
GAM1511 LOC220988 3'	GTAAAAATCTGCCACAGAAGGA 90848	CCA TTC	
	TCCT GTGGCG TTTTAC		
	AGGA CACCGT AAAAATG		
	AGA CT_		
GAM1511 LOC221596 3'	TAAAAACCTCACACTGGAGAGA 91981	_ GCGTTC	
	TC CTCCAGTG TTTTTA		
	AG GAGGTCAC AAAAAT		
	A ACTCC_		
GAM1511 LOC255190 3'	GTAAAAATCTGCCACAGAAGGA 97689	CCA TTC	
	TCCT GTGGCG TTTTAC		
	AGGA CACCGT AAAAATG		
	AGA CT_		
GAM1511 LOC91796 3'	AAAAAGAACAAGGCTGGA 67207	GGC	
	TCCAGT GTTCTTTTT		

			AGGTCG CAAGAAAAA		
			GAA		
GAM1511	LOC92539	5'	TAAAAAGTGTCAGTG	69639	TT
			CAGTGGCG CTTTTTA		
			GTCAGTGT GAAAAAT		
			—		
GAM1511	LOC93444	3'	GAACCCACTGGAAGA	72387	C C
			TC TCCAGTGG GTTC		
			AG AGGTCACC CAAG		
			A —		
GAM1511	LOC93538	5'	GTAAAGCTTCAGCGACTGAAGG	72562	C G GTTCT
	A		TCCT CAGT GC TTTTAC		
			AGGA GTCA CG GAAATG		
			A G ACTTC		
GAM1512	CLCN5	5'	TGAAATACCTAAGCTGCTCCAA	3595	_____
			TTGGAGCAG GTTTCA		
			AACCTCGTC TAAAGT		
			GAATCCA		
GAM1512	FLRT2	5'	ATTGAAAAATGAGGTCTGC	25056	GT CTC
			GCAG TTCATT CAAT		
			CGTC GAGTAA GTTA		
			TG AAA		
GAM1512	IL17	3'	TGGGGAAAATGAAACCCTCC	9333	CA —
			GGAG GGTTTCAT TCTCCA		
			CCTC CCAAAGTA AGGGGT		
			— AA		
GAM1512	NLGN1	5'	TGAAGATGCTGCTCCAA	30026	G_
			TTGGAGCAG TTTCA		
			AACCTCGTC GAAGT		
			GTA		
GAM1512	POLG	3'	GTGATAAACCTGCTCCAA	10682	—
			TTGGAGCAGGTT TCAT		
			AACCTCGTCCAA AGTG		
			AT		
GAM1512	TPK1	3'	GGAGAACCTGTCCAA	42384	G TTCAT
			TTGGA CAGGT TCTCC		
			AACCT GTCCA AGAGG		
			— —		
GAM1512	C1orf8	5'	GAGAATGAAACCCTC	16832	CA
			GAG GGTTTCATTCTC		

CTC CCAAAGTAAGAG

GAM1512 CLIC6 3' TGGAGAACATGTTCCAA 82536 G TTCAT  
 TTGGAGCA GT TCTCCA  
 ||||| || |||||  
 AACCTTGT CA AGAGGT  
 A \_\_\_\_\_

GAM1512 CLIPR-59 3' TGGAGAATTTCAATGCCCCGA 31374 A GGTTTC  
 TTGG GCA ATTCTCCA  
 ||| ||| |||||  
 AGCC CGT TAAGAGGT  
 C AACTT\_

GAM1512 DKFZP547L112 3' TGGAGAACTCTTGCTCCA 66532 TTTCA  
 TGGAGCAGG TTCTCCA  
 ||||| |||||  
 ACCTCGTTC AAGAGGT  
 TC\_\_\_\_\_

GAM1512 EPS8R3 5' GGACCACCTGCTCCAA 55701 TTCATTC  
 TTGGAGCAGGT TCC  
 ||||| |||  
 AACCTCGTCCA AGG  
 CC\_\_\_\_\_

GAM1512 EPS8R3 5' GGACCACCTGCTCCAA 57404 TTCATTC  
 TTGGAGCAGGT TCC  
 ||||| |||  
 AACCTCGTCCA AGG  
 CC\_\_\_\_\_

GAM1512 FLJ20552 3' AGAACAAAAGTCTGCTCCAA 35389 G CA  
 TTGGAGCAG TTT TTCT  
 ||||| ||| |||  
 AACCTCGTC AAA AAGA  
 \_ AC

GAM1512 FLJ22865 5' TGGAGAAAAGTCTCTAA 47071 GTTTCA  
 TTGGAGCAG TTCTCCA  
 ||||| |||||  
 AATCTCGTC AAGAGGT  
 AA\_\_\_\_\_

GAM1512 KIAA0372 5' ATTGAAATTTGTTACCTACTCC 27663 C TT TTCTC  
 AA TTGGAG AGGT CA CAAT  
 ||||| ||| |||  
 AACCTC TCCA GT GTTA  
 A TT TAAA

GAM1512 PRO0132 5' ATGAAACCACTCCAA 26101 CA  
 TTGGAG GGTTTCAT  
 ||||| |||||  
 AACCTC CCAAAGTA  
 A\_

GAM1512 TEX27 3' AGAGTGGAACCCGCTGCAA 41658 G A  
 TTG AGC GGTTTCATTCT  
 ||| ||| |||||



AAC TCG CCAAGGTGAGA  
G C  
GAM1512 LOC149373 3' ATTGGGGTGATGATACCCACCC 79312 AGCA T \_  
CAA TTGG GGT TCATT CTCCAAT  
|||| ||| ||||| |||||  
AACC CCA AGTAG GGGGTTA  
CCAC T T  
GAM1512 LOC152687 3' TTGGAGAATATTGCTCC 80643 GTTTC  
GGAGCAG ATTCTCCAA  
||||| |||||  
CCTCGTT TAAGAGGTT  
A\_\_\_\_  
GAM1512 LOC51202 3' ATTGGAGAATGAAACCTGCTCC 33017  
AA TTGGAGCAGGTTTCATTCTCCAAT  
||||||| |||||  
AACCTCGTCCAAAGTAAGAGGTTA  
  
GAM1513 ARF3 3' TACTGTCACCCTGCC 8008 A A  
GG CAGG TGACAGTG  
|| ||| |||||  
CC GTCC ACTGTCAT  
\_ C  
GAM1513 CTGF 3' AGCGTGCTCACTGACCTGCC 8574 A ATGA A  
GG CAGG CAGTGAGCAC CT  
|| ||| ||||| ||  
CC GTCC GTCACCTCGTG GA  
\_ A\_\_\_\_ C  
GAM1513 KLK13 3' TGTACCGGCTTCCATCCTGTC 31532 AC GAGC  
GACAGGATG AGT ACA  
||||||| ||| |||  
CTGTCCTAC TCG TGT  
CT GCCA  
GAM1513 MGAT1 3' GCTCACTGCCTCCTGCC 10009 A TGA  
GG CAGGA CAGTGAGC  
|| ||| |||||  
CC GTCCT GTCACCTCG  
\_ CC\_  
GAM1513 C9orf7 3' GCCCACTGTCACCCTGCC 34175 A A A  
GG CAGG TGACAGTG GC  
|| ||| ||||| ||  
CC GTCC ACTGTCAC CG  
\_ C C  
GAM1513 CDK5RAP3 5' AGTGTGCTGCCCCCACCACCCAC 47279 ACA A ACA G  
C GG GG TG GT AGCACACT  
|| ||| || |||||  
CC CC AC CG TCGTGTGA  
ACC C CCC \_  
GAM1513 CNNM4 3' AGCGTGAGAGGTCATCCTGCC 39471 A AGTGAG A  
GG CAGGATGAC CAC CT  
|| ||||| ||| ||

		CC GTCCTACTG	GTG GA	
		— GAGA— C		
GAM1513	DKFZP564D166	3' CACCTTCATCCTGTCC	47670	CA
		GGACAGGATGA	GTG	
		CCTGTCCTACT	CAC	
		TC		
GAM1513	FBXO24	3' GTGCCTATACATCCTGTCC	24094	ACA A
		GGACAGGATG	GTG GCAC	
		CCTGTCCTAC	TAT CGTG	
		A— C		
GAM1513	FLJ12800	3' CATTGTCACCCTTCC	43229	C A
		GGA AGG	TGACAGTG	
		CCT TCC	ACTGTTAC	
		— C		
GAM1513	KIAA0433	3' TGTACTCACTGTGGAGGTC	30840	AGGATG C
		GAC	ACAGTGAG ACA	
		CTG	TGTCACTC TGT	
		GAGG—	A	
GAM1513	KIAA1432	5' AGTGTACTCACTGTAAACCCT	66746	ATG— C
		AGG	ACAGTGAG ACACT	
		TCC	TGTCACTC TGTGA	
		CAAA	A	
GAM1513	KIAA1878	3' GCACACTCTGTATCTCCTGTCC	91713	TG— — A
		GGACAGGA	ACA GTG GC	
		CCTGTCCT	TGT CAC CG	
		CTA	CT A	
GAM1513	MGC24976	3' GCACACTCTTCCATCCTGTCC	58115	AC— A
		GGACAGGATG	AGTG GC	
		CCTGTCCTAC	TCAC CG	
		CTTC	A	
GAM1513	PADI3	3' GCTCCACCCACCATCCTGTCC	32661	ACA— —
		GGACAGGATG	GT GAGC	
		CCTGTCCTAC	CA CTCG	
		CACC	CC	
GAM1513	PRO2521	3' GCCACTACCATCCTGTC	37592	AC A
		GACAGGATG	AGTG GC	
		CTGTCCTAC	TCAC CG	
		CA	—	
GAM1513	VPS39	3' GTGGCCCTGCCTCCTGTCC	62850	TGA TGA A
		GGACAGGA	CAG GC CAC	

CCTGTCCT GTC CG GTG  
 CC\_ C\_\_ \_  
 GAM1513 ZNF317 3' CTCCTGTGCATCTGCC 72014 A G TG  
 GG CAG ATGACAG AG  
 || ||| ||||| ||  
 CC GTC TACTGTC TC  
 \_ \_ CT  
 GAM1513 LOC119180 3' TGCCTGTGTCATCTTGTCC 73964 G GA  
 GGACAGGATGACA T GCA  
 ||||| |||  
 CCTGTTCTACTGT G CGT  
 \_ TC  
 GAM1513 LOC144563 5' GCAAAACCGCCATCTTGTCC 76890 ACA GA\_  
 GGACAGGATG GT GC  
 ||||| || ||  
 CCTGTTCTAC CA CG  
 CGC AAA  
 GAM1513 LOC145955 5' GCTCACTGCCACCCTCC 83594 CA A A  
 GGA GG TG CAGTGAGC  
 ||| ||| |||||  
 CCT CC AC GTCACTCG  
 \_ C C  
 GAM1513 LOC147111 3' GTATGCTCACTGCCCTCCTGCC 83948 A TGA C  
 GG CAGGA CAGTGAGCA AC  
 || ||| ||||| ||  
 CC GTCCT GTCACTCGT TG  
 \_ CCC A  
 GAM1513 LOC158434 5' GTGTCCTTCATCCTGCC 86824 A C T G  
 GG CAGGATGA AG GA CAC  
 || ||||| || |||  
 CC GTCCTACT TC CT GTG  
 \_ \_ \_  
 GAM1513 LOC158969 3' CTCCTGTCCCCCATCC 82059 CA AT  
 GGA GG GACAGTGAG  
 ||| || |||||  
 CCT CC CTGTCACTC  
 AC C\_  
 GAM1513 LOC159765 5' GCTCAACCGTCATCCTCC 82197 CA AG\_  
 GGA GGATGAC TGAGC  
 ||| ||||| |||  
 CCT CCTACTG ACTCG  
 \_ CCA  
 GAM1513 LOC163231 5' TGCTCACTGTCAACCCTCTCC 82445 C A  
 GGA AGG TGACAGTGAGCA  
 ||| ||| |||||  
 CCT TCC ACTGTCACTCGT  
 C C  
 GAM1513 LOC169436 5' AGCGTGCCCTGAAGCTCCTGTC 82738 TGA\_ TGA A  
 C GGACAGGA CAG GCAC CT  
 ||||| ||| ||| ||

			CCTGTCCT GTC CGTG GA		
			CGAA C__ C		
GAM1513	LOC255030	5'	GTGAGCTATCATCCTGTCT 97270	C	GA
			GGACAGGATGA AGT GC		
			TCTGTCCTACT TCG TG		
			A AG		
GAM1513	LOC84569	3'	TGCCTGTGTCATCTTGTCC 91378	G	GA
			GGACAGGATGACA T GCA		
			CCTGTTCTACTGT G CGT		
			_ TC		
GAM1513	LOC93496	3'	AGTATGCTAGTCATCCTTCC 72429	C	AGTG C
			GGA AGGATGAC AGCA ACT		
			CCT TCCTACTG TCGT TGA		
			_ A__ A		
GAM1514	BAI2	3'	GCCCCTCAGCCACTGGAA 8118	A	A TTCT
			TTC CAGTGGCT AG GC		
			AAG GTCACCGA TC CG		
			_ C CC__		
GAM1514	BTG2	3'	GCAAGGTTAGCAACTGTGAA 22213	G	G C
			TTCACAGT GCTAA TT TGC		
			AAGTGTCA CGATT GA ACG		
			A G _		
GAM1514	CABC1	3'	GTGCAAAACCCAGAAACATGAA 39657	CA	GG AA C
			TTCA GT CT GTT TGCAC		
			AAGT CA GA CAA ACGTG		
			A_ AA CC A		
GAM1514	CYP8B1	3'	TGCAGAACTTGGCATCTG 15276	TG	
			CAG GCTAAGTTCTGCA		
			GTC CGGTTCAAGACGT		
			TA		
GAM1514	DSCR3	3'	GCAAAGTGCTAGCCACTGGAA 20180	A	A TC__
			TTC CAGTGGCTA GT TGC		
			AAG GTCACCGAT CG ACG		
			_ _ TGAA		
GAM1514	FADD	3'	GTAGCCCAGCACTGTGAA 13797	G	AAGTT
			TTCACAGTG CT CTGC		
			AAGTGTAC GA GATG		
			_ CCC__		
GAM1514	GBA	3'	TGCAGAACTGGGCCCGTGGA 76339	AGT	A
			TTACAC GGCT AGTTCTGCA		

AGGTG CCGG TCAAGACGT  
 C\_\_ G  
 GAM1514 GEMIN5 5' GGTTGCTACTTAGCCACTGGAA 89166 A TCT \_  
 TTC CAGTGGCTAAGT GCA CC  
 ||| ||||| ||| ||  
 AAG GTCACCGATTCA CGT GG  
 \_ T\_\_ T  
 GAM1514 NOS1 3' GTGCATGAAACCACTGGAA 5252 A CTAAG \_  
 TTC CAGTGG TTC TGCAC  
 ||| ||||| ||| |||||  
 AAG GTCACC AAG ACGTG  
 \_ A\_\_ T  
 GAM1514 SORBS1 3' GCACAAAAATAGCCATTGT 31156 AG\_ C  
 ACAGTGGCTA TT TGC  
 ||||| || |||  
 TGTTACCGAT AA ACG  
 AAA C  
 GAM1514 SORD 3' TGCAGAACTTTCTCTTTTGAA 11873 C T CT  
 TTCA AG GG AAGTTCTGCA  
 ||| || || |||||  
 AAGT TT TC TTCAAGACGT  
 T C T\_  
 GAM1514 WNT3A 3' GCCTCTGCCACTGTGAA 52435 TA TTCT  
 TTCACAGTGGC AG GC  
 ||||| || ||  
 AAGTGTACCG TC CG  
 TC \_\_\_\_  
 GAM1514 C9orf5 3' GTACAGAACTTGGTCAT 49282 C  
 GTGGCTAAGTTCTG AC  
 ||||| || ||  
 TACTGGTTCAAGAC TG  
 A  
 GAM1514 CABIN1 3' GCCCGCCTTAGCCATGTGAA 24481 G TTCT  
 TTCACA TGGCTAAG GC  
 ||||| ||||| ||  
 AAGTGT ACCGATTC CG  
 \_ CGCC  
 GAM1514 DKFZP564D172 3' GATGTGGCCAACACTGTGAA 49388 \_\_\_\_ AGT  
 TTCACAGT GGCTA TC  
 ||||| ||||| ||  
 AAGTGTCA CCGGT AG  
 CAA GT\_  
 GAM1514 DORFIN 3' GTGCAGAACTTGTACCA 31261 C\_  
 TGG TAAGTTCTGCAC  
 ||| |||||  
 ACC GTTCAAGACGTG  
 AT  
 GAM1514 EFS2 5' GGTGCGGGGCAGCCACCGCTGA 19626 CA\_ AA  
 A  
 TTCA GTGGCT GTTCTGCACC  
 ||| ||||| |||||

		AAGT CACCGA CGGGGCGTGG	
		CGC _	
GAM1514 FLJ10035	3'	GGCACAGAACTTAGCAAC 35748 G	CA
		GT GCTAAGTTCTG CC	
		CA CGATTCAAGAC GG	
		A AC	
GAM1514 FLJ12586	3'	TGCTTCTAATTCAGCCACTGTG 44881	A CT_
	AA	TTCACAGTGGCT AGTT GCA	
		AAGTGTACCGA TTAA CGT	
		C TCTT	
GAM1514 FLJ12800	3'	TGCAGAAGCAGAGCCACTGTGA 43236	AA _
	A	TTCACAGTGGCT GTT CTGCA	
		AAGTGTACCGA CGA GACGT	
		GA A	
GAM1514 FLJ12934	3'	GCACTTACAAGCACTGTGAA 43200	G AA TC_
		TTCACAGTG CT GT TGC	
		AAGTGTAC GA CA ACG	
		_ A_ TTC	
GAM1514 FLJ14621	3'	GCACACCACACTGGCCACTGT 51472	A TC_____
		ACAGTGGCTA GT TGC	
		TGTCACCGGT CA ACG	
		_ CACCAC	
GAM1514 FOXP1	5'	GACACAGAGCCACTGTG 51067	AA _
		CACAGTGGCT GT TC	
		GTGTCACCGA CA AG	
		GA C	
GAM1514 KIAA0062	3'	GCCTTAGCCACTGTGGA 70240	TTCT
		TTCACAGTGGCTAAG GC	
		AGGTGTACCGATTG CG	
		_____	
GAM1514 KIAA0450	5'	GGCTTCCCAGCCACTGTGA 27643	_____
		TCACAGTGGCT AAGTT	
		AGTGTACCGA TTCGG	
		CCC	
GAM1514 KIAA1494	3'	GCATGCATTAGCCACT 68459	_ TC
		AGTGGCTAA GT TGC	
		TCACCGATT CG ACG	
		A T_	
GAM1514 KIAA1828	3'	GGTGCAGAACCGTCCAC 73779	CTAA
		GTGG GTTCTGCACC	

CACC CAAGACGTGG  
 TGC\_  
 GAM1514 KIAA1853 3' GCAAGTACAGCCACTGT 69394 AA T \_  
 ACAGTGGCT GT CT GC  
 ||||| || ||  
 TGTCACCGA CA GA CG  
 \_ T A  
 GAM1514 MGC12458 3' GGTGCAGAACGAACCACTCGAA 50321 AC CTAA  
 TTC AGTGG GTTCTGCACC  
 || ||| |||||  
 AAG TCACC CAAGACGTGG  
 C\_ AAG\_  
 GAM1514 MGC14801 3' TGCGGAGCCCAGCACTGTGAA 51120 G AA  
 TTCACAGTG CT GTTCTGCA  
 ||||| || |||||  
 AAGTGTCA C GA CGAGGCGT  
 \_ CC  
 GAM1514 MGC35558 3' CAGAAACACCGACTGTGAA 58776 \_ CTAAG  
 TTCACAGT GG TTCTG  
 ||||| || |||  
 AAGTGTCA CC AAGAC  
 G ACA\_  
 GAM1514 P1P373C6 5' GGTGCAGAGGACGACCCTG 38904 T CTAAG  
 CAG GG TTCTGCACC  
 || || |||||  
 GTC CC GAGACGTGG  
 \_ AGCAG  
 GAM1514 RAD51 3' TGCAGAACTTAATCTGGA 56022 A TGGC  
 TC CAG TAAGTTCTGCA  
 || ||| |||||  
 AG GTC ATTCAAGACGT  
 \_ TA\_  
 GAM1514 RAD51 3' TGCAGAACTTAATCTGGA 11228 A TGGC  
 TC CAG TAAGTTCTGCA  
 || ||| |||||  
 AG GTC ATTCAAGACGT  
 \_ TA\_  
 GAM1514 TIX1 3' GTGCAGAACCTGCTGT 61747 TG CTAA  
 ACAG G GTTCTGCAC  
 ||| | |||||  
 TGTC C CAAGACGTG  
 GT \_\_\_\_  
 GAM1514 LOC116166 3' TGCAGAACTTTCTCTTTTGAA 59764 C T CT  
 TTCA AG GG AAGTTCTGCA  
 ||| || |||||  
 AAGT TT TC TTCAAGACGT  
 T C T\_  
 GAM1514 LOC144481 3' CAGGAGCCACTGAGAA 83096 A AAGT  
 TTC CAGTGGCT TCTG  
 || ||||| |||

AAG GTCACCGA GGAC  
 A \_\_\_\_\_  
 GAM1514 LOC144970 5' GGTGCTGCACTTGACCACTGT 76983 C TCT \_  
 GAA TTCACAGTGG TAAGT GCA CC  
 ||||| ||| ||| ||  
 AAGTGTCAACC GTTCA CGT GG  
 A CGT T  
 GAM1514 LOC149117 3' CAGCACCTACTGTGAA 84352 CTAA T  
 TTCACAGTGG GT CTG  
 ||||| || |||  
 AAGTGTCAATC CA GAC  
 \_\_\_\_\_ C  
 GAM1514 LOC149319 5' GTGGAGGCTCAGCCACTGTGAG 79302 A T G  
 TTCACAGTGGCT AGT CT CAC  
 ||||| ||| ||| |||  
 GAGTGTCAACCGA TCG GA GTG  
 C \_ G  
 GAM1514 LOC149320 3' GGCGCACAGAAAGTCACTGTGAA 70694 AAGTTC A  
 TTCACAGTGGCT TGC CC  
 ||||| ||| |||  
 AAGTGTCACTGA ACG GG  
 AGAC\_\_ C  
 GAM1514 LOC219942 3' GTGCAGAACTCACT 93349 GCTA  
 AGTG AGTTCTGCAC  
 ||| |||||  
 TCAC TCAAGACGTG  
 \_\_\_\_\_  
 GAM1514 LOC254045 3' CAGGAGCCACTGAGAA 96505 A AAGT  
 TTC CAGTGGCT TCTG  
 ||| ||||| |||  
 AAG GTCACCGA GGAC  
 A \_\_\_\_\_  
 GAM1515 AMPD3 3' GGTGCTCAATAAATGCATATTG 4900 CAA C  
 AA TTCAA GT TTTATTGAGCACC  
 |||| || |||||  
 AAGTT CG AAATAACTCGTGG  
 ATA T  
 GAM1515 CHRND 3' TGCTCAATGGCTCCCCTGAA 5638 ACA\_ TTT  
 TTCA AGTC ATTGAGCA  
 ||| ||| |||||  
 AAGT TCGG TAACTCGT  
 CCCC \_\_\_\_\_  
 GAM1515 CNTN3 3' GGTTTTCAAAAAATTGTTGAA 66696 GTC A C  
 TTCAACAA TTT TTGAG ACC  
 ||||| ||| ||| |||  
 AAGTTGTT AAA AACTT TGG  
 \_\_\_\_\_ A T  
 GAM1515 CRYBA2 3' CTCAATAAAGGTTCTGAA 54044 ACA GT  
 TTCA A CTTTATTGAG  
 ||| | |||||



		AAGT T GAAATAACTC	
		CC_TG	
GAM1515 CRYBA2	3'	CTCAATAAAGGTTCTGAA 54045	ACA GT
		TTCA A CTTTATTGAG	
		AAGT T GAAATAACTC	
		CC_TG	
GAM1515 CRYBA2	3'	CTCAATAAAGGTTCTGAA 17798	ACA GT
		TTCA A CTTTATTGAG	
		AAGT T GAAATAACTC	
		CC_TG	
GAM1515 CYP46	3'	TGCTCAATAAATGTGTGTTGA 21897	AG C
		TCAACA T TTTATTGAGCA	
		AGTTGT G AAATAACTCGT	
		GT T	
GAM1515 DLEU1	3'	CTCAATAAATCTTTGATGAA 19694	A TC
		TTCA CAAG TTTATTGAG	
		AAGT GTTT AAATAACTC	
		A CT	
GAM1515 EIF1A	3'	AATAAAATACTTGTTGAA 88599	C_
		TTCAACAAGT TTTATT	
		AAGTTGTTCA AAATAA	
		TA	
GAM1515 GABPB1	3'	TTGATAAAGATTGTTGAA 17908	G TG
		TTCAACAA TCTTTAT A	
		AAGTTGTT AGAAATA T	
		_ GT	
GAM1515 GCNT1	3'	GTGCTCAGGGACTT 7654	TTA
		AAGTCT TTGAGCAC	
		TTCAGG GACTCGTG	
		—	
GAM1515 GNRHR	5'	GTGCTCAACAGTGTGTTTGAA 4642	_ AGT TTA
		TTCAA CA CT TTGAGCAC	
		AAGTT GT GA AACTCGTG	
		T GT_ C__	
GAM1515 GUCY1B3	3'	GCACCCAATAAATATTTGTTGA 5966	C A__
A		TTCAACAAGT TTTATTG GC	
		AAGTTGTTTA AAATAAC CG	
		T CCA	
GAM1515 MEF2D	3'	GGTGCTCAATAAATGAATG 96915	AG _
		CA TC TTTATTGAGCACC	

			GT AG AAATAACTCGTGG		
			A_ T		
GAM1515	MEF2D	3'	GGCACTCAATAAATGCT	96914	C CA
			AGT TTTATTGAG CC		
			TCG AAATAACTC GG		
			T AC		
GAM1515	NFATC1	3'	GCAGACAAAGACTTTTGAA	20486	C A GA
			TTCAA AAGTCTTT TT GC		
			AAGTT TTCAGAAA AG CG		
			_ C A_		
GAM1515	PAG	3'	GGTACTTCTAGACTTGTT	37405	TTATT C
			AACAAGTCT GAG ACC		
			TTG TTCAGA TTC TGG		
			TC__ A		
GAM1515	PBX3	3'	GGTGCTGCACAGACTTGT	20566	TTAT _
			ACAAGTCT TG AGCACC		
			TG TTCAGA AC TCGTGG		
			C__ G		
GAM1515	PLA2G2D	3'	GGTGCTCAATTCATGCCTGTGA	24798	A A CTTT
	A		TTCA CA GT ATTGAGCACC		
			AAGT GT CG TAACTCGTGG		
			_ C TACT		
GAM1515	PLA2G4C	3'	GTGCTCAATAAATGCTTGCTGA	73415	A C
			TCA CAAGT TTTATTGAGCAC		
			AGT GTTCG AAATAACTCGTG		
			C T		
GAM1515	PML	3'	GGCTGCTCAATAAACACTTGTT	52678	C _
	GAA		TTCAACAAGT TTTATTGAGCA CC		
			AAGTTGTTCA AAATAACTCGT GG		
			C C		
GAM1515	PML	3'	GGCTGCTCAATAAACACTTGTT	52663	C _
	GAA		TTCAACAAGT TTTATTGAGCA CC		
			AAGTTGTTCA AAATAACTCGT GG		
			C C		
GAM1515	PML	3'	GGCTGCTCAATAAACACTTGTT	52669	C _
	GAA		TTCAACAAGT TTTATTGAGCA CC		
			AAGTTGTTCA AAATAACTCGT GG		
			C C		
GAM1515	PML	3'	GGCTGCTCAATAAACACTTGTT	52675	C _
	GAA		TTCAACAAGT TTTATTGAGCA CC		

			AAGTTGTTCA AAATAACTCGT GG		
			C C		
GAM1515 PX19	3'	CTCAATAAACTTGTGAA	25087	C	
		TTCAACAAGT TTTATTGAG			
		AAGTTGTTCA AAATAACTC			
		T			
GAM1515 SNAP25	3'	TGCTCAATGTGCTGTTGA	11834	A CTT	
		TCAACA GT TATTGAGCA			
		AGTTGT CG GTAACCTCGT			
		_ T _			
GAM1515 SNAP25	3'	TGCTCAATGTGCTGTTGA	55527	A CTT	
		TCAACA GT TATTGAGCA			
		AGTTGT CG GTAACCTCGT			
		_ T _			
GAM1515 SOD3	5'	GCACCCAATAAACATTTGTTG	11863	C A _	
		CAACAAGT TTTATTG GC			
		GTTGTTTA AAATAAC CG			
		C CCA			
GAM1515 TLR9	3'	GGCACTCAATAAATGCT	33851	C CA	
		AGT TTTATTGAG CC			
		TCG AAATAACTC GG			
		T AC			
GAM1515 YWHAZ	3'	TGCTCAATAAATATTG	12706	GTC	
		CAA TTTATTGAGCA			
		GTT AAATAACTCGT			
		AT _			
GAM1515 Z39IG	3'	GGTGCTCAATAAATATCT	23435	TC _	
		AG TTTATTGAGCACC			
		TC AAATAACTCGTGG			
		TAT			
GAM1515 ZNF2	3'	GGTGCTCAATAAATATTT	40806	C	
		AAGT TTTATTGAGCACC			
		TTTA AAATAACTCGTGG			
		T			
GAM1515 AKAP6	3'	GGTATTCAATAAAAATTTACTG	14992	AC C C	
AA		TTCA AAGT TTTATTGAG ACC			
		AAGT TTTA AAATAACTT TGG			
		CA A A			
GAM1515 CROC4	3'	GTCTTCAATAAAGACTCTTGAA	21020	CA C	
		TTCAA AGTCTTTATTGAG AC			

AAGTT TCAGAAATAACTT TG  
 C\_ C  
 GAM1515 DIS3 3' GGGCACTCAATAAATGTTGA 30232 AGTC CA  
 TCAACA TTTATTGAG CC  
 ||||| ||||| ||  
 AGTTGT AAATAACTC GG  
 AC  
 GAM1515 DKFZp434A1520 3' TGCTCAATAGATGTTTGTGAA 61118 TC  
 TTCAACAAG TTTATTGAGCA  
 ||||| |||||  
 AAGTTGTTT AGATAACTCGT  
 GT  
 GAM1515 E2F6 3' GTGCTCAATAAATGTCTGAA 8717 \_ AGTC  
 TTCA ACA TTTATTGAGCAC  
 ||| || |||||  
 AAGT TGT AAATAACTCGTG  
 C  
 GAM1515 FLJ13352 3' GGTGCTCAATAACTGTTTGTG 44757 TCT  
 CAACAAG TTATTGAGCACC  
 ||||| |||||  
 GTTGTTT AATAACTCGTGG  
 GTC  
 GAM1515 FLJ20255 3' TGCTCAATAAAGCTATTCAGTG 34800 ACA\_ T  
 AA TTCA AG CTTTATTGAGCA  
 ||| || |||||  
 AAGT TC GAAATAACTCGT  
 GACTTA \_  
 GAM1515 FLJ20276 5' TGCAAAAATAAAGACCTTTGAA 34832 CAA GA\_  
 TTCAA GTCTTTATT GCA  
 ||||| ||||| |||  
 AAGTT CAGAAATAA CGT  
 TC\_ AAA  
 GAM1515 FLJ21820 3' GATAAAGAATTGTTGAA 41623 G  
 TTCAACAA TCTTTATT  
 ||||| |||||  
 AAGTTGTT AGAAATAG  
 A  
 GAM1515 GIT2 3' TAATAAAACTTGTTGA 57582 C  
 TCAACAAGT TTTATTG  
 ||||| |||||  
 AGTTGTTCA AAATAAT  
 A  
 GAM1515 GOA 3' TGCTCAATAAACACTTGTTGAA 78078 C  
 TTCAACAAGT TTTATTGAGCA  
 ||||| |||||  
 AAGTTGTTCA AAATAACTCGT  
 C  
 GAM1515 KIAA0830 3' TGCTCAATAAAGTAATTACTGA 69704 AC GT\_  
 TCA AA CTTTATTGAGCA  
 ||| || |||||

		AGT TT GAAATAACTCGT			
		CA AAT			
GAM1515 KIAA0924	3'	CTCAGACTTGTGGAA	29715	A	TTATT
		TTC ACAAGTCT	GAG		
		AAG TGTTCAGA	CTC		
		G			
GAM1515 KIAA1161	5'	CTTCCTAGAGACTTGTT	81750		TT
		AACAAGTCTTTA	GAG		
		TTGTTCAGAGAT	TTC		
		CC			
GAM1515 KIAA1184	3'	GGCGCTCAATAAATGTTGAA	42616	AGTC	A
		TTCAACA TTTATTGAGC	CC		
		AAGTTGT AAATAACTCG	GG		
			C		
GAM1515 KIAA1219	3'	GGCGCCCAGTAAATACTTGTTG	61370	C	A A
AA		TTCAACAAGT TTTATTG	GC CC		
		AAGTTGTTCA AAATGAC	CG GG		
		T C C			
GAM1515 KIAA1497	3'	GTGCTCAATAAAATGATT	67516		
		AGTC TTTATTGAGCAC			
		TTAG AAATAACTCGTG			
		TA			
GAM1515 KIAA1877	3'	GTACAGTTAAGACTTGTTG	66174	T A	
		CAACAAGTCTT ATTG	GC		
		GTTGTTCAGAA TGAC	TG		
		T A			
GAM1515 KLK15	3'	GGCGCTCAAGGTCACCTGTT	33999	A CTTTA	A
		AACA GT TTGAGC	CC		
		TTGT CA AACTCG	GG		
		C CTGG_ C			
GAM1515 KLK15	3'	GGCGCTCAAGGTCACCTGTT	56748	A CTTTA	A
		AACA GT TTGAGC	CC		
		TTGT CA AACTCG	GG		
		C CTGG_ C			
GAM1515 KLK15	3'	GGCGCTCAAGGTCACCTGTT	56746	A CTTTA	A
		AACA GT TTGAGC	CC		
		TTGT CA AACTCG	GG		
		C CTGG_ C			
GAM1515 KLK15	3'	GGCGCTCAAGGTCACCTGTT	43435	A CTTTA	A
		AACA GT TTGAGC	CC		

TTGT CA AACTCG GG  
 C CTGG\_ C  
 GAM1515 LEC3 3' GGCACCTCATTGTGGCCTTGTTG 30861 T T T CA  
 AA TTCAACAAG CT TA TGAG CC  
 ||||| || || || ||  
 AAGTTGTTT GG GT ACTC GG  
 C T T AC  
 GAM1515 MGC32043 3' CTCAATAAATGTTTGTG 58048 TC  
 AACAAAG TTTATTGAG  
 ||||| |||||  
 TTGTTT AAATAACTC  
 GT  
 GAM1515 MGC5576 3' GGCACCTCAATAAAGATTTGCAG 43922 AA CA  
 AA TTC CAAGTCTTTATTGAG CC  
 || ||||| ||||| ||  
 AAG GTTTAGAAATAACTC GG  
 AC AC  
 GAM1515 OSBPL11 3' GGTGCTCAACACTTGTT 42891 CTTTA  
 AACAAAGT TTGAGCACC  
 ||||| |||||  
 TTGTTCA AACTCGTGG  
 C\_\_\_\_  
 GAM1515 PDGFC 3' TGCAAAGACTTTTTGAA 32501 C ATTGA  
 TTCAA AAGTCTTT GCA  
 ||||| ||||| ||  
 AAGTT TTCAGAAA CGT  
 T \_\_\_\_\_  
 GAM1515 RHOBTB3 3' TGTAAGTCAAAGACTTGTT 29745 \_ GA  
 AACAAAGTCTTT ATT GCA  
 ||||| ||||| ||  
 TTGTTTCAGAAA TGA TGT  
 C A\_  
 GAM1515 SC65 3' GGTGCTCAATAAATGTTTGTG 21293 TC  
 CAACAAG TTTATTGAGCACC  
 ||||| ||||| |||||  
 GTTGTTT AAATAACTCGTGG  
 GT  
 GAM1515 SH3BGRL2 3' TAAAGAACTTGTTGAA 48888 \_  
 TTCAACAAGT CTTTA  
 ||||| |||||  
 AAGTTGTTCA GAAAT  
 A  
 GAM1515 TRIM26 3' GGTGCTCAATAAAGACTTGTTG 12892  
 AA TTCAACAAGTCTTTATTGAGCACC  
 ||||| ||||| ||||| |||||  
 AAGTTGTTTCAGAAATAACTCGTGG  
 GAM1515 VEST1 5' TAATAAAGACTTCTGAA 53687 AC  
 TTCA AAGTCTTTATTG  
 ||||| ||||| |||||

		AAGT TTCAGAAATAAT		
		C_		
GAM1515	ZFP95	3' TGCCCAATAAATATTTGTTGA 59025	C	A
		TCAACAAGT TTTATTG GCA		
		AGTTGTTTA AAATAAC CGT		
		T C		
GAM1515	ZFP95	3' TGCCCAATAAATATTTGTTGA 27381	C	A
		TCAACAAGT TTTATTG GCA		
		AGTTGTTTA AAATAAC CGT		
		T C		
GAM1515	LOC145482	3' GGCAGTGAAGATTTGTTG 77231		G CA
	AA	TTCAACAAGTCTTTATT AG CC		
		AAGTTGTTTAGAAATGA TC GG		
		G AC		
GAM1515	LOC145482	3' GGCAGTTGTAAAGATTTGTT 77232		T CA
		AACAAGTCTTTAT GAG CC		
		TTGTTTAGAAATG TTC GG		
		T AC		
GAM1515	LOC148645	5' GGTGCTCAGAAAACGTGCT 84184	C_	A
		AGT TTT TTGAGCACC		
		TCG AAA GACTCGTGG		
		TGC A		
GAM1515	LOC149535	3' GTGCTCAATAAATGTGT 79419	AGTC	
		ACA TTTATTGAGCAC		
		TGT AAATAACTCGTG		
		GT_		
GAM1515	LOC150630	3' GTGCTCAATAAATACTGAGTGA 85111	ACA	C
	A	TTCA AGT TTTATTGAGCAC		
		AAGT TCA AAATAACTCGTG		
		GAG T		
GAM1515	LOC152225	5' GGTGCTCAATAAAAGCTTGTT 85594	TC	
		AACAAG TTTATTGAGCACC		
		TTGTTC AAATAACTCGTGG		
		GA		
GAM1515	LOC154141	5' GTGCTGAGAAGACTTGT 86172	AT G	
		ACAAGTCTTT T AGCAC		
		TGTTTCAGAAG A TCGTG		
		_ G		
GAM1515	LOC154562	3' GGCAGTCAATAAATACTTGTT 81092	C	CA
		AACAAGT TTTATTGAG CC		

		TTGTTCA AAATAACTC GG		
		T AC		
GAM1515	LOC157660 3'	GGCACTCAACAAATATTTGTTG 86509	C A	CA
	AA	TTCAACAAGT TTT TTGAG CC		
		AAGTTGTTTA AAA AACTC GG		
		T C AC		
GAM1515	LOC158310 3'	GGTGCTCAATAAATATCTGCCG 86760	AA AG C	
	A	TC CA T TTTATTGAGCACC		
		AG GT A AAATAACTCGTGG		
		CC CT T		
GAM1515	LOC197125 3'	GGCACTCAGTAAATACTTGTTG 87904	C	CA
	AA	TTCAACAAGT TTTATTGAG CC		
		AAGTTGTTCA AAATGACTC GG		
		T AC		
GAM1515	LOC203411 3'	TGCTCAGTCAGACCTGTT 90632	A TT	
		AACA GTCT ATTGAGCA		
		TTGT CAGA TGA CTGT		
		C C_		
GAM1515	LOC256338 3'	CTCAATAAATAATTGTTGAA 94610	GTC	
		TTCAACAA TTTATTGAG		
		AAGTTGTT AAATAACTC		
		AAT		
GAM1515	LOC257494 3'	GGTGCTCAATAAAGACTTGTTG 97796		
	AA	TTCAACAAGTCTTTATTGAGCACC		
		AAGTTGTT CAGAAATAACTCGTGG		
GAM1515	LOC56267 3'	TGCTAAGAGTTGTTGAA 39016	G TATTG	
		TTCAACAA TCTT AGCA		
		AAGTTGTT AGAA TCGT		
		G _		
GAM1515	LOC90874 5'	GGCTCGGACTTGTTGAA 64259	A TTATT A	
		TTCA CAAGTCT GAGC C		
		AAGT GTTCAGG CTCG G		
		G _ C		
GAM1515	LOC91907 3'	GTGCTCAATAAAATGATT 67494	_	
		AGTC TTTATTGAGCAC		
		TTAG AAATAACTCGTG		
		TA		
GAM1516	ADAMTS8 5'	TCGGGCCGCCAGCACCTG 22886	_ ATAAG	
		CAG TGCTGGC CTGA		



			GTC ACGACCG	GGCT		
			C CCG__			
GAM1516 BAP1	3'	TCAGGGACCCAGCACTGG	16219	CATAAG		
		CCAGTGCTGG	CTGA			
		GGTCACGACC	GA CT			
		CAGG__				
GAM1516 BF	5'	TTCAGCTTGGACACTG	8140	CTGGCA		
		CAGTG TAAGCTGAA				
		GTCAC GTTCGACTT				
		AG__				
GAM1516 C1QB	3'	TTCAACTCTGTGTCCCAGCACT	4923	A _ _ C		
		GGC G CCAGTGCTGG	CATA AG TGAA			
		C GGTACGACC GTGT TC ACTT				
		_ CT C A				
GAM1516 CHC1	3'	CAGCCCTGAGCACTGTGTC	7020	_ _ CATAA		
		GAC CAGTGCT GG	GCTG			
		CTG GTCACGA CC	CGAC			
		T GT ____				
GAM1516 CMRF35	5'	CAGAGCTGTCAGCACCGG	21929	A TAAG		
		CC GTGCTGGCA	CTG			
		GG CACGACTGT	GAC			
		C CGA_				
GAM1516 EPHB6	3'	TCAGCCCTGGACACTGGTC	15466	_ TG CATAA		
		GACCA GTG C G	GCTGA			
		CTGGTCAC G C	CGACT			
		A GT C__				
GAM1516 EVPL	5'	CAGCCTGAGCCAGCACT	8803	A A		
		AGTGCTGGC TA	GCTG			
		TCACGACCG GT	CGAC			
		A C				
GAM1516 GARP	3'	CAGCCCAGCACTGG	18594	CATAA		
		CCAGTGCTGG	GCTG			
		GGTCACGACC	CGAC			
		_____				
GAM1516 GJB5	3'	CAGCTCGACGGCACTGG	17945	GCATA		
		CCAGTGCTG	AGCTG			
		GGTCACGGC	TCGAC			
		AGC__				
GAM1516 GPR81	3'	CTTACCAGCATTAGTC	50757	C CA		
		GAC AGTGCTGG	TAAG			

CTG TTACGACC ATTG  
 A    \_\_\_  
 GAM1516 IFI16  5' AGCAAGCCAGCACTAGTC  71221  C    ATAA  
                   GAC AGTGCTGGC  GCT  
                   ||| |||||   |||  
                   CTG TCACGACCG  CGA  
                   A    AA\_\_\_  
 GAM1516 KRT4  3' CAGCTGGGCCCAGCACTGGT  9635        \_ATA  
                   ACCAGTGCTGG C  AGCTG  
                   ||||||| |   |||  
                   TGGTCACGACC G  TCGAC  
                   C GG\_  
 GAM1516 MAP3K9 3' TTCAGCTTCCCAAACACCAGT 60709  CA  C\_  CAT  
                   AC GTG TGG  AAGCTGAA  
                   || ||| |||   |||||  
                   TG CAC ACC  TTCGACTT  
                   AC AA  C\_\_\_  
 GAM1516 MGAT5  5' TCAGCTTACAGTTCCTG  10028  T\_  GCA  
                   CAG GCTG  TAAGCTGA  
                   ||| |||   |||||  
                   GTC TGAC  ATTCGACT  
                   CT  \_\_\_  
 GAM1516 MOCS1  3' TTCAGCTTAACAGTTGCCCGGT 92037  A\_  \_  GCA  
                   C            GACC GTG CTG  TAAGCTGAA  
                   |||| ||| |||   |||||  
                   CTGG CGT GAC  ATTCGACTT  
                   CC T  A\_\_\_  
 GAM1516 P23    3' TCAGCTTATACCCGGGCT  21719  G  C\_  
                   AGT CTGG  ATAAGCTGA  
                   ||| |||   |||||  
                   TCG GGCC  TATTCGACT  
                   \_  CA  
 GAM1516 PFKFB4 3' TCAGCCACATGCAACACTGTGT 15874  \_  CTG  AA\_  
                   C            GAC CAGTG  GCAT  GCTGA  
                   ||| |||   |||   |||  
                   CTG GTCAC  CGTA  CGACT  
                   T  AA\_  CAC  
 GAM1516 PTPRK  3' TTCAGCCTGTGGCCCAGCACTG 11125        \_\_\_ A  
                   GTC            GACCAGTGCTGG  CATA GCTGAA  
                   ||||||| ||| |||||  
                   CTGGTCACGACC GTGT CGACTT  
                   CG  C  
 GAM1516 RNPEPL1 3' CGGATGCCAGCACCTG  36676  \_  AAG  
                   CAG TGCTGGCAT  CTG  
                   ||| |||||   |||  
                   GTC ACGACCGTA  GGC  
                   C    \_\_\_  
 GAM1516 UBE2L3 3' TCAGCCCTGGCACTGGC  12507  A  TG CATAA  
                   G CCAGTGC G  GCTGA  
                   | ||||| |   |||

C GGTACAG C CGACT  
 \_ GT C\_  
 GAM1516 APXL2 5' CAGCCTCAGCACTCATC 75185 CC CATAA  
 GA AGTGCTGG GCTG  
 || ||||| |||  
 CT TCACGACT CGAC  
 AC C\_  
 GAM1516 ARHGEF9 3' TTCAGCTTACCAAGCA 30824 \_ CA  
 TGCT GG TAAGCTGAA  
 |||| || |||||  
 ACGA CC ATTCGACTT  
 A \_  
 GAM1516 CEGP1 3' TTCAGCTTCCTCTAGCCCGG 40589 AGT CAT  
 CC GCTGG AAGCTGAA  
 || |||| |||||  
 GG CGATC TTCGACTT  
 CC\_ TCC  
 GAM1516 DKFZp547D155 3' CAGCCCTGAGACCACTGGTC 70435 CTGG TAA  
 GACCAGTG CA GCTG  
 ||||| || |||  
 CTGGTCAC GT CGAC  
 CAGA CC\_  
 GAM1516 DKFZP727G051 3' TTCAGCCCATCAACCAGCATTG 69483 CATAA\_  
 GTC GACCAGTGCTGG GCTGAA  
 ||||| |||||  
 CTGGTTACGACC CGACTT  
 AACTACC  
 GAM1516 DUSP14 5' CACTGTCACCAGCACTGCTC 22834 C CATA C  
 GA CAGTGCTGG AG TG  
 || ||||| || ||  
 CT GTCACGACC TC AC  
 C ACTG \_  
 GAM1516 FLJ10206 5' CAGCTTATGCCAGGAGTC 35898 CAGTG  
 GAC CTGGCATAAGCTG  
 || |||||  
 CTG GACCGTATTCGAC  
 AG\_  
 GAM1516 FLJ20967 5' GGCGCCCAGCACTGGTT 41962 CATAA  
 GACCAGTGCTGG GCT  
 ||||| |||  
 TTGGTCACGACC CGG  
 CG\_  
 GAM1516 FLJ22569 3' TTCAGCTTACTAACTG 43679 GC CA  
 CAGT TGG TAAGCTGAA  
 |||| || |||||  
 GTCA ATC ATTCGACTT  
 A\_ \_  
 GAM1516 FOXN4 3' TTCAGCTTGGACACACTGG 75574 C GCA  
 CCAGTG TG TAAGCTGAA  
 |||| || |||||

			GGTCAC AC GTTCGACTT		
			_ AG_		
GAM1516	GW112	3'	TTCAACTGAAGCCAGCACTGGT 21194	ATA	C
	T		GACCA GTGCTGGC AG TGAA		
			TTGGTCACGACCG TC ACTT		
			AAG A		
GAM1516	HOOK2	3'	CAGCTCACATGGCGCCCAGCAC 25256	___	A_
	TGG		CCAGTGTGCTGG CAT AGCTG		
			GGTCACGACC GTA TCGAC		
			CGCG CAC		
GAM1516	jdp2	3'	TTCAGCACAGCCAGCAT 55327	ATAA	
			GTGCTGGC GCTGAA		
			TACGACCG CGACTT		
			ACA_		
GAM1516	KIAA0767	3'	TCTGCTGCCAGCACAGG 60632	A	TAA T
			CC GTGCTGGCA GC GA		
			GG CACGACCGT CG CT		
			A _ T		
GAM1516	KIAA0923	3'	TCAGCTTGATGCATGGTC 25838	G	TGGCA
			GACCA TGC TAAGCTGA		
			CTGGT ACG GTTCGACT		
			_ TA_		
GAM1516	KIAA0982	3'	TTCAGTGTGTTGCCAGCAC 25852	TA_	C
			GTGCTGGCA AG TGAA		
			CACGACCGT TC ACTT		
			TTG _		
GAM1516	KIAA1000	3'	TTCAGCTTTGCAAAGTACTGG 65281	G_	T
			CCAGTGTGCT GCA AAGCTGAA		
			GGTCATGA CGT TTCGACTT		
			AA _		
GAM1516	MAP3K3	3'	TCAGCCTGGGCGCTGGTC 9999	GG	TAA
			GACCA GTGCT CA GCTGA		
			CTGGTCGCGG GT CGACT		
			_ C_		
GAM1516	MGC16037	5'	CTTGTCCAGCACTAGTC 51821	C	C
			GAC AGTGTGCTGG ATAAG		
			CTG TCACGACC TGTC		
			A _		
GAM1516	MIDORI	3'	TCAGCTTATCCTGCAACT 73792	_	T C
			AGT GC GG ATAAGCTGA		

		TCA CG CC TATTCGACT		
		A T _		
GAM1516 MtFMT	5'	CAGTGGCGAGCACTGG	57651	G ATAA
		CCAGTGCT GC GCTG		
		GGTCACGA CG TGAC		
		G G__		
GAM1516 PCDH16	5'	TCAGTTCCAACCACTGG	72826	C_ CATA
		CCAGTG TGG AGCTGA		
		GGTCAC ACC TTGACT		
		CA ____		
GAM1516 QKI	3'	CAGCTTATCAACTCGTC	65439	C GCTGGC
		GAC AGT ATAAGCTG		
		CTG TCA TATTCGAC		
		C AC__		
GAM1516 TNRC6	3'	CAACTTTTAGCACTG	70506	CAT C
		CAGTGCTGG AAG TG		
		GTCACGATT TTC AC		
		__ A		
GAM1516 TOB2	3'	CAGCCCAGGCCAGCACTG	95618	ATAA
		CAGTGCTGGC GCTG		
		GTCACGACCG CGAC		
		GACC		
GAM1516 TU12B1-TY	3'	TCAGCCCACAGCACTGTC	33406	C GCATAA
		GAC AGTGCTG GCTGA		
		CTG TCACGAC CGACT		
		_ ACC__		
GAM1516 TUSP	3'	TCAGCCTAAGAGCGCAGCACTG	39641	_ A__ A
		CAGTGCTG GC TA GCTGA		
		GTCACGAC CG AT CGACT		
		G AGA C		
GAM1516 USP19	3'	TCAGCTTATGCATCTGGT	88959	TGCTG
		ACCAG GCATAAGCTGA		
		TGGTC CGTATTCGACT		
		TA__		
GAM1516 ZD52F10	3'	CAGCCTGTGCCAGCCCTGG	52819	T A
		CCAG GCTGGCATA GCTG		
		GGTC CGACCGTGT CGAC		
		C C		
GAM1516 LOC145268	3'	TCAGCTTACAAGAGCCACTG	77062	_ GGCA
		CAGTG CT TAAGCTGA		

GTCAC GA ATTCGACT  
 C GAAC  
 GAM1516 LOC149296 5' CAGCTTATGGGCAGCA 79256 G\_  
 TGCTG CATAAGCTG  
 |||| |||||  
 ACGAC GTATTCGAC  
 GG  
 GAM1516 LOC161877 5' TCAGGGCAGGCCAGCGCTGG 82326 ATAAG  
 CCAGTGCTGGC CTGA  
 ||||| |||  
 GGTCGCGACCG GACT  
 GACGG  
 GAM1516 LOC163115 5' TCAGCCCCTGACAGCACTGG 82413 G TAA  
 CCAGTGCTG CA GCTGA  
 ||||| || ||||  
 GGTCACGAC GT CGACT  
 A CCC  
 GAM1516 LOC196500 3' TCAGCTCACTCAGTGGTC 87744 AGT CATA  
 GACC GCTGG AGCTGA  
 ||| |||| ||||  
 CTGG TGA CTGACT  
 \_ CAC\_  
 GAM1516 LOC197287 3' TCAGCTCATGTGTTTTGCACTG 60865 T\_ \_  
 CAGTGC GGCATA AGCTGA  
 |||| |||| ||||  
 GTCACG TTGTGT TCGACT  
 TT AC  
 GAM1516 LOC200470 5' TCAGCCTGCGGCGCTGG 90069 G TAA  
 CCAGTGCTG CA GCTGA  
 ||||| || ||||  
 GGTCGCGGC GT CGACT  
 \_ C\_  
 GAM1516 LOC221584 3' CAGCTTATGTGGCAC 93828 G  
 GTGCTG CATAAGCTG  
 |||| |||||  
 CACGGT GTATTCGAC  
 \_  
 GAM1516 LOC51716 3' CAGCTCATGGCCCTAGCA 32787 \_ A  
 TGCTGG CAT AGCTG  
 |||| || ||||  
 ACGATC GTA TCGAC  
 CCG C  
 GAM1516 LOC92196 5' CAGAGCACCAGCACTGGC 68456 A CATAAG  
 G CCAGTGCTGG CTG  
 | ||||| |||  
 C GGTCACGACC GAC  
 \_ ACGA\_  
 GAM1517 EGR2 3' CAACAAACACTACCACC 4627 CA C  
 GG GTGGTGTTTG TG  
 || ||||| ||

CC CATCACAAAC AC  
 AC A  
 GAM1517 GALGT 3' CCAACAAACCCACCACC 7614 CA T C  
 GG GTGG GTTTG TGG  
 || ||| ||||| ||  
 CC CACC CAAAC ACC  
 AC C A  
 GAM1517 NME4 3' GCCACCAACTTCAGTGCCT 17203 G T TTGC  
 AGGCA TGG GT TGGTGGC  
 ||||| ||| || |||||  
 TCCGT ACT CA ACCACCG  
 G T \_\_\_\_  
 GAM1517 TCF3 3' AGCCACCAGCAAATTGTGCCT 70727 GTGGT  
 AGGCA GTTTGCTGGTGGCT  
 ||||| ||||| |||||  
 TCCGT TAAACGACCACCGA  
 GT\_\_\_\_  
 GAM1517 TNFRSF8 3' CCACCAGGCCACAGCC 6957 A T TTG  
 GGC GTGG GT CTGGTGG  
 ||| ||||| || |||||  
 CCG CACC CG GACCACC  
 A \_ \_\_\_\_  
 GAM1517 TRPM6 3' ACCTGTAAAACACCACTCCT 34525 C \_ T  
 AGG AGTGGTGTTT GC GGT  
 ||| ||||| ||| |||  
 TCC TCACCACAAA TG CCA  
 \_ A T  
 GAM1517 XK 3' AGCCACCAGCCTCCCACTGACT 40798 G TGTTT  
 AG CAGTGG GCTGGTGGCT  
 || ||||| |||||  
 TC GTCACC CGACCACCGA  
 A CTC\_\_\_\_  
 GAM1517 DKFZP434M131 3' GCCACCATCACCCTGACC 69136 \_ TTTGC  
 GG CAGTGGTG TGGTGGC  
 || ||||| |||||  
 CC GTCACCAC ACCACCG  
 A T\_\_\_\_  
 GAM1517 FLJ20514 3' AGACAAATACCACTACCT 35336 C \_  
 AGG AGTGGTGTTTG CT  
 ||| ||||| ||| |||  
 TCC TCACCATAAAC GA  
 A A  
 GAM1517 KIAA0397 3' AGCCACCAACCGACCCAC 61670 T TGC  
 GTGG GTT TGGTGGCT  
 ||||| ||| |||||  
 CACC CAG ACCACCGA  
 C CCA  
 GAM1517 KIAA0537 5' CCTGCAAACACCACCGCCT 29246 A T  
 AGGC GTGGTGTTTGC GG  
 ||||| ||||| ||| |||

		TCCG CACCACAAACG CC		
		C T		
GAM1517 KIAA0987	3'	CCACCAGTACCACCACCACT	24562	TT__
		AGTGGTG TGCTGGTGG		
		TCACCAC ATGACCACC		
		CACC		
GAM1517 MGC21621	3'	AGCCACCAGCAAACAGACCCTG	58793	T __
		CAG GGT GTTTGCTGGTGGCT		
		GTC CCA CAAACGACCACCGA		
		_ GA		
GAM1517 PRSS25	3'	CCACCAGCACTGACTCC	25112	T __
		GG GTT TGCTGGTGG		
		CC CAG ACGACCACC		
		T TC		
GAM1517 PRSS25	3'	CCACCAGCACTGACTCC	59021	T __
		GG GTT TGCTGGTGG		
		CC CAG ACGACCACC		
		T TC		
GAM1517 SMCR5	5'	AGCCACCAGCCAGCCACTGCT	58591	GTTT
		GGCAGTGGT GCTGGTGGCT		
		TCGTCACCG CGACCACCGA		
		AC__		
GAM1517 LOC149041	3'	CACAAACACCACTACT	79139	C C
		GG AGTGGTGTGTTG TG		
		TC TCACCACAAAC AC		
		A _		
GAM1517 LOC150577	3'	AGCCACCATCGTACCACTGC	85071	TT C
		GCAGTGGTG TG TGGTGGCT		
		CGTCACCAT GC ACCACCGA		
		_ T		
GAM1517 LOC158147	3'	GCCACCATCACCCTGTC	69523	TTTGC
		GGCAGTGGTG TGGTGGC		
		CTGTCACCAC ACCACCG		
		T__		
GAM1517 LOC162333	5'	CCACCAGCTTCATCACTGC	87126	TTT
		GCAGTGGTG GCTGGTGG		
		CGTCACTAC CGACCACC		
		TT_		
GAM1517 LOC203078	3'	CCACCGCCACCACCACC	89276	CA TTT T
		GG GTGGTG GC GGTGG		



CC CACCAC CG CCACC  
 AC    — —  
 GAM1517 LOC220370 3' ATCTTACAAATCACCCTGCC 92823    — CT\_  
 GGCAGTGGTG TTTG GGT  
 ||||| ||| |||  
 CCGTCACCAC AAAC CTA  
       T ATT  
 GAM1517 LOC90515 3' CCACCAACACCATGCCT 63122 G TTGC  
 AGGCA TGGTGT TGGTGG  
 |||| |||| ||||  
 TCCGT ACCACA ACCACC  
  
 — —  
 GAM1517 LOC90529 3' AGCCACCAGCCCACCCTGCC 63159 T TTT  
 GGCAG GGTG GCTGGTGGCT  
 |||| ||| |||||  
 CCGTC CCAC CGACCACCGA  
       — C—  
 GAM1518 FKBP1B 3' CTAGCCTGCTCTGCCACTGGGA 14647 A AA TC\_  
       C GTC CAGTGGCA AGT TTAG  
       || ||||| ||| |||  
       CAG GTCACCGT TCG GATC  
       G C\_ TCC  
 GAM1518 FKBP1B 3' CTAGCCTGCTCTGCCACTGGGA 14647 A AA TC\_  
       C GTC CAGTGGCA AGT TTAG  
       || ||||| ||| |||  
       CAG GTCACCGT TCG GATC  
       G C\_ TCC  
 GAM1518 FKBP1B 3' CTAGCCTGCTCTGCCACTGGGA 54007 A AA TC\_  
       C GTC CAGTGGCA AGT TTAG  
       || ||||| ||| |||  
       CAG GTCACCGT TCG GATC  
       G C\_ TCC  
 GAM1518 FKBP1B 3' CTAGCCTGCTCTGCCACTGGGA 54007 A AA TC\_  
       C GTC CAGTGGCA AGT TTAG  
       || ||||| ||| |||  
       CAG GTCACCGT TCG GATC  
       G C\_ TCC  
 GAM1518 KLF4 5' TCTAAGAACTTTTGTATAC 14892 —  
       GTG GCAAAAGTTCTTAGA  
       || |||||  
       CAT TGTTTTCAAGAATCT  
       A  
 GAM1518 KLF4 5' TCTAAGAACTTTTGTATAC 14892 —  
       GTG GCAAAAGTTCTTAGA  
       || |||||  
       CAT TGTTTTCAAGAATCT  
       A  
 GAM1518 PIN1L 3' ACTCCCTGCCACTGTCAC 20618 C AA\_  
       GT ACAGTGGCA AGT  
       || ||||| |||

			CA TGTCACCGT TCA		
			C CCC		
GAM1518	PIN1L	3'	ACTCCCTGCCACTGTCAC 20618	C	AA_
			GT ACAGTGGCA AGT		
			CA TGTCACCGT TCA		
			C CCC		
GAM1518	PON2	3'	ACTTCTGGCACTGTGAC 4333	G A	
			GTCACAGTG CA AAGT		
			CAGTGTAC GT TTCA		
			G C		
GAM1518	PON2	3'	ACTTCTGGCACTGTGAC 4333	G A	
			GTCACAGTG CA AAGT		
			CAGTGTAC GT TTCA		
			G C		
GAM1518	PPP4C	3'	TCTGGCCCTCGCACCCTGTGA 10765		CAAA TT T
	C		GTCACAGTGG AG CT AGA		
			CAGTGTACC TC GG TCT		
			ACGC CC _		
GAM1518	PPP4C	3'	TCTGGCCCTCGCACCCTGTGA 10765		CAAA TT T
	C		GTCACAGTGG AG CT AGA		
			CAGTGTACC TC GG TCT		
			ACGC CC _		
GAM1518	BAG2	3'	CTATAATTTACCACTGTGA 91028	CAA	CT
			TCACAGTGG AAGTT TAG		
			AGTGTACC TTAA ATC		
			A_ T_		
GAM1518	BAG2	3'	CTATAATTTACCACTGTGA 91028	CAA	CT
			TCACAGTGG AAGTT TAG		
			AGTGTACC TTAA ATC		
			A_ T_		
GAM1518	DKFZP434F0318	3'	CTTTTCCCATCACTGTGAC 48011		C__
			GTCACAGTGG AAAAG		
			CAGTGTCACT TTTTC		
			ACCC		
GAM1518	DKFZP434F0318	3'	CTTTTCCCATCACTGTGAC 48011		C__
			GTCACAGTGG AAAAG		
			CAGTGTCACT TTTTC		
			ACCC		
GAM1518	DKFZP566J091	3'	TTTTTGTCCTGTGAC 48128		
			GTCACAGTGGCAAAAG		

CAGTGTCACTGTTTTT

GAM1518 DKFZP566J091 3' TTTTGTCACTGTGAC 48128  
GTCACAGTGGCAAAAG  
|||||||  
CAGTGTCACTGTTTTT

GAM1518 FBP17 3' CTGTCACTTCGCCACCGTG 72790 A AA TCT  
CAC GTGGC AAGT TAG  
||| ||| ||| |||  
GTG CACCG TTCA GTC  
C C\_ CT\_

GAM1518 FBP17 3' CTGTCACTTCGCCACCGTG 72790 A AA TCT  
CAC GTGGC AAGT TAG  
||| ||| ||| |||  
GTG CACCG TTCA GTC  
C C\_ CT\_

GAM1518 FLJ10377 3' AAGGGCACTGCCACTGTG 36079 AAA  
CACAGTGGCA GTTCTT  
||||||| |||||  
GTGTCACCGT CGGGAA  
CA\_

GAM1518 FLJ10377 3' AAGGGCACTGCCACTGTG 36079 AAA  
CACAGTGGCA GTTCTT  
||||||| |||||  
GTGTCACCGT CGGGAA  
CA\_

GAM1518 FLJ14816 3' CTATTCTCTTTGCCACCCTGAC 51635 CA \_ TTCT  
GTCA GTGGCAAA AG TAG  
||| ||||| || |||  
CAGT CACCGTTT TC ATC  
CC C TT\_

GAM1518 FLJ14816 3' CTATTCTCTTTGCCACCCTGAC 51635 CA \_ TTCT  
GTCA GTGGCAAA AG TAG  
||| ||||| || |||  
CAGT CACCGTTT TC ATC  
CC C TT\_

GAM1518 HEI10 3' TCTAAGATCATGCCACTG 41000 AAAGT  
CAGTGGCA TCTTAGA  
||||| |||||  
GTCACCGT AGAATCT  
ACT\_

GAM1518 HEI10 3' TCTAAGATCATGCCACTG 41000 AAAGT  
CAGTGGCA TCTTAGA  
||||| |||||  
GTCACCGT AGAATCT  
ACT\_

GAM1518 HRMT1L3 3' GGGCTCTGCCACTGGAC 39076 A AA  
GTC CAGTGGCA AGTTC  
||| ||||| |||||

			CAG GTCACCGT TCGGG		
			— C—		
GAM1518	HRMT1L3	3'	GGGCTCTGCCACTGGAC	39076	A AA
			GTC CAGTGGCA AGTTC		
			CAG GTCACCGT TCGGG		
			— C—		
GAM1518	KIAA0450	5'	TCTAAATGGCTTCCCAGCCACT	27650	AA— C—
			GTGAC		
			GTCACAGTGGC AAGTT TTAGA		
			CAGTGTACCG TTCGG AATCT		
			ACCC TA		
GAM1518	KIAA0450	5'	TCTAAATGGCTTCCCAGCCACT	27650	AA— C—
			GTGAC		
			GTCACAGTGGC AAGTT TTAGA		
			CAGTGTACCG TTCGG AATCT		
			ACCC TA		
GAM1518	KIAA1813	5'	CTGAGCCTCTGCCACCATGGC	70297	CA AA TT
			GTCA GTGGCA AG CTTAG		
			CGGT CACCGT TC GAGTC		
			AC C— C—		
GAM1518	KIAA1813	5'	CTGAGCCTCTGCCACCATGGC	70297	CA AA TT
			GTCA GTGGCA AG CTTAG		
			CGGT CACCGT TC GAGTC		
			AC C— C—		
GAM1518	KIAA1872	3'	TCCAAGATCATGCCACTG	62946	AAAGT A
			CAGTGGCA TCTT GA		
			GTCACCGT AGAA CT		
			ACT— C		
GAM1518	KIAA1872	3'	TCCAAGATCATGCCACTG	62946	AAAGT A
			CAGTGGCA TCTT GA		
			GTCACCGT AGAA CT		
			ACT— C		
GAM1518	LRPPRC	3'	CTTCTGCCACTGTGGC	55706	A
			GTCACAGTGGCA AAG		
			CGGTGTCACCGT TTC		
			C		
GAM1518	LRPPRC	3'	CTTCTGCCACTGTGGC	55706	A
			GTCACAGTGGCA AAG		
			CGGTGTCACCGT TTC		
			C		
GAM1518	MGC10067	3'	TCCAAGAAGTCTTGCTTTTAT	58940	GT— — A
			G		
			CA GGCAA AAGTTCTT GA		

		GT TCGTT TTCAAGAA CT		
		ATTT C C		
GAM1518	MGC10067	3' TCCAAGAACTTCTTGCTTTTAT 58940	GT__ _	A
	G	CA GGCAA AAGTTCTT GA		
		GT TCGTT TTCAAGAA CT		
		ATTT C C		
GAM1518	MGC1842	5' AGCAGCTCTACCACTGGGAC 65639	A CAAA _	
		GTC CAGTGG AGTT CT		
		CAG GTCACC TCGA GA		
		G ATC_ C		
GAM1518	MGC1842	5' AGCAGCTCTACCACTGGGAC 65639	A CAAA _	
		GTC CAGTGG AGTT CT		
		CAG GTCACC TCGA GA		
		G ATC_ C		
GAM1518	MGC2477	5' TCTAAGAATCACCACCATGGC 44071	CA CAAAA	
		GTCA GTGG GTTCTTAGA		
		CGGT CACC TAAGAATCT		
		AC AC__		
GAM1518	MGC2477	5' TCTAAGAATCACCACCATGGC 44071	CA CAAAA	
		GTCA GTGG GTTCTTAGA		
		CGGT CACC TAAGAATCT		
		AC AC__		
GAM1518	OS4	3' GCTTCCCACTGTGAC 19185	CAA	
		GTCACAGTGG AAGT		
		CAGTGTCAACC TTCG		
		C_		
GAM1518	OS4	3' GCTTCCCACTGTGAC 19185	CAA	
		GTCACAGTGG AAGT		
		CAGTGTCAACC TTCG		
		C_		
GAM1518	P5-1	3' AGGCCCTCCACTGTGAC 21915	CAAA TT	
		GTCACAGTGG AG CTT		
		CAGTGTCAACC TC GGA		
		__ CC		
GAM1518	P5-1	3' AGGCCCTCCACTGTGAC 21915	CAAA TT	
		GTCACAGTGG AG CTT		
		CAGTGTCAACC TC GGA		
		__ CC		
GAM1518	PCDH20	3' TCTGTTTGCTTTACCACTG 43132	CA TCT	
		CAGTGG AAAGT TAGA		

			GTCACC TTTCG GTCT		
			A_ TTT		
GAM1518	PCDH20	3'	TCTGTTTGCTTTACCACTG 43132	CA	TCT
			CAGTGG AAAGT TAGA		
			GTCACC TTTCG GTCT		
			A_ TTT		
GAM1518	PPFIBP2	3'	AGGGACTTCTGCCACAGTGAC 76598	A	A
			GTCAC GTGGCA AAGTTCTT		
			CAGTG CACCGT TTCAGGGA		
			A C		
GAM1518	PPFIBP2	3'	AGGGACTTCTGCCACAGTGAC 76598	A	A
			GTCAC GTGGCA AAGTTCTT		
			CAGTG CACCGT TTCAGGGA		
			A C		
GAM1518	PTD012	5'	TCTGGGTGTTTTGCTACCGTGA 25895	A	GTT
	C		GTCAC GTGGCAAAA CTTAGA		
			CAGTG CATCGTTTT GGGTCT		
			C GT_		
GAM1518	PTD012	5'	TCTGGGTGTTTTGCTACCGTGA 25895	A	GTT
	C		GTCAC GTGGCAAAA CTTAGA		
			CAGTG CATCGTTTT GGGTCT		
			C GT_		
GAM1518	THTPA	3'	TCTAATCTGACTTTGCCACTGT 44263	A	C__
	G		CACAGTGGCAAA GTT TTAGA		
			GTGTCACCGTTT CAG AATCT		
			_ TCT		
GAM1518	THTPA	3'	TCTAATCTGACTTTGCCACTGT 44263	A	C__
	G		CACAGTGGCAAA GTT TTAGA		
			GTGTCACCGTTT CAG AATCT		
			_ TCT		
GAM1518	LOC144231	5'	CTGGCTCCTACCACTGGAC 83013	A	CAAA TCT
			GTC CAGTGG AGT TAG		
			CAG GTCACC TCG GTC		
			_ ATCC _		
GAM1518	LOC144231	5'	CTGGCTCCTACCACTGGAC 83013	A	CAAA TCT
			GTC CAGTGG AGT TAG		
			CAG GTCACC TCG GTC		
			_ ATCC _		
GAM1518	LOC146176	3'	CTAAGAATACCACTGGAC 77697	A	CAAAA
			GTC CAGTGG GTTCTTAG		

		CAG GTCACC	TAAGAATC		
		— A—			
GAM1518	LOC146176 3'	CTAAGAATACCACTGGAC	77697	A	CAAAA
		GTC CAGTGG	GTTCTTAG		
		CAG GTCACC	TAAGAATC		
		— A—			
GAM1518	LOC150737 3'	TCTAAGAACTTTTACCCCAGGA	79997	ACAGT	C
		TC	GG AAAAGTTCTTAGA		
		AG	CC TTTTCAAGAATCT		
		GACC_	A		
GAM1518	LOC150737 3'	TCTAAGAACTTTTACCCCAGGA	79997	ACAGT	C
		TC	GG AAAAGTTCTTAGA		
		AG	CC TTTTCAAGAATCT		
		GACC_	A		
GAM1518	LOC158987 3'	CTTCTGCCATTGTGAC	86962	A	
		GTCACAGTGGCA	AAG		
		CAGTGTTACCGT	TTC		
		C			
GAM1518	LOC158987 3'	CTTCTGCCATTGTGAC	86962	A	
		GTCACAGTGGCA	AAG		
		CAGTGTTACCGT	TTC		
		C			
GAM1518	LOC92609 3'	TCTAAAAACCCCTCGCTGTG	72851	CAAAA	C
		CACAGTGG	GTT TTAGA		
		GTGTCGCT	CAA AATCT		
		CC_	A		
GAM1518	LOC92609 3'	TCTAAAAACCCCTCGCTGTG	72851	CAAAA	C
		CACAGTGG	GTT TTAGA		
		GTGTCGCT	CAA AATCT		
		CC_	A		
GAM1518	LOC93268 5'	CTGGCCCTCACCACTGTG	71878	CAAA	TT T
		CACAGTGG	AG CT AG		
		GTGTCACC	TC GG TC		
		AC_	CC _		
GAM1518	LOC93268 5'	CTGGCCCTCACCACTGTG	71878	CAAA	TT T
		CACAGTGG	AG CT AG		
		GTGTCACC	TC GG TC		
		AC_	CC _		
GAM1519	PIN 3'	CACACCCAGTGATCCATCC	13630	AT_	C
		GGAT	TTATTGGG GTG		

			CCTA AGTGACCC CAC		
			CCT A		
GAM1519	TCF2	3'	CACACTGTAAATATCC 4856	TG C	
			GGATATTTAT GG GTG		
			CCTATAAATG TC CAC		
			__ A		
GAM1519	TRIM9	3'	GCACAAAAATATCCG 30760	A G	
			CGGATATTT TTG GC		
			GCCTATAAA AAC CG		
			_ A		
GAM1519	XRCC3	3'	GCACAGGCTGAAATATCC 18339	ATTG __	
			GGATATTT GGC GTGC		
			CCTATAAA TCG CACG		
			G__ GA		
GAM1519	C21orf25	3'	GCACACCATTGAATATCC 63549	TTG C	
			GGATATTTA GG GTGC		
			CCTATAAGT CC CACG		
			TTA A		
GAM1519	LOC123855	3'	GCACGCTTGGAATACCC 75629	A TA TG	
			GG TATT T GGCGTGC		
			CC ATAA G TCGCACG		
			C __ GT		
GAM1519	LOC145693	3'	CACGCCCAAATGACCCAGTGA 77348	AC_ A TAT	
			TCA GG TATT TGGGCGTG		
			AGT CC GTAA ACCCGCAC		
			GAC A __		
GAM1519	LOC158310	3'	GCTCAATAAATATCTG 86755		
			CGGATATTTATTGGGC		
			GTCTATAAATAACTCG		
GAM1519	LOC51652	3'	ACAATCAATAAACCTCCATTGA 32188	C TA GC	
			TCAA GGA TTTATTGG GT		
			AGTT CCT AAATAACT CA		
			A CC AA		
GAM1520	CNGA1	3'	CAACTGATAATGTGCAAA 59507	GC A	
			TTTGCACATTA TAG TTG		
			AAACGTGTAAT GTC AAC		
			A_ _		
GAM1520	ESRRG	3'	TGGCAGTCTTATGTGCAAA 66396	TAGCT	
			TTTGCACAT AGATTGCCA		



			AAACGTGTA	TCTGACGGT	
			T_____		
GAM1520	KCNJ3	3'	GCAATAATGTGCAAA	9525	GCTAGA
			TTTGCACATTA	TTGC	
			AAACGTGTAAT	AACG	
			_____		
GAM1520	SDC2	3'	GCAAATTAATGTGTAAA	67132	CTAGA
			TTTGCACATTAG	TTGC	
			AAATGTGTAATT	AACG	
			A_____		
GAM1520	USP9X	3'	ATGGCCTGATGCTAATGTGTAA	16206	TAGATT
	A		TTTGCACATTAGC	GCCAT	
			AAATGTGTAATCG	CGGTA	
			TAGTC_		
GAM1520	AMOTL1	3'	GGCAAGTAATGTGCAAA	73650	G AGAT
			TTTGCACATTA CT	TGCC	
			AAACGTGTAAT GA	ACGG	
			_____		
GAM1520	BCAR3	3'	AGTAATAATGTGCAAA	13098	_____
			TTTGCACATTA	GCT	
			AAACGTGTAAT	TGA	
			AA		
GAM1520	DKFZP434B044	3'	TGACAATTAAATGTGCAGA	48930	AGCTA C
			TTTGCACATT	GATTG CA	
			AGACGTGTAA	TTAAC GT	
			A_____ A		
GAM1520	MGC3184	3'	ATGACATTTTCTAATGTGCAGA	48235	CT T C
			TTTGCACATTAG	AGA TG CAT	
			AGACGTGTAATC	TTT AC GTA	
			_____ T A		
GAM1520	PTD012	3'	ATGGCAATCTAGCTAATGTGCA	25891	
	AA		TTTGCACATTAGCTAGATTGCCAT		
			AAACGTGTAATCGATCTAACGGTA		
			_____		
GAM1521	ALDH1B1	3'	CAAGGCTACAGACTGTATGA	5488	C GTC
			TCAT ACAGTCTG	TCTTG	
			AGTA TGTCAGAC	GGAAC	
			_____ ATC		
GAM1521	ASPH	3'	CAAAAGATGGCTGTGAT	50615	TG C
			ATCACAGTC	GTCT TTG	

			TAGTGTCCG TAGA AAC		
			— A		
GAM1521	ASPH	3'	CAAAAGATGGCTGTGAT 50628	TG	C
			ATCACAGTC GTCT TTG		
			TAGTGTCCG TAGA AAC		
			— A		
GAM1521	BACH1	3'	CAAGAGACAAAGAAATGA 6798	CAG	G_
			TCA TCT GTCTCTTG		
			AGT AGA CAGAGAAC		
			AA_ AA		
GAM1521	CLECSF5	5'	AGGCAGAGACTGTGAAGA 25126	A	G_
			TC TCACAGTCT GTCT		
			AG AGTGTGAGA CGGA		
			A GA		
GAM1521	CRTL1	3'	CAAGTTACCAAACTGTGAT 8543	C_	CT
			ATCACAGT TGGT CTTG		
			TAGTGTCA ACCA GAAC		
			AA TT		
GAM1521	DDX10	3'	AAGAGACTATGATGG 15295	CAGTC	
			TCATCA TGGTCTCTT		
			GGTAGT ATCAGAGAA		
			—		
GAM1521	DIAPH2	3'	GACCTGACTGTGATGA 22067	T	
			TCATCACAGTC GGTC		
			AGTAGTGTGAG CCAG		
			T		
GAM1521	DLG5	5'	CAAGAAATCCTGTGATGA 82912	TCT	C
			TCATCACAG GGT TCTTG		
			AGTAGTGTG CTA AGAAC		
			— A		
GAM1521	GRIN2B	3'	AAGAGGCTATGTGA 5902	GTC	
			TCACA TGGTCTCTT		
			AGTGT ATCGGAGAA		
			—		
GAM1521	HSPA6	5'	CAAGAGCATCAACCCTGATGA 76331	CA	C _
			TCATCA GT TGGT CTCTTG		
			AGTAGT CA ACTA GAGAAC		
			CC _ C		
GAM1521	HTR1E	5'	CAAGAGACCACATAGCTG 6010	C_	
			CAGT TGGTCTCTTG		

			GTCG ACCAGAGAAC		
			ATAC		
GAM1521	IL13RA2	3'	CAAGAGACATGGTATTG	5321	_ _
			CAGT CTG GTCTCTTG		
			GTTA GGT CAGAGAAC		
			T A		
GAM1521	IL24	5'	AGACATGACTGTGATGA	22441	TG
			TCATCACAGTC GTCT		
			AGTAGTGTGTCAG CAGA		
			TA		
GAM1521	KCNS3	3'	CAAGAGAGAGTTGTGAT	9587	T GG
			ATCACAG CT TCTCTTG		
			TAGTGTT GA AGAGAAC		
			_ G_		
GAM1521	PPARGC1	3'	CAAGAGACAGAATGAT	25158	CAG G
			ATCA TCTG TCTCTTG		
			TAGT AGAC AGAGAAC		
			A__ _		
GAM1521	RFXANK	5'	CAAGAAAGGGGCTGTGTGA	13559	T GGTC
			TCA CACAGTCT TCTTG		
			AGT GTGTCGGG AGAAC		
			_ GAA_		
GAM1521	RFXANK	5'	CAAGAAAGGGGCTGTGTGA	56237	T GGTC
			TCA CACAGTCT TCTTG		
			AGT GTGTCGGG AGAAC		
			_ GAA_		
GAM1521	RPS6KA5	3'	CAAGAAATGACTCATACTGTGA	16466	C _ _
	TGA		TCATCACAGT TG GTC TCTTG		
			AGTAGTGTCA AC CAG AGAAC		
			T T TAA		
GAM1521	TRPM6	5'	CAAAGGATGTCTGTGATGA	34531	TCTG TC
			TCATCACAG GTC TTG		
			AGTAGTGTGTC TAG AAC		
			TG__ GA		
GAM1521	UGT2B7	3'	AGAAAGATTGTGATG	6538	GG
			CATCACAGTCT TCT		
			GTAGTGTTAGA AGA		
			A_		
GAM1521	WISP1	3'	CAAGAGGTACTGTAATGG	13940	C CTGG
			TCAT ACAGT TCTCTTG		

			GGTA TGTCA GGAGAAC		
			A T__		
GAM1521	WNT1	3'	CAAAAGGGCAGCTGTGATGA 18310	T G C	
			TCATCACAG CTG TCT TTG		
			AGTAGTGTC GAC GGA AAC		
			_ G A		
GAM1521	ZNF22	3'	CAAGTGTCAGACTCTAATGA 91462	CAC TCT	
			TCAT AGTCTGG CTTG		
			AGTA TCAGACT GAAC		
			ATC GT_		
GAM1521	ARHGEF9	3'	GGGAGTATCAGACTATGATGA 30815	C _	
			TCATCA AGTCTGGT CTCTT		
			AGTAGT TCAGACTA GAGGG		
			A T		
GAM1521	FLJ10520	3'	CAAGAGACTTAACTATGA 36210	C CT	
			TCA AGT GGTCTCTTG		
			AGT TCA TCAGAGAAC		
			A AT		
GAM1521	FLJ11110	3'	CAAGAGACCAAAAAGATGG 37060	ACAGTC	
			TCATC TGGTCTCTTG		
			GGTAG ACCAGAGAAC		
			AAAA__		
GAM1521	FLJ20618	5'	CAAAAGACTTAAAGACTGTGGTG 35456	_ C	
	A		TCATCACAGTCT GGTCT TTG		
			AGTGGTGTGAGA TCAGA AAC		
			AT A		
GAM1521	FLJ21839	5'	GACCAGACTGTGCTGA 41549	T	
			TCA CACAGTCTGGTC		
			AGT GTGTCAGACCAG		
			C		
GAM1521	FLJ22843	5'	CAAGATTTATGACTGTGATG 47225	TGGTC	
			CATCACAGTC TCTTG		
			GTAGTGTGAG AGAAC		
			TATTT		
GAM1521	FLJ30681	3'	CAAGAGACCAGAAGGATGA 91783	ACAG	
			TCATC TCTGGTCTCTTG		
			AGTAG AGACCAGAGAAC		
			GA__		
GAM1521	GABARAPL1	3'	AAGAGACCCACTGTAATTGA 48598	TC_ CT	
			TCA ACAGT GGTCTCTT		

AGT TGTCA CCAGAGAA  
 TAA C\_  
 GAM1521 KIAA0022 3' CAAGAGGCCTCTGGTAATGA 29661 CA\_ TCT  
 TCAT CAG GGTCTCTTG  
 ||| ||| |||||  
 AGTA GTC CCGGAGAAC  
 ATG T\_  
 GAM1521 KIAA1069 3' CAAGAAGGGCGTGAAG 67933 A \_ G \_  
 A TC TCACAGTC TG TCT CTTG  
 || ||||| || ||| |||  
 AG AGTGTGAG GC GGA GAAC  
 A T G A  
 GAM1521 LGI2 3' CAAGAGACCAGATGGTG 36398 A  
 CAC GTCTGGTCTCTTG  
 ||| |||||  
 GTG TAGACCAGAGAAC  
 G  
 GAM1521 MBLL39 5' CAAGAGACTCGGACGTTGA 19249 CA \_  
 TCA GTCTG GTCTCTTG  
 ||| ||||| |||||  
 AGT CAGGC CAGAGAAC  
 TG T  
 GAM1521 MBLL39 5' CAAGAGACTCGGACGTTGA 58606 CA \_  
 TCA GTCTG GTCTCTTG  
 ||| ||||| |||||  
 AGT CAGGC CAGAGAAC  
 TG T  
 GAM1521 MGC16179 3' CAAGAGACGTCTTGTGTGA 51301 T TCTG  
 TCA CACAG GTCTCTTG  
 ||| ||||| |||||  
 AGT GTGTT CAGAGAAC  
 \_ CTG\_  
 GAM1521 MGC2376 3' AAGAGATGTGAGATGA 43699 ACAG TG  
 TCATC TC GTCTCTT  
 ||||| || |||||  
 AGTAG AG TAGAGAA  
 \_ TG  
 GAM1521 MGC4707 3' CAAGCTGACAGACTGTGCTGA 44116 T G T\_  
 TCA CACAGTCTG TC CTTG  
 ||| ||||| || |||  
 AGT GTGTCAGAC AG GAAC  
 C \_ TC  
 GAM1521 NAP1L2 3' CAAGAAATGTACACTGTGGT 41734 C \_ C  
 ATCACAGT TG GT TCTTG  
 ||||| || || |||||  
 TGGTGTCA AT TA AGAAC  
 C G A  
 GAM1521 p25 3' CAAGAGACACGAAGTGCCGA 22845 AT AG TG  
 TC CAC TC GTCTCTTG  
 || ||| || |||||

AG GTG AG CAGAGAAC  
 CC A\_ CA  
 GAM1521 PCDH10 3' CAAGAGAAATTGTGAT 51986 CTGG  
 ATCACAGT TCTCTTG  
 ||||| |||||  
 TAGTGTTA AGAGAAC  
 A\_\_\_\_  
 GAM1521 SDS3 3' CAAGTTGGGGGGGACTGTGATGA 69224 GG T\_  
 TCATCACAGTCT TC CTTG  
 ||||| || ||||  
 AGTAGTGTGAGG GG GAAC  
 GG TT  
 GAM1521 SLC5A6 3' CAAGAAACCAGGGCCATGA 40831 CA \_ C  
 TCA GTC TGGT TCTTG  
 || || || || ||||  
 AGT CGG ACCA AGAAC  
 AC G A  
 GAM1521 STX3A 3' GAGGGACCAGGATGA 14805 ACAGT  
 TCATC CTGGTCTCTT  
 |||| |||||  
 AGTAG GACCAGGGAG  
 \_\_\_\_\_  
 GAM1521 LOC114987 3' CAAGAGACACTCACTGGA 59120 A CTG\_  
 TC CAGT GTCTCTTG  
 || || |||||  
 AG GTCA CAGAGAAC  
 \_ CTCA  
 GAM1521 LOC121838 5' CAAAAGACCAGGGTGTACGA 75995 ATC G C  
 TC ACA TCTGGTCT TTG  
 || || ||||| ||  
 AG TGT GGACCAGA AAC  
 CAT G A  
 GAM1521 LOC131965 3' CAAGAGGCGGAGACTGCAGTGA 75028 CA G\_  
 TCAT CAGTCT GTCTCTTG  
 |||| |||| |||||  
 AGTG GTCAGA CGGAGAAC  
 AC GG  
 GAM1521 LOC143287 3' CAAGAGATGGACCAAAATGA 82928 CACA G  
 TCAT GTCTG TCTCTTG  
 |||| |||| |||||  
 AGTA CAGGT AGAGAAC  
 AAAC \_  
 GAM1521 LOC144742 3' AAGAGACCCTGAATGA 76938 CA TCT  
 TCAT CAG GGTCTCTT  
 |||| || |||||  
 AGTA GTC CCAGAGAA  
 A\_ \_\_\_\_  
 GAM1521 LOC146050 3' CAAAGGATAGACTGTAAGGA 77630 ATC G TC  
 TC ACAGTCTG TC TTG  
 || ||||| || |||

AG TGT CAGAT AG AAC  
 GAA \_ GA  
 GAM1521 LOC147664 3' CAAGAGAGGGGAGACCCTGATGA 78404 CA GG\_  
 TCATCA GTCT TCTCTTG  
 ||||| ||| |||||  
 AGTAGT CAGA AGAGAAC  
 CC GGG  
 GAM1521 LOC148824 3' CAAGAAGGGGGGCTGTGGT 84225 GG \_  
 ATCACAGTCT TCT CTTG  
 ||||| ||| |||  
 TGGTGTGCGG GGA GAAC  
 \_ A  
 GAM1521 LOC155036 5' CAAGAGGTGCACTGCGGTGA 86336 A CTGG  
 TCATC CAGT TCTCTTG  
 ||||| ||| |||||  
 AGTGG GTCA GGAGAAC  
 C CGT\_  
 GAM1521 LOC157621 3' CAAGGGCCTTCAAACCTGTGATG 86494 CT\_\_ T  
 G TCATCACAGT GGTC CTTG  
 ||||| ||| |||  
 GGTAGTGTCA CCGG GAAC  
 AACTT \_  
 GAM1521 LOC157918 3' CAAGCATT CAGACTGGACGA 86642 A A TCT  
 TC TC CAGTCTGG CTTG  
 || ||||| |||  
 AG AG GTCAGACT GAAC  
 C \_ TAC  
 GAM1521 LOC158427 3' CAAGAGACGCACATGATG 57677 CAGTC \_  
 CATCA TG GTCTCTTG  
 |||| || |||||  
 GTAGT AC CAGAGAAC  
 AC\_\_ G  
 GAM1521 LOC158863 3' AAGAGCTCTGTGATG 86920 TCT T  
 CATCACAG GG CTCTT  
 ||||| || |||||  
 GTAGTGTC TC GAGAA  
 \_ \_  
 GAM1521 LOC200316 5' AAGAGGGGAGACTGGGA 88761 A GG  
 TC CAGTCT TCTCTT  
 || ||||| |||||  
 AG GTCAGA GGAGAA  
 G G\_  
 GAM1521 LOC201595 3' CAAGTGACAAAATGTGATGA 88978 GTCTG T  
 TCATCACA GTC CTTG  
 ||||| ||| |||  
 AGTAGTGT CAG GAAC  
 AAAA\_ T  
 GAM1521 LOC203197 3' AAGGGGCCTGTGATG 89281 GTCT  
 CATCACA GGTCTCTT  
 ||||| |||||

GTAGTGT CCGGGGAA

GAM1521 LOC219988 5' GAGAGGCCTAGTGATGA 91622 AGTCT  
TCATCAC GGTCTCTT  
||||| |||||  
AGTAGTG CCGGAGAG  
AT\_\_

GAM1521 LOC220763 5' GGACAGCTGTGATGA 73347 T G  
TCATCACAG CTG TCT  
||||||| ||| |||  
AGTAGTGTC GAC AGG

GAM1521 LOC255000 3' CAAGTGAGACTGTGA 96830 TGG T  
TCACAGTC TC CTTG  
||||||| || |||  
AGTGTCAG AG GAAC  
\_\_ T

GAM1521 LOC93052 5' AGAACCAAAGTGTGATG 71256 C C  
CATCACAGT TGGT TCT  
||||||| ||||| |||  
GTAGTGTCA ACCA AGA  
A \_

GAM1522 GSTM5 3' ACATCATCCCTCCCGCATCGA 5954 A TCTTCA  
TCGA GT GGATGATGT  
||| || |||||  
AGCT CG CCTACTACA  
A CCCCTC

GAM1522 H4FG 3' GTCTCCTGAGAACTTC 13050 T T  
GAAGTTCT CAGGA GAT  
||||||| ||||| |||  
CTTCAAGA GTCCT CTG

GAM1522 MYLK 3' ACACTCTCCAAAGAACTTGA 97017 G CA T \_  
TC AAGTTCTT GGA GA TGT  
|| ||||| ||| ||| |||  
AG TTCAAGAA CCT CT ACA  
\_ A\_ \_ C

GAM1522 RFPL2 5' TGACTTTCCCAATAGAACTTC 21727 TCA\_ TGAT  
GAAGTTCT GGA GTCA  
||||||| ||| |||  
CTTCAAGA CCT CAGT  
TAAC TT\_\_

GAM1522 RFPL3 5' TGACTTTCCCAATAGAACTTC 21722 TCA\_ TGAT  
GAAGTTCT GGA GTCA  
||||||| ||| |||  
CTTCAAGA CCT CAGT  
TAAC TT\_\_

GAM1522 CD36L1 3' TGACATCATCCTATGGACT 18567 TTC  
AGTTC AGGATGATGTCA  
||||| |||||



		TCAGG TCCTACTACAGT		
		TA_		
GAM1522	FLJ10385	5' ATCCCTGAGAACTTCGA 36083	T	AT
		TCGAAGTTCT CAGG GAT		
		AGCTTCAAGA GTCC CTA		
		— —		
GAM1522	FLJ11029	5' ACATCATCCTGGAAGTTC 60970	TT	
		GAAGTTC CAGGATGATGT		
		CTTCAAG GTCCTACTACA		
		—		
GAM1522	FLJ21007	5' TGACATCATCCTGATTGCTCTC 47926	_	TCT
		GA AGT TCAGGATGATGTCA		
		CT TCG AGTCCTACTACAGT		
		C TT_		
GAM1522	KIAA1649	5' GACACCATCCTGAAGGC 50261	T	A
		GT CTTCAGGATG TGTC		
		CG GAAGTCCTAC ACAG		
		— C		
GAM1522	LOC112724	5' ACATCATCCTGGCCTGCCGA 56488	AA	TCT
		TCG GT TCAGGATGATGT		
		AGC CG GGTCCTACTACA		
		— TCC		
GAM1522	LOC145188	3' ATCCCAAAGACTTCGA 77045	T	CA
		TCGAAGT CTT GGAT		
		AGCTTCA GAA CCTA		
		— AC		
GAM1522	LOC146237	5' TGACATCAGAGGAGAACCCGA 83635	AA	AGGA
		TCG GTTCTTC TGATGTCA		
		AGC CAAGAGG ACTACAGT		
		C_ AG_		
GAM1522	LOC196549	5' TGACATTAGAGGAAGACTTC 59235	T	AGGA
		GAAGT CTTC TGATGTCA		
		CTTCA GAAG ATTACAGT		
		— GAG_		
GAM1522	LOC203221	5' TGAAGAACCTGAAGAACT 89547		ATGATG
		AGTTCTTCAGG TCA		
		TCAAGAAGTCC AGT		
		AAGA_		
GAM1523	BACH1	3' ACTCAGAATACAGTGGCATGAG 6797	GA	GG AC
		TTCA GT ACT ATTCTGAGT		

GAGT CG TGA TAAGACTCA  
 A\_ G\_ CA  
 GAM1523 HD 3' ACCCAGAATGTAGCATCTGAG 9179 GTGGA A  
 TTCAGA CTACATTCTG GT  
 ||||| ||||| ||  
 GAGTCT GATGTAAGAC CA  
 AC\_\_ C  
 GAM1523 ITGA2 3' ACTCAGAATATAACATTT 9370 GACTAC  
 GAGTG ATTCTGAGT  
 ||||| |||||  
 TTTAC TAAGACTCA  
 AATA\_\_  
 GAM1523 KRT2A 3' ACCCAGACTCTCCCACTCCAGA 4707 A\_ ACTACAT A  
 A TTC GAGTGG TCTG GT  
 ||| ||||| ||| ||  
 AAG CTCACC AGAC CA  
 AC CTCTC\_\_ C  
 GAM1523 PP 3' ACTCAGAATGTTATCCATCT 40895 G CT  
 AGA TGA ACATTCTGAGT  
 ||| ||| |||||  
 TCT ACCT TGTAAGACTCA  
 \_ AT  
 GAM1523 CL25084 3' ACTCAGAATGGTTTACTCT 31656 TA  
 AGAGTGGAC CATTCTGAGT  
 ||||| |||||  
 TCTCATTTG GTAAGACTCA  
 \_  
 GAM1523 DKFZp434O0320 3' ACTCAAATGCAACTGCTGACT 83688 \_ ACTA\_\_ C  
 TTGAA TTCAGAGT GG CATT TGAGT  
 ||||| || ||| |||||  
 AAGTTTCA TC GTAA ACTCA  
 G GTCAAC A  
 GAM1523 FAPP2 3' ACTCAGAACATAATACCTGAG 50968 A GACTACA  
 TTCAG GTG TTCTGAGT  
 ||||| ||| |||||  
 GAGTC CAT AAGACTCA  
 \_ AATAC\_\_  
 GAM1523 HSNV1 3' ACTCAGAATGGGACACTCT 34001 GACTA  
 AGAGTG CATTCTGAGT  
 ||||| |||||  
 TCTCAC GTAAGACTCA  
 AG\_\_  
 GAM1523 TRPV5 5' ACTCAGAGTCCCAGCCCCA 39046 A\_ AC\_  
 TGG CT ATTCTGAGT  
 ||| || |||||  
 ACC GA TGAGACTCA  
 CC CCC  
 GAM1523 LOC131308 3' ACTCAGAATGGTGAGCCCTGAA 75001 A GG TA  
 TTCAG GT AC CATTCTGAGT  
 ||||| || || |||||

AAGTC CG TG GTAAGACTCA  
 C AG \_\_\_\_  
 GAM1523 LOC220739 3' TGCAGGCCCACTCTGAA 92938 A\_ A  
 TTCAGAGTGG CT CA  
 ||||| ||  
 AAGTCTCACC GA GT  
 CG C  
 GAM1523 LOC91974 5' ACTGCAGATACAGTTCACTCTG 67747 ACAT \_  
 AA TTCAGAGTGGACT TCTG AGT  
 ||||| |||  
 AAGTCTCACTTGA AGAC TCA  
 CAT\_ G  
 GAM1523 LOC92346 5' ACTCAGAACATCTAAAGATCTG 57639 GTGGACTACA  
 AA TTCAGA TTCTGAGT  
 |||| |||||  
 AAGTCT AAGACTCA  
 AGAAATCTAC  
 GAM1524 ADAMTS8 5' TCGGGCCGCCAGCACCTG 22886 \_ ATAAG  
 CAG TGCTGGC CTGA  
 || ||||| |||  
 GTC ACGACCG GGCT  
 C CCG\_\_\_\_  
 GAM1524 BAP1 3' TCAGGGACCCAGCACTGG 16219 CATAAG  
 CCAGTGCTGG CTGA  
 ||||| |||  
 GGTCACGACC GACT  
 CAGG\_\_\_\_  
 GAM1524 BF 5' TTCAGCTTGACACTG 8140 CTGGCA  
 CAGTG TAAGCTGAA  
 |||| |||||  
 GTCAC GTTCGACTT  
 AG\_\_\_\_  
 GAM1524 C1QB 3' TTCAACTCTGTGTCCCACT 4923 A \_ \_ C  
 GGC G CCAGTGCTGG CATA AG TGAA  
 | ||||| ||| |||  
 C GGTCACGACC GTGT TC ACTT  
 \_ CT C A  
 GAM1524 CHC1 3' CAGCCCTGAGCACTGTGTC 7020 \_ \_ CATAA  
 GAC CAGTGCT GG GCTG  
 || ||||| || |||  
 CTG GTCACGA CC CGAC  
 T GT \_\_\_\_\_  
 GAM1524 CMRF35 5' CAGAGCTGTCAGCACCGG 21929 A TAAG  
 CC GTGCTGGCA CTG  
 || ||||| |||  
 GG CACGACTGT GAC  
 C CGA\_  
 GAM1524 EPHB6 3' TCAGCCCTGGACACTGGTC 15466 \_ TG CATAA  
 GACCAGTG C G GCTGA  
 ||||| | | ||||

			CTGGTCAC G C CGACT		
			A GT C_____		
GAM1524	EVPL	5'	CAGCCTGAGCCAGCACT	8803	A A
			AGTGCTGGC TA GCTG		
			TCACGACCG GT CGAC		
			A C		
GAM1524	GARP	3'	CAGCCCAGCACTGG	18594	CATAA
			CCAGTGCTGG GCTG		
			GGTCACGACC CGAC		
			_____		
GAM1524	GJB5	3'	CAGCTCGACGGCACTGG	17945	GCATA
			CCAGTGCTG AGCTG		
			GGTCACGGC TCGAC		
			AGC__		
GAM1524	GPR81	3'	CTTACCAGCATTAGTC	50757	C CA
			GAC AGTGCTGG TAAG		
			CTG TTACGACC ATTC		
			A _		
GAM1524	IFI16	5'	AGCAAGCCAGCACTAGTC	71221	C ATAA
			GAC AGTGCTGGC GCT		
			CTG TCACGACCG CGA		
			A AA__		
GAM1524	KRT4	3'	CAGCTGGGCCCAGCACTGGT	9635	_ATA
			ACCAGTGCTGG C AGCTG		
			TGGTCACGACC G TCGAC		
			C GG_		
GAM1524	MAP3K9	3'	TTCAGCTTCCCAAACACCAGT	60709	CA C_ CAT
			AC GTG TGG AAGCTGAA		
			TG CAC ACC TTCGACTT		
			AC AA C__		
GAM1524	MGAT5	5'	TCAGCTTACAGTTCCTG	10028	T_ GCA
			CAG GCTG TAAGCTGA		
			GTC TGAC ATTCGACT		
			CT _		
GAM1524	MOCS1	3'	TTCAGCTTAACAGTTGCCCGGT	92037	A_ _ GCA
	C		GACC GTG CTG TAAGCTGAA		
			CTGG CGT GAC ATTCGACTT		
			CC T A__		
GAM1524	P23	3'	TCAGCTTATACCCGGGCT	21719	G C_
			AGT CTGG ATAAGCTGA		

TCG GGCC TATTCGACT  
 \_ CA  
 GAM1524 PFKFB4 3' TCAGCCACATGCAACACTGTGT 15874 \_ CTG AA\_  
 C GAC CAGTG GCAT GCTGA  
 ||| |||| ||| ||||  
 CTG GTCAC CGTA CGACT  
 T AA\_ CAC  
 GAM1524 PTPRK 3' TTCAGCCTGTGGCCCAGCACTG 11125 \_ A  
 GTC GACCAGTGCTGG CATA GCTGAA  
 ||||| ||| |||||  
 CTGGTCACGACC GTGT CGACTT  
 CG C  
 GAM1524 RNPEPL1 3' CGGATGCCAGCACCTG 36676 \_ AAG  
 CAG TGCTGGCAT CTG  
 ||| ||||| |||  
 GTC ACGACCGTA GGC  
 C \_  
 GAM1524 UBE2L3 3' TCAGCCCTGGCACTGGC 12507 A TG CATAA  
 G CCAGTGC G GCTGA  
 | ||||| | ||||  
 C GGTACAG C CGACT  
 \_ GTC \_  
 GAM1524 APXL2 5' CAGCCTCAGCACTCATC 75185 CC CATAA  
 GA AGTGCTGG GCTG  
 || ||||| |||  
 CT TCACGACT CGAC  
 AC C \_  
 GAM1524 ARHGEF9 3' TTCAGCTTACCAAGCA 30824 \_ CA  
 TGCT GG TAAGCTGAA  
 |||| || |||||  
 ACGA CC ATTCGACTT  
 A \_  
 GAM1524 CEGP1 3' TTCAGCTTCCTCTAGCCCGG 40589 AGT CAT  
 CC GCTGG AAGCTGAA  
 || |||| |||||  
 GG CGATC TTCGACTT  
 CC\_ TCC  
 GAM1524 DKFZp547D155 3' CAGCCCTGAGACCACTGGTC 70435 CTGG TAA  
 GACCAGTG CA GCTG  
 ||||| || |||  
 CTGGTCAC GT CGAC  
 CAGA CC\_  
 GAM1524 DKFZP727G051 3' TTCAGCCCATCAACCAGCATTG 69483 CATAA\_  
 GTC GACCAGTGCTGG GCTGAA  
 ||||| ||| |||||  
 CTGGTTACGACC CGACTT  
 AACTACC  
 GAM1524 DUSP14 5' CACTGTCACCAGCACTGCTC 22834 C CATA C  
 GA CAGTGCTGG AG TG  
 || ||||| || ||

CT GTCACGACC TC AC  
 C ACTG \_  
 GAM1524 FLJ10206 5' CAGCTTATGCCAGGAGTC 35898 CAGTG  
 GAC CTGGCATAAGCTG  
 ||| |||||  
 CTG GACCGTATTCGAC  
 AG\_\_  
 GAM1524 FLJ20967 5' GGCGCCCAGCACTGGTT 41962 CATAA  
 GACCAGTGCTGG GCT  
 ||||| |||  
 TTGGTCACGACC CGG  
 CG\_\_  
 GAM1524 FLJ22569 3' TTCAGCTTACTAAACTG 43679 GC CA  
 CAGT TGG TAAGCTGAA  
 ||| ||| |||||  
 GTCA ATC ATTCGACTT  
 A\_ \_  
 GAM1524 FOXN4 3' TTCAGCTTGGACACACTGG 75574 C GCA  
 CCAGTG TG TAAGCTGAA  
 ||||| || |||||  
 GGTCAC AC GTTCGACTT  
 \_ AG\_  
 GAM1524 GW112 3' TTCAACTGAAGCCAGCACTGGT 21194 ATA C  
 T GACCAGTGCTGGC AG TGAA  
 ||||| || |||||  
 TTGGTCACGACCG TC ACTT  
 AAG A  
 GAM1524 HOOK2 3' CAGCTCACATGGCGCCCAGCAC 25256 \_\_\_\_ A\_  
 TGG CCAGTGCTGG CAT AGCTG  
 ||||| ||| |||||  
 GGTCACGACC GTA TCGAC  
 CGCG CAC  
 GAM1524 jdp2 3' TTCAGCACAGCCAGCAT 55327 ATAA  
 GTGCTGGC GCTGAA  
 ||||| |||||  
 TACGACCG CGACTT  
 ACA\_  
 GAM1524 KIAA0767 3' TCTGCTGCCAGCACAGG 60632 A TAA T  
 CC GTGCTGGCA GC GA  
 || ||||| |||  
 GG CACGACCGT CG CT  
 A \_\_\_\_ T  
 GAM1524 KIAA0923 3' TCAGCTTGATGCATGGTC 25838 G TGGCA  
 GACCA TGC TAAGCTGA  
 ||||| ||| |||||  
 CTGGT ACG GTTCGACT  
 \_ TA\_\_  
 GAM1524 KIAA0982 3' TTCACTGTTTGCCAGCAC 25852 TA\_ C  
 GTGCTGGCA AG TGAA  
 ||||| || |||||

			CACGACCGT TC ACTT		
			TTG _		
GAM1524 KIAA1000	3'	TTCAGCTTTGCAAAGTACTGG	65281	G_ T	
		CCAGTGCT GCA AAGCTGAA			
		GGTCATGA CGT TTCGACTT			
		AA _			
GAM1524 MAP3K3	3'	TCAGCCTGGGCGCTGGTC	9999	GG TAA	
		GACCAGTGCT CA GCTGA			
		CTGGTCGCGG GT CGACT			
		_ C _			
GAM1524 MGC16037	5'	CTTGTCCAGCACTAGTC	51821	C C	
		GAC AGTGCTGG ATAAG			
		CTG TCACGACC TGTC			
		A _			
GAM1524 MIDORI	3'	TCAGCTTATCCTGCAACT	73792	_ T C	
		AGT GC GG ATAAGCTGA			
		TCA CG CC TATTCGACT			
		A T _			
GAM1524 MtFMT	5'	CAGTGGCGAGCACTGG	57651	G ATAA	
		CCAGTGCT GC GCTG			
		GGTCACGA CG TGAC			
		G G _			
GAM1524 PCDH16	5'	TCAGTTCCAACCACTGG	72826	C_ CATA	
		CCAGTG TGG AGCTGA			
		GGTCAC ACC TTGACT			
		CA _			
GAM1524 QKI	3'	CAGCTTATCAACTCGTC	65439	C GCTGGC	
		GAC AGT ATAAGCTG			
		CTG TCA TATTCGAC			
		C AC _			
GAM1524 TNRC6	3'	CAACTTTTAGCACTG	70506	CAT C	
		CAGTGCTGG AAG TG			
		GTCACGATT TTC AC			
		_ A			
GAM1524 TOB2	3'	CAGCCCAGGCCAGCACTG	95618	ATAA	
		CAGTGCTGGC GCTG			
		GTCACGACCG CGAC			
		GACC			
GAM1524 TU12B1-TY	3'	TCAGCCCACAGCACTGTC	33406	C GCATAA	
		GAC AGTGCTG GCTGA			

		CTG TCACGAC	CGACT		
		— ACC—			
GAM1524	TUSP	3' TCAGCCTAAGAGCGCAGCACTG	39641	— A—	A
		CAGTGCTG GC TA GCTGA			
		GTCACGAC CG AT CGACT			
		G AGA C			
GAM1524	USP19	3' TCAGCTTATGCATCTGGT	88959	TGCTG	
		ACCAG GCATAAGCTGA			
		TGGTC CGTATTCGACT			
		TA—			
GAM1524	ZD52F10	3' CAGCCTGTGCCAGCCCTGG	52819	T	A
		CCAG GCTGGCATA GCTG			
		GGTC CGACCGTGT CGAC			
		C C			
GAM1524	LOC145268	3' TCAGCTTACAAGAGCCACTG	77062	— GGCA	
		CAGTG CT TAAGCTGA			
		GTCAC GA ATTCGACT			
		C GAAC			
GAM1524	LOC149296	5' CAGCTTATGGGCAGCA	79256	G—	
		TGCTG CATAAGCTG			
		ACGAC GTATTCGAC			
		GG			
GAM1524	LOC161877	5' TCAGGGCAGGCCAGCGCTGG	82326	ATAAG	
		CCAGTGCTGGC CTGA			
		GGTCGCGACCG GACT			
		GACGG			
GAM1524	LOC163115	5' TCAGCCCCTGACAGCACTGG	82413	G TAA	
		CCAGTGCTG CA GCTGA			
		GGTCACGAC GT CGACT			
		A CCC			
GAM1524	LOC196500	3' TCAGCTCACTCAGTGGTC	87744	AGT	CATA
		GACC GCTGG AGCTGA			
		CTGG TGA CT TCGACT			
		— CAC—			
GAM1524	LOC197287	3' TCAGCTCATGTGTTTTGCACTG	60865	T—	—
		CAGTGC GGCATA AGCTGA			
		GTCACG TTGTGT TCGACT			
		TT AC			
GAM1524	LOC200470	5' TCAGCCTGCGGCGCTGG	90069	G TAA	
		CCAGTGCTG CA GCTGA			



GGTCGCGGC GT CGACT  
\_ C\_  
GAM1524 LOC221584 3' CAGCTTATGTGGCAC 93828 G  
GTGCTG CATAAGCTG  
||||| |||||  
CACGGT GTATTCGAC  
  
GAM1524 LOC51716 3' CAGCTCATGGCCCTAGCA 32787 \_ A  
TGCTGG CAT AGCTG  
||||| ||| |||||  
ACGATC GTA TCGAC  
CCG C  
GAM1524 LOC92196 5' CAGAGCACCAGCACTGGC 68456 A CATAAG  
G CCAGTGCTGG CTG  
| ||||| |||  
C GGTACGACC GAC  
\_ ACGA\_  
GAM1525 AF1Q 3' TCAAGCCCCTTCCTTTCCA 22368 T AAA A  
TGGAA GGAA GC TGA  
||||| ||| |||  
ACCTT CCTT CG ACT  
T CCC A  
GAM1525 ALX3 3' CACCTCTTTTCCATTCC 21419 CATGAA  
GGAATGGAAAAAG GTG  
||||||| |||  
CCTTACCTTTTTC CAC  
TC\_  
GAM1525 AP2B1 3' TCATGCTTCCCCCTTTCCA 7065 T AAA  
TGGAA GG AAGCATGA  
||||| || |||||  
ACCTT CC TTCGTACT  
T CCC  
GAM1525 CKTSF1B1 3' TCAGCTCATTTCCATTCCA 25370 A\_ A  
TGGAATGGAAA AGC TGA  
||||||| ||| |||  
ACCTTACCTTT TCG ACT  
AC \_  
GAM1525 KCNJ15 3' CACTATCTCTTTCCATTCC 9543 A C GA  
GAATGGAAA AG AT AGTG  
||||||| || |||  
CTTACCTTT TC TA TCAC  
C \_ \_  
GAM1525 KCNJ6 5' CACTCTTATCTTTCCCACTTC 9529 A AA C \_  
A TGGAA TGG AAAG ATGA AGTG  
||||| ||| ||| |||  
ACTT ACC TTTC TATT TCAC  
C CC \_ C  
GAM1525 NOTCH3 3' ACTTCACTGCATTCCA 4743 AAA \_  
TGGAA GCA TGAAGT  
||||| ||| |||||

			ACCTT CGT ACTTCA		
			A__ C		
GAM1525	RAI14	3'	ATGCTCCTTCCATTCC 31478	AA	
			GGAATGGAA AGCAT		
			CCTTACCTT TCGTA		
			CC		
GAM1525	SRC	3'	TCACTTCCTTGCCCCATTTC 18287	AAAAA T_	
			TGGAATGG GCA GAAGTGA		
			ACTTTACC CGT CTTCACT		
			CC__ TC		
GAM1525	TEM8	3'	CACTAATTCCTCTCCATTCTA 36327	AAA CATGA	
			TGGAATGGA AG AGTG		
			ATCTTACCT TC TCAC		
			C__ CTAA		
GAM1525	ABLM	3'	CATGCTTTTTCTATCCCA 9760	A	
			TGG ATGGAAAAAGCATG		
			ACC TATCTTTTTCGTAC		
			C		
GAM1525	ABLM	3'	CATGCTTTTTCTATCCCA 22021	A	
			TGG ATGGAAAAAGCATG		
			ACC TATCTTTTTCGTAC		
			C		
GAM1525	AFAP	3'	TCAGGGCTCTTTCCATTCTA 41308	A A_	
			TGGAATGGAAA AGC TGA		
			ATCTTACCTTT TCG ACT		
			C GG		
GAM1525	BANP	5'	CACCTTGTTTTTCCACTC 66215	A G TGAA	
			GA TGGAAAA CA GTG		
			CT ACCTTTTT GT CAC		
			C _ TC__		
GAM1525	C1orf19	3'	CACCTCTGTTTACTTTTTCTC 68189	AT ____ T	
	TCCA		TGGA GGAAAAAG CA GAAGTG		
			ACCT CCTTTTTC GT CTTAC		
			CT ATTT _		
GAM1525	CLSTN3	3'	CACCTCATTTCCATTTC 28205	AAAGC A	
			TGGAATGGAA ATGA GTG		
			ACTTTACCTT TACT CAC		
			____ C		
GAM1525	FADS1	3'	TCACTTCATACTTCTAAATCA 25485	AA AAA C	
			TGG TGGA AG ATGAAGTGA		

		ACT ATCT TC TACTTCACT	
		AA ____ A	
GAM1525	FLJ12387	3' CACTCCAGCTCCATCCC 43065	A AAAA A A
		GG ATGGA GC TG AGTG	
		CC TACCT CG AC TCAC	
		C ____ _ C	
GAM1525	FLJ21313	3' TCACTTATACTTCCTCCTCCC 43691	AAT A_ CATG
	A	TGG GGAA AAG AAGTGA	
		ACC CCTT TTC TTCACT	
		CT_ CC ATA_	
GAM1525	HXCP2	3' CACTTCATTTGTTCCATTCC 50833	AAAGC
		GGAATGGAA ATGAAGTG	
		CCTTACCTT TACTTCAC	
		GTT__	
GAM1525	ITGA10	5' CACCATCACTCCTCCCATTCC 59375	AAAA CA A_
		GGAATGG AG TGA GTG	
		CCTTACC TC ACT CAC	
		CTCC __ AC	
GAM1525	KIAA0370	3' CACCTTCTCACCATTCCA 73205	AAAAAGCAT _
		TGGAATGG GAAG TG	
		ACCTTACC CTTC AC	
		ACT____ C	
GAM1525	KIAA0429	5' CACTCCCATCCCCATTCC 28551	AAAAAGC A_
		GGAATGG ATG AGTG	
		CCTTACC TAC TCAC	
		CC____ CC	
GAM1525	KIAA0481	3' CAGGGCCCTTCCATTCCA 71845	AAA A_
		TGGAATGGAA GC TG	
		ACCTTACCTT CG AC	
		CC_ GG	
GAM1525	KIAA1016	5' CACTTCATCATCCCCACCA 91732	AAT AAAAGC
		TGG GGA ATGAAGTG	
		ACC CCT TACTTCAC	
		ACC AC____	
GAM1525	KIAA1045	3' TCACGCTTCTCCCTATTCCA 71059	AAA_ A
		TGGAATGG AAGC TGA	
		ACCTTATC TTCG ACT	
		CCTC C	
GAM1525	KIAA1550	3' CACTTCACACCGATTCC 66552	_ AAAAAGCA
		GGAAT GG TGAAGTG	

			CCTTA CC	ACTTCAC		
			G AC_____			
GAM1525	KIAA1674	3'	CACCTAAGCTTTCCATTC	68775	AA	ATGAA
			GAATGGAA AGC	GTG		
			CTTACCTT TCG	CAC		
			__ AATC_			
GAM1525	MGC20460	5'	CACCTGCTTTTCCCTCCA	53844	AT	TGAA
			TGGA GGAAAAAGCA	GTG		
			ACCT CCTTTTTCGT	CAC		
			C_ C_			
GAM1525	MGC4294	3'	CACTTTCTTCCCTATTCCA	44230	AAA	CAT
			TGGAATGG AAG	GAAGTG		
			ACCTTATC TTC	TTTCAC		
			CC_ _			
GAM1525	MIC2L1	3'	TCACTTCAGTCTTCCCCATCCC	48827	A	AA AG A
	A		TGG ATGG AA C	TGAAGTGA		
			ACC TACC TT G	ACTTCACT		
			C CC CT_			
GAM1525	MRPL4	3'	TCACCTGGCCCCCTTCATTCCA	31982	AAAA	ATGAA
			TGGAATGGA GC	GTGA		
			ACCTTACTT CG	CACT		
			CCCC GTC_			
GAM1525	OSTF1	3'	CTGTTGCTTTTGCCATTCCA	24725	A	TGA
			TGGAATGG AAAAGCA	AG		
			ACCTTACC TTTTCGT	TC		
			G TG_			
GAM1525	PALMD	3'	CACCCCTTCTTCCATTC	34811	A	CATGAA
			GAATGGAA AAG	GTG		
			CTTACCTT TTC	CAC		
			C CC_			
GAM1525	PMX2B	5'	CACTCCAGCCACCTTCTCCATA	14078	_ A A_ A A	
	TCCA		TGGA ATGGA AA	GC TG AGTG		
			ACCT TACCT TT	CG AC TCAC		
			A C CCAC _ C			
GAM1525	RAI15	3'	TGCTTTCCCCATTCCA	66670	AA	
			TGGAATGG AAAGCA			
			ACCTTACC TTTTCGT			
			CC			
GAM1525	SMARCF1	3'	TCACCTCACGCCTTTCTGTTCC	37444	AA A A	
			GGAATGGAAA GC	TGA GTGA		

			CCTTGTCTTT CG ACT CACT		
			C_ C C		
GAM1525	SMARCF1	3'	TCACCTCACGCCTTTCTGTTCC 57492	AA A A	
			GGAATGGAAA GC TGA GTGA		
			CCTTGTCTTT CG ACT CACT		
			C_ C C		
GAM1525	SMARCF1	3'	TCACCTCACGCCTTTCTGTTCC 20046	AA A A	
			GGAATGGAAA GC TGA GTGA		
			CCTTGTCTTT CG ACT CACT		
			C_ C C		
GAM1525	SPRY1	3'	TCACCCCATGCTTCTCACCA 65006	AAA_ AA	
			TGG AAGCATG GTGA		
			ACC TTCGTAC CACT		
			ACTC CC		
GAM1525	SR-BP1	3'	TCAGCGTCTTCCATTCCA 19636	AAA A	
			TGGAATGGAA GC TGA		
			ACCTTACCTT CG ACT		
			CTG _		
GAM1525	SV2B	3'	CACTTCATGTTCTACCCCA 29295	AA AAAA	
			TGG TGGA GCATGAAGTG		
			ACC ATCT TGTACTTCAC		
			CC _		
GAM1525	ZFP	3'	ACTTCCTCCATTTC A 37845	AAAAGCAT	
			TGGAATGGA GAAGT		
			ACTTTACCT CTTCA		
			C _		
GAM1525	LOC115207	3'	CACTCCATGCTTTCTCTACTCC 56598	A A A	
			GGA TGGA AAAGCATG AGTG		
			CCT ATCT TTTCGTAC TCAC		
			C C C		
GAM1525	LOC144231	5'	GCAGCAGCTTTTCCACCCCA 83015	AA A A AA	
			TGG TGGAAAA GC TG GT		
			ACC ACCTTTT CG AC CG		
			CC _ _ GA		
GAM1525	LOC145508	3'	TCTGCTTCTACCATCCCA 77260	A AAA T	
			TGG ATGG AAGCA GA		
			ACC TACC TTCGT CT		
			C ATC _		
GAM1525	LOC150372	5'	CACTGCCCCCCCATTCTA 79790	AAAAA TGAA	
			TGGAATGG GCA GTG		

	ATCTTACC CGT CAC	
	CCCC_ ____	
GAM1525 LOC150577 3'	TCACTTCACACCCACCTCCA 85080	A_ AAAAAGCA
	TGGA TGG TGAAGTGA	
	ACCT ACC ACTTCACT	
	CC CAC_____	
GAM1525 LOC157247 5'	TATGCCTTGTCCATTCCA 81375	A A
	TGGAATGGA AA GCATG	
	ACCTTACCT TT CGTAT	
	G C	
GAM1525 LOC162962 3'	CACTCCCTTTTTCCTTCCA 82374	T CAT A
	TGGAA GGAAAAAG GA GTG	
	ACCTT CCTTTTTC CT CAC	
	CC_ _	
GAM1525 LOC219848 3'	ACTCTCTTCCATTCC 91491	AAAGCAT _
	GGAATGGAA GA AGT	
	CCTTACCTT CT TCA	
	_____ C	
GAM1525 LOC221511 3'	TCACTTCATGTGAAACTACTC 90990	A AAAAA
CA	TGGA TGG GCATGAAGTGA	
	ACCT ATC TGTACTTCACT	
	C AAAAG	
GAM1525 LOC253980 3'	TCACTTTGGCCCTTCTCCACCC 95075	AA A A_ A
A	TGG TGGAA AA GC TGAAGTGA	
	ACC ACCT TT CG GTTTCACT	
	C_ C CC _	
GAM1525 LOC257569 3'	TCACTTCATGTGAAACTACTC 97831	A AAAAA
CA	TGGA TGG GCATGAAGTGA	
	ACCT ATC TGTACTTCACT	
	C AAAAG	
GAM1525 LOC90393 3'	CATGCTGTCTTCCATTCCA 62621	AA_
	TGGAATGGAA AGCATG	
	ACCTTACCTT TCGTAC	
	CTG	
GAM1525 LOC90750 3'	TCACTTTTCCTTTTCTATTCCA 63924	A CAT
	TGGAATGGAAAA G GAAGTGA	
	ACCTTATCTTTT C TTTCACT	
	_CT_	
GAM1525 LOC92078 3'	CACCTGCTTCCTCCACCCCA 67976	AA AA TGAA
	TGG TGGAA AAGCA GTG	

ACC ACCT TTCGT CAC  
 CC CC C\_\_\_  
 GAM1526 ABCB11 5' TCTGGCTTCCTCAAATTC 13618 A ATGA  
 GAATTTGA GAAG AGA  
 ||||| ||| ||  
 CTTAAACT CTTC TCT  
 C GG\_\_\_  
 GAM1526 APC 3' CTTCATCTTCTTGTTGCA 3477 G TTG  
 TG AAT AAGAAGATGAAG  
 || ||| |||||  
 AC TTG TTCTTCTACTTC  
 G \_\_\_  
 GAM1526 ATP1B2 3' CTTCCCAGAATATCCTTCAAGT 8049 AA AA\_\_\_  
 TCCA GGAATTTGAAG GATG GAAG  
 ||||| ||| |||  
 CCTTGAAGTTC CTAT CTTC  
 \_\_\_ AAGACC  
 GAM1526 CA4 3' TCAGCTCTCCAAGTTCCA 5552 A AGA  
 TGGAATTTG AGA TGA  
 ||||| ||| ||  
 ACCTTGAAC TCT ACT  
 C CG\_\_\_  
 GAM1526 CEP1 5' CTTCCGTTTCGTTCTTCAAAACC 22816 AA \_ T\_\_\_  
 CA TGG TTTGAAGAA GA GAAG  
 ||| ||||| || |||  
 ACC AAAGTTCTT CT CTTC  
 CA G TGC  
 GAM1526 CEP2 3' CTTCATCTTCTCCTTCAA 23227 \_\_\_  
 TTGA AGAAGATGAAG  
 ||| |||||  
 AACT TCTTCTACTTC  
 TCC  
 GAM1526 FBLN5 3' CTTCTTCACCTCTTCCACTCC 20916 ATTT A A  
 GGA GAAGA G TGAAGAAG  
 ||| ||||| |||||  
 CCT CTCT C ACTTCTTC  
 CAC\_ \_C  
 GAM1526 GAC1 3' TCCCCATCTTCTCTTGCCCA 20945 AATTT \_ AA  
 TGG GA AGAAGATG GA  
 ||| || ||||| ||  
 ACC CT TCTTCTAC CT  
 CGT\_ C CC  
 GAM1526 GATA4 3' CTTCCCTCCTCAAATTCC 9005 A AGAT  
 GGAATTTGA GA GAAG  
 ||||| || |||  
 CCTTAAACT CT CTTC  
 C CC\_\_\_  
 GAM1526 MGA 3' TTCTTTATCCCAAATCCCA 62812 A AAGAA  
 TGG ATTTG GATGAAGAA  
 ||| ||||| |||||

		ACC TAAAC CTATTTCTT		
		C C_____		
GAM1526 PIK3R3	3'	TCGTTTCCTTACAAATTCCA 61064	_	A
		TGGAATTTG AAG AGATGA		
		ACCTTAAAC TTC TTTGCT		
		A C		
GAM1526 POU2F2	3'	TCTTCATCCTCATCCTCC 10692	ATTT	A A
		GGA GA GA GATGAAGA		
		CCT CT CT CTACTTCT		
		C_____ A C		
GAM1526 PTPRS	3'	TCCTTTCCTTCCAATTCCA 11141	T	A T
		TGGAATT GAAG AGA GA		
		ACCTTAA CTTC TTT CT		
		C C C		
GAM1526 PTPRS	3'	TCCTTTCCTTCCAATTCCA 55651	T	A T
		TGGAATT GAAG AGA GA		
		ACCTTAA CTTC TTT CT		
		C C C		
GAM1526 PTPRS	3'	TCCTTTCCTTCCAATTCCA 55645	T	A T
		TGGAATT GAAG AGA GA		
		ACCTTAA CTTC TTT CT		
		C C C		
GAM1526 PTPRS	3'	TCCTTTCCTTCCAATTCCA 55648	T	A T
		TGGAATT GAAG AGA GA		
		ACCTTAA CTTC TTT CT		
		C C C		
GAM1526 SELL	3'	TCCCCACCTTCTTCAGCCACC 5393	AAT	A AA
		GG TTGAAGAAG TG GA		
		CC GACTTCTTC AC CT		
		ACC C CC		
GAM1526 TEM7	3'	CTTTTCTTCCTCAAATTC 39885	A	T
		GAATTTGA GAAGA GAAG		
		CTTAAACT CTTCT TTTC		
		C T		
GAM1526 WT1	3'	TTCTTCATCCAACCTTCCA 44357	T	AAGAA
		TGGAA TTG GATGAAGAA		
		ACCTT AAC CTACTTCTT		
		C _____		
GAM1526 WT1	3'	TTCTTCATCCAACCTTCCA 44367	T	AAGAA
		TGGAA TTG GATGAAGAA		



ACCTT AAC CTACTTCTT  
 C \_\_\_\_\_  
 GAM1526 WT1 3' TTCTTCATCCAACCTTCCA 44377 T AAGAA  
 TGGAA TTG GATGAAGAA  
 ||||| ||| |||||  
 ACCTT AAC CTACTTCTT  
 C \_\_\_\_\_  
 GAM1526 WT1 3' TTCTTCATCCAACCTTCCA 4592 T AAGAA  
 TGGAA TTG GATGAAGAA  
 ||||| ||| |||||  
 ACCTT AAC CTACTTCTT  
 C \_\_\_\_\_  
 GAM1526 AD-003 5' CTTCCCATCTTCTTC 25931 AA  
 GAAGAAGATG GAAG  
 ||||| |||  
 CTTCTTCTAC CTTC  
 CC  
 GAM1526 CEACAM7 3' CTTCTAGCTCCTTCAATCCCA 22557 AAT A AT\_  
 TGG TTGAAG AG GAAG  
 ||| ||||| || |||  
 ACC AACTTC TC CTTC  
 CT\_ C GAT  
 GAM1526 CSMD1 3' CTTCTTTGTCCTCAATTTCCA 73120 T AGAA TG  
 TGGAA TTGA GA AAGAAG  
 ||||| ||| || |||||  
 ACCTT AACT CT TTCTTC  
 T C\_\_ GT  
 GAM1526 DDX34 3' CATGTCTCCAGATTCCA 27979 A AG  
 TGGAATTTG AGA ATG  
 ||||| ||| |||  
 ACCTTAGAC TCT TAC  
 C G\_  
 GAM1526 DKFZP434B205 3' CTTCTTCATCTTCCTGGACGTC 75320 ATTTGAA  
 GA GAAGATGAAGAAG  
 || |||||  
 CT CTTCTACTTCTTC  
 GCAGGTC  
 GAM1526 FENS-1 3' CTTCCCTTTCCCCCAAATTCC 40439 AA\_ AT  
 GGAATTTG GAAG GAAG  
 ||||| ||| |||  
 CCTTAAAC CTTT CTTC  
 CCC CC  
 GAM1526 FLJ13262 3' ATCCTCTCCAAATTCC 46155 A A  
 GGAATTTG AGA GAT  
 ||||| ||| |||  
 CCTTAAAC TCT CTA  
 C C  
 GAM1526 FLJ20170 3' TCACCTTCTTCAACTCCA 34672 AT A  
 TGGA TTGAAGAAG TGA  
 ||| ||||| |||

ACCT AACTTCTTC ACT  
 C\_ C  
 GAM1526 FLJ20375 3' CTTCTCCCTGCTAAATTCCA 35085 A\_ AA T  
 TGGAATTTG AG GA GAAG  
 ||||| || ||||  
 ACCTTAAAT TC CT CTTC  
 CG C\_ \_  
 GAM1526 FLJ20802 3' CTTCTTCACCTTTGCATCC 35669 ATT AA A  
 GGA TG GAAG TGAAGAAG  
 || || |||| |||||  
 CCT AC TTTC ACTTCTTC  
 \_ G\_ C  
 GAM1526 FLJ22055 3' CTTCATCTTCTGCTCCA 45496 ATTTGA  
 TGGA AGAAGATGAAG  
 ||| |||||  
 ACCT TCTTCTACTTC  
 CG\_  
 GAM1526 HUMAGCGB 5' CTATGCCTTCCTCAAGTTCCA 25231 A AT A  
 TGGAATTTGA GAAG G AG  
 ||||| ||| ||  
 ACCTTGA ACT CTTC T TC  
 C CG A  
 GAM1526 INA 3' CACCTCCTTCAATTCCA 51187 T A A  
 TGGAATT GAAG AG TG  
 ||||| ||| ||  
 ACCTTAA CTTC TC AC  
 \_ C C  
 GAM1526 KIAA0451 5' TCATAATTCTCAAATTCCA 29114 AG AG  
 TGGAATTTGA A ATGA  
 ||||| | |||  
 ACCTTAAACT T TACT  
 CT AA  
 GAM1526 KIAA0972 5' CTTCTTCATCCCCTTGCCCA 30010 AATTG AA  
 TGG AAG GATGAAGAAG  
 || || |||||  
 ACC TTC CTACTTCTTC  
 CG\_ CC  
 GAM1526 MGC15854 5' TTCCCCATCTTCTCCTCTA 58852 ATTT A AA  
 TGGA GA GAAGATG GAA  
 ||| || ||||| |||  
 ATCT CT CTTCTAC CTT  
 C\_ \_ CC  
 GAM1526 MGC17998 3' TTCCTCATCTTCTGGTCC 58746 ATTTGA A  
 GGA AGAAGATGA GAA  
 || ||||| |||  
 CCT TCTTCTACT CTT  
 GG\_ C  
 GAM1526 MIL1 3' TCTTCACCCCCAGGTTCC 31097 AAGAAGA  
 GGAATTTG TGAAGA  
 ||||| ||||

CCTTGGAC ACTTCT  
 CCCC\_\_\_\_  
 GAM1526 NYD-SP21 3' CTTCAGCTTCCTCAAATTC 50873 A A  
 GAATTTGA GAAG TGAAG  
 ||||| ||| |||||  
 CTTAAACT CTTC ACTTC  
 C G  
 GAM1526 PCDH19 3' TTCTTCATCCAAAATTGCA 63713 G GAAGAA  
 TG AATTT GATGAAGAA  
 || ||||| |||||  
 AC TTAAA CTACTTCTT  
 G AC\_\_\_\_  
 GAM1526 PEG10 3' CTTCACCGTCTTCAAACCTCCA 30525 A AGA  
 TGA TTTGAAGA TGAAG  
 ||| ||||| |||||  
 ACCT AAACCTTCT ACTTC  
 C GCC  
 GAM1526 TRIM16 3' TCATCTTCTAGTGCCA 21343 A TGA  
 TGG ATT AGAAGATGA  
 ||| ||| |||||  
 ACC TGA TCTTCTACT  
 G \_\_\_\_  
 GAM1526 LOC124245 3' CTCCATCTTCTTCCCTGGCC 58152 AATTT A  
 GG GAAGAAGATG AG  
 || ||||| ||  
 CC CTTCTTCTAC TC  
 GGTCC C  
 GAM1526 LOC144231 5' ATCTTCCTCAAACCTTCA 83011 A A  
 TGA TTTGA GAAGAT  
 ||| ||||| |||||  
 ACTT AAACCT CTTCTA  
 C C  
 GAM1526 LOC145739 3' TCATTCTTCAAAGCCCA 77443 AA AG  
 TGG TTTGAAGA ATGA  
 ||| ||||| |||||  
 ACC AAACCTTCT TACT  
 CG \_\_\_\_  
 GAM1526 LOC146856 3' CTTCTTTTTTCTTCTTCAACC 82802 AT T\_ \_  
 TCCA TGA TTGAAGAAGA GAAG AAG  
 ||| ||||| |||||  
 ACCT AACTTCTTCT TTTC TTC  
 CC TT C  
 GAM1526 LOC147166 3' TCATCTTCTAGTGCCA 78290 A TGA  
 TGG ATT AGAAGATGA  
 ||| ||| |||||  
 ACC TGA TCTTCTACT  
 G \_\_\_\_  
 GAM1526 LOC151124 5' TCTGTTCTTCCCCAAATTCC 85234 AA TGA  
 GGAATTTG GAAGA AGA  
 ||||| ||||| |||

	CCTTAAAC CTTCT TCT	
	CC TG_	
GAM1526 LOC151405 5'	CTTCTTCATGACACCAAATCCA 85337	A AAGAAG
	TGGA TTTG ATGAAGAAG	
	ACCT AAAC TACTTCTTC	
	_ CACAG_	
GAM1526 LOC151438 5'	CTTCTGGGACCAAATTCCA 85365	A_____
	TGGAATTTG AGAAG	
	ACCTTAAAC TCTTC	
	CAGGG	
GAM1526 LOC153469 3'	CTTCATCTTCTCCTCA 80841	___
	TGA AGAAGATGAAG	
	ACT TCTTCTACTTC	
	CC	
GAM1526 LOC157909 5'	CTTCTCAGACTTAAAATTCCA 81627	G AAGA A
	TGGAATTT AAG TGA GAAG	
	ACCTTAAA TTC ACT CTTC	
	A AG_ _	
GAM1526 LOC165140 5'	TCTTCATCTTCTGCATCCA 82467	ATT A
	TGGA TG AGAAGATGAAGA	
	ACCT AC TCTTCTACTTCT	
	___ G	
GAM1526 LOC169831 5'	CTTCTTCATCTTCCCTTC 82783	___
	GAA GAAGATGAAGAAG	
	CTT CTTCTACTTCTTC	
	CC	
GAM1526 LOC197414 3'	CTTGGCTTCTTCAAACGCCA 88066	AA ATG
	TGG TTTGAAGAAG AAG	
	ACC AAACCTTCTTC TTC	
	GC GG_	
GAM1526 LOC219894 3'	CTTCCCAACTTCTTCAAATTC 93281	A AA
	GAATTTGAAGAAG TG GAAG	
	CTTAAACTTCTTC AC CTTC	
	A C_	
GAM1526 LOC255040 3'	CTTCCTTTTGCTCCAAATTCC 96382	A _ T
	GGAATTTG AG AAGA GAAG	
	CCTTAAAC TC TTTT CTTC	
	C G C	
GAM1526 LOC255041 3'	CTTCCTTTTGCTCCAAATTCC 96388	A _ T
	GGAATTTG AG AAGA GAAG	

CCTTAAAC TC TTTT CTTC  
 C G C  
 GAM1526 LOC90371 5' TCTTCATCCTCCTCTACC 62504 AATT A A  
 GG GA GA GATGAAGA  
 || || || || || || || ||  
 CC CT CT CTACTTCT  
 AT\_\_ C C  
 GAM1526 LOC92539 5' TCCTCTCTTCAAGTCCCA 69643 A A T  
 TGG ATTTGAAGA GA GA  
 ||| ||||| || ||  
 ACC TGAACCTTCT CT CT  
 C \_ C  
 GAM1527 ATP1A2 3' CTCCCAAAGGCTGTCATTTC 5523 TTG A A  
 TGAAATGACA GT TTTG GAG  
 ||||| || ||| |||  
 ACTTTACTGT CG AAAC CTC  
 \_ G C  
 GAM1527 CACNB1 3' CTCCTGTGCCAATGTCA 5571 TT  
 TGACATTGGTAT GAG  
 ||||| |||  
 ACTGTAACCGTG CTC  
 TC  
 GAM1527 MBNL 3' ATACCAATGTAATTTC 40725 G  
 TGAAAT ACATTGGTAT  
 |||| |||||  
 ACTTTA TGTAACCATA  
 A  
 GAM1527 SLC13A3 3' CTCTCAAAGGGCTGTCACCATC 60468 AA\_ TTG A\_  
 A TGA TGACA GT TTTGAGAG  
 || ||| || |||||  
 ACT ACTGT CG AAACCTCTC  
 ACC \_ GG  
 GAM1527 CSTF2 3' CTCTCAGAACAAAATCACTTCA 7174 A CA GTA  
 TGAA TGA TTG TTTGAGAG  
 ||| || ||| |||||  
 ACTT ACT AAC AGACTCTC  
 C AA A\_  
 GAM1527 FLJ10989 3' CTAGAACACCATTGTCATCTCA 36948 A T A G  
 TGA ATGACA TGGT TTT AG  
 || |||| ||| || ||  
 ACT TACTGT ACCA AAG TC  
 C T C A  
 GAM1527 HTR3A 3' TTTCCAATGCCAATTCA 6028 C T  
 TGA ATTGGTATT GAGA  
 || ||||| |||  
 ACT TAACCGTAA CTTT  
 \_ C  
 GAM1527 KIAA0368 3' CTCTATTGACCAATGTATTTC 65164 A ATTTG  
 TGAAATG CATTGGT AGAG  
 ||||| ||||| |||

ACTTTAT GTAACCA TCTC  
 \_ GTTA\_  
 GAM1527 KIAA0843 3' CTCTTTTGGCCAATGTCTTTT 30111 T ATTT  
 CA TGAAA GACATTGGT GAGAG  
 |||| ||||| ||||  
 ACTTT CTGTAACCG TTCTC  
 T GTTT  
 GAM1527 MGC4643 3' TCTCAAATATTGATCTCA 51156 C TG  
 TGA AT GTATTTGAGA  
 ||| || |||||  
 ACT TA TATAAACTCT  
 C GT  
 GAM1527 SIRPB1 3' CTCTGCTCAATGTCACTTCA 20250 A \_ TTT  
 TGAA TGACATTG GTA GAG  
 ||| ||||| ||| |||  
 ACTT ACTGTAAC CGT CTC  
 C T \_  
 GAM1527 LOC121504 3' CTCCCAAAGTGCTGGCATTTC 74096 ACA TG GA\_  
 TGAAATG T GTATTT GAG  
 ||||| | ||||| |||  
 ACTTTAC G CGTGAA CTC  
 \_ GT ACC  
 GAM1527 LOC126282 3' CAAACACCAATGTCACCTC 74469 AA A  
 GA TGACATTGGT TTTG  
 || ||||| ||||  
 CT ACTGTAACCA AAAC  
 CC C  
 GAM1527 LOC221140 3' CTCTCAAATACCATGATGT 93488 \_  
 ACAT TGGTATTTGAGAG  
 ||| |||||  
 TGTA ACCATAAACTCTC  
 GT  
 GAM1527 LOC221399 5' CTCTCAAAAAGGCAACGTTATT 93848 A GTA\_  
 TCA TGAAATGAC TTG TTTGAGAG  
 ||||| ||| |||||  
 ACTTTATTG AAC AAACCTCTC  
 C GGAA  
 GAM1528 ADAM10 3' CTTTTACCACAAATTGAAAT 6619 GTA CT  
 ATTTCAATT TGGT GAG  
 ||||| ||| |||  
 TAAAGTTAA ACCA TTC  
 AC\_ TT  
 GAM1528 JTB 3' TCTCAGACAGTGAAAGTGAAAT 21963 ATTG G  
 G CATTTCA TAT GTCTGAGA  
 ||||| ||| |||||  
 GTAAAGT GTG CAGACTCT  
 GAAA A  
 GAM1528 DREV1 3' TCTCAGGTTCTCAGAATTGAAA 32071 GTAT\_ GT  
 TTTCAATT G CTGAGA  
 ||||| | |||||

	AAAGTTAA	T	GA	CTCT	
			GA	CTC	TG
GAM1528	FLJ10482	3'	CTCAGACCTTAGCTTGAAG	36161	TT AT_
			TTTCAA	GT	GGTCTGAG
			GAAGTT	CG	CCAGACTC
			_		ATT
GAM1528	FLJ21977	5'	TCTCAGACCTTACTAAAATG	49886	CAATT T
			CATTT	GTA	GGTCTGAGA
			GTAAA	CAT	CCAGACTCT
			AT_		T
GAM1528	FLJ22202	3'	CTCTCTGTACAATTGGAA	45990	TCT
			TTTCAATTGTATGG		GAG
			AAGGTTAACATGTC		CTC
			T_		
GAM1528	FLJ23510	3'	TCTCAGACAGTGACTGAAATG	45290	ATTG G
			CATTTCA	TAT	GTCTGAGA
			GTAAAGT	GTG	CAGACTCT
			CA_		A
GAM1528	FLJ25416	5'	CTCAGACCACGGTGTGAA	58810	_ AT
			TTCA	ATTGT	GGTCTGAG
			AAGT	TGGCA	CCAGACTC
			G		_
GAM1528	HMG4	3'	TCTCAGAACTGAATTGAAAT	20980	GTATGG
			ATTTCAATT		TCTGAGA
			TAAAGTTAA		AGACTCT
			GTCAA_		
GAM1528	KIAA1577	3'	CTCAAAAAAATAATTGAAATG	64476	ATGGTC
			CATTTCAATTGT		TGAG
			GTAAAGTTAATA		ACTC
			AAAAAA		
GAM1528	MGC11257	3'	CTCAGACCACACAGGGTG	50371	A_ A
			CA	TTGT	TGGTCTGAG
			GT	GACA	ACCAGACTC
			GG		C
GAM1528	MGC2376	3'	CTCAGACCTACTGAA	43703	ATT T
			TTCA	GTA	GGTCTGAG
			AAGT	CAT	CCAGACTC
			_		-
GAM1528	MGC2848	3'	CTCATATACAATGAAATG	51892	A GTC
			CATTTCA	TTGTATG	TGAG

GTAAAGT AACATAT ACTC

GAM1528 PCDH10 3' GTCCACATCATACAAT 51995 C A  
ATTGTATGGT TG GAC  
||||||| || |||  
TAACATACTA AC CTG

C \_  
GAM1528 SCYB11 3' TCTTGGACACATCTGAAAT 87445 AT ATG TG  
ATTTCA TGT GTC AGA  
||||| ||| ||| |||  
TAAAGT ACA CAG TCT

CT \_ GT  
GAM1528 LOC124989 5' CTCTGTGCACAATTGAAATG 74384 ATG CT\_  
CATTTCAATTGT GT GAG  
||||||| || |||  
GTAAAGTTAACA CG CTC

\_ TGT  
GAM1528 LOC148426 3' TCTCAGACCCCTACAAT 84153 T\_  
ATTGTA GGTCTGAGA  
||||| |||||  
TAACAT CCAGACTCT

CC  
GAM1528 LOC196411 3' GTCCTGGAAATAGCAATTGAAA 87679 ATGG GA  
TTTCAATTGT TCT GAC  
||||||| ||| |||  
AAAGTTAACG AGG CTG

ATAA TC  
GAM1528 LOC202020 3' CTCAGTGAACAAATTGAAA 89135 ATGGTC  
TTTCAATTGT TGAG  
||||||| |||  
AAAGTTAACA ACTC

AAGTC\_  
GAM1528 LOC219673 5' ACTATACAACCTGAAATG 93018 A  
CATTTCA TTGTATGGT  
||||| |||||  
GTAAAGT AACATATCA

C  
GAM1529 APBB2 3' GATATGAAAAGAAGCATGAA 72466 GGTGG \_ C  
TTCAT GCT CT TTCATATC  
||||| ||| || |||||  
AAGTA CGA GA AAGTATAG

\_ A A  
GAM1529 SFRP2 3' AGGAAAAGCCCACCCGAA 72067 AT C\_  
TTC GGTGGGCT TCTT  
||| ||||| |||  
AAG CCACCCGA AGGA

C\_ AA  
GAM1529 SLC24A1 3' GATATGAAAAAAACCCAAACAT 16376 G\_ CTCTC  
ATG TGGG TTCATATC  
||| ||| |||||



		TAC ACCC AAGTATAG		
		AA AAAAA		
GAM1529	SORCS1	3' GACTGGGCAAAGCCCACTAT	53584	___ T_
		ATGGTGGGCT CTC TC		
		TATCACCCGA GGG AG		
		AAC TC		
GAM1529	ZNF146	3' GAGAAAGCCCATCACGAA	23086 A C	
		TTC TGGTGGGCT TCTT		
		AAG ACTACCCGA AGAG		
		C A		
GAM1529	DKFZP761C169	3' ATATGAAGAAAACCAAGAA	67809 A GGGCTC	
		TTC TGGT TCTTCATAT		
		AAG ACCA AGAAGTATA		
		A AA___		
GAM1529	KIAA1708	3' ATACGATGCAGCCCACCAT	67030 CTCT A	
		ATGGTGGGCT TC TAT		
		TACCACCCGA AG ATA		
		CGT_ C		
GAM1529	MGC3178	3' GAAGCCAGAGCCCACATGAA	47987 G _	
		TTCATG TGGGCTCT CTTC		
		AAGTAC ACCCGAGA GAAG		
		_ CC		
GAM1529	PP1201	3' ATATGAAAAGAGCCTATTCGA	42186 AT C	
		TC GGTGGGCTCT TTCATAT		
		AG TTATCCGAGA AAGTATA		
		C_ A		
GAM1529	UGT2B10	3' GATACAAAAAGAGCCTATTA	6543 C CA	
		TGGTGGGCTCT TT TATC		
		ATTATCCGAGA AA ATAG		
		A AC		
GAM1529	LOC137964	5' GATATGAACTCTCTACCATGAA	75283 CTCTC	
		TTCATGGTGGG TTCATATC		
		AAGTACCATCT AAGTATAG		
		CTC__		
GAM1529	LOC153525	5' ATATGAAGAAAAAATACACCA	86045 GGCTC__	
		TGGTG TCTTCATAT		
		ACCAC AGAAGTATA		
		ATAAAAA		
GAM1529	LOC222484	3' GATATGAAGAGAACCACACCA	94340 _ C	
		TGGTG GG TCTCTTCATATC		

ACCAC CC AGAGAAGTATAG  
 A A  
 GAM1529 LOC90841 3' ATACAAAGATGCCAGCATGAA 64191 G G TC CA  
 TTCATG TGG C TCTT TAT  
 ||||| ||| | ||| |||  
 AAGTAC ACC G AGAA ATA  
 G \_ T\_ AC  
 GAM1529 LOC91373 3' ATGAAGAGAGCTATGA 65833 GGTG  
 TCAT GGCTCTCTTCAT  
 ||| |||||  
 AGTA TCGAGAGAAGTA  
  
 GAM1530 CDR1 3' TTGATTTACTGGAAGACTT 14513 T TGA C  
 AAGTCTTCCA GT AGA CAA  
 ||||| || ||| |||  
 TTCAGAAGGT CA TTT GTT  
 \_ \_ \_ A  
 GAM1530 CTSZ 3' TCTTCAGCAGAGGACTT 62118 CA  
 AAGTCTTC TGTTGAAGA  
 ||||| |||||  
 TTCAGGAG ACGACTTCT  
  
 GAM1530 CUL4B 3' TCTTCAACCTGAGAAGATTT 13143 \_ T  
 AAGTCTTC CA GTTGAAGA  
 ||||| || |||||  
 TTTAGAAG GT CAACTTCT  
 A C  
 GAM1530 GPR86 3' TGGTACACTTGGAAGACT 43653 T TGAAG  
 AGTCTTCCA GT ACCA  
 ||||| || |||  
 TCAGAAGGT CA TGGT  
 T CA \_  
 GAM1530 LANCL1 3' TTAACCCCAGGAAGATTT 20216 AT\_  
 AAGTCTTCC GTTGA  
 ||||| |||  
 TTTAGAAGG CAATT  
 ACCC  
 GAM1530 MKI67 3' CTTGGTCTCTTGGAATACTT 10044 C ATGTT A  
 AAGT TTCC GA GACCAAG  
 ||| ||| || |||||  
 TTCA AAGG CT CTGGTTC  
 T GTT \_ \_  
 GAM1530 NCOA6 5' CTTGTGTTTCATCAACAATGGAA 25964 \_ A\_ \_  
 GACT AGTCTTCCAT GTTGA GAC CAAG  
 ||||| |||| ||| |||  
 TCAGAAGGTA CAACT TTG GTTC  
 A AC T  
 GAM1530 RNF12 5' CTTGTTCATCAATATGGAAAAC 32279 C A C  
 T AGT TTCCATGTTGA GA CAAG  
 ||| ||||| || |||

		TCA AAGGTATAACT CT GTTC	
		A A T	
GAM1530	SERPINE1	3' CTTGGCCTCTCCTTGGAGGAC 5195	TGTT A A
		GTCTTCCA GA G CCAAG	
		CAGGAGGT CT C GGTC	
		TCCT _ C	
GAM1530	WSX1	3' CTTGGCCCCCATGGGGAAGAC 16733	ATGT AAGA
		GTCTTCC TG CCAAG	
		CAGAAGG AC GGTC	
		GGT_ CCCC	
GAM1530	B3GALT6	3' GGTCTGCGTTTGGGAGAC 54612	TGT A
		GTCTTCCA TG AGACC	
		CAGAGGGT GC TCTGG	
		TT_ G	
GAM1530	CBX1	3' TTGGTCTCAGGAGAAGATT 22329	CATG A
		AGTCTTC TTGA GACCAA	
		TTAGAAG GACT CTGGTT	
		AG_ _	
GAM1530	CD109	3' TGATCTTTGTGTGGAAGAT 56050	TG T C
		GTCTTCCA T GAAGA CA	
		TAGAAGGT G TTTCT GT	
		GT_ A	
GAM1530	CHST4	3' TCACATAGAAGACTT 19304	C T
		AAGTCTTC ATGT GA	
		TTCAGAAG TACA CT	
		A _	
GAM1530	FLJ13081	3' TTGGTCTTGCAGAAAAG 45754	CCA TG
		CTT TGT AAGACCAA	
		GAA ACG TTCTGGTT	
		AAG _	
GAM1530	FLJ20344	5' TGTCTCAGAAGACTT 35019	CATGT A C
		AAGTCTTC TGA GAC A	
		TTCAGAAG ACT CTG T	
		_ _ A	
GAM1530	FLJ22127	3' GGCCTTAGGGTGGAGACTT 42886	T G A A
		AAGTCT CCAT TTGA G CC	
		TTCAGA GGTG GATT C GG	
		_ G _ C	
GAM1530	FLJ32786	3' TGATCCTAACATGGAAAAC 58319	C AA C
		GT TTCCATGTTG GA CA	

	CA AAGGTACAAT CT GT		
	A C_ A		
GAM1530 H_GS165L15.1	3' CTCAGACCTGGAAGACT 16926	T	GA
	AGTCTTCCA GTT AG		
	TCAGAAGGT CAG TC		
	C AC		
GAM1530 KIAA0247	3' CTTGGCCGAGGATGGAAGATTT 28399	G	GAAGA
	AAGTCTTCCAT TT CCAAG		
	TTTAGAAGGTA GA GGTTTC		
	G GCC__		
GAM1530 KIAA0660	3' TCGTTAGCATGGAAGACTT 24516	A	
	AAGTCTTCCATGTTGA GA		
	TTCAGAAGGTACGATT CT		
	G		
GAM1530 KIAA1016	3' TTGAAAATATGGAAGAC 91735	GAAGAC	
	GTCTTCCATGTT CAA		
	CAGAAGGTATAA GTT		
	AA__		
GAM1530 KIAA1300	3' TCGGTCAGATGGAAGAC 62866	G	A_
	GTCTTCCAT TTGA GA		
	CAGAAGGTA GACT CT		
	_ GG		
GAM1530 KIAA1634	3' CTTGGTCTTTCCTTAAAAAGAC 63388	CCATGTT	
TT	AAGTCTT GAAGACCAAG		
	TTCAGAA TTTCTGGTTC		
	AAATTCC		
GAM1530 KIAA1735	3' TGGGCAACATAGGAAGACT 87631	_	AAGA
	AGTCTTCC ATGTTG CCA		
	TCAGAAGG TACAAC GGT		
	A G__		
GAM1530 KIAA1786	3' CTTGGTCTCAGTATTGAAAAC 66028	C C	A
T	AAGT TTC ATGTTGA GACCAAG		
	TTCA AAG TATGACT CTGGTTC		
	A T _		
GAM1530 KIAA1862	3' CTTGGACATGGAAGAC 68928	G	
	GTCTTCCATGTT AAG		
	CAGAAGGTACAG TTC		
	G		
GAM1530 NPTXR	3' CTGGACACGGGAGACTT 54177	A	GA
	AAGTCTTCC TGTT AG		

TTCAGAGGG ACAG TC  
 C G\_  
 GAM1530 NPTXR 3' CTGGACACGGGAGACTT 26641 A GA  
 AAGTCTTCC TGTT AG  
 ||||| ||| ||  
 TTCAGAGGG ACAG TC  
 C G\_  
 GAM1530 PGRMC1 3' CTGAGAGACAAGGAAGACTT 21894 A GA\_  
 AAGTCTTCC TGTT AG  
 ||||| ||| ||  
 TTCAGAAGG ACAG TC  
 A AGAG  
 GAM1530 RIP5 3' CTTGGAAGTTGGAAGAC 38125 T GAAGA  
 GTCTTCCA GTT CCAAG  
 ||||| ||| ||||  
 CAGAAGGT CAA GGTTC  
 T \_\_\_\_\_  
 GAM1530 SEF 3' CTTGGTCTCCCCTGTGGAA 69465 GTTGA  
 TTCCAT AGACCAAG  
 ||||| |||||  
 AAGGTG TCTGGTTC  
 TCCCC  
 GAM1530 SMARCF1 3' TCTGCCTACATAGAAGACTT 57493 C TGA\_  
 AAGTCTTC ATGT AGA  
 ||||| ||| ||  
 TTCAGAAG TACA TCT  
 A TCCG  
 GAM1530 SMARCF1 3' TCTGCCTACATAGAAGACTT 37446 C TGA\_  
 AAGTCTTC ATGT AGA  
 ||||| ||| ||  
 TTCAGAAG TACA TCT  
 A TCCG  
 GAM1530 SMARCF1 3' TCTGCCTACATAGAAGACTT 20047 C TGA\_  
 AAGTCTTC ATGT AGA  
 ||||| ||| ||  
 TTCAGAAG TACA TCT  
 A TCCG  
 GAM1530 SMCR5 3' TCAGCCCTGGAAGACT 58596 T\_  
 AGTCTTCCA GTTGA  
 ||||| ||||  
 TCAGAAGGT CGACT  
 CC  
 GAM1530 TRPC3 5' CTTAGTCTTCAACCTAAGTACT 12395 \_ CCAT C  
 T AAGT CTT GTTGAAGAC AAG  
 ||| ||| ||||| |||  
 TTCA GAA CAACTTCTG TTC  
 T TC\_ A  
 GAM1530 LOC127162 3' CTTAGTCTTTGAGGAAAAC 74637 C ATG TG C  
 GT TTCC T AAGAC AAG  
 || ||| | ||||| |||

	CA AAGG A TTCTG TTC	
	A ____ GT A	
GAM1530 LOC129401 3'	CTTCAGCACAGAAAAC 56283	C CA
	AGT TTC TGTGAAG	
	TCA AAG ACGACTTC	
	A AC	
GAM1530 LOC142927 3'	CTTGATCTTTGGCTTGAAGA 76426	T TG C
	TCTTCCA GT AAGA CAAG	
	AGAAGGT CG TTCT GTTC	
	T GT A	
GAM1530 LOC145748 3'	GGATGCAACACAGAAGGCTT 83467	CA AAGA
	AAGTCTTC TGTTG CC	
	TTCGGAAG ACAAC GG	
	AC GTA_	
GAM1530 LOC148887 3'	CTTGCCGAAAGCACAGAAGAC 84237	CA GAAGA
	GTCTTC TGTT CCAAG	
	CAGAAG ACGA GGTTTC	
	AC AAGCC	
GAM1530 LOC154789 5'	CTTCAACCTAGAAGACT 81134	CAT
	AGTCTTC GTTGAAG	
	TCAGAAG CAACTTC	
	ATC	
GAM1530 LOC157623 5'	CTTAGTCTCGGAATATGGAAGA 81496	GA_ C
	TCTTCCATGTT AGAC AAG	
	AGAAGGTATAA TCTG TTC	
	GGC A	
GAM1530 LOC220758 5'	CTTGAAAATGGAAGAC 90785	G G
	GTCTTCCAT TT AAG	
	CAGAAGGTA AA TTC	
	A G	
GAM1530 LOC220963 3'	CTTGCTAGTAAACAGAAGACTT 91448	CA GAAGAC
	AAGTCTTC TGTT CAAG	
	TTCAGAAG ACAA GTTC	
	__ ATGATC	
GAM1530 LOC221189 3'	TGGCCAGACAGAGGACTT 93573	CA GAAGA
	AAGTCTTC TGTT CCA	
	TTCAGGAG ACAG GGT	
	__ ACC__	
GAM1530 LOC221448 3'	TCAACATGGAAACTT 93800	C
	AAGT TTCCATGTTGA	

TTCA AAGGTACAAC

GAM1530 LOC253228 3' TGGTACAGGAAGACTT 95943 A TGAAG  
AAGTCTTCC TGT ACCA  
||||||| ||| ||||  
TTCAGAAGG ACA TGGT

GAM1530 LOC256979 5' TCGATCATGGAAGATT 96046 \_  
AGTCTTCCATG TTGA  
||||||| ||||  
TTAGAAGGTAC AGCT

T  
GAM1530 LOC91263 5' GGTCTCAACACAGAAGACTT 65382 CA A  
AAGTCTTC TGTGTA GACC  
||||||| ||||| ||||  
TTCAGAAG ACAACT CTGG  
AC \_

GAM1530 LOC92997 5' TCAGCTCAGGAAGACTT 71092 AT\_  
AAGTCTTCC GTTGA  
||||||| ||||  
TTCAGAAGG CGACT  
ACT

GAM1531 ACCN1 3' TATTAAAAGCTGGTCTTGTGGA 6584 \_ TA CC  
AA  
TTTTTCAC GGCCA GCTT AATA  
||||||| ||||| ||||| ||||  
AAAGGTG CTGGT CGAA TTAT  
TT \_ AA

GAM1531 IRF2 5' TTGGTAGCGTGAAAA 9358 GGCCATA T  
TTTTTCAC GCT CCAA  
||||||| ||| ||||  
AAAAGTG CGA GGTT  
\_ T

GAM1531 PABPN1 5' ATTGGAAGCTGTCCAGGAAAA 16174 AC CC  
TTTTTC GG ATAGCTTCCAAT  
||||| || ||||| |||||  
AAAAG CC TGTCGAAGGTTA  
GA \_

GAM1531 TPO 5' GAGTTACAGCCGTGAAAA 5046 CA  
TTTTTCACGGC TAGCTT  
||||||| |||||  
AAAAGTGCCG ATTGAG  
AC

GAM1531 ARHU 3' TATTAGAAGCTATATTAGCTG 41079 C\_ C  
CGGC ATAGCTTC AATA  
||| ||||| ||||  
GTCG TATCGAAG TTAT  
ATTA A

GAM1531 FLJ12998 3' ATTGGTTTTGCCGTGAAAA 42835 CATAGCTT  
TTTTTCACGGC CCAAT  
||||||| ||||

AAAAGTGCCG GGTTA  
 TTTT\_\_\_\_  
 GAM1531 GNB4 3' AGCCTATAGCTGTGAAAA 41267 C \_  
 TTTTCACGGC ATAG CT  
 ||||| ||| ||  
 AAAAGTGTCTG TATC GA  
 A C  
 GAM1531 LOC150418 3' GAGTCGGCCGTGAAGA 65509 ATA  
 TTTTCACGGCC GCTT  
 ||||| |||  
 AGAAGTGCCGG TGAG  
 C\_\_\_\_  
 GAM1531 LOC199957 3' GAGTCGGCCGTGAAGA 88505 ATA  
 TTTTCACGGCC GCTT  
 ||||| |||  
 AGAAGTGCCGG TGAG  
 C\_\_\_\_  
 GAM1531 LOC91431 5' ATTGGAAATGCAAGGCCGTGGA 56922 ATA \_\_\_\_  
 AA TTTTCACGGCC GC TTCCAAT  
 ||||| || |||||  
 AAAGGTGCCGG CG AAGGTTA  
 AA\_ TA  
 GAM1532 AF1Q 3' TCTGACTCGACATCTTGTCCT 22369 CGCATG  
 GGGACAAGATGTTG CAGA  
 ||||| |||  
 CCCTGTTCTACAGC GTCT  
 TCA\_\_\_\_  
 GAM1532 EN2 5' CTGCATGCGCGCAGCTCTCGCC 7461 ACA T \_\_\_\_  
 C GGG AGA GT TGCGCATGCAG  
 || ||| || |||||  
 CCC TCT CG GCGCGTACGTC  
 GC\_ \_ AC  
 GAM1532 SLC22A12 3' CGCACTGCCACTTGTCCC 58068 ATGT C \_ A  
 GGGACAAG TG GCA TGC G  
 ||||| || ||| |||  
 CCCTGTTC AC CGT ACG C  
 \_\_\_\_ \_ C C  
 GAM1532 ZNF76 3' TCTGCATGGCCACTCTTGCCC 12813 A T T G  
 GGG CAAGA GT GC CATGCAGA  
 || |||| || || |||||  
 CCC GTTCT CA CG GTACGTCT  
 \_ \_ C \_  
 GAM1532 C9orf7 3' CTGGGTCAGCAGCATCCCACCC 34171 ACAA GC G  
 GGG GATGTTGC AT CAG  
 || ||||| || |||  
 CCC CTACGACG TG GTC  
 ACC\_ AC G  
 GAM1532 CAMK2G 3' CTGCATGCAGCCCTCCCGCCC 68964 ACAA TGTT \_  
 GGG GA GC GCATGCAG  
 || || || |||||



CCC CT CG CGTACGTC  
 GCC\_ CC\_ A  
 GAM1532 DDX34 3' CTGCATGCGCCCTCACGCCC 27981 ACAA TGTT  
 GGG GA GCGCATGCAG  
 ||| || |||||  
 CCC CT CGCGTACGTC  
 GCA\_ CCC\_  
 GAM1532 DKFZp547E052 3' TCTGCTATAACACATCTTGCCC 50100 A TGCGCAT  
 GGG CAAGATGT GCAGA  
 ||| ||||| ||||  
 CCC GTTCTACA CGTCT  
 \_ CAATAT\_  
 GAM1532 FBXO21 3' TCTGCATGCAGTATTCTCACCC 53242 ACA TGT \_  
 GGG AGA TGC GCATGCAGA  
 ||| ||| ||| |||||  
 CCC TCT ATG CGTACGTCT  
 AC\_ T\_ A  
 GAM1532 FEM-2 3' CTGCATGCCAGCCTTACCCC 27578 AC AT C  
 GGG AAG GTTG GCATGCAG  
 ||| ||| ||| |||||  
 CCC TTC CGAC CGTACGTC  
 CA \_ C  
 GAM1532 FLJ12681 3' CAGGCCAACCCTTGTCCT 42872 AT C A  
 GGGACAAG GTTG GC TG  
 ||||| ||| ||  
 CCCTGTTC CAAC CG AC  
 C\_ \_ G  
 GAM1532 GNB4 3' CTGCATCTGAACATCTTTCCC 41268 C G C  
 GGGA AAGATGTT CG ATGCAG  
 ||| ||||| || |||||  
 CCCT TTCTACAA GT TACGTC  
 \_ \_ C  
 GAM1532 HSJ1 3' TCTGCATGCTGAGCCCCATC 22138 TT \_\_\_\_  
 GATG GC GCATGCAGA  
 ||| || |||||  
 CTAC CG CGTACGTCT  
 CC AGT  
 GAM1532 NYD-SP17 5' TCTGTTTTCCAACACCTTGCCT 50879 A A CGCAT  
 GGG CAAG TGTTG GCAGA  
 ||| ||| |||| ||||  
 TCC GTTC ACAAC TGTCT  
 \_ C CTTT\_  
 GAM1532 SLC17A6 3' GCACAACATCTCATCCT 39744 CA C  
 GGGA AGATGTTG GC  
 ||| ||||| ||  
 TCCT TCTACAAC CG  
 AC A  
 GAM1532 TRPV5 5' CTGCATGCACACACACCACC 39047 GACAAGA \_ C  
 GG TGT TG GCATGCAG  
 || ||| || |||||

CC ACA AC CGTACGTC  
 ACC\_\_\_ C A  
 GAM1532 LOC148987 3' TGGGCAGCATCCTATCCC 79122 CAA G  
 GGA GATGTTGC CA  
 ||| ||||| ||  
 CCCT CTACGACG GT  
 ATC G  
 GAM1532 LOC152641 5' TCTGCATGCGCATTCTCGCGC 80635 ACAA TGT\_  
 C GG GA TGCGCATGCAGA  
 || || |||||  
 CC CT ACGCGTACGTCT  
 GCG\_ CCTT  
 GAM1532 LOC253980 3' GCCAACACTTGTCCC 95072 A C  
 GGGACAAG TGTTG GC  
 ||||| ||||| ||  
 CCCTGTTT ACAAC CG  
  
 GAM1532 LOC254556 3' TGCCTAACATCTGCC 94619 A A C  
 GGG CA GATGTTG GCA  
 ||| || ||||| |||  
 CCC GT CTACAAT CGT  
 \_ \_ C  
 GAM1533 EPHB1 5' ACACTCCTGCCACGC 15437 A\_  
 GCGTG CAGGAGTGT  
 |||| |||||  
 CGCAC GTCCTCACA  
 CC  
 GAM1533 IRTA2 3' CACACTCCTCCACCTGTCTCA 48402 T C AC  
 TGAGA CAG GTG AGGAGTGTG  
 |||| ||| ||| |||||  
 ACTCT GTC CAC TCCTCACAC  
 \_ \_ C\_  
 GAM1533 KIR2DL4 3' CACACTCCTTTGCTTATCCCA 9612 A C TGAC  
 TG GAT AGCG AGGAGTGTG  
 || ||| ||| |||||  
 AC CTA TCGT TCCTCACAC  
 C T T\_  
 GAM1533 MSN 3' CACACTCCTACACCTAACTCA 60252 ATC C AC  
 TGAG AG GTG AGGAGTGTG  
 ||| || ||| |||||  
 ACTC TC CAC TCCTCACAC  
 AA\_ \_ A\_  
 GAM1533 AMOTL1 3' CACCTTCCCACGCTGATCCCA 73649 A ACA T  
 TG GATCAGCGTG GGAG GTG  
 || ||||| ||| |||  
 AC CTAGTCGCAC CCTT CAC  
 C \_ C  
 GAM1533 DKFZP564D172 3' CACACTCCAAAGCCGATTTC 49385 A GTGACA  
 TGAGATC GC GGAGTGTG  
 ||||| || |||||

ACTTTAG CG CCTCACAC  
 C AAA\_\_\_\_  
 GAM1533 MOST2 5' CACACTCCTGCTCACTAGC 39676 \_\_\_\_  
 GC GTGA CAGGAGTGTG  
 || ||| |||||  
 CG CACT GTCCTCACAC  
 AT C  
 GAM1533 SNT-2 3' CACACTCCTGTCCTCTGA 21839 CGT  
 TCAG GACAGGAGTGTG  
 ||| |||||  
 AGTC CTGTCCTCACAC  
 TC\_  
 GAM1533 TED 3' CACACTCCCGTTTGGCCCTCA 31631 ATCA GT A  
 TGAG GC GAC GGAGTGTG  
 ||| || ||| |||||  
 ACTC CG TTG CCTCACAC  
 C\_\_\_\_ GT C  
 GAM1533 LOC132720 3' CACACTCCCCACCAAATAATCT 75063 CAGC\_\_\_\_ ACA  
 CA TGAGAT GTG GGAGTGTG  
 ||||| || |||||  
 ACTCTA CAC CCTCACAC  
 ATAAAC C\_\_\_\_  
 GAM1533 LOC219842 5' CACTCCTGCCAAGCTGACCTCA 93267 A G A  
 TGAG TCAGC TG CAGGAGTGTG  
 ||| |||| || |||||  
 ACTC AGTCG AC GTCCTCAC  
 C A C  
 GAM1534 SLC17A4 3' CAACAGTTCTTCATGTAGC 18525 CAGT  
 GCTGC TGAAGAACTGTTG  
 |||| |||||  
 CGATG ACTTCTTGACAAC  
 T\_\_\_\_  
 GAM1534 CITED1 5' CAACAGCTCCAGCTGGCAGC 14729 AA A  
 GCTGCCAGTTG GA CTGTTG  
 ||||| || |||||  
 CGACGGTCGAC CT GACAAC  
 \_\_\_\_ C  
 GAM1534 FLJ10900 5' CAACAGTTCTTGCTGAAGCAGT 65590 \_\_\_\_ TG  
 T AGCTGC CAGT AAGAACTGTTG  
 |||| ||| |||||  
 TTGACG GTCG TTCTTGACAAC  
 AA \_\_\_\_  
 GAM1534 HS6ST 3' CAACAGTTCCTTTGCCAGCAGC 62025 CA T A  
 GCTGC GT GA GAACTGTTG  
 |||| || || |||||  
 CGACG CG TT CTTGACAAC  
 AC T C  
 GAM1534 MGC4638 3' CAACAGTTCTTCAAGTG 48939 G  
 CA TTGAAGAACTGTTG  
 || |||||

		GT AACTTCTTGACAAC	
		G	
GAM1534	ZNF262	3' TTCCCCAATGGCAGCTT 17492	G AA
		AAGCTGCCA TTG GAA	
		TTCGACGGT AAC CTT	
		_ CC	
GAM1534	LOC115051	3' CAACAGTTCTTTGCCAGCAGC 60036	CA T A
		GCTGC GT GA GAACTGTTG	
		CGACG CG TT CTTGACAAC	
		AC T C	
GAM1534	LOC143153	3' CAGCCTCAAGCTGGCAGC 76463	GA AA
		GCTGCCAGTT AG CTG	
		CGACGGTCGA TC GAC	
		AC C_	
GAM1534	LOC168512	5' CAACAGCCTCTCTGGCAGCTT 82714	TTGA A_
		AAGCTGCCAG AGA CTGTTG	
		TTCGACGGTC TCT GACAAC	
		___ CC	
GAM1534	LOC199923	3' AACAGTTCCAGACCAGC 88494	CCA GAA
		GCTG GTT GAACTGTT	
		CGAC CAG CTTGACAA	
		___ AC_	
GAM1534	LOC199926	3' TAGTCCTTCAACTCACAGCTT 89880	CC A
		AAGCTG AGTTGAAG ACTG	
		TTCGAC TCAACTTC TGAT	
		AC C	
GAM1534	LOC202316	3' TAGTCCTTCAACTCACAGCTT 90340	CC A
		AAGCTG AGTTGAAG ACTG	
		TTCGAC TCAACTTC TGAT	
		AC C	
GAM1534	LOC221479	3' CAACAACCTACAGCAGCAGC 92222	CA A AAC
		GCTGC GTTG AG TGTTG	
		CGACG CGAC TC ACAAC	
		A_ A A_	
GAM1535	ARNT2	3' AAACAACCCGTGCATCCCTGC 29450	A TTTTA
		GTA GGAT GGGTTGTTT	
		CGT CCTA CCCAACAAA	
		C CGTG_	
GAM1535	LCT	3' AACCGTAAAAATCCTT 9697	G
		AAGGATTTTTA GGTT	

TTCCTAAAAAT CCAA  
 G  
 GAM1535 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
 GTAAGGATTTTTAGGGTTGTTT  
 |||||  
 CATTCTAAAAATCCCAACAAA

GAM1535 FBXO30 3' AACTAAAAAAATCCTGAC 49573 A AG  
 GTAGGATTTTT GGTT  
 || ||||| |||  
 CATCCTAAAAA TCAA  
 G AA

GAM1535 KIAA0494 3' AACAACCCTTACTTAC 28736 GATTTTT  
 GTAAG AGGGTTGTT  
 |||| |||||  
 CATTCTCCCAACAA  
 AT\_\_\_\_\_

GAM1535 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
 TAAG TTTTGGGTTGTTT  
 ||| ||| |||||  
 GTTC AAAA CCAACAAA  
 \_\_\_\_ C

GAM1535 SMT3H2 3' AACAACATAAAAAATCCTTGC 22670 GG  
 GTAAGGATTTTTA GTTGTT  
 ||||| |||||  
 CGTTCCTAAAAAT CAACAA  
 A\_

GAM1535 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_  
 GTAAGGATTTTT GGGTT  
 ||||| |||||  
 CGTTCCTAAAAA TCCAA  
 GTA

GAM1535 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
 GGAT TTGGGTTGTTT  
 ||| || |||||  
 CCTG AA CCAACAAA  
 T\_ C

GAM1535 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
 C GTA GGATTTTT TTGTTT  
 ||| ||||| |||||  
 CGT CCTAAAAA AACAAA  
 C GATAA

GAM1535 LOC148089 3' GGCCCTAAAAATTCCTAC 78637 A  
 GTA GGATTTTTAGGGTT  
 ||| |||||  
 CATCTTAAAAATCCCGG  
 C

GAM1535 LOC154547 3' AACAACATAAAAAATCCTTGC 76050 GG  
 GTAAGGATTTTTA GTTGTT  
 ||||| |||||

CGTTCCTAAAAAT CAACAA  
A\_  
GAM1535 LOC158104 3' ACAGCCAAAAATCCTTA 60313 AG  
TAAGGATTTTT GGTGT  
||||||| |||||  
ATTCCTAAAAA CCGACA

—  
GAM1535 LOC205880 5' AAACAACCATCATCCTGAC 90709 A TTTTAG  
GT AGGAT GGTGT  
|| ||||| |||||  
CA TCCTA CCAACAAA  
G CTA—

GAM1535 LOC221561 3' AACAAACATAAAAAATCCTTGC 92130 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_  
GAM1535 LOC257591 3' AACAAACATAAAAAATCCTTGC 97840 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_  
GAM1535 LOC51145 3' AGCTAAAATCCTTAC 32393 TAG  
GTAAGGATTTT GTT  
||||||| |||  
CATTCCTAAAA TCGA

—  
GAM1536 NFATC1 3' CGAGCACCCACTCCTAGTTGCC 20484 GT\_\_ TT  
ACA TGTGGCAAC AGT GTGCTCG  
||||||| ||| |||||  
ACACCGTTG TCA CACGAGC  
ATCC CC

GAM1536 BZW2 3' AGCACAATACCTAGGTTACCAC 25884 C G T\_\_  
A TGTGG AAC TAG TTGTGCT  
||||| ||| |||||  
ACACC TTG ATC AACACGA  
A G CAT

GAM1536 C21orf6 3' ACGAAGATGCCAGTTGCCACA 33742 \_\_ G\_  
TGTGGCAAC GTA TTTGT  
||||||| ||| |||||  
ACACCGTTG CGT AAGCA  
AC AG

GAM1536 DKFZP564K0822 3' GCAAGCACAGATGCTGCCAC 94047 AC G C  
GTGGCA GTA TTTGTGCT GC  
||||| ||| ||||| ||  
CACCGT CGT AGACACGA CG  
— — A

GAM1536 FLJ11000 3' ACAAACAAACGCTGCCAC 36959 A A\_  
GTGGCA CGT GTTTGT  
||||| ||| |||||

			CACCGT GCA CAAACA		
			C AA		
GAM1536	FLJ20147	3'	ACAAGCATGAGCCAC	34633	AA A
			GTGGC CGT GTTTGT		
			CACCG GTA CGAACA		
			A_ _		
GAM1536	G4	5'	GCAAAC TACTTGCCACA	90993	C
			TGTGGCAA GTAGTTTGT		
			ACACCGTT CATCAAACG		
			—		
GAM1536	INPP5E	3'	GCAAACAATGTCGCCACA	73109	A A
			TGTGGC ACGT GTTTGT		
			ACACCG TGTA CAAACG		
			C A		
GAM1536	KIAA1237	5'	ACAAACAACCTTGCCACA	80462	C A
			TGTGGCAA GT GTTTGT		
			ACACCGTT CA CAAACA		
			C A		
GAM1536	MGC2541	3'	GCAAGAAGGCCAGTTGCCACA	54750	GTA TG__
			TGTGGCAAC GTT TGC		
			ACACCGTTG CGG ACG		
			ACC AAGA		
GAM1536	SB52	3'	TGTAAACTACATTGCCATA	56363	C GT
			TGTGGCAA GTAGTTT G		
			ATACCGTT CATCAA T		
			A TG		
GAM1536	SOX6	3'	ACGAACAAGGTTGCCACA	52825	GTA
			TGTGGCAAC GTTTGT		
			ACACCGTTG CAAGCA		
			GAA		
GAM1536	LOC149910	3'	GCAAATAACCCATTGCCACA	79533	C__ A
			TGTGGCAA GT GTTTGT		
			ACACCGTT CA TAAACG		
			ACC A		
GAM1536	LOC157869	5'	ACAAGCTACGTCTCCACA	81624	CA
			TGTGG ACGTAGTTTGT		
			ACACC TGCATCGAACA		
			TC		
GAM1536	LOC158476	3'	ACAAACTACATTATCACA	86834	GC C
			TGTG AA GTAGTTTGT		

		ACAC TT CATCAAACA		
		TA A		
GAM1536	LOC257554 5'	GCAAACACTTGCCACA	97693	C
		TGTGGCAA GTAGTTTGT		
		ACACCGTT CATCAAACG		
		—		
GAM1537	OTX1 5'	AGCAAGACAAGCCACTCCGA	27303	AA C ATA
		TC AG GGCT GTTTTGCT		
		AG TC CCGA CAGAACGA		
		CC A A__		
GAM1537	TTN 5'	AGCAAAACTACACAGTCTTGA	55916	AG GGCTA
		TCAA C TAGTTTTGCT		
		AGTT G ATCAAAACGA		
		CT ACAC_		
GAM1537	TTN 5'	AGCAAAACTACACAGTCTTGA	55934	AG GGCTA
		TCAA C TAGTTTTGCT		
		AGTT G ATCAAAACGA		
		CT ACAC_		
GAM1537	TTN 5'	AGCAAAACTACACAGTCTTGA	55924	AG GGCTA
		TCAA C TAGTTTTGCT		
		AGTT G ATCAAAACGA		
		CT ACAC_		
GAM1537	TTN 5'	AGCAAAACTACACAGTCTTGA	55946	AG GGCTA
		TCAA C TAGTTTTGCT		
		AGTT G ATCAAAACGA		
		CT ACAC_		
GAM1537	ARPP-19 3'	CAAACTATACCTCT	21789	C C
		AG GG TATAGTTTTG		
		TC CC ATATCAAAAC		
		T _		
GAM1537	BET3 3'	GCAAACTCACTTTGA	26964	C GCTAT
		TCAAAG G AGTTTTGC		
		AGTTTC C TCAAAACG		
		A _____		
GAM1537	C12orf22 3'	AGCAAACTATTCTTCT	47975	C CT
		AG GG ATAGTTTTGCT		
		TC TC TATCAAAACGA		
		T T_		
GAM1537	C14orf4 5'	AGCGCAGCCGCTTCGAG	67332	A ATA
		TTC AAGCGGCT GTT		



GAG TTCGCCGA CGA  
 C CG\_  
 GAM1537 CDCA1 3' CAAAACTAGTTACCTTTGAA 48658 CGGCTA  
 TTCAAAG TAGTTTTG  
 ||||| |||||  
 AAGTTTC ATCAAAAC  
 CATTG\_  
 GAM1537 DKFZP564C196 3' GTACAACCTGCTTTGAA 70068 CTATA T  
 TTCAAAGCGG GTT TGC  
 ||||| |||||  
 AAGTTTCGTC CAA ATG  
 C  
 GAM1537 FLJ21276 3' AGCAGATAACCTGCTTTGAA 44913 CTATAGT  
 TTCAAAGCGG TTTGCT  
 ||||| |||||  
 AAGTTTCGTC AGACGA  
 CAAT\_  
 GAM1537 FLJ21308 3' CAAAATTAACCCTTTGAA 44866 C CTA  
 TTCAAAG GG TAGTTTTG  
 ||||| |||||  
 AAGTTTC CC ATTAAAC  
 A\_  
 GAM1537 FLJ22457 3' AGCAAACTGTCAGCT 46083 \_  
 GGCT ATAGTTTTGCT  
 |||| |||||  
 TCGA TGTCAAAACGA  
 C  
 GAM1537 LOC145501 3' AGCCCCCAGATGGCCGCCCTGA 77250 AA AGTTTT  
 A TTCA GCGGCTAT GCT  
 |||| ||||| |||  
 AAGT CGCCGTA CGA  
 CC GACCCC  
 GAM1537 LOC221477 3' CAAAACTGTAGGGCT 92149 GG  
 AGC CTATAGTTTTG  
 |||| |||||  
 TCG GATGTCAAAAC  
 G\_  
 GAM1538 APM1 3' TACCCTAAACTCTCTGGG 16600 ACTCA T  
 TCCAGAGA AGG GTG  
 ||||| |||||  
 GGGTCTCT TCC CAT  
 CAAA\_ \_  
 GAM1538 APPBP2 3' TTGCATTAAAGTTCCCTAGGA 21086 \_ A CA TG  
 TCC AG GAACT AGGTG A  
 |||| ||||| |||||  
 AGG TC CTTGA TTTAC T  
 A C A\_ GT  
 GAM1538 AQP6 5' CATGCTTGAGTCCCCTGGG 53915 AGA G  
 TCCAG ACTCAAG TGTG  
 |||| ||||| |||||

		GGGTC TGAGTTC GTAC		
		CCC _		
GAM1538	ARAF1	3' CACTCAGAACCTCTCTGGA 63937	AC_	AA
		TCCAGAGA TC GGTG		
		AGGTCTCT AG TCAC		
		CCA AC		
GAM1538	C8orf1	3' TACTGGCTTGAATTTTCTGGA 15087	C	G_
		TCCAGAGAA TCAAG T GTG		
		AGGTCTTTT AGTTC G CAT		
		A G T		
GAM1538	CA12	3' CACTTCGGCTCTCTGGA 6875	A	CA
		TCCAGAGA CT AGGTG		
		AGGTCTCT GG TTCAC		
		C C_		
GAM1538	CANX	3' ATTCACACCTCTGTCCCTC 87480	A_	TCA
		GAG AC AGGTGTGAAT		
		CTC TG TCCACACTTA		
		CC TC_		
GAM1538	CEP1	5' TAGACCCCGAACTCTTTGGA 22817	AC	AA G
		TCCAGAGA TC GGT TG		
		AGGTTTCT AG CCA AT		
		CA CC G		
GAM1538	FCAR	3' TTCCTCGCTAGAGTTCTCCAGA 55807	CA	AA T_
		TC GAGAACTC GGTG GAA		
		AG CTCTTGAG TCGC CTT		
		AC A_ TC		
GAM1538	FCAR	3' TTCCTCGCTAGAGTTCTCCAGA 55817	CA	AA T_
		TC GAGAACTC GGTG GAA		
		AG CTCTTGAG TCGC CTT		
		AC A_ TC		
GAM1538	HMGCR	3' ATTCACACAGGGCTCTTGGA 5972	_	AA CAAG
		TCCA GAG CT GTGTGAAT		
		AGGT CTC GA CACACTTA		
		T GG _		
GAM1538	MME	3' TACTCTTGTTGAGTTCTATAGA 6143	CAG	_ T
		TC AGAACTCAA GG GTG		
		AG TCTTGAGTT TC CAT		
		ATA GT T		
GAM1538	MME	3' TACTCTTGTTGAGTTCTATAGA 23490	CAG	_ T
		TC AGAACTCAA GG GTG		

		AG TCTTGAGTT TC CAT		
		ATA GT T		
GAM1538 MME	3'	TACTCTTGTTGAGTTCTATAGA 23500	CAG	___ T
		TC AGAACTCAA GG GTG		
		AG TCTTGAGTT TC CAT		
		ATA GT T		
GAM1538 MME	3'	TACTCTTGTTGAGTTCTATAGA 23512	CAG	___ T
		TC AGAACTCAA GG GTG		
		AG TCTTGAGTT TC CAT		
		ATA GT T		
GAM1538 NEU3	3'	CACCTGAACTCTCTGGA 21846	AC	A
		TCCAGAGA TCA GGTG		
		AGGTCTCT AGT CCAC		
		CA _		
GAM1538 P53AIP1	3'	CACCCACTGAACTTTCTGGA 42080	AC	A_ T
		TCCAGAGA TCA GG GTG		
		AGGTCTTT AGT CC CAC		
		CA CA _		
GAM1538 PAICS	3'	TACCTTTAGTTCTCTG 21260	C	
		CAGAGAACT AAGGTG		
		GTCTCTTGA TTCCAT		
		T		
GAM1538 PIR51	3'	CACTTTTTGTTAAGTTCTTTAG 21364	C	___ T
A		TC AGAGAACT CAAGG GTG		
		AG TTTCTTGA GTTTT CAC		
		A ATT T		
GAM1538 PLSCR1	5'	CATCGCCTGGCCCCGGCTCTCT 40856	A	CA_____ _
GGA		TCCAGAGA CT AGGTG TG		
		AGGTCTCT GG TCCGC AC		
		C CCCCGG T		
GAM1538 PTPN1	3'	TATTCACACCTCACGCTCTGGA 11050	AACTCA	
		TCCAGAG AGGTGTGAATA		
		AGGTCTC TCCACACTTAT		
		GCAC__		
GAM1538 RAP1A	3'	GTTTGCACAAAGTTCCCTGGA 11248	A	CAAG TG
		TCCAG GAACT GTG AAT		
		AGGTC CTTGA CAC TTG		
		C A__ GT		
GAM1538 SYT4	3'	CACTATATTTGAGTTCTT 62435	GT__	
		GAGAACTCAAG GTG		

		TTCTTGAGTTT CAC		
		ATAT		
GAM1538	TCTA	3' TAGGCCCTGAGTTTTCTG 42241	A G	
		CAGAGAACTCA GGT TG		
		GTCTTTTGAGT CCG AT		
		C G		
GAM1538	VAT1	3' CACCCTTCACTGAGTTCTCTGG 21044	_____ T	
	A	TCCAGAGAACTCA AGG GTG		
		AGGTCTCTTGAGT TCC CAC		
		CACT _		
GAM1538	ZFH4	5' CACCTCAGCTCCCTGGA 45294	A A CA	
		TCCAG GA CT AGGTG		
		AGGTC CT GA TCCAC		
		C C C_		
GAM1538	ZFP103	5' TATTCGAGCTCTCTGGA 19026	A AA T	
		TCCAGAGA CTC GG GTG		
		AGGTCTCT GAG CC TAT		
		C _ T		
GAM1538	ZNF202	3' TTGCAGCCAAGTCCCTGG 12913	A CAA _ TG	
		CCAG GAACT GG TG A		
		GGTC CTTGA CC AC T		
		C A_ G GT		
GAM1538	C1orf25	5' ATTCACGTCAGTTCTCTG 72532	CAA GT	
		CAGAGAACT G GTGAAT		
		GTCTCTTGA C CACTTA		
		____ TG		
GAM1538	C20orf177	3' TACTTTTGAGTTCTC 62154	T	
		GAGAACTCAAGG GTG		
		CTCTTGAGTTTT CAT		
		-		
GAM1538	CG012	3' GCAGTCTGAGTTCTTCAGA 83221	CA A _	
		TC GAGAACTCA GG TGT		
		AG TTCTTGAGT CT ACG		
		AC _ G		
GAM1538	CRK7	3' TTCCATCCAGTTCTCTG 33256	CAA T	
		CAGAGAACT GGTG GAA		
		GTCTCTTGA CTAC CTT		
		C_ _		
GAM1538	DIO2	3' ATTCACACTGTTGTCCTT 25678	A TCAA	
		GAG AC GGTGTGAAT		

TTC TG TCACACTTA  
 C TTG\_  
 GAM1538 DIO2 3' ATTCACACTGTTGTCCTT 5826 A TCAA  
 GAG AC GGTGTGAAT  
 ||| || |||||  
 TTC TG TCACACTTA  
 C TTG\_  
 GAM1538 DKFZP434A043 3' CACACTTAAACTCTGTGGA 31187 G ACTCA  
 TCCA AGA AGGTGTG  
 |||| || |||||  
 AGGT TCT TTCACAC  
 G CAAA\_  
 GAM1538 DKFZp434F1819 3' TCACACCTCCTTTTTG 50009 ACTCA  
 CAGAGA AGGTGTGA  
 |||| |||||  
 GTTTTT TCCACACT  
 CC\_  
 GAM1538 DPCR1 3' CATCTCTGAGTTCTCAGGA 55120 A \_  
 TCC GAGAACTCA AGGTG  
 || ||||| ||||  
 AGG CTCTTGAGT TCTAC  
 A C  
 GAM1538 FLJ10898 3' ATTCACACTGATTTTGTCTGGA 59421 G CTCAA  
 TCCAGA AA GGTGTGAAT  
 |||| || |||||  
 AGGTCT TT TCACACTTA  
 G TTAG\_  
 GAM1538 FLJ11193 3' TATTTTGAATCTCTG 37154 AC  
 CAGAGA TCAAGGTG  
 |||| |||||  
 GTCTCT AGTTTTAT  
 A\_  
 GAM1538 FLJ13769 3' CACTCAAGCTCTCTGGA 46603 A CAA  
 TCCAGAGA CT GGTG  
 ||||| || ||||  
 AGGTCTCT GA TCAC  
 C AC\_  
 GAM1538 FLJ13782 3' GCCTGAGCTTTCTGGA 46169 A A  
 TCCAGAGA CTCA GGT  
 ||||| |||| ||||  
 AGGTCTTT GAGT CCG  
 C \_  
 GAM1538 FLJ20555 3' CAGACCTCAGCTCTCTGGA 35393 A CA G  
 TCCAGAGA CT AGGT TG  
 ||||| || |||| ||  
 AGGTCTCT GA TCCA AC  
 C C\_ G  
 GAM1538 FLJ23142 3' TTTTGAGTTCCTAGA 44727 C A  
 TC AG GAACTCAAGG  
 || || |||||

AG TC CTTGAGTTTT  
 A \_  
 GAM1538 FLJ30092 5' TATTCACACCTCACTTCCTG 58691 A CTCA  
 CAG GAA AGGTGTGAATA  
 ||| ||| |||||  
 GTC CTT TCCACACTTAT  
 \_ CAC\_  
 GAM1538 GRID1 3' TATTCAAGCAAGTTCTCTAGG 68501 \_ CAAG G  
 CC AGAGAACT GT TGAATA  
 || ||||| || |||||  
 GG TCTCTTGA CG ACTTAT  
 A A\_\_ A  
 GAM1538 HPCAL4 3' CATCTTGTGCCCTCTGGA 32732 AACT  
 TCCAGAG CAAGGTG  
 ||||| |||||  
 AGGTCTC GTTCTAC  
 CCGT  
 GAM1538 KIAA0229 3' CATTTTGATTCTCTG 92423 C  
 CAGAGAA TCAAGGTG  
 ||||| |||||  
 GTCTCTT AGTTTAC  
 \_  
 GAM1538 KIAA0295 3' GCCTTGGGTTCTCCAGA 68105 CA  
 TC GAGAACTCAAGGT  
 || |||||  
 AG CTCTTGGGTTCCG  
 AC  
 GAM1538 KIAA0420 3' TACCCTGCACTCTCTGGA 63366 ACTCA T  
 TCCAGAGA AGG GTG  
 ||||| ||| |||  
 AGGTCTCT TCC CAT  
 CACG\_ \_  
 GAM1538 KIAA0565 3' TATTTTAAAGTCTCTGGA 66897 ACTC  
 TCCAGAGA AAGGTG  
 ||||| |||||  
 AGGTCTCT TTTTAT  
 GAAT  
 GAM1538 KIAA1036 3' CATCTTGGTCCTCCGGA 29816 A A T  
 TCC GAG AC CAAGGTG  
 ||| ||| || |||||  
 AGG CTC TG GTTCTAC  
 C C \_  
 GAM1538 KIAA1240 3' TATTCATGTTTGAGTTC 66737 G TG  
 GAACTCAA G TGAATA  
 ||||| | |||||  
 CTTGAGTT T ACTTAT  
 \_ GT  
 GAM1538 KIAA1297 5' CACTGCAGCCCGAGTTCTCTGG 72170 AA \_\_\_\_  
 CCAGAGAACTC GGT GTG  
 ||||| ||| |||

			GGTCTCTTGAG CCG CAC		
			C_ ACGT		
GAM1538	KIAA1579	3'	CACTTTGATTTCCCTGGA 36605	A C	
			TCCAG GAA TCAAGGTG		
			AGGTC CTT AGTTTCAC		
			C T		
GAM1538	MAB21L2	5'	TTCGCAGCTCTCTGGA 21233	ACTCAA G	
			TCCAGAGA G TGTGAA		
			AGGTCTCT C ACGCTT		
			_____G		
GAM1538	MAP2K6	5'	CATCTTGATTCCCTG 10868	A C	
			CAG GAA TCAAGGTG		
			GTC CTT AGTTCTAC		
			C _		
GAM1538	MGC21688	3'	ATTCACGCAGAGCTCTCTG 58265	A AAG	
			CAGAGA CTC GTGTGAAT		
			GTCTCT GAG CGCACTTA		
			C A_		
GAM1538	MMPL1	3'	TATTCCTCTGTGTGTTCTCTGG 14722	T A TGT	
	A		TCCAGAGAAC CA GG GAATA		
			AGGTCTCTTG GT TC CTTAT		
			T G TC_		
GAM1538	NDUFB6	3'	ATTTACTGAATTTTCTGGA 10197	C AGGT	
			TCCAGAGAA TCA GTGAAT		
			AGGTCTTTT AGT CATTTA		
			A _____		
GAM1538	SSB-4	3'	CACTGACTCACAGTTCTCTGGA 55097	CA_ GT_	
			TCCAGAGAACT AG GTG		
			AGGTCTCTTGA TC CAC		
			CAC AGT		
GAM1538	STAM2	3'	TTCAAGCTAGTTCTCTG 19570	CAA G	
			CAGAGAACT GGT TGAA		
			GTCTCTTGA TCG ACTT		
			_____A		
GAM1538	SYT12	3'	TAGCTTGAGTTCCCTAGA 94740	C A G	
			TC AG GAACTCAAG TG		
			AG TC CTTGAGTTC AT		
			A C G		
GAM1538	TED	3'	TATTCACACCTTTCCATCCCTG 31643	A ACTC	
			CAG GA AAGGTGTGAATA		

			GTC CT TTCCACACTTAT		
			C ACCT		
GAM1538	TRAD	3'	CACTCCGTGCAGTTCTCTG	22951	_ A T
			CAGAGAACT CA GG GTG		
			GTCTCTTGA GT CC CAC		
			C G T		
GAM1538	TRIM22	3'	CATCTACAAGTTCTCTGGA	20286	CA_
			TCCAGAGAACT AGGTG		
			AGGTCTCTTGA TCTAC		
			ACA		
GAM1538	TUB	3'	ATTCAGAACTTCAAGTTCTCTT	12425	C CA G_
	GA		TC AGAGAACT AGGT TGAAT		
			AG TCTCTTGA TTCA ACTTA		
			T AC AG		
GAM1538	LOC120939	3'	CATCTCTCGAGTTCTTGGA	76250	G A GT
			TCCA AGAACTC AG GTG		
			AGGT TCTTGAG TC TAC		
			_ C TC		
GAM1538	LOC122258	3'	CACGCCACGTTCTCTG	59141	TCAA
			CAGAGAAC GGTGTG		
			GTCTCTTG CCGCAC		
			CAC_		
GAM1538	LOC124842	3'	CACCTTCCTGAGTTCTCAGGA	75658	A ____
			TCC GAGAACTCA AGGTG		
			AGG CTCTTGAGT TCCAC		
			A CCT		
GAM1538	LOC138050	5'	TCCATAATGAACTTCTCTGGA	75299	C_ AG T
			TCCAGAGAA TCA GTG GA		
			AGGTCTCTT AGT TAC CT		
			CA AA _		
GAM1538	LOC146839	5'	ATTCTCTTGAGTTTTCTAGA	83806	C TGT
			TC AGAGAACTCAAGG GAAT		
			AG TCTTTTGAGTTCT CTTA		
			A ____		
GAM1538	LOC150095	5'	CACACCTTCCCTCTCTG	84855	ACTC
			CAGAGA AAGGTGTG		
			GTCTCT TTCCACAC		
			CCC_		
GAM1538	LOC151094	3'	CACGCTTGTTCCCT	65293	A CA
			AG GAACT AGGTGTG		



	TC CTTGG TTCGCAC	
	C _	
GAM1538 LOC153603 3'	CATCTTCGAGCTCTCTGGA 80900	A _
	TCCAGAGA CTC AAGGTG	
	AGGTCTCT GAG TTCTAC	
	C C	
GAM1538 LOC153811 3'	ATTCACACAGCTCCCTGGG 80942	A A CAAG
	TCCAG GA CT GTGTGAAT	
	GGGTC CT GA CACACTTA	
	C C _	
GAM1538 LOC163341 3'	CATCTTGAGCCCCCTTGGA 82119	AGAA
	TCCAG CTCAAGGTG	
	AGGTT GAGTTCTAC	
	CCCC	
GAM1538 LOC199800 5'	CACCCAGTGAGGTCTCTGGA 89856	A A_ T
	TCCAGAGA CTCA GG GTG	
	AGGTCTCT GAGT CC CAC	
	G GA _	
GAM1538 LOC254439 3'	TTCACAGCTCTCTGGA 94749	ACTCAA G
	TCCAGAGA G TGTGAA	
	AGGTCTCT C ACACTT	
	_ G	
GAM1538 LOC255465 3'	GCCTTGAGTCTCTGGA 97289	A
	TCCAGAGA CTCAAGGT	
	AGGTCTCT GAGTTCCG	
	-	
GAM1538 LOC256207 3'	TATTTTCAAGTCTCTGGA 95176	ACTC
	TCCAGAGA AAGGTG	
	AGGTCTCT TTTTAT	
	GAAC	
GAM1538 LOC257354 3'	TACCCTGCACTCTCTGGA 95099	ACTCA T
	TCCAGAGA AGG GTG	
	AGGTCTCT TCC CAT	
	CACG_ _	
GAM1538 LOC91308 3'	TGTGCCTTAAGTTCTCT 65568	C TG
	AGAGAACT AAGG TG	
	TCTCTTGA TTCC GT	
	A GT	
GAM1538 LOC91695 5'	TATTCCAATCAAGTTCTCTG 66971	CAAGG T
	CAGAGAACT TG GAATA	

GTCTCTTGA AC CTTAT  
 ACTA\_ \_  
 GAM1538 LOC93259 5' TACAGCCTTGAGTTCCTTGGA 71826 A \_  
 TCCAG GAACTCAAGG TGTG  
 ||||| |||||  
 AGGTT CTTGAGTTCC ACAT  
 C G  
 GAM1539 ADAM20 5' TTTTCAGCACTGCAGCT 13770 CA  
 AGCTGC TGCTGAAGA  
 ||||| |||||  
 TCGACG ACGACTTTT  
 TC  
 GAM1539 DDEF2 3' ATGAACTGTTTGTATGGCAGC 13951 TGA\_ AAC  
 GCTGCCATGC AG TCAT  
 ||||| || |||||  
 CGACGGTATG TC AGTA  
 TTTG A\_  
 GAM1539 LIPA 3' ATGAGCTCTCAATTTTCATGGCA 4079 C\_ A A  
 G CTGCCATG TGA GA CTCAT  
 ||||| || |||||  
 GACGGTAC ACT CT GAGTA  
 TTTA \_ C  
 GAM1539 NFE2L1 3' AGCTCTCAGCCACAGGCAGCTT 12167 AT\_ A A  
 AAGCTGCC GCTGA GA CT  
 ||||| ||||| |||||  
 TTCGACGG C GACT CT GA  
 ACAC \_ C  
 GAM1539 NRCAM 3' TGAGTTCATTATGACAGT 17209 C CTGAA  
 GCTG CATG GAACTCA  
 ||||| |||||  
 TGAC GTAT CTTGAGT  
 A TA\_  
 GAM1539 PCLO 3' TTCCTCAGCATGGCAGCTT 94229 A  
 AAGCTGCCATGCTGA GAA  
 ||||| ||||| |||||  
 TTCGACGGTACGACT CTT  
 C  
 GAM1539 PLA2G2D 3' GTTCCTCAGCATGGAGCT 24800 G A  
 AGCT CCATGCTGA GAAC  
 ||||| ||||| |||||  
 TCGA GGTACGACT CTTG  
 \_ C  
 GAM1539 ARHGEF15 3' TCTAGGTCATGGCAGTT 30262 \_ GA  
 AGCTGCCATG CT AGA  
 ||||| || |||||  
 TTGACGGTAC GG TCT  
 T A\_  
 GAM1539 C21orf109 3' ATGAGCCTGAAGACTGCATGGC 57266 TGA\_ AA  
 A TGCCATGC AG CTCAT  
 ||||| || |||||

ACGGTACG TC GAGTA  
 TCAGAAG C\_  
 GAM1539 DKFZp434N074 5' GAGTCCCTTCCTGGAGC 62648 G TGCT A\_  
 GCT CCA GAAG ACTC  
 ||| ||| ||| |||  
 CGA GGT CTTC TGAG  
 \_ C\_\_ CC  
 GAM1539 DNAJA3 3' ATGAGTTCTTCCTGACAGGTT 60484 G C TGCT  
 AA CTG CA GAAGAACTCAT  
 || ||| || |||||  
 TT GAC GT CTTCTTGAGTA  
 G A C\_\_  
 GAM1539 FLJ10898 5' ATGAATTCTTCACTTCAGCAGC 59419 CATGC C  
 GCTGC TGAAGAA TCAT  
 |||| ||||| ||||  
 CGACG ACTTCTT AGTA  
 ACTTC A  
 GAM1539 FLJ13189 3' TTCTTCAGCATAATTGCT 45988 TGCC  
 AGC ATGCTGAAGAA  
 || |||||  
 TCG TACGACTTCTT  
 TTAA  
 GAM1539 KIAA0323 3' AGTTCTTTTGGCAACT 63256 C TGCT  
 AG TGCCA GAAGAACT  
 || |||| |||||  
 TC ACGGT TTTCTTGA  
 A \_\_\_\_  
 GAM1539 KIAA0376 5' TGAGTTCCTGAGGCAGTCC 65603 A ATGCTGAA  
 A GCTGCC GAACTCA  
 | |||| |||||  
 C TGACGG CTTGAGT  
 C AGTC\_\_  
 GAM1539 KIAA1613 3' ATGAATAGAAGCATGGCACTT 64813 C GAAGAAC  
 AAG TGCCATGCT TCAT  
 || ||||| |||  
 TTC ACGGTACGA AGTA  
 \_ AGATA\_\_  
 GAM1539 MAD4 3' ATGAGCTCTGCTGCGGCAGCTT 21269 AT TGA A  
 AAGCTGCC GC AGA CTCAT  
 ||||| || ||| ||||  
 TTCGACGG CG TCT GAGTA  
 \_ TCG C  
 GAM1539 NPD009 3' ATGAGTTCCTGAGACATGC 95045 C \_ GAA  
 GC ATG CT GAACTCAT  
 || ||| || |||||  
 CG TAC GA CTTGAGTA  
 \_ A GTC  
 GAM1539 PRO1584 3' ATGAGTTCCTGCAGGAGC 37724 G A TGAA  
 GCT CC TGC GAACTCAT  
 ||| || |||||

			CGA GG ACG CTTGAGTA		
			— — TC—		
GAM1539	ST7L	3'	TCCTCAGCATGAAGCT	57571	GC A
			AGCT CATGCTGA GA		
			TCGA GTACGACT CT		
			A_ C		
GAM1539	STK16	5'	GAGCTCTTCGGTAGC	72117	ATGCT A
			GCTGCC GAAGA CTC		
			CGATGG CTTCT GAG		
			_____ C		
GAM1539	LOC123242	5'	TCTTCCCACATGGCAGC	75603	CT_
			GCTGCCATG GAAGA		
			CGACGGTAC CTTCT		
			ACC		
GAM1539	LOC124599	3'	TCCTCAGCATGACAGCTT	75655	C A
			AAGCTG CATGCTGA GA		
			TTCGAC GTACGACT CT		
			A C		
GAM1539	LOC150383	3'	CTTCAGCAGGGCAGCT	79813	A
			AGCTGCC TGCTGAAG		
			TCGACGG ACGACTTC		
			G		
GAM1539	LOC157292	3'	GAGAGCTACATGGCAGC	86415	CTGA AA
			GCTGCCATG AG CTC		
			CGACGGTAC TC GAG		
			A_ GA		
GAM1539	LOC158235	3'	AGTCTGGGCATGGTAACT	86699	C GA A
			AG TGCCATGCT AGA CT		
			TC ATGGTACGG TCT GA		
			A G_ _		
GAM1539	LOC162333	5'	ATGGGAGCAGGATGGCAGC	87121	G AAGAA
			GCTGCCAT CTG CTCAT		
			CGACGGTA GAC GGGTA		
			G GA_		
GAM1539	LOC220394	5'	CTTCAGCAGGGCAGCTT	92822	A
			AAGCTGCC TGCTGAAG		
			TTCGACGG ACGACTTC		
			G		
GAM1539	LOC221463	3'	GAGATAGCAGCTTGGCAGCT	92071	T AAGAA
			AGCTGCCA GCTG CTC		

TCGACGGT CGAC GAG  
 T GATA\_  
 GAM1539 LOC221692 3' ATGAACCCTCTGACGGTGGCAG 92235 AT A\_ AC\_  
 CT AGCTGCC GCTG AGA TCAT  
 ||||| ||| || |||  
 TCGACGG TGGC TCT AGTA  
 \_ AG CCA  
 GAM1539 LOC253001 5' TCTTCCCACATGGCAGC 96260 CT\_  
 GCTGCCATG GAAGA  
 ||||| |||  
 CGACGGTAC CTTCT  
 ACC  
 GAM1539 LOC51312 3' ATGAGTTCCTGCAGGAGC 37713 G A TGAA  
 GCT CC TGC GAACTCAT  
 ||| ||| |||||  
 CGA GG ACG CTTGAGTA  
 \_ \_ TC\_  
 GAM1540 CLCN5 5' TGAAATACCTAAGCTGCTCCAA 3595 \_\_\_\_\_  
 TTGGAGCAG GTTTCA  
 ||||| |||  
 AACCTCGTC TAAAGT  
 GAATCCA  
 GAM1540 FLRT2 5' ATTGAAAAATGAGGTCTGC 25056 GT CTC  
 GCAG TTCATT CAAT  
 ||| ||||| |||  
 CGTC GAGTAA GTTA  
 TG AAA  
 GAM1540 IL17 3' TGGGGAAAATGAAACCCTCC 9333 CA \_  
 GGAG GGTTTCAT TCTCCA  
 ||| ||||| |||||  
 CCTC CCAAAGTA AGGGGT  
 \_ AA  
 GAM1540 NLGN1 5' TGAAGATGCTGCTCCAA 30026 G\_  
 TTGGAGCAG TTTCA  
 ||||| |||  
 AACCTCGTC GAAGT  
 GTA  
 GAM1540 POLG 3' GTGATAAACCTGCTCCAA 10682 \_  
 TTGGAGCAGGTT TCAT  
 ||||| |||  
 AACCTCGTCCAA AGTG  
 AT  
 GAM1540 TPK1 3' GGAGAACCTGTCCAA 42384 G TTCAT  
 TTGGA CAGGT TCTCC  
 ||| ||||| |||  
 AACCT GTCCA AGAGG  
 \_ \_  
 GAM1540 C1orf8 5' GAGAATGAAACCCTC 16832 CA  
 GAG GGTTTCATTCTC  
 ||| |||||

CTC CCAAAGTAAGAG

GAM1540 CLIC6 3' TGGAGAACATGTTCCAA 82536 G TTCAT  
 TTGGAGCA GT TCTCCA  
 ||||| || |||||  
 AACCTTGT CA AGAGGT  
 A \_\_\_\_\_

GAM1540 CLIPR-59 3' TGGAGAATTTCAATGCCCCGA 31374 A GGTTTC  
 TTGG GCA ATTCTCCA  
 ||| ||| |||||  
 AGCC CGT TAAGAGGT  
 C AACTT\_

GAM1540 DKFZP547L112 3' TGGAGAACTCTTGCTCCA 66532 TTTCA  
 TGGAGCAGG TTCTCCA  
 ||||| |||||  
 ACCTCGTTC AAGAGGT  
 TC\_\_\_\_\_

GAM1540 EPS8R3 5' GGACCACCTGCTCCAA 55701 TTCATTC  
 TTGGAGCAGGT TCC  
 ||||| |||  
 AACCTCGTCCA AGG  
 CC\_\_\_\_\_

GAM1540 EPS8R3 5' GGACCACCTGCTCCAA 57404 TTCATTC  
 TTGGAGCAGGT TCC  
 ||||| |||  
 AACCTCGTCCA AGG  
 CC\_\_\_\_\_

GAM1540 FLJ20552 3' AGAACAAAAGTCTGCTCCAA 35389 G CA  
 TTGGAGCAG TTT TTCT  
 ||||| ||| |||  
 AACCTCGTC AAA AAGA  
 \_ AC

GAM1540 FLJ22865 5' TGGAGAAAAGTCTCTAA 47071 GTTTCA  
 TTGGAGCAG TTCTCCA  
 ||||| |||||  
 AATCTCGTC AAGAGGT  
 AA\_\_\_\_\_

GAM1540 KIAA0372 5' ATTGAAATTTGTTACCTACTCC 27663 C TT TTCTC  
 AA TTGGAG AGGT CA CAAT  
 ||||| ||| ||| |||  
 AACCTC TCCA GT GTTA  
 A TT TAAA

GAM1540 PRO0132 5' ATGAAACCACTCCAA 26101 CA  
 TTGGAG GGTTTCAT  
 ||||| |||||  
 AACCTC CCAAAGTA  
 A\_

GAM1540 TEX27 3' AGAGTGGAACCCGCTGCAA 41658 G A  
 TTG AGC GGTTTCATTCT  
 ||| ||| ||||| |||||

AAC TCG CCAAGGTGAGA  
 G C  
 GAM1540 LOC149373 3' ATTGGGGTGATGATACCCACCC 79312 AGCA T \_  
 CAA TTGG GGT TCATT CTCCAAT  
 |||| ||| |||| |||||  
 AACC CCA AGTAG GGGGTTA  
 CCAC T T  
 GAM1540 LOC152687 3' TTGGAGAATATTGCTCC 80643 GTTTC  
 GGAGCAG ATTCTCCAA  
 ||||| |||||  
 CCTCGTT TAAGAGGTT  
 A\_\_\_\_  
 GAM1540 LOC51202 3' ATTGGAGAATGAAACCTGCTCC 33017  
 AA TTGGAGCAGGTTTCATTCTCCAAT  
 ||||| |||||  
 AACCTCGTCCAAAGTAAGAGGTTA  
  
 GAM1541 CARPX 3' CACACACACAAGCACTTG 39417 GACTCCA  
 CAAGTGCTTG TGTG  
 ||||| |||  
 GTTCACGAAC ACAC  
 ACAC\_\_\_\_  
 GAM1541 C20orf112 3' AGCCCACTCCAAGCACCTGA 54639 A CTCCA \_  
 TCA GTGCTTGGA TGTG CT  
 || ||||| ||| ||  
 AGT CACGAACCT ACAC GA  
 C C\_\_\_\_ C  
 GAM1541 DNAJC8 3' AGCACACAGAGCAGCATCTGA 26558 AG TGGA CA  
 TCA TGCT CTC TGTGCT  
 || ||| || |||||  
 AGT ACGA GAG ACACGA  
 CT C\_\_\_\_ AC  
 GAM1541 GGA2 3' GGCTTTGAAGTCCAAGCAGCTG 30476 AG C TGT  
 A TCA TGCTTGGA CT CA GCT  
 || ||||| || |||  
 AGT ACGAACCTGA GT CGG  
 CG A TT\_  
 GAM1541 GGA2 3' GGCTTTGAAGTCCAAGCAGCTG 56890 AG C TGT  
 A TCA TGCTTGGA CT CA GCT  
 || ||||| || |||  
 AGT ACGAACCTGA GT CGG  
 CG A TT\_  
 GAM1541 KIAA0976 3' AGTATGAATCCAAGCAATTGA 29886 G C CAT  
 TCAA TGCTTGGA TC GTGCT  
 ||| ||||| || ||||  
 AGTT ACGAACCT AG TATGA  
 A A \_\_\_\_  
 GAM1541 MGC5590 3' ATGAAGCCCAAGAACCTGA 43924 A G A C  
 TCA GT CTTGG CT CAT  
 ||| || |||| || |||

			AGT CA GAACC GA GTA		
			C A C A		
GAM1541	NUDE1	3'	CACATGGGCTAGTACTTGA 34567	T A T	
			TCAAGTGCT GG C CCATGTG		
			AGTTCATGA TC G GGTACAC		
			— — —		
GAM1541	RNF40	3'	GGAGCCCAGAGCACTTGA 28716	_ A	
			TCAAGTGCT TGG CTCC		
			AGTTCACGA ACC GAGG		
			G C		
GAM1541	TRIM2	3'	CACATGCTATGAGCACTCGA 30940	A	GACTC
			TC AGTGCTTG CATGTG		
			AG TCACGAGT GTACAC		
			C ATC_		
GAM1541	LOC154092	3'	ACAATAGTCTAAGCACTT 86158		CCA
			AAGTGCTTGGACT TGT		
			TTCACGAATCTGA ACA		
			TA_		
GAM1541	LOC164955	3'	GCCAAATCCAAGAACTT 82459	G	CTCCA T
			AAGT CTTGGA TG GC		
			TTCA GAACCT AC CG		
			A AA_ _		
GAM1541	LOC89958	3'	CGCCTGGAATCCCAGCACTTGA 60920		T C T
			TCAAGTGCT GGA TCCA GTG		
			AGTTCACGA CCT AGGT CGC		
			C A C		
GAM1542	TNFAIP1	3'	CATCAGCTGAGGACAGCAAACCT 40917	AG	G
	CC		GGA TTGCTG CTTCAGCTGATG		
			CCT AACGAC GGAGTCGACTAC		
			CA A		
GAM1542	C1orf2	3'	CAGCTGGTTGGGACCAGCAGCC 21681	AA	_ _
	CCC		GG GTTGCTGG CT TCAGCTG		
			CC CGACGACC GG GGTCGAC		
			CC A GTT		
GAM1542	C1orf2	3'	CAGCTGGTTGGGACCAGCAGCC 94622	AA	_ _
	CCC		GG GTTGCTGG CT TCAGCTG		
			CC CGACGACC GG GGTCGAC		
			CC A GTT		
GAM1542	C20orf59	3'	CATCCCTAGCCAGCAGCTCC 41992	A	TC CT
			GGA GTTGCTGGCT AG GATG		



CCT CGACGACCGA TC CTAC  
 \_ \_ C\_  
 GAM1542 FLJ20079 3' CATTCTGGTAAACCAGCAGCCT 34490 A CT\_\_ CT  
 CC GGA GTTGCTGG TCAG GATG  
 ||| ||||| ||| |||  
 CCT CGACGACC GGTC TTAC  
 C AAAT \_  
 GAM1542 SSAT2 3' CATCAGCTGAAGCACTCTTC 56041 TTGCTG  
 GAAG GCTTCAGCTGATG  
 ||| |||||  
 CTTC CGAAGTCGACTAC  
 TCA\_\_  
 GAM1542 SYNJ2 3' ATCAGCTTAAGCAATTCC 61763 GTTGCTG C  
 GGAA GCTT AGCTGAT  
 ||| ||| |||||  
 CCTT CGAA TCGACTA  
 AA\_\_\_\_\_ T  
 GAM1542 LOC162333 5' CTGAAGCCAGCAATTCC 87131 G  
 GGAA TTGCTGGCTTCAG  
 ||| |||||  
 CCTT AACGACCGAAGTC  
 \_  
 GAM1542 LOC222060 5' CACCTCCCACCAGCAACCCCC 94104 AA CTTC C  
 GG GTTGCTGG AG TG  
 || ||||| |||  
 CC CAACGACC TC AC  
 CC ACCC C  
 GAM1542 LOC255650 3' CATCAGCCCCAGGCAACTTCC 96711 \_ CTTCA  
 GGAAGTTGC TGG GCTGATG  
 ||||| ||| |||||  
 CCTTCAACG ACC CGACTAC  
 G C\_\_  
 GAM1543 CARPX 3' CTGTCAAGAAATCAATAAATGT 39421 TGT\_\_  
 G CAC TTGATTCTTGACAG  
 ||| |||||  
 GTG AACTAAAGAACTGTC  
 TAAAT  
 GAM1543 ELK4 3' TTATAAAACAAACAGTGAT 41419 A CT  
 ATCACTGTTTG TTT TGA  
 ||||| ||| |||  
 TAGTGACAAAC AAA ATT  
 \_ AT  
 GAM1543 KCNK6 3' TGTCCCCAGACAGTGATG 16698 ATTTCTT  
 CATCACTGTTTG GACA  
 ||||| |||  
 GTAGTGACAGAC CTGT  
 CC\_\_\_\_\_  
 GAM1543 LRAT 3' CTGTCAAGAATCACAAA 60104 AT\_  
 TTTG TTCTTGACAG  
 ||| |||||

			AAAC AAGAACTGTC		
			ACT		
GAM1543	MAN2A2	3'	CTGTTTCAGAAACCAACAGTGA	20396	T A T_
		TG	CATCACTGTT G TTTCT GACAG		
			GTAGTGACAA C AAAGA TTGTC		
			_C CT		
GAM1543	PCP4	3'	CTGTCAAGAAATTAAAAG	20572	G
			CT TTTGATTTCTTGACAG		
			GA AAATTAAAGAACTGTC		
			—		
GAM1543	PHTF1	3'	TCAAGGAAAGTGATG	21732	GTTTGA
			CATCACT TTTCTTGA		
			GTAGTGA AAGGAACT		
			—————		
GAM1543	XPR1	3'	CTGTCAAGAAACAGCAGT	16426	T A
			ACTGTT G TTTCTTGACAG		
			TGACGA C AAAGAACTGTC		
			— —		
GAM1543	C9orf5	3'	AAATTAGCAGCAGTGATG	49271	—
			CATCACTGTT TGATTT		
			GTAGTGACGA ATTAAA		
			CG		
GAM1543	FHX	3'	TCAAGGGTGAAAGTGATG	37306	GTTTGAT
			CATCACT TTCTTGA		
			GTAGTGA GGGAAC		
			AAGT—		
GAM1543	FLJ12643	3'	GTCAAGAAAGAAAATA	82786	GA
			TGTTT TTTCTTGAC		
			ATAAA AAAGAACTG		
			AG		
GAM1543	FLJ13031	5'	TCAAAAAACGAAACAGTGAT	45198	_ A C
			ATCACTGTTT G TTT TTGA		
			TAGTGACAAA C AAA AACT		
			G A A		
GAM1543	FLJ22833	3'	AGTAATCAAACAGTGATG	43098	T
			CATCACTGTTTGATT CT		
			GTAGTGACAAACTAA GA		
			T		
GAM1543	KIAA1559	3'	GTCAAGAAAAAGGAAACA	73072	GA_
			TGTTT TTTCTTGAC		

ACAA AAAGAACTG  
 GGAA  
 GAM1543 KIAA1958 3' AAGAAACCAACATGAT 81896 C A  
 ATCA TGTTTG TTTCTT  
 ||| ||||| |||||  
 TAGT ACAAAC AAAGAA  
 \_ C  
 GAM1543 LOC149711 5' CTGCCAAAAAATGAGATAGTG 84680 G C A  
 CACTGTTT ATTT TTG CAG  
 ||||| ||| ||| |||  
 GTGATAGA TAAA AAC GTC  
 G A C  
 GAM1543 LOC201799 3' CTGCCAAGAAGACACAGTGA 89060 TT A A  
 TCACTGT G TTTCTTG CAG  
 ||||| | ||||| |||  
 AGTGACA C GAAGAAC GTC  
 \_ A C  
 GAM1543 LOC253263 3' CTGCCATCCCCCAAACAGTGA 97031 ATTTCT A  
 TCACTGTTTG TG CAG  
 ||||| || |||  
 AGTGACAAAC AC GTC  
 CCCCT\_ C  
 GAM1543 LOC56959 5' TGTCTATCAAACAGTG 81928 TTCTT  
 CACTGTTTGAT GACA  
 ||||| |||  
 GTGACAAACTA CTGT  
 T\_\_\_\_  
 GAM1544 AQP3 3' TTCACGATCCACCCTTTC 59593 T\_ \_  
 GAAA GTGG TCGTGAA  
 ||| ||| |||||  
 CTTT CACC AGCACTT  
 CC T  
 GAM1544 ARSB 3' TCACGACTCTTGTC 3502 AATGTG  
 GACAAGA GTCGTGA  
 ||||| |||||  
 CTGTTCT CAGCACT  
 \_\_\_\_\_  
 GAM1544 B4GALT5 3' TTTTCACAAAAATAGTCCTTTG 16519 AAA\_ GGTC  
 TCA TGACAAG TGT GTGAAAA  
 ||||| || |||||  
 ACTGTTT ATA CACTTTT  
 CCTG AAAA  
 GAM1544 CHRNA3 3' TCGTTACCCATTTCTT 5610 T CG  
 AAGAAATG GGT TGA  
 ||||| ||| |||  
 TTCTTTAC CCA GCT  
 \_ TT  
 GAM1544 DRD1 3' TTACAACCACATTTCTGGCCA 5840 ACA C  
 TG AGAAATGTGGT GTGA  
 || ||||| ||||| |||

AC TCTTTACACCA CATT  
 CGG A  
 GAM1544 FUT1 3' TCTGATCACATCCCCTGTC 3798 AGAA T  
 GACA ATGTGGTTCG GA  
 ||| ||||| ||  
 CTGT TACACTAGT CT  
 CCCC \_  
 GAM1544 IRF1 3' GCCACATTTCTGATCA 64345 CA  
 TGA AGAAATGTGGT  
 || |||||  
 ACT TCTTTACACCG  
 AG  
 GAM1544 MAP3K8 5' TCACGACCACCTCATG 17791 A AAT  
 CA GA GTGGTTCGTGA  
 || || |||||  
 GT CT CACCAGCACT  
 A C\_  
 GAM1544 NGFR 3' TTCTGACCACACTTCCTGTC 10231 A A T  
 GACA GAA TGTGGTCG GAA  
 ||| || ||||| ||  
 CTGT CTT ACACCAGT CTT  
 C C \_  
 GAM1544 OLR1 3' TTCACAACAGTTCTTGTTA 10341 ATGTG C  
 TGACAAGAA GT GTGAA  
 ||||| || ||||  
 ATTGTTCTT CA CACTT  
 GA\_\_ A  
 GAM1544 POU4F1 3' CACTGAAAACATTTTTGTCA 20660 A GG \_  
 TGACAAGAA TGT TC GTG  
 ||||| || || ||  
 ACTGTTTTT ACA AG CAC  
 \_ AA T  
 GAM1544 SMP1 3' TTTCACATGAATAATTTTTGTC 26705 A GGTC  
 A TGACAAGAA TGT GTGAAA  
 ||||| || ||||  
 ACTGTTTTT ATA CACTTT  
 A AGTA  
 GAM1544 ZNF264 3' TTCTATTAACATTTCTTTTCA 12769 C GGTCGT  
 TGA AAGAAATGT GAA  
 || ||||| ||  
 ACT TTCTTTACA CTT  
 T ATTAT\_  
 GAM1544 C20orf175 3' CGAGCTCCACGTTTCCTGCCA 55063 A A \_  
 TG CA GAAATGTGG TCG  
 || || ||||| ||  
 AC GT CTTTGCACC AGC  
 C C TCG  
 GAM1544 CAPNS2 3' TTTCACAACCCTACATATTCT 50323 CA \_ C  
 GATCA TGA AGAAATGT GGT GTGAAA  
 || ||||| || |||||

ACT TCTTTATA CCA CACTTT  
 AG CATC A  
 GAM1544 CLDN6 3' TTTACACTCACATTTTATCA 41041 CA \_ C  
 TGA AGAAATGTG GT GTGAA  
 ||| ||||| || |||||  
 ACT TTTTACAC CA CATT  
 A\_ T\_  
 GAM1544 DKFZP564L0864 3' GCACCAATTTCTTGCCA 72555 A G C  
 TG CAAGAAAT TGGT GT  
 || ||||| ||| ||  
 AC GTTCTTTA ACCA CG  
 C \_ \_  
 GAM1544 DKFZP566B183 3' TTTCCATAAACATTTCTTTTCA 31330 C GGTCGT  
 TGA AAGAAATGT GAAA  
 ||| ||||| |||  
 ACT TTCTTTACA CTTT  
 T AATAC\_  
 GAM1544 GTF2E1 3' TACAGACCTCTTGTCA 18616 AATGT \_  
 TGACAAGA GGTC GTG  
 ||||| ||| |||  
 ACTGTTCT CCAG CAT  
 \_ A  
 GAM1544 KIAA0089 3' TTTTAATTCACATTTCTT 69967 TCG  
 AAGAAATGTGG TGAAA  
 ||||| |||  
 TTCTTTACACT ATTT  
 TA\_  
 GAM1544 KIAA0373 5' TTTTCAAAGTAACATTTCTT 28015 GGTCG  
 AAGAAATGT TGAAAA  
 ||||| |||  
 TTCTTTACA ACTTTT  
 ATGAA  
 GAM1544 KIAA1813 3' TTTTCACACTGTAAATTTCTTG 70314 \_ TG C  
 T ACAAGAAAT G GT GTGAAAA  
 ||||| | |||||  
 TGTTCTTTA T CA CACTTTT  
 AA GT \_  
 GAM1544 KIAA1951 3' TTCCAGGCTTCTCTTGTC 73766 AATGT GT  
 TGACAAGA GGTC GAA  
 ||||| ||| |||  
 ACTGTTCT TCGG CTT  
 CT\_ AC  
 GAM1544 MGC4170 3' TTCACCATTTCTTGTC 44227 TGGTC  
 GACAAGAAATG GTGAA  
 ||||| |||  
 CTGTTCTTTAC CACTT  
 \_  
 GAM1544 NRN1 3' CACTGCACATTTCTCCTCA 33432 CA GTC  
 TGA AGAAATGTG GTG  
 ||| ||||| |||

ACT TCTTTACAC CAC  
 CC GT\_  
 GAM1544 PLA2G12 3' TTTTCACAACCACATTT 48028 C  
 AAATGTGGT GTGAAAA  
 ||||| |||||  
 TTTACACCA CACTTTT  
 A  
 GAM1544 PPY2 3' CACTCCACATTCCTGGCCA 40819 ACA A TC  
 TG AG AATGTGG GTG  
 || ||||| |||  
 AC TC TTACACC CAC  
 CGG C T\_  
 GAM1544 ZNF31 3' TTTGTAGACCACATTTCTGT 64992 A \_TG  
 A TGACA GAAATGTGGTC G AA  
 |||| ||||| |||  
 ATTGT CTTTACACCAG T TT  
 C A GT  
 GAM1544 LOC115219 3' CACGACAACGGGTCCTCA 73295 CAA AA G  
 TGA GA TGT GTCGTG  
 ||| || |||||  
 ACT CT GCA CAGCAC  
 C\_ GG A  
 GAM1544 LOC120376 5' TTCAGAGCATTTCTTTCA 75986 C GG G  
 TGA AAGAAATGT TC TGAA  
 ||| ||||| || ||||  
 ACT TTCTTTACG AG ACTT  
 - - -  
 GAM1544 LOC133418 3' TTTTCATATACATTTTGTGCCA 75094 A GTC  
 TG CAAGAAATGTG GTGAAA  
 || ||||| |||||  
 AC GTTTTACAT TACTTT  
 C A\_  
 GAM1544 LOC151199 3' TTAAAACCACAGCTCTTGCCA 80174 A AA CG  
 TG CAAGA TGTGGT TGA  
 || |||| ||||| |||  
 AC GTTCT ACACCA ATT  
 C CG AA  
 GAM1544 LOC152317 5' TCACACTGACTTTTGTCA 85649 AATG C  
 TGACAAGA TGGT GTGA  
 ||||| |||||  
 ACTGTTTT GTCA CACT  
 CA\_ \_  
 GAM1544 LOC152674 3' TTCAACCCACCCTCTTGTC 85841 AAT TCG  
 TGACAAGA GTGG TGAA  
 ||||| ||| ||||  
 ACTGTTCT CACC ACTT  
 CC\_ CA\_  
 GAM1544 LOC152845 5' CATGACCACATTTTCA 60330 CAA  
 TGA GAAATGTGGTCGTG  
 ||| |||||

ACT TTTTACACCAGTAC

GAM1544 LOC154743 3' TTTAGTCCACATTGTCTTGTCA 81118 \_ TCG  
TGACAAGA AATGTGG TGAA  
||||| ||||| |||  
ACTGTTCT TTACACC ATTT  
G TG\_  
GAM1544 LOC165476 5' TTCACGGCACCTTCT 87201 AT G  
AGAA GTG TCGTGAA  
||| ||| |||||  
TCTT CAC GGCACCT  
C \_  
GAM1544 LOC254266 5' TTTTCGGTCACACATCTTATCA 97356 C AA GT T  
TGA AAGA TGTG CG GAA  
||| ||| ||| |||  
ACT TTCT ACAC GC TTT  
A AC TG T  
GAM1544 LOC255919 3' TTTCATTCTTACATTTCTAATC 95043 CA TC  
A TGA AGAAATGTGG GTGAAA  
||| ||||| |||||  
ACT TCTTTACATT TACTTT  
AA CT  
GAM1544 LOC51754 5' CACGGCCACATCTCTGTCA 71027 A A  
TGACA GA ATGTGGTCGTG  
||||| ||| |||||  
ACTGT CT TACACCGGCAC  
\_ C  
GAM1544 LOC55862 3' ACCTCATTTCTTGCCA 37485 A T  
TG CAAGAAATG GGT  
||| ||||| |||  
AC GTTCTTTAC CCA  
C T  
GAM1544 LOC55954 3' CACGTGGTCACTTTTCTCATCA 38877 CA T GT \_  
TGA AGAAA GTG C GTG  
||| ||||| ||| | |||  
ACT TCTTT CAC G CAC  
AC T TG TG  
GAM1545 B3GNT3 3' CCCACCTGGTACTGTT 26517 TACTAA A  
AACAGTATC AG TGGG  
||||| ||| |||  
TTGTCATGG TC ACCC  
\_ C  
GAM1545 CSPG3 3' AGCCCATTTGACTTAGAACTGT 15227 A CTAAA  
T AACAGT TCTA GATGGGCT  
||||| ||| |||||  
TTGTCA AGAT TTACCCGA  
A TCAG\_  
GAM1545 EVA1 3' AGCCCATCTCTAATGAGGACT 58572 A AC\_ A  
AGT TCT TA AGATGGGCT  
||| ||| ||| |||||

			TCA GGA AT TCTACCCGA		
			_ GTA C		
GAM1545 ID4	3'	CTTTAATAGATACTGT	7754	C	
		ACAGTATCTA TAAAG			
		TGTCATAGAT ATTTC			
		A			
GAM1545 RAD51C	3'	TTTAGAGATACTGTT	54255	A	
		AACAGTATCT CTAAA			
		TTGTCATAGA GATTT			
		-			
GAM1545 RHO	3'	AGCCCATCTTCAGCAGTTGCT	5018	T A A	
		AGTA CT CT AAGATGGGCT			
		TCGT GA GA TTCTACCCGA			
		T C C			
GAM1545 STAR	3'	CTCATTAGTAGACATGTT	4445	GTA AAG	
		AACA TCTACTA ATGGG			
		TTGT AGATGAT TACTC			
		AC_ _			
GAM1545 CD109	3'	AGTGGTCTCAGTAGATACT	56046	AA GG	
		AGTATCTACT AGAT GCT			
		TCATAGATGA TCTG TGA			
		C_ G_			
GAM1545 FLJ00024	3'	AGCCCATCCCTGGGACCTGC	63747	TCTA AA	
		GTA CTA GATGGGCT			
		CGT GGT CTACCCGA			
		CCAG CC			
GAM1545 FLJ20666	3'	GCTTACCACAGATACTGTT	37089	ACTAAAGA	
		AACAGTATCT TGGGC			
		TTGTCATAGA ATTCG			
		CACC_			
GAM1545 FLJ20666	3'	GCTTACCACAGATACTGTT	35510	ACTAAAGA	
		AACAGTATCT TGGGC			
		TTGTCATAGA ATTCG			
		CACC_			
GAM1545 FLJ22969	3'	GGCTCAGCAGATGCTGT	68657	ACTAAAGA	
		ACAGTATCT TGGGCT			
		TGTCGTAGA ACTCGG			
		CG_			
GAM1545 GGTLA1	5'	AGCCCATCTCTGTCCCATTGT	14657	ATCT TAA	
		ACAGT AC AGATGGGCT			



			TGTTA TG TCTACCCGA		
			CCC_ TC_		
GAM1545	KIAA0240	3'	TTTAGTAGATTCTGTT 92443	T	
			AACAG ATCTACTAAA		
			TTGTC TAGATGATTT		
			T		
GAM1545	KIAA1028	3'	TTTATTAGATACTGTT 91952	C	
			AACAGTATCTA TAAA		
			TTGTCATAGAT ATTT		
			T		
GAM1545	KIAA1332	3'	CATCAAAAGATACTGTT 71163	ACTAAA	
			AACAGTATCT GATG		
			TTGTCATAGA CTAC		
			AAA_		
GAM1545	KIAA1497	3'	ATCTTTAGTAGACACT 67503	A	
			AGT TCTACTAAAGAT		
			TCA AGATGATTTCTA		
			C		
GAM1545	KIAA1858	3'	AGCCCATCTCTAGCACACCTTG 67133	TATCTA A	
			CAG CTA AGATGGGCT		
			GTT GAT TCTACCCGA		
			CCACAC C		
GAM1545	p25	3'	GCCCATCCAGGACACTCC 22851	C A ACTAAA	
			A AGT TCT GATGGGC		
			C TCA AGG CTACCCG		
			C C AC_		
GAM1545	PME-1	3'	AGCCCATCTTTTCTGTGACTGT 32351	ATCTACT	
			ACAGT AAAGATGGGCT		
			TGTCA TTTCTACCCGA		
			GTGTCT_		
GAM1545	PRO0628	3'	AGCCCATCTTCTGTACTGCT 26205	TC TA	
			AGTA TAC AAGATGGGCT		
			TCGT ATG TTCTACCCGA		
			C_ TC		
GAM1545	LOC122728	3'	AGCCCATCTGCTGTATTACTG 74150	TC TAA	
			CAGTA TAC AGATGGGCT		
			GTCAT ATG TCTACCCGA		
			T_ TCG		
GAM1545	LOC130507	3'	ATCTCTAGTAAATACTGTT 74948	C A	
			AACAGTAT TACTA AGAT		

	TTGTCATA ATGAT TCTA	
	A C	
GAM1545 LOC144110 3'	AGCCTGGGGCAGCAGGTA	A AAAGA
	CTG 76672	
	CAGTATCT CT TGGGCT	
	GTCATGGA GA GTCCGA	
	C CGGG_	
GAM1545 LOC145368 3'	AGCCCATCTGCTGTATTACTG 77092	TC TAA
	CAGTA TAC AGATGGGCT	
	GTCAT ATG TCTACCCGA	
	T_ TCG	
GAM1545 LOC149830 3'	CCCATCTCTAAGGCAGGATGCT 84724	A__ AA_
G	CAGTATCT CT AGATGGG	
	GTCGTAGG GA TCTACCC	
	ACG ATC	
GAM1545 LOC150236 5'	AGCCCATCCCCCAGTTCACT 79680	ATCT AAA_
	AGT ACT GATGGGCT	
	TCA TGA CTACCCGA	
	CT__ CCCC	
GAM1545 LOC150279 3'	CCCATGAGGCTCAGATGCTGTT 79667	ACTAAAG
	AACAGTATCT ATGGG	
	TTGTCGTAGA TACCC	
	CTCGGAG	
GAM1545 LOC150423 3'	AGCCCATCTCCTGTATTACTG 79863	TC TAA
	CAGTA TAC AGATGGGCT	
	GTCAT ATG TCTACCCGA	
	T_ TCC	
GAM1545 LOC151405 5'	AGATGGGCTTTAGTAAAGACTG 85334	ATC ATGGG
T	ACAGT TACTAAAG CT	
	TGTCA ATGATTTC GA	
	GAA GGGTA	
GAM1545 LOC151473 3'	AGCCCATCTCTAGACTCTCGT 80250	_ TA CTA
	AC AG TCTA AGATGGGCT	
	TG TC AGAT TCTACCCGA	
	C TC C__	
GAM1545 LOC153196 5'	AGCCCATCCTTGGGACCCTACT 85953	TCTA_ A
	AGTA CTAAGATGGGCT	
	TCAT GGTT CTACCCGA	
	CCCAG C	
GAM1545 LOC221002 3'	AGCCCATTCAGATAAAACTG 91475	__ ACTAAA
	CAGT ATCT GATGGGCT	

GTCA TAGA TTACCCGA  
 AAA C\_\_\_\_  
 GAM1545 LOC255290 5' AGCCCATCTCTGTCCCATTGT 95607 ATCT TAA  
 ACAGT AC AGATGGGCT  
 |||| | |||||  
 TGTTA TG TCTACCCGA  
 CCC\_ TC\_  
 GAM1545 LOC91907 3' ATCTTTAGTAGACACT 67493 A  
 AGT TCTACTAAAGAT  
 || |||||  
 TCA AGATGATTTCTA  
 C  
 GAM1546 B4GALT1 3' CAAGAGTCAGAACTGTAGA 7666 GTCAA TG  
 TCTACAGT TG TCTTG  
 ||||| || ||||  
 AGATGTCA AC AGAAC  
 AG\_\_ TG  
 GAM1546 DGKA 3' CAAAACACATACATTG 7201 CA C  
 CAGTGT ATGTGT TTG  
 |||| |||| |  
 GTTACA TACACA AAC  
 \_ A  
 GAM1546 MTMR6 3' CTCAAAACACAATTTGCACTGT 93549 C \_ C  
 A TACAGTGT AAT GTGT TTGAG  
 ||||| || || ||||  
 ATGTCACG TTA CACA AACTC  
 T A A  
 GAM1546 SLC4A4 3' CTCAAGACACAGACACCCACAG 13635 ACA\_ AA  
 A TCT GTGTC TGTGTCTTGAG  
 || |||| |||||  
 AGA CACAG ACACAGAACTC  
 CACC \_  
 GAM1546 CUL4A 3' CTCAAGACTTCAACCTGCAGA 13153 A T CAA T\_  
 TCT CAG GT TG GTCTTGAG  
 || || || || |||||  
 AGA GTC CA AC CAGAACTC  
 C \_ \_ TT  
 GAM1546 FLJ11301 3' CAAGACACTAGCACTGTAGA 37226 CAAT  
 TCTACAGTGT GTGTCTTG  
 ||||| |||||  
 AGATGTCACG CACAGAAC  
 AT\_  
 GAM1546 GPR105 3' GACACACCCACACCGTAGA 29655 A CAA  
 TCTAC GTGT TGTGTC  
 |||| || ||||  
 AGATG CACA ACACAG  
 C CCC  
 GAM1546 LAP1B 5' CTCAAGACACACCATGGGC 64584 AA\_  
 GTC TGTGTCTTGAG  
 || |||||

			CGG ACACAGAACTC		
			GTACC		
GAM1546	PRDM10	3'	CTCAAGACACATTGACACTGTA	39578	
	GA		TCTACAGTGTCAATGTGTCTTGAG		
			AGATGTCACAGTTACACAGAACTC		
GAM1546	SEMA3C	3'	CTCTTCTACATTGACAC	21061	TCTT
			GTGTCAATGTG	GAG	
			CACAGTTACAT	CTC	
			CTT_		
GAM1546	LOC255654	3'	GACATCCACACTGTAGA	96887	CAAT
			TCTACAGTGT	GTGTC	
			AGATGTCACA	TACAG	
			CC_		
GAM1546	LOC96652	3'	CTCAAGACAGGACACTGCGGA	65467	TA AATG
			TC CAGTGTC	TGTCTTGAG	
			AG GTCACAG	ACAGAACTC	
			GC	G_	
GAM1547	SLC17A4	3'	CAACAGTTCTTCATGTAGC	18525	CAGT
			GCTGC	TGAAGAACTGTTG	
			CGATG	ACTTCTTGACAAC	
			T_		
GAM1547	CITED1	5'	CAACAGCTCCAGCTGGCAGC	14729	AA A
			GCTGCCAGTTG	GA CTGTTG	
			CGACGGTCGAC	CT GACAAC	
			_ C		
GAM1547	FLJ10900	5'	CAACAGTTCTTGCTGAAGCAGT	65590	_ TG
	T		AGCTGC	CAGT AAGAACTGTTG	
			TTGACG	GTCG TTCTTGACAAC	
			AA	_	
GAM1547	HS6ST	3'	CAACAGTTCCTTTGCCAGCAGC	62025	CA T A
			GCTGC	GT GA GAACTGTTG	
			CGACG	CG TT CTTGACAAC	
			AC	T C	
GAM1547	MGC4638	3'	CAACAGTTCTTCAAGTG	48939	G
			CA TTGAAGAACTGTTG		
			GT AACTTCTTGACAAC		
			G		
GAM1547	ZNF262	3'	TTCCCCAATGGCAGCTT	17492	G AA
			AAGCTGCCA	TTG GAA	

	TTCGACGGT AAC CTT	
	_ CC	
GAM1547 LOC115051 3'	CAACAGTTCCTTTGCCAGCAGC 60036	CA T A
	GCTGC GT GA GAACTGTTG	
	CGACG CG TT CTTGACAAC	
	AC T C	
GAM1547 LOC143153 3'	CAGCCTCAAGCTGGCAGC 76463	GA AA
	GCTGCCAGTT AG CTG	
	CGACGGTCGA TC GAC	
	AC C_	
GAM1547 LOC168512 5'	CAACAGCCTCTCTGGCAGCTT 82714	TTGA A_
	AAGCTGCCAG AGA CTGTTG	
	TTCGACGGTC TCT GACAAC	
	_____ CC	
GAM1547 LOC199923 3'	AACAGTTCCAGACCAGC 88494	CCA GAA
	GCTG GTT GAACTGTT	
	CGAC CAG CTTGACAA	
	_____ AC_	
GAM1547 LOC199926 3'	TAGTCCTTCAACTCACAGCTT 89880	CC A
	AAGCTG AGTTGAAG ACTG	
	TTCGAC TCAACTTC TGAT	
	AC C	
GAM1547 LOC202316 3'	TAGTCCTTCAACTCACAGCTT 90340	CC A
	AAGCTG AGTTGAAG ACTG	
	TTCGAC TCAACTTC TGAT	
	AC C	
GAM1547 LOC221479 3'	CAACAACACTACAGCAGCAGC 92222	CA A AAC
	GCTGC GTTG AG TGTTG	
	CGACG CGAC TC ACAAC	
	A_ A A_	
GAM1548 ABCG1 3'	CCTAGAACCGCGTTGGGTT 16982	TAGATCA
	AACCCG GTTCTAGG	
	TTGGGT CAAGATCC	
	TGCGC_	
GAM1548 ADORA2A 3'	CCTAGACTCTCCTAGGGTT 5433	G ATC T
	AACCC TAG AGT CTAGG	
	TTGGG ATC TCA GATCC	
	_ CTC _	
GAM1548 AIM1 3'	CCCAGGCTGATCTCG 91819	T T A
	CG AGATCAGT CT GG	

GC TCTAGTCG GA CC  
 \_ \_ C  
 GAM1548 B4GALT5 3' CCCAGGCTGGTCTCG 16495 T T A  
 CG AGATCAGT CT GG  
 || ||||| || ||  
 GC TCTGGTCG GA CC  
 \_ \_ C  
 GAM1548 CBFA2T2 3' CCCAGAGGCTGATCTGC 17460 \_ A  
 GTAGATCAGT TCT GG  
 ||||| || ||  
 CGTCTAGTCG AGA CC  
 G C  
 GAM1548 CBFB 3' CCCAGGCTGGTCTCG 43141 T T A  
 CG AGATCAGT CT GG  
 || ||||| || ||  
 GC TCTGGTCG GA CC  
 \_ \_ C  
 GAM1548 CBFB 3' CCCAGGCTGGTCTCG 8274 T T A  
 CG AGATCAGT CT GG  
 || ||||| || ||  
 GC TCTGGTCG GA CC  
 \_ \_ C  
 GAM1548 CIT 3' CCTAGGGCTAGACCTA 69745 A \_  
 TAG TC AGTTCTAGG  
 ||| || |||||  
 ATC AG TCGGGATCC  
 C A  
 GAM1548 CRLF1 3' CCTAGAACCCCTGCCAGGG 16452 \_ ATCA  
 CCC GTAG GTTCTAGG  
 ||| ||| |||||  
 GGG CGTC CAAGATCC  
 AC CC\_  
 GAM1548 DMPK 3' CCTAGAAGTGTCTTCG 15323 T T  
 CG AGA CAGTTCTAGG  
 || ||| |||||  
 GC TCT GTCAAGATCC  
 T \_  
 GAM1548 EDAR 5' CCCAGAACTGGATGG 42265 AGA A  
 CCGT TCAGTTCT GG  
 ||| ||||| ||  
 GGTA GGTCAAGA CC  
 \_ C  
 GAM1548 EPHB3 5' CCTAGAGCTGCCACGG 15455 AGAT  
 CCGT CAGTTCTAGG  
 ||| |||||  
 GGCA GTCGAGATCC  
 CC\_  
 GAM1548 GAB2 3' CCCAGAACTCTGGAGCTACAGG 54449 C A \_ A  
 CC GTAG TC AGTTCT GG  
 || ||| || ||||| ||

			GG CATC AG TCAAGA CC			
			A G GTC C			
GAM1548	GAB2	3'	CCCAGAACTCTGGAGCTACAGG 24492	C	A ____	A
			CC GTAG TC AGTTCT GG			
			GG CATC AG TCAAGA CC			
			A G GTC C			
GAM1548	GRM6	3'	CCCAGGCTGGTCTCG 5929	T	T A	
			CG AGATCAGT CT GG			
			GC TCTGGTCG GA CC			
			— — C			
GAM1548	ITGAL	3'	CCCAGAACTGGA CT CAGG 9389	GT A	A	
			CC AG TCAGTTCT GG			
			GG TC GGTCAAGA CC			
			AC A C			
GAM1548	MIPOL1	5'	CCCAGACTGGTCTCG 77066	T	T A	
			CG AGATCAGT CT GG			
			GC TCTGGTCA GA CC			
			— — C			
GAM1548	MTR	3'	CCTAAAATTGATCTATGG 4208		C	
			CCGTAGATCAGTT TAGG			
			GGTATCTAGTTAA ATCC			
			A			
GAM1548	NGFR	3'	CCTAGAATCAGCCTAGGGGT 10224	G	ATCA	
			ACCC TAG GTTCTAGG			
			TGGG ATC TAAGATCC			
			G CGAC			
GAM1548	RFXANK	3'	CCCAGAACTGACTTCAAAGG 13561	GT ____	A	A
			CC AG TCAGTTCT GG			
			GG TC AGTCAAGA CC			
			AACT _ C			
GAM1548	RFXANK	3'	CCCAGAACTGACTTCAAAGG 56239	GT ____	A	A
			CC AG TCAGTTCT GG			
			GG TC AGTCAAGA CC			
			AACT _ C			
GAM1548	SLC3A2	5'	CCCAGACTGGTCTCG 9983	T	T A	
			CG AGATCAGT CT GG			
			GC TCTGGTCA GA CC			
			— — C			
GAM1548	TEM5	3'	CCAAGGTCTGACCTAGGGTT 51318	G	A TT A	
			AACCC TAG TCAG CT GG			

				TTGGG ATC AGTC GA CC		
				_ C TG A		
GAM1548	WHSC1	5'	CCCAGGCTGGTCTCG	29907	T	T A
			CG AGATCAGT CT GG			
			GC TCTGGTCG GA CC			
			_ _ C			
GAM1548	WHSC1	5'	CCCAGGCTGGTCTCG	23656	T	T A
			CG AGATCAGT CT GG			
			GC TCTGGTCG GA CC			
			_ _ C			
GAM1548	WHSC1	5'	CCCAGGCTGGTCTCG	55842	T	T A
			CG AGATCAGT CT GG			
			GC TCTGGTCG GA CC			
			_ _ C			
GAM1548	WHSC1	5'	CCCAGGCTGGTCTCG	55825	T	T A
			CG AGATCAGT CT GG			
			GC TCTGGTCG GA CC			
			_ _ C			
GAM1548	ZFX	5'	CCCAGGCTGGTCTCG	12717	T	T A
			CG AGATCAGT CT GG			
			GC TCTGGTCG GA CC			
			_ _ C			
GAM1548	ALDH9	5'	CCTAGAACCGATCCCGTGG	5512	_ TA	A
			CC CG GATC GTTCTAGG			
			GG GC CTAG CAAGATCC			
			T C_ C			
GAM1548	C22orf19	3'	CCCAGGCTGGTCTCG	13418	T	T A
			CG AGATCAGT CT GG			
			GC TCTGGTCG GA CC			
			_ _ C			
GAM1548	CBX6	3'	CTAGAACTAGGGTT	26612	G	ATCAG
			AACCC TAG TTCTAG			
			TTGGG ATC AAGATC			
			_ A_			
GAM1548	CHL1	3'	CCTAGAGAACTGTCCAAGGGTT	21745	GTA T	_
			AACCC GA CAGT TCTAGG			
			TTGGG CT GTCA AGATCC			
			AAC _ AG			
GAM1548	CIP29	3'	CCCAGGCTGGTCTCG	50402	T	T A
			CG AGATCAGT CT GG			



GC TCTGGTCG GA CC  
 \_ \_ C  
 GAM1548 FLJ10483 3' CCTAGAACCTCTACAGGT 36168 C TCA  
 ACC GTAGA GTTCTAGG  
 ||| |||| |||||  
 TGG CATCT CAAGATCC  
 A C\_

GAM1548 FLJ10815 3' CTGGAATCCACGGGT 36694 A CAGT  
 ACCCGT GAT TCTAG  
 ||||| || ||||  
 TGGGCA CTA AGGTC  
 C \_

GAM1548 FLJ10898 5' CCCAGAGGTAGATCGACAGGTT 59427 C A AG\_ A  
 AACC GT GATC TTCT GG  
 ||| || ||| ||| ||  
 TTGG CA CTAG GAGA CC  
 A G ATG C

GAM1548 FLJ11715 3' CCCAGGCTGGTCTCG 44669 T T A  
 CG AGATCAGT CT GG  
 || ||||| || ||  
 GC TCTGGTCG GA CC  
 \_ \_ C

GAM1548 FLJ12448 3' CCTAGAACTGTCTGAGG 43176 G T  
 CC TAGA CAGTTCTAGG  
 || ||| |||||  
 GG GTCT GTCAAGATCC  
 A \_

GAM1548 FLJ20147 3' CCCAGACTGGTCTCG 34637 T T A  
 CG AGATCAGT CT GG  
 || ||||| || ||  
 GC TCTGGTCA GA CC  
 \_ \_ C

GAM1548 FLJ30532 3' CCTCAGATGATCTAC 58543 GT \_  
 GTAGATCA TCT AGG  
 ||||| ||| |||  
 CATCTAGT AGA TCC  
 \_ C

GAM1548 FLJ32334 3' CCCAGGCTGGTCTCG 57981 T T A  
 CG AGATCAGT CT GG  
 || ||||| || ||  
 GC TCTGGTCG GA CC  
 \_ \_ C

GAM1548 KIAA0205 3' CCTGAATAATCTATGGGTT 29579 CA T  
 AACCCGTAGAT GTTC AGG  
 ||||| ||| |||  
 TTGGGTATCTA TAAG TCC  
 A\_ \_

GAM1548 KIAA0268 3' CCCAGAACTGAAGATGG 70001 AGA A  
 CCGT TCAGTTCT GG  
 ||| ||||| ||

GGTA AGTCAAGA CC  
GA\_ C  
GAM1548 KIAA0318 3' CCTACGTCATCTATGGGTT 68950 CAGTTC  
AACCCGTAGAT TAGG  
||||||| |||  
TTGGGTATCTA ATCC  
CTGC\_\_  
GAM1548 KIAA0552 3' CCTAGAACCTGGGCCTAGG 28311 G A\_ \_  
CC TAG TCAG TTCTAGG  
|| ||| |||||  
GG ATC GGTC AAGATCC  
\_ CG C  
GAM1548 KIAA0710 3' CCCAGAACTGGGAGATGG 29566 AGA A  
CCGT TCAGTTCT GG  
||| ||||| ||  
GGTA GGTCAAGA CC  
GAG C  
GAM1548 KIAA0907 3' CCCAGAACTGGTTGC 30172 G A  
GTA ATCAGTTCT GG  
||| ||||| ||  
CGT TGGTCAAGA CC  
\_ C  
GAM1548 KIAA1157 3' AGCTTATCTACGGGTT 72237 C  
AACCCGTAGAT AGTT  
||||||| |||  
TTGGGCATCTA TCGA  
T  
GAM1548 KIAA1671 3' CCCAGGCTGGTCTCG 65669 T T A  
CG AGATCAGT CT GG  
|| ||||| || ||  
GC TCTGGTCG GA CC  
\_ \_ C  
GAM1548 KIAA1715 3' CCTGAGCATGATCTAC 68118 \_ T  
GTAGATCA GTTC AGG  
|||||| ||| |||  
CATCTAGT CGAG TCC  
A \_  
GAM1548 KIAA1814 3' CCTAGAGCAGTCTCCAGGG 70360 GT\_ CA  
CCC AGAT GTTCTAGG  
||| ||| |||||  
GGG TCTG CGAGATCC  
ACC A\_  
GAM1548 LIECG3 3' CCCAGGCTGGTCTCG 87409 T T A  
CG AGATCAGT CT GG  
|| ||||| || ||  
GC TCTGGTCG GA CC  
\_ \_ C  
GAM1548 MGC10812 3' CCTAGAACTTTTGCCAGT 48666 CC TC  
AC GTAGA AGTTCTAGG  
|| ||||| |||||

				TG CGTTT TCAAGATCC			
				AC _			
GAM1548	PELI1	5'	CCCAGGCTGGTCTCG	40258	T	T	A
			CG AGATCAGT CT GG				
			GC TCTGGTCG GA CC				
			_ _ C				
GAM1548	PGGT1B	5'	AGTGCTGATCTAGGG	17230	G	T	
			CCC TAGATCAGT CT				
			GGG ATCTAGTCG GA				
			_ T				
GAM1548	PIP3-E	3'	CCTAGAACTGGGAGATG	66803	AGA		
			CGT TCAGTTCTAGG				
			GTA GGTCAAGATCC				
			GAG				
GAM1548	PIP5K2B	3'	CCTCAGAACTGAGCCACAGG	13070	C	AGA	_
			CC GT TCAGTTCT AGG				
			GG CA AGTCAAGA TCC				
			A CCG C				
GAM1548	PTDSS1	3'	CCTAGAACTGAGAGGG	28571	GTAGA		
			CCC TCAGTTCTAGG				
			GGG AGTCAAGATCC				
			AG__				
GAM1548	PYPAF3	3'	CCTGGGATCGCTCTACG	57539	TCA		
			CGTAGA GTTCTAGG				
			GCATCT TAGGGTCC				
			CGC				
GAM1548	SDS3	3'	CCCAGAGGCTGATCTGC	69226	_	A	
			GTAGATCAGT TCT GG				
			CGTCTAGTCG AGA CC				
			G C				
GAM1548	SRF	3'	CCCAGAACTGGCTGGG	11943	GT	A	A
			CCC AG TCAGTTCT GG				
			GGG TC GGTCAAGA CC				
			_ _ C				
GAM1548	TRIM2	5'	CCCAGTTGTCTGCGGG	30941	T	TT	A
			CCCGTAGA CAG CT GG				
			GGGCGTCT GTT GA CC				
			_ _ C				
GAM1548	TSPEAR	3'	CCTAGGGCATCCCGGG	58719	TA	CA	
			CCCG GAT GTTCTAGG				

GGGC CTA CGGGATCC  
C\_ \_

GAM1548 LOC113026 3' CCCAGGCTGGTCTCG 55899 T T A  
CG AGATCAGT CT GG  
|| ||||| || ||  
GC TCTGGTCG GA CC  
\_ \_ C

GAM1548 LOC125144 3' CCCAGGCTGGTCTCAGG 74393 GT T A  
CC AGATCAGT CT GG  
|| ||||| || ||  
GG TCTGGTCG GA CC  
AC \_ C

GAM1548 LOC126549 5' CCTAGAACTGGCTGC 75708 A  
GTAG TCAGTTCTAGG  
|||| |||||  
CGTC GGTCAAGATCC  
\_

GAM1548 LOC126661 3' CCCAGGCTGGTCTCG 74547 T T A  
CG AGATCAGT CT GG  
|| ||||| || ||  
GC TCTGGTCG GA CC  
\_ \_ C

GAM1548 LOC127702 3' CCTGGGACACCTACAGG 75458 C ATCA  
CC GTAG GTTCTAGG  
|| ||| |||||  
GG CATC CAGGGTCC  
A CA\_

GAM1548 LOC143920 3' CCCAGAGTCCTATCTAGGGT 76624 G C \_ A  
ACCC TAGAT AG TTCT GG  
|||| |||| || ||| ||  
TGGG ATCTA TC GAGA CC  
\_ \_ CT C

GAM1548 LOC145725 3' CCCAGGCTGGTCTCG 77403 T T A  
CG AGATCAGT CT GG  
|| ||||| || ||  
GC TCTGGTCG GA CC  
\_ \_ C

GAM1548 LOC145732 3' CCCAGGCTGGTCTCG 77425 T T A  
CG AGATCAGT CT GG  
|| ||||| || ||  
GC TCTGGTCG GA CC  
\_ \_ C

GAM1548 LOC146733 3' CCTGGCTTGATCTACAGGT 83759 C TT  
ACC GTAGATCAG CTAGG  
||| ||||| ||||  
TGG CATCTAGTT GGTCC  
A C\_

GAM1548 LOC154877 3' CCCAGGCTGGTCTCG 86286 T T A  
CG AGATCAGT CT GG  
|| ||||| || ||

			GC TCTGGTCG GA CC		
			— — C		
GAM1548	LOC154881	3'	CCCAGAACAGAAGAAGGGTT	81170	GTAGA A A
			AACCC TC GTTCT GG		
			TTGGG AG CAAGA CC		
			AAGA_ A C		
GAM1548	LOC163998	5'	CCCAGAACTGGATGG	87053	AGA A
			CCGT TCAGTTCT GG		
			GGTA GGTCAAGA CC		
			— C		
GAM1548	LOC170261	3'	CTGCAGCCTACGGGT	82582	ATCA C
			ACCCGTAG GTT TAG		
			TGGGCATC CGA GTC		
			— C		
GAM1548	LOC196463	3'	CCTAGAGTGGGTCACG	87710	A AG
			CGT GATC TTCTAGG		
			GCA CTGG GAGATCC		
			— GT		
GAM1548	LOC196957	3'	CCCAGGCTGGTCTCG	87820	T T A
			CG AGATCAGT CT GG		
			GC TCTGGTCG GA CC		
			— — C		
GAM1548	LOC196961	3'	CCCAGGCTGGTCTCG	87841	T T A
			CG AGATCAGT CT GG		
			GC TCTGGTCG GA CC		
			— — C		
GAM1548	LOC197138	3'	CCCAGGCTGGTCTCG	87914	T T A
			CG AGATCAGT CT GG		
			GC TCTGGTCG GA CC		
			— — C		
GAM1548	LOC197423	5'	CCCAGAACTGATAGTGC	77857	G_ A
			GTA ATCAGTTCT GG		
			CGT TAGTCAAGA CC		
			GA C		
GAM1548	LOC200268	3'	CCCAGGCTGGTCTCG	88681	T T A
			CG AGATCAGT CT GG		
			GC TCTGGTCG GA CC		
			— — C		
GAM1548	LOC200339	3'	AACTGATCTACAGGT	90022	C
			AACC GTAGATCAGTT		

TTGG CATCTAGTCAA

A

GAM1548 LOC219653 3' CCCAGAACTGAACACTAGGT 91292 CG A\_\_ A

ACC TAG TCAGTTCT GG

||| ||| ||||| ||

TGG ATC AGTCAAGA CC

\_\_ ACA C

GAM1548 LOC220565 5' CCCAGAACTGATAGTGC 90748 G\_ A

GTA ATCAGTTCT GG

||| ||||| ||

CGT TAGTCAAGA CC

GA C

GAM1548 LOC221895 3' CCTATTGATATCTGCGG 92524 \_\_ TCT

CCGTAGA TCAGT AGG

||||| |||| ||

GGCGTCT AGTTA TCC

AT \_\_

GAM1548 LOC221960 3' CCCAGGCTGGTCTCG 91081 T T A

CG AGATCAGT CT GG

|| ||||| || ||

GC TCTGGTCG GA CC

\_ \_ C

GAM1548 LOC253228 3' CTAGTGCTGACCTACGGG 95940 A T

CCCGTAG TCAGT CTAG

||||| |||| |||

GGGCATC AGTCG GATC

C T

GAM1548 LOC254181 5' CCCAGAACTGGCTCAGG 97583 GT A A

CC AG TCAGTTCT GG

|| || ||||| ||

GG TC GGTCAAGA CC

AC \_ C

GAM1548 LOC257051 3' CTGCAGCCTACGGGT 96316 ATCA C

ACCGTAG GTT TAG

||||| ||| ||

TGGGCATC CGA GTC

\_\_ C

GAM1548 LOC51226 3' CCCAGAACTGACTCCTAAGG 33150 G A\_\_ A

CC TAG TCAGTTCT GG

|| ||| ||||| ||

GG ATC AGTCAAGA CC

A CTC C

GAM1548 LOC51622 3' CCCAGGCTGGTCTCG 31566 T T A

CG AGATCAGT CT GG

|| ||||| || ||

GC TCTGGTCG GA CC

\_ \_ C

GAM1548 LOC90139 3' CCCAGAACTGAGGCTTGG 55402 T A\_ A

CCG AG TCAGTTCT GG

||| || ||||| ||

GGT TC AGTCAAGA CC  
\_ GG \_ C  
GAM1548 LOC90979 3' CCTGCAGGCTGATCCAGGG 64525 GTA C\_  
CCC GATCAGTT TAGG  
||| ||||| |||  
GGG CTAGTCGG GTCC  
AC\_ AC  
GAM1548 LOC91012 5' CCCAGGCTGGTCTCGG 64639 T T A  
CCG AGATCAGT CT GG  
||| ||||| || ||  
GGC TCTGGTCG GA CC  
\_ \_ C  
GAM1548 LOC92568 5' CTGGAGATTCTACGGG 69772 TCAG  
CCCGTAGA TTCTAG  
||||| |||||  
GGGCATCT GAGGTC  
TA\_  
GAM1548 LOC93550 5' CCTAGAACTGGAATAC 72584 GA  
GTA TCAGTTCTAGG  
||| |||||  
CAT GGTCAAGATCC  
AA  
GAM1548 LOC93550 5' GGTGCTGATCTCCGAGT 72586 C T T  
AC CG AGATCAGT CT  
|| || ||||| ||  
TG GC TCTAGTCG GG  
A C T  
GAM1549 ADRA2A 3' AAAAGACAAATGGGCCTGCC 5449 CT \_  
GGC GGTTC TTTGTCTTT  
||| |||| |||||  
CCG CCGGG AAACAGAAAA  
T\_ T  
GAM1549 MSL3L1 5' GAAGAACCAGAGCTTCA 22308 GC  
TGAAG CTGGTTCTTT  
|||| |||||  
ACTTC GACCAAGAAG  
GA  
GAM1549 TEM7 3' AAAAGACAAGGCAAAGCCCGC 39879 CT \_\_\_\_  
GC GGTT CTTTGTCTTT  
|| ||| |||||  
CG CCGA GGAACAGAAAA  
C\_ AAC  
GAM1549 FLJ10315 3' AAAAGACAAAAAATCCACC 36016 CC TTC\_  
GG TGG TTTGTCTTT  
|| ||| |||||  
CC ACC AAACAGAAAA  
\_ TAAAA  
GAM1549 FLJ12577 5' AAAGACAGACAAGGCTTCA 48153 G G CTT  
TGAAG CCT GTT TGTCTTT  
|||| ||| ||| |||||

ACTTC GGA CAG ACAGAAA  
 \_ A \_  
 GAM1549 KIAA1656 3' AAAAGACATGGGACAGGCCTGC 65777 A G T  
 A TG AGGCCTG TTCT TGTCTTTT  
 || ||||| ||| |||||  
 AC TCCGGAC AGGG ACAGAAAA  
 G \_ T  
 GAM1549 MGC26684 3' AAGGAACCAGGCCCTCA 57989 A  
 TGA GGCCTGGTTCTTT  
 ||| |||||  
 ACT CCGGACCAAGGAA  
 C  
 GAM1549 S164 5' AAAAGACAAAAACGGGACC 60774 \_ GTTC  
 GG CCTG TTTGTCTTTT  
 || ||| |||||  
 CC GGC AACAGAAAA  
 A AAA\_  
 GAM1549 SMARCF1 3' AAAAGACAAAGCTCTGCCTACA 37429 A CT TT  
 TG AGGC GG CTTTGTCTTTT  
 || ||| || |||||  
 AC TCCG TC GAAACAGAAAA  
 A \_ TC  
 GAM1549 SMARCF1 3' AAAAGACAAAGCTCTGCCTACA 20033 A CT TT  
 TG AGGC GG CTTTGTCTTTT  
 || ||| || |||||  
 AC TCCG TC GAAACAGAAAA  
 A \_ TC  
 GAM1549 SMARCF1 3' AAAAGACAAAGCTCTGCCTACA 57479 A CT TT  
 TG AGGC GG CTTTGTCTTTT  
 || ||| || |||||  
 AC TCCG TC GAAACAGAAAA  
 A \_ TC  
 GAM1549 TP53INP1 5' AAAAGACATCCAGCCAACTCT 72947 AG CC CTT  
 CA TGA G TGGT TGTCTTTT  
 ||| | ||| |||||  
 ACT C ACCGA ACAGAAAA  
 CT AA CCT  
 GAM1549 TP53INP1 5' AAAAGACATCCAGCCAACTCT 52720 AG CC CTT  
 CA TGA G TGGT TGTCTTTT  
 ||| | ||| |||||  
 ACT C ACCGA ACAGAAAA  
 CT AA CCT  
 GAM1549 LOC170037 5' AAAAGACGGTCCAAAGCC 87243 C\_ TTCT  
 GGC TGG TTGTCTTTT  
 ||| || |||||  
 CCG ACC GGCAGAAAA  
 AA T\_  
 GAM1549 LOC196527 3' AAAAGACAGGGAGCCAGGCCCT 87752 A  
 C GA GGCCTGGTTCTTTGTCTTTT  
 || |||||



			CT CCGGACCGAGGGACAGAAAA			
			C			
GAM1550	BAZ2B	3'	GAAGCACACCCAAAGAATTTTC	25620	GC	A A
	A		TGAAAA CTTTGGGT GTG TTC			
			ACTTTT GAAACCCA CAC AAG			
			AA _ G			
GAM1550	CD2AP	3'	ACCCAAAGCTTTTCA	24014	C	
			TGAAAAGC TTTGGGT			
			ACTTTTCG AAACCCA			
			-			
GAM1550	COX11	3'	GAATCATATTTAAAGGCTGCCC	15191	AAA	G
	A		TG AGCCTTTGGGTA TGATTC			
			AC TCGGAAATTTAT ACTAAG			
			CCG _			
GAM1550	EHD4	3'	ATTGTCCAAAGAGTCCTCA	57689	AAA _	GT
			TGA GC CTTTGG AGT			
			ACT TG GAAACC TTA			
			CC_ A TG			
GAM1550	GNG5	3'	GAATCTTTCAAAGGTTTCCCA	17949	AA	TAGT
			TG AAGCCTTTGGG GATTC			
			AC TTTGGAAACTT CTAAG			
			CC T__			
GAM1550	DKFZP564O1664	3'	GAATAGCCACCCAAAG	47937	A G	
			CTTTGGGT GT ATTC			
			GAAACCCA CG TAAG			
			C A			
GAM1550	FLJ30567	3'	ACCTTCAAAGGCTTCCCA	58822	AA	_
			TG AAGCCTTTG GGT			
			AC TTCGGAAAC CCA			
			CC TT			
GAM1550	H2BFK	3'	ACGACCCAAAGGCTCTTC	13049	A	A
			GAA AGCCTTTGGGT GT			
			CTT TCGGAAACCCA CA			
			C G			
GAM1550	HERPUD1	3'	TGCCCAAGGCTTCTCA	28020	A	T
			TGA AAGCCTT GGGTA			
			ACT TTCGGAA CCCGT			
			C _			
GAM1550	IDI2	3'	AATCACTATTTCAACCTTTTCA	52693	CCT	_
			TGAAAAG TTGGG TAGTGATT			

		ACTTTTC AACTT ATCACTAA		
		C_ T		
GAM1550 KIAA0182	3'	GCAACCCAAAGGCTTTTC 72028	A	
		GAAAAGCCTTTGGGT GT		
		CTTTTCGGAAACCCA CG		
		A		
GAM1550 KIAA0493	3'	GAATCACTTTTTAGACTTTTCA 64275	CC	T
		TGAAAAG TTTGGG AGTGATTC		
		ACTTTTC AGATTT TCACTAAG		
		_ T		
GAM1550 KIAA1046	3'	ACCCAAAGGCCTTTCA 29988	A	
		TGAAA GCCTTTGGGT		
		ACTTT CGGAAACCCA		
		C		
GAM1550 KIAA1906	3'	GTCAGCCAAAAGCTTTTCA 73198	C	GTAG
		TGAAAAGC TTTGG TGAT		
		ACTTTTCG AAACC ACTG		
		A G_		
GAM1550 MBD2	3'	ACTACCCAAAGGTCTTCA 31715	AA	
		TGAA GCCTTTGGGTAGT		
		ACTT TGGAAACCCATCA		
		C_		
GAM1550 SIRPB1	3'	GAATCACTCCAGAAGATCCTTT 20252	AGC_	G T
CA		TGAAA CTTT GG AGTGATTC		
		ACTTT GAAG CC TCACTAAG		
		CCTA A _		
GAM1550 STAG2	3'	TACCAAAAGGCTTTTCA 70567	A	G
		TGAAA GCCTTT GGTA		
		ACTTT CGGAAA CCAT		
		_ A		
GAM1550 LOC164955	3'	AATCACCATCTGAAGCTTTT 82456	C TG	A
		AAAAGC TT GGT GTGATT		
		TTTTCG AA CTA CACTAA		
		_ GT C		
GAM1550 LOC201164	3'	ACCACCCAGAGACCCTTCA 88110	AAGC	A
		TGAA CTTTGGGT GT		
		ACTT GAGACCCA CA		
		CCCA C		
GAM1550 LOC219653	3'	GAGCACACCAAAGGCT 91294	GTA	A
		AGCCTTTGG GTG TTC		

			TCGGAAACC CAC GAG		
			A__ _		
GAM1551	ADH1B	3'	CTTAGACATAAAAGTAAAAT 72644	C	CAC
			ATTT ACTTT TGTCTGAG		
			TAAA TGAAA ACAGATTC		
			A T__		
GAM1551	AHR	3'	ATCTCAGATGTTAAAATAAATG 7875	CAC	C T
			CATTT TTT AC GTCTGAGAT		
			GTAAA AAA TG TAGACTCTA		
			TA_ T _		
GAM1551	FDFT1	3'	TAGGAAAGTGAAATG 15518	A	
			CATTTCACTTTC CTG		
			GTAAAGTGAAAG GAT		
			-		
GAM1551	JTB	3'	ATCTCAGACAGTGAAAGTGAAA 21959		
	TG		CATTTCACTTTCACTGTCTGAGAT		
			GTAAAGTGAAAGTGACAGACTCTA		
GAM1551	KLF4	3'	TCCCAGACAGTGGATATG 14891	CT	A
			CA TTCACTGTCTG GA		
			GT AGGTGACAGAC CT		
			AT C		
GAM1551	PHYH	3'	ACAGTAAAAGTGAAAT 20608	C	
			ATTTCACTTT ACTGT		
			TAAAGTGAAA TGACA		
			A		
GAM1551	PKD2	3'	TCCAGGTTGAAAGTGAAA 60096	CTG	A
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T__ _		
GAM1551	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1551	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA	CTG
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1551	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT	CT
			TTCAC TTTCA GT GAG		

AAGTGAAAGT CA CTC  
 CT \_  
 GAM1551 EIF2C2 3' ATCTTCTGAGAGTGAAAAG 71946 G T\_  
 CTTTCACT TC GAGAT  
 ||||| || ||||  
 GAAAGTGA AG TTCTA  
 G TC  
 GAM1551 FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802 ACTTTCACT  
 G CATTTC GTCTGAGAT  
 |||| | |||||  
 GTAAAG CAGACTCTA  
 AAACATTT\_  
 GAM1551 FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281 CTT  
 CATTTCA TCACTGTCTGAGAT  
 |||| | |||||  
 GTAAAGT AGTGACAGACTCTA  
 C\_  
 GAM1551 KIAA0984 3' TTTGTCCAGTGAAAATGAA 65534 C TC  
 TTCA TTTCACTG TGAG  
 ||| ||||| |||  
 AAGT AAAGTGAC GTTT  
 A CT  
 GAM1551 KLHL6 3' ATCTCAGAGCAGGAAA 55299 A \_  
 TTTC CTG TCTGAGAT  
 ||| ||| |||||  
 AAAG GAC AGACTCTA  
 \_ G  
 GAM1551 NIR3 3' GCAGTGAAAGTGCAAT 66242 T  
 ATT CACTTTCACTGT  
 ||| |||||  
 TAA GTGAAAGTGACG  
 C  
 GAM1551 PORIMIN 3' ATCTCAGAGGGCCAAAGTGAA 53598 CA G  
 TTCACTTT CT TCTGAGAT  
 ||||| || |||||  
 AAGTGAAA GG AGACTCTA  
 CC G  
 GAM1551 PP35 3' ATCTCAGACTGAAA 22814 CT  
 TTTCA GTCTGAGAT  
 |||| | |||||  
 AAAGT CAGACTCTA  
 \_  
 GAM1551 PRTD-NY3 3' CTCATTGCAATAAGTGAAATG 48148 TCAC C\_  
 CATTTCACTT TGT TGAG  
 ||||| || |||  
 GTAAAGTGAA ACG ACTC  
 TA\_\_ TT  
 GAM1551 SEP15 3' TCCTACAGTAAGAGTGAAA 14934 C CT  
 TTTCACTTT ACTGT GA  
 ||||| |||| ||

		AAAGTGAGA TGACA CT	
		A TC	
GAM1551	SFXN2	3' CTCAGGGGAAAAAAGTGAAA 73941	CACTG
		TTTCACTTT TCTGAG	
		AAAGTGAAA GGA CTC	
		AAAGG	
GAM1551	LOC149703	3' ATCTCAGACAGCCGTTTGAAAA 84647	ACTTTCA
		TTTC CTGTCTGAGAT	
		AAAG GACAGACTCTA	
		GTTTGCC	
GAM1551	LOC154007	3' ATCTCAAACCCTTTAGTGAAA 81015	TTCACT C
		TTTCACT GT TGAGAT	
		AAAGTGA CA ACTCTA	
		TTTCC_ A	
GAM1551	LOC155004	3' TCATTTAAGTGAAAGGAAA 81226	A GTC_
		TTTC CTTTCACT TGA	
		AAAG GAAAGTGA ACT	
		_ ATTT	
GAM1551	LOC222134	5' ACAGTGAAGTGAAATG 94136	T
		CATTTCACTT CACTGT	
		GTAAAGTGAA GTGACA	
		-	
GAM1552	A1BG	3' TCACAGCAACCTCTACCTC 55432	A
		GAGGTAGAGGTTGC GTGA	
		CTCCATCTCCAACG CACT	
		A	
GAM1552	ACVR1	5' CACTGCAGCCTCCACCTC 6603	A
		GAGGT GAGGTTGCAGTG	
		CTCCA CTCCGACGTCAC	
		C	
GAM1552	ADRB3	3' CTTTCCACAACCTCTACCTT 3435	CAGT
		GAGGTAGAGGTTG GAG	
		TTCCATCTCCAAC TTC	
		ACCT	
GAM1552	AHR	3' TCACTGCAACCTCTACCTC 7883	
		GAGGTAGAGGTTGCAGTGA	
		CTCCATCTCCAACGTCACT	
GAM1552	AIM1	3' TCACTGCAGCCTCTACCTC 91826	
		GAGGTAGAGGTTGCAGTGA	

CTCCATCTCCGACGTCACT

GAM1552 ALDH1B1 3' TCACTGCAACCTCCGCCTC 5496 TA  
GAGG GAGGTTGCAGTGA  
|||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 AP3B2 5' CGCCGCAACCTCCTCCTC 16187 TA A  
GAGG GAGGTTGC GTG  
|||||  
CTCC CTCCAACG CGC  
TC C

GAM1552 APPBP2 3' TCACTGCAACCTCCGCCTC 21082 TA  
GAGG GAGGTTGCAGTGA  
|||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 AQP6 3' TCGGCTCACTGCAACCTCTACC 53944  
TC GAGGTAGAGGTTGCAGTGAGTCGA  
|||||  
CTCCATCTCCAACGTCACTCGGCT

GAM1552 AQP6 3' TCGGCTCACTGCAACCTCTACC 7964  
TC GAGGTAGAGGTTGCAGTGAGTCGA  
|||||  
CTCCATCTCCAACGTCACTCGGCT

GAM1552 ARCN1 3' TCACTGCAACCTCCGCCTC 7985 TA  
GAGG GAGGTTGCAGTGA  
|||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 ATP8B2 3' TCAGCTCACTGCAACCTCCACC 65237 A C  
TC GAGGT GAGGTTGCAGTGAGT GA  
|||||  
CTCCA CTCCAACGTCACTCG CT  
C A

GAM1552 BRIP1 3' TCACTGCAACCTTCACCTC 49400 AG  
GAGGT AGGTTGCAGTGA  
|||||  
CTCCA TCCAACGTCACT  
CT

GAM1552 C7 3' CTGCAACCTCCGCCTC 5161 TA  
GAGG GAGGTTGCAG  
|||||  
CTCC CTCCAACGTC  
GC

GAM1552 CAMLG 3' TCACCGCAACCTCCACCTT 8243 A A  
GAGGT GAGGTTGC GTGA  
|||||

			TTCCA CTCCAACG CACT		
			C C		
GAM1552	CCNF	3'	TCAACTCACTGTAACCTCCGCC 8325	TA	C
	TC		GAGG GAGGTTGCAGTGAGT GA		
			CTCC CTCCAATGTCACTCA CT		
			GC A		
GAM1552	CDH17	3'	TCACTGCAACCTCCGCCTC 14507	TA	
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	CIAS1	5'	TCACTGCAGCCTCCACCTC 16903	A	
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCGACGTCACT		
			C		
GAM1552	CLECSF12	3'	TCACCGCAACCTCCGCC 76700	TA A	
			GG GAGGTTGC GTGA		
			CC CTCCAACG CACT		
			GC C		
GAM1552	CLECSF12	3'	TCGACTCACTGCAGCTATCTC 76703	AGA	
			GAGGT GGTTCAGTGAGTCGA		
			CTCTA TCGACGTCACTCAGCT		
			—		
GAM1552	CRTAP	3'	TCACTGCAACCTCCGCCTC 21039	TA	
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	CSNK2A2	5'	TCAGCTCACTGCAACCTCCACC 8568	A	C
	TC		GAGGT GAGGTTGCAGTGAGT GA		
			CTCCA CTCCAACGTCACTCG CT		
			C A		
GAM1552	CXCL16	3'	TCGGCTCACTGCAACCCCATC 41927	AGA	
	TC		GAGGT GGTTCAGTGAGTCGA		
			CTCTA CCAACGTCACTCGGCT		
			CCC		
GAM1552	CYLN2	3'	CTGCAGCCTCCACCTC 12632	A	
			GAGGT GAGGTTGCAG		
			CTCCA CTCCGACGTC		
			C		
GAM1552	CYP1A2	3'	TCAGCTCACTGCAACCTCCACC 69128	A	C
	TC		GAGGT GAGGTTGCAGTGAGT GA		

			CTCCA CTCCAACGTCAGTCG CT		
			C            A		
GAM1552	CYP1A2	3'	TCAGCTCACTGCAACCTCCACC 5708	A	C
	TC		GAGGT GAGGTTGCAGTGAGT GA		
			CTCCA CTCCAACGTCAGTCG CT		
			C            A		
GAM1552	CYP1A2	3'	TCAGTCAACCTCTGCCTC 5705		
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCAGT		
GAM1552	CYP1A2	3'	TCAGTCAACCTCTGCCTC 69125		
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCAGT		
GAM1552	CYP2B6	3'	TCGGCTCACTGCAACCTCCACC 5742	A	
			GGT GAGGTTGCAGTGAGTCGA		
			CCA CTCCAACGTCAGTCGGCT		
			C		
GAM1552	CYP4F3	3'	TCATTGCAACCTCCGCCTC 6124	TA	
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTTACT		
			GC		
GAM1552	CYP8B1	3'	TCAGTACAACCTCTGCCTC 15270		C
			GAGGTAGAGGTTG AGTGA		
			CTCCGTCTCCAAC TCACT		
			A		
GAM1552	CYP8B1	3'	TCAGTCAACCTCTGCCTC 15272		
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCAGT		
GAM1552	DFFB	3'	TCAGTCAACCTCCGCCTC 87393	TA	
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCAGT		
			GC		
GAM1552	DISC1	3'	TCGGCTCACTGCAACCTCTACC 37895		
	TC		GAGGTAGAGGTTGCAGTGAGTCGA		
			CTCCATCTCCAACGTCAGTCGGCT		
GAM1552	DSCR3	3'	TCAGCTCACTGCAACCTCCACC 20193	A	C
	TC		GAGGT GAGGTTGCAGTGAGT GA		



			CTCCA CTCCAACGTCAGTCTG CT		
			C            A		
GAM1552 EHD2	3'	TCAGTCACTGCAACCTCCACC 27500	A		C
TC		GAGGT GAGGTTGCAGTGAGT GA			
		CTCCA CTCCAACGTCAGTCTG CT			
		C            A			
GAM1552 EPB72	3'	TCAGTCACTGCAACCTCCGCCTC 14610	TA		
		GAGG GAGGTTGCAGTGA			
		CTCC CTCCAACGTCAGT			
		GC			
GAM1552 F2RL2	3'	TCATTGCAACCTCTGCCTC 14626			
		GAGGTAGAGGTTGCAGTGA			
		CTCCGTCTCCAACGTTACT			
GAM1552 FANCF	3'	TCAGTGCAACCTCTGCCTC 42679		G	
		GAGGTAGAGGTTGCA TGA			
		CTCCGTCTCCAACGT ACT			
		G			
GAM1552 FCAR	3'	TCGACTCACTGCAACCTTCGCC 55816	TA		
TC		GAGG GAGGTTGCAGTGAGTCGA			
		CTCC TTCCAACGTCAGTCTCAGCT			
		GC			
GAM1552 FCAR	3'	TCGACTCACTGCAACCTTCGCC 55804	TA		
TC		GAGG GAGGTTGCAGTGAGTCGA			
		CTCC TTCCAACGTCAGTCTCAGCT			
		GC			
GAM1552 FEZ1	3'	TCAGTCACTGCAACCTCCACCTC 42579	A		
		GAGGT GAGGTTGCAGTGA			
		CTCCA CTCCAACGTCAGT			
		C			
GAM1552 FGF5	3'	TCGGCTCACTGCAACCTCCAAC 15550	GTA		
TC		GAG GAGGTTGCAGTGAGTCGA			
		CTC CTCCAACGTCAGTCTGGCT			
		AAC			
GAM1552 FGF5	3'	TCGGCTCACTGCAACCTCCAAC 52495	GTA		
TC		GAG GAGGTTGCAGTGAGTCGA			
		CTC CTCCAACGTCAGTCTGGCT			
		AAC			
GAM1552 FHL2	5'	TCAGTCACTGCAAGCTCTACC 7567	G		C
TC		GAGGTAGAG TTGCAGTGAGT GA			

			CTCCATCTC AACGTCACG CT		
			G A		
GAM1552	FZD4	3'	TCACTGCAACCTCTGCCTC 24149 GAGGTAGAGGTTGCAGTGA       CTCCGTCTCCAACGTCACG		
GAM1552	G6PC	3'	TCACTGCAACCTCTTCCTC 3834 GAGG AGAGGTTGCAGTGA           CTCC TCTCCAACGTCACG T	T	
GAM1552	GHR C	3'	TGACTCACTGCAATCTCCACCT 3891 GAGGT GAGGTTGCAGTGAGTCG            CTCCA CTCTAACGTCACGTCAGT C	A	
GAM1552	GM2A	3'	TCACTGCAACCTCCGCCTC 67784 GAGG GAGGTTGCAGTGA           CTCC CTCCAACGTCACG GC	TA	
GAM1552	GNE	3'	TCAATGCAACCTCTGCC 18484 GGTAGAGGTTGCA TGA           CCGTCTCCAACGTC ACT A	G	
GAM1552	GPR4	3'	TCACTGCAGCCTCCACCTC 59907 GAGGT GAGGTTGCAGTGA            CTCCA CTCCGACGTCACG C	A	
GAM1552	GPR56	5'	TCATCGTAACCTCCACCTC 19073 GAGGT GAGGTTGC GTGA                CTCCA CTCCAATG TACT C C	A	A
GAM1552	GPR81	3'	TCACTGCAACCTCTGCCTC 50765 GAGGTAGAGGTTGCAGTGA       CTCCGTCTCCAACGTCACG		
GAM1552	GRAF	3'	TCACTGCAACCTCCGCCTC 30576 GAGG GAGGTTGCAGTGA           CTCC CTCCAACGTCACG GC	TA	
GAM1552	HTR1E	5'	TCATTGCAACCTCCGCCTC 6015 GAGG GAGGTTGCAGTGA 	TA	

		CTCC CTCCAACGTTACT	
		GC	
GAM1552 IL11	3'	TCACTGCAAGCTCCACCTC 5337	A G
		GAGGT GAG TTGCAGTGA	
		CTCCA CTC AACGTCACT	
		C G	
GAM1552 INMT	3'	TCGACTCACTGCAAGCTCCGCC 22279	TA G
TC		GAGG GAG TTGCAGTGAGTCGA	
		CTCC CTC AACGTCACTCAGCT	
		GC G	
GAM1552 ITGAM	3'	TCACTGCAACCTCCGCCTC 71842	TA
		GAGG GAGGTTGCAGTGA	
		CTCC CTCCAACGTCACT	
		GC	
GAM1552 KMO	3'	TCACTGCAACCTCTGCCTC 13455	
		GAGGTAGAGGTTGCAGTGA	
		CTCCGTCTCCAACGTCACT	
GAM1552 LILRA3	3'	TCACTGCAACCTCCGCCTC 95310	TA
		GAGG GAGGTTGCAGTGA	
		CTCC CTCCAACGTCACT	
		GC	
GAM1552 LNK	3'	TCACTGCAACCTCCACCTT 18470	A
		GAGGT GAGGTTGCAGTGA	
		TTCCA CTCCAACGTCACT	
		C	
GAM1552 LSS	3'	CTCAACCTCTATCTC 9816	C
		GAGGTAGAGGTTG AG	
		CTCTATCTCCAAC TC	
GAM1552 LYZ	3'	TCGGCTCACTGCAACCTCCACC 4111	A
TC		GAGGT GAGGTTGCAGTGAGTCGA	
		CTCCA CTCCAACGTCACTCGGCT	
		C	
GAM1552 MAK	3'	TACTGCAACCTCCACCTC 19767	A
		GAGGT GAGGTTGCAGTG	
		CTCCA CTCCAACGTCAT	
		C	
GAM1552 MEF2A	5'	TCACTGCAACCTCCGCCTC 18784	TA
		GAGG GAGGTTGCAGTGA	

			CTCC CTCCAACGTCACT		
			GC		
GAM1552	MEFV	3'	TA	CTACTGCAACCTCCGCCTC 4150	TA
				GAGG GAGGTTGCAGTGA	
				CTCC CTCCAACGTCACT	
				GC	
GAM1552	MEFV	3'	TA	CTAGCTCACTGCAACCTCCACC 4154	A
	TC			GAGGT GAGGTTGCAGTGAGT GA	C
				CTCCA CTCCAACGTCACTCG CT	
				C A	
GAM1552	MHC2TA	3'	TA	CTACTGCAACCTCCGCCTC 4188	TA
				GAGG GAGGTTGCAGTGA	
				CTCC CTCCAACGTCACT	
				GC	
GAM1552	MICB	3'		CTACTGCAACCTCTGCCTC 19832	
				GAGGTAGAGGTTGCAGTGA	
				CTCCGTCTCCAACGTCACT	
GAM1552	MPL	3'	TA	CTAGCTCACTGCAACCTCCACC 18156	A
	TC			GAGGT GAGGTTGCAGTGAGT GA	C
				CTCCA CTCCAACGTCACTCG CT	
				C A	
GAM1552	MPL	3'		CTACTGCAACCTCTGCCTC 18154	
				GAGGTAGAGGTTGCAGTGA	
				CTCCGTCTCCAACGTCACT	
GAM1552	MRPL49	3'		CTACTGCAACTTCCACCTC 69574	A
				GAGGT GAGGTTGCAGTGA	
				CTCCA CTTCAACGTCACT	
				C	
GAM1552	MYCL2	3'		CTACTGCAACCTCTGCCTC 18188	
				GAGGTAGAGGTTGCAGTGA	
				CTCCGTCTCCAACGTCACT	
GAM1552	NDRG3	3'		CTACTGCAACCTCTGCC 49303	
				GGTAGAGGTTGCAGTGA	
				CCGTCTCCAACGTCACT	
GAM1552	NQO1	3'		CTACTGCAACCTCTGCCTC 6165	
				GAGGTAGAGGTTGCAGTGA	

CTCCGTCTCCAACGTCAC

GAM1552 PCDHB11 3' TCACTGCAACCTCTGCCTC 38420  
GAGGTAGAGGTTGCAGTGA  
|||||  
CTCCGTCTCCAACGTCAC

GAM1552 PCDHB16 3' TCACTGCAACCTCTGCCTC 40554  
GAGGTAGAGGTTGCAGTGA  
|||||  
CTCCGTCTCCAACGTCAC

GAM1552 PCDHB9 3' TCACTGCAACCTCCGCCTC 38947 TA  
GAGG GAGGTTGCAGTGA  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1552 PDCL 3' TCGGCTCACTGCAACCTCCACC 18219 A  
TC GAGGT GAGGTTGCAGTGAGTCGA  
|||||  
CTCCA CTCCAACGTCACCTCGGCT  
C

GAM1552 PDE6B 3' TCAGCTCACTGCAACCTCCACC 4290 A C  
TC GAGGT GAGGTTGCAGTGAGT GA  
||||| ||  
CTCCA CTCCAACGTCACCTCG CT  
C A

GAM1552 PER2 3' TCACTGCAACCTCTGCCTC 43043  
GAGGTAGAGGTTGCAGTGA  
|||||  
CTCCGTCTCCAACGTCAC

GAM1552 PIGR 3' TCACTGCAACCTCCGCCTC 72606 TA  
GAGG GAGGTTGCAGTGA  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1552 PIK3C2B 3' TCGACTCACTGCAAAATCTGCC 10578 GG  
TC GAGGTAGA TTGCAGTGAGTCGA  
||||| |||||  
CTCCGTCT AACGTCACCTCAGCT  
AA

GAM1552 PON1 3' TCACTGCAACTTCTACCTC 4804  
GAGGTAGAGGTTGCAGTGA  
|||||  
CTCCATCTTCAACGTCAC

GAM1552 PSMB2 3' TCACTGCAACCTCCGCCTC 10953 TA  
GAGG GAGGTTGCAGTGA  
||| |||||

			CTCC CTCCAACGTCACT		
			GC		
GAM1552	RAB36	3'	TCAGTGCAACCTCTGCCTC	16973	G
			GAGGTAGAGGTTGCA TGA		
			CTCCGTCTCCAACGT ACT		
			G		
GAM1552	RAB36	3'	TCACGTACACCCCCACCTC	16972	AGA _ A
			GAGGT GGT TGC GTGA		
			CTCCA CCA ATG CACT		
			CCC C _		
GAM1552	RHD	3'	TCACTGCAACCTCCGCCTC	32623	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	RHD	3'	TCACTGCAACCTCCGCCTC	32314	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	RHD	3'	TCACTGCAACCTCTACCTC	32316	
			GAGGTAGAGGTTGCAGTGA		
			CTCCATCTCCAACGTCACT		
GAM1552	RHD	3'	TCACTGCAACCTCTACCTC	32625	
			GAGGTAGAGGTTGCAGTGA		
			CTCCATCTCCAACGTCACT		
GAM1552	RPH3AL	3'	TCACTGCAACCTCCACCTC	22755	A
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCAACGTCACT		
			C		
GAM1552	SAS	3'	TCACCGCAACCTCTGCCTC	19959	A
			GAGGTAGAGGTTGC GTGA		
			CTCCGTCTCCAACG CACT		
			C		
GAM1552	SEDL	3'	TCACTGCAACCTCCACCTC	27355	A
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCAACGTCACT		
			C		
GAM1552	SEDL	3'	TCACTGCAACCTCCGCCTC	27359	TA
			GAGG GAGGTTGCAGTGA		

			CTCC CTCCAACGTCACT			
			GC			
GAM1552	SEDL	3'	TCAGTGCACCTCCACCTC	27356	A	
			GAGGT GAGGTTGCAGTGA			
			CTCCA CTCCAACGTCACT			
			C			
GAM1552	SEPN1	3'	TCAGTGCACCTCCACCTC	66378	A	
			GAGGT GAGGTTGCAGTGA			
			CTCCA CTCCAACGTCACT			
			C			
GAM1552	SERPINB9	3'	TCAGTGCACCTCCTCCTC	14763	TA	
			GAGG GAGGTTGCAGTGA			
			CTCC CTCCAACGTCACT			
			TC			
GAM1552	SHOX	3'	TCGACTCACTGCAACCTCCGCC	22547	TA	
	TC		GAGG GAGGTTGCAGTGAGTCGA			
			CTCC CTCCAACGTCACTCAGCT			
			GC			
GAM1552	SIL	3'	TCAGTGCACCTCTGCCTC	11695		
			GAGGTAGAGGTTGCAGTGA			
			CTCCGTCTCCAACGTCACT			
GAM1552	SLA2	3'	TCAGCTCACTGCAACCTCCATC	49907	A	C
	TC		GAGGT GAGGTTGCAGTGAGT GA			
			CTCTA CTCCAACGTCACTCG CT			
			C A			
GAM1552	SLC14A2	5'	TCAGTGCACCTCCACCTC	23139	A	
			GAGGT GAGGTTGCAGTGA			
			CTCCA CTCCAACGTCACT			
			C			
GAM1552	SLC15A1	3'	TCAGTGCACCTCCGCCTC	17406	TA	
			GAGG GAGGTTGCAGTGA			
			CTCC CTCCAACGTCACT			
			GC			
GAM1552	SMAC	5'	TCAGTGCACCTCTGCCTC	57216		
			GAGGTAGAGGTTGCAGTGA			
			CTCCGTCTCCAACGTCACT			
GAM1552	SNAP23	3'	TCAGTGCACCTCCGCCTC	55467	TA	
			GAGG GAGGTTGCAGTGA			

			CTCC CTCCAACGTCACT		
			GC		
GAM1552	SNAP23	3'	TCACTGCAACCTCCGCCTC	13814	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	SNX15	3'	TCACTGCAACCTCCACCTC	73748	A
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCAACGTCACT		
			C		
GAM1552	SPN	3'	TCACTGCAACCTCTGCCTC	11925	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCACT		
GAM1552	SS18	3'	TCACTGCAACCTCCGCCTC	18888	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	STAU	5'	TCGGCTCACTGCAACCTCCACC	16011	A
	TC		GAGGT GAGGTTGCAGTGAGTCGA		
			CTCCA CTCCAACGTCACTCGGCT		
			C		
GAM1552	STAU	5'	CACTGCAACCTCCACCTC	15997	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCAACGTCAC		
			C		
GAM1552	SULT2B1	5'	TCACTGCAACCTCCGCCTC	16030	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	TAF4	3'	TCGTTGCACCCCCACCTC	12092	AGA T
			GAGGT GG TGCAGTGA		
			CTCCA CC ACGTTGCT		
			CC_ C		
GAM1552	TAPBP	3'	TACTGCAACCTCCGCCTC	12134	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAT		
			GC		
GAM1552	TAT	3'	TCGGCTCACTGCAACCTCCACC	4477	A
	TC		GAGGT GAGGTTGCAGTGAGTCGA		



			CTCCA CTCCAACGTC	ACTCGGCT		
			C			
GAM1552	TBXA2R	3'	TC	ACTGCAACCTCCGCCTC	6502	TA
				GAGG GAGGTTGCAGTGA		
				CTCC CTCCAACGTC		
				ACT		
				GC		
GAM1552	TBXA2R	3'	TC	AGCTCACTGCAACCTCCACC	6505	A C
			TC	GAGGT GAGGTTGCAGTGAGT		
				GAGT GA		
				CTCCA CTCCAACGTC		
				ACTCG CT		
				C A		
GAM1552	TMC1	5'	TCT	CTGCAACCTCCGCCTC	56906	TA T
				GAGG GAGGTTGCAG		
				GA		
				CTCC CTCCAACGTC		
				CT		
				GC T		
GAM1552	TNFRSF10B	3'	TC	AGTGCAACCTCCGCCTC	13878	TA G
				GAGG GAGGTTGCA		
				TGA		
				CTCC CTCCAACGTC		
				ACT		
				GC G		
GAM1552	TPMT	3'	TC	ACTGCAACCTCTGCCTC	4544	
				GAGGTAGAGGTTGCAGTGA		
				CTCCGTCTCCAACGTC		
				ACT		
GAM1552	TRIM9	5'	TC	ACTGCAACCTCCGCCTC	30765	TA
				GAGG GAGGTTGCAGTGA		
				CTCC CTCCAACGTC		
				ACT		
				GC		
GAM1552	TRPM6	3'	TC	ACTGCAACCTCTGCCTC	34545	
				GAGGTAGAGGTTGCAGTGA		
				CTCCGTCTCCAACGTC		
				ACT		
GAM1552	TRPV1	3'	CT	GCAACCTCCGCCTC	54866	TA
				GAGG GAGGTTGCAG		
				CTCC CTCCAACGTC		
				ACT		
				GC		
GAM1552	TRPV1	3'	CT	GCAACCTCCGCCTC	38080	TA
				GAGG GAGGTTGCAG		
				CTCC CTCCAACGTC		
				ACT		
				GC		
GAM1552	TRPV1	3'	TC	ACTGCAACCTCTGCCTC	54878	
				GAGGTAGAGGTTGCAGTGA		

CTCCGTCTCCAACGTCACT

GAM1552 TRPV1 3' TCACTGCAACCTCTGCCTC 38095  
GAGGTAGAGGTTGCAGTGA  
|||||||  
CTCCGTCTCCAACGTCACT

GAM1552 TRPV1 3' CTGCAACCTCCGCCTC 54801 TA  
GAGG GAGGTTGCAG  
||| |||||  
CTCC CTCCAACGTC  
GC

GAM1552 TRPV1 3' TCACTGCAACCTCTGCCTC 54813  
GAGGTAGAGGTTGCAGTGA  
|||||||  
CTCCGTCTCCAACGTCACT

GAM1552 TRPV1 3' CTGCAACCTCCGCCTC 54834 TA  
GAGG GAGGTTGCAG  
||| |||||  
CTCC CTCCAACGTC  
GC

GAM1552 TRPV1 3' TCACTGCAACCTCTGCCTC 54845  
GAGGTAGAGGTTGCAGTGA  
|||||||  
CTCCGTCTCCAACGTCACT

GAM1552 TUFT1 3' TCACTGCAACCTCTGCCTC 39263  
GAGGTAGAGGTTGCAGTGA  
|||||||  
CTCCGTCTCCAACGTCACT

GAM1552 VENTX2 3' TCACTGCAACCTCCGCCTC 27117 TA  
GAGG GAGGTTGCAGTGA  
||| |||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 VHL 3' TCACTGCAACCTCTGCCTC 5084  
GAGGTAGAGGTTGCAGTGA  
|||||||  
CTCCGTCTCCAACGTCACT

GAM1552 ZIC1 5' TCGACTCACCCTCCCTCCTCCT 12725 TA TTGCA  
C GAGG GAGG GTGAGTCGA  
||| ||| |||||  
CTCC CTCC CACTCAGCT  
TC CTCC\_

GAM1552 ZNF133 5' TCAACTCACTGCAACCTCCACC 12839 A C  
GGT GAGGTTGCAGTGAGT GA  
||| ||||| ||

			CCA CTCCAACGTCACTCA CT		
			C            A		
GAM1552	ZNF264	3'	TCTCTGCAACCTCTGCCTC	12767	T
			GAGGTAGAGGTTGCAG GA		
			CTCCGTCTCCAACGTC CT		
			T		
GAM1552	ZNF264	3'	TCACTGCAACCTCCGCCTC	12764	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	20D7-FC4	5'	TCACTGCAGCCTCCACCTC	60908	A
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCGACGTCACT		
			C		
GAM1552	ARHF	3'	TCACTGCAAGCTCCACCTC	38748	A G
			GAGGT GAG TTGCAGTGA		
			CTCCA CTC AACGTCACT		
			C G		
GAM1552	ARHGAP5	5'	TCGGCTCACCACAACCCCCACC	77081	AGA CA
	TC		GAGGT GGTG GTGAGTCGA		
			CTCCA CCAAC CACTCGGCT		
			CCC AC		
GAM1552	ARPP-19	3'	TCACTGCAACCTCTGCCTC	21801	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCACT		
GAM1552	ASB16	5'	TCACTGCAACCTCCGCCTC	69943	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	ASE-1	3'	TCACTGCAACCTCCGCCTC	23953	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	ATP1B4	3'	TCGGCTCACTGCAACCTCCACC	23829	A
	TC		GAGGT GAGGTTGCAGTGAGTCGA		
			CTCCA CTCCAACGTCACTCGGCT		
			C		
GAM1552	BA108L7.2	3'	TCACTGCAACCTCTGCCTC	48266	
			GAGGTAGAGGTTGCAGTGA		

CTCCGTCTCCAACGTCACT

GAM1552 BAG5 3' TCAGCTCACTGCAACCTCCACC 16853 A C  
TC GAGGT GAGGTTGCAGTGAGT GA  
||||| ||||| ||  
CTCCA CTCCAACGTCAGTCTG CT  
C A

GAM1552 BNIP-S 3' TCACTGCAACCTCCGCCTC 56266 TA  
GAGG GAGGTTGCAGTGA  
||||| |||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 BTN3A1 3' CTGCAACCTCCACCTC 22918 A  
GAGGT GAGGTTGCAG  
||||| |||||  
CTCCA CTCCAACGTC  
C

GAM1552 C1orf24 3' TCACTGCAACCTCCGCCTC 53725 TA  
GAGG GAGGTTGCAGTGA  
||||| |||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 C1QTNF6 3' TCACTGCAACCTCTGCCTC 49150  
GAGGTAGAGGTTGCAGTGA  
||||| |||||  
CTCCGTCTCCAACGTCACT

GAM1552 C21orf25 3' TACTGCAACCTCCACCTC 63556 A  
GAGGT GAGGTTGCAGTG  
||||| |||||  
CTCCA CTCCAACGTCAT  
C

GAM1552 C3F 3' TCAGCTCACC GCAACCTCCACC 19298 A A C  
TC GAGGT GAGGTTGC GTGAGT GA  
||||| ||||| ||||| ||  
CTCCA CTCCAACG CACTCG CT  
C C A

GAM1552 C9orf9 3' TCACTGCAACCTCCGCCTC 38525 TA  
GAGG GAGGTTGCAGTGA  
||||| |||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 C9orf9 3' TCACTGCAACCTCCACCTC 38523 A  
GAGGT GAGGTTGCAGTGA  
||||| |||||  
CTCCA CTCCAACGTCACT  
C

GAM1552 CEACAM8 3' TCAACTCACTGCAAGCTCCGCC 8424 TA G C  
TC GAGG GAG TTGCAGTGAGT GA  
||||| ||||| ||||| ||

			CTCC CTC AACGTC	ACTCA CT		
			GC G	A		
GAM1552	CENPH	3'	TC	ACTGCAACCTCTGCCTC	43276	
				GAGGTAGAGGTTGCAGTGA		
				CTCCGTCTCCAACGTC	ACT	
GAM1552	CHRA1	3'	TC	ACTGCAACCTCCGCCTC	33876	TA
				GAGG GAGGTTGCAGTGA		
				CTCC CTCCAACGTC	ACT	
				GC		
GAM1552	CLSTN2	3'	ACT	CACTGTGCGTCTCCTC	42119	T G T
				GAGG AGA GT GCAGTGAGT		
				CTCC TCT CG TGTC	ACTCA	
				- G -		
GAM1552	CPSF2	3'	TC	ACCGCAACCTCTGCCTC	61598	A
				GAGGTAGAGGTTGC	GTGA	
				CTCCGTCTCCAACG	CACT	
				C		
GAM1552	DBR1	3'	TC	ACCGCAACCTCCGCCTC	32537	TA A
				GAGG GAGGTTGC	GTGA	
				CTCC CTCCAACG	CACT	
				GC C		
GAM1552	DKFZp434A2417	3'	TC	ACTGCAACTTCCACCTC	66107	A
				GAGGT GAGGTTGCAGTGA		
				CTCCA CTTCAACGTC	ACT	
				C		
GAM1552	DKFZP434C212	3'	TC	ACTGCAACCTCCACCTC	68918	A
				GAGGT GAGGTTGCAGTGA		
				CTCCA CTCCAACGTC	ACT	
				C		
GAM1552	DKFZp434E2220	5'	TC	ACTGCAACCTCCGCCTC	34302	TA
				GAGG GAGGTTGCAGTGA		
				CTCC CTCCAACGTC	ACT	
				GC		
GAM1552	DKFZp547H025	3'	TC	AGCTCACTGCAACCTCCACC	39366	A C
	TC			GAGGT GAGGTTGCAGTGAGT	GA	
				CTCCA CTCCAACGTC	ACTCG CT	
				C A		
GAM1552	DKFZP564O0523	3'	TC	GGCTCACTGCAACCTCCACC	49520	A
	TC			GAGGT GAGGTTGCAGTGAGTCGA		

			CTCCA CTCCAACGTC	ACTCGGCT		
			C			
GAM1552	DKFZp761J139	5'	TCACTGCAACGTCCACCTC	50118	A	G
			GAGGT GA GTTGCAGTGA			
			CTCCA CT CAACGTC			
			C			
GAM1552	DKFZp761N1114	3'	TCACTGCAACCTCCGCCTC	79024	TA	
			GAGG GAGGTTGCAGTGA			
			CTCC CTCCAACGTC			
			GC			
GAM1552	DKFZp762P2111	3'	TCACTGCAACCTCCGCCTC	86363	TA	
			GAGG GAGGTTGCAGTGA			
			CTCC CTCCAACGTC			
			GC			
GAM1552	DRIL2	3'	TCAATAAACCTCTACCTC	21329		GCAG
			GAGGTAGAGGTT TGA			
			CTCCATCTCCAA ACT			
			ATA_			
GAM1552	DSCR6	3'	TCACTGCAACCTCCACTTC	38552	A	
			GAGGT GAGGTTGCAGTGA			
			CTTCA CTCCAACGTC			
			C			
GAM1552	EREG	3'	TCGGCTCACTGCAACCTCACCT	7513	A	
	C		GAGGT GAGGTTGCAGTGAGTCGA			
			CTCCA CTCCAACGTC			
			ACTCGGCT			
			-			
GAM1552	FBP17	3'	TCGGCTCACTACAACCTCCACC	72810	A	C
	TC		GAGGT GAGGTTG AGTGAGTCGA			
			CTCCA CTCCAAC TCACTCGGCT			
			C A			
GAM1552	FER1L4	3'	TCGGCTGACTGCAACCTCCACC	47362	A	G
	TC		GAGGT GAGGTTGCAGT AGTCGA			
			CTCCA CTCCAACGTCA TCGGCT			
			C G			
GAM1552	FER1L4	3'	TCGGCTGACTGCAACCTCCACC	47361	A	G
	TC		GAGGT GAGGTTGCAGT AGTCGA			
			CTCCA CTCCAACGTCA TCGGCT			
			C G			
GAM1552	FLJ00024	5'	TCACTGCAACCTCTGCCTC	63766		
			GAGGTAGAGGTTGCAGTGA			

CTCCGTCTCCAACGTCACT

GAM1552 FLJ10232 3' TCACTGCAACCTCCGCCTC 35929 TA  
GAGG GAGGTTGCAGTGA  
|||| |||||||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 FLJ10346 5' TCGGCTCACTGCAAGCTCCACC 36050 A G  
TC GAGGT GAG TTGCAGTGAGTCGA  
|||| ||| |||||||||  
CTCCA CTC AACGTCACTCGGCT  
C G

GAM1552 FLJ10535 3' TCACTGCAACCTCTGCCTC 36248  
GAGGTAGAGGTTGCAGTGA  
|||||||||||  
CTCCGTCTCCAACGTCACT

GAM1552 FLJ10922 3' TCACTGCAACCTCCGCCTC 36879 TA  
GAGG GAGGTTGCAGTGA  
|||| |||||||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 FLJ11004 5' TCGGCTCACTGCAACCTCTACC 36973  
TC GAGGTAGAGGTTGCAGTGAGTCGA  
|||||||||||  
CTCCATCTCCAACGTCACTCGGCT

GAM1552 FLJ11106 5' TCTTGCAACCTCACCTC 37055 A T  
GAGGT GAGGTTGCAG GA  
|||| |||||| ||  
CTCCA CTCCAACGTT CT

GAM1552 FLJ12363 3' TCAGCTCACTGCAACCTCCACC 49692 A C  
TC GAGGT GAGGTTGCAGTGAGT GA  
|||| ||||||||| ||  
CTCCA CTCCAACGTCACTCG CT  
C A

GAM1552 FLJ12409 3' TCACTGCAACCTCCGCCTC 47052 TA  
GAGG GAGGTTGCAGTGA  
|||| |||||||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 FLJ12572 5' TCACTGCAACCTCTGCCTC 43255  
GAGGTAGAGGTTGCAGTGA  
|||||||||||  
CTCCGTCTCCAACGTCACT

GAM1552 FLJ12649 3' TCACTGCAACCTCCGCCTC 44785 TA  
GAGG GAGGTTGCAGTGA  
|||| |||||||||

			CTCC CTCCAACGTCACT		
			GC		
GAM1552	FLJ12668	3'	TCACTGCAACCTCCATCTC	46524	A
			GAGGT GAGGTTGCAGTGA		
			CTCTA CTCCAACGTCACT		
			C		
GAM1552	FLJ12687	3'	TCACTGCAACCTCCGCCTC	46202	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	FLJ12747	3'	TCACTGCAACCTCTGCCTC	49724	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCACT		
GAM1552	FLJ12973	3'	TCACCGCAACCTCCGCCTC	46107	TA A
			GAGG GAGGTTGC GTGA		
			CTCC CTCCAACG CACT		
			GC C		
GAM1552	FLJ12975	3'	TCACCACAACCTCCTCCTC	69590	TA CA
			GAGG GAGGTTG GTGA		
			CTCC CTCCAAC CACT		
			TC AC		
GAM1552	FLJ13072	5'	TCACTGCAACCTCTGCCTC	89826	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCACT		
GAM1552	FLJ13197	3'	TCGGCTCACTGCAACCTCTACC	44865	
	TC		GAGGTAGAGGTTGCAGTGAGTCGA		
			CTCCATCTCCAACGTCACTCGGCT		
GAM1552	FLJ14950	3'	TCACTGCAACCTCCACCTC	51727	A
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCAACGTCACT		
			C		
GAM1552	FLJ14957	3'	TCACTGCAACCTCTGCCTC	51758	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCACT		
GAM1552	FLJ20004	3'	TCATTGCAACCTCCGCCTC	95299	TA
			GAGG GAGGTTGCAGTGA		



		CTCC CTCCAACGTTACT		
		GC		
GAM1552	FLJ20034	3' TCACTGCAACCTCTGCCTC	34384	
		GAGGTAGAGGTTGCAGTGA		
		CTCCGTCTCCAACGTC		
GAM1552	FLJ20045	3' TCACTGCAACCTCTGCCTC	34428	
		GAGGTAGAGGTTGCAGTGA		
		CTCCGTCTCCAACGTC		
GAM1552	FLJ20079	3' TCACCGCAACCTCCACCTC	34500	A A
		GAGGT GAGGTTGC GTGA		
		CTCCA CTCCAACG CACT		
		C C		
GAM1552	FLJ20342	3' TCACTGCAACCTCTGCCTC	34993	
		GAGGTAGAGGTTGCAGTGA		
		CTCCGTCTCCAACGTC		
GAM1552	FLJ20344	3' TCACTGCAACCTCCGCCTC	35016	TA
		GAGG GAGGTTGCAGTGA		
		CTCC CTCCAACGTC		
		GC		
GAM1552	FLJ20507	3' TCACTGCAACCTCTGCCTC	35298	
		GAGGTAGAGGTTGCAGTGA		
		CTCCGTCTCCAACGTC		
GAM1552	FLJ20507	3' TCACTGCAACCTCTGCCTC	60233	
		GAGGTAGAGGTTGCAGTGA		
		CTCCGTCTCCAACGTC		
GAM1552	FLJ20511	3' TCGGCTCACTGCAAGCTCCACC	35332	A G
	TC	GAGGT GAG TTGCAGTGAGTCGA		
		CTCCA CTC AACGTC		
		C G		
GAM1552	FLJ20813	3' TCACTGCAACTCCACCTC	35689	A G
		GAGGT GAG TTGCAGTGA		
		CTCCA CTC AACGTC		
		C _		
GAM1552	FLJ21302	3' TCACTGCAACCTCCGCCTC	43219	TA
		GAGG GAGGTTGCAGTGA		

CTCC CTCCAACGTCACT  
 GC  
 GAM1552 FLJ22002 3' TCACTGCAACCTCCGCCTC 45776 TA  
 GAGG GAGGTTGCAGTGA  
 |||| |||||  
 CTCC CTCCAACGTCACT  
 GC  
 GAM1552 FLJ22531 5' TCGGCTCACTGCAACCTCCACC 45035 A  
 TC GAGGT GAGGTTGCAGTGAGTCGA  
 |||| |||||  
 CTCCA CTCCAACGTCACTCGGCT  
 C  
 GAM1552 FLJ22794 3' TCACTGCAACTTCCACCTC 91611 A  
 GAGGT GAGGTTGCAGTGA  
 |||| |||||  
 CTCCA CTTCAACGTCACT  
 C  
 GAM1552 FLJ22965 3' TCACTGCAACCTCCGCCTC 42053 TA  
 GAGG GAGGTTGCAGTGA  
 |||| |||||  
 CTCC CTCCAACGTCACT  
 GC  
 GAM1552 FLJ22969 3' TCACTGCAACCTCTGCCTC 68661  
 GAGGTAGAGGTTGCAGTGA  
 |||||  
 CTCCGTCTCCAACGTCACT  
  
 GAM1552 FLJ23024 3' TCACTGCAACCTCTGCCTC 46273  
 GAGGTAGAGGTTGCAGTGA  
 |||||  
 CTCCGTCTCCAACGTCACT  
  
 GAM1552 FLJ23392 3' TCACTGCAACCTCTGCCTC 45544  
 GAGGTAGAGGTTGCAGTGA  
 |||||  
 CTCCGTCTCCAACGTCACT  
  
 GAM1552 FLJ23563 3' TCACTGCAACCTCTGCCTC 67599  
 GAGGTAGAGGTTGCAGTGA  
 |||||  
 CTCCGTCTCCAACGTCACT  
  
 GAM1552 FLJ31101 3' TCACTGCAACCTCTGCCTC 35717  
 GAGGTAGAGGTTGCAGTGA  
 |||||  
 CTCCGTCTCCAACGTCACT  
  
 GAM1552 FLJ32865 3' TCACTGCAACCTCTGCCTC 58181  
 GAGGTAGAGGTTGCAGTGA  
 |||||

CTCCGTCTCCAACGTCACT

GAM1552 GAL3ST-4 3' TCACTGCAACCTCTGCCTC 44941  
GAGGTAGAGGTTGCAGTGA  
|||||  
CTCCGTCTCCAACGTCACT

GAM1552 GMPPB 5' TCGGCTCACTGCAACCTCCACC 95755 A  
TC GAGGT GAGGTTGCAGTGAGTCGA  
|||||  
CTCCA CTCCAACGTCACTCGGCT  
C

GAM1552 GNG4 3' TCAGCTCACTGCGACCTCCACC 15624 A C  
TC GAGGT GAGGTTGCAGTGAGT GA  
|||||  
CTCCA CTCCAGCGTCACTCG CT  
C A

GAM1552 GP5 3' TCACGGGCCCCGCAACCCCTCCT 15656 T A A\_ GA C  
C GAGG AG GGTTGC GT GT GA  
|||||  
CTCC TC CCAACG CG CA CT  
\_ C CC GG \_

GAM1552 GREB1 3' TCACTGCAACCTCTGCCTC 27885  
GAGGTAGAGGTTGCAGTGA  
|||||  
CTCCGTCTCCAACGTCACT

GAM1552 GRWD 3' TCACTGCAACCTCCGCCTC 48972 TA  
GAGG GAGGTTGCAGTGA  
|||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 GTF2E1 3' TCACTGCAACCTCTGCCTC 18618  
GAGGTAGAGGTTGCAGTGA  
|||||  
CTCCGTCTCCAACGTCACT

GAM1552 GTPBG3 3' TCGGCTTACTGCAACCTCCACC 50912 A  
TC GAGGT GAGGTTGCAGTGAGTCGA  
|||||  
CTCCA CTCCAACGTCATTCTGGCT  
C

GAM1552 GTPBG3 3' TCACTGCAACCTCCATCTC 50909 A  
GAGGT GAGGTTGCAGTGA  
|||||  
CTCTA CTCCAACGTCACT  
C

GAM1552 H-plk 5' TCGACTCACTGCAACCTCCACC 31813 A  
TC GAGGT GAGGTTGCAGTGAGTCGA  
|||||

			CTCCA CTCCAACGTC	ACTCAGCT	
			C		
GAM1552	HRH4	3'	TA	CTACTGCAACCTCTGCCTC	41256
				GAGGTAGAGGTTGCAGTGA	
				CTCCGTCTCCAACGTC	ACT
GAM1552	HSPC065	3'	TA	CTACTGCAACCTCCACCTC	26323
				GAGGT GAGGTTGCAGTGA	A
				CTCCA CTCCAACGTC	ACT
				C	
GAM1552	HSPC065	3'	TC	GCTGCAACCTCCTCCTC	26326
				GAGG GAGGTTGCAGTGA	TA
				CTCC CTCCAACGTC	GCT
				TC	
GAM1552	ICK	3'	TCT	CTGCAACCTCTGCCTC	29934
				GAGGTAGAGGTTGCAG	GA
				CTCCGTCTCCAACGTC	CT
				T	
GAM1552	JAM1	5'	TA	CTACTGCAACCTCCTCCTC	57933
				GAGG GAGGTTGCAGTGA	TA
				CTCC CTCCAACGTC	ACT
				TC	
GAM1552	JM11	3'	TA	CTACTGCAACCTCTGCCTC	53268
				GAGGTAGAGGTTGCAGTGA	
				CTCCGTCTCCAACGTC	ACT
GAM1552	KIAA0063	3'	TC	GCGTCACTGCAACCTCCACC	29644
				GAGGT GAGGTTGCAGTGAGTCGA	A
				CTCCA CTCCAACGTC	ACTCGGCT
				C	
GAM1552	KIAA0391	3'	TA	CTACTGCAACCTCTGCCTC	27920
				GAGGTAGAGGTTGCAGTGA	
				CTCCGTCTCCAACGTC	ACT
GAM1552	KIAA0426	3'	TA	CTACTGCAACCTCCGCCTC	28264
				GAGG GAGGTTGCAGTGA	TA
				CTCC CTCCAACGTC	ACT
				GC	
GAM1552	KIAA0459	3'	TC	GCGTCACTGCAACCTCCACC	61009
				GAGGT GAGGTTGCAGTGAGTCGA	A

CTCCA CTCCAACGTCAGTCTCGGCT  
C  
GAM1552 KIAA0469 3' TCACTGCAGCCTCCACCTC 29350 A  
GAGGT GAGGTTGCAGTGA  
||||| |||||||||  
CTCCA CTCCGACGTCAGT  
C  
GAM1552 KIAA0513 3' TCTACTCACTGCAACCTCCACC 28378 A C  
TC GAGGT GAGGTTGCAGTGAGT GA  
||||| ||||||||| ||  
CTCCA CTCCAACGTCAGTCA CT  
C T  
GAM1552 KIAA0513 5' TCACTGCAGCCTCCACCTC 28372 A  
GAGGT GAGGTTGCAGTGA  
||||| |||||||||  
CTCCA CTCCGACGTCAGT  
C  
GAM1552 KIAA0527 3' TCACTGCAACCTCTGCCTC 95808  
GAGGTAGAGGTTGCAGTGA  
||||| |||||||||  
CTCCGTCTCCAACGTCAGT  
GAM1552 KIAA0544 3' CACGCACCTCTACC 70893 T A  
GGTAGAGGT GC GTG  
||||| || |||  
CCATCTCCA CG CAC  
— —  
GAM1552 KIAA0544 3' TCACTGCAACCTCCGCCTC 70908 TA  
GAGG GAGGTTGCAGTGA  
||||| |||||||||  
CTCC CTCCAACGTCAGT  
GC  
GAM1552 KIAA0557 3' TCACCACAACCTCCACCTC 78008 A CA  
GAGGT GAGGTTG GTGA  
||||| ||||| |||  
CTCCA CTCCAAC CACT  
C AC  
GAM1552 KIAA0561 3' TCACTGCAACCTCCGCCTC 65895 TA  
GAGG GAGGTTGCAGTGA  
||||| |||||||||  
CTCC CTCCAACGTCAGT  
GC  
GAM1552 KIAA0562 3' CTGCAACCTCCGCCTC 28152 TA  
GAGG GAGGTTGCAG  
||||| |||||||||  
CTCC CTCCAACGTC  
GC  
GAM1552 KIAA0563 5' TCACTGCAACCTCTGCCTC 29192  
GAGGTAGAGGTTGCAGTGA  
||||| |||||||||

CTCCGTCTCCAACGTCACT

GAM1552 KIAA0594 3' TCGGCTTACTGCAACCTCCGCC 64906 TA  
TC GAGG GAGGTTGCAGTGAGTCGA

|||||  
CTCC CTCCAACGTCATTTCGGCT  
GC

GAM1552 KIAA0599 3' TCACTGCAACCTCCGCCTC 77190 TA  
GAGG GAGGTTGCAGTGA

|||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 KIAA0599 3' TACTGCAACCTCCGCCTC 77189 TA  
GAGG GAGGTTGCAGTG

|||||  
CTCC CTCCAACGTCAT  
GC

GAM1552 KIAA0630 3' TTTACCACCACCTCTACC 89400 TGCA  
GGTAGAGGT GTGAG

|||||  
CCATCTCCA CATT  
CCAC

GAM1552 KIAA0720 3' TCACTGCAACCTCTGCCTC 62329  
GAGGTAGAGGTTGCAGTGA

|||||  
CTCCGTCTCCAACGTCACT

GAM1552 KIAA0841 3' TCACTGCAACCTCTGCCTC 71398  
GAGGTAGAGGTTGCAGTGA

|||||  
CTCCGTCTCCAACGTCACT

GAM1552 KIAA0841 3' TCACTGCAACCTCCGCCTC 71396 TA  
GAGG GAGGTTGCAGTGA

|||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 KIAA0924 3' TCACTGCAACCCCGCC 29722 AGA  
GGT GGTTGCAGTGA

|||  
CCG CCAACGTCACT  
CCC

GAM1552 KIAA1041 3' TCACTGCAACCTCCGCCTC 30139 TA  
GAGG GAGGTTGCAGTGA

|||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 KIAA1054 3' TCACTGCAACCTCCGCCTC 68449 TA  
GAGG GAGGTTGCAGTGA

|||||

		CTCC CTCCAACGTCACT			
		GC			
GAM1552	KIAA1161	5' TCACTGCAACCCCTCCTC	81760	T A	
		GAGG AG GGTTGCAGTGA			
		CTCC TC CCAACGTCACT			
		_ C			
GAM1552	KIAA1170	3' TCACTGCAACCTCCGCCTC	69860	TA	
		GAGG GAGGTTGCAGTGA			
		CTCC CTCCAACGTCACT			
		GC			
GAM1552	KIAA1193	3' TCACTGCAACCTCCGCCTC	67648	TA	
		GAGG GAGGTTGCAGTGA			
		CTCC CTCCAACGTCACT			
		GC			
GAM1552	KIAA1198	3' TCACCGCAACCTCCGCCTC	63332	TA	A
		GAGG GAGGTTGC GTGA			
		CTCC CTCCAACG CACT			
		GC C			
GAM1552	KIAA1198	3' TCACTGCAACCTCCACTTC	63334	A	
		GAGGT GAGGTTGCAGTGA			
		CTTCA CTCCAACGTCACT			
		C			
GAM1552	KIAA1209	3' TCACTGCAGCCTCCACCTC	60761	A	
		GAGGT GAGGTTGCAGTGA			
		CTCCA CTCCGACGTCACT			
		C			
GAM1552	KIAA1257	3' TCACCGCAACCTCCGCCTC	62757	TA	A
		GAGG GAGGTTGC GTGA			
		CTCC CTCCAACG CACT			
		GC C			
GAM1552	KIAA1320	5' TCACTGCAACCTCTGCCTC	69309		
		GAGGTAGAGGTTGCAGTGA			
		CTCGTCTCCAACGTCACT			
GAM1552	KIAA1373	3' TCAGCTCACTGCAACCTCCACC	70952	A	C
	TC	GAGGT GAGGTTGCAGTGAGT GA			
		CTCCA CTCCAACGTCACTCG CT			
		C A			
GAM1552	KIAA1497	5' TCACTGCAACCTCTGCCTC	67520		
		GAGGTAGAGGTTGCAGTGA			

CTCCGTCTCCAACGTCACT

GAM1552	KIAA1508	3'	TC	ACTGCAACCTCCGCCTC	61891	TA	
				GAGG GAGGTTGCAGTGA			
				CTCC CTCCAACGTCACT			
				GC			
GAM1552	KIAA1571	3'	TC	ACCGCAACCTCCACCTC	60960	A	A
				GAGGT GAGGTTGC GTGA			
				CTCCA CTCCAACG CACT			
				C C			
GAM1552	KIAA1615	3'	GAT	CACTGCAACCTCCACCTC	68712	A	G
				GAGGT GAGGTTGCAGTGA TC			
				CTCCA CTCCAACGTCACT AG			
				C —			
GAM1552	KIAA1655	3'	TC	ACTGTAACCTCCACCTC	66624	A	
				GAGGT GAGGTTGCAGTGA			
				CTCCA CTCCAATGTCACT			
				C			
GAM1552	KIAA1655	3'	TC	ATTGCAACCTCCGCCTC	66628	TA	
				GAGG GAGGTTGCAGTGA			
				CTCC CTCCAACGTTACT			
				GC			
GAM1552	KIAA1737	3'	TC	ACTGCAACCTCCGCCTC	67362	TA	
				GAGG GAGGTTGCAGTGA			
				CTCC CTCCAACGTCACT			
				GC			
GAM1552	KIAA1784	3'	TC	ACTGCAACCTCCGCCTC	65154	TA	
				GAGG GAGGTTGCAGTGA			
				CTCC CTCCAACGTCACT			
				GC			
GAM1552	KIAA1922	5'	TC	ACTGCAACCTCCGCCTC	73641	TA	
				GAGG GAGGTTGCAGTGA			
				CTCC CTCCAACGTCACT			
				GC			
GAM1552	KIAA1956	3'	TC	ACTGCAGCCTCCACCTC	78440	A	
				GAGGT GAGGTTGCAGTGA			
				CTCCA CTCCGACGTCACT			
				C			
GAM1552	KIAA1971	3'	TAC	TGCAACCTCCACCTC	74227	A	
				GAGGT GAGGTTGCAGTG			



			CTCCA CTCCAACGTCAT		
			C		
GAM1552	KLK7	3'	TCACTGCAACCTCCGCCTC	17296	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	KLK7	3'	TCACTGCAACCTCCGCCTC	57736	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	MCLC	3'	TCGGCTCACTGCAACCTCCACC	30695	A
	TC		GAGGT GAGGTTGCAGTGAGTCGA		
			CTCCA CTCCAACGTCACTCGGCT		
			C		
GAM1552	MEF-2	3'	TCACTGCAACCTCCGCCTC	64395	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	MGC12518	3'	TACTGCAACCTCTGCC	64083	
			GGTAGAGGTTGCAGTG		
			CCGTCTCCAACGTCAT		
GAM1552	MGC13138	3'	TCACTGCAACCTCTGCCTC	53023	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCACT		
GAM1552	MGC14836	3'	TCACTGCAACCTCCGCCTC	53039	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	MGC1842	3'	TACTACAACCTCCGCCTC	65657	TA C
			GAGG GAGGTTG AGTG		
			CTCC CTCCAAC TCAT		
			GC A		
GAM1552	MGC2474	3'	TCGACTCACTGCAACTTCCACC	43732	A
	TC		GAGGT GAGGTTGCAGTGAGTCGA		
			CTCCA CTTCAACGTCACTCAGCT		
			C		
GAM1552	MGC29891	3'	TCACTGCAACCTCCGCCTC	58216	TA
			GAGG GAGGTTGCAGTGA		

			CTCC CTCCAACGTCACT		
			GC		
GAM1552	MGC3113	3'	TCACTGCAGCCTCCACCTC	43850	A
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCGACGTCACT		
			C		
GAM1552	MGC3329	3'	TCACTGCAACCCCCGCCTC	44019	AGA
			GAGGT GGTTCAGTGA		
			CTCCG CCAACGTCACT		
			CCC		
GAM1552	MGC5149	3'	TCACTGCAACCTCTGCCTC	72297	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCACT		
GAM1552	MGC9912	3'	TCGGCTCACTGCAACCTCCACC	54724	A
	TC		GAGGT GAGGTTGCAGTGAGTCGA		
			CTCCA CTCCAACGTCACTCGGCT		
			C		
GAM1552	MLZE	5'	TCACTGCAACCTCTGCCTC	48625	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCACT		
GAM1552	MMPL1	3'	TCACTGCAGCCTCCACCTC	14724	A
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCGACGTCACT		
			C		
GAM1552	moblak	3'	TCACTGCATCCTCCACCTC	55511	A T
			GAGGT GAGG TGCAGTGA		
			CTCCA CTCC ACGTCACT		
			C T		
GAM1552	MOCS3	3'	TCACTGCAACCTCCGCCTC	27158	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	MRPL44	3'	TCGGCTCACTGCAACCTCCACC	43328	A
	TC		GAGGT GAGGTTGCAGTGAGTCGA		
			CTCCA CTCCAACGTCACTCGGCT		
			C		
GAM1552	MtFMT	3'	TCACTGCAACCTCCGCCTC	57657	TA
			GAGG GAGGTTGCAGTGA		

			CTCC CTCCAACGTCACT			
			GC			
GAM1552	NDUFB1	5'	TCACTGCAACCTCTGCCTC	15819		
			GAGGTAGAGGTTGCAGTGA			
			CTCCGTCTCCAACGTCACT			
GAM1552	NDUFC2	3'	TCGGCTCACTGCAACCTCCACC	15844	A	
	TC		GAGGT GAGGTTGCAGTGAGTCGA			
			CTCCA CTCCAACGTCACTCGGCT			
			C			
GAM1552	Nup43	3'	TCGGCTCACTGCAACCTCCACC	45011	A	
	TC		GAGGT GAGGTTGCAGTGAGTCGA			
			CTCCA CTCCAACGTCACTCGGCT			
			C			
GAM1552	OR51E2	3'	TCACTGCAACCTCCAC	47797	A	
			GT GAGGTTGCAGTGA			
			CA CTCCAACGTCACT			
			C			
GAM1552	OSBPL2	3'	TCACCGCAACCTCCGCCTC	57870	TA	A
			GAGG GAGGTTGC GTGA			
			CTCC CTCCAACG CACT			
			GC C			
GAM1552	OSBPL2	3'	TCACCGCAACCTCCGCCTC	29219	TA	A
			GAGG GAGGTTGC GTGA			
			CTCC CTCCAACG CACT			
			GC C			
GAM1552	PASK	5'	TCACTGCAACCTCTGCCTC	30724		
			GAGGTAGAGGTTGCAGTGA			
			CTCCGTCTCCAACGTCACT			
GAM1552	PELI1	5'	TCACTGCAACCTCCTCCTC	40283	TA	
			GAGG GAGGTTGCAGTGA			
			CTCC CTCCAACGTCACT			
			TC			
GAM1552	PELI1	5'	TCACTGCAACCTCTGCCTC	40285		
			GAGGTAGAGGTTGCAGTGA			
			CTCCGTCTCCAACGTCACT			
GAM1552	PIP3-E	3'	TCACTGCAACCTCTGCCTC	66812		
			GAGGTAGAGGTTGCAGTGA			

CTCCGTCTCCAACGTCACT

GAM1552 PRO0365 5' TCAGCTCACTGCAACCTCCACC 26170 A C  
TC GAGGT GAGGTTGCAGTGAGT GA

||||| |||||||||||| ||  
CTCCA CTCCAACGTCACTCG CT  
C A

GAM1552 PRO1992 5' TCACTGCAACCTCTGCCTC 26061  
GAGGTAGAGGTTGCAGTGA  
||||| ||||||||||||  
CTCCGTCTCCAACGTCACT

GAM1552 PRO2955 3' TCACTGCAACCTCTGCCTC 37645  
GAGGTAGAGGTTGCAGTGA  
||||| ||||||||||||  
CTCCGTCTCCAACGTCACT

GAM1552 PSTPIP2 3' TCACTGCAACCTCTGCCTC 44396  
GAGGTAGAGGTTGCAGTGA  
||||| ||||||||||||  
CTCCGTCTCCAACGTCACT

GAM1552 RAB21 3' TCGGCTCACTGCAAGCTCCACC 30393 A G  
TC GAGGT GAG TTGCAGTGAGTCGA

||||| ||| ||||||||||||  
CTCCA CTC AACGTCACTCGGCT  
C G

GAM1552 RAB33B 3' TCACTGCAACCTCCGCCTC 48506 TA  
GAGG GAGGTTGCAGTGA  
||||| ||||||||||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 RAI 5' TCACTGCAACCTCCGCCTC 21886 TA  
GAGG GAGGTTGCAGTGA  
||||| ||||||||||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 RNF20 3' CACCAAACCTCTACCTC 38965 GCA  
GAGGTAGAGGTT GTG  
||||| ||| ||  
CTCCATCTCCAA CAC  
AC\_

GAM1552 RNF8 3' TCAGCTCACTGCAACCTCCACC 14241 A C  
TC GAGGT GAGGTTGCAGTGAGT GA

||||| |||||||||||| ||  
CTCCA CTCCAACGTCACTCG CT  
C A

GAM1552 RNO2 5' TCACTGCAACCTCCACCTT 52776 A  
GAGGT GAGGTTGCAGTGA  
||||| ||||||||||||

			TTCCA CTCCAACGTC		
			C		
GAM1552	SC4MOL	3'	TCACTGCAACCTCTGCCTC	22161	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTC		
GAM1552	SCAMP-4	3'	TCACTGCAACCTCTGCCTC	54399	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTC		
GAM1552	SCYA16	3'	TCACTGTAACCTCCACCTC	15967	A
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCAATGT		
			C		
GAM1552	SCYA22	3'	TCGGCTCACTACAACCTCGACC	90963	A C
	TC		GAGGT GAGGTTG AGTGAGTCGA		
			CTCCA CTCCAAC TCACTCGGCT		
			G A		
GAM1552	SERF1B	3'	CATGCAACCTCTGCCTC	43412	G
			GAGGTAGAGGTTGCA TG		
			CTCCGTCTCCAACGT AC		
GAM1552	SERF1B	3'	TCACTGCAACCTCCGCCTC	43422	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTC		
			GC		
GAM1552	SIRPB1	3'	TCACTGCAACCCCGCCTC	20263	AGA
			GAGGT GGTTCAGTGA		
			CTCCG CCAACGTC		
			CCC		
GAM1552	SLC11A1	3'	TCATTGCAACCTCCACCTT	59460	A
			GAGGT GAGGTTGCAGTGA		
			TTCCA CTCCAACGTT		
			C		
GAM1552	SLC2A10	3'	TCACTGCAACCTCCACTTC	47827	A
			GAGGT GAGGTTGCAGTGA		
			CTTCA CTCCAACGTC		
			C		
GAM1552	SP2	3'	CGCCACAACCTCTCCTC	11887	T CA
			GAGG AGAGGTTG GTG		

			CTCC TCTCCAAC CGC		
			— AC		
GAM1552	STAF65(gamma)	3'	TCGACTCACTGCAACCTCTGCC 29446		
	TC		GAGGTAGAGGTTGCAGTGAGTCGA		
			CTCCGTCTCCAACGTCAGCT		
GAM1552	SUN1	3'	TCACTGCAGCCTCCACCTC 47161	A	
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCGACGTCAGT		
			C		
GAM1552	SYT13	3'	TCACTGCAACCTCCGCCTC 93458	TA	
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCAGT		
			GC		
GAM1552	TOR1B	3'	TCAACTCACTGCAACCTCCGCT 27205	TA	C
			GG GAGGTTGCAGTGAGT GA		
			TC CTCCAACGTCAGTCA CT		
			GC A		
GAM1552	TRIM5	3'	TCGGTTCAGTCAACCTCCACC 52306	A	GT
	TC		GAGGT GAGGTTGCAGTGA CGA		
			CTCCA CTCCAACGTCAGT GCT		
			C TG		
GAM1552	TRIM6	3'	TCACTGCAACCTCTGCCTC 54144		
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCAGT		
GAM1552	TU12B1-TY	3'	TCACTGCAACCTCTGCCTC 33404		
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCAGT		
GAM1552	TUCAN	3'	TCACTGCAACCTCTGCCTC 30281		
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCAGT		
GAM1552	UBF-fl	3'	TCACTGCAACCTCTGCCTC 51571		
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCAGT		
GAM1552	USP22	3'	TCGGCTCACTGCAACCTCCACC 68028	A	
	TC		GAGGT GAGGTTGCAGTGAGTCGA		

			CTCCA CTCCAACGTCACCTCGGCT		
			C		
GAM1552	VDU1	3'	TCACTGCAGCCTCCACCTC	30426	A
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCGACGTCACCT		
			C		
GAM1552	VPS33A	3'	TCACCTCACTGCAACCTCCACC	43343	A
			GAGGT GAGGTTGCAGTGAG		TC
			CTCCA CTCCAACGTCACCTC		CT
			C		
			CA		
GAM1552	WBSCR20A	5'	TCACCGCAACCTCTGCCTC	49656	A
			GAGGTAGAGGTTGC		
			CTCCGTCTCCAACG		CACT
			C		
GAM1552	ZNF364	3'	CTTCTCCAACCTCTACC	66771	C T
			GGTAGAGGTTG		AG GAG
			CCATCTCCAAC		TC TTC
			C		
			_		
GAM1552	ZTL1	3'	TCACTGCAACCTCTGCCTC	43919	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCACCT		
GAM1552	LOC112724	5'	TCGGCTCACTGCAACCTCCACC	56503	A
			GAGGT GAGGTTGCAGTGAGTCGA		
			CTCCA CTCCAACGTCACCTCGGCT		
			C		
GAM1552	LOC113675	5'	TCACTGCAACCTCCGCCTC	56572	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACCT		
			GC		
GAM1552	LOC115219	5'	TCACTGCAACCTCCGCCTC	73320	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACCT		
			GC		
GAM1552	LOC116411	5'	TCGCTACAACCTCCACCTC	73874	A C
			GAGGT GAGGTTG		AGTGA
			CTCCA CTCCAAC		TCGCT
			C		A
GAM1552	LOC119392	3'	TCACTGCAACCTCTGCCTC	59138	
			GAGGTAGAGGTTGCAGTGA		

## CTCCGTCTCCAACGTCACT

GAM1552	LOC120114	3'	TCAGCTCACTGCAATCTCCACC	75539	A	C
		TC	GAGGT GAGGTTGCAGTGAGT GA			
			CTCCA CTCTAACGTCACTCG CT			
			C A			
GAM1552	LOC120939	3'	TCACTGTAACCTCCACCTC	76260	A	
			GAGGT GAGGTTGCAGTGA			
			CTCCA CTCCAATGTCACT			
			C			
GAM1552	LOC126364	3'	TCACTGCAACCTCCGCCTC	75698	TA	
			GAGG GAGGTTGCAGTGA			
			CTCC CTCCAACGTCACT			
			GC			
GAM1552	LOC126661	3'	TCACTGCAACCTCCGCCTC	74557	TA	
			GAGG GAGGTTGCAGTGA			
			CTCC CTCCAACGTCACT			
			GC			
GAM1552	LOC128077	3'	TCACTGCAACCTCCGCCTC	74718	TA	
			GAGG GAGGTTGCAGTGA			
			CTCC CTCCAACGTCACT			
			GC			
GAM1552	LOC128077	3'	TCACTGCAACCTCTGCCTC	74720		
			GAGGTAGAGGTTGCAGTGA			
			CTCCGTCTCCAACGTCACT			
GAM1552	LOC128387	3'	TCACTGCAACCTCCACTTC	74752	A	
			GAGGT GAGGTTGCAGTGA			
			CTTCA CTCCAACGTCACT			
			C			
GAM1552	LOC128989	3'	TCACTGCAACCTCCGCCTC	74816	TA	
			GAGG GAGGTTGCAGTGA			
			CTCC CTCCAACGTCACT			
			GC			
GAM1552	LOC130813	3'	TCACCGCAACCTCCGCCTC	75776	TA	A
			GAGG GAGGTTGC GTGA			
			CTCC CTCCAACG CACT			
			GC C			
GAM1552	LOC132625	3'	TCACTGCAACCTCCACCTC	75913	A	
			GAGGT GAGGTTGCAGTGA			



	CTCCA CTCCAACGTCACT		
	C		
GAM1552 LOC135154 3'	ACTCACTGCAACTTCCGCC 75211	TA	
	GG GAGGTTGCAGTGAGT		
	CC CTTCAACGTCACTCA		
	GC		
GAM1552 LOC135293 3'	TCACTGCAACCTCTGCCTC 76191		
	GAGGTAGAGGTTGCAGTGA		
	CTCCGTCTCCAACGTCACT		
GAM1552 LOC135763 3'	TCACTGCAACCTCCGCCTC 56792	TA	
	GAGG GAGGTTGCAGTGA		
	CTCC CTCCAACGTCACT		
	GC		
GAM1552 LOC142913 5'	CACTGCAGCCTCCACCTC 76414	A	
	GAGGT GAGGTTGCAGTG		
	CTCCA CTCCGACGTCAC		
	C		
GAM1552 LOC143187 3'	TCACTGCAACCTCCACCTC 59101	A	
	GAGGT GAGGTTGCAGTGA		
	CTCCA CTCCAACGTCACT		
	C		
GAM1552 LOC143241 5'	TCACTGCAACCTCTGCCTC 57179		
	GAGGTAGAGGTTGCAGTGA		
	CTCCGTCTCCAACGTCACT		
GAM1552 LOC144248 5'	CGCTCACTGCAACCTCCACCTC 76736	A	T
	GAGGT GAGGTTGCAGTGAG CG		
	CTCCA CTCCAACGTCACTC GC		
	C		
GAM1552 LOC144317 5'	TCAACTCACTGCAACCTCTTCC 76798	T	C
TC	GAGG AGAGGTTGCAGTGAGT GA		
	CTCC TCTCCAACGTCACTCA CT		
	T A		
GAM1552 LOC144524 5'	TCAGTCACTGCAACCTCCACC 83137	A	C
TC	GAGGT GAGGTTGCAGTGAGT GA		
	CTCCA CTCCAACGTCACTCG CT		
	C A		
GAM1552 LOC145268 5'	TCACTGCAACCTCCACCC 77061	A A	
	G GGT GAGGTTGCAGTGA		

		C CCA CTCCAACGTCACT		
		— C		
GAM1552	LOC145725 3'	TCACTGCAGCCTCCACCTC	77414	A
		GAGGT GAGGTTGCAGTGA		
		CTCCA CTCCGACGTCACT		
		C		
GAM1552	LOC145732 3'	TCACTGCAGCCTCCACCTC	77436	A
		GAGGT GAGGTTGCAGTGA		
		CTCCA CTCCGACGTCACT		
		C		
GAM1552	LOC145757 5'	TCACTACAACCTCTGCCTC	77473	C
		GAGGTAGAGGTTG AGTGA		
		CTCCGTCTCCAAC TCACT		
		A		
GAM1552	LOC146229 3'	CTGCAACCTCCACCTC	77749	A
		GAGGT GAGGTTGCAG		
		CTCCA CTCCAACGTC		
		C		
GAM1552	LOC146229 3'	TCACTGCAACCTCCACCTC	77771	A
		GAGGT GAGGTTGCAGTGA		
		CTCCA CTCCAACGTCACT		
		C		
GAM1552	LOC146784 5'	TCGGTCACTGCAACCTCCACC	78128	A
	TC	GAGGT GAGGTTGCAGTGAGTCGA		
		CTCCA CTCCAACGTCACTCGGCT		
		C		
GAM1552	LOC146839 3'	TCACCACAACCTCCGCCTC	83815	TA CA
		GAGG GAGGTTG GTGA		
		CTCC CTCCAAC CACT		
		GC AC		
GAM1552	LOC146901 3'	TCATTGCAACCTCCACCTT	83848	A
		GAGGT GAGGTTGCAGTGA		
		TTCCA CTCCAACGTTACT		
		C		
GAM1552	LOC146909 3'	TCACTGCAACCTCCGCCTC	78183	TA
		GAGG GAGGTTGCAGTGA		
		CTCC CTCCAACGTCACT		
		GC		
GAM1552	LOC146952 5'	TCAGTCACTGCAACCTCCACC	83874	A C
	TC	GAGGT GAGGTTGCAGTGAGT GA		

		CTCCA CTCCAACGTC	ACTCG CT		
		C	A		
GAM1552	LOC147071 5'	TC	ACTGCAACCTCTGCCTC	73005	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTC	ACT	
GAM1552	LOC147407 3'	TC	ACTGCAACCTCCGCCTC	76326	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTC	ACT	
			GC		
GAM1552	LOC147817 3'	TC	ACTGCAACCTCCACCTC	78504	A
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCAACGTC	ACT	
			C		
GAM1552	LOC147990 3'	TC	ACTACAACCTCTGCCTC	84100	C
			GAGGTAGAGGTTG	AGTGA	
			CTCCGTCTCCAAC	TC	ACT
			A		
GAM1552	LOC148137 3'	TC	ACGGCAACCTCCACCTC	58439	A A
			GAGGT GAGGTTGC	GTGA	
			CTCCA CTCCAACG	CACT	
			C	G	
GAM1552	LOC148189 5'	TC	GGCTCACTGCAACCTCCACC	78725	A
	TC		GAGGT GAGGTTGCAGTGAGTCGA		
			CTCCA CTCCAACGTC	ACTCGGCT	
			C		
GAM1552	LOC148198 3'	TC	AGCTCACTGCAACCTCCATC	70690	A C
	TC		GAGGT GAGGTTGCAGTGAGT	GA	
			CTCTA CTCCAACGTC	ACTCG CT	
			C	A	
GAM1552	LOC148709 3'	TC	ACTACAACCTCCGCCTC	78950	TA C
			GAGG GAGGTTG	AGTGA	
			CTCC CTCCAAC	TC	ACT
			GC	A	
GAM1552	LOC148918 5'	ACT	CAGCTTCTTCTACCTC	79053	TT AG
			GAGGTAGAGG	GC	TGAGT
			CTCCATCTTC	CG	ACTCA
			TT	—	
GAM1552	LOC148918 5'	TC	ACTGCAGCCTCCACCTC	79082	A
			GAGGT GAGGTTGCAGTGA		

	CTCCA CTCCGACGTCACT		
	C		
GAM1552 LOC149506 3'	TCACTGCAACCTCTGCCTC 84477		
	GAGGTAGAGGTTGCAGTGA		
	CTCCGTCTCCAACGTCACT		
GAM1552 LOC149506 3'	TCACTGCAACTTCCACCTC 84479	A	
	GAGGT GAGGTTGCAGTGA		
	CTCCA CTTCAACGTCACT		
	C		
GAM1552 LOC149577 3'	TCGGCTCACCACAACCTCCACC 84524	A	CA
TC	GAGGT GAGGTTG GTGAGTCGA		
	CTCCA CTCCAAC CACTCGGCT		
	C AC		
GAM1552 LOC150397 3'	TCATTGCAACCTCCGCCTC 79850	TA	
	GAGG GAGGTTGCAGTGA		
	CTCC CTCCAACGTTACT		
	GC		
GAM1552 LOC150519 3'	CTGCAACCTGCCACCTC 79915	AG_	
	GAGGT AGGTTGCAG		
	CTCCA TCCAACGTC		
	CCG		
GAM1552 LOC150696 3'	TCACTGCAGCCTCCACCTC 58487	A	
	GAGGT GAGGTTGCAGTGA		
	CTCCA CTCCGACGTCACT		
	C		
GAM1552 LOC150960 3'	TCGCTGCAACCTCCGCCTC 80072	TA	
	GAGG GAGGTTGCAGTGA		
	CTCC CTCCAACGTCGCT		
	GC		
GAM1552 LOC151057 3'	TCACTGCAACCTCTGCCTC 85215		
	GAGGTAGAGGTTGCAGTGA		
	CTCCGTCTCCAACGTCACT		
GAM1552 LOC151201 3'	TCAGCTCACTGCAACCTCCACC 85292	A	C
TC	GAGGT GAGGTTGCAGTGAGT GA		
	CTCCA CTCCAACGTCACTCG CT		
	C A		
GAM1552 LOC151475 5'	TCACTGCAACCTCTGCCTC 85418		
	GAGGTAGAGGTTGCAGTGA		

CTCCGTCTCCAACGTCACT

GAM1552 LOC151475 5' TCACTGCAACCTCCACCTC 85416 A  
GAGGT GAGGTTGCAGTGA  
||||| |||||||||  
CTCCA CTCCAACGTCACT  
C

GAM1552 LOC151826 3' TCACTGCAACCTCCGCCTC 80365 TA  
GAGG GAGGTTGCAGTGA  
||| |||||||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 LOC151877 3' TCGGCTCACTACAACCACCACC 85509 AGA C  
TC GAGGT GGTG AGTGAGTCGA  
|||| ||| |||||||  
CTCCA CCAAC TCACTCGGCT  
CCA A

GAM1552 LOC152343 3' TCGACTCAGTGCAACCTCCGCC 80573 TA G  
TC GAGG GAGGTTGCA TGAGTCGA  
||| ||||| |||||  
CTCC CTCCAACGT ACTCAGCT  
GC G

GAM1552 LOC152445 3' TCACTGCAACCTCTGCCTC 85760  
GAGGTAGAGGTTGCAGTGA  
|||||||||||  
CTCCGTCTCCAACGTCACT

GAM1552 LOC152582 5' TCACCGCAACCTCTGCCTC 85793 A  
GAGGTAGAGGTTGC GTGA  
||||||||||| |||  
CTCCGTCTCCAACG CACT  
C

GAM1552 LOC152620 3' TCACTACAACCTCTGCCTC 60086 C  
GAGGTAGAGGTTG AGTGA  
||||||||||| |||  
CTCCGTCTCCAAC TCACT  
A

GAM1552 LOC152719 5' TCACTGCAACCTCTGCCTC 85855  
GAGGTAGAGGTTGCAGTGA  
|||||||||||  
CTCCGTCTCCAACGTCACT

GAM1552 LOC152794 5' TCACTGCAACCTCTACCTC 80682  
GAGGTAGAGGTTGCAGTGA  
|||||||||||  
CTCCATCTCCAACGTCACT

GAM1552 LOC152851 3' TCGCTGCAACCTCCACCC 80716 A A  
G GGT GAGGTTGCAGTGA  
| ||| |||||||||

C CCA CTCCAACGTCGCT  
 \_ C  
 GAM1552 LOC153077 3' TCACTGCAACCTCCGCCTC 85916 TA  
 GAGG GAGGTTGCAGTGA  
 |||| |||||  
 CTCC CTCCAACGTCACT  
 GC  
 GAM1552 LOC153688 3' TCGGCTCACTGCAACCTCCACC 86124 A  
 TC GAGGT GAGGTTGCAGTGAGTCGA  
 |||| |||||  
 CTCCA CTCCAACGTCACTCGGCT  
 C  
 GAM1552 LOC153883 5' TCACTGCAACCTCCACC 80986 A  
 GGT GAGGTTGCAGTGA  
 || |||||  
 CCA CTCCAACGTCACT  
 C  
 GAM1552 LOC154075 3' TCACTGCAACCTCCGCCTC 81048 TA  
 GAGG GAGGTTGCAGTGA  
 |||| |||||  
 CTCC CTCCAACGTCACT  
 GC  
 GAM1552 LOC154282 5' TCGGCTCACTGCAACCTCCACC 86211 A  
 TC GAGGT GAGGTTGCAGTGAGTCGA  
 |||| |||||  
 CTCCA CTCCAACGTCACTCGGCT  
 C  
 GAM1552 LOC154877 3' TCAGCTCACTGCAACCTCTACC 86311 C  
 TC GAGGTAGAGGTTGCAGTGAGT GA  
 ||||| ||  
 CTCCATCTCCAACGTCACTCG CT  
 A  
 GAM1552 LOC157247 5' TCAGCTCACTGCAACCTCCACC 81377 A C  
 GGT GAGGTTGCAGTGAGT GA  
 || ||||| ||  
 CCA CTCCAACGTCACTCG CT  
 C A  
 GAM1552 LOC157798 5' TCACTGCAACCTCCGCCTC 86551 TA  
 GAGG GAGGTTGCAGTGA  
 |||| |||||  
 CTCC CTCCAACGTCACT  
 GC  
 GAM1552 LOC157858 5' TCACTGCAACCTCTGCCTC 86602  
 GAGGTAGAGGTTGCAGTGA  
 |||||  
 CTCCGTCTCCAACGTCACT  
  
 GAM1552 LOC158476 3' TCACTGCAACCTCCGCC 86851 TA  
 GG GAGGTTGCAGTGA  
 || |||||

	CC CTCCAACGTCACT		
	GC		
GAM1552 LOC158668 3'	TCACTGCAACCTCTGCCTC 69374		
	GAGGTAGAGGTTGCAGTGA		
	CTCCGTCTCCAACGTCACT		
GAM1552 LOC158865 5'	TCACTGCAACCTCTGCCTC 86940		
	GAGGTAGAGGTTGCAGTGA		
	CTCCGTCTCCAACGTCACT		
GAM1552 LOC161829 3'	TCACTGCAACCTCCGCCTC 82321	TA	
	GAGG GAGGTTGCAGTGA		
	CTCC CTCCAACGTCACT		
	GC		
GAM1552 LOC196047 5'	TCACTGCAACCTCCGCCTC 89610	TA	
	GAGG GAGGTTGCAGTGA		
	CTCC CTCCAACGTCACT		
	GC		
GAM1552 LOC196264 3'	TCACTGCAACCTCTGCCTC 87613		
	GAGGTAGAGGTTGCAGTGA		
	CTCCGTCTCCAACGTCACT		
GAM1552 LOC196411 3'	TCACTGCAACCTCCGCCTC 87685	TA	
	GAGG GAGGTTGCAGTGA		
	CTCC CTCCAACGTCACT		
	GC		
GAM1552 LOC196529 3'	CGCTCACTGCAACCTCCACCTC 87772	A	T
	GAGGT GAGGTTGCAGTGAG CG		
	CTCCA CTCCAACGTCACTC GC		
	C		
	—		
GAM1552 LOC196761 3'	TCAACCCACAACACCTCTGCC 89557	T CA	A C
	GGTAGAGGT G GTG GT GA		
	CCGTCTCCA C CAC CA CT		
	— AA C A		
GAM1552 LOC196957 3'	TCACTGCAGCCTCCACCTC 87829	A	
	GAGGT GAGGTTGCAGTGA		
	CTCCA CTCCGACGTCACT		
	C		
GAM1552 LOC196961 3'	TCACTGCAGCCTCCACCTC 87850	A	
	GAGGT GAGGTTGCAGTGA		

	CTCCA CTCCGACGTCACT		
	C		
GAM1552 LOC197138 3'	TCAGTGCAGCCTCCACCTC	87923	A
	GAGGT GAGGTTGCAGTGA		
	CTCCA CTCCGACGTCACT		
	C		
GAM1552 LOC197358 3'	CTGCAACCTCCGCCTC	88032	TA
	GAGG GAGGTTGCAG		
	CTCC CTCCAACGTC		
	GC		
GAM1552 LOC199699 3'	TCAGTCACTGCAAGCTCCACC	88313	A G C
TC	GAGGT GAG TTGCAGTGAGT GA		
	CTCCA CTC AACGTCAGTCT		
	C G A		
GAM1552 LOC199786 3'	TCAGTGCACCTCCGCCTC	88391	TA
	GAGG GAGGTTGCAGTGA		
	CTCC CTCCAACGTCAGT		
	GC		
GAM1552 LOC200014 3'	TCGCTGCAACCCCCACCTC	88542	AGA
	GAGGT GGTTCAGTGA		
	CTCCA CCAACGTCGCT		
	CCC		
GAM1552 LOC200169 5'	TCAGTGCACCTCTGCCTC	89957	
	GAGGTAGAGGTTGCAGTGA		
	CTCCGTCTCCAACGTCAGT		
GAM1552 LOC200268 3'	TCAGTGCACCTCTGCCTC	88691	
	GAGGTAGAGGTTGCAGTGA		
	CTCCGTCTCCAACGTCAGT		
GAM1552 LOC200310 3'	TCAGTACAACCTCTGCCTC	65741	C
	GAGGTAGAGGTTG AGTGA		
	CTCCGTCTCCAAC TCACT		
	A		
GAM1552 LOC200314 3'	TCAGTGCACCTCCACCTC	90016	A
	GAGGT GAGGTTGCAGTGA		
	CTCCA CTCCAACGTCAGT		
	C		
GAM1552 LOC200339 3'	TCAGTGCACCTCTGCCTC	90039	
	GAGGTAGAGGTTGCAGTGA		



CTCCGTCTCCAACGTCACT

GAM1552 LOC200845 5' TCACTGCAACCTCCGCCTC 88906 TA  
GAGG GAGGTTGCAGTGA  
|||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 LOC200860 3' TCACTGCAACCTCCACCTC 90175 A  
GAGGT GAGGTTGCAGTGA  
|||||  
CTCCA CTCCAACGTCACT  
C

GAM1552 LOC201173 5' TCACTGCAACCTCTGCCTC 87334  
GAGGTAGAGGTTGCAGTGA  
|||||  
CTCCGTCTCCAACGTCACT

GAM1552 LOC201220 5' TCACTGCAACCTCTGCCTC 87355  
GAGGTAGAGGTTGCAGTGA  
|||||  
CTCCGTCTCCAACGTCACT

GAM1552 LOC201294 3' TCACTGCAACCTCCGCCTC 88219 TA  
GAGG GAGGTTGCAGTGA  
|||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 LOC201294 3' TCACTGCAACCTCCGCCTC 88220 TA  
GAGG GAGGTTGCAGTGA  
|||||  
CTCC CTCCAACGTCACT  
GC

GAM1552 LOC201411 3' TCACTGCAACCTCTGCCTC 62960  
GAGGTAGAGGTTGCAGTGA  
|||||  
CTCCGTCTCCAACGTCACT

GAM1552 LOC201626 3' TCACTGCAACCTCCGCC 88996 TA  
GG GAGGTTGCAGTGA  
|||  
CC CTCCAACGTCACT  
GC

GAM1552 LOC201627 3' TCGGCTGACTGCAACCTCCACC 89027 A G  
TC GAGGT GAGGTTGCAGT AGTCGA  
|||||  
CTCCA CTCCAACGTCA TCGGCT  
C G

GAM1552 LOC202025 3' TCACTGCAACCTCCGCCTC 90297 TA  
GAGG GAGGTTGCAGTGA  
|||||

	CTCC CTCCAACGTCACT		
	GC		
GAM1552 LOC202934 3'	TCACTACAACCTCTGCCTC	90428	C
	GAGGTAGAGGTTG AGTGA		
	CTCCGTCTCCAAC TCACT		
	A		
GAM1552 LOC203297 5'	TCACTGCAACCTCTGCCTC	75353	
	GAGGTAGAGGTTGCAGTGA		
	CTCCGTCTCCAACGTCACT		
GAM1552 LOC203350 3'	TCAACTGACTGCAACCTCCGCC	90571	TA G C
TC	GAGG GAGGTTGCAGT AGT GA		
	CTCC CTCCAACGTCA TCA CT		
	GC G A		
GAM1552 LOC204804 3'	TCACTGCAACCTCGACCTC	89485	A
	GAGGT GAGGTTGCAGTGA		
	CTCCA CTCCAACGTCACT		
	G		
GAM1552 LOC204804 3'	TCGGCTCACTGCCACCTCCACC	89488	A T
TC	GAGGT GAGGT GCAGTGAGTCGA		
	CTCCA CTCCA CGTCACTCGGCT		
	C C		
GAM1552 LOC219735 3'	TCACTGCAACCTCTGCCTC	93115	
	GAGGTAGAGGTTGCAGTGA		
	CTCCGTCTCCAACGTCACT		
GAM1552 LOC219894 3'	TCACTGCAAGCTCCACCTC	93287	A G
	GAGGT GAG TTGCAGTGA		
	CTCCA CTC AACGTCACT		
	C G		
GAM1552 LOC220662 3'	TCACTGCAACCTCCACCTC	91179	A
	GAGGT GAGGTTGCAGTGA		
	CTCCA CTCCAACGTCACT		
	C		
GAM1552 LOC220662 3'	TCACTGCAACCTCCACTTC	91181	A
	GAGGT GAGGTTGCAGTGA		
	CTTCA CTCCAACGTCACT		
	C		
GAM1552 LOC220846 3'	CTTTCCACAACCTCTACCTT	90816	CAGT
	GAGGTAGAGGTTG GAG		

		TTCCATCTCCAAC	TTC		
		ACCT			
GAM1552	LOC221035 3'	TC	ACTACAACCTCTGCCTC	93169	C
			GAGGTAGAGGTTG AGTGA		
			CTCCGTCTCCAAC TCACT		
			A		
GAM1552	LOC221174 5'	TC	AGCTCACTGCGACCTCCACC	93506	A C
			GAGGT GAGGTTGCAGTGAGT GA		
			CTCCA CTCCAGCGTCACTCG CT		
			C A		
GAM1552	LOC221271 3'	TC	ACTGCAACCTCTGCCTC	91874	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCACT		
GAM1552	LOC221296 3'	TC	CGGCTCACTGCAACCTCCACC	91972	A
			GAGGT GAGGTTGCAGTGAGTCGA		
			CTCCA CTCCAACGTCACTCGGCT		
			C		
GAM1552	LOC221663 5'	TC	ACTGCAACCTCCACCTC	93822	A
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCAACGTCACT		
			C		
GAM1552	LOC221715 5'	AC	CAAATGCCTCTACCTT	93747	TGCAG A
			GAGGTAGAGGT TG GT		
			TTCCATCTCCG AC CA		
			TAA__ C		
GAM1552	LOC222070 5'	TC	ACTGCAACCTCTGCCTC	94160	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCACT		
GAM1552	LOC253612 5'	TC	ACTGCAACCTCCGCCTC	96756	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	LOC253664 3'	TC	ATTGCAACCTCTGCCTC	94815	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTTACT		
GAM1552	LOC253666 5'	TC	ACTGCAACCTCCGCCTC	95067	TA
			GAGG GAGGTTGCAGTGA		

CTCC CTCCAACGTCACT  
 GC  
 GAM1552 LOC253779 3' TCACTGCAACCTCCGCCTC 97145 TA  
 GAGG GAGGTTGCAGTGA  
 |||| |||||  
 CTCC CTCCAACGTCACT  
 GC  
 GAM1552 LOC255004 3' CGACCCAATCCCCCTACCC 95549 A A TTGCAG A  
 G GGTAG GG TG GTCG  
 | |||| || || ||||  
 C CCATC CC AC CAGC  
 \_ \_ CCTA\_ C  
 GAM1552 LOC255497 3' TCACTGCAACCTCCGCCTC 97194 TA  
 GAGG GAGGTTGCAGTGA  
 |||| |||||  
 CTCC CTCCAACGTCACT  
 GC  
 GAM1552 LOC256267 3' TCACTGCAACCTCCGCCTC 96807 TA  
 GAGG GAGGTTGCAGTGA  
 |||| |||||  
 CTCC CTCCAACGTCACT  
 GC  
 GAM1552 LOC256306 3' TCAGTCACTGCAACCTCCACC 96698 A C  
 TC GAGGT GAGGTTGCAGTGAGT GA  
 |||| ||||| ||  
 CTCCA CTCCAACGTCAGTCTG CT  
 C A  
 GAM1552 LOC51200 3' TCACCACAACCTCTGCCTC 33002 CA  
 GAGGTAGAGGTTG GTGA  
 ||||| ||||  
 CTCCGTCTCCAAC CACT  
 AC  
 GAM1552 LOC51219 5' TCACCGCAACCTCCGCCTC 33126 TA A  
 GAGG GAGGTTGC GTGA  
 |||| ||||| ||||  
 CTCC CTCCAACG CACT  
 GC C  
 GAM1552 LOC51696 3' TCACTGCAACCTCTGCCTC 32556  
 GAGGTAGAGGTTGCAGTGA  
 |||||  
 CTCCGTCTCCAACGTCACT  
  
 GAM1552 LOC57107 3' TCACTGCAACCTCCGCCTC 39842 TA  
 GAGG GAGGTTGCAGTGA  
 |||| |||||  
 CTCC CTCCAACGTCACT  
 GC  
 GAM1552 LOC57146 3' TCGGCTCACTGCAACCTCCAAC 39930 GTA  
 TC GAG GAGGTTGCAGTGAGTCGA  
 || |||||

			CTC CTCCAACGTCACTCGGCT		
			AAC		
GAM1552	LOC64102	5'	CGACTCACTTGCAACTCCACCT 42171	A G	—
		C	GAGGT GAG TTGCA GTGAGTCG		
			CTCCA CTC AACGT CACTCAGC		
			C _ T		
GAM1552	LOC81034	3'	TCAGCTCACTGCAACCTCCACC 47858	A	C
		TC	GAGGT GAGGTTGCAGTGAGT GA		
			CTCCA CTCCAACGTCACTCG CT		
			C A		
GAM1552	LOC89932	3'	TCACTGCAACCTCCACCTC 60815	A	
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCAACGTCACT		
			C		
GAM1552	LOC90288	3'	TCTTCTCACTGCAACCTCCACC 62109	A	TC
		TC	GAGGT GAGGTTGCAGTGAG GA		
			CTCCA CTCCAACGTCACTC CT		
			C TT		
GAM1552	LOC90333	3'	TCACTGCAACCTCCTCCTC 62299	TA	
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			TC		
GAM1552	LOC90333	5'	TCACTGCAACCTCCACTTC 62297	A	
			GAGGT GAGGTTGCAGTGA		
			CTTCA CTCCAACGTCACT		
			C		
GAM1552	LOC90371	5'	TCACTGCAACCTCCACCTC 62502	A	
			GAGGT GAGGTTGCAGTGA		
			CTCCA CTCCAACGTCACT		
			C		
GAM1552	LOC90408	5'	TCACTGCAACCTCTACCTC 62667		
			GAGGTAGAGGTTGCAGTGA		
			CTCCATCTCCAACGTCACT		
GAM1552	LOC90459	3'	TCACTGCAACCTCCGCCTC 62892	TA	
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	LOC90485	3'	TCACTGCAACCTCCGCCTC 63025	TA	
			GAGG GAGGTTGCAGTGA		

				CTCC	CTCCAACGTC	ACT			
				GC					
GAM1552	LOC90591	3'	TCAGCTCACTGCAAGCTCCACC	63442		A	G		C
		TC	GAGGT GAG TTGCAGTGAGT GA						
			CTCCA CTC AACGTC	ACTCG CT					
			C G A						
GAM1552	LOC90591	3'	TCAGTGCACCTCCACCTC	63440		A	T		
			GAGGT GAGGT GCAGTGA						
			CTCCA CTCCA CGTCACT						
			C C						
GAM1552	LOC91115	3'	TCGGCTCACTGCAACCTCCACC	64956		A			
		TC	GAGGT GAGGTTGCAGTGAGTCGA						
			CTCCA CTCCAACGTC	ACTCGGCT					
			C						
GAM1552	LOC91115	3'	TCAGTGCACCTCCGCCTC	64950		TA			
			GAGG GAGGTTGCAGTGA						
			CTCC CTCCAACGTC	ACT					
			GC						
GAM1552	LOC91291	5'	TCAGCTCACTGCAACCTCGACC	65485		A			C
		TC	GAGGT GAGGTTGCAGTGAGT GA						
			CTCCA CTCCAACGTC	ACTCG CT					
			G A						
GAM1552	LOC91373	3'	ACTCATCCTCTGCC	65830		TTGCA			
			GGTAGAGG GTGAGT						
			CCGTCTCC TACTCA						
GAM1552	LOC92267	3'	TCAGCTCACTGCAACCTCCACC	68625		A			C
		TC	GAGGT GAGGTTGCAGTGAGT GA						
			CTCCA CTCCAACGTC	ACTCG CT					
			C A						
GAM1552	LOC92303	3'	TCAACTCACTGCAACCTCTGCC	68825					C
			GGTAGAGGTTGCAGTGAGT GA						
			CCGTCTCCAACGTC	ACTCA CT					
			A						
GAM1552	LOC92466	3'	TCAGTGCACCTCCGCCTC	69432		TA			
			GAGG GAGGTTGCAGTGA						
			CTCC CTCCAACGTC	ACT					
			GC						
GAM1552	LOC92661	5'	TCAGTGCACCTCCACCTC	70085		A	G		
			GAGGT GAG TTGCAGTGA						

			CTCCA CTC AACGTCACT		
			C G		
GAM1552	LOC92689	3'	TCACTGCAACCTCCGCCTC	70228	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	LOC92697	5'	TCACCGCAACCTCCGCCTC	70278	TA A
			GAGG GAGGTTGC GTGA		
			CTCC CTCCAACG CACT		
			GC C		
GAM1552	LOC92697	5'	TCGCTACAACCTCCACCTC	70283	A C
			GAGGT GAGGTTG AGTGA		
			CTCCA CTCCAAC TCGCT		
			C A		
GAM1552	LOC92841	3'	TCACCGCAACCTCCTCCTC	70721	TA A
			GAGG GAGGTTGC GTGA		
			CTCC CTCCAACG CACT		
			TC C		
GAM1552	LOC93132	5'	TCACTGCAACCTCCGCCTC	71500	TA
			GAGG GAGGTTGCAGTGA		
			CTCC CTCCAACGTCACT		
			GC		
GAM1552	LOC93349	3'	TCACTGCAACCTCTGCCTC	56464	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCACT		
GAM1552	LOC93408	5'	TCACTGCAACCTCTGCCTC	56482	
			GAGGTAGAGGTTGCAGTGA		
			CTCCGTCTCCAACGTCACT		
GAM1553	ARNT2	3'	AAACAACCCGTGCATCCCTGC	29450	A TTTA
			GTA GGAT GGGTTGTTT		
			CGT CCTA CCAACAAA		
			C CGTG_		
GAM1553	LCT	3'	AACCGTAAAAATCCTT	9697	G
			AAGGATTTTTA GGTT		
			TTCCTAAAAAT CCAA		
			G		
GAM1553	RPL15	3'	AAACAACCCTAAAAATCCTTAC	11382	
			GTAAGGATTTTATAGGGTTGTTT		

CATTCCTAAAAATCCCAACAAA

GAM1553 FBXO30 3' AACTAAAAAATCCTGAC 49573 A AG  
GT AGGATTTTT GTT  
|| ||||| |||  
CA TCCTAAAAA TCAA  
G AA

GAM1553 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTT  
GTAAG AGGGTTGTT  
|||| |||||  
CATTC TCCCAACAA  
AT\_\_\_\_

GAM1553 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
TAAG TTTT GGGTTGTT  
||| ||| |||||  
GTTC AAAA CCAACAAA  
\_\_\_\_ C

GAM1553 SMT3H2 3' AACACATAAAAAATCCTTGC 22670 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1553 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
GTAAGGATTTTT GGGTT  
||||||| |||||  
CGTTCCTAAAAA TCCAA  
GTA

GAM1553 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
GGAT TT GGGTTGTT  
||| || |||||  
CCTG AA CCAACAAA  
T\_ C

GAM1553 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
C GTA GGATTTTT TTGTTT  
|| ||||| |||||  
CGT CCTAAAAA AACAAA  
C GATAA

GAM1553 LOC148089 3' GGCCCTAAAAATTCCTAC 78637 A  
GTA GGATTTTTAGGGTT  
|| |||||  
CAT CTAAAAATCCCGG  
C

GAM1553 LOC154547 3' AACACATAAAAAATCCTTGC 76050 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1553 LOC158104 3' ACAGCCAAAAATCCTTA 60313 AG  
TAAGGATTTTT GGTGT  
||||||| |||||



ATTCCTAAAAA CCGACA

GAM1553 LOC205880 5' AAACAACCATCATCCTGAC 90709 A TTTTAG  
GT AGGAT GGTGTGTT  
|| |||| |||||  
CA TCCTA CCAACAAA  
G CTA\_\_

GAM1553 LOC221561 3' AACAAACATAAAAAATCCTTGC 92130 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1553 LOC257591 3' AACAAACATAAAAAATCCTTGC 97840 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1553 LOC51145 3' AGCTAAAATCCTTAC 32393 TAG  
GTAAGGATTTT GTT  
||||||| |||  
CATTCCTAAAA TCGA

GAM1554 ATP11A 3' GCCACGCCGGCAGCTTC 77031 A AT\_  
GAAGCTGCC GGC GC  
||||||| ||| ||  
CTTCGACGG CCG CG  
\_ CAC

GAM1554 BAP1 3' AGCGAGGTACTGCAGCTTC 16213 CAG A\_  
GAAGCTGC GC TGCT  
||||||| || ||||  
CTTCGACG TG GCGA  
TCA GA

GAM1554 BCL7B 3' GCTGCTGGCAGCTTC 8134 G T  
GAAGCTGCCAG CA GC  
||||||| ||| ||  
CTTCGACGGTC GT CG

GAM1554 C18orf1 5' GCCTCGCCCGGCGGCTTC 60245 A AT\_  
GAAGCTGCC GGC GC  
||||||| ||| ||  
CTTCGGCGG CCG CG  
C CTC

GAM1554 CIS4 5' GCAGCCTTGCAGCCTC 14877 A C A  
GA GCTGC AGGC TGC  
|| |||| |||| |||  
CT CGACG TCCG ACG  
C T \_

GAM1554 DSCR3 3' TGTGCCCAGCAGTTTC 20198 CA  
GAAGCTGC GGCATG  
||||||| |||||

			CTTTGACG CCGTGT		
			AC		
GAM1554	EGFL4	5'	GCCGGCCCCGGCAGCTTC 61813	A	AT
			GAAGCTGCC GGC GC		
			CTTCGACGG CCG CG		
			C GC		
GAM1554	EMS1	3'	GTCACGCGGCAGCTTC 17854	AG	A _
			GAAGCTGCC GC TG C		
			CTTCGACGG CG AC G		
			_ C T		
GAM1554	EMS1	3'	GTCACGCGGCAGCTTC 56754	AG	A _
			GAAGCTGCC GC TG C		
			CTTCGACGG CG AC G		
			_ C T		
GAM1554	ETS2	3'	TGGCGCCTGGCAGTCC 17881	A	AT
			A GCTGCCAGGC GCTA		
			C TGACGGTCCG CGGT		
			C _		
GAM1554	FUT4	3'	TGTGGCCCGTGCAGCTTC 8963	CA	CAT
			GAAGCTGC GG GCTATA		
			CTTCGACG CC CGGTGT		
			TG _		
GAM1554	GNA11	5'	GCACCGGCCTGGGCAGCTTC 76100	_	A _
			GAAGCTGCC AGGC TGC		
			CTTCGACGG TCCG ACG		
			G GCC		
GAM1554	GRLF1	3'	GTACAGCCCGGCTGGCGGCCTC 78563	A	G AT_ A
			GA GCTGCCAG C GCT TAC		
			CT CGGCGGTC G CGA ATG		
			C _ GCC C		
GAM1554	HAS3	3'	GTATGGCCTGACAGCT 18042	C	_
			AGCTG CAGGC ATGC		
			TCGAC GTCCG TATG		
			A G		
GAM1554	HMG20A	3'	GCATCACGCCTAGCAGTTTC 36539	C	_
			GAAGCTGC AGGC ATGC		
			CTTTGACG TCCG TACG		
			A CAC		
GAM1554	HPS4	5'	TGGGATGCCTGGCTACT 41989	CT	G
			AG GCCAGGCAT CTA		

			TC CGGTCCGTA GGT		
			AT G		
GAM1554	IKBKB	3'	GTACAGCCATGGCAGCT 63210	_ A_	
			AGCTGCCA GGC TGC		
			TCGACGGT CCG ATG		
			A AC		
GAM1554	KCNJ5	3'	GTGGCATCAGCAGCTTC 6097	CAGGC	
			GAAGCTGC ATGCTAT		
			CTTCGACG TACGGTG		
			AC__		
GAM1554	MBD3	3'	GCAGTGGGCTGGCAGCTTC 14095	G_ _	
			GAAGCTGCCAG CA TGC		
			CTTCGACGGTC GT ACG		
			GG G		
GAM1554	MFI2	3'	GCACCTGGCAGCTTT 52814	CA	
			GAAGCTGCCAGG TGC		
			TTTCGACGGTCC ACG		
			—		
GAM1554	MYLK	3'	GCAGATGTCTAGCAGCTTC 97020	C _	
			GAAGCTGC AGGCA TGC		
			CTTCGACG TCTGT ACG		
			A AG		
GAM1554	PCDH12	5'	GCACAGGTTCTTGCAGCTTC 33422	C _ A_	
			GAAGCTGC AGG C TGC		
			CTTCGACG TCT G ACG		
			T T GAC		
GAM1554	PEX1	3'	TATGCTTAGCAGCTTC 4877	C	
			GAAGCTGC AGGCATG		
			CTTCGACG TTCGTAT		
			A		
GAM1554	SGCA	3'	GCTGCTGGCAGCCTC 3428	A G T	
			GA GCTGCCAG CA GC		
			CT CGACGGTC GT CG		
			C _ _		
GAM1554	SLC3A1	3'	TACAGCATGCTGCTT 62247	TGCCA A	
			AAGC GGCATGCT TA		
			TTCG TCGTACGA AT		
			— C		
GAM1554	SPON1	5'	GCCAGCCTGGCAGCCTC 62451	A AT	
			GA GCTGCCAGGC GC		

		CT CGACGGTCCG CG	
		C AC	
GAM1554 TAF1C	3'	AGCGGCCGTTGGCAGCT 19056	___ A
		AGCTGCCA GGC TGCT	
		TCGACGGT CCG GCGA	
		TG _	
GAM1554 UBE2I	5'	GGCGGCTCTAGCAGCTTC 12492	C _ A
		GAAGCTGC AG GC TGCT	
		CTTCGACG TC CG GCGG	
		A T _	
GAM1554 UBE4A	3'	AGCTATTCCCAGCAGCTTC 16555	CA C _
		GAAGCTGC GG AT GCT	
		CTTCGACG CC TA CGA	
		AC T T	
GAM1554 XKRY	5'	AGCAAAATCTGGCAGCT 16253	CA_
		AGCTGCCAGG TGCT	
		TCGACGGTCT ACGA	
		AAA	
GAM1554 XKRY	5'	AGCAAAATCTGGCAGCT 60014	CA_
		AGCTGCCAGG TGCT	
		TCGACGGTCT ACGA	
		AAA	
GAM1554 ZFH1B	3'	CGTGCCTGACGCTTC 28924	T C
		GAAGC G CAGGCATG	
		CTTCG C GTCCGTGC	
		_ A	
GAM1554 AKAP6	3'	GTATAGCATGTAGCAGCTTC 14993	CAG
		GAAGCTGC GCATGCTATAC	
		CTTCGACG TGTACGATATG	
		A_	
GAM1554 AP1S2	3'	GCACACTTTACAGCAGCTTC 14040	C___ CA
		GAAGCTGC AGG TGC	
		CTTCGACG TTC ACG	
		ACAT AC	
GAM1554 BRPF3	3'	GTATGGCCGGCAGCTTC 92323	A _
		GAAGCTGCC GGC ATGC	
		CTTCGACGG CCG TATG	
		_ G	
GAM1554 C16orf44	3'	GTACAACCTTAGCAGCTTT 45316	C CA_
		GAAGCTGC AGG TGC	

TTTTCGACG TTC ATG  
 A AAC  
 GAM1554 CGI-96 3' CATGGCCTGCAGCTTC 31661 C \_  
 GAAGCTGC AGGC ATG  
 ||||| ||| ||  
 CTTTCGACG TCCG TAC  
 \_ G  
 GAM1554 DKFZp434F1719 3' GTCTGCCTGGCTGCCTC 50003 A T T  
 GA GC GCCAGGCA GC  
 || || ||||| ||  
 CT CG CGGTCCGT TG  
 C T C  
 GAM1554 DKFZP564C1940 5' GCATTGCCAGCCTGGCAATTTTC 25903 C \_\_\_\_  
 GAAG TGCCAGGC ATGC  
 ||| ||||| |||  
 CTTT ACGGTCCG TACG  
 A ACCGT  
 GAM1554 DKFZP564O0423 3' GCACCTCTGAACCCGCAGCTTC 91690 \_\_\_\_ CA  
 GAAGCTGC CAGG TGC  
 ||||| ||| ||  
 CTTTCGACG GTCT ACG  
 CCCAA CC  
 GAM1554 DKFZP564P1916 5' GTAGATGTGCAGCTTC 31608 CAG G  
 GAAGCTGC GCAT CTAT  
 ||||| ||| |||  
 CTTTCGACG TGTA GATG  
 \_ \_  
 GAM1554 DKFZP761F241 3' GCAGTGCCTGGCAGTCC 48797 A \_  
 A GCTGCCAGGCA TGC  
 | ||||| |||  
 C TGACGGTCCGT ACG  
 C G  
 GAM1554 DNAL4 3' GCTACCTGGCAGTTTC 19218 CAT  
 GAAGCTGCCAGG GC  
 ||||| ||  
 CTTTGACGGTCC CG  
 AT\_  
 GAM1554 ERAP140 3' GCATACTGGCAGTTTC 75206 GC  
 GAAGCTGCCAG ATGC  
 ||||| |||  
 CTTTGACGGTC TACG  
 A\_  
 GAM1554 FEM1B 5' GCAGCGCCTGGCACTTC 31024 C A\_  
 GAAG TGCCAGGC TGC  
 ||| ||||| ||  
 CTTT ACGGTCCG ACG  
 \_ CG  
 GAM1554 FLJ10824 5' GTGTGCTGGCAGCTTC 72575 G  
 GAAGCTGCCAG CATGC  
 ||||| |||

CTTCGACGGTC GTGTG

GAM1554 FLJ10898 5' GCACTTTGCCAGCAGCTTC 59433 CA \_\_\_\_  
GAAGCTGC GGCA TGC  
||||||| ||| |||  
CTTCGACG CCGT ACG  
A\_ TTC

GAM1554 FLJ10979 3' GCATTTGCCTGGCAGCTTT 36934 \_\_\_\_  
GAAGCTGCCAGGCA TGC  
||||||| |||  
TTTCGACGGTCCGT ACG  
TT

GAM1554 FLJ11151 3' GCATCTTCTCAGCAGCTTC 67876 C\_\_ C  
GAAGCTGC AGG ATGC  
||||||| ||| |||  
CTTCGACG TTC TACG  
ACTC \_

GAM1554 FLJ12150 3' GCATGGCCTGGCAGCT 45349 \_  
AGCTGCCAGGC ATGC  
||||||| |||  
TCGACGGTCCG TACG  
G

GAM1554 FLJ12387 3' CACGCCTGCAGCTTC 43064 C A  
GAAGCTGC AGGC TG  
||||||| ||| ||  
CTTCGACG TCCG AC  
\_ C

GAM1554 FLJ14957 3' AGCATGCCAGCTCCTC 51737 \_\_ GCCA  
GA AGCT GGCATGCT  
|| ||| |||||  
CT TCGA CCGTACGA  
CC \_\_\_\_

GAM1554 FLJ14966 3' GCACGCATGGCAGCTTC 51769 G A  
GAAGCTGCCA GC TGC  
||||||| || |||  
CTTCGACGGT CG ACG  
A C

GAM1554 FLJ23047 3' TATGTCTGCAACTTC 44627 C C  
GAAG TGC AGGCATG  
||| ||| |||||  
CTTC ACG TCTGTAT  
A \_

GAM1554 HSNV1 3' GTATGCCTGGGAGCCTC 34012 A G  
GA GCT CCAGGCATGC  
|| ||| |||||  
CT CGA GGTCCGTATG  
C G

GAM1554 ING4 3' ATAGCATGGGGGCAGT 59703 AGG  
GCTGCC CATGCTAT  
||||| |||||

			TGACGG	GTACGATA		
			GG_			
GAM1554	KIAA0140	3'	AGCGGGTGTGTCAGCCTC	27804	A	C G A
			GA GCTG CA GC TGCT			
			CT CGAC GT TG GCGA			
			C T G G			
GAM1554	KIAA0376	3'	AGCGCCTGGCAGTT	65596	AT	
			AGCTGCCAGGC GCT			
			TTGACGGTCCG CGA			
			—			
GAM1554	KIAA0450	5'	AGTGGCCAGCAGCTTC	27617	CA	A
			GAAGCTGC GGC TGCT			
			CTTCGACG CCG GTGA			
			A_ _			
GAM1554	KIAA0682	3'	AGCATGCTATCACTTC	29362	C	CCA
			GAAG TG GGCATGCT			
			CTTC AC TCGTACGA			
			_ TA_			
GAM1554	KIAA1184	3'	GTCTGCCTGGCAAGTTC	42617	GC	T
			GAA TGCCAGGCA GC			
			CTT ACGGTCCGT TG			
			GA C			
GAM1554	KIAA1404	3'	TAGCATGCCAGCAGCTTC	61992	CA	
			GAAGCTGC GGCATGCTA			
			CTTCGACG CCGTACGAT			
			A_			
GAM1554	KIAA1530	5'	GCCTCGCCTGGCGCTTC	67952	T	AT_
			GAAGC GCCAGGC GC			
			CTTCG CGGTCCG CG			
			_ CTC			
GAM1554	KIAA1600	3'	AGCATGCTTGTACTT	71441	C	C
			AAG TGC AGGCATGCT			
			TTC ATG TTCGTACGA			
			— —			
GAM1554	KIAA1622	5'	GCCGCCTGGCAGCCTC	54261	A	AT
			GA GCTGCCAGGC GC			
			CT CGACGGTCCG CG			
			C C_			
GAM1554	KIAA1622	5'	GCCGCCTGGCAGCCTC	40560	A	AT
			GA GCTGCCAGGC GC			

			CT CGACGGTCCG CG		
			C C_		
GAM1554	LANO	5'	GTAGCGCCTGGCGC 47191	T	AT
			GC GCCAGGC GCTAT		
			CG CGGTCCG CGATG		
			— —		
GAM1554	MAGE-E1	3'	AGCACCTAGGCGGCTTC 47941	_	CA
			GAAGCTGCC AGG TGCT		
			CTTCGGCGG TCC ACGA		
			A C_		
GAM1554	MAGEA1	3'	GCGTCCAGCAGCTTC 17159	CA	C
			GAAGCTGC GG ATGC		
			CTTCGACG CC TGCG		
			A_ _		
GAM1554	MGC26766	3'	GCCTCTGCCTGGCAGCT 58820	T_	
			AGCTGCCAGGCA GC		
			TCGACGGTCCGT CG		
			CTC		
GAM1554	MGC4832	3'	GCTGCCTGGTAGCTTC 59003	T	
			GAAGCTGCCAGGCA GC		
			CTTCGATGGTCCGT CG		
			—		
GAM1554	NET-7	3'	GCCTGCCATGGCAGCT 24709	_	T
			AGCTGCCA GGCA GC		
			TCGACGGT CCGT CG		
			A C		
GAM1554	OSBPL7	3'	GCAAAATGCCTGCAGCTTC 34808	C	___
			GAAGCTGC AGGCA TGC		
			CTTCGACG TCCGT ACG		
			— AAA		
GAM1554	phorbolin-1	5'	GTATCGCTGACTCAGCAGCTTC 88782	CA _	T T
			GAAGCTGC GG CA GC ATAC		
			CTTCGACG TC GT CG TATG		
			AC A _ C		
GAM1554	PL6	3'	GTACATCAGCTGGCAGC 22832	GC_	C
			GCTGCCAG ATG TAT		
			CGACGGTC TAC ATG		
			GAC _		
GAM1554	RIL	3'	GTGGGGTGCTGGCAGCCTC 13489	A	G G
			GA GCTGCCAG CAT CTAT		



			CT CGACGGTC GTG GGTG		
			C _ G		
GAM1554	RP4-622L5	3'	GTAGATGCCTGGCACT	38932	C G
			AG TGCCAGGCAT CTAT		
			TC ACGGTCCGTA GATG		
			_ _		
GAM1554	SIAT8C	5'	GCAGCCTGGCAGCCTC	31882	A A
			GA GCTGCCAGGC TGC		
			CT CGACGGTCCG ACG		
			C _		
GAM1554	SLC38A1	3'	ATAGGCCCAGCAGCTTT	47721	CA ATG
			GAAGCTGC GGC CTAT		
			TTTCGACG CCG GATA		
			AC _		
GAM1554	SMARCF1	3'	GTATAGCACTATGGTGCCTTC	37442	_ GGCA
			GAAGC TGCCA TGCTATAC		
			CTTCG GTGGT ACGATATG		
			C ATC_		
GAM1554	SSB-3	5'	GCAGGGCCTGGCACTTC	55095	C A_
			GAAG TGCCAGGC TGC		
			CTTC ACGGTCCG ACG		
			_ GG		
GAM1554	TXNL2	3'	AGCTGCAGTAGCTTC	21548	CAG T
			GAAGCTGC GCA GCT		
			CTTCGATG CGT CGA		
			A _ _		
GAM1554	ZAK	3'	GCATAGCCTGACAGCT	56129	C _
			AGCTG CAGGC ATGC		
			TCGAC GTCCG TACG		
			A A		
GAM1554	ZF	5'	GCTGCTGGCAGCCTC	41089	A G T
			GA GCTGCCAG CA GC		
			CT CGACGGTC GT CG		
			C _ _		
GAM1554	LOC112724	3'	GCCATGCCCGCAGCTTC	56498	CA _
			GAAGCTGC GGCATG C		
			CTTCGACG CCGTAC G		
			C_ C		
GAM1554	LOC115939	3'	ATGGGCCTGGCAGCCTC	73662	A ATG
			GA GCTGCCAGGC CTAT		

		CT CGACGGTCCG GGTA		
		C     —		
GAM1554	LOC124460 3'	ATAGCATGGACTTAGCT 76038	CC	G_
		AGCTG AG CATGCTAT		
		TCGAT TC GTACGATA		
		— AG		
GAM1554	LOC125268 3'	AGGTGCTGGCAGCT 76067	G	G
		AGCTGCCAG CAT CT		
		TCGACGGTC GTG GA		
		— —		
GAM1554	LOC128936 3'	ATGGCACCTTGCAGCTTC 75788	C	CA
		GAAGCTGC AGG TGCTAT		
		CTTCGACG TCC ACGGTA		
		T —		
GAM1554	LOC129011 5'	AGCATGCCTTTGGGTGC 74863	T	—
		GC GCC AGGCATGCT		
		CG TGG TCCGTACGA		
		— GTT		
GAM1554	LOC131831 5'	GCTCGCCTAGCGGCTTC 75010	C	AT
		GAAGCTGC AGGC GC		
		CTTCGGCG TCCG CG		
		A CT		
GAM1554	LOC131870 3'	GCACCCTGGCAGGTTC 75019	G	CA
		GAA CTGCCAGG TGC		
		CTT GACGGTCC ACG		
		G C_		
GAM1554	LOC139296 5'	TGGAAGGCCTGGCAGCTTC 75830		ATG
		GAAGCTGCCAGGC CTA		
		CTTCGACGGTCCG GGT		
		GAA		
GAM1554	LOC146562 3'	GCAGCCTGGCGGCCTC 57533	A	A
		GA GCTGCCAGGC TGC		
		CT CGGCGGTCCG ACG		
		C —		
GAM1554	LOC148166 5'	GCCCAGCCTGGCAGCTTC 78692		AT_
		GAAGCTGCCAGGC GC		
		CTTCGACGGTCCG CG		
		ACC		
GAM1554	LOC148710 5'	GCATCCCAGTAGCTTC 84196	CA	C
		GAAGCTGC GG ATGC		

	CTTCGATG CC TACG	
	AC _	
GAM1554 LOC149182 3'	GTACCTGGCAGCTTC 84376	CA
	GAAGCTGCCAGG TGC	
	CTTCGACGGTCC ATG	
	—	
GAM1554 LOC149386 3'	ATAGCATGCTGACCTTC 84402	CTGCCA
	GAAG GGCATGCTAT	
	CTTC TCGTACGATA	
	CAG _	
GAM1554 LOC150225 3'	GGAATCCCAGCAGTTTC 85002	CA C G
	GAAGCTGC GG AT CT	
	CTTTGACG CC TA GG	
	AC _ A	
GAM1554 LOC151534 3'	GCTGGTGCCTTGCAGCTTC 56685	C _
	GAAGCTGC AGGCAT GC	
	CTTCGACG TCCGTG CG	
	T GT	
GAM1554 LOC153768 5'	GCGCATGGCAGCTTC 56715	G AT
	GAAGCTGCCA GC GC	
	CTTCGACGGT CG CG	
	A _	
GAM1554 LOC154007 3'	TGTGCCTGCAGCCTC 81024	A C
	GA GCTGC AGGCATG	
	CT CGACG TCCGTGT	
	C _	
GAM1554 LOC168512 5'	AGCCTCTCTGGCAGCTTT 82712	CAT
	GAAGCTGCCAGG GCT	
	TTTCGACGGTCT CGA	
	CTC	
GAM1554 LOC197423 5'	GCACAGTCTGCAGCTTC 77860	C A_
	GAAGCTGC AGGC TGC	
	CTTCGACG TCTG ACG	
	_ AC	
GAM1554 LOC199920 5'	GTATAGCATATTTGTTCAATTC 88492	GCTGC C
	GAA CAGG ATGCTATAC	
	CTT GTTT TACGATATG	
	A ACTT A	
GAM1554 LOC200205 3'	GCCAGCACTGGCAGCTTC 88626	_ AT
	GAAGCTGCCAG GC GC	

		CTTCGACGGTC CG CG		
		A AC		
GAM1554	LOC200268 3'	AGTGAGCCGGTAGCTTC	88675	A A
		GAAGCTGCC GGC TGCT		
		CTTCGATGG CCG GTGA		
		_ A		
GAM1554	LOC219700 5'	GTAGCCTGGCAGTCC	93067	A A
		A GCTGCCAGGC TGC		
		C TGACGGTCCG ATG		
		C _		
GAM1554	LOC220776 3'	ATAGCATGCAGCGGT	68384	CAG
		GCTGC GCATGCTAT		
		TGGCG CGTACGATA		
		A _		
GAM1554	LOC221037 3'	GTATAGCATATGTCACAGCT	93157	CCA _
		AGCTG GGCA TGCTATAC		
		TCGAC CTGT ACGATATG		
		A _ AT		
GAM1554	LOC221424 3'	GCATGGGGGCTCTGGCAGCT	93627	_____
		AGCTGCCAGG CATGC		
		TCGACGGTCT GTACG		
		CGGGG		
GAM1554	LOC222057 3'	GCAGCTGGCAGCCTC	92775	A G A
		GA GCTGCCAG C TGC		
		CT CGACGGTC G ACG		
		C _ _		
GAM1554	LOC223009 5'	GCATCTTGGCAGCCTC	94376	A C
		GA GCTGCCAGG ATGC		
		CT CGACGGTTC TACG		
		C _		
GAM1554	LOC253502 5'	GCATGGGCCCAGCGGCTTC	94580	CA _
		GAAGCTGC GGC ATGC		
		CTTCGGCG CCG TACG		
		AC GG		
GAM1554	LOC253725 5'	GCCTGTGCTGGCAGCCTC	94701	A _ T
		GA GCTGCCAG GCA GC		
		CT CGACGGTC TGT CG		
		C G C		
GAM1554	LOC255158 3'	GTATAGCATGTGTATCTTC	96171	C CAG
		GAAG TGC GCATGCTATAC		

CTTC ATG TGTACGATATG  
 T \_\_\_\_  
 GAM1554 LOC255326 3' ATAGCATGTTAGTTTC 96371 CCAG  
 GAAGCTG GCATGCTAT  
 ||||| |||||  
 CTTTGAT TGTACGATA  
  
 \_\_\_\_  
 GAM1554 LOC255759 5' AGCACCTGGCAGGCT 97479 \_ CA  
 AGC TGCCAGG TGCT  
 || ||||| ||  
 TCG ACGGTCC ACGA  
 G \_\_\_\_  
 GAM1554 LOC255975 5' GCTGCTGGCAGCCTC 95896 A G T  
 GA GCTGCCAG CA GC  
 || ||||| ||  
 CT CGACGGTC GT CG  
 C \_ \_  
 GAM1554 LOC256337 5' GCCTGTGCTGGCAGCCTC 94696 A \_ T  
 GA GCTGCCAG GCA GC  
 || ||||| ||  
 CT CGACGGTC TGT CG  
 C G C  
 GAM1554 LOC51337 3' GCCTCTCCTGGCAGCTTC 33588 CAT\_  
 GAAGCTGCCAGG GC  
 ||||| ||  
 CTTGACGGTCC CG  
 TCTC  
 GAM1554 LOC91149 3' ATAGCATGCTTTTGCTC 65070 A TGCC  
 GA GC AGGCATGCTAT  
 || |||||  
 CT CG TTCGTACGATA  
 \_ TT\_  
 GAM1554 LOC91409 3' GCATTTCTGACACTTC 65957 C C C\_  
 GAAG TG CAGG ATGC  
 ||| || |||  
 CTTC AC GTCC TACG  
 \_ A TT  
 GAM1554 LOC92492 5' ATGGAGAGCCAGCAGCTTC 69525 CA ATG  
 GAAGCTGC GGC CTAT  
 ||||| || |||  
 CTTGACG CCG GGTA  
 A\_ AGA  
 GAM1555 ATP2B2 3' GCTTAAATTGCTCT 8067 TAACAG  
 AGAGCAATT AGGC  
 ||||| |||  
 TCTCGTTAAA TTCG  
  
 \_\_\_\_  
 GAM1555 AXIN1 3' AGGGCCTCTGTCAATTGT 60849 TTA  
 GCAATT ACAGAGGCCCT  
 |||| |||||

			TGTTAA TGTCTCCGGGA		
			C__		
GAM1555 CRP	3'	GGCCATTAGAATTGC	71629	CAGA	
		GCAATTTTAA	GGCC		
		CGTTAAGATT	CCGG		
		A__			
GAM1555 DACH	3'	AGGACCTATGAAAATTGTCT	54968	G AACAG C	
		AGA CAATTTT	AGG CCT		
		TCT GTTAAAA	TCC GGA		
		_ GTA__ A			
GAM1555 FPGS	3'	AGGGCCTCTGCCTGGGACACTG	17080	A__ A_	
C		GCA TTTTA	CAGAGGCCCT		
		CGT AGGGT	GTCTCCGGGA		
		CAC CC			
GAM1555 HLA-E	3'	GGGCCTCTGAATCTGTCTG	91025	G AT TAA	
		CAGA CA TT	CAGAGGCCC		
		GTCT GT AA	GTCTCCGGG		
		_ CT _			
GAM1555 HOXB3	5'	TTGTAAAATTGCTTTG	9264		
		CAGAGCAATTTTAACAG			
		GTTTCGTTAAAATTGTT			
GAM1555 HOXC5	3'	AGGGCCCCCACAGTTGCTCT	38490	TTAACAGA	
		AGAGCAATT	GGCCCT		
		TCTCGTTGA	CCGGGA		
		CACCC__			
GAM1555 IHPK1	3'	GGGCCTCTGGTGGCTCTG	95760	AATTTTAA	
		CAGAGC	CAGAGGCC		
		GTCTCG	GTCTCCGGG		
		GTG__			
GAM1555 IL22RA2	3'	CCCATGAAAATTGCTC	53690	AA GA	
		GAGCAATTTT	CA GG		
		CTCGTTAAAA	GT CC		
		_ AC			
GAM1555 LY64	3'	GCTTAGCAAAAATTGCTCT	18756	AACAG	
		AGAGCAATTTT	AGGC		
		TCTCGTTAAAA	TTCG		
		CGA__			
GAM1555 MASP1	3'	AGGGCCTCTGCATTGTTGCTC	57469	TTTAA	
		GAGCAAT	CAGAGGCCCT		

		CTCGTTG	GTCTCCGGGA		
		TTAC_			
GAM1555	MYO1D	3'	AGGGCCTCTGACCACCGCTCTG 71765	AATTTTAA	
			CAGAGC CAGAGGCCCT		
			GTCTCG GTCTCCGGGA		
			CCACCA_		
GAM1555	PFKFB4	3'	AGGGCCTCTACCATCCTCTCTG 15865	CAATTTTAAAC	
			CAGAG AGAGGCCCT		
			GTCTC TCTCCGGGA		
			TCCTACCA_		
GAM1555	PPP2R4	3'	GCCTCTGTTTTGCACCTG 60559	A_ TTTT	
			CAG GCAA AACAGAGGC		
			GTC CGTT TTGTCTCCG		
			CA _		
GAM1555	RPL15	3'	TCTGTAAAACTAGTCTG 11385	GCAA	
			CAGA TTTTAACAGA		
			GTCT AAAATTGTCT		
			GATC		
GAM1555	SRD5A1	3'	TTGTAAAAATTCTCT 6461	C	
			AGAG AATTTTAACAG		
			TCTC TAAAAATTGTT		
			-		
GAM1555	XYLB	3'	AGGGCCTCTCTTACTTGC 17557	TTT C	
			GCAA TAA AGAGGCCCT		
			CGTT ATT TCTCCGGGA		
			C_ C		
GAM1555	ZNF267	5'	GACCTCTGTTGCTCTG 12735	ATTTTA CC	
			CAGAGCA ACAGAGG C		
			GTCTCGT TGTCTCC G		
			AA		
GAM1555	ARTS-1	3'	CTCTTTTAAAATTGCTCTG 33184	C	
			CAGAGCAATTTTAA AGAG		
			GTCTCGTTAAAATT TCTC		
			T		
GAM1555	C1orf25	3'	GGCTCACATGTTAAAATGACCC 72536	AGCA GA_	
	TG		CAG ATTTTAACA GGCC		
			GTC TAAAATTGT TCGG		
			CCAG ACAC		
GAM1555	C22orf5	3'	AGGGCCCCTGGGCACCGCTTCT 24339	_ AATTTTAA A	
	G		CAGA GC CAG GGCCCT		

			GTCT CG	GTC CCGGGA		
			T CCACGG__ C			
GAM1555	CD109	3'	AGGAGCATACTGAAAATTGCCC	56045	A	AA AG__
	TG		CAG GCAATTTT	CAG GC CCT		
			GTC CGTTAAAA	GTC CG GGA		
			C __ ATA A			
GAM1555	FKHL18	3'	AGGGCCTCTTGGGATTTACTCT	79553	C_	AC
	G		CAGAG AATTTTA	AGAGGCCCT		
			GTCTC TTAGGGT	TCTCCGGGA		
			AT __			
GAM1555	FLJ22054	3'	CCATCTGTAAAAATTACCTG	94393	AGC	_
			CAG AATTTTAACAGA	GG		
			GTC TAAAAATTGTCT	CC		
			CA_ A			
GAM1555	FLJ23074	3'	GCCTTAGAAAAATTGCCTG	46818	A	AACA
			CAG GCAATTTT	GAGGC		
			GTC CGTTAAAA	TTCCG		
			_ GA__			
GAM1555	FLJ30473	3'	GGCCTCTGCTGCCACTG	58463	A_	ATTTTAA
			CAG GCA	CAGAGGCC		
			GTC CGT	GTCTCCGG		
			AC C_____			
GAM1555	FOXJ1	3'	GGCCTCTGGGGTCTTTGCCTG	7574	A	TTTTAA
			CAG GCAA	CAGAGGCC		
			GTC CGTT	GTCTCCGG		
			_ TCTGGG			
GAM1555	KIAA0514	3'	GCCTAAAATTGCACT	28086	A	AACAG
			AG GCAATTTT	AGGC		
			TC CGTTAAAA	TCCG		
			A _____			
GAM1555	KIAA0543	3'	AGAGCCCCCAGAGGCATTGTTC	68931		TTTAACAGA C
	TG		CAGAGCAAT	GGC CT		
			GTCTTGTTA	CCG GA		
			CGGAGACCC	A		
GAM1555	KIAA1546	3'	GGCCTCTGGATTTTGCTC	67909		TTTTAA
			GAGCAA	CAGAGGCC		
			CTCGTT	GTCTCCGG		
			TTAG__			
GAM1555	KRTHB2	3'	AGGGCCTCTGCCCTGAACATCT	52285		GCAATTTTAA
	G		CAGA	CAGAGGCCCT		



GTCT GTCTCCGGGA  
 ACAAGTCCC\_  
 GAM1555 LIPI 3' CTCATGTTAAATCACTT 79566 CA \_  
 GAG ATTTTAACA GAG  
 ||| ||||| |||  
 TTC TAAAATTGT CTC  
 AC A  
 GAM1555 MGC15606 5' AGGACCTCTGGTCAAAATTGCC 58874 A AA\_ C  
 TG CAG GCAATTTT CAGAGG CCT  
 ||| ||||| ||||| |||  
 GTC CGTTAAAA GTCTCC GGA  
 \_ CTG A  
 GAM1555 MGC20255 3' GCCTCTGCTACGGAGCGCTTCT 53443 \_ AA \_ A  
 G CAGA GC TTT TA CAGAGGC  
 |||| || ||| || |||||  
 GTCT CG AGG AT GTCTCCG  
 T CG C C  
 GAM1555 MGC2742 5' AGGGCCTCTGTCTCCATCTCTG 43744 CAATTTTA  
 CAGAG ACAGAGGCCCT  
 |||| |||||  
 GTCTC TGTCTCCGGGA  
 TACCTC\_  
 GAM1555 NLP\_1 3' TGTTTAAAATTGCTTTG 23710 \_  
 CAGAGCAATTTTAA CA  
 ||||| ||||| ||  
 GTTTCGTTAAAATT GT  
 T  
 GAM1555 PIK4CA 3' AGGGCCTCTGCCCCATGTGCCC 54123 A ATTTTAA  
 T AG GCA CAGAGGCCCT  
 || ||| |||||  
 TC CGT GTCTCCGGGA  
 C GTACCCC  
 GAM1555 PIK4CA 3' AGGGCCTCTGCCCCATGTGCCC 10592 A ATTTTAA  
 T AG GCA CAGAGGCCCT  
 || ||| |||||  
 TC CGT GTCTCCGGGA  
 C GTACCCC  
 GAM1555 SLC21A14 5' TTGTTCAAAATTGCTGTG 33833 G \_  
 CA AGCAATTTT AACAG  
 || ||||| |||||  
 GT TCGTTAAAA TTGTT  
 G C  
 GAM1555 TSGA14 3' GCCCACTGAAAATTGCCTG 38047 A AA A\_  
 CAG GCAATTTT CAG GGC  
 ||| ||||| ||| |||  
 GTC CGTTAAAA GTC CCG  
 \_ \_ AC  
 GAM1555 LOC124411 5' GACCTCTGTACTCTG 74284 CAATTT CC  
 CAGAG TAACAGAGG C  
 |||| ||||| |

	GTCTC	ATTGTCTCC	G	
	_____	AA		
GAM1555	LOC139221	3'	TGTTAAAATTGCACTG	75827 A
			CAG GCAATTTTAACA	
			GTC CGTTAAAATTGT	
			A	
GAM1555	LOC144501	3'	AGGGCCTCTGTTCTCCTCT	83103 CAATTTT
			AGAG AACAGAGGCCCT	
			TCTC TTGTCTCCGGGA	
			CTC_____	
GAM1555	LOC148183	3'	GGGCCCCTGTGTTCTCTG	84121 C TTTA A
			CAGAG AAT ACAG GCCCC	
			GTCTC TTG TGTC CCGGG	
			- _____ C	
GAM1555	LOC149134	5'	GGGCCTCTGTCAGCACTG	84363 A AATTTTA
			CAG GC ACAGAGGCCCC	
			GTC CG TGTCTCCGGG	
			A AC_____	
GAM1555	LOC149910	3'	AGGGCCTCTGCCCAGGCTCT	79528 AATTTTAA
			AGAGC CAGAGGCCCT	
			TCTCG GTCTCCGGGA	
			GACCC_____	
GAM1555	LOC160156	5'	AGGGCCTCCGTTCCCTGAGCTC	82206 AATTTT A
			GAGC AAC GAGGCCCT	
			CTCG TTG CTCCGGGA	
			AGTCCC C	
GAM1555	LOC160414	5'	GCCAAAATTGTTCTG	87067 AACAGA
			CAGAGCAATTTT GGC	
			GTCTTGTTAAAA CCG	
			_____	
GAM1555	LOC162952	5'	AGGGCCTCTACACCTGCTC	82378 ATTTTAAC
			GAGCA AGAGGCCCT	
			CTCGT TCTCCGGGA	
			CCACA_____	
GAM1555	LOC196214	5'	AGGGCTTATGCAAAATTGT	89615 AA G
			GCAATTTT CA AGGCCCT	
			TGTTAAAA GT TTCGGGA	
			C_ A	
GAM1555	LOC220686	3'	AGGGCCTCTGCCCCATGTGCCC	92920 A ATTTTAA
			AG GCA CAGAGGCCCT	

T

		TC CGT    GTCTCCGGA	
		C   GTACCCC	
GAM1555	LOC257476 3'	GGGCCTCTGGTGGCTCTG    61255	AATTTTAA
		CAGAGC    CAGAGGCC	
		GTCTCG    GTCTCCGGG	
		GTG_____	
GAM1555	LOC257539 3'	GGGCCTCTGAATCTGTCTG    97703	G AT TAA
		CAGA CA TT CAGAGGCC	
		GTCT GT AA GTCTCCGGG	
		_ CT _	
GAM1555	LOC257578 3'	GGGCCTCTGAATCTGTCTG    97823	G AT TAA
		CAGA CA TT CAGAGGCC	
		GTCT GT AA GTCTCCGGG	
		_ CT _	
GAM1555	LOC90092 5'	GGCACCAAGTCAAAGTTACTCT 61412	C   A AGAG_
	G	CAGAG AATTTT AC    GCC	
		GTCTC TTGAAA TG    CGG	
		A   C AACCA	
GAM1556	ABCA1    3'	GTTGACAGAATGGTGC    18550	GAAA
		GCACCATTT    TTAAC	
		CGTGGTAAG    AGTTG	
		AC_	
GAM1556	COL4A1    3'	TAATGTCACAACATGGTGCTA 8464	T_   A
		TAGCACCAT    TGA ATTA	
		ATCGTGGTA    ACT TAAT	
		CAAC G	
GAM1556	DDX4    3'	TGATACAAATGGTGTTA    38755	AA
		TAGCACCATTG ATTA	
		ATTGTGGTAAAC TAGT	
		A_	
GAM1556	DDX4    3'	TGATACAAATGGTGTTA    44323	AA
		TAGCACCATTG ATTA	
		ATTGTGGTAAAC TAGT	
		A_	
GAM1556	NMI    3'	GTTTCAAATGGTGCTG    16265	
		TAGCACCATTGAAAT	
		GTCGTGGTAAACTTTG	
GAM1556	NR3C1    3'	TTGGTTAATCTTTCCTGATGGT 3927	T_   _
		ACCATT GAA ATTAACCAA	

			TGGTAG CTT TAATTGGTT	
			TC TC	
GAM1556	PIK3CD	3'	TTAGTTTGAAATGGTGC 17253	G
			GCACCATTT AAATTAA	
			CGTGGTAAA TTTGATT	
			G	
GAM1556	PPP3CB	3'	TTGGTTAAACTAAATGG 40902	AAA
			CCATTTG TTAACCAA	
			GGTAAAT AATTGGTT	
			CA_	
GAM1556	ROBO1	3'	TTGATTTTATAATTGGTGCTA 56089	TT__
			TAGCACCA TGAAATTAA	
			ATCGTGGT ATTTTAGTT	
			TAAT	
GAM1556	ROBO1	3'	TTGATTTTATAATTGGTGCTA 11375	TT__
			TAGCACCA TGAAATTAA	
			ATCGTGGT ATTTTAGTT	
			TAAT	
GAM1556	SERPINB9	3'	TGGTAATAAATGGTGCTA 14770	AAATTA
			TAGCACCATTG ACCA	
			ATCGTGGTAAAT TGGT	
			AA_____	
GAM1556	SLC4A8	3'	TAATTGCAAATGGTGCTG 16777	A
			TAGCACCATTG AATTA	
			GTCGTGGTAAAC TTAAT	
			G	
GAM1556	TCL1A	3'	TGGTCTCACATGGTGCTA 41739	T AATTA
			TAGCACCAT TGA ACCA	
			ATCGTGGTA ACT TGGT	
			C C_____	
GAM1556	TCTEL1	3'	ATTTCAAAGGTGCTA 21507	A
			TAGCACC TTTGAAAT	
			ATCGTGG AAAC TTTA	
			-	
GAM1556	ZNF236	3'	TTAGTATCGTCAATGGTGC 23720	_ A
			GCACCATT TGA ATTA	
			CGTGGTAA GCT TGATT	
			CT A	
GAM1556	BTN2A2	3'	TGGTTAATTTTAGATG 22783	
			CATTTGAAATTAACCA	

GTAGATTTTAATTGGT

GAM1556 COASTER 3' TGGTTAAAGGGAATGGTGT 31449 GAAA  
GCACCATT TTAACCA  
||||| |||||  
TGTGGTAAG AATTGGT  
GGA\_

GAM1556 FHX 3' TTGGAGGTTTTAAATGGTGCT 37311 \_ AA  
A TAGCACCATT GAAATT CCAA  
||||| ||||| |||||  
ATCGTGGTAAA TTTTGG GGTT  
A A\_

GAM1556 FIBL-6 3' TTGATCCCAAATGGTGCT 72917 AA  
AGCACCATTG ATTAA  
||||| |||||  
TCGTGGTAAAC TAGTT  
CC

GAM1556 FLJ10891 3' TTAATTTTGGTGCTG 36808 TTT  
TAGCACCA GAAATTAA  
||||| |||||  
GTCGTGGT TTTTAATT

GAM1556 FNBP3 3' TTAATTATAGTGGTGCTA 80154 TGA  
TAGCACCATT AATTAA  
||||| |||||  
ATCGTGGTGA TTAATT  
TA\_

GAM1556 HYPH 3' TTGGTTAACTTTACAAATG 94902 \_ \_  
CATTTG AAA TTAACCAA  
||||| |||||  
GTAAAC TTT AATTGGTT  
A C

GAM1556 KIAA1169 5' TTGGTTAACTAAGGATTGTGCT 35454 C GAAA  
A TAGCAC ATTT TTAACCAA  
||||| |||||  
ATCGTG TAGG AATTGGTT  
T AATC

GAM1556 KIAA1979 3' TAATTTTGGTGCTG 88290 TTT  
TAGCACCA GAAATTA  
||||| |||||  
GTCGTGGT TTTTAAT

GAM1556 P5-1 3' TGGCTAATTCAGTGCT 21920 CATT A  
AGCAC TGAAATTA CCA  
||||| ||||| |||||  
TCGTG ACTTTAAT GGT

GAM1556 PCDH19 3' GTTTCAAATGGTGTTA 63706  
TAGCACCATTGAAAT  
|||||

ATTGTGGTAAACTTTG

GAM1556 YAP1 3' GTTAATTTTAAAATGGT 20356 —  
ACCATTT GAAATTAAC  
||||| |||||||  
TGGTAAA TTTTAATTG  
AT

GAM1556 ZNF282 3' TGGGCCTCCCAATTGGTGCTA 89219 T AAATTAA  
TAGCACCA TTG CCA  
||||| ||| |||  
ATCGTGGT AAC GGT  
T CCTCCG\_

GAM1556 LOC144871 3' TAATTTCAAATGACGTTA 83204 AC  
TAGC CATTTGAAATTA  
||| |||||||||  
ATTG GTAAACTTTAAT  
CA

GAM1556 LOC145694 5' TGGCGCATTTCAAACGGGC 83423 A A TAA  
GC CC TTTGAAAT CCA  
|| ||||||| |||  
CG GG AAACTTTA GGT  
\_ C CGC

GAM1556 LOC148371 3' TGGTTAATGATAATAATGC 78807 CC TGAA  
GCA ATT ATTAACCA  
||| ||| |||||||  
CGT TAA TAATTGGT  
AA TAG\_

GAM1556 LOC151057 3' TGACTAAGGAAGATGGTGCTA 85218 GAAA AC  
TAGCACCATT TTA CA  
||||||||| ||| |||  
ATCGTGGTAGA AAT GT  
AGG\_ CA

GAM1556 LOC151473 3' ATTTTAAATGGTGCTA 80252  
TAGCACCATTGAAAT  
|||||||||||  
ATCGTGGTAAATTTTA

GAM1556 LOC154834 3' TGGTTAATTCCTGTGC 86269 CATTT A  
GCAC GAA TTAACCA  
||| ||| |||||||  
CGTG CTT AATTGGT  
TC\_\_ \_

GAM1556 LOC161589 3' TGGTTAATGACAACGATGC 82283 CCAT AA  
GCA TTG ATTAACCA  
||| ||| |||||||  
CGT AAC TAATTGGT  
AGC\_ AG

GAM1556 LOC202460 5' AATTTCAAACGTGCTA 89176 CA  
TAGCAC TTTGAAATT  
||||| |||||||

ATCGTG AAAC TTAA  
 C\_  
 GAM1556 LOC221495 3' TTGGTTAATTT CATAAAGT 93869 CATT  
 AC TGAAATTAACCAA  
 || |||||  
 TG ACTTTAATTGGTT  
 AAAT  
 GAM1556 LOC222128 5' TTGGCTAATTCAAGG TAGTGC 92718 CA\_ A A  
 GCAC TTTGAA TTA CCAA  
 ||| ||||| ||| ||||  
 CGTG GAACTT AAT GGTT  
 ATG \_ C  
 GAM1556 LOC90333 3' TAATTTTGGTGCTG 62296 TTT  
 TAGCACCA GAAATTA  
 ||||| |||||  
 GTCGTGGT TTTTAAT  
  
 GAM1557 ADAMTS8 5' TCGGGCCGCCAGCACCTG 22886 \_ ATAAG  
 CAG TGCTGGC CTGA  
 ||| ||||| |||  
 GTC ACGACCG GGCT  
 C CCG\_  
 GAM1557 BAP1 3' TCAGGGACCCAGCACTGG 16219 CATAAG  
 CCAGTGCTGG CTGA  
 ||||| |||  
 GGTCACGACC GACT  
 CAGG\_  
 GAM1557 BF 5' TTCAGCTTG GACACTG 8140 CTGGCA  
 CAGTG TAAGCTGAA  
 |||| |||||  
 GTCAC GTTCGACTT  
 AG\_  
 GAM1557 C1QB 3' TTCAACTCTGTGTCC CAGCACT 4923 A \_ \_ C  
 GGC G CCAGTGCTGG CATA AG TGAA  
 | ||||| ||| || |||  
 C GGTCACGACC GTGT TC ACTT  
 \_ CT C A  
 GAM1557 CHC1 3' CAGCCCTGAGCACTGTGTC 7020 \_ \_ CATAA  
 GAC CAGTGCT GG GCTG  
 ||| ||||| || |||  
 CTG GTCACGA CC CGAC  
 T GT\_  
 GAM1557 CMRF35 5' CAGAGCTGTCAGCACCGG 21929 A TAAG  
 CC GTGCTGGCA CTG  
 || ||||| |||  
 GG CACGACTGT GAC  
 C CGA\_  
 GAM1557 EPHB6 3' TCAGCCCTGGACACTGGTC 15466 \_ TG CATAA  
 GACCAGTG C G GCTGA  
 ||||| | | ||||

			CTGGTCAC G C CGACT		
			A GT C_____		
GAM1557	EVPL	5'	CAGCCTGAGCCAGCACT	8803	A A
			AGTGCTGGC TA GCTG		
			TCACGACCG GT CGAC		
			A C		
GAM1557	GARP	3'	CAGCCCAGCACTGG	18594	CATAA
			CCAGTGCTGG GCTG		
			GGTCACGACC CGAC		
			_____		
GAM1557	GJB5	3'	CAGCTCGACGGCACTGG	17945	GCATA
			CCAGTGCTG AGCTG		
			GGTCACGGC TCGAC		
			AGC__		
GAM1557	GPR81	3'	CTTACCAGCATTAGTC	50757	C CA
			GAC AGTGCTGG TAAG		
			CTG TTACGACC ATTC		
			A _		
GAM1557	IFI16	5'	AGCAAGCCAGCACTAGTC	71221	C ATAA
			GAC AGTGCTGGC GCT		
			CTG TCACGACCG CGA		
			A AA__		
GAM1557	KRT4	3'	CAGCTGGGCCCAGCACTGGT	9635	_ATA
			ACCAGTGCTGG C AGCTG		
			TGGTCACGACC G TCGAC		
			C GG_		
GAM1557	MAP3K9	3'	TTCAGCTTCCCAAACACCAGT	60709	CA C_ CAT
			AC GTG TGG AAGCTGAA		
			TG CAC ACC TTCGACTT		
			AC AA C__		
GAM1557	MGAT5	5'	TCAGCTTACAGTTCCTG	10028	T_ GCA
			CAG GCTG TAAGCTGA		
			GTC TGAC ATTCGACT		
			CT _		
GAM1557	MOCS1	3'	TTCAGCTTAACAGTTGCCCGGT	92037	A_ _ GCA
	C		GACC GTG CTG TAAGCTGAA		
			CTGG CGT GAC ATTCGACTT		
			CC T A__		
GAM1557	P23	3'	TCAGCTTATACCCGGGCT	21719	G C_
			AGT CTGG ATAAGCTGA		



TCG GGCC TATTCGACT  
 \_ CA  
 GAM1557 PFKFB4 3' TCAGCCACATGCAACACTGTGT 15874 \_ CTG AA\_  
 C GAC CAGTG GCAT GCTGA  
 ||| |||| ||| ||||  
 CTG GTCAC CGTA CGACT  
 T AA\_ CAC  
 GAM1557 PTPRK 3' TTCAGCCTGTGGCCCAGCACTG 11125 \_ A  
 GTC GACCAGTGCTGG CATA GCTGAA  
 ||||| ||| |||||  
 CTGGTCACGACC GTGT CGACTT  
 CG C  
 GAM1557 RNPEPL1 3' CGGATGCCAGCACCTG 36676 \_ AAG  
 CAG TGCTGGCAT CTG  
 ||| ||||| |||  
 GTC ACGACCGTA GGC  
 C \_  
 GAM1557 UBE2L3 3' TCAGCCCTGGCACTGGC 12507 A TG CATAA  
 G CCAGTGC G GCTGA  
 | ||||| | ||||  
 C GGTACAG C CGACT  
 \_ GTC \_  
 GAM1557 APXL2 5' CAGCCTCAGCACTCATC 75185 CC CATAA  
 GA AGTGCTGG GCTG  
 || ||||| |||  
 CT TCACGACT CGAC  
 AC C \_  
 GAM1557 ARHGEF9 3' TTCAGCTTACCAAGCA 30824 \_ CA  
 TGCT GG TAAGCTGAA  
 |||| || |||||  
 ACGA CC ATTCGACTT  
 A \_  
 GAM1557 CEGP1 3' TTCAGCTTCCTCTAGCCCGG 40589 AGT CAT  
 CC GCTGG AAGCTGAA  
 || |||| |||||  
 GG CGATC TTCGACTT  
 CC\_ TCC  
 GAM1557 DKFZp547D155 3' CAGCCCTGAGACCACTGGTC 70435 CTGG TAA  
 GACCAGTG CA GCTG  
 ||||| || |||  
 CTGGTCAC GT CGAC  
 CAGA CC\_  
 GAM1557 DKFZP727G051 3' TTCAGCCCATCAACCAGCATTG 69483 CATAA\_  
 GTC GACCAGTGCTGG GCTGAA  
 ||||| ||| |||||  
 CTGGTTACGACC CGACTT  
 AACTACC  
 GAM1557 DUSP14 5' CACTGTCACCAGCACTGCTC 22834 C CATA C  
 GA CAGTGCTGG AG TG  
 || ||||| || ||

CT GTCACGACC TC AC  
 C ACTG \_  
 GAM1557 FLJ10206 5' CAGCTTATGCCAGGAGTC 35898 CAGTG  
 GAC CTGGCATAAGCTG  
 ||| |||||  
 CTG GACCGTATTCGAC  
 AG\_\_  
 GAM1557 FLJ20967 5' GGCGCCCAGCACTGGTT 41962 CATAA  
 GACCAGTGCTGG GCT  
 ||||| |||  
 TTGGTCACGACC CGG  
 CG\_\_  
 GAM1557 FLJ22569 3' TTCAGCTTACTAAACTG 43679 GC CA  
 CAGT TGG TAAGCTGAA  
 ||| ||| |||||  
 GTCA ATC ATTCGACTT  
 A\_ \_  
 GAM1557 FOXN4 3' TTCAGCTTGGACACACTGG 75574 C GCA  
 CCAGTG TG TAAGCTGAA  
 ||||| || |||||  
 GGTCAC AC GTTCGACTT  
 \_ AG\_  
 GAM1557 GW112 3' TTCAACTGAAGCCAGCACTGGT 21194 ATA C  
 T GACCAGTGCTGGC AG TGAA  
 ||||| || |||||  
 TTGGTCACGACCG TC ACTT  
 AAG A  
 GAM1557 HOOK2 3' CAGCTCACATGGCGCCCAGCAC 25256 \_\_\_\_ A\_  
 TGG CCAGTGCTGG CAT AGCTG  
 ||||| ||| |||||  
 GGTCACGACC GTA TCGAC  
 CGCG CAC  
 GAM1557 jdp2 3' TTCAGCACAGCCAGCAT 55327 ATAA  
 GTGCTGGC GCTGAA  
 ||||| |||||  
 TACGACCG CGACTT  
 ACA\_  
 GAM1557 KIAA0767 3' TCTGCTGCCAGCACAGG 60632 A TAA T  
 CC GTGCTGGCA GC GA  
 || ||||| |||  
 GG CACGACCGT CG CT  
 A \_\_\_\_ T  
 GAM1557 KIAA0923 3' TCAGCTTGATGCATGGTC 25838 G TGGCA  
 GACCA TGC TAAGCTGA  
 ||||| ||| |||||  
 CTGGT ACG GTTCGACT  
 \_ TA\_\_  
 GAM1557 KIAA0982 3' TTCACTGTTTGCCAGCAC 25852 TA\_ C  
 GTGCTGGCA AG TGAA  
 ||||| || |||||

CACGACCGT TC ACTT  
TTG \_  
GAM1557 KIAA1000 3' TTCAGCTTTGCAAAGTACTGG 65281 G\_ T  
CCAGTGCT GCA AAGCTGAA  
||||||| ||| |||||||  
GGTCATGA CGT TTCGACTT  
AA \_  
GAM1557 MAP3K3 3' TCAGCCTGGGCGCTGGTC 9999 GG TAA  
GACCAGTGCT CA GCTGA  
||||||| || |||||  
CTGGTCGCGG GT CGACT  
\_ C\_  
GAM1557 MGC16037 5' CTTGTCCAGCACTAGTC 51821 C C  
GAC AGTGCTGG ATAAG  
||| ||||||| |||||  
CTG TCACGACC TGTC  
A \_  
GAM1557 MIDORI 3' TCAGCTTATCCTGCAACT 73792 \_ T C  
AGT GC GG ATAAGCTGA  
||| ||| |||||||  
TCA CG CC TATTCGACT  
A T \_  
GAM1557 MtFMT 5' CAGTGGCGAGCACTGG 57651 G ATAA  
CCAGTGCT GC GCTG  
||||||| || |||||  
GGTCACGA CG TGAC  
G G\_  
GAM1557 PCDH16 5' TCAGTTCCAACCACTGG 72826 C\_ CATA  
CCAGTG TGG AGCTGA  
||||||| ||| |||||||  
GGTCAC ACC TTGACT  
CA \_  
GAM1557 QKI 3' CAGCTTATCAACTCGTC 65439 C GCTGGC  
GAC AGT ATAAGCTG  
||| ||| |||||||  
CTG TCA TATTCGAC  
C AC\_  
GAM1557 TNRC6 3' CAACTTTTAGCACTG 70506 CAT C  
CAGTGCTGG AAG TG  
||||||| ||| ||  
GTCACGATT TTC AC  
\_ A  
GAM1557 TOB2 3' CAGCCCAGGCCAGCACTG 95618 ATAA  
CAGTGCTGGC GCTG  
||||||| |||||  
GTCACGACCG CGAC  
GACC  
GAM1557 TU12B1-TY 3' TCAGCCCACAGCACTGTC 33406 C GCATAA  
GAC AGTGCTG GCTGA  
||| ||||||| |||||

CTG TCACGAC CGACT  
 \_ ACC\_  
 GAM1557 TUSP 3' TCAGCCTAAGAGCGCAGCACTG 39641 \_ A\_ A  
 CAGTGCTG GC TA GCTGA  
 ||||| || |||||  
 GTCACGAC CG AT CGACT  
 G AGA C  
 GAM1557 USP19 3' TCAGCTTATGCATCTGGT 88959 TGCTG  
 ACCAG GCATAAGCTGA  
 |||| |||||  
 TGGTC CGTATTCGACT  
 TA\_  
 GAM1557 ZD52F10 3' CAGCCTGTGCCAGCCCTGG 52819 T A  
 CCAG GCTGGCATA GCTG  
 ||| ||||| |||  
 GGTC CGACCGTGT CGAC  
 C C  
 GAM1557 LOC145268 3' TCAGCTTACAAGAGCCACTG 77062 \_ GGCA  
 CAGTG CT TAAGCTGA  
 |||| || |||||  
 GTCAC GA ATTCGACT  
 C GAAC  
 GAM1557 LOC149296 5' CAGCTTATGGGCAGCA 79256 G\_  
 TGCTG CATAAGCTG  
 |||| |||||  
 ACGAC GTATTCGAC  
 GG  
 GAM1557 LOC161877 5' TCAGGGCAGGCCAGCGCTGG 82326 ATAAG  
 CCAGTGCTGGC CTGA  
 ||||| |||  
 GGTCGCGACCG GACT  
 GACGG  
 GAM1557 LOC163115 5' TCAGCCCCTGACAGCACTGG 82413 G TAA  
 CCAGTGCTG CA GCTGA  
 ||||| || |||||  
 GGTCACGAC GT CGACT  
 A CCC  
 GAM1557 LOC196500 3' TCAGCTCACTCAGTGGTC 87744 AGT CATA  
 GACC GCTGG AGCTGA  
 ||| |||| |||||  
 CTGG TGA CT TCGACT  
 \_ CAC\_  
 GAM1557 LOC197287 3' TCAGCTCATGTGTTTTGCACTG 60865 T\_ \_  
 CAGTGC GGCATA AGCTGA  
 |||| |||| |||||  
 GTCACG TTGTGT TCGACT  
 TT AC  
 GAM1557 LOC200470 5' TCAGCCTGCGGCGCTGG 90069 G TAA  
 CCAGTGCTG CA GCTGA  
 ||||| || |||||

GGTCGCGGC GT CGACT  
\_ C\_  
GAM1557 LOC221584 3' CAGCTTATGTGGCAC 93828 G  
GTGCTG CATAAGCTG  
||||| |||||  
CACGGT GTATTCGAC  
  
GAM1557 LOC51716 3' CAGCTCATGGCCCTAGCA 32787 \_ A  
TGCTGG CAT AGCTG  
||||| ||| |||||  
ACGATC GTA TCGAC  
CCG C  
GAM1557 LOC92196 5' CAGAGCACCAGCACTGGC 68456 A CATAAG  
G CCAGTGCTGG CTG  
| ||||| |||  
C GGTCACGACC GAC  
\_ ACGA\_  
GAM1558 ABCB11 5' TCTGGCTTCCTCAAATTC 13618 A ATGA  
GAATTTGA GAAG AGA  
||||| ||| |||  
CTTAAACT CTTC TCT  
C GG\_  
GAM1558 APC 3' CTTCATCTTCTTGTTGCA 3477 G TTG  
TG AAT AAGAAGATGAAG  
|| ||| |||||  
AC TTG TTCTTCTACTTC  
G \_  
GAM1558 ATP1B2 3' CTTCCCAGAATATCCTTCAAGT 8049 AA AA\_  
TCCA GGAATTTGAAG GATG GAAG  
||||||| ||| |||  
CCTTGA ACTTC CTAT CTTC  
\_ AAGACC  
GAM1558 CA4 3' TCAGCTCTCCAAGTTCCA 5552 A AGA  
TGGAATTTG AGA TGA  
||||||| ||| |||  
ACCTTGAAC TCT ACT  
C CG\_  
GAM1558 CEP1 5' CTTCCGTTTCGTTCTTCAAAACC 22816 AA \_ T\_  
CA TGG TTTGAAGAA GA GAAG  
||| ||||| || |||  
ACC AA ACTTCTT CT CTTC  
CA G TGC  
GAM1558 CEP2 3' CTTCATCTTCTCCTTCAA 23227 \_  
TTGA AGAAGATGAAG  
||| |||||  
AACT TCTTCTACTTC  
TCC  
GAM1558 FBLN5 3' CTTCTTCACCTCTTCCACTCC 20916 ATTT A A  
GGA GAAGA G TGAAGAAG  
||| ||||| |||||

			CCT CTTCT C ACTTCTTC		
			CAC_ _ C		
GAM1558	GAC1	3'	TCCCCATCTTCTCTGCCCCA 20945	AATTT _	AA
			TGG GA AGAAGATG GA		
			ACC CT TCTTCTAC CT		
			CGT_ C CC		
GAM1558	GATA4	3'	CTCCCTCCTCAAATTCC 9005	A AGAT	
			GGAATTTGA GA GAAG		
			CCTTAAACT CT CTTC		
			C CC_		
GAM1558	MGA	3'	TTCTTTATCCCAAATCCCA 62812	A AAGAA	
			TGG ATTTG GATGAAGAA		
			ACC TAAAC CTATTTCTT		
			C C_		
GAM1558	PIK3R3	3'	TCGTTTCCTTACAAATTCCA 61064	_ A	
			TGGAATTTG AAG AGATGA		
			ACCTTAAAC TTC TTTGCT		
			A C		
GAM1558	POU2F2	3'	TCTTCATCCTCATCCTCC 10692	ATTT A A	
			GGA GA GA GATGAAGA		
			CCT CT CT CTACTTCT		
			C_ A C		
GAM1558	PTPRS	3'	TCCTTTCCTTCCAATTCCA 11141	T A T	
			TGGAATT GAAG AGA GA		
			ACCTTAA CTTC TTT CT		
			C C C		
GAM1558	PTPRS	3'	TCCTTTCCTTCCAATTCCA 55648	T A T	
			TGGAATT GAAG AGA GA		
			ACCTTAA CTTC TTT CT		
			C C C		
GAM1558	PTPRS	3'	TCCTTTCCTTCCAATTCCA 55651	T A T	
			TGGAATT GAAG AGA GA		
			ACCTTAA CTTC TTT CT		
			C C C		
GAM1558	PTPRS	3'	TCCTTTCCTTCCAATTCCA 55645	T A T	
			TGGAATT GAAG AGA GA		
			ACCTTAA CTTC TTT CT		
			C C C		
GAM1558	SELL	3'	TCCCCACCTTCTTCAGCCACC 5393	AAT A AA	
			GG TTGAAGAAG TG GA		

CC GACTTCTTC AC CT  
 ACC C CC  
 GAM1558 TEM7 3' CTTTTTCTTCCTCAAATTC 39885 A T  
 GAATTTGA GAAGA GAAG  
 ||||| |||| ||||  
 CTTAAACT CTTCT TTTC  
 C T  
 GAM1558 WT1 3' TTCTTCATCCAACCTTCCA 44357 T AAGAA  
 TGGAA TTG GATGAAGAA  
 |||| || |||||  
 ACCTT AAC CTA CTACTTCTT  
 C \_\_\_\_  
 GAM1558 WT1 3' TTCTTCATCCAACCTTCCA 44367 T AAGAA  
 TGGAA TTG GATGAAGAA  
 |||| || |||||  
 ACCTT AAC CTA CTACTTCTT  
 C \_\_\_\_  
 GAM1558 WT1 3' TTCTTCATCCAACCTTCCA 44377 T AAGAA  
 TGGAA TTG GATGAAGAA  
 |||| || |||||  
 ACCTT AAC CTA CTACTTCTT  
 C \_\_\_\_  
 GAM1558 WT1 3' TTCTTCATCCAACCTTCCA 4592 T AAGAA  
 TGGAA TTG GATGAAGAA  
 |||| || |||||  
 ACCTT AAC CTA CTACTTCTT  
 C \_\_\_\_  
 GAM1558 AD-003 5' CTTCCCATCTTCTTC 25931 AA  
 GAAGAAGATG GAAG  
 ||||| ||||  
 CTTCTTCTAC CTTC  
 CC  
 GAM1558 CEACAM7 3' CTTCTAGCTCCTTCAATCCCA 22557 AAT A AT\_  
 TGG TTGAAG AG GAAG  
 || |||| || ||||  
 ACC AACTTC TC CTTC  
 CT\_ C GAT  
 GAM1558 CSMD1 3' CTTCTTTGTCCTCAATTTCCA 73120 T AGAA TG  
 TGGAA TTGA GA AAGAAG  
 |||| || || ||||  
 ACCTT AACT CT TTCTTC  
 T C\_\_ GT  
 GAM1558 DDX34 3' CATGTCTCCAGATTCCA 27979 A AG  
 TGAATTTG AGA ATG  
 ||||| || ||  
 ACCTTAGAC TCT TAC  
 C G\_  
 GAM1558 DKFZP434B205 3' CTTCTTCATCTTCCTGGACGTC 75320 ATTTGAA  
 GA GAAGATGAAGAAG  
 || |||||

CT CTTCTACTTCTTC  
 GCAGGTC  
 GAM1558 FENS-1 3' CTTCCCTTTCCCCCAAATTCC 40439 AA\_ AT  
 GGAATTTG GAAG GAAG  
 ||||| ||| |||  
 CCTTAAAC CTTT CTTC  
 CCC CC  
 GAM1558 FLJ13262 3' ATCCTCTCCAAATTCC 46155 A A  
 GGAATTTG AGA GAT  
 ||||| ||| |||  
 CCTTAAAC TCT CTA  
 C C  
 GAM1558 FLJ20170 3' TCACCTTCTTCAACTCCA 34672 AT A  
 TGGA TTGAAGAAG TGA  
 ||| ||||| |||  
 ACCT AACTTCTTC ACT  
 C\_ C  
 GAM1558 FLJ20375 3' CTTCTCCCTGCTAAATTCCA 35085 A\_ AA T  
 TGGAATTTG AG GA GAAG  
 ||||| || |||||  
 ACCTTAAAT TC CT CTTC  
 CG C\_ \_  
 GAM1558 FLJ20802 3' CTTCTTCACCTTTGCATCC 35669 ATT AA A  
 GGA TG GAAG TGAAGAAG  
 ||| || ||||| |||||  
 CCT AC TTTC ACTTCTTC  
 \_ G\_ C  
 GAM1558 FLJ22055 3' CTTTCATCTTCTGCTCCA 45496 ATTTGA  
 TGGA AGAAGATGAAG  
 ||| ||||| |||||  
 ACCT TCTTCTACTTC  
 CG\_\_\_\_  
 GAM1558 HUMAGCGB 5' CTATGCCTTCCTCAAGTTCCA 25231 A AT A  
 TGGAATTTGA GAAG G AG  
 ||||| ||| | |||  
 ACCTTGAAC CTTC T TC  
 C CG A  
 GAM1558 INA 3' CACCTCCTTCAATTCCA 51187 T A A  
 TGGAATT GAAG AG TG  
 ||||| ||| || |||  
 ACCTTAA CTTC TC AC  
 \_ C C  
 GAM1558 KIAA0451 5' TCATAATTCTCAAATTCCA 29114 AG AG  
 TGGAATTTGA A ATGA  
 ||||| | |||  
 ACCTTAAACT T TACT  
 CT AA  
 GAM1558 KIAA0972 5' CTTCTTCATCCCCTTGCCCA 30010 AATTG AA  
 TGG AAG GATGAAGAAG  
 || ||| ||||| |||||



		ACC	TTC	CTACTTCTTC			
		CG		CC			
GAM1558	MGC15854	5'	TTCCCCATCTTCTCCTCTA	58852	ATTT	A	AA
			TGGA GA GAAGATG GAA				
			ATCT CT CTTCTAC CTT				
			C				
GAM1558	MGC17998	3'	TTCCTCATCTTCTGGTCC	58746	ATTTGA		A
			GGA AGAAGATGA GAA				
			CCT TCTTCTACT CTT				
			GG				
GAM1558	MIL1	3'	TCTTCACCCCCAGGTTCC	31097	AAGAAGA		
			GGAATTTG TGAAGA				
			CCTTGGAC ACTTCT				
			CCCC				
GAM1558	NYD-SP21	3'	CTTCAGCTTCTCCTCAAATTC	50873	A	A	
			GAATTTGA GAAG TGAAG				
			CTTAAACT CTTC ACTTC				
			C G				
GAM1558	PCDH19	3'	TTCTTCATCCAAAATTGCA	63713	G	GAAGAA	
			TG AATTT GATGAAGAA				
			AC TTAAA CTACTTCTT				
			G AC				
GAM1558	PEG10	3'	CTTCACCGTCTTCAAACCTCCA	30525	A	AGA	
			TGGA TTTGAAGA TGAAG				
			ACCT AAACCTTCT ACTTC				
			C GCC				
GAM1558	TRIM16	3'	TCATCTTCTAGTGCCA	21343	A	TGA	
			TGG ATT AGAAGATGA				
			ACC TGA TCTTCTACT				
			G				
GAM1558	LOC124245	3'	CTCCATCTTCTTCCCTGGCC	58152	AATTT		A
			GG GAAGAAGATG AG				
			CC CTTCTTCTAC TC				
			GGTCC C				
GAM1558	LOC144231	5'	ATCTTCCTCAAACCTTCA	83011	A	A	
			TGGA TTTGA GAAGAT				
			ACTT AAACCT CTTCTA				
			C C				
GAM1558	LOC145739	3'	TCATTCTTCAAAGCCCA	77443	AA	AG	
			TGG TTTGAAGA ATGA				

ACC AAAC TTCT TACT  
 CG \_  
 GAM1558 LOC146856 3' CTTCTTTTTTTCTTCTTCAACC 82802 AT T\_ \_  
 TCCA TGGG TTGAAGAAGA GAAG AAG  
 ||| ||||| ||| |||  
 ACCT AAC TTCTTCT TTTC TTC  
 CC TT C  
 GAM1558 LOC147166 3' TCATCTTCTAGTGCCA 78290 A TGA  
 TGG ATT AGAAGATGA  
 ||| ||| |||||  
 ACC TGA TCTTCTACT  
 G \_  
 GAM1558 LOC151124 5' TCTGTTCTTCCCCAAATTCC 85234 AA TGA  
 GGAATTTG GAAGA AGA  
 ||||| ||| |||  
 CCTTAAAC CTTCT TCT  
 CC TG\_  
 GAM1558 LOC151405 5' CTTCTTCATGACACCAAATCCA 85337 A AAGAAG  
 TGGG TTTG ATGAAGAAG  
 ||| ||| |||||  
 ACCT AAAC TACTTCTTC  
 \_ CACAG\_  
 GAM1558 LOC151438 5' CTTCTGGGACCAAATCCA 85365 A\_\_\_\_  
 TGGGATTTG AGAAG  
 ||||| |||  
 ACCTTAAAC TCTTC  
 CAGGG  
 GAM1558 LOC153469 3' CTTTCATCTTCTCCTCA 80841 \_  
 TGA AGAAGATGAAG  
 ||| |||||  
 ACT TCTTCTACTTC  
 CC  
 GAM1558 LOC157909 5' CTTCTCAGACTTAAAATTCCA 81627 G AAGA A  
 TGGGATTT AAG TGA GAAG  
 ||||| ||| ||| |||  
 ACCTTAAA TTC ACT CTTC  
 A AG\_ \_  
 GAM1558 LOC165140 5' TCTTCATCTTCTGCATCCA 82467 ATT A  
 TGGG TG AGAAGATGAAGA  
 ||| ||| |||||  
 ACCT AC TCTTCTACTTCT  
 \_ G  
 GAM1558 LOC169831 5' CTTCTTCATCTTCCCTTC 82783 \_  
 GAA GAAGATGAAGAAG  
 ||| |||||  
 CTT CTCTACTTCTTC  
 CC  
 GAM1558 LOC197414 3' CTTGGCTTCTTCAAACGCCA 88066 AA ATG  
 TGG TTTGAAGAAG AAG  
 ||| ||||| |||

		ACC AA	ACTTCTTC	TTC		
		GC	GG_			
GAM1558	LOC219894 3'	CTTCCCA	ACTTCTTCAAATTC	93281	A	AA
		GAATTTGA	AAGAAG TG GAAG			
		CTTAA	ACTTCTTC AC CTTC			
		A	C_			
GAM1558	LOC255040 3'	CTTCCTTTT	GCTCCAAATTCC	96382	A _	T
		GGAATTTG	AG AAGA GAAG			
		CCTTAAAC	TC TTTT CTTC			
		C G	C			
GAM1558	LOC255041 3'	CTTCCTTTT	GCTCCAAATTCC	96388	A _	T
		GGAATTTG	AG AAGA GAAG			
		CCTTAAAC	TC TTTT CTTC			
		C G	C			
GAM1558	LOC90371 5'	TCTTCATC	CTCTCTACC	62504	AATTT A	A
		GG	GA GA GATGAAGA			
		CC	CT CT CTACTTCT			
		AT__	C C			
GAM1558	LOC92539 5'	TCCTCTCTT	CAAGTCCCA	69643	A	A T
		TGG ATTTGA	AGA GA GA			
		ACC TGA	ACTTCT CT CT			
		C	_ C			
GAM1559	DIAPH2 5'	ATCGGCAG	CTTCCCGGGC	23599	GAA	T
		GCC	GGA GCTGCCGAT			
		CGG	CCT CGACGGCTA			
		GC_	T			
GAM1559	DIAPH2 5'	ATCGGCAG	CTTCCCGGGC	22062	GAA	T
		GCC	GGA GCTGCCGAT			
		CGG	CCT CGACGGCTA			
		GC_	T			
GAM1559	DSC3 3'	GGTTTTCC	ACCATCCTTCAGCG	8679	C	C CC_
	TG	CACGC	GAAGGATG TG GATC			
		GTGCG	CTTCCTAC AC TTGG			
		A	C CTT			
GAM1559	DSC3 3'	GGTTTTCC	ACCATCCTTCAGCG	44344	C	C CC_
	TG	CACGC	GAAGGATG TG GATC			
		GTGCG	CTTCCTAC AC TTGG			
		A	C CTT			
GAM1559	FBN1 3'	GGATCAC	CAGTGCATCCTTC	64401	_	CC
		GAAGGATGC	TG GATCC			

CTTCTACG AC CTAGG  
 TG CA  
 GAM1559 LEF1 5' CGGCGTTCTCCGCGCG 32757 \_ A  
 CGC CG AGGATGCTG  
 ||| || |||||  
 GCG GC TCTTGCGGC  
 C C  
 GAM1559 LYL1 5' GGCCAGCATCCTCCGGC 18759 A \_  
 GCCG AGGATGCTG CC  
 ||| ||||| ||  
 CGGC TCCTACGAC GG  
 C C  
 GAM1559 PAX3 3' GGATCAAGGTCCCTTCATGCG 4768 C\_ AT GCC  
 CGC GAAGG GCT GATCC  
 || |||| || ||||  
 GCG CTTCC TGG CTAGG  
 TA C\_ AA\_  
 GAM1559 CIDEB 3' GATCAAGATGTCCCCCAGGC 27043 GAA\_ \_ GCC  
 GCC GGATG CT GATC  
 || |||| || ||||  
 CGG CCTGT GA CTAG  
 ACCC A A\_  
 GAM1559 DKFZp434G171 3' GGATGTCAGCATCCCCCG 79435 AA C G  
 CG GGATGCTG C ATCC  
 || ||||| ||||  
 GC CCTACGAC G TAGG  
 CC T\_  
 GAM1559 OSBPL1A 5' GGATCGGCTCGCCTCGGC 35909 A A CT  
 GCCGA GG TG GCCGATCC  
 |||| || |||||  
 CGGCT CC GC CGGCTAGG  
 \_ \_ T\_  
 GAM1559 SDC3 3' GGCCCCAGCATCCCCCAGGTG 27757 GAA\_ \_  
 CGCC GGATGCT GCC  
 ||| ||||| ||  
 GTGG CCTACGA CGG  
 ACCC CCC  
 GAM1559 TRAP95 3' GCAGCATCGTGGAGTG 65537 G AAG  
 CAC CCG GATGCTGC  
 ||| || |||||  
 GTG GGT CTACGACG  
 A G\_  
 GAM1559 USP25 5' GGACCGGCAGCAAAGGAACGTG 25443 \_ GAAGGA A  
 CACG CC TGCTGCCG TCC  
 ||| || ||||| ||  
 GTGC GG ACGACGGC AGG  
 AA AA\_ C  
 GAM1559 LOC134875 5' ATCAAAGGCTCCTTCGGGTG 75933 G T GCC  
 CAC CCGAAGGA GCT GAT  
 ||| ||||| || ||

GTG GGCTTCCT CGG CTA  
 \_ \_ AAA  
 GAM1559 LOC167147 5' GGACTTATAGCATCCCCAGGT 82673 GAA\_ CCGA  
 G CGCC GGATGCTG TCC  
 |||| ||||| ||  
 GTGG CCTACGAT AGG  
 ACCC ATTC  
 GAM1559 LOC90632 5' GATCGGCGCGCACCCCAGAGTG 63648 CGAA A \_  
 CGC GG TGC TGCCGATC  
 || || || |||||  
 GTG CC ACG GCGGCTAG  
 AGAC C C  
 GAM1559 LOC93268 3' CAGTTGTCCTTCAATGTG 71877 CC \_  
 CACG GAAGGATG CTG  
 |||| ||||| ||  
 GTGT CTTCTGT GAC  
 AA T  
 GAM1560 ACN 5' AACACCCAAGCGCCCC 30367 AAA T ATCA  
 GGGGC G CT GGTGTT  
 |||| || |||||  
 CCCCC C GA CCACAA  
 \_ \_ AC\_  
 GAM1560 CLCN6 3' AAACACCTCTCTCTCCCC 41379 CAA TCTATC  
 GGGG AG AGGTGTTT  
 |||| || |||||  
 CCCC TC TCCACAAA  
 \_ TCTC\_  
 GAM1560 CLCN6 3' AAACACCTCTCTCTCCCC 41394 CAA TCTATC  
 GGGG AG AGGTGTTT  
 |||| || |||||  
 CCCC TC TCCACAAA  
 \_ TCTC\_  
 GAM1560 CLCN6 3' AAACACCTCTCTCTCCCC 7072 CAA TCTATC  
 GGGG AG AGGTGTTT  
 |||| || |||||  
 CCCC TC TCCACAAA  
 \_ TCTC\_  
 GAM1560 CNTN3 3' TATCTGATCAGACTTTGCCCC 66698 \_  
 GGGGCAAAGTCT ATCAGGTG  
 ||||| |||||  
 CCCCCGTTTCAGA TAGTCTAT  
 C  
 GAM1560 CSRP1 3' CAAACACCTTTCCCTTTGCCCT 14526 TCTATC  
 GGGGCAAAG AGGTGTTTG  
 ||||| |||||  
 TCCCGTTTC TCCACAAAC  
 CCTT\_  
 GAM1560 MYCL2 3' TGATAGATTTTGCCCC 18191  
 GGGGCAAAGTCTATCA  
 |||||

CCCCGTTTTAGATAGT

GAM1560	NTSR1	3'	ACTTCCTGCCAAACTTTGCCCC	10284	CTAT	T_
			GGGGCAAAGT CAGG GT			
			CCCCGTTTCA GTCC CA			
			AACC TT			
GAM1560	RAB26	3'	CAAGTGGACAGACTTTGCC	26822	A	AGG_
			GGCAAAGTCT TC TG			
			CCGTTTCAGA AG AC			
			C GTGA			
GAM1560	STK10	3'	CCTGATAGACCTGCCCC	19984	AA	
			GGGGCA GTCTATCAGG			
			CCCCGT CAGATAGTCC			
			C_			
GAM1560	TCTA	3'	CAAACACCCACATACCTGGCCC	42234	AAA	CTATCA
			GGGC GT GGTGTTTG			
			CCCG CA CCACAAAC			
			GTC TACAC_			
GAM1560	ELKS	3'	CAAACACTACAACTTCATCCC	30502	CA	CTATCA
			GGGG AAGT GGTGTTTG			
			CCCT TTCA TCACAAAC			
			AC AACA__			
GAM1560	FLJ23537	3'	CAAACACCTGCCTCTCTTCAAC	46023	GCA	TCTAT
	CC		GGG AAG CAGGTGTTTG			
			CCC TTC GTCCACAAAC			
			AAC TCTCC			
GAM1560	KIAA0433	5'	CAAACACCTCACCCCTGCCTC	30835	AAGTCTATC	
			GGGGCA AGGTGTTTG			
			CTCCGT TCCACAAAC			
			CCCCAC__			
GAM1560	KIAA0450	3'	CACTGCTGATGACTTTGCCCC	27620	T	__
			GGGGCAAAGTC ATCAG GTG			
			CCCCGTTTCAG TAGTC CAC			
			_ GT			
GAM1560	LEAP-2	5'	AAATATAAACTTTGCCCC	53739	CTATCAG	
			GGGGCAAAGT GTGTTT			
			CCCCGTTTCA TATAAA			
			AA_____			
GAM1560	LOC147077	3'	CACCTCCTAATAGACTTAGCCC	78249	A	C__
	C		GGGGC AAGTCTAT AGGTG			

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          CCCCCG TTCAGATA  TCCAC
            A   ATCC
GAM1561 CABC1  5' GCACAAACAGACGCTC  39654  CTGGC
          GAGC  TCTGTTTGTGC
          |||  |||||
          CTCG  AGACAAACACG
            C____
GAM1561 CEACAM5 3' AACAGAGCAAGACTCCA  15153  C G
          TGGAG CT GCTCTGTT
          |||| || |||||
          ACCTC GA CGAGACAA
            A A
GAM1561 F2R    3' AACAGAGCAAGACTCCA  8831   C G
          TGGAG CT GCTCTGTT
          |||| || |||||
          ACCTC GA CGAGACAA
            A A
GAM1561 FGFR2  3' GACAGAGCGAGACTCCA  43377  C G
          TGGAG CT GCTCTGTT
          |||| || |||||
          ACCTC GA CGAGACAG
            A G
GAM1561 FGFR2  3' GACAGAGCGAGACTCCA  43383  C G
          TGGAG CT GCTCTGTT
          |||| || |||||
          ACCTC GA CGAGACAG
            A G
GAM1561 FUT6   3' GACAGAGCAAGACTCCA  3812   C G
          TGGAG CT GCTCTGTT
          |||| || |||||
          ACCTC GA CGAGACAG
            A A
GAM1561 GCLM   5' GGCGCAGACCAGGCTCCA  9026   C  TTGT _
          TGGAGCCTGG TCTGT  GC C
          ||||| ||||  ||
          ACCTCGGACC AGACG  CG G
            _  ____ A
GAM1561 GPC1   3' GGCTGCAGAGCCCGGCCCA  9103  A T  TTGT
          TGG GCC GGCTCTGT  GCC
          ||| ||| |||||  |||
          ACC CGG CCGAGACG  CGG
            C C  T____
GAM1561 HPSE   3' CAAACAGGCCAGGCTCCA  21890  T
          TGGAGCCTGGC CTGTTTG
          ||||| |||||
          ACCTCGGACCG GACAAAC
            _
GAM1561 IFIT4  3' AACAGAGCAAGACTCCA  70918  C G
          TGGAG CT GCTCTGTT
          |||| || |||||

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			ACCTC GA CGAGACAA		
			A A		
GAM1561	KCNJ5	3'	GACAGAGCGAGACTCCA	6091	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A G		
GAM1561	LY94	3'	GACAGAGCGAGACTCCA	16705	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A G		
GAM1561	LZTS1	3'	ACAGAGCCTGGCCCCA	40676	A T
			TGG GCC GGCTCTGT		
			ACC CGG CCGAGACA		
			C T		
GAM1561	MSH3	3'	AACAGAGCAAGACTCCA	10116	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A A		
GAM1561	POLH	3'	AACAGAGCGAGACTCCA	21461	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1561	PRKAB1	3'	GCACACCACCAGGCTCCA	20736	CTC TT
			TGGAGCCTGG TG TGTGC		
			ACCTCGGACC AC ACACG		
			___ C_		
GAM1561	SIGLEC6	3'	AACAGAGCGAGACTCCA	59925	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1561	SLC10A2	5'	AGCAGAGCCAGGGCCCA	4840	AG
			TGG CCTGGCTCTGTT		
			ACC GGACCGAGACGA		
			CG		
GAM1561	SNRPN	5'	CAAGCAAAAACCAGGCTCCA	43005	CTC_
			TGGAGCCTGG TGTTTG		
			ACCTCGGACC ACGAAC		
			AAAA		
GAM1561	SNRPN	5'	CAAGCAAAAACCAGGCTCCA	43013	CTC_
			TGGAGCCTGG TGTTTG		



			ACCTCGGACC	ACGAAC		
			AAAA			
GAM1561	SNRPN	5'	CAAGCAAAAACCAGGCTCCA	42991	CTC_	
			TGGAGCCTGG	TGTTTG		
			ACCTCGGACC	ACGAAC		
			AAAA			
GAM1561	SNRPN	5'	CAAGCAAAAACCAGGCTCCA	42998	CTC_	
			TGGAGCCTGG	TGTTTG		
			ACCTCGGACC	ACGAAC		
			AAAA			
GAM1561	TNFSF11	5'	CAGGAGCCAAAGCCGGGCTCCA	13512	CT_	G
			TGGAGCCTGGCT	GTTT TG		
			ACCTCGGGCCGA	CGAG AC		
			AAC	G		
GAM1561	TSNAX	3'	GGTAACAGAGCAAGACTCCA	20002	C G	TTG
			TGGAG CT	GCTCTGT TGCC		
			ACCTC GA	CGAGACA ATGG		
			A A	___		
GAM1561	UBE2L3	3'	GCCTTTGCAGAGTCAAGCTCCA	12503	C	TTGT
			TGGAGC	TGGCTCTGT GC		
			ACCTCG	ACTGAGACG CG		
			A	TTTC		
GAM1561	ZNF264	3'	AACAGAGCGAGACTCCA	12738	C G	
			TGGAG CT	GCTCTGTT		
			ACCTC GA	CGAGACAA		
			A G			
GAM1561	ARNTL2	3'	GACAGAGCGAGACTCCA	39466	C G	
			TGGAG CT	GCTCTGTT		
			ACCTC GA	CGAGACAG		
			A G			
GAM1561	C22orf5	3'	GGATCAGAGCCAGACACCA	24344	AGC	TTTGTG
			TGG	CTGGCTCTG CC		
			ACC	GACCGAGAC GG		
			ACA	TA___		
GAM1561	DKFZp547C176	3'	GACAGAGCAAGACTCCA	67223	C G	
			TGGAG CT	GCTCTGTT		
			ACCTC GA	CGAGACAG		
			A A			
GAM1561	DKFZp564K142	3'	AACAGAGCGAGACTCCA	49522	C G	
			TGGAG CT	GCTCTGTT		

			ACCTC GA CGAGACAA			
			A G			
GAM1561	FADS1	3'	GACAGAGCAAGACTCCA	25477	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1561	FLJ12298	3'	AACAGAGCGAGACTCCA	49664	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A G			
GAM1561	FLJ14117	3'	AACAGAGCAAGACTCCA	42896	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A A			
GAM1561	FLJ14251	3'	GGTAACAGAGCGAGACTCCA	45977	C G	TTG
			TGGAG CT GCTCTGT TGCC			
			ACCTC GA CGAGACA ATGG			
			A G —			
GAM1561	FLJ14327	3'	AACAGAGCTAGACTCCA	46127	C	
			TGGAG CTGGCTCTGTT			
			ACCTC GATCGAGACAA			
			A			
GAM1561	FLJ14566	5'	GGCCACAGAGCCAGCCCCA	51446	A C	TT T
			TGG GC TGGCTCTGT G GCC			
			ACC CG ACCGAGACA C CGG			
			C _ _ _			
GAM1561	FLJ20084	3'	AACAGAGCGAGACTCCA	34511	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A G			
GAM1561	FLJ20306	3'	GACAGAGCAAGACTCCA	34917	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1561	FLJ20456	3'	GGTAACAGAGCTAGACTCCA	35215	C	TTG
			TGGAG CTGGCTCTGT TGCC			
			ACCTC GATCGAGACA ATGG			
			A —			
GAM1561	FLJ22054	3'	AACAGAGCAAGACTCCA	94391	C G	
			TGGAG CT GCTCTGTT			

			ACCTC GA CGAGACAA			
			A A			
GAM1561	FLJ22393	5'	AGCAGGAACCAGGCTCCA	47058	C_	
			TGGAGCCTGG TCTGTT			
			ACCTCGGACC GGACGA			
			AA			
GAM1561	FLJ23598	3'	GCCAAGAGCCAGCTCCA	45522	C	GTT T
			TGGAGC TGGCTCT TG GC			
			ACCTCG ACCGAGA AC CG			
			— — —			
GAM1561	FLJ31168	3'	GACAGAGCGAGACTCCA	58502	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1561	GP5	3'	GACAGAGCGAGACTCCA	15646	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1561	GTPBP5	3'	GACAGAGCAAGACTCCA	65357	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1561	HIC	3'	AACAGAGCGAGACTCCA	67444	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A G			
GAM1561	ING1-like	3'	GACAGAGCGAGACTCCA	54156	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1561	KBRAS2	3'	AACAGAGCAAGACTCCA	34191	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A A			
GAM1561	KIAA0189	3'	CAGGAGCAGAGCCAGGCCCA	28273	A	G
			TGG GCCTGGCTCTGTTT TG			
			ACC CGGACCGAGACGAG AC			
			— G			
GAM1561	KIAA0472	3'	AGCAGAGCAAGACTCCA	71853	C G	
			TGGAG CT GCTCTGTT			

		ACCTC GA CGAGACGA		
		A A		
GAM1561	KIAA0563	3' GACAGAGCAAGACTCCA	29188	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1561	KIAA0565	3' GACAGAGCAAGACTCCA	66890	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1561	KIAA0648	3' CAAACAGAAGCAGGCTCCA	82651	GC
		TGGAGCCTG TCTGTTTG		
		ACCTCGGAC AGACAAAC		
		GA		
GAM1561	KIAA0924	3' AACAGAGCGAGACTCCA	29712	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAA		
		A G		
GAM1561	KIAA1028	3' CAGAGCACAGGCTCCA	91934	_
		TGGAGCCTG GCTCTG		
		ACCTCGGAC CGAGAC		
		A		
GAM1561	KIAA1719	3' GGCCAGGGCCAGGCCCCA	68169	A TTTGT
		TGG GCCTGGCTCTG	GCC	
		ACC CGGACCGGGAC	CGG	
		C		
GAM1561	KIAA1940	3' GGTCTCAGAACCAAGGCTCCA	79988	_ C TTTGT
		TGGAGCCT GG TCTG	GCC	
		ACCTCGGA CC AGAC	TGG	
		A A TC_		
GAM1561	LGI2	3' CAAATCAAAGCCAGGCTC	36397	C _
		GAGCCTGGCT TG TTTG		
		CTCGGACCGA AC AAAC		
		A T		
GAM1561	MGC10200	3' AACAGAGCGAGACTCCA	58980	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAA		
		A G		
GAM1561	MGC2705	5' GCACCAAGCCAGGCTCC	51113	C TTT
		GGAGCCTGGCT TG GTGC		

CCTCGGACCGA AC CACG

— — —  
GAM1561 MGC4562 3' AACAGAGCGAGACTCCA 55908 C G  
TGGAG CT GCTCTGTT  
||||| || |||||  
ACCTC GA CGAGACAA  
A G  
GAM1561 MGC4663 3' AACAGAGCCAGACTCC 44501 C  
GGAG CTGGCTCTGTT  
|||| |||||  
CCTC GACCGAGACAA  
A  
GAM1561 NPTXR 3' AACAGAGCAAGACTCCA 54171 C G  
TGGAG CT GCTCTGTT  
||||| || |||||  
ACCTC GA CGAGACAA  
A A  
GAM1561 NPTXR 3' AACAGAGCAAGACTCCA 26635 C G  
TGGAG CT GCTCTGTT  
||||| || |||||  
ACCTC GA CGAGACAA  
A A  
GAM1561 OR7C1 5' AACAGAGCCAAGTCCA 82428 G C  
TGGA C TGGCTCTGTT  
|||| | |||||  
ACCT G ACCGAGACAA  
\_ A  
GAM1561 POFUT1 3' AACAGAGCGAGACTCCA 70462 C G  
TGGAG CT GCTCTGTT  
||||| || |||||  
ACCTC GA CGAGACAA  
A G  
GAM1561 PTK6 3' GACAGAGCGAGACTCCA 19936 C G  
TGGAG CT GCTCTGTT  
||||| || |||||  
ACCTC GA CGAGACAG  
A G  
GAM1561 RASGRF2 3' GCACGAAGCCAGGCTCC 61042 CTGT  
GGAGCCTGGCT TTGTGC  
||||||| |||||  
CCTCGGACCGA AGCACG  
— — —  
GAM1561 SC65 3' GACAGAGCGAGACTCCA 21289 C G  
TGGAG CT GCTCTGTT  
||||| || |||||  
ACCTC GA CGAGACAG  
A G  
GAM1561 SNURF 3' CAAGCAAAAACCAGGCTCCA 19052 CTC\_  
TGGAGCCTGG TGTTTG  
||||||| |||||

			ACCTCGGACC	ACGAAC		
			AAAA			
GAM1561	TMG4	3'	GACAGAGCAAGACTCCA	43989	C	G
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1561	WBSCR23	3'	GACAGAGCAAGACTCCA	46762	C	G
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1561	WIRE	3'	GACAGAGCCAGACTCC	78305	C	
			GGAG CTGGCTCTGTT			
			CCTC GACCGAGACAG			
			A			
GAM1561	WSB1	3'	AACAGAGCGAGACTCCA	56138	C	G
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A G			
GAM1561	WSB1	3'	AACAGAGCGAGACTCCA	56144	C	G
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A G			
GAM1561	LOC115704	3'	CAGCCAGAGCCAGGCCCC	73541	A	T
			GG GCCTGGCTCTG TTG			
			CC CGGACCGAGAC GAC			
			C C			
GAM1561	LOC124220	5'	GGCACAACCAGACGCC	59146	_	T
			GGC TCTG TTGTGCC			
			CCG AGAC AACACGG			
			C C			
GAM1561	LOC127262	3'	GACAGAGCGAGACTCCA	76110	C	G
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1561	LOC129563	3'	AGCAGAGCAGGCCCCA	74878	A	G
			TGG GCCTG CTCTGTT			
			ACC CGGAC GAGACGA			
			C _			
GAM1561	LOC129880	3'	AACAGAGCAAGACTCCA	74900	C	G
			TGGAG CT GCTCTGTT			

	ACCTC GA CGAGACAA		
	A A		
GAM1561 LOC143196 3'	AACAGAGCGAGACTCCA	82903	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAA		
	A G		
GAM1561 LOC144319 3'	GGCACAAACAGGCGCCCC	83057	A CTG T
	GG GC GC CTGTTTGTGCC		
	CC CG CG GACAAACACGG		
	C _ _		
GAM1561 LOC145216 3'	GACAGAGCAAGACTCCA	83267	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1561 LOC145820 3'	GACAGAGCAAGACTCCA	77514	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1561 LOC146227 3'	GGTCAGAGCCAGACCCC	77711	AGC TTTGT
	GG CTGGCTCTG GCC		
	CC GACCGAGAC TGG		
	CCA _ _ _		
GAM1561 LOC146713 3'	AACAGAGCAAGACTCCA	83720	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAA		
	A A		
GAM1561 LOC147071 3'	GACAGAGCAAGACTCCA	72999	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1561 LOC147649 3'	GACAGAGCGAGACTCCA	78414	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A G		
GAM1561 LOC148936 3'	AACAGAGCAAGACTCCA	84286	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAA		
	A A		
GAM1561 LOC149803 5'	CAGGCAGAGCAAGCTCCA	79538	CTG
	TGGAGC GCTCTGTTTG		

		ACCTCG CGAGACGGAC		
		AA_		
GAM1561	LOC150299 3'	GACAGAGCAAGACTCCA	84970	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1561	LOC151429 3'	GACAGAGCAAGACTCCA	85353	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1561	LOC151904 3'	AACAGAGCGAGACTCCA	80382	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAA		
		A G		
GAM1561	LOC158292 5'	GACAGAGCGAGACTCCA	86730	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A G		
GAM1561	LOC162137 5'	CAAGCAGGCCAAGCCCCA	87111	A C T
		TGG GC TGGC CTGTTTG		
		ACC CG ACCG GACGAAC		
		C A _		
GAM1561	LOC163033 5'	CGACCAGGACCAAGCCCCA	82396	A C CT T
		TGG GC TGG CTG TTG		
		ACC CG ACC GAC AGC		
		C A AG C		
GAM1561	LOC163682 3'	ACACTCAAAGCCGGGCTCCA	87020	C TT
		TGGAGCCTGGCT TG TGT		
		ACCTCGGGCCGA AC ACA		
		A TC		
GAM1561	LOC200261 3'	GCACAAACCTCTGGAGGCCCA	88655	A GGCTCT
		TGG GCCT GTTTGTGC		
		ACC CGGA CAAACACG		
		_ GGTCTC		
GAM1561	LOC201173 3'	GACAGAGCAAGACTCCA	87329	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1561	LOC201182 5'	AACAGAGCAAGACTCCA	89760	C G
		TGGAG CT GCTCTGTT		



		ACCTC GA CGAGACAA		
		A A		
GAM1561	LOC219627 3'	GACAGAGCGAGACTCCA	92178	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A G		
GAM1561	LOC221543 5'	GACAGAGCAAGACTCCA	93742	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1561	LOC221943 5'	GACAGAGCAAGACTCCA	93989	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1561	LOC222160 5'	GACAGAGCAAGACTCCA	94127	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1561	LOC253039 5'	GGCTCCAAAACCAGGCTCTA	96159	CTCTG T_
		TGGAGCCTGG TTTG GCC		
		ATCTCGGACC AAAC CGG		
		A_____ CT		
GAM1561	LOC254659 3'	AAACAGAGCAAGACTCCA	95109	C G
		TGGAG CT GCTCTGTTT		
		ACCTC GA CGAGACAAA		
		A A		
GAM1561	LOC256158 5'	AACATCGAGCCAGGCCCA	97639	A _
		TGG GCCTGGCTC TGTT		
		ACC CGGACCGAG ACAA		
		_ CT		
GAM1561	LOC256207 3'	GACAGAGCAAGACTCCA	95169	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1561	LOC257596 5'	GACAGAGCAAGACTCCA	97935	C G
		TGGAG CT GCTCTGTT		
		ACCTC GA CGAGACAG		
		A A		
GAM1561	LOC56963 3'	GCACAAAGCCAGGCTTCA	71455	CTGT
		TGGAGCCTGGCT TTGTGC		

ACTTCGGACCGA AACACG

GAM1561 LOC91149 3' GCTGAACCAAGAGCCAGACTCCA 65079 C \_ T  
TGGAG CTGGCTCTG TTTG GC  
||||| ||||| ||||| ||  
ACCTC GACCGAGAC AAGT CG  
A C \_

GAM1561 LOC91409 3' AGGCAAGGCCAGGCCCCA 65951 A TC  
TGG GCCTGGC TGTTT  
||| ||||| |||||  
ACC CGGACCG ACGGA  
C GA

GAM1561 LOC91862 3' GGTGACAGAGCGAGACTCCA 53470 C G TGT  
TGGAG CT GCTCTGTT GCC  
||||| || ||||| |||  
ACCTC GA CGAGACAG TGG  
A G \_

GAM1561 LOC92482 3' AACAGAGCAAGACTCCA 69485 C G  
TGGAG CT GCTCTGTT  
||||| || |||||  
ACCTC GA CGAGACAA  
A A

GAM1562 ABCC3 3' AGAAGCTGCTACCCCTACATCA 39148 TA\_ T GTG  
TGATGTAG AGC GT CT  
||||| ||| || ||  
ACTACATC TCG CG GA  
CCCA T AA\_

GAM1562 NBS1 3' GAGGCTGGCCTCTACATCA 69499 TAA T G  
TGATGTAG GCTG GT CTC  
||||| ||| || |||  
ACTACATC CGGT CG GAG  
TC\_ \_ \_

GAM1562 PIP5K1A 3' AGCACACAGCACACA 13054 A AA  
TGT GT GCTGTGTGCT  
||| || |||||  
ACA CA CGACACACGA

GAM1562 PLN 3' TGCAGCTTGCCACATCA 10650 A  
TGATGT GTAAGCTGTG  
||||| |||||  
ACTACA CGTTCGACGT  
C

GAM1562 RAG2 3' AGCAAGATCTACTACATC 82200 AG\_ GTG  
GATGTAGTA CT TGCT  
||||| || |||  
CTACATCAT GA ACGA  
CTA \_

GAM1562 TSN 3' AGCACACACAAAATAAATCA 16103 G GTAAGC  
TGAT TA TGTGTGCT  
||| || |||||

ACTA AT ACACACGA  
 A AAAAC\_  
 GAM1562 ZNF236 3' GGAGCACATGCAGACACACCA 23715 A A AA T  
 TG TGT GT GC GTGTGCTCC  
 || ||| || || |||||  
 AC ACA CA CG TACACGAGG  
 C \_ GA \_  
 GAM1562 BIKE 3' GAAAACATGGGCTACTACATTA 34185 AG GC  
 TGATGTAGTA CTGTGT TC  
 ||||| ||||| ||  
 ATTACATCAT GGTACA AG  
 CG AA  
 GAM1562 C11orf15 3' AGCACACAGCTCAAAGTCA 40219 GTAGTA  
 TGAT AGCTGTGTGCT  
 ||| |||||  
 ACTG TCGACACACGA  
 AAAC\_  
 GAM1562 C17orf31 5' GAGAACCTTCTACATCA 34124 T CTGT G  
 TGATGTAG AAG GT CTC  
 ||||| || |||||  
 ACTACATC TTC CA GAG  
 \_ \_ \_ A  
 GAM1562 DKFZP586D2223 3' GAGCAGTTGCCTACCACAT 37682 A A TGTG  
 ATGT GTA GC TGCTC  
 ||| ||| || |||||  
 TACA CAT CG ACGAG  
 C C TTG\_  
 GAM1562 FLJ11722 3' AGCAGGAATCCTACATCA 46388 TAAG GTG  
 TGATGTAG CT TGCT  
 ||||| || |||||  
 ACTACATC GG ACGA  
 CTAA \_  
 GAM1562 GENX-3414 3' AGCACTTTTACTACAT 14145 CTGT  
 ATGTAGTAAG GTGCT  
 ||||| |||||  
 TACATCATTT CACGA  
 TT\_  
 GAM1562 JM11 3' GGAGCACACAGCTGAC 53265 A  
 GT AGCTGTGTGCTCC  
 || |||||  
 CA TCGACACACGAGG  
 G  
 GAM1562 KIAA0261 3' ACAGTTACTACATCA 68176 G  
 TGATGTAGTAA CTGT  
 ||||| |||||  
 ACTACATCATT GACA  
 \_  
 GAM1562 KIAA0416 3' AGCACACACACACACA 31463 A A AAGC  
 TG TGT GT TGTGTGCT  
 || ||| || |||||

AC ACA CA ACACACGA  
 \_ \_ CAC\_  
 GAM1562 KIAA1635 3' AGCACAAAGTAAATTATACATCA 67859 GTAA\_\_ G  
 TGATGTA GCT TGTGCT  
 ||||| || |||||  
 ACTACAT TGA ACACGA  
 ATTAAA \_  
 GAM1562 KIAA1644 3' CACACAAGTACATACATGCA 85025 \_ \_ AGC  
 TG ATGTA GTA TGTGTG  
 || ||||| || |||||  
 AC TACAT CAT ACACAC  
 G A GA\_  
 GAM1562 LHFP 3' AGCACACAAGCACATACA 19334 GTAA \_  
 TGTA GCT GTGTGCT  
 ||| || |||||  
 ACAT CGA CACACGA  
 ACA\_ A  
 GAM1562 MGC5601 5' ATCCAACCTTACTACATCA 47505 C TG  
 TGATGTAGTAAG TG T  
 ||||| || ||  
 ACTACATCATTC AC A  
 A CT  
 GAM1562 PRO0611 5' ACCAGCTTATTACACCA 26005 A T  
 TG TGTAGTAAGCTG GT  
 || ||||| || ||  
 AC ACATTATTCGAC CA  
 C \_  
 GAM1562 SFXN2 3' GAGCACACAGGCACACAT 73945 A AAG  
 ATGT GT CTGTGTGCTC  
 ||| || |||||  
 TACA CA GACACACGAG  
 \_ CG\_  
 GAM1562 SYNPO2 3' GAGCACACAATTATTAGCATCA 71894 \_ GC  
 TGATGT AGTAA TGTGTGCTC  
 ||||| ||| |||||  
 ACTACG TTATT ACACACGAG  
 A A\_  
 GAM1562 LOC138654 5' GAGCCTCATTCTGACTACATCA 75948 A CT T\_  
 TGATGTAGT AG GTG GCTC  
 ||||| || || |||  
 ACTACATCA TC TAC CGAG  
 G T\_ TC  
 GAM1562 LOC145815 5' AGAACACAAACTACATC 83516 AAGC G  
 GATGTAGT TGTGT CT  
 ||||| ||| ||  
 CTACATCA ACACA GA  
 A\_\_ A  
 GAM1562 LOC145980 5' CACACAGCTCCATTTCAT 83599 T A\_  
 ATG AGT AGCTGTGTG  
 ||| || |||||

			TAC TTA TCGACACAC		
			T CC		
GAM1562	LOC151568	5'	GGGAGCACGGGCTTCTACACC	56702	A TAA G
	A		TG TGTA GCT TGTGCTCCC		
			AC ACATC CGG GCACGAGGG		
			C TTC _		
GAM1562	LOC200953	5'	AGCACACAGTGGACACG	90205	A AA
			TGT GT GCTGTGTGCT		
			GCA CA TGACACACGA		
			_ GG		
GAM1562	LOC90139	3'	GGAACACACAGAGGTGCACATC	55403	A AG_ C
	A		TGATGT GTA CTGTGTG TCC		
			ACTACA CGT GACACAC AGG		
			_ GGA A		
GAM1563	CNGA1	3'	CAACTGATAATGTGCAAA	59507	GC A
			TTTGCACATTA TAG TTG		
			AAACGTGTAAT GTC AAC		
			A_ _		
GAM1563	ESRRG	3'	TGGCAGTCTTATGTGCAAA	66396	TAGCT
			TTTGCACAT AGATTGCCA		
			AAACGTGTA TCTGACGGT		
			T_		
GAM1563	KCNJ3	3'	GCAATAATGTGCAAA	9525	GCTAGA
			TTTGCACATTA TTGC		
			AAACGTGTAAT AACG		
GAM1563	SDC2	3'	GCAAATTAATGTGTAAA	67132	CTAGA
			TTTGCACATTAG TTGC		
			AAATGTGTAATT AACG		
			A_		
GAM1563	USP9X	3'	ATGGCCTGATGCTAATGTGTAA	16206	TAGATT
	A		TTTGCACATTAGC GCCAT		
			AAATGTGTAATCG CGGTA		
			TAGTC_		
GAM1563	AMOTL1	3'	GGCAAGTAATGTGCAAA	73650	G AGAT
			TTTGCACATTA CT TGCC		
			AAACGTGTAAT GA ACGG		
GAM1563	BCAR3	3'	AGTAATAATGTGCAAA	13098	_
			TTTGCACATTA GCT		

AAACGTGTAAT TGA  
 AA  
 GAM1563 DKFZP434B044 3' TGACAATTAAATGTGCAGA 48930 AGCTA C  
 TTTGCACATT GATTG CA  
 ||||| |||||  
 AGACGTGTAA TTAAC GT  
 A\_\_\_\_ A  
 GAM1563 MGC3184 3' ATGACATTTTCTAATGTGCAGA 48235 CT T C  
 TTTGCACATTAG AGA TG CAT  
 ||||| |||||  
 AGACGTGTAATC TTT AC GTA  
 \_\_\_\_ T A  
 GAM1563 PTD012 3' ATGGCAATCTAGCTAATGTGCA 25891  
 AA TTTGCACATTAGCTAGATTGCCAT  
 |||||  
 AAACGTGTAATCGATCTAACGGTA  
  
 GAM1564 ATP7A 3' ACCAAAAAAAAAAGGCC 3515 C\_\_\_\_  
 GGCCTT TTTTGGT  
 ||||| |||||  
 CCGGAA AAAAACCA  
 AAAA  
 GAM1564 BAZ2B 3' ACCAAAAAGAACTTTACTGT 25617 C CC\_  
 ACA TGG TTCTTTTGGT  
 ||| |||||  
 TGT ATT AAGAAAAACCA  
 C TCA  
 GAM1564 DBT 3' ACCAAAAAGCCAAGTGTGGTG 8606 \_ CTTC  
 TACCACACT GGC TTTTGGT  
 ||||| |||||  
 GTGGTGTGA CCG AAAAACCA  
 A \_\_\_\_  
 GAM1564 DIAPH2 3' ACCAAAAAAGTATATAGTG 22060 GC\_\_ C  
 CACTG CTT TTTTGGT  
 |||| |||||  
 GTGAT GAA AAAAACCA  
 ATAT \_  
 GAM1564 PTP4A2 3' ACCAAAAAACAGCAGTG 12980 G CTTC  
 CACTG C TTTTGGT  
 |||| | |||||  
 GTGAC G AAAAACCA  
 \_ACAA  
 GAM1564 SNX9 3' ACCAAAAAGAAAGAGTT 32588 \_ \_  
 GGC CTT CTTTGGT  
 ||| |||||  
 TTG GAA GAAAAACCA  
 A A  
 GAM1564 YES1 3' CCAAAAAAGGAAGTTGG 18350 C GG CT  
 CCA ACT CCTT TTTTGG  
 ||| |||||

GGT TGA GGAA AAAACC  
 \_ A\_ \_  
 GAM1564 C6orf25 3' ACCAAAAAAAAAAGGCC 56251 C\_\_\_\_  
 GGCCTT TTTTGGT  
 ||||| |||||  
 CCGGAA AAAAACCA  
 AAAA  
 GAM1564 DKFZp547M236 5' ACCAAAAAACTCCAAATGGTA 38033 CAC CCTTC  
 TACCA TGG TTTTGGT  
 |||| | |||||  
 ATGGT ACC AAAAACCA  
 AA\_ TCA\_  
 GAM1564 FLJ13162 3' GGAAAAGCCAGTGTCTGTA 46559 C C\_  
 TAC AACTGGC TTCT  
 || ||||| |||  
 ATG TGTGACCG AAGG  
 C AA  
 GAM1564 FLJ14346 3' ACCAGCGAGACCAGTGTGGTG 46706 CCT T  
 TACCACACTGG TCTT TTGGT  
 ||||| ||| ||||  
 GTGGTGTGACC AGAG GACCA  
 \_ C  
 GAM1564 GNB4 3' ACCAAAAAAAAAAGTGGGGGTGG 41266 A G C C  
 CCAC CT GC TT TTTTGGT  
 ||| || || |||||  
 GGTG GG TG AA AAAAACCA  
 G G A A  
 GAM1564 GS3955 5' ACCAAAAAAAGGGGGTGCAG 41314 \_ \_  
 CTG GCCTTCT TTTTGGT  
 || ||||| |||||  
 GAC TGGGGGA AAAACCA  
 G AA  
 GAM1564 KIAA1691 3' ACCAAAAAGGGGGAATATGGG 92550 A CTGG  
 CC CA CCTTCTTTTGGT  
 || |||||  
 GG GT GGGGAAAAACCA  
 \_ ATAA  
 GAM1564 KIAA1813 3' AGAGAAAGCCAGATGG 70287 CA C  
 CCA CTGGC TTCTT  
 || |||| |||||  
 GGT GACCG AAGAGA  
 A\_ A  
 GAM1564 MISS 3' ACCAAAAAAAGCCCTGGTA 58026 CACT CTTC\_  
 TACCA GGC TTTTGGT  
 |||| | |||||  
 ATGGT CCG AAAAACCA  
 C\_ AAAAA  
 GAM1564 PDZ- 3' ACTCTTCTGAAGGCCAACGTGG 64998 AC TTTT  
 CCAC TGGCCTTC GGT  
 ||| ||||| ||

GGTG ACCGGAAG TCA  
CA TCTTC

GAM1564 TGIF2 3' ACCAAAAAAAAAGGCAGGG 41445 ACACTG C  
CC GCCTT TTTTGGT  
|| |||| |||||  
GG CGGAA AAAAACCA  
GA\_\_ A

GAM1564 TUCAN 3' ACCAAAAAGAAAATGAGGGTA 30265 ACACTGGCC  
TACC TTCTTTTGGT  
|||| |||||  
ATGG AAGAAAAACCA  
GAGTAA\_\_

GAM1564 VIT1 3' ACCAAAAAGAAAGTGGC 37969 \_\_  
GCC TTCTTTTGGT  
||| |||||  
CGG AAGAAAAACCA  
TGA

GAM1564 LOC144348 5' CCAAAAAAGGAGACGG 76804 GC \_  
CTG CTTCTTTT GG  
||| ||||| ||  
GGC GAGGAAAA CC  
A\_ A

GAM1564 LOC146229 3' GGAGAAGGCCGCGGTGGTA 77765 A  
TACCAC CTGGCCTTCTTT  
||||| |||||  
ATGGTG GGCCGGAAGAGG  
C

GAM1564 LOC147699 3' ACCAAAAAGAAAAAGCC 78465 C\_\_  
GGC TTCTTTTGGT  
||| |||||  
CCG AAGAAAAACCA  
AAAA

GAM1564 LOC151057 3' ACCAAAAAGGTCCAAATGTG 85201 C\_ CCT  
CACA TGG TCTTTTGGT  
|||| ||| |||||  
GTGT ACC GGAAAAACCA  
AA T\_\_

GAM1564 LOC196418 5' CCAAAAAAGGAGACGG 87693 GC \_  
CTG CTTCTTTT GG  
||| ||||| ||  
GGC GAGGAAAA CC  
A\_ A

GAM1564 LOC200316 3' ACCAAAAAAGCCAGATGTGG 88762 \_ C C  
TG TACCACA CTGGC TT TTTTGGT  
||||| |||| || |||||  
GTGGTGT GACCG AA AAAAACCA  
A \_ A

GAM1564 LOC200399 5' ACCAAAAAAGCCCAG 88803 C C  
CTGG CTT TTTTGGT  
|||| ||| |||||



GACC GAA AAAAACCA  
 C \_  
 GAM1564 LOC253039 3' ACCAAGAAAGACCAGCGTGG 96151 A C CT  
 CCAC CTGG CTT TTTTGGT  
 |||| |||| || |||||  
 GGTG GACC GAA AGAACCA  
 C A \_  
 GAM1564 LOC254351 3' ACTTTGGAAGGCCGAGTGTGG 94992 \_ TTTT  
 CCACACT GGCCTTCT GGT  
 ||||| ||||| ||  
 GGTGTGA CCGGAAGG TCA  
 G TT\_  
 GAM1564 LOC257017 5' ACCAAAAAGAGACAGCGTG 97371 A GC T  
 CAC CTG CT CTTTTTGGT  
 ||| ||| || |||||  
 GTG GAC GA GAAAAACCA  
 C A\_ \_  
 GAM1565 AQP3 3' TTCACGATCCACCCTTTC 59593 T\_ \_  
 GAAA GTGG TCGTGAA  
 |||| |||| |||||  
 CTTT CACC AGCACTT  
 CC T  
 GAM1565 ARSB 3' TCACGACTCTTGTC 3502 AATGTG  
 GACAAGA GTCGTGA  
 ||||| |||||  
 CTGTTCT CAGCACT  
 \_\_\_\_\_  
 GAM1565 B4GALT5 3' TTTTCACAAAAATAGTCCTTTG 16519 AAA\_ GGTC  
 TCA TGACAAG TGT GTGAAAA  
 ||||| || |||||  
 ACTGTTT ATA CACTTTT  
 CCTG AAAA  
 GAM1565 CHRNA3 3' TCGTTACCCATTTCTT 5610 T CG  
 AAGAAATG GGT TGA  
 ||||| ||| |||  
 TTCTTTAC CCA GCT  
 \_ TT  
 GAM1565 DRD1 3' TTACAACCACATTTCTGGCCA 5840 ACA C  
 TG AGAAATGTGGT GTGA  
 || ||||| |||||  
 AC TCTTTACACCA CATT  
 CGG A  
 GAM1565 FUT1 3' TCTGATCACATCCCCTGTC 3798 AGAA T  
 GACA ATGTGGTGTG GA  
 |||| ||||| ||  
 CTGT TACACTAGT CT  
 CCCC \_  
 GAM1565 IRF1 3' GCCACATTTCTGATCA 64345 CA  
 TGA AGAAATGTGGT  
 ||| ||||| |||||

ACT TCTTTACACCG  
 AG  
 GAM1565 MAP3K8 5' TCACGACCACCTCATG 17791 A AAT  
 CA GA GTGGTCTGTA  
 || || |||||  
 GT CT CACCAGCACT  
 A C\_\_  
 GAM1565 NGFR 3' TTCTGACCACACTTCCTGTC 10231 A A T  
 GACA GAA TGTGGTCG GAA  
 |||| || ||||| ||  
 CTGT CTT ACACCAGT CTT  
 C C \_  
 GAM1565 OLR1 3' TTCACAACAGTTCTTGTTA 10341 ATGTG C  
 TGACAAGAA GT GTGAA  
 ||||| || ||||  
 ATTGTTCTT CA CACTT  
 GA\_\_ A  
 GAM1565 POU4F1 3' CACTGAAAACATTTTTGTCA 20660 A GG \_  
 TGACAAGAA TGT TC GTG  
 ||||| || || ||  
 ACTGTTTTT ACA AG CAC  
 \_ AA T  
 GAM1565 SMP1 3' TTTACATGAATAATTTTTGTC 26705 A GGTC  
 A TGACAAGAA TGT GTGAAA  
 ||||| || ||||  
 ACTGTTTTT ATA CACTTT  
 A AGTA  
 GAM1565 ZNF264 3' TTCTATTAACATTTCTTTTCA 12769 C GGTCGT  
 TGA AAGAAATGT GAA  
 || ||||| ||  
 ACT TTCTTTACA CTT  
 T ATTAT\_  
 GAM1565 C20orf175 3' CGAGCTCCACGTTTCCTGCCA 55063 A A \_\_\_\_  
 TG CA GAAATGTGG TCG  
 || || ||||| ||  
 AC GT CTTTGCACC AGC  
 C C TCG  
 GAM1565 CAPNS2 3' TTTCACAACCCTACATATTCT 50323 CA \_\_\_\_ C  
 GATCA TGA AGAAATGT GGT GTGAAA  
 || ||||| || |||||  
 ACT TCTTTATA CCA CACTTT  
 AG CATC A  
 GAM1565 CLDN6 3' TTTACACTCACATTTTATCA 41041 CA \_ C  
 TGA AGAAATGTG GT GTGAA  
 || ||||| || ||||  
 ACT TTTTACAC CA CATT  
 A\_ T\_  
 GAM1565 DKFZP564L0864 3' GCACCAATTTCTTGCCA 72555 A G C  
 TG CAAGAAAT TGGT GT  
 || ||||| || ||

AC GTTCTTTA ACCA CG  
 C \_ \_  
 GAM1565 DKFZP566B183 3' TTTCCATAAACATTTCTTTTCA 31330 C GGTCGT  
 TGA AAGAAATGT GAAA  
 ||| ||||| |||  
 ACT TTCTTTACA CTTT  
 T AATAC\_  
 GAM1565 GTF2E1 3' TACAGACCTCTTGTCA 18616 AATGT \_  
 TGACAAGA GGTC GTG  
 ||||| ||| |||  
 ACTGTTCT CCAG CAT  
 \_ A  
 GAM1565 KIAA0089 3' TTTTAATTCACATTTCTT 69967 TCG  
 AAGAAATGTGG TGAAA  
 ||||| |||  
 TTCTTTACACT ATTTT  
 TA\_  
 GAM1565 KIAA0373 5' TTTTCAAAGTAACATTTCTT 28015 GGTCG  
 AAGAAATGT TGAAAA  
 ||||| |||  
 TTCTTTACA ACTTTT  
 ATGAA  
 GAM1565 KIAA1813 3' TTTTCACACTGTAAATTTCTTG 70314 \_ TG C  
 T ACAAGAAAT G GT GTGAAAA  
 ||||| | |||||  
 TGTTCCTTA T CA CACTTTT  
 AA GT \_  
 GAM1565 KIAA1951 3' TTCCAGGCTTCTCTTGTCA 73766 AATGT GT  
 TGACAAGA GGTC GAA  
 ||||| ||| |||  
 ACTGTTCT TCGG CTT  
 CT\_ AC  
 GAM1565 MGC4170 3' TTCACCATTTCTTGTC 44227 TGGTC  
 GACAAGAAATG GTGAA  
 ||||| |||  
 CTGTTCTTTAC CACTT  
 \_  
 GAM1565 NRN1 3' CACTGCACATTTCTCCTCA 33432 CA GTC  
 TGA AGAAATGTG GTG  
 ||| ||||| |||  
 ACT TCTTTACAC CAC  
 CC GT\_  
 GAM1565 PLA2G12 3' TTTTCACAACCACATTT 48028 C  
 AAATGTGGT GTGAAAA  
 ||||| |||||  
 TTTACACCA CACTTTT  
 A  
 GAM1565 PPY2 3' CACTCCACATTCCTGGCCA 40819 ACA A TC  
 TG AG AATGTGG GTG  
 || ||||| |||

			AC TC TTACACC CAC		
			CGG C T_		
GAM1565	ZNF31	3'	TTTGTAGACCACATTTCTGT	64992	A _TG
	A		TGACA GAAATGTGGTC G AA		
			ATTGT CTTTACACCAG T TT		
			C A GT		
GAM1565	LOC115219	3'	CACGACAACGGGTCCTCA	73295	CAA AA G
			TGA GA TGT GTCGTG		
			ACT CT GCA CAGCAC		
			C_ GG A		
GAM1565	LOC120376	5'	TTCAGAGCATTCTTTCA	75986	C GG G
			TGA AAGAAATGT TC TGAA		
			ACT TTCTTTACG AG ACTT		
			- - -		
GAM1565	LOC133418	3'	TTTCATATACATTTTTTGCCA	75094	A GTC
			TG CAAGAAATGTG GTGAAA		
			AC GTTTTTTACAT TACTTT		
			C A_		
GAM1565	LOC151199	3'	TTAAAACACAGCTCTTGCCA	80174	A AA CG
			TG CAAGA TGTGGT TGA		
			AC GTTCT ACACCA ATT		
			C CG AA		
GAM1565	LOC152317	5'	TCACACTGACTTTTGTCA	85649	AATG C
			TGACAAGA TGGT GTGA		
			ACTGTTTT GTCA CACT		
			CA_ -		
GAM1565	LOC152674	3'	TTCAACCCACCCTCTTGTC	85841	AAT TCG
			TGACAAGA GTGG TGAA		
			ACTGTTCT CACC ACTT		
			CC_ CA_		
GAM1565	LOC152845	5'	CATGACCACATTTTTCA	60330	CAA
			TGA GAAATGTGGTCGTG		
			ACT TTTACACCAGTAC		
			-		
GAM1565	LOC154743	3'	TTTAGTCCACATTGTCTTGTC	81118	_ TCG
			TGACAAGA AATGTGG TGAA		
			ACTGTTCT TTACACC ATTT		
			G TG_		
GAM1565	LOC165476	5'	TTCACGGCACCTTCT	87201	AT G
			AGAA GTG TCGTGAA		

TCTT CAC GGCACCTT  
 C\_ \_  
 GAM1565 LOC254266 5' TTTTCGGTCACACATCTTATCA 97356 C AA GT T  
 TGA AAGA TGTG CG GAA  
 ||| ||| ||| |||  
 ACT TTCT ACAC GC TTT  
 A AC TG T  
 GAM1565 LOC255919 3' TTTCATTCTTACATTTCTAATC 95043 CA TC  
 A TGA AGAAATGTGG GTGAAA  
 ||| ||||| |||||  
 ACT TCTTTACATT TACTTT  
 AA CT  
 GAM1565 LOC51754 5' CACGGCCACATCTCTGTCA 71027 A A  
 TGACA GA ATGTGGTCGTG  
 ||||| || |||||  
 ACTGT CT TACACCGGCAC  
 \_ C  
 GAM1565 LOC55862 3' ACCTCATTTCTTGCCA 37485 A T  
 TG CAAGAAATG GGT  
 || ||||| |||  
 AC GTTCTTTAC CCA  
 C T  
 GAM1565 LOC55954 3' CACGTGGTCACTTTTCTCATCA 38877 CA T GT \_  
 TGA AGAAA GTG C GTG  
 ||| ||||| ||| | |||  
 ACT TCTTT CAC G CAC  
 AC T TG TG  
 GAM1566 ACP2 3' AGAAAGTTCTAGACTG 7851 GC TC  
 CAGT CT AGAACTTTCT  
 ||||| || |||||  
 GTCA GA TCTTGAAAGA  
 \_ \_  
 GAM1566 APTX 5' AAGAGAAAGAGATCAGGCA 34655 TCAGAA  
 TGCCT CTTTCTCTT  
 ||||| |||||  
 ACGGA GAAAGAGAA  
 CTAGA\_  
 GAM1566 BCL7A 3' AGGCTGTCTCCTTAAGGCACTG 40637 C A\_ TT  
 CAGTGCCTT AG AC TCT  
 ||||| || |||  
 GTCACGGAA TC TG GGA  
 T CTC TC  
 GAM1566 CLC 3' AAGAGAAAATACTGAAAGCACA 25105 A C AAC  
 GG CC GTGC TTCAG TTTCTCTT  
 || ||||| |||||  
 GG CACG AAGTC AAAGAGAA  
 A A ATA  
 GAM1566 CNK 3' AAGCCCTGAAGGCCTG 14517 T AA  
 CAG GCCTTCAG CTT  
 ||| ||||| |||

			GTC CGGAAGTC GAA		
			— CC		
GAM1566 COL4A3	3'	AAGTGCAGGTTCTGAGGGCACC 48549	A	TCT	
GG		CC GTGCCTTCAGAACTT CTT			
		GG CACGGGAGTCTTGGA GAA			
		C CGT			
GAM1566 CSPG4	3'	AAGAGAGACCTGGAGACAC 8570	C	AAC	
		GTG CTTCAG TTTCTCTT			
		CAC GAGGTC AGAGAGAA			
		A C__			
GAM1566 CYP1B1	3'	AAGAGAAAAGAGAGAAACACTG 3651	CC	AGAAC	
		CAGTG TTC TTTCTCTT			
		GTCAC AAG AAAGAGAA			
		A_ AGAGA			
GAM1566 DLG3	3'	AAGAGAAAAGAGGAGGACTG 40880	G	AGAAC	
		CAGT CCTTC TTTCTCTT			
		GTCA GGAGG AAAGAGAA			
		— AGA__			
GAM1566 DLG5	5'	AGGCAGACTCTGAAGGC 82909	A_	T	
		GCCTTCAGA CT TCT			
		CGGAAGTCT GA GGA			
		CA C			
GAM1566 FLT1	3'	AAGAGAAACCGGGAGAAGGCAT 8910	AGAAC_		
		GTGCCTTC TTTCTCTT			
		TACGGAAG AAAGAGAA			
		AGGGCC			
GAM1566 GRB10	3'	AGAGAAAATGGCACCTGG 17971	_	TTCAGAAC	
		CCAG TGCC TTTCTCT			
		GGTC ACGG AAAGAGA			
		C TA_____			
GAM1566 LFG	3'	AAGAGAAAAGGAGCCAAGAACT 76711	GC	CAGAA _	
GG		CCAGT CTT CTTT CTCTT			
		GGTCA GAA GAAA GAGAA			
		A_ CCGAG A			
GAM1566 MAN2A2	3'	AAGAGAAAGTTCATTCAC 20391	CCTTCA		
		GTG GAACTTTCTCTT			
		CAC CTTGAAAGAGAA			
		TTA__			
GAM1566 NLGN3	3'	AAGAAAAGTTCTTAAACACT 38596	CC C	C	
		AGTG TT AGAACTTT TCTT			

		TCAC AA TCTTGAAA AGAA	
		AA T _	
GAM1566 NPAS1	5'	AAGGTCTCCCGAGGGCACT 59879	A_ _
		AGTGCCTTC GA ACTTT	
		TCACGGGAG CT TGGAA	
		CC C	
GAM1566 PLAG1	3'	AGTGTGTTCCAAAGGCATT 10605	CA TTT
		AGTGCCTT GAAC CT	
		TTACGGAA CTTG GA	
		AC TGT	
GAM1566 PLXNA1	3'	AGAAAAATGAAGGCAGTGG 72309	G GAAC
		CCA TGCCTTCA TTTCT	
		GGT ACGGAAGT AAAGA	
		G A_	
GAM1566 PPP4R1	3'	AAGAGAAAGTACAGTAAACACT 17620	CCTTCAGA
		AGTG ACTTTCTCTT	
		TCAC TGAAAGAGAA	
		AAATGACA	
GAM1566 ACYP2	3'	AAGAGAAAAATTGTAACACACT 56612	CC _ AAC
G		CAGTG TT CAG TTTCTCTT	
		GTCAC AA GTT AAAGAGAA	
		AC T AA_	
GAM1566 B3GNT6	3'	AGAAATCAGATGAAGGCAT 22503	GAAC_
		GTGCCTTCA TTTCT	
		TACGGAAGT AAAGA	
		AGACT	
GAM1566 BAG5	3'	AAGAGAAGGGATAAAGGAC 16835	G CAGAA
		GT CCTT CTTTCTCTT	
		CA GGAA GGAAGAGAA	
		_ ATAG_	
GAM1566 BIVM	3'	AAGAGAAAAGACTCAAGAACT 34665	GC C AAC
G		CAGT CTT AG TTTCTCTT	
		GTCA GAA TC AAAGAGAA	
		AA C AGA	
GAM1566 C15orf5	3'	AGAGAAAAGAAAGCAC 48195	C AGAAC
		GTGC TTC TTTCTCT	
		CACG AAG AAAGAGA	
		A A_	
GAM1566 C20orf80	5'	AAGAGAAGAAGATGAAGAAAC 65282	GC GAAC
		GT CTTCA TTTCTCTT	

CA GAAGT GAAGAGAA  
 AA AGAA  
 GAM1566 CLSTN1 3' AGTTCTGAGGACACTGG 30103 C  
 CCAGTG CTTCAGAACT  
 ||||| |||||  
 GGTCAC GGAGTCTTGA  
 A  
 GAM1566 DKFZP434P0111 3' AAGAGAAAGTTTCTGCAC 67368 CTTCA  
 GTGC GAACTTTCTCTT  
 ||| |||||  
 CACG TTTGAAAGAGAA  
 TC\_\_  
 GAM1566 DORFIN 5' AGAATTCTCTGAAGGAAC 31257 G ACT  
 GT CCTTCAGA TTCT  
 || ||||| |||  
 CA GGAAGTCT AAGA  
 A CTT  
 GAM1566 FLJ10300 5' AAGAGAAAGATGAAGACTCTG 35997 TGC GAA  
 CAG CTTCA CTTTCTCTT  
 ||| ||||| |||||  
 GTC GAAGT GAAAGAGAA  
 TCA A\_\_  
 GAM1566 FLJ20373 3' AAGAGAAGAAGGAAAGGCACAG 35070 A \_AGAAC  
 G CC GTGCCTT C TTTCTCTT  
 || ||||| | |||||  
 GG CACGGAA G GAAGAGAA  
 A A GAA\_\_  
 GAM1566 FLJ23511 5' AGAGAAAAACAAGGCAT 49956 CAGAAC  
 GTGCCTT TTTCTCT  
 ||||| |||||  
 TACGGAA AAAGAGA  
 CAA\_\_  
 GAM1566 FLJ30681 3' AGAGAAGAAAGACCACTGG 91782 CCT AGAAC  
 CCAGTG TC TTTCTCT  
 ||||| || |||||  
 GGTCAC AG GAAGAGA  
 C\_\_ AAA\_\_  
 GAM1566 HDAC11 3' GAGCTATAGGCACTGG 45717 TC AACTTT  
 CCAGTGCCT AG CTC  
 ||||| || |||  
 GGTCACGGA TC GAG  
 TA \_\_\_\_\_  
 GAM1566 IKKE 5' AGTGAGCCCTGAAAGCTCTGG 25745 T C AA T  
 CCAG GC TTCAG CTT CT  
 ||| || |||| ||| ||  
 GGTC CG AAGTC GAG GA  
 T A CC T  
 GAM1566 KIAA0680 3' AGAGAAAATTGAAGCAT 28232 C AAC  
 GTGC TTCAG TTTCTCT  
 ||| |||| |||||



TACG AAGTT AAAGAGA  
 \_ A\_  
 GAM1566 KIAA1228 3' AGGGGGTGATTCTGAGGCACTG 65035 T \_\_\_\_ TT  
 CAGTGCCT CAGA ACT CT  
 ||||| ||| ||  
 GTCACGGA GTCT TGG GA  
 \_ TAG GG  
 GAM1566 KIAA1300 5' AGGAACCCTGAAGGCA 62860 AAC  
 TGCCTTCAG TTTCT  
 ||||| ||||  
 ACGGAAGTC AAGGA  
 CC\_  
 GAM1566 KIAA1805 3' AAGAGAAAGTAGAAGCAGCA 79966 \_\_\_\_ AGA  
 TGC CTTC ACTTTCTCTT  
 || ||| |||||  
 ACG GAAG TGAAAGAGAA  
 AC A\_  
 GAM1566 LENG1 5' AAGAGAAAGCTCTGGGCATCCT 84074 \_\_\_\_ TT A  
 G CAG TGCC CAGA CTTTCTCTT  
 || ||| ||| |||||  
 GTC ACGG GTCT GAAAGAGAA  
 CT \_ C  
 GAM1566 LHX6 3' AAGAGAAAAGTCTGGGGTCA 26854 C AC  
 TG CTTCAGA TTTCTCTT  
 || ||||| |||||  
 AC GGGGTCT AAAGAGAA  
 T CA  
 GAM1566 N4BP3 3' AGCTCCAGAAGGCACTGG 66250 A\_ A  
 CCAGTGCCTTC GA CT  
 ||||| || ||  
 GGTCACGGAAG CT GA  
 AC C  
 GAM1566 NASP 3' AGAGGGTGAAGAACTG 67966 GC AGA  
 CAGT CTTC ACTTTCT  
 ||| ||| |||||  
 GTCA GAAG TGGGAGA  
 AA \_  
 GAM1566 SMARCF1 3' AAAATTCTGAAGGAC 57480 G C  
 GT CCTTCAGAA TTT  
 || ||||| |||  
 CA GGAAGTCTT AAA  
 \_ A  
 GAM1566 SMARCF1 3' AAAATTCTGAAGGAC 37430 G C  
 GT CCTTCAGAA TTT  
 || ||||| |||  
 CA GGAAGTCTT AAA  
 \_ A  
 GAM1566 SMARCF1 3' AAAATTCTGAAGGAC 20034 G C  
 GT CCTTCAGAA TTT  
 || ||||| |||

CA GGAAGTCTT AAA  
 — A  
 GAM1566 TED 3' AAGAGAAAGTCCAGGGACTGG 31630 G TCA A  
 CCAGT CCT GA CTTTCTCTT  
 ||||| ||| || |||||  
 GGTCA GGA CT GAAAGAGAA  
 G C\_\_ \_  
 GAM1566 TGIF2 3' AGAAGGGTGCTGAAGGC 41447 AA\_  
 GCCTTCAG CTTTCT  
 ||||| |||||  
 CGGAAGTC GGAAGA  
 GTG  
 GAM1566 WBSCR20A 3' AAGAGAAAGAAGAGACAGCA 35958 CT AGAA  
 TGC TC CTTTCTCTT  
 ||| || |||||  
 ACG AG GAAAGAGAA  
 AC AGAA  
 GAM1566 LOC115273 3' AGAAAGTTCTGATGGCCAGG 73356 AGT T  
 CC GCC TCAGAACTTTCT  
 || ||| |||||  
 GG CGG AGTCTTGAAAGA  
 AC\_ T  
 GAM1566 LOC145761 5' AAGAGAAAGTGGAAGGCATGG 83472 G AGA  
 CCA TGCCTTC ACTTTCTCTT  
 ||| ||||| |||||  
 GGT ACGGAAG TGAAAGAGAA  
 \_ G\_\_  
 GAM1566 LOC146179 5' AGAAAGTTTTGGGCCT 77700 T TT  
 AG GCC CAGAACTTTCT  
 || ||| |||||  
 TC CGG GTTTTGAAAGA  
 — —  
 GAM1566 LOC147072 3' AAGAGAAAGTGAGAAGAACTG 60407 GC AGA  
 CAGT CTTC ACTTTCTCTT  
 |||| ||| |||||  
 GTCA GAAG TGAAAGAGAA  
 AA AG\_  
 GAM1566 LOC148758 5' AGAAAGTTCTGAGAAAC 78962 GCC  
 GT TTCAGAACTTTCT  
 || |||||  
 CA GAGTCTTGAAAGA  
 AA\_  
 GAM1566 LOC148932 3' AGGAATCTGAAGGCACTGG 79103 AC  
 CCAGTGCCTTCAGA TTTCT  
 ||||| |||||  
 GGTCACGGAAGTCT AAGGA  
 —  
 GAM1566 LOC149386 5' AAGTTTTGAAAGCACT 84400 C  
 AGTGC TTCAGAACTT  
 ||||| |||||

TCACG AAGTTTTGAA  
 A  
 GAM1566 LOC150139 3' AGAAAATAGAAAAAGGCGCTGG 79583 CAGAAC\_  
 CCAGTGCCTT TTTCT  
 ||||| ||||  
 GGTCGCGGAA AAAGA  
 AAAGATA  
 GAM1566 LOC152756 3' AAGATGCAGTTCTGAAAACCTG 85871 TGCC TTC  
 CAG TTCAGAACT TCTT  
 || ||||| ||||  
 GTC AAGTCTTGA AGAA  
 CAA\_ CGT  
 GAM1566 LOC162333 5' AAGAGAAAGCGATGACACTG 87114 CCT GAA  
 CAGTG TCA CTTTCTCTT  
 |||| || |||||  
 GTCAC AGT GAAAGAGAA  
 \_ AGC  
 GAM1566 LOC199221 3' AAGAGAAGCTCGAAAGCATGG 80347 G C A A T  
 CCA TGC TTC GA CTT CTCTT  
 || || || || || ||||  
 GGT ACG AAG CT GAA GAGAA  
 \_ A \_ C \_  
 GAM1566 LOC203339 3' AGAGAAAATTGGGCCTG 90542 T TCAGAAC  
 CAG GCCT TTTCTCT  
 || || || ||||  
 GTC CGGG AAAGAGA  
 \_ TTA\_  
 GAM1566 LOC255017 3' AGAAAGAGGAACTGG 94624 G TCAGAA  
 CCAGT CCT CTTTCT  
 |||| || ||||  
 GGTCA GGA GAAAGA  
 A \_  
 GAM1566 LOC256021 3' AAGAGAAACAAAGACAACACTG 96512 CCT AGAAC  
 G CCAGTG TC TTTCTCTT  
 |||| || |||||  
 GGTCAC AG AAAGAGAA  
 AAC AAAC\_  
 GAM1566 LOC90139 3' AGAATCCCGAAGGCAT 55396 A\_ ACT  
 GTGCCTTC GA TTCT  
 ||||| || ||||  
 TACGGAAG CT AAGA  
 CC \_  
 GAM1567 AQP3 3' TTCACGATCCACCCTTTC 59593 T\_ \_  
 GAAA GTGG TCGTGAA  
 || || || |||||  
 CTTT CACC AGCACTT  
 CC T  
 GAM1567 ARSB 3' TCACGACTCTTGTC 3502 AATGTG  
 GACAAGA GTCGTGA  
 ||||| |||||

CTGTTCT CAGCACT

GAM1567 B4GALT5 3' TTTTCACAAAAATAGTCCTTTG 16519 AAA\_ GGTC  
TCA TGACAAG TGT GTGAAAA

||||| ||| |||||  
ACTGTTT ATA CACTTTT  
CCTG AAAA

GAM1567 CHRNA3 3' TCGTTACCCATTTCTT 5610 T CG  
AAGAAATG GGT TGA

||||| ||| |||  
TTCTTTAC CCA GCT  
\_ TT

GAM1567 DRD1 3' TTACAACCACATTTCTGGCCA 5840 ACA C  
TG AGAAATGTGGT GTGA

|| ||||| |||  
AC TCTTTACACCA CATT  
CGG A

GAM1567 FUT1 3' TCTGATCACATCCCCTGTC 3798 AGAA T  
GACA ATGTGGTCG GA

||| ||||| ||  
CTGT TACACTAGT CT  
CCCC \_

GAM1567 IRF1 3' GCCACATTTCTGATCA 64345 CA  
TGA AGAAATGTGGT

||| |||||  
ACT TCTTTACACCG  
AG

GAM1567 MAP3K8 5' TCACGACCACCTCATG 17791 A AAT  
CA GA GTGGTCGTGA

|| || |||||  
GT CT CACCAGCACT  
A C\_

GAM1567 NGFR 3' TTCTGACCACACTTCCTGTC 10231 A A T  
GACA GAA TGTGGTCG GAA

||| ||| ||||| |||  
CTGT CTT ACACCAGT CTT  
C C \_

GAM1567 OLR1 3' TTCACAACAGTTCTTGTTA 10341 ATGTG C  
TGACAAGAA GT GTGAA

||||| || |||  
ATTGTTCTT CA CACTT  
GA\_ A

GAM1567 POU4F1 3' CACTGAAAACATTTTGTCA 20660 A GG \_  
TGACAAGAA TGT TC GTG

||||| ||| || |||  
ACTGTTTTT ACA AG CAC  
\_ AA T

GAM1567 SMP1 3' TTTACATGAATAATTTTGTGTC 26705 A GGTC  
A TGACAAGAA TGT GTGAAA

||||| ||| |||||

ACTGTTTTT ATA CACTTT  
 A AGTA  
 GAM1567 ZNF264 3' TTCTATTAACATTTCTTTTCA 12769 C GGTCGT  
 TGA AAGAAATGT GAA  
 ||| ||||| |||  
 ACT TTCTTTACA CTT  
 T ATTAT\_  
 GAM1567 C20orf175 3' CGAGCTCCACGTTTCCTGCCA 55063 A A \_\_\_\_  
 TG CA GAAATGTGG TCG  
 || || ||||| |||  
 AC GT CTTTGCACC AGC  
 C C TCG  
 GAM1567 CAPNS2 3' TTTCACAACCCTACATATTTCT 50323 CA \_\_\_\_ C  
 GATCA TGA AGAAATGT GGT GTGAAA  
 ||| ||||| ||| |||||  
 ACT TCTTTATA CCA CACTTT  
 AG CATC A  
 GAM1567 CLDN6 3' TTTACTCACAATTTTATCA 41041 CA \_ C  
 TGA AGAAATGTG GT GTGAA  
 ||| ||||| || |||||  
 ACT TTTTACAC CA CATTT  
 A\_ T\_  
 GAM1567 DKFZP564L0864 3' GCACCAATTTCTTGCCA 72555 A G C  
 TG CAAGAAAT TGGT GT  
 || ||||| |||| ||  
 AC GTTCTTTA ACCA CG  
 C \_ \_  
 GAM1567 DKFZP566B183 3' TTTCCATAAACATTTCTTTTCA 31330 C GGTCGT  
 TGA AAGAAATGT GAAA  
 ||| ||||| |||  
 ACT TTCTTTACA CTTT  
 T AATAC\_  
 GAM1567 GTF2E1 3' TACAGACCTCTTGTCA 18616 AATGT \_  
 TGACAAGA GGTC GTG  
 ||||| |||| |||  
 ACTGTTCT CCAG CAT  
 \_ A  
 GAM1567 KIAA0089 3' TTTTAATTCACATTTCTT 69967 TCG  
 AAGAAATGTGG TGAAA  
 ||||| ||||  
 TTCTTTACACT ATTTT  
 TA\_  
 GAM1567 KIAA0373 5' TTTTCAAAGTAACATTTCTT 28015 GGTCG  
 AAGAAATGT TGAAAA  
 ||||| |||||  
 TTCTTTACA ACTTTT  
 ATGAA  
 GAM1567 KIAA1813 3' TTTTCACACTGTAAATTTCTTG 70314 \_ TG C  
 T ACAAGAAAT G GT GTGAAAA  
 ||||| | || |||||

			TGTTCTTTA T CA CACTTTT		
			AA GT _		
GAM1567	KIAA1951	3'	TTCCAGGCTTCTCTTGTC	73766	AATGT GT
			TGACAAGA GGTC GAA		
			ACTGTTCT TCGG CTT		
			CT__ AC		
GAM1567	MGC4170	3'	TTCACCATTTCTTGTC	44227	TGGTC
			GACAAGAAATG GTGAA		
			CTGTTCTTTAC CACTT		
			_____		
GAM1567	NRN1	3'	CACTGCACATTTCTCCTCA	33432	CA GTC
			TGA AGAAATGTG GTG		
			ACT TCTTTACAC CAC		
			CC GT_		
GAM1567	PLA2G12	3'	TTTTCACAACCACATTT	48028	C
			AAATGTGGT GTGAAAA		
			TTTACACCA CACTTTT		
			A		
GAM1567	PPY2	3'	CACTCCACATTCCTGGCCA	40819	ACA A TC
			TG AG AATGTGG GTG		
			AC TC TTACACC CAC		
			CGG C T_		
GAM1567	ZNF31	3'	TTTGTAGACCACATTTCTGTT	64992	A _TG
	A		TGACA GAAATGTGGTC G AA		
			ATTGT CTTTACACCAG T TT		
			C A GT		
GAM1567	LOC115219	3'	CACGACAACGGGTCCTCA	73295	CAA AA G
			TGA GA TGT GTCGTG		
			ACT CT GCA CAGCAC		
			C__ GG A		
GAM1567	LOC120376	5'	TTCAGAGCATTTCTTTCA	75986	C GG G
			TGA AAGAAATGT TC TGAA		
			ACT TTCTTTACG AG ACTT		
			— — —		
GAM1567	LOC133418	3'	TTTCATATACATTTTTTGCCA	75094	A GTC
			TG CAAGAAATGTG GTGAAA		
			AC GTTTTTTACAT TACTTT		
			C A__		
GAM1567	LOC151199	3'	TTAAAACCACAGCTCTTGCCA	80174	A AA CG
			TG CAAGA TGTGGT TGA		

AC GTTCT ACACCA ATT  
 C CG AA  
 GAM1567 LOC152317 5' TCACACTGACTTTTGTCA 85649 AATG C  
 TGACAAGA TGGT GTGA  
 ||||| ||| |||  
 ACTGTTTT GTCA CACT  
 CA\_\_ \_  
 GAM1567 LOC152674 3' TTCAACCCACCCTCTTGTCA 85841 AAT TCG  
 TGACAAGA GTGG TGAA  
 ||||| ||| |||  
 ACTGTTCT CACC ACTT  
 CC\_ CA\_  
 GAM1567 LOC152845 5' CATGACCACATTTTTCA 60330 CAA  
 TGA GAAATGTGGTCGTG  
 || |||||  
 ACT TTTTACACCAGTAC  
 \_  
 GAM1567 LOC154743 3' TTTAGTCCACATTGTCTTGTCA 81118 \_ TCG  
 TGACAAGA AATGTGG TGAA  
 ||||| ||||| |||  
 ACTGTTCT TTACACC ATTT  
 G TG\_  
 GAM1567 LOC165476 5' TTCACGGCACCTTCT 87201 AT G  
 AGAA GTG TCGTGAA  
 ||| ||| |||||  
 TCTT CAC GGCATT  
 C\_ \_  
 GAM1567 LOC254266 5' TTTTCGGTCACACATCTTATCA 97356 C AA GT T  
 TGA AAGA TGTG CG GAA  
 ||| ||| ||| |||  
 ACT TTCT ACAC GC TTT  
 A AC TG T  
 GAM1567 LOC255919 3' TTTCATTCTTACATTTCTAATC 95043 CA TC  
 A TGA AGAAATGTGG GTGAAA  
 ||| ||||| |||||  
 ACT TCTTTACATT TACTTT  
 AA CT  
 GAM1567 LOC51754 5' CACGGCCACATCTCTGTCA 71027 A A  
 TGACA GA ATGTGGTCGTG  
 ||||| || |||||  
 ACTGT CT TACACCGGCAC  
 \_ C  
 GAM1567 LOC55862 3' ACCTCATTCTTGCCA 37485 A T  
 TG CAAGAAATG GGT  
 || ||||| |||  
 AC GTTCTTTAC CCA  
 C T  
 GAM1567 LOC55954 3' CACGTGGTCACTTTTCTCATCA 38877 CA T GT \_  
 TGA AGAAA GTG C GTG  
 ||| ||||| ||| | |||

ACT TCTTT CAC G CAC  
 AC T TG TG  
 GAM1568 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
 GTA GGAT GGGTTGTTT  
 ||| ||| |||||  
 CGT CCTA CCCAACAAA  
 C CGTG\_  
 GAM1568 LCT 3' AACCGTAAAAATCCTT 9697 G  
 AAGGATTTTTTA GGTT  
 ||||| |||  
 TTCCTAAAAAT CCAA  
 G  
 GAM1568 RPL15 3' AAACAACCCCTAAAAATCCTTAC 11382  
 GTAAGGATTTTTTAGGGTTGTTT  
 |||||  
 CATTCTAAAAATCCCAACAAA  
  
 GAM1568 FBXO30 3' AACTAAAAAATCCTGAC 49573 A AG  
 GT AGGATTTTTT GGTT  
 || ||||| |||  
 CA TCCTAAAAA TCAA  
 G AA  
 GAM1568 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTTT  
 GTAAG AGGGTTGTT  
 ||| |||||  
 CATTCT TCCCAACAA  
 AT\_\_\_\_  
 GAM1568 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
 TAAG TTTT GGGTTGTTT  
 ||| ||| |||||  
 GTTC AAAA CCCAACAAA  
 \_\_\_\_ C  
 GAM1568 SMT3H2 3' AACCAACATAAAAAATCCTTGC 22670 GG  
 GTAAGGATTTTTTA GTTGTT  
 ||||| |||  
 CGTTCCTAAAAAT CAACAA  
 A\_  
 GAM1568 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
 GTAAGGATTTTTT GGGTT  
 ||||| |||  
 CGTTCCTAAAAA TCCAA  
 GTA  
 GAM1568 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
 GGAT TT GGGTTGTTT  
 ||| || |||||  
 CCTG AA CCCAACAAA  
 T\_ C  
 GAM1568 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
 C GTA GGATTTTT TTGTTT  
 || ||||| |||



		CGT CCTAAAAA AACAAA		
		C GATAA		
GAM1568	LOC148089 3'	GGCCCTAAAAATTCCTAC	78637	A
		GTA GGATTTTTAGGGTT		
		CAT CTTAAAAATCCCGG		
		C		
GAM1568	LOC154547 3'	AACAACATAAAAAATCCTTGC	76050	GG
		GTAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1568	LOC158104 3'	ACAGCCAAAAATCCTTA	60313	AG
		TAAGGATTTTT GTTGT		
		ATTCCTAAAAA CCGACA		
		—		
GAM1568	LOC205880 5'	AAACAACCATCATCCTGAC	90709	A TTTAG
		GT AGGAT GGTGTTT		
		CA TCCTA CCAACAAA		
		G CTA_		
GAM1568	LOC221561 3'	AACAACATAAAAAATCCTTGC	92130	GG
		GTAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1568	LOC257591 3'	AACAACATAAAAAATCCTTGC	97840	GG
		GTAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1568	LOC51145 3'	AGCTAAAATCCTTAC	32393	TAG
		GTAAGGATTTT GTT		
		CATTCCTAAAA TCGA		
		—		
GAM1569	ARNT2 3'	AAACAACCCGTGCATCCCTGC	29450	A TTTTA
		GTA GGAT GGGTTGTTT		
		CGT CCTA CCAACAAA		
		C CGTG_		
GAM1569	LCT 3'	AACCGTAAAAATCCTT	9697	G
		AAGGATTTTTTA GTT		
		TTCTAAAAAT CCAA		
		G		
GAM1569	RPL15 3'	AAACAACCCTAAAAATCCTTAC	11382	
		GTAAGGATTTTTAGGGTTGTTT		

CATTCCTAAAAATCCCAACAAA

GAM1569 FBXO30 3' AACTAAAAAATCCTGAC 49573 A AG  
GT AGGATTTTT GTT  
|| ||||| |||  
CA TCCTAAAAA TCAA  
G AA

GAM1569 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTT  
GTAAG AGGGTTGTT  
|||| |||||  
CATTC TCCCAACAA  
AT\_\_\_\_

GAM1569 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
TAAG TTTT GGGTTGTT  
||| ||| |||||  
GTTC AAAA CCAACAAA  
\_\_\_ C

GAM1569 SMT3H2 3' AACACATAAAAAATCCTTGC 22670 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1569 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
GTAAGGATTTTT GGGTT  
||||||| |||||  
CGTTCCTAAAAA TCCAA  
GTA

GAM1569 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
GGAT TT GGGTTGTT  
||| || |||||  
CCTG AA CCAACAAA  
T\_ C

GAM1569 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
C GTA GGATTTTT TTGTTT  
|| ||||| |||||  
CGT CCTAAAAA AACAAA  
C GATAA

GAM1569 LOC148089 3' GGCCCTAAAAATTCCTAC 78637 A  
GTA GGATTTTTAGGGTT  
|| |||||  
CAT CTAAAAATCCCGG  
C

GAM1569 LOC154547 3' AACACATAAAAAATCCTTGC 76050 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1569 LOC158104 3' ACAGCCAAAAATCCTTA 60313 AG  
TAAGGATTTTT GGTGT  
||||||| |||||

ATTCCTAAAAA CCGACA

GAM1569 LOC205880 5' AAACAACCATCATCCTGAC 90709 A TTTTAG  
GT AGGAT GGTGTGTT  
|| |||| |||||  
CA TCCTA CCAACAAA  
G CTA\_\_

GAM1569 LOC221561 3' AACAAACATAAAAAATCCTTGC 92130 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA

A\_  
GAM1569 LOC257591 3' AACAAACATAAAAAATCCTTGC 97840 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA

A\_  
GAM1569 LOC51145 3' AGCTAAAATCCTTAC 32393 TAG  
GTAAGGATTTT GTT  
||||||| |||  
CATTCCTAAAA TCGA

GAM1570 ADCY7 3' AGGCATGCAGATGGCTGTG 6636 AC GC  
CACAGCCA TTTGTG GCCT  
|||||| |||| |||  
GTGTCGGT AGACGT CGGA

\_\_ A\_  
GAM1570 APXL 3' GGTGAAGCTGGCTGTG 7930 ACTTT GG  
CACAGCCA GT CGCC  
|||||| || |||  
GTGTCGGT CG GTGG

\_\_ AA  
GAM1570 INPPL1 3' GGCACCACGAAGCTGTG 7803 CAAC C  
CACAGC TTTGTGG GCC  
|||| ||||| |||  
GTGTCTG AAGCACC CGG

\_\_ A  
GAM1570 LGR6 5' AGGCGCCAACACCTTGACTG 84199 C CTTTG  
CAG CAA TGGCGCCT  
||| ||| |||||  
GTC GTT ACCGCGGA  
A CCACA

GAM1570 SH3GL3 5' GTTCCACAAAGCCAGCCAGTA 11636 ACA CAA C  
TAC GC CTTTGTGG GC  
||| || ||||| ||  
ATG CG GAAACACC TG  
AC\_ ACC T

GAM1570 SIAT8E 5' AGGCGCCAAGTCGGC 59857 A TTG  
GCC ACT TGGCGCCT  
||| ||| |||||

			CGG TGA ACCGCGGA		
			C ____		
GAM1570 SRM	3'	GCCTATACCAGCTGTGTA	11956	CAACTT	C
		TACACAGC TGTGG GC			
		ATGTGTCG ATATC CG			
		ACC ____ _			
GAM1570 WISP2	5'	AGGCTCAAAGCTGGCTCTG	13932	C A	TGGC
		CA AGCCA CTTTG GCCT			
		GT TCGGT GAAAC CGGA			
		C C T ____			
GAM1570 ACAS2	3'	CAGGGAGGCAGCTGTGTA	37932	CAA	G
		TACACAGC CTTT TG			
		ATGTGTCG GAGG AC			
		ACG G			
GAM1570 ACAS2	3'	CAGGGAGGCAGCTGTGTA	57702	CAA	G
		TACACAGC CTTT TG			
		ATGTGTCG GAGG AC			
		ACG G			
GAM1570 BRD1	3'	ATAAAGTTATGCTGTGTA	27414	C_	
		TACACAGC AACTTTGT			
		ATGTGTCG TTGAAATA			
		TA			
GAM1570 CARD9	3'	AGGCGCAGCTACTGGCCGTG	42283	A	ACTTT G
		CAC GCCA GT GCGCCT			
		GTG CGGT CG CGCGGA			
		C CAT ____ A			
GAM1570 CASKIN1	3'	AGGCGCTGCCGTGCGCTGTCA	40397	C	A TTT TG
		A ACAGCC AC G GCGCCT			
		A TGTCGG TG C CGCGGA			
		C C C ____ GT			
GAM1570 CNOT7	3'	CAGGAAAATTGGTTGTG	53983	C_	G
		CACAGCCAA TTT TG			
		GTGTTGGTT AAG AC			
		AA G			
GAM1570 EHM2	3'	ACAAGTTGGCTGTTA	38910	C	T
		A ACAGCCAACTT GT			
		A TGTCGGTTGAA CA			
		T ____			
GAM1570 FLJ10508	3'	ACTGAGAAATGGCTGTGTA	36198	A ____	T
		TACACAGCCA CTT GT			

			ATGTGTCGGT	GAG CA		
			AAA T			
GAM1570	FLJ14721	3'	GGCACACAGGGGCT	51585	AAC	C
			AGCC TTTGTGG GCC			
			TCGG GGACACC CGG			
			_____ A			
GAM1570	FLJ22004	3'	TGCTATGTAGCTGTGTA	47214	CA	TTT
			TACACAGC AC GTGGCG			
			ATGTGTCG TG TATCGT			
			A_ _____			
GAM1570	HCBP6	3'	GTTGGAAAGTTGGCTG	80902	G	
			CAGCCAACCTT TGGC			
			GTCGGTTGAAA GTTG			
			G			
GAM1570	KIAA0527	3'	ACAAAGTTAGCTTTGTA	95787	C	C
			TACA AGC AACTTTGT			
			ATGT TCG TTGAAACA			
			T A			
GAM1570	KIAA0648	3'	TCAAGAGTTGGCTGTGTA	82657	G	
			TACACAGCCAACCTT TGG			
			ATGTGTCGGTTGAGA ACT			
			_____			
GAM1570	KIAA1157	3'	AGGCTTTGTGAAGTCAGCTGTG	72238	CA	TG C
			CACAGC ACTTTG G GCCT			
			GTGTCG TGAAGT T CGGA			
			AC GT T			
GAM1570	KIAA1979	3'	CGCATTGGTTGGCTGTGT	88276	T_	
			ACACAGCCAAC TGTG			
			TGTGTCGGTTGG ACGC			
			TT			
GAM1570	KIAA1987	3'	GGAGCCAGGCTGTGTA	88019	AACTTTG	G
			TACACAGCC TGGC CC			
			ATGTGTCGG ACCG GG			
			_____ A			
GAM1570	MAPK8IP3	3'	GCCAGTATAAGTCAGCTGTG	52985	CA	TG_
			CACAGC ACTT TGGC			
			GTGTCG TGAA ACCG			
			AC TATG			
GAM1570	MCM10	3'	GCAAAGGATTGGCTGTGTA	37573	_____	
			TACACAGCCAA CTTTGT			

ATGTGTCGGTT GAAACG  
 AG  
 GAM1570 PSR 3' CCACAGAGCCAGCTGTGTA 65179 CAA  
 TACACAGC CTTTGTGG  
 ||||| |||||  
 ATGTGTCG GAGACACC  
 ACC  
 GAM1570 TRIM28 5' GGCAGCAGTTGGCCGTG 19267 A TTGTG \_  
 CAC GCCAACT GC GCC  
 || ||||| || |||  
 GTG CGGTTGA CG CGG  
 C \_ \_ A  
 GAM1570 ZNF263 5' AGGCGCCGAGCCGGC 19222 AA TG  
 GCC CTT TGGCGCCT  
 || || |||||  
 CGG GAG GCCGCGGA  
 CC \_  
 GAM1570 LOC118672 5' AGGCGCCAATCCTACTGGCTG 73922 ACTTTG\_  
 CAGCCA TGGCGCCT  
 ||||| |||||  
 GTCGGT ACCGCGGA  
 CATCCTA  
 GAM1570 LOC149997 5' GCCATAAACTGGCTG 76341 AC  
 CAGCCA TTTGTGGC  
 ||||| |||||  
 GTCGGT AAATACCG  
 CA  
 GAM1570 LOC151126 3' CATTTTtagTTGCTGTGTA 80125 C TT\_  
 TACACAGC AACT GTG  
 ||||| ||| |||  
 ATGTGTCG TTGA TAC  
 \_ TTTT  
 GAM1570 LOC158852 5' AGGCGCCACAACCTCACTG 82032 CCAACT  
 CAG TTGTGGCGCCT  
 || |||||  
 GTC AACACCGCGGA  
 ACTTC\_  
 GAM1570 LOC170221 3' AGGCGCCGCTCCCTGGCT 82576 ACTTT  
 AGCCA GTGGCGCCT  
 ||||| |||||  
 TCGGT CGCCGCGGA  
 CCCT\_  
 GAM1570 LOC201292 5' GCAGTTGCTAAGCCGGCTGTGT 88188 AA T TG \_  
 G TACACAGCC CTT G GC GC  
 ||||| ||| || ||  
 GTGTGTCGG GAA C TG CG  
 CC T GT A  
 GAM1570 LOC221154 5' GCGCCGCCTAGCTGCGCT 93546 \_ A TT  
 AGC CA CT GTGGCGC  
 || || || |||||

		TCG GT GA CGCCGCG		
		C C TC		
GAM1570	LOC221296 3'	AGGCAAAGAAAGTTGGCCTGT	91955	GTGGC
		ACAG CCAACTTT GCCT		
		TGTC GGTGAAG CGGA		
		C AAA_		
GAM1570	LOC221576 3'	GGGCATGCAAAGCCGGCTGTGT	93705	AA GC
	G	TACACAGCC CTTTGTG GCCT		
		GTGTGTCGG GAAACGT CGGG		
		CC A_		
GAM1570	LOC257122 5'	AGGCGCCACAACCTCACTG	96212	CCAAC
		CAG TTGTGGCGCCT		
		GTC AACACCGCGGA		
		ACTTC_		
GAM1570	LOC257515 3'	GGGCATGCAAAGCCGGCTGTGT	97785	AA GC
	G	TACACAGCC CTTTGTG GCCT		
		GTGTGTCGG GAAACGT CGGG		
		CC A_		
GAM1570	LOC257572 3'	GGGCATGCAAAGCCGGCTGTGT	97914	AA GC
	G	TACACAGCC CTTTGTG GCCT		
		GTGTGTCGG GAAACGT CGGG		
		CC A_		
GAM1571	CTSB 3'	CCTCCGTGATCCATCCAT	64726	T ACA
		GTG ATG GATCACGGAGG		
		TAC TAC CTAGTGCCTCC		
		C _		
GAM1571	EPHA3 3'	CCTTTTCCTGTTCATACACT	17869	_ ATCAC
		AGTGTATGA CAG GGAGG		
		TCACATACT GTC TTTCC		
		T CT_		
GAM1571	C20orf20 3'	CTCCGTGCCACGCACTGA	36854	TA ACAGAT
		TCAGTG TG CACGGAG		
		AGTCAC AC GTGCCTC		
		GC C_		
GAM1571	DKFZP586I2223 3'	CCTCCGTGTCTGTCATACACTG	31267	T
	A	TCAGTGTATGACAGA CACGGAGG		
		AGTCACATACTGTCT GTGCCTCC		
		-		
GAM1571	DKFZP586I2223 3'	CCTCCGTGTCTGTCATACACTG	54909	T
	A	TCAGTGTATGACAGA CACGGAGG		

AGTCACATACTGTCT GTGCCTCC

GAM1571 DKFZP586I2223 3' CCTCCGTGTCTGTCATACTG 54918 T  
A TCAGTGTATGACAGA CACGGAGG  
||||||| |||||  
AGTCACATACTGTCT GTGCCTCC

GAM1571 KNSL5 3' CCTCAGCTACATCATACTGA 56730 CAGATCACG  
TCAGTGTATGA GAGG  
||||||| |||  
AGTCACATACT CTCC  
ACATCGA\_\_

GAM1571 KNSL5 3' CCTCAGCTACATCATACTGA 16774 CAGATCACG  
TCAGTGTATGA GAGG  
||||||| |||  
AGTCACATACT CTCC  
ACATCGA\_\_

GAM1571 KRTAP2-4 3' CCCCACAGAGCAATACACTGA 52590 GACAGA AC\_ A  
TCAGTGTAT TC GG GG  
||||||| || |||  
AGTCACATA AG CC CC  
ACG\_\_ ACA \_

GAM1571 NINJ2 3' CCTCCGTGATCTGCCAGGC 59711 A A  
GT TG CAGATCACGGAGG  
|| || |||||  
CG AC GTCTAGTGCCTCC  
G C

GAM1571 NINJ2 3' CCTCCGTGATCTGCCAGGC 33281 A A  
GT TG CAGATCACGGAGG  
|| || |||||  
CG AC GTCTAGTGCCTCC  
G C

GAM1572 ADH1B 3' CTTAGACATAAAGTAAAAT 72644 C CAC  
ATTT ACTTT TGTCTGAG  
|||| |||||  
TAAA TGAAA ACAGATTC  
A T\_\_

GAM1572 AHR 3' ATCTCAGATGTTAAATAAATG 7875 CAC C T  
CATTT TTT AC GTCTGAGAT  
|||| ||| || |||||  
GTAAA AAA TG TAGACTCTA  
TA\_ T \_

GAM1572 FDFT1 3' TAGGAAAGTGAAATG 15518 A  
CATTTCACTTTC CTG  
||||||| |||  
GTAAAGTGAAAG GAT

GAM1572 JTB 3' ATCTCAGACAGTGAAAGTGAAA 21959  
TG CATTTCACTTTCAGTGTCTGAGAT  
|||||||



GTAAAGTGAAAGTGACAGACTCTA

GAM1572	KLF4	3'	TCCCAGACAGTGGATATG	14891	CT	A
			CA TTCACTGTCTG GA			
			GT AGGTGACAGAC CT			
			AT C			
GAM1572	PHYH	3'	ACAGTAAAAGTGAAAT	20608		C
			ATTTCACTTT ACTGT			
			TAAAGTGAAA TGACA			
			A			
GAM1572	PKD2	3'	TCCAGGTTGAAAGTGAAA	60096	CTG	A
			TTTCACTTTCA TCTG GA			
			AAAGTGAAAGT GGAC CT			
			T_ _			
GAM1572	WRN	3'	GGGCAGTGAAAATGAAA	5098		C
			TTTCA TTTCACTGTCT			
			AAAGT AAAGTGACGGG			
			A			
GAM1572	ZNF216	3'	ATCTGCACAGCAAAGTGAAA	20017	CA	CTG
			TTTCACTTT CTGT AGAT			
			AAAGTGAAA GACA TCTA			
			C_ CG_			
GAM1572	CG012	5'	CTCACTCTGAAAGTGAA	83218	CT	CT
			TTCAC TTTCA GT GAG			
			AAGTGAAAGT CA CTC			
			CT _			
GAM1572	EIF2C2	3'	ATCTTCTGAGAGTGAAAG	71946	G	T_
			CTTTCACT TC GAGAT			
			GAAAGTGA AG TTCTA			
			G TC			
GAM1572	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT	45802	ACTTTCACT	
	G		CATTTT GTCTGAGAT			
			GTAAAG CAGACTCTA			
			AAACATTT_			
GAM1572	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG	45281	CTT	
			CATTTCA TCACTGTCTGAGAT			
			GTAAAGT AGTGACAGACTCTA			
			C_			
GAM1572	KIAA0984	3'	TTTGTCCAGTGAAAATGAA	65534	C	TC
			TTCA TTTCACTG TGAG			

			AAGT AAAGTGAC GTTT		
			A CT		
GAM1572	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A _	
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1572	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T	
			ATT CACTTTCACTGT		
			TAA GTGAAAGTGACG		
			C		
GAM1572	PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA 53598	CA G	
			TTCAC TTT CT TCTGAGAT		
			AAGTGAAA GG AGACTCTA		
			CC G		
GAM1572	PP35	3'	ATCTCAGACTGAAA 22814	CT	
			TTTCA GTCTGAGAT		
			AAAGT CAGACTCTA		
			—		
GAM1572	PRTD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148	TCAC C_	
			CATTTCACTT TGT TGAG		
			GTAAAGTGAA ACG ACTC		
			TA__ TT		
GAM1572	SEP15	3'	TCCTACAGTAAGAGTGAAA 14934	C CT	
			TTTCACTTT ACTGT GA		
			AAAGTGAGA TGACA CT		
			A TC		
GAM1572	SFXN2	3'	CTCAGGGGAAAAAAGTGAAA 73941	CACTG	
			TTTCACTTT TCTGAG		
			AAAGTGAAA GGA CTC		
			AAAGG		
GAM1572	LOC149703	3'	ATCTCAGACAGCCGTTTGAAA 84647	ACTTTCA	
			TTTC CTGTCTGAGAT		
			AAAG GACAGACTCTA		
			GTTTGCC		
GAM1572	LOC154007	3'	ATCTCAAACCCTTTAGTGAAA 81015	TTCAC T C	
			TTTCACT GT TGAGAT		
			AAAGTGA CA ACTCTA		
			TTTCC_ A		
GAM1572	LOC155004	3'	TCATTTAAGTGAAAAGGAAA 81226	A GTC_	
			TTTC CTTTCACT TGA		

			AAAG GAAAGTGA	ACT	
			—	ATTT	
GAM1572	LOC222134	5'	ACAGTGAAGTGAAATG	94136	T
			CATTTCACTT	CACTGT	
			GTAAAGTGAA	GTGACA	
			—		
GAM1573	CNGA1	3'	CAACTGATAATGTGCAAA	59507	GC A
			TTTGCACATTA	TAG TTG	
			AAACGTGTAAT	GTC AAC	
			A_	—	
GAM1573	ESRRG	3'	TGGCAGTCTTATGTGCAAA	66396	TAGCT
			TTTGCACAT	AGATTGCCA	
			AAACGTGTA	TCTGACGGT	
			T_		
GAM1573	KCNJ3	3'	GCAATAATGTGCAAA	9525	GCTAGA
			TTTGCACATTA	TTGC	
			AAACGTGTAAT	AACG	
			—		
GAM1573	SDC2	3'	GCAAATTAATGTGTAAA	67132	CTAGA
			TTTGCACATTAG	TTGC	
			AAATGTGTAATT	AACG	
			A_		
GAM1573	USP9X	3'	ATGGCCTGATGCTAATGTGTAA	16206	TAGATT
	A		TTTGCACATTAGC	GCCAT	
			AAATGTGTAATCG	CGGTA	
			TAGTC_		
GAM1573	AMOTL1	3'	GGCAAGTAATGTGCAAA	73650	G AGAT
			TTTGCACATTA CT	TGCC	
			AAACGTGTAAT GA	ACGG	
			—		
GAM1573	BCAR3	3'	AGTAATAATGTGCAAA	13098	—
			TTTGCACATTA	GCT	
			AAACGTGTAAT	TGA	
			AA		
GAM1573	DKFZP434B044	3'	TGACAATTAAATGTGCAGA	48930	AGCTA C
			TTTGCACATT	GATTG CA	
			AGACGTGTAA	TTAAC GT	
			A_	A	
GAM1573	MGC3184	3'	ATGACATTTTCTAATGTGCAGA	48235	CT T C
			TTTGCACATTAG	AGA TG CAT	

AGACGTGTAATC TTT AC GTA  
 \_ T A  
 GAM1573 PTD012 3' ATGGCAATCTAGCTAATGTGCA 25891  
 AA TTTGCACATTAGCTAGATTGCCAT  
 |||||  
 AAACGTGTAATCGATCTAACGGTA

GAM1574 PSG1 3' ACCTATTTTGCAAACAACT 22602 C A\_  
 AGT TG GTAAGATAGGT  
 ||| || |||||  
 TCA AC CGTTTTATCCA  
 A AAA

GAM1574 DKFZP564D0462 3' ACCTAACTCTCAGACT 70495 TA A  
 AGTCTGAG AG TAGGT  
 ||||| || |||||  
 TCAGACTC TC ATCCA  
 \_ A

GAM1574 FLJ10852 3' ACCCAAACCTCTCAATCTGATT 38733 TC TAAGATA  
 TG CAAATCAG TGAG GGT  
 ||||| ||| |||  
 GTTTAGTC ACTC CCA  
 TA TCAAAAC

GAM1574 FLJ12221 3' CTTACCCAGACTGGCTTG 62550 AT A  
 CAA CAGTCTG GTAAG  
 ||| ||||| |||||  
 GTT GTCAGAC CATTG  
 CG C

GAM1574 KIAA0179 3' ACCTGCGAACATCAGACTGACT 64823 A GTAAGA  
 TG CAA TCAGTCTGA TAGGT  
 ||| ||||| |||||  
 GTT AGTCAGACT GTCCA  
 C ACAAGC

GAM1574 KIAA0316 3' ACCTGCGAGACCCAGATGACTT 69668 A G A AAGA  
 G CAA TCA TCTG GT TAGGT  
 ||| ||| ||||| ||| |||||  
 GTT AGT AGAC CA GTCCA  
 C \_ C GAGC

GAM1574 KIAA0551 3' TCTTACTCAAATGATTTG 66840 GTC  
 CAAATCA TGAGTAAGA  
 ||||| |||||  
 GTTTAGT ACTCATTCT  
 AA\_

GAM1574 KIAA0630 5' ACCCAGATTTGCACTCAGACAG 89388 A A\_ A\_  
 AT ATC GTCTGAGT AGAT GGT  
 ||| ||||| ||| |||  
 TAG CAGACTCA TTTA CCA  
 A CG GAC

GAM1574 KIAA1530 3' CCGCACTCAGCTGATTTG 67949 T AAGATA  
 CAAATCAG CTGAGT GG  
 ||||| ||||| ||

			GTTTAGTC GACTCA	CC	
			— CG—		
GAM1574	NIR3	3'	ACCTCCCACTCAGACTGG	66235	AAGAT
			TCAGTCTGAGT	AGGT	
			GGTCAGACTCA	TCCA	
			CCC—		
GAM1574	SLAM	3'	ACCTATCTCACACACTGA	11709	CT A A
			TCAGT G GT AGATAGGT		
			AGTCA C CA TCTATCCA		
			— A C		
GAM1574	SLC37A1	3'	ACCCATGATGTTCCGGA	38559	— AG A
			TCAGTCTG AGTA AT GGT		
			AGTCAGGC TTGT TA CCA		
			C AG C		
GAM1574	LOC126964	3'	ACCTATTTTCCAAATCTGATTT	74611	TCTGAGT
			AAATCAG AAGATAGGT		
			TTTAGTC TTTTATCCA		
			TAAACC—		
GAM1574	LOC150333	5'	ACCTATCAGTAAAAGACTATTT	85018	C GAGTAA
	G		CAAAT AGTCT GATAGGT		
			GTTTA TCAGA CTATCCA		
			— AAATGA		
GAM1574	LOC255654	5'	ACCTATCCACCAGATTGA	96885	A AA
			TCAGTCTG GT GATAGGT		
			AGTTAGAC CA CTATCCA		
			— C—		
GAM1575	PSG1	3'	ACCTATTTTGCAAACAACT	22602	C A—
			AGT TG GTAAGATAGGT		
			TCA AC CGTTTTATCCA		
			A AAA		
GAM1575	DKFZP564D0462	3'	ACCTAACTCTCAGACT	70495	TA A
			AGTCTGAG AG TAGGT		
			TCAGACTC TC ATCCA		
			— A		
GAM1575	FLJ10852	3'	ACCCAAAACCTCTCAATCTGATT	38733	TC TAAGATA
	TG		CAAATCAG TGAG GGT		
			GTTTAGTC ACTC CCA		
			TA TCAAAAC		
GAM1575	FLJ12221	3'	CTTACCCAGACTGGCTTG	62550	AT A
			CAA CAGTCTG GTAAG		

		GTT GTCAGAC CATTG		
		CG C		
GAM1575 KIAA0179	3'	ACCTGCGAACATCAGACTGACT 64823	A	GTAAGA
	TG	CAA TCAGTCTGA TAGGT		
		GTT AGTCAGACT GTCCA		
		C ACAAGC		
GAM1575 KIAA0316	3'	ACCTGCGAGACCCAGATGACTT 69668	A G	A AAGA
	G	CAA TCA TCTG GT TAGGT		
		GTT AGT AGAC CA GTCCA		
		C _ C GAGC		
GAM1575 KIAA0551	3'	TCTTACTCAAATGATTTG 66840	GTC	
		CAAATCA TGAGTAAGA		
		GTTTAGT ACTCATTCT		
		AA_		
GAM1575 KIAA0630	5'	ACCCAGATTTGCACTCAGACAG 89388	A	A_ A__
	AT	ATC GTCTGAGT AGAT GGT		
		TAG CAGACTCA TTTA CCA		
		A CG GAC		
GAM1575 KIAA1530	3'	CCGCACTCAGCTGATTTG 67949	T	AAGATA
		CAAATCAG CTGAGT GG		
		GTTTAGTC GACTCA CC		
		_ CG__		
GAM1575 NIR3	3'	ACCTCCCACTCAGACTGG 66235	AAGAT	
		TCAGTCTGAGT AGGT		
		GGTCAGACTCA TCCA		
		CCC_		
GAM1575 SLAM	3'	ACCTATCTCACACACTGA 11709	CT A A	
		TCAGT G GT AGATAGGT		
		AGTCA C CA TCTATCCA		
		_ A C		
GAM1575 SLC37A1	3'	ACCCATGATGTTCCGGAAGTGA 38559	_ AG A	
		TCAGTCTG AGTA AT GGT		
		AGTCAGGC TTGT TA CCA		
		C AG C		
GAM1575 LOC126964	3'	ACCTATTTTCCAAATCTGATTT 74611	TCTGAGT	
		AAATCAG AAGATAGGT		
		TTTAGTC TTTTATCCA		
		TAAACC_		
GAM1575 LOC150333	5'	ACCTATCAGTAAAAGACTATTT 85018	C	GAGTAA
	G	CAAAT AGTCT GATAGGT		

			GTTTA TCAGA CTATCCA		
			_ AAATGA		
GAM1575	LOC255654	5'	ACCTATCCACCAGATTGA 96885	A AA	
			TCAGTCTG GT GATAGGT		
			AGTTAGAC CA CTATCCA		
			_ C_		
GAM1576	ADAM20	5'	GCACTGCAGCTCTGA 13767	A AT	
			TCA AGCTGCAG TGC		
			AGT TCGACGTC ACG		
			C _		
GAM1576	ANXA9	5'	CACAGGCAATCTACCAGGC 13102	GC_	
			GCT AGATTGCCTGTG		
			CGG TCTAACGGACAC		
			ACCA		
GAM1576	E2F1	3'	CACCTTGTCTCTGCAGCCCTGG 84796	AA TTGCCT	
			TCA GCTGCAGA GTG		
			GGT CGACGTCT CAC		
			CC CTGTTT		
GAM1576	E2F1	3'	CAATCTGCACTTTGA 84795	C	
			TCAAAG TGCAGATTG		
			AGTTTC ACGTCTAAC		
			-		
GAM1576	FPRL1	5'	CACTGCATTTGCAGCCTTGA 7590	A T CT	
			TCAA GCTGCAGAT GC GTG		
			AGTT CGACGTTTA CG CAC		
			C _ T_		
GAM1576	FSHPRH1	5'	CACGGCTCTCTGCAGC 22114	TT T	
			GCTGCAGA GCC GTG		
			CGACGTCT CGG CAC		
			CT _		
GAM1576	IL10RA	3'	CACAGGCATGGAAGCTGTGA 59641	A GCAGAT	
			TCA AGCT TGCCTGTG		
			AGT TCGA ACGGACAC		
			G AGGT_		
GAM1576	ITGA6	3'	CACAGGTGCAACAGACTTGA 3983	AG CAGATT	
			TCAA CTG GCCTGTG		
			AGTT GAC TGGACAC		
			CA AACG_		
GAM1576	ITPKA	3'	CATGTGGACCTGCAGCTTTG 9415	ATTG _	
			CAAAGCTGCAG CC TGTG		

			GTTTCGACGTC	GG GTAC	
			CA__ T		
GAM1576	LILRB4	3'	CAGGACCTGCAGCTTTG	22431	ATTG
			CAAAGCTGCAG	CCTG	
			GTTTCGACGTC	GGAC	
			CA__		
GAM1576	MBD3	3'	CACAGGCACCCAGCTTTGG	14093	CAGAT
			TCAAAGCTG	TGCCTGTG	
			GGTTTCGAC	ACGGACAC	
			CC__		
GAM1576	MPP3	3'	CACAGGCAAGCTGACCCT	8635	CTG A
			AG CAG	TTGCCTGTG	
			TC GTC	AACGGACAC	
			CCA	G	
GAM1576	NR1I2	3'	CAAAGTGCAGCTGTGA	13963	A A
			TCA AGCTGCAG	TTG	
			AGT TCGACGTC	AAC	
			G	A	
GAM1576	NR1I2	3'	CAAAGTGCAGCTGTGA	41826	A A
			TCA AGCTGCAG	TTG	
			AGT TCGACGTC	AAC	
			G	A	
GAM1576	OCM	3'	CACAGGCAATGCCTCT	20546	CT GA
			AG GCA	TTGCCTGTG	
			TC CGT	AACGGACAC	
			TC	__	
GAM1576	OGDH	3'	CACAGAAAGGGCAGCTT	91105	AGA GC
			AAGCTGC	TT CTGTG	
			TTCGACG	AA GACAC	
			GG_	A_	
GAM1576	PACE4	3'	GGGAATCCACAGCTCTGG	10403	A CA G
			TCA AGCTG	GATT CC	
			GGT TCGAC	CTAA GG	
			C	AC G	
GAM1576	PACE4	3'	GGGAATCCACAGCTCTGG	56348	A CA G
			TCA AGCTG	GATT CC	
			GGT TCGAC	CTAA GG	
			C	AC G	
GAM1576	PIGK	3'	GGAATCCTGCAGCTTT	66701	_ G
			AAAGCTGCAG	ATT CC	



		TTTCGACGTC TAA GG	
		C _	
GAM1576 STARD4	3'	CACAGCTCACTGCAGCTTTGA 57510	ATT C
		TCAAAGCTGCAG GC TGTG	
		AGTTTCGACGTC CG ACAC	
		ACT _	
GAM1576 UBE4A	3'	CACAAGCAAGTGTGTAGCTT 16561	G _ C
		AAGCTGCA ATT GC TGTG	
		TTCGATGT TGA CG ACAC	
		G A A	
GAM1576 BIRC8	5'	CAGGTTTATCCGCAGCTTT 52904	A T_
		AAAGCTGC GAT GCCTG	
		TTTCGACG CTA TGGAC	
		C TT	
GAM1576 C11orf9	3'	CACTCATTCTCAGCTTTGA 25207	C T CCT
		TCAAAGCTG AGA TG GTG	
		AGTTTCGAC TCT AC CAC	
		_ T T_	
GAM1576 C20orf98	3'	CACAGGCAATTACTAGC 71512	CA
		GCTG GATTGCCTGTG	
		CGAT TTAACGGACAC	
		CA	
GAM1576 C6orf5	3'	GCTCACTGCAGCTTTGA 31354	ATT
		TCAAAGCTGCAG GC	
		AGTTTCGACGTC CG	
		ACT	
GAM1576 CHST3	3'	ACAGACAATCTGCCGT 14963	T C
		GC GCAGATTG CTGT	
		TG CGTCTAAC GACA	
		C A	
GAM1576 DKFZP434B103	3'	CACAGGCAGAGGGCAGCT 31588	AGA
		AGCTGC TTGCCTGTG	
		TCGACG GACGGACAC	
		GGA	
GAM1576 FLJ10813	3'	TAATCTGCCACTTTGA 36686	CT
		TCAAAG GCAGATTG	
		AGTTTC CGTCTAAT	
		AC	
GAM1576 FLJ12168	3'	CACAGGCACTTTAGC 45184	C AT
		GCTG AG TGCCTGTG	

CGAT TC ACGGACAC  
 T \_\_\_\_  
 GAM1576 FLJ12331 3' CAATCAGTGCAGTTTGA 46475 G \_\_\_\_  
 TCAAA CTGCA GATTG  
 ||||| ||||| |||||  
 AGTTT GACGT CTAAC  
 \_ GA  
 GAM1576 FLJ12650 3' CACAGGCATGGAGCT 44524 G GAT  
 AGCT CA TGCCTGTG  
 ||||| || |||||  
 TCGA GT ACGGACAC  
 G \_\_\_\_  
 GAM1576 FLJ14082 5' CACATGGAGAGCTGCAGCT 46670 ATTG \_  
 AGCTGCAG CC TGTG  
 ||||| || |||||  
 TCGACGTC GG ACAC  
 GAGA T  
 GAM1576 FLJ14326 5' CATCCTGCCCCAGCTTTGA 49804 \_\_\_\_ AT  
 TCAAAGCT GCAG TG  
 ||||| ||||| |||||  
 AGTTTCGA CGTC AC  
 CCC CT  
 GAM1576 FLJ20249 3' CACAGTCCTTTCTGCAGCTT 79424 TTGC\_  
 AAGCTGCAGA CTGTG  
 ||||| ||||| |||||  
 TTCGACGTCT GACAC  
 TTCCT  
 GAM1576 FLJ20436 3' CACAGGCAACCCAGACT 35167 \_ CAGA  
 AG CTG TTGCCTGTG  
 || ||||| |||||  
 TC GAC AACGGACAC  
 A CC\_  
 GAM1576 FLJ21945 3' ACAGGCAATGTCTGCA 47313 \_\_\_\_  
 TGCAGAT TGCCTGT  
 ||||| ||||| |||||  
 ACGTCTG ACGGACA  
 TA  
 GAM1576 FLJ22037 5' CACAAGTTCCTGCAGCT 93913 ATT C  
 AGCTGCAG GC TGTG  
 ||||| || |||||  
 TCGACGTC TG ACAC  
 CT\_ A  
 GAM1576 FLJ23185 3' CACAGGCCACCGGCTCCAGCTT 46828 C ATT\_\_\_\_  
 TGA TCAAAGCTG AG GCCTGTG  
 ||||| || ||||| |||||  
 AGTTTCGAC TC CGGACAC  
 C GGCCAC  
 GAM1576 FLJ23563 5' CACGGTCACCCACAGCTTTGA 67590 CAGAT C  
 TCAAAGCTG TG CTGTG  
 ||||| || ||||| |||||

AGTTTCGAC AC GGCAC  
 ACCC\_ T  
 GAM1576 KIAA0544 3' CACAAGCTGCGTGCGAGCTCTGG 70888 A GATT C  
 TCA AGCTGCA GC TGTG  
 ||| ||||| || ||||  
 GGT TCGACGT CG ACAC  
 C GCGT A  
 GAM1576 KIAA0557 3' CAGACATCTGTAGCCCTGA 77991 AA T C  
 TCA GCTGCAGAT G CTG  
 ||| ||||| ||| |||  
 AGT CGATGTCTA C GAC  
 CC \_A  
 GAM1576 KIAA0844 3' CACAGGCAAGCACCT 30198 C AGA  
 AG TGC TTGCCTGTG  
 || ||| ||||| |||  
 TC ACG AACGGACAC  
 C \_  
 GAM1576 KIAA1348 3' CACAAAAATCTGCAAATTTGA 68574 GC GCC  
 TCAAA TGCAGATT TGTG  
 |||| ||||| |||  
 AGTTT ACGTCTAA ACAC  
 AA AA\_  
 GAM1576 KIAA1579 3' CACAAATTGCTGCAGTCTGA 36604 AA ATTGCC  
 TCA GCTGCAG TGTG  
 ||| ||||| |||  
 AGT TGACGTC ACAC  
 C\_ GTTAA\_  
 GAM1576 KIAA1712 5' CACAGAGAAGCTCCCAGCTTTG 67532 C\_ A GC  
 A TCAAAGCTG AG TT CTGTG  
 ||||| || || |||||  
 AGTTTCGAC TC AA GACAC  
 CC G GA  
 GAM1576 MGC20258 5' CAGGAATCTGCAGCCTGGA 58150 AAA G  
 TC GCTGCAGATT CCTG  
 || ||||| ||| |||  
 AG CGACGTCTAA GGAC  
 GTC \_  
 GAM1576 MGC5528 3' CACAGGCAATGCTCACT 44043 C C \_  
 AG TG AG ATTGCCTGTG  
 || || || ||||| |||  
 TC AC TC TAACGGACAC  
 \_ \_ G  
 GAM1576 MIC2L1 3' CACTGGAATCTGCAGC 48820 G T  
 GCTGCAGATT CC GTG  
 ||||| || |||  
 CGACGTCTAA GG CAC  
 \_ T  
 GAM1576 MYO5C 3' ACAGGTGACAGCTGTGA 38104 A CAGA TG  
 TCA AGCTG T CCTGT  
 ||| |||| | ||||

			AGT TCGAC A GGACA		
			G ____ GT		
GAM1576	OSR2	3'	CAGCCGCACCTGCAGCT 53805	AT ____	
			AGCTGCAG TGC CTG		
			TCGACGTC ACG GAC		
			C_ CC		
GAM1576	PLSCR3	3'	CACAGGCATATCAGCTTT 39792	CAGAT	
			AAAGCTG TGCCTGTG		
			TTTCGAC ACGGACAC		
			TAT__		
GAM1576	PLSCR3	3'	CACAGGCATATCAGCTTT 90759	CAGAT	
			AAAGCTG TGCCTGTG		
			TTTCGAC ACGGACAC		
			TAT__		
GAM1576	STATI2	3'	CACAGGCCTCACTGCAATTTGA 94550	GC ATT_	
			TCAAA TGCAG GCCTGTG		
			AGTTT ACGTC CGGACAC		
			A_ ACTC		
GAM1576	STATI2	3'	CACAGGCCTCACTGCAATTTGA 13920	GC ATT_	
			TCAAA TGCAG GCCTGTG		
			AGTTT ACGTC CGGACAC		
			A_ ACTC		
GAM1576	TRIM11	3'	CACAGTTCCTGCAGCTTTG 72830	ATTGC	
			CAAAGCTGCAG CTGTG		
			GTTTCGACGTC GACAC		
			CTT__		
GAM1576	LOC115574	3'	CACAGGTCATGTCTGCAGC 73464	--	
			GCTGCAGAT TG CCTGTG		
			CGACGTCTG AC GGACAC		
			T T		
GAM1576	LOC124976	3'	CGATCTGCAGCTTTGA 74378		
			TCAAAGCTGCAGATTG		
			AGTTTCGACGTCTAGC		
GAM1576	LOC130471	3'	GCACTGCAGCTCTGA 74941	A AT	
			TCA AGCTGCAG TGC		
			AGT TCGACGTC ACG		
			C ____		
GAM1576	LOC145501	3'	CACAGGAGGCTATCTGTAGC 77251	TG__	
			GCTGCAGAT CCTGTG		

			CGATGTCTA	GGACAC		
			TCGGA			
GAM1576	LOC146819	3'	CACATTATTTTGCAGCTCTGA	78150	A	TTGCC
			TCA AGCTGCAGA	TGTG		
			AGT TCGACGTTT	ACAC		
			C	TATT_		
GAM1576	LOC146821	3'	CACATTATTTTGCAGCTCTGA	78142	A	TTGCC
			TCA AGCTGCAGA	TGTG		
			AGT TCGACGTTT	ACAC		
			C	TATT_		
GAM1576	LOC150005	5'	CACAGGCACCAGCTCTGA	84817	A	CAGAT
			TCA AGCTG	TGCCTGTG		
			AGT TCGAC	ACGGACAC		
			C	C_		
GAM1576	LOC150005	3'	CACAGGCAGGGGTAGC	84818	AGA	
			GCTGC	TTGCCTGTG		
			CGATG	GACGGACAC		
			GG_			
GAM1576	LOC151318	3'	CACAGGCAATCTACCTTCTGA	80225	_	CTGC
			TCA AAG	AGATTGCCTGTG		
			AGT TTC	TCTAACGGACAC		
			C	CA_		
GAM1576	LOC151907	3'	CAGTTATCTAAGCTTTGA	80397	GC	TGC
			TCAAAGCT	AGAT CTG		
			AGTTTCGA	TCTA GAC		
			A_	TT_		
GAM1576	LOC163724	5'	CACACCAGCTGCAGCTT	82152	A	CC
			AAGCTGCAG	TTG TGTG		
			TTCGACGTC	GAC ACAC		
			_	C_		
GAM1576	LOC168667	3'	CACCCTCGTATCTGCAGCCTGA	92756	AA	_ CCT
			TCA GCTGCAGAT	TG GTG		
			AGT CGACGTCTA	GC CAC		
			C_	T TCC		
GAM1576	LOC201324	3'	CACATCAGCTGCAGCT	68561	A	CC
			AGCTGCAG	TTG TGTG		
			TCGACGTC	GAC ACAC		
			_	T_		
GAM1576	LOC219818	3'	CAGTCTTATTACAGCTTTGA	90887	C_	
			TCAAAGCTG	AGATTG		

		AGTTTCGAC	TCTGAC		
		ATTAT			
GAM1576	LOC220980	3'	ACATACTGCAGTTTGA	93141	G ATTGCC
			TCAAA CTGCAG	TGT	
			AGTTT GACGTC	ACA	
			— AT—		
GAM1576	LOC221576	3'	AATCTGCAAGCTTTGA	93700	—
			TCAAAGCT GCAGATT		
			AGTTTCGA CGTCTAA		
			A		
GAM1576	LOC254962	3'	CACAGGCAATCTTGCTTCT	96614	CT _
			AG GCA GATTGCCTGTG		
			TC CGT CTAACGGACAC		
			TT T		
GAM1576	LOC255299	5'	CAACCTGGAGCTTTGA	97464	G A
			TCAAAGCT CAG TTG		
			AGTTTCGA GTC AAC		
			G C		
GAM1576	LOC255545	3'	CAGTTATCTAAGCTTTGA	95706	GC TGC
			TCAAAGCT AGAT CTG		
			AGTTTCGA TCTA GAC		
			A_ TT_		
GAM1576	LOC256940	3'	CACAGGTTTTCTGCAGT	96492	TT
			GCTGCAGA GCCTGTG		
			TGACGTCT TGGACAC		
			TT		
GAM1576	LOC257319	3'	ACATGCTGCAGCTTGA	95771	A ATTGCC
			TCAA GCTGCAG	TGT	
			AGTT CGACGTC	ACA	
			— GT—		
GAM1576	LOC257515	3'	AATCTGCAAGCTTTGA	97780	—
			TCAAAGCT GCAGATT		
			AGTTTCGA CGTCTAA		
			A		
GAM1576	LOC257572	3'	AATCTGCAAGCTTTGA	97909	—
			TCAAAGCT GCAGATT		
			AGTTTCGA CGTCTAA		
			A		
GAM1576	LOC51075	3'	CACAAGCCTGAGGTGCAGCTTT	31989	GA _ C
			AAAGCTGCA TT GC TGTG		

TTTCGACGT AG CG ACAC  
 GG TC A  
 GAM1576 LOC56267 3' CACAGATTTTACAGCTTTGG 39010 C TTGC  
 TCAAAGCTG AGA CTGTG  
 ||||| || ||||  
 GGTTCGAC TTT GACAC  
 A TA\_\_  
 GAM1576 LOC90139 3' CACAGGCGTGACAGTTCTGA 55401 A \_ GAT  
 TCA AGCTG CA TGCCTGTG  
 || |||| || |||||  
 AGT TTGAC GT GCGGACAC  
 C A \_\_\_\_  
 GAM1577 ABCB11 5' TCTGGCTTCCTCAAATTC 13618 A ATGA  
 GAATTTGA GAAG AGA  
 ||||| ||| |||  
 CTTAAACT CTTC TCT  
 C GG\_\_  
 GAM1577 APC 3' CTTTCATCTTCTTGTTGCA 3477 G TTG  
 TG AAT AAGAAGATGAAG  
 || ||| |||||  
 AC TTG TTCTTCTACTTC  
 G \_\_\_\_  
 GAM1577 ATP1B2 3' CTTCCCAGAATATCCTTCAAGT 8049 AA AA\_\_\_\_  
 TCCA GGAATTTGAAG GATG GAAG  
 ||||| ||| |||  
 CCTTGAAGCTTC CTAT CTTC  
 \_ AAGACC  
 GAM1577 CA4 3' TCAGCTCTCCAAGTTCCA 5552 A AGA  
 TGGAATTTG AGA TGA  
 ||||| ||| |||  
 ACCTTGAAC TCT ACT  
 C CG\_  
 GAM1577 CEP1 5' CTTCCGTTTCGTTCTTCAAAACC 22816 AA \_ T\_\_  
 CA TGG TTTGAAGAA GA GAAG  
 || ||||| || |||  
 ACC AAATTCTT CT CTTC  
 CA G TGC  
 GAM1577 CEP2 3' CTTTCATCTTCTCCTTCAA 23227 \_\_\_\_  
 TTGA AGAAGATGAAG  
 ||| |||||  
 AACT TCTTCTACTTC  
 TCC  
 GAM1577 FBLN5 3' CTTCTTCACCTCTTCCACTCC 20916 ATTT A A  
 GGA GAAGA G TGAAGAAG  
 || |||| | |||||  
 CCT CTTCT C ACTTCTTC  
 CAC\_ \_ C  
 GAM1577 GAC1 3' TCCCCATCTTCTCTCTGCCCA 20945 AATTT \_ AA  
 TGG GA AGAAGATG GA  
 || || ||||| ||

			ACC CT TCTTCTAC CT		
			CGT__ C CC		
GAM1577	GATA4	3'	CTTCCCTCCTCAAATTCC 9005	A	AGAT
			GGAATTTGA GA GAAG		
			CCTTAAACT CT CTTC		
			C CC__		
GAM1577	MGA	3'	TTCTTTATCCCAAATCCCA 62812	A	AAGAA
			TGG ATTTG GATGAAGAA		
			ACC TAAAC CTATTTCTT		
			C C__		
GAM1577	PIK3R3	3'	TCGTTTCCTTACAAATTCCA 61064	_	A
			TGGAATTTG AAG AGATGA		
			ACCTTAAAC TTC TTTGCT		
			A C		
GAM1577	POU2F2	3'	TCTTCATCCTCATCCTCC 10692	ATTT	A A
			GGA GA GA GATGAAGA		
			CCT CT CT CTACTTCT		
			C__ A C		
GAM1577	PTPRS	3'	TCCTTTCCTTCCAATTCCA 11141	T	A T
			TGGAATT GAAG AGA GA		
			ACCTTAA CTTC TTT CT		
			C C C		
GAM1577	PTPRS	3'	TCCTTTCCTTCCAATTCCA 55645	T	A T
			TGGAATT GAAG AGA GA		
			ACCTTAA CTTC TTT CT		
			C C C		
GAM1577	PTPRS	3'	TCCTTTCCTTCCAATTCCA 55648	T	A T
			TGGAATT GAAG AGA GA		
			ACCTTAA CTTC TTT CT		
			C C C		
GAM1577	PTPRS	3'	TCCTTTCCTTCCAATTCCA 55651	T	A T
			TGGAATT GAAG AGA GA		
			ACCTTAA CTTC TTT CT		
			C C C		
GAM1577	SELL	3'	TCCCCACCTTCTTCAGCCACC 5393	AAT	A AA
			GG TTGAAGAAG TG GA		
			CC GACTTCTTC AC CT		
			ACC C CC		
GAM1577	TEM7	3'	CTTTTTCTTCCTCAAATTC 39885	A	T
			GAATTTGA GAAGA GAAG		



CTTAAACT CTTCT TTTC  
C T

GAM1577 WT1 3' TTCTTCATCCAACCTTCCA 44357 T AAGAA  
TGGAA TTG GATGAAGAA  
||||| ||| |||||  
ACCTT AAC CTACTTCTT  
C \_\_\_\_\_

GAM1577 WT1 3' TTCTTCATCCAACCTTCCA 44367 T AAGAA  
TGGAA TTG GATGAAGAA  
||||| ||| |||||  
ACCTT AAC CTACTTCTT  
C \_\_\_\_\_

GAM1577 WT1 3' TTCTTCATCCAACCTTCCA 44377 T AAGAA  
TGGAA TTG GATGAAGAA  
||||| ||| |||||  
ACCTT AAC CTACTTCTT  
C \_\_\_\_\_

GAM1577 WT1 3' TTCTTCATCCAACCTTCCA 4592 T AAGAA  
TGGAA TTG GATGAAGAA  
||||| ||| |||||  
ACCTT AAC CTACTTCTT  
C \_\_\_\_\_

GAM1577 AD-003 5' CTTCCCATCTTCTTC 25931 AA  
GAAGAAGATG GAAG  
||||||| |||  
CTTCTTCTAC CTTC  
CC

GAM1577 CEACAM7 3' CTTCTAGCTCCTTCAATCCCA 22557 AAT A AT\_  
TGG TTGAAG AG GAAG  
||| ||||| || |||||  
ACC AACTTC TC CTTC  
CT\_ C GAT

GAM1577 CSMD1 3' CTTCTTTGTCCTCAATTTCCA 73120 T AGAA TG  
TGGAA TTGA GA AAGAAG  
||||| ||| || |||||  
ACCTT AACT CT TTCTTC  
T C\_ GT

GAM1577 DDX34 3' CATGTCTCCAGATTCCA 27979 A AG  
TGGAATTTG AGA ATG  
||||||| ||| |||  
ACCTTAGAC TCT TAC  
C G\_

GAM1577 DKFZP434B205 3' CTTCTTCATCTTCCTGGACGTC 75320 ATTTGAA  
GA GAAGATGAAGAAG  
|| |||||  
CT CTTCTACTTCTTC  
GCAGGTC

GAM1577 FENS-1 3' CTTCCCTTTCCCCCAAATTCC 40439 AA\_ AT  
GGAATTTG GAAG GAAG  
||||||| ||| |||

CCTTAAAC CTTT CTTC  
 CCC CC  
 GAM1577 FLJ13262 3' ATCCTCTCCAAATTCC 46155 A A  
 GGAATTTG AGA GAT  
 ||||| ||| |||  
 CCTTAAAC TCT CTA  
 C C  
 GAM1577 FLJ20170 3' TCACCTTCTTCAACTCCA 34672 AT A  
 TGGA TTGAAGAAG TGA  
 ||| ||||| |||  
 ACCT AACTTCTTC ACT  
 C\_ C  
 GAM1577 FLJ20375 3' CTTCTCCCTGCTAAATTCCA 35085 A\_ AA T  
 TGGAATTTG AG GA GAAG  
 ||||| || |||  
 ACCTTAAAT TC CT CTTC  
 CG C\_ \_  
 GAM1577 FLJ20802 3' CTTCTTCACCTTTGCATCC 35669 ATT AA A  
 GGA TG GAAG TGAAGAAG  
 ||| || |||||  
 CCT AC TTTC ACTTCTTC  
 \_ G\_ C  
 GAM1577 FLJ22055 3' CTTTCATCTTCTGCTCCA 45496 ATTTGA  
 TGGA AGAAGATGAAG  
 ||| |||||  
 ACCT TCTTCTACTTC  
 CG\_  
 GAM1577 HUMAGCGB 5' CTATGCCTTCCTCAAGTTCCA 25231 A AT A  
 TGGAATTTGA GAAG G AG  
 ||||| ||| |||  
 ACCTTGAAC TTT T TC  
 C CG A  
 GAM1577 INA 3' CACCTCCTTCAATTCCA 51187 T A A  
 TGGAATT GAAG AG TG  
 ||||| ||| |||  
 ACCTTAA CTTC TC AC  
 \_ C C  
 GAM1577 KIAA0451 5' TCATAATTCTCAAATTCCA 29114 AG AG  
 TGGAATTTGA A ATGA  
 ||||| | |||  
 ACCTTAAACT T TACT  
 CT AA  
 GAM1577 KIAA0972 5' CTTCTTCATCCCTTGCCCA 30010 AATTTG AA  
 TGG AAG GATGAAGAAG  
 ||| ||| |||||  
 ACC TTC CTACTTCTTC  
 CG\_ CC  
 GAM1577 MGC15854 5' TTCCCCATCTTCTCCTCTA 58852 ATTT A AA  
 TGGA GA GAAGATG GAA  
 ||| || ||||| |||

ATCT CT CTTCTAC CTT  
 C\_\_ \_ CC  
 GAM1577 MGC17998 3' TTCCTCATCTTCTGGTCC 58746 ATTTGA A  
 GGA AGAAGATGA GAA  
 ||| ||||| |||  
 CCT TCTTCTACT CTT  
 GG\_\_ C  
 GAM1577 MIL1 3' TCTTCACCCCCAGGTTCC 31097 AAGAAGA  
 GGAATTTG TGAAGA  
 ||||| |||||  
 CCTTGGAC ACTTCT  
 CCCC\_\_  
 GAM1577 NYD-SP21 3' CTTCAGCTTCCTCAAATTC 50873 A A  
 GAATTTGA GAAG TGAAG  
 ||||| ||| |||||  
 CTTAAACT CTTC ACTTC  
 C G  
 GAM1577 PCDH19 3' TTCTTCATCCAAAATTGCA 63713 G GAAGAA  
 TG AATTT GATGAAGAA  
 || ||||| |||||  
 AC TTAAA CTACTTCTT  
 G AC\_\_  
 GAM1577 PEG10 3' CTTCACCGTCTTCAAACCTCCA 30525 A AGA  
 TGGA TTTGAAGA TGAAG  
 ||| ||||| |||||  
 ACCT AAACCTTCT ACTTC  
 C GCC  
 GAM1577 TRIM16 3' TCATCTTCTAGTGCCA 21343 A TGA  
 TGG ATT AGAAGATGA  
 ||| ||| |||||  
 ACC TGA TCTTCTACT  
 G \_\_  
 GAM1577 LOC124245 3' CTCCATCTTCTTCCCTGGCC 58152 AATTT A  
 GG GAAGAAGATG AG  
 || ||||| |||  
 CC CTTCTTCTAC TC  
 GGTCC C  
 GAM1577 LOC144231 5' ATCTTCCTCAAACCTTCA 83011 A A  
 TGGA TTTGA GAAGAT  
 ||| ||||| |||||  
 ACTT AAACCT CTTCTA  
 C C  
 GAM1577 LOC145739 3' TCATTCTTCAAAGCCCA 77443 AA AG  
 TGG TTTGAAGA ATGA  
 ||| ||||| |||  
 ACC AAACCTTCT TACT  
 CG \_\_  
 GAM1577 LOC146856 3' CTTCTTTTTTCTTCTTCAACC 82802 AT T\_ \_  
 TCCA TGGA TTGAAGAAGA GAAG AAG  
 ||| ||||| ||| |||

ACCT AACTTCTTCT TTTC TTC  
 CC TT C  
 GAM1577 LOC147166 3' TCATCTTCTAGTGCCA 78290 A TGA  
 TGG ATT AGAAGATGA  
 ||| ||| |||||  
 ACC TGA TCTTCTACT  
 G \_\_\_\_  
 GAM1577 LOC151124 5' TCTGTTCTTCCCCAAATTCC 85234 AA TGA  
 GGAATTTG GAAGA AGA  
 ||||| ||||| |||  
 CCTTAAAC CTTCT TCT  
 CC TG\_  
 GAM1577 LOC151405 5' CTTCTTCATGACACCAAATCCA 85337 A AAGAAG  
 TGGA TTTG ATGAAGAAG  
 ||| ||| |||||  
 ACCT AAAC TACTTCTTC  
 \_ CACAG\_  
 GAM1577 LOC151438 5' CTTCTGGGACCAAATTCCA 85365 A\_\_\_\_  
 TGGAATTTG AGAAG  
 ||||| |||||  
 ACCTTAAAC TCTTC  
 CAGGG  
 GAM1577 LOC153469 3' CTTTCATCTTCTCCTCA 80841 \_\_\_\_  
 TGA AGAAGATGAAG  
 ||| |||||  
 ACT TCTTCTACTTC  
 CC  
 GAM1577 LOC157909 5' CTTCTCAGACTTAAAATTCCA 81627 G AAGA A  
 TGGAATTT AAG TGA GAAG  
 ||||| ||| ||| |||  
 ACCTTAAA TTC ACT CTTC  
 A AG\_\_ \_  
 GAM1577 LOC165140 5' TCTTCATCTTCTGCATCCA 82467 ATT A  
 TGGA TG AGAAGATGAAGA  
 ||| ||| |||||  
 ACCT AC TCTTCTACTTCT  
 \_\_\_\_ G  
 GAM1577 LOC169831 5' CTTCTTCATCTTCCCTTC 82783 \_\_\_\_  
 GAA GAAGATGAAGAAG  
 ||| |||||  
 CTT CTTCTACTTCTTC  
 CC  
 GAM1577 LOC197414 3' CTTGGCTTCTTCAAACGCCA 88066 AA ATG  
 TGG TTTGAAGAAG AAG  
 ||| ||||| |||  
 ACC AAATTCTTC TTC  
 GC GG\_  
 GAM1577 LOC219894 3' CTTCCCAACTTCTTCAAATTC 93281 A AA  
 GAATTTGAAGAAG TG GAAG  
 ||||| ||| |||

		CTTAAACTTCTTC AC CTTC		
		A C_		
GAM1577	LOC255040	3' CTTCTTTTGCTCCAAATTCC 96382	A _ T	
		GGAATTTG AG AAGA GAAG		
		CCTTAAAC TC TTTT CTTC		
		C G C		
GAM1577	LOC255041	3' CTTCTTTTGCTCCAAATTCC 96388	A _ T	
		GGAATTTG AG AAGA GAAG		
		CCTTAAAC TC TTTT CTTC		
		C G C		
GAM1577	LOC90371	5' TCTTCATCCTCCTCTACC 62504	AATTT A A	
		GG GA GA GATGAAGA		
		CC CT CT CTACTTCT		
		AT__ C C		
GAM1577	LOC92539	5' TCCTCTCTTCAAGTCCCA 69643	A A T	
		TGG ATTTGAAGA GA GA		
		ACC TGAATTCT CT CT		
		C _ C		
GAM1578	ACCN1	3' CATGTCGTTCTTCTCTCC 6582	A AT CAC	
		GGA AGAA GG CGACATG		
		CCT TCTT CT GCTGTAC		
		C _ T__		
GAM1578	BCL11A	3' CCACATCGATGGTTCTTTCTA 43160	ATGG C CA	
		TGGAAAGAA CA CGA TGG		
		ATCTTTCTT GT GCT ACC		
		G__ A AC		
GAM1578	CD79B	3' CCAGAGCTGCCATTTGTCTCCA 41208	AAG CCGACA	
		TGGA AAATGGCA TGG		
		ACCT TTTACCGT ACC		
		CTG CGAG__		
GAM1578	CD79B	3' CCAGAGCTGCCATTTGTCTCCA 5272	AAG CCGACA	
		TGGA AAATGGCA TGG		
		ACCT TTTACCGT ACC		
		CTG CGAG__		
GAM1578	COL5A3	3' CCTTTTGGTGCTACCCCTCCCC 31693	AA AAA CAT	
	A	TGG AG TGGCACCGA GG		
		ACC TC ATCGTGGTT CC		
		CC CCC TT_		
GAM1578	CYP2B6	3' TGGTGCCATCTCTGTCCA 5743	A A	
		TGGA AGA ATGGCACCG		

		ACCT TCT TACCGTGGT		
		G C		
GAM1578 DTNB	3'	CCAGAGGCACATTCCTCTCCA 41578	A A	GCA GACA
		TGGA AG AATG CC TGG		
		ACCT TC TTAC GG ACC		
		C C AC_ AG__		
GAM1578 DTNB	3'	CCAGAGGCACATTCCTCTCCA 52500	A A	GCA GACA
		TGGA AG AATG CC TGG		
		ACCT TC TTAC GG ACC		
		C C AC_ AG__		
GAM1578 EGFL5	3'	CCGAGATGGCGCCATTTCACTC 86615	AA	A ACA
CA		TGGA GAAATGGC CCG TGG		
		ACCT CTTTACCG GGT GCC		
		CA C AGA		
GAM1578 PRKAG1	3'	CCATTTAGTGACATTTCTTCCC 10799	A	G CG C
A		TGG AAGAAATG CAC A ATGG		
		ACC TTCTTTAC GTG T TACC		
		C A AT_		
GAM1578 PSEN1	3'	TGTGATTGCCATTTCTTCCCA 23628	A	CCG
		TGG AAGAAATGGCA ACA		
		ACC TTCTTTACCGT TGT		
		C TAG		
GAM1578 PSEN1	3'	TGTGATTGCCATTTCTTCCCA 3426	A	CCG
		TGG AAGAAATGGCA ACA		
		ACC TTCTTTACCGT TGT		
		C TAG		
GAM1578 C20orf102	3'	CCATGTCGGCCCTCTTTCCA 54615	AAT CA	
		TGGAAAGA GG CCGACATGG		
		ACCTTTCT CC GGCTGTACC		
		__ C_		
GAM1578 CAMKK2	3'	GGCAATGCCATTTCTCCCCA 21586	AA	A_____
		TGG AGAAATGGC CC		
		ACC TCTTTACCG GG		
		CC TAAC		
GAM1578 FBXO9	3'	CCAAGATCGTGCCATTCCACTC 53101	AAGA	C CA_
CA		TGGA AATGGCAC GA TGG		
		ACCT TTACCGTG CT ACC		
		CACC _ AGA		
GAM1578 FLJ13057	3'	CATGTTCAATTTCTTTCCA 42454	_	GCACC
		TGGAAAGAAA TG GACATG		

ACCTTTCTTT AC TTGTAC  
 T \_\_\_\_\_  
 GAM1578 FLJ13057 3' CATGTTCAATTTCTTTCCA 95647 \_ GCACC  
 TGGAAAGAAA TG GACATG  
 ||||| || |||||  
 ACCTTTCTTT AC TTGTAC  
 T \_\_\_\_\_  
 GAM1578 FLJ13072 3' CCATATCAGTGTCTGTTTCT 89805 \_ C C  
 AGAAAT GGCAC GA ATGG  
 ||||| ||||| || |||||  
 TCTTTG CTGTG CT TACC  
 T A A  
 GAM1578 FLJ23499 3' CGGTGCCATTGCTCTCCA 42819 A A  
 TGGA AG AATGGCACCG  
 ||| || |||||  
 ACCT TC TTACCGTGGC  
 C G  
 GAM1578 KIAA0276 3' CCACTATTTTACCATTCTTTG 70963 G CACCGACA  
 CA TG AAAGAAATGG TGG  
 || ||||| |||  
 AC TTTCTTTACC ACC  
 G ATTTTATC  
 GAM1578 KIAA1161 5' CCACGCCAGCCATTTCTCTTT 81743 \_ AC\_ ACA  
 CTA GGAAAGA AATGGC CG TGG  
 ||||| ||||| || |||  
 TCTTTCT TTACCG GC ACC  
 CTT ACC \_  
 GAM1578 MGC10960 3' GGTGCCATCCTCTCCA 51008 A AA  
 TGGA AG ATGGCACC  
 ||||| || |||||  
 ACCT TC TACCGTGG  
 C C\_  
 GAM1578 MGC13170 3' CATGTTGCACTTCTGCCCA 51145 AA A GCAC  
 TGG AGAA TG CGACATG  
 ||| ||||| || |||||  
 ACC TCTT AC GTTGTAC  
 CG C \_  
 GAM1578 NCKX3 3' CCATCATCACCATCTCTTTCT 40350 A CACCGAC  
 GGAAAGA ATGG ATGG  
 ||||| ||||| |||  
 TCTTTCT TACC TACC  
 C ACTAC\_  
 GAM1578 PLEK2 3' TGGTGCCATTTCCTTCC 33190 A  
 GGAA GAAATGGCACCG  
 ||||| |||||  
 CCTT CTTTACCGTGGT  
 C  
 GAM1578 RDH-E2 3' GTGCCCTTCTTTCCA 57272 AT  
 TGGAAAGAA GGCAC  
 ||||| |||||

			ACCTTTCTT CCGTG		
			C_		
GAM1578	RPL34	3'	CCAGTTGTGTGCATCTCTTTCC 6395	A G _ A	
	A		TGGAAAGA ATG CAC CGAC TGG		
			ACCTTTCT TAC GTG GTTG ACC		
			C _ T _		
GAM1578	RPL34	3'	CCAGTTGTGTGCATCTCTTTCC 53245	A G _ A	
	A		TGGAAAGA ATG CAC CGAC TGG		
			ACCTTTCT TAC GTG GTTG ACC		
			C _ T _		
GAM1578	LOC147664	3'	CCAAGATCGTGCCATTCCACTC 78406	AAGA C CA_	
	CA		TGGA AATGGCAC GA TGG		
			ACCT TTACCGTG CT ACC		
			CACC _ AGA		
GAM1578	LOC151361	3'	CACGTCACTGTTCTTTCCA 85319	AATG CC A	
			TGGAAAGA GCA GAC TG		
			ACCTTTCT TGT CTG AC		
			_ CA C		
GAM1578	LOC256267	5'	CCAATATTGTGCCATTGCTTTC 96800	A CGACA	
	CA		TGGAAAG AATGGCAC TGG		
			ACCTTTC TTACCGTG ACC		
			G TTATA		
GAM1578	LOC257481	3'	GGTAGCACCATTTCCTTTC 61110	C_	
			GAAAGAAATGG ACC		
			CTTTCCTTACC TGG		
			ACGA		
GAM1578	LOC91035	3'	CCAAGCGCGTGCCATTTCACTC 64666	AA _ ACA	
	CA		TGGA GAAATGGCAC CG TGG		
			ACCT CTTTACCGTG GC ACC		
			CA C GA_		
GAM1578	LOC92466	5'	CCAATATTGTGCCATTGCTTTC 69425	A CGACA	
	CA		TGGAAAG AATGGCAC TGG		
			ACCTTTC TTACCGTG ACC		
			G TTATA		
GAM1579	ADH1B	3'	TGACAAAGCCTCAATTA 72647	C T	
			TAA TGA GCTTTGTCA		
			ATT ACT CGAAACAGT		
			A C		
GAM1579	CNTN3	3'	GAAGACTTAACCAGTATCA 66694	TT C	
			TGATGCT GT AAGTCTTC		



		ACTATGA CA TTCAGAAG		
		C_ A		
GAM1579	GPR18	5' AAGAGACAAAGCAGCAATTA	17958	C A AAG
		TAA TG TGCTTTGTC TCTT		
		ATT AC ACGAAACAG AGAA		
		A G _		
GAM1579	IFNG	5' GAGAAAGATCAGTTA	5240	G G
		TAACTGAT CTTT TC		
		ATTGACTA GAAA AG		
		_ G		
GAM1579	MGST3	3' ACTTACCTGGCATCAG	15758	TT C
		CTGATGCT GT AAGT		
		GACTACGG CA TTCA		
		TC _		
GAM1579	AP1GBP1	3' AAGACTCTGCATCAGT	54513	TTTGTCA
		ACTGATGC AGTCTT		
		TGACTACG TCAGAA		
		TC_		
GAM1579	AP1GBP1	3' AAGACTCTGCATCAGT	54527	TTTGTCA
		ACTGATGC AGTCTT		
		TGACTACG TCAGAA		
		TC_		
GAM1579	AP1GBP1	3' AAGACTCTGCATCAGT	23387	TTTGTCA
		ACTGATGC AGTCTT		
		TGACTACG TCAGAA		
		TC_		
GAM1579	EDR1	5' GAAGACTTGGGTGCACAG	15382	A TTTG
		CTG TGC TCAAGTCTTC		
		GAC ACG GGTTCAGAAG		
		_ TG_		
GAM1579	FLJ10252	3' AAGACCTACCATCGCATCAGT	35946	TT TCAA
		ACTGATGC TG GTCTT		
		TGACTACG AC CAGAA		
		CT CATC		
GAM1579	PRSS12	3' AAGACTTGACAAGAAATC	13245	GC
		GAT TTTGTCAAGTCTT		
		CTA GAACAGTTCAGAA		
		AA		
GAM1579	LOC203411	5' ACTTCTTACAAAAGCATCA	90626	_ C_
		TGATGCTTT GT AAGT		

			ACTACGAAA CA TTCA		
			A TTC		
GAM1579	LOC220883	5'	GAAAACTTGACAAGCGAGT 91259	GA T C	
			ACT TGCTT GTCAAGT TTC		
			TGA GCGAA CAGTTCA AAG		
			— — A		
GAM1580	ADH4	3'	TAAAAAGATTTTTACTGGA 5408	CGT	
			TCCAGTGG TCTTTTTA		
			AGGTCATT AGAAAAAT		
			TTT		
GAM1580	B4GALT2	3'	AGTAAAAACGTGAATGGA 47580	GTG CT	
			TCCA GCGTT TTTTACT		
			AGGT TGCAA AAAATGA		
			AAG —		
GAM1580	CTBP1	3'	AAAAAGAAACCTGAAGGAG 67941	AGT_ CG	
			CTCC GG TTCTTTTT		
			GAGG CC AAGAAAAA		
			AAGT AA		
GAM1580	ENPP3	3'	TAAAAAGAACAGCAGAGAG 17226	CAGTG _	
			CTC GC GTTCTTTTTA		
			GAG CG CAAGAAAAAT		
			AGA_ A		
GAM1580	F8	3'	TAAAAAATAAGTCAGGAGGA 3732	AG GTTC_	
			TCCTCC TGGC TTTTTA		
			AGGAGG ACTG AAAAAT		
			— AATAA		
GAM1580	GK	3'	AGCAAAAAGAATGCTAT 3911	A	
			GTGGCGTTCTTTTT CT		
			TATCGTAAGAAAAA GA		
			C		
GAM1580	ID4	3'	GAAAAAAGCCACCGGAGGA 7755	A GTTC	
			TCCTCC GTGGC TTTTT		
			AGGAGG CACCG AAAAG		
			C AAA_		
GAM1580	PITX1	3'	GAAAAAGACGTCGGAG 10599	AGT T A	
			CTCC GGCGT CTTTTT C		
			GAGG CTGCA GAAAAA G		
			— — C		
GAM1580	TDG	3'	GAAAAAGATGCTGGAG 12191	GCGT A	
			CTCCAGTG TCTTTTT C		

GAGGTCGT AGAAAAA G  
 \_\_\_\_\_ C  
 GAM1580 XRCC2 3' AGCAAAAAGAACAAAGCTGGAG 18318 GGC A  
 G CCTCCAGT GTTCTTTTT CT  
 ||||| ||||| ||  
 GGAGGTCG CAAGAAAAA GA  
 AAA C  
 GAM1580 DKFZP727M111 5' AAAAGGAAAAGCCCTGAAG 31401 C T G\_  
 CT CAG GGC TTCTTTTT  
 || ||| |||||  
 GA GTC CCG AAGGAAAA  
 A \_ AA  
 GAM1580 ELKS 3' AGTGGTCAACGCCCTGGAAGA 30501 C T CTTT  
 TC TCCAG GCGGT TTACT  
 || ||| ||||| ||||  
 AG AGGTC CCGCAA GGTGA  
 A \_ CT\_  
 GAM1580 FLJ10648 3' AGCAAAAAGAACAAAGTCCTGG 36378 T \_ A  
 AGGA TCCTCCAG GGC GTTCTTTTT CT  
 ||||| || ||||| ||  
 AGGAGGTC CTG CAAGAAAAA GA  
 \_ AAA C  
 GAM1580 FLJ20151 3' AAAGACCCTGGAGGA 34648 T CGT  
 TCCTCCAG GG TCTTT  
 ||||| || ||||  
 AGGAGGTC CC AGAAA  
 \_ \_  
 GAM1580 FLJ20435 3' TAAAAAGAGCCATCTGGAGGA 35162 \_ GT  
 TCCTCCAG TGGC TCTTTTTA  
 ||||| ||| |||||  
 AGGAGGTC ACCG AGAAAAAT  
 T \_  
 GAM1580 MDS024 3' AAAAAGAATTGCCAAGGA 41522 AG \_  
 TCC TGGCG TTCTTTTT  
 || ||| |||||  
 AGG ACCGT AAGAAAAA  
 A\_ T  
 GAM1580 ShrmL 5' AGAGCGCCACTGAAGGA 40463 C  
 TCCT CAGTGGCGTTCT  
 ||| |||||  
 AGGA GTCACCGCGAGA  
 A  
 GAM1580 SIAT8C 5' TAAAAAGCCCCACAGAGGA 31883 CA C C  
 TCCTC GTGG GTT TTTTTA  
 |||| ||| ||| |||||  
 AGGAG CACC CGA AAAAAT  
 A\_ C \_  
 GAM1580 VEST1 5' AAAAAGATGCACTGGGGA 53678 T G T  
 TCC CCAGTG CGT CTTTTT  
 || ||||| ||| |||||

AGG GGTCAC GTA GAAAAA

GAM1580 ZFD25 5' AAAAAGAGCCCTGGA 32573 T GT  
TCCAG GGC TCTTTT  
||||| ||| |||||  
AGGTC CCG AGAAAAA

GAM1580 LOC124626 3' AGTAAGACCAAACCACTGGA 74313 CGTTCT  
TCCAGTGG TTTTACT  
||||||| |||||  
AGGTCACC AGAATGA  
AAACC\_

GAM1580 LOC144577 3' TAAAAAGAAGCCACAAAGAG 76902 CA\_ G  
CTC GTGGC TTCTTTTTA  
||| ||||| |||||  
GAG CACCG AAGAAAAAT  
AAA \_

GAM1580 LOC145837 5' AGCAAAAAGAACCAAAGAGGA 83542 CAG CG A  
TCCTC TGG TTCTTTTT CT  
||||| ||| ||||| ||  
AGGAG ACC AAGAAAAA GA  
AA\_ \_ C

GAM1580 LOC151194 3' TAAAAAACTGGGGA 59215 T GGC GTTC  
TCC CCAGT TTTTTA  
||| ||||| |||||  
AGG GGTC AAAAAAT  
\_ A\_

GAM1580 LOC154789 5' AGTAAAATCTCAGGCCACTAGA 81131 C GTTCT\_  
G CTC AGTGGC TTTTACT  
||| ||||| |||||  
GAG TCACCG AAAATGA  
A GACTCT

GAM1580 LOC197322 3' AAAGACTCCACTGGAGGA 89736 C T  
TCCTCCAGTGG GT CTTT  
||||||| || |||||  
AGGAGGTCACC CA GAAA  
T \_

GAM1580 LOC221596 3' TAAAAACCTCACACTGGAGAGA 91980 \_ GCGTTC  
TC CTCCAGTG TTTTTA  
|| ||||| |||||  
AG GAGGTCAC AAAAAAT  
A ACTCC\_

GAM1580 LOC91796 3' AGCAAAAAGAACAAGGCTGGA 67208 GGC A  
TCCAGT GTTCTTTTT CT  
||||| ||||| ||  
AGGTCG CAAGAAAAA GA  
GAA C

GAM1580 LOC92539 5' TAAAAAGTGTCCTG 69638 TT  
CAGTGGCG CTTTTTA  
||||||| |||||

GTCACTGT GAAAAAT

GAM1581 TNFAIP1 3' CATCAGCTGAGGACAGCAAAC 40917 AG G  
CC GGA TTGCTG CTTCAGCTGATG

||| ||||| |||||  
CCT AACGAC GGAGTCGACTAC  
CA A

GAM1581 C1orf2 3' CAGCTGGTTGGGACCAGCAGCC 21681 AA \_ \_  
CCC GG GTTGCTGG CT TCAGCTG

|| ||||| || |||||  
CC CGACGACC GG GGTCGAC  
CC A GTT

GAM1581 C1orf2 3' CAGCTGGTTGGGACCAGCAGCC 94622 AA \_ \_  
CCC GG GTTGCTGG CT TCAGCTG

|| ||||| || |||||  
CC CGACGACC GG GGTCGAC  
CC A GTT

GAM1581 C20orf59 3' CATCCCTAGCCAGCAGCTCC 41992 A TC CT  
GGA GTTGCTGGCT AG GATG

||| ||||| || ||||  
CCT CGACGACCGA TC CTAC  
\_ \_ C\_

GAM1581 FLJ20079 3' CATTCTGGTAAACCAGCAGCCT 34490 A CT\_ CT  
CC GGA GTTGCTGG TCAG GATG

||| ||||| ||| ||||  
CCT CGACGACC GGTC TTAC  
C AAAT \_

GAM1581 SSAT2 3' CATCAGCTGAAGCACTCTTC 56041 TTGCTG  
GAAG GCTTCAGCTGATG

||| |||||  
CTTC CGAAGTCGACTAC  
TCA\_

GAM1581 SYNJ2 3' ATCAGCTTAAGCAATTCC 61763 GTTGCTG C  
GGAA GCTT AGCTGAT

||| ||| |||||  
CCTT CGAA TCGACTA  
AA\_ T

GAM1581 LOC162333 5' CTGAAGCCAGCAATTCC 87131 G  
GGAA TTGCTGGCTTCAG

||| |||||  
CCTT AACGACCGAAGTC

GAM1581 LOC222060 5' CACCTCCCACCAGCAACCCCC 94104 AA CTTC C  
GG GTTGCTGG AG TG

|| ||||| ||  
CC CAACGACC TC AC  
CC ACCC C

GAM1581 LOC255650 3' CATCAGCCCCAGGCAACTTCC 96711 \_ CTTCA  
GGAAGTTGC TGG GCTGATG

||||| ||| |||||

CCTTCAACG ACC CGACTAC  
 G C\_\_\_\_  
 GAM1582 ADAM11 3' ATTCAAACCAAAGCTGCC 9966 GTACA C  
 GGCAGCTT GGT TTGAAT  
 ||||| |||||  
 CCGTCGAA CCA AACTTA  
 A\_\_\_\_ \_  
 GAM1582 ADAM11 3' ATTCAAACCAAAGCTGCC 41212 GTACA C  
 GGCAGCTT GGT TTGAAT  
 ||||| |||||  
 CCGTCGAA CCA AACTTA  
 A\_\_\_\_ \_  
 GAM1582 B3GALT5 3' GACCTGCTGTACAGACTGCC 52558 CT \_\_\_\_  
 GGCAG TGTACA GGTC  
 |||| |||| ||||  
 CCGTC ACATGT CCAG  
 AG CGT  
 GAM1582 B3GALT5 3' GACCTGCTGTACAGACTGCC 52563 CT \_\_\_\_  
 GGCAG TGTACA GGTC  
 |||| |||| ||||  
 CCGTC ACATGT CCAG  
 AG CGT  
 GAM1582 B3GALT5 3' GACCTGCTGTACAGACTGCC 52571 CT \_\_\_\_  
 GGCAG TGTACA GGTC  
 |||| |||| ||||  
 CCGTC ACATGT CCAG  
 AG CGT  
 GAM1582 B3GALT5 3' GACCTGCTGTACAGACTGCC 52578 CT \_\_\_\_  
 GGCAG TGTACA GGTC  
 |||| |||| ||||  
 CCGTC ACATGT CCAG  
 AG CGT  
 GAM1582 B3GALT5 3' GACCTGCTGTACAGACTGCC 20220 CT \_\_\_\_  
 GGCAG TGTACA GGTC  
 |||| |||| ||||  
 CCGTC ACATGT CCAG  
 AG CGT  
 GAM1582 FRAP1 3' ATTCAAGACCTGACCGCT 17097 TT A  
 AGC GT CAGGTCTTGAAT  
 || |||||  
 TCG CA GTCCAGAACTTA  
 C\_ \_  
 GAM1582 GARP 3' TCAAGACCTTGTGTTTGCTGTC 18602 TTGT \_  
 GGCAGC ACA GGTCTTGA  
 |||| |||||  
 CTGTCG TGT CCAGAACT  
 TTT\_ T  
 GAM1582 KIAA0789 3' TCAAGACCCCTGGTTACC 63687 C TGTACA  
 GG AGCT GGTCTTGA  
 || |||||

CC TTGG CCAGAACT  
 A TCC\_\_\_\_  
 GAM1582 KIAA1157 3' TTCAGCCTGTCAAGCTGCC 72253 T CT  
 GGCAGCTTG ACAGGT TGAA  
 ||||| ||||| ||||  
 CCGTCGAAC TGTCCG ACTT

— —  
 GAM1582 KREMEN 3' TCAAGACCCTCAGGACTGGCC 49409 \_ \_ TACA  
 GGC AG CTTG GGTCTTGA  
 ||| || ||||| |||||  
 CCG TC GGAC CCAGAACT  
 G A TC\_\_\_\_

GAM1582 SLC12A8 3' TCAAGACCCATCCTCCC 44903 C CT TACA  
 GG AG TG GGTCTTGA  
 || || || |||||  
 CC TC AC CCAGAACT  
 C CT \_\_\_\_\_

GAM1582 LOC147136 3' TCAAGACTGTGAGCTGCC 78270 TG ACA  
 GGCAGCT T GGTCTTGA  
 ||||| | |||||  
 CCGTCGA G TCAGAACT  
 GT \_\_\_\_\_

GAM1582 LOC151178 5' AAGACCCACCAAGCTGCC 80147 TACA  
 GGCAGCTTG GGTCTT  
 ||||| |||||  
 CCGTCGAAC CCAGAA  
 CAC\_

GAM1582 LOC201931 3' ACCTGACAAGCTGCC 89107 A  
 GGCAGCTTGT CAGGT  
 ||||| |||||  
 CCGTCGAACA GTCCA

—  
 GAM1582 LOC253216 3' GGACCTGCCAAGCTGCC 94961 TA  
 GGCAGCTTG CAGGTCT  
 ||||| |||||  
 CCGTCGAAC GTCCAGG  
 C\_

GAM1583 DMRT2 3' CACAACAAGCAACAAGAACA 21614 CTATC\_  
 TGTTC CTTGTTGTG  
 |||| |||||  
 ACAAG GAACAACAC  
 AACAAC

GAM1583 F8 3' CACAACAAAATGTAAACAGGG 3725 G CC CC  
 CCC TGTT TAT TTGTTGTG  
 || ||| || |||||  
 GGG ACAA GTA AACAACAC  
 \_ T\_ AA

GAM1583 GJB3 3' TAAGAGACAGGAACACAGG 43770 C A \_  
 CC GTGTTCTC TC CTTG  
 || ||||| || |||

			GG CACAAGGA AG GAAT		
			A C A		
GAM1583	SH3BP2	3'	CAAGGACAGGAACACTGGT	11593	C A
			ACC GTGTTCTCCT TCCTTG		
			TGG CACAAGGA AGGAAC		
			T C		
GAM1583	TEM8	3'	CACCCAGGGATAAAAACA	49851	CC TT
			TGTT TATCCTTG GTG		
			ACAA ATAGGGAC CAC		
			AA C_		
GAM1583	ZNF216	3'	CACAGATAATAGGAACA	20018	CCTTG
			TGTTCTAT TTGTG		
			ACAAGGATA GACAC		
			ATA__		
GAM1583	C20orf142	3'	AAGGAGCAGAAACACAGGT	74763	C C A_
			ACC GTGTT CT TCCTT		
			TGG CACAA GA AGGAA		
			A A CG		
GAM1583	C20orf59	3'	CACACGAGCAGAGAGGAACAC	41991	A __ T
			GTGTTCTCCT TC CTTGT GTG		
			CACAAGGA AG GAGCA CAC		
			G AC _		
GAM1583	CLSTN2	3'	CACAACAAGGACAACAAGGACA	42126	T A____
	C		GTGT CCT TCCTTGTTGTG		
			CACA GGA AGGAACAACAC		
			_ ACAAC		
GAM1583	CLSTN2	3'	CACAACAAGGACAGTCACAAC	42127	_ TC A
			GT GT CT TCCTTGTTGTG		
			CA CA GA AGGAACAACAC		
			A CT C		
GAM1583	CLSTN2	3'	CACAACAAGGACAGTCACAACA	42128	CG__ TC A
	AGG		CC TGT CT TCCTTGTTGTG		
			GG ACA GA AGGAACAACAC		
			AACA CT C		
GAM1583	FLJ10101	5'	CGGGGAGACAGGAACACGGG	45264	A__
			CCCGTGTTCCT TCCTTG		
			GGGCACAAGGA AGGGGC		
			CAG		
GAM1583	HEYL	3'	CACTCAGGACAGGAACAAGG	27391	G A TTT
			CC TGTTCTCCT TCCT G GTG		



			GG ACAAGGA AGGA C CAC	
			A C _T_	
GAM1583	INPP4B	3'	TAATAAACAGGAACAC 13915	ATCC
			GTGTTTCCT TTGTTG	
			CACAAGGA AATAAT	
			CA__	
GAM1583	KIAA0391	3'	CAAGAGACAGGAACAC 27906	A _
			GTGTTTCCT TC CTTG	
			CACAAGGA AG GAAC	
			C A	
GAM1583	KIAA1376	3'	CACAACAAGGAACAAAACA 63621	CCTA
			TGTT TCCTTGTTGTG	
			ACAA AGGAACAACAC	
			AACA	
GAM1583	KIAA1494	3'	CACAACAAAGTAGCAC 68457	C ATCC
			GTGTT CT TTGTTGTG	
			CACGA GA AACAACAC	
			T ____	
GAM1583	LOC147639	3'	CACAATAACAGGGACAC 78378	ATCC
			GTGTTTCCT TTGTTGTG	
			CACAGGGA AATAACAC	
			C__	
GAM1583	LOC219529	3'	ACAGGATAACAGGAACAC 92964	__ T
			GTGTTTCCT ATCCT GT	
			CACAAGGA TAGGA CA	
			CAA _	
GAM1584	ADH4	3'	TAAAAAGATTTTACTGGA 5408	CGT
			TCCAGTGG TCTTTTAA	
			AGGTCATT AGAAAAAT	
			TTT	
GAM1584	B4GALT2	3'	AGTAAAAAACGTGAATGGA 47580	GTG CT
			TCCA GCGTT TTTTACT	
			AGGT TGCAA AAAATGA	
			AAG _	
GAM1584	CTBP1	3'	AAAAAGAAAACCTGAAGGAG 67941	AGT_ CG
			CTCC GG TTCTTTTT	
			GAGG CC AAGAAAAA	
			AAGT AA	
GAM1584	ENPP3	3'	TAAAAAGAACAGCAGAGAG 17226	CAGTG _
			CTC GC GTTCTTTTAA	

			GAG CG CAAGAAAAAT		
			AGA__ A		
GAM1584 F8	3'	TAAAAAATAAGTCAGGAGGA 3732		AG	GTTC_
		TCCTCC TGGC TTTTTA			
		AGGAGG ACTG AAAAAT			
		__ AATAA			
GAM1584 GK	3'	AGCAAAAAGAATGCTAT 3911		A	
		GTGGCGTTCTTTTT CT			
		TATCGTAAGAAAAA GA			
		C			
GAM1584 ID4	3'	GAAAAAAGCCACCGGAGGA 7755		A	GTTC
		TCCTCC GTGGC TTTT			
		AGGAGG CACCG AAAAG			
		C AAA_			
GAM1584 PITX1	3'	GAAAAAGACGTCGGAG 10599	AGT T A		
		CTCC GCGT CTTTTT C			
		GAGG CTGCA GAAAAA G			
		__ _ C			
GAM1584 TDG	3'	GAAAAAGATGCTGGAG 12191	GCGT A		
		CTCCAGTG TCTTTT C			
		GAGGTCGT AGAAAAA G			
		__ C			
GAM1584 XRCC2	3'	AGCAAAAAGAACAAAGCTGGAG 18318	GGC A		
G		CCTCCAGT GTTCTTTT CT			
		GGAGGTCG CAAGAAAAA GA			
		AAA C			
GAM1584 DKFZP727M111	5'	AAAAGGAAAAGCCCTGAAG 31401	C T G_		
		CT CAG GGC TTCTTTT			
		GA GTC CCG AAGGAAAA			
		A _ AA			
GAM1584 ELKS	3'	AGTGGTCAACGCCCTGGAAGA 30501	C T CTTT		
		TC TCCAG GCGT TTACT			
		AG AGGTC CCGCAA GGTGA			
		A _ CT_			
GAM1584 FLJ10648	3'	AGCAAAAAGAACAAAGTCCTGG 36378	T _ A		
AGGA		TCCTCCAG GGC GTTCTTTT CT			
		AGGAGGTC CTG CAAGAAAAA GA			
		_ AAA C			
GAM1584 FLJ20151	3'	AAAGACCCTGGAGGA 34648	T CGT		
		TCCTCCAG GG TCTTT			

AGGAGGTC CC AGAAA

GAM1584 FLJ20435 3' TAAAAAGAGCCATCTGGAGGA 35162 \_ GT  
TCCTCCAG TGGC TCTTTTTA  
||||||| ||| |||||||  
AGGAGGTC ACCG AGAAAAAT

T \_  
GAM1584 MDS024 3' AAAAAGAATTGCCAAGGA 41522 AG \_  
TCC TGGCG TTCTTTTT  
||| ||||| |||||||  
AGG ACCGT AAGAAAAA

A\_ T  
GAM1584 ShrmL 5' AGAGCGCCACTGAAGGA 40463 C  
TCCT CAGTGGCGTTCT  
||| |||||||||  
AGGA GTCACCGCGAGA  
A

GAM1584 SIAT8C 5' TAAAAAAGCCCCACAGAGGA 31883 CA C C  
TCCTC GTGG GTT TTTTTA  
||||| ||| ||| |||||  
AGGAG CACC CGA AAAAAT  
A\_ C \_

GAM1584 VEST1 5' AAAAAGATGCACTGGGGA 53678 T G T  
TCC CCAGTG CGT CTTTTT  
||| ||||| ||| |||||  
AGG GGTCAC GTA GAAAAA

\_ \_ \_  
GAM1584 ZFD25 5' AAAAAGAGCCCTGGA 32573 T GT  
TCCAG GGC TCTTTTT  
||||| ||| |||||||  
AGGTC CCG AGAAAAA

\_ \_  
GAM1584 LOC124626 3' AGTAAGACCAAACCACTGGA 74313 CGTTCT  
TCCAGTGG TTTTACT  
||||||| |||||||  
AGGTCACC AGAATGA  
AAACC\_

GAM1584 LOC144577 3' TAAAAAGAAGCCACAAAGAG 76902 CA\_ G  
CTC GTGGC TTCTTTTTA  
||| ||||| |||||||  
GAG CACCG AAGAAAAAT  
AAA \_

GAM1584 LOC145837 5' AGCAAAAAGAACCAAAGAGGA 83542 CAG CG A  
TCCTC TGG TTCTTTTT CT  
||||| ||| ||||||| ||  
AGGAG ACC AAGAAAAA GA  
AA\_ \_ C

GAM1584 LOC151194 3' TAAAAAACTGGGGA 59215 T GGC GTTC  
TCC CCAGT TTTTTA  
||| ||||| |||||||

		AGG GGTCA	AAAAAT		
		— A —			
GAM1584	LOC154789 5'	AGTAAATCTCAGGCCACTAGA	81131	C	GTTCT_
	G	CTC AGTGGC	TTTTACT		
		GAG TCACCG	AAAATGA		
		A	GACTCT		
GAM1584	LOC197322 3'	AAAGACTCCACTGGAGGA	89736	C T	
		TCCTCCAGTGG	GT CTTT		
		AGGAGGTCACC	CA GAAA		
		T —			
GAM1584	LOC221596 3'	TAAAAACCTCACACTGGAGAGA	91980	—	GCGTTC
		TC CTCCAGTG	TTTTTA		
		AG GAGGTCAC	AAAAAT		
		A	ACTCC_		
GAM1584	LOC91796 3'	AGCAAAAAGAACAAGGCTGGA	67208	GGC	A
		TCCAGT	GTTCTTTTT CT		
		AGGTCG	CAAGAAAAA GA		
		GAA	C		
GAM1584	LOC92539 5'	TAAAAGTGTCAGTG	69638	TT	
		CAGTGGCG	CTTTTTA		
		GTCAGTGT	GAAAAAT		
		—			
GAM1585	CCR9	3' GATCTGCAGGTCTTGCCA	21815	A	GTTG A
		TGG CAAGAT	GCA ATC		
		ACC GTTCTG	CGT TAG		
		— GA — C			
GAM1585	CCR9	3' GATCTGCAGGTCTTGCCA	48299	A	GTTG A
		TGG CAAGAT	GCA ATC		
		ACC GTTCTG	CGT TAG		
		— GA — C			
GAM1585	MAPK9	3' GTAATTTGGTGTCTGTCCA	57413	A TG TGG	C
		TGGACA GA T	CAAAT AC		
		ACCTGT CT G	GTTTA TG		
		— GT — A			
GAM1585	MAPK9	3' GTAATTTGGTGTCTGTCCA	57423	A TG TGG	C
		TGGACA GA T	CAAAT AC		
		ACCTGT CT G	GTTTA TG		
		— GT — A			
GAM1585	MAPK9	3' GTAATTTGGTGTCTGTCCA	57418	A TG TGG	C
		TGGACA GA T	CAAAT AC		

ACCTGT CT G GTTTA TG  
 \_ GT \_ A  
 GAM1585 MAPK9 3' GTAATTTGGTGTCTGTCCA 10853 A TG TGG C  
 TGGACA GA T CAAAT AC  
 ||||| || | ||||| ||  
 ACCTGT CT G GTTTA TG  
 \_ GT \_ A  
 GAM1585 TCF2 3' AGTGATTTGCCAAAGTG 21371 AGATG  
 CA TTGGCAAATCACT  
 || ||||| |||||  
 GT AACCGTTTAGTGA  
 GA \_  
 GAM1585 AAK1 3' TGAGAAAACATTTTGCCCA 29857 A GGCAAA  
 TGG CAAGATGTT TCA  
 ||| ||||| |||  
 ACC GTTTTACAA AGT  
 C AAG \_  
 GAM1585 ATP8A1 3' TGACCTGGTATCTTGCCA 20339 A TT CAAA  
 TGG CAAGATG GG TCA  
 ||| ||||| || |||  
 ACC GTTCTAT TC AGT  
 \_ GG C \_  
 GAM1585 CBX1 3' TGATTTGCTTCTATGTCCA 22328 \_ TGTT  
 TGGACA AGA GGCAAATCA  
 ||||| ||| ||||| |||  
 ACCTGT TCT TCGTTTAGT  
 A \_  
 GAM1585 CSMD1 3' AGCGATCTTCAACCTTGTCTA 52641 AT CAA A  
 TGGACAAG GTTGG ATC CT  
 ||||| ||||| ||| |||  
 ATCTGTTT CAACT TAG GA  
 \_ TC \_ C  
 GAM1585 DCNP1 3' TGCCAACACTCCATCCA 55629 CA \_ A  
 TGGA AG TGTTGGCA  
 |||| || ||||| |||  
 ACCT TC ACAACCGT  
 ACC \_  
 GAM1585 DKFZP564F013 3' ATTTGCCAAGTGTCCA 94205 AGATG  
 TGGACA TTGGCAAAT  
 ||||| ||||| |||  
 ACCTGT AACCGTTTA  
 G \_  
 GAM1585 DKFZP566C243 5' GCCCACATCTTGCCCA 31170 A T  
 TGG CAAGATGT GGC  
 ||| ||||| ||| |||  
 ACC GTTCTACA CCG  
 C C  
 GAM1585 EIF5 3' TGACAGTGCAACATCTTAACCA 8761 AC G AA\_  
 TGG AAGATGTTG CA TCA  
 ||| ||||| || |||

ACC TTCTACAAC GT AGT  
 AA \_ GAC  
 GAM1585 IDI2 3' GTGACTCGACGTTTATCCA 52697 CA CAAA  
 TGGAGATGTTGG TCAC  
 |||| ||||| ||||  
 ACCT TTTGCAGCT AGTG  
 A\_ C\_\_  
 GAM1585 KIAA0022 3' AGTGATTTTAAGCATCCCGTC 29659 AA GGC  
 GAC GATGTT AAATCACT  
 ||| ||||| |||||  
 CTG CTACGA TTTAGTGA  
 CC AT\_  
 GAM1585 KIAA0429 3' TTGCCAATGTGTTTACCA 28564 AC G  
 TGG AAATGTTGGCAA  
 ||| |||||  
 ACC TT TGTAACCGTT  
 AT G  
 GAM1585 KIAA1939 3' AGTAATTTGCTGAGCATCATCC 45761 CAA \_ C  
 A TGGAGATGTT GGCAAAT ACT  
 |||| ||||| ||||| ||||  
 ACCT CTACGA TCGTTTA TGA  
 A\_ G A  
 GAM1585 NMT2 3' GTGATGGTACATTTGTCCA 16668 A TGGCAA  
 TGGACA GATGT ATCAC  
 ||||| ||||| |||||  
 ACCTGT TTACA TAGTG  
 \_ TGG\_\_  
 GAM1585 PBEF 3' AGTGATTTAACAGTCTTTCCA 19233 C GT GC  
 TGGAAAGAT TG AAATCACT  
 |||| ||||| |||||  
 ACCT TTCTG AC TTTAGTGA  
 \_ \_ AA  
 GAM1585 LOC148823 3' TGCCAACATCTCCCCA 59212 ACA  
 TGG AGATGTTGGCA  
 ||| |||||  
 ACC TCTACAACCGT  
 CC\_  
 GAM1585 LOC153910 3' AGTGATCCACCAACATGGCATC 80994 CAAG CAA  
 T GGA ATGTTGG ATCACT  
 ||| ||||| |||||  
 TCT TACAACC TAGTGA  
 ACGG ACC  
 GAM1586 CDH10 3' TAGTTCTCCCTTAAGCAACCT 22058 CG CAGTGT A  
 AGG GCT GA GAACTA  
 ||| ||| |||||  
 TCC CGA CTCTTGAT  
 AA ATTCC\_ \_  
 GAM1586 DACH 3' TAGTTCTTCCATAACCACT 54971 C CTCA T  
 AGG GG GTG GAAGAACTA  
 ||| || |||||

TCC CC TAC CTTCTTGAT  
 A AA\_\_ \_  
 GAM1586 HPS1 3' TCTTCCAGAGCTGCCT 3969 AG T  
 AGGCGGCTC TG GAAGA  
 ||||| || ||||  
 TCCGTCGAG AC CTTCT

— —  
 GAM1586 PCK1 5' TCTTCAGGCTGCCT 52264 CAGTG  
 AGGCGGCT TGAAGA  
 ||||| ||||  
 TCCGTCGG ACTTCT

— —  
 GAM1586 RORB 5' AGCTCTTCGCCGACCACCT 22606 C C AGT A  
 AGG GG TC GTGAAGA CT  
 ||| || ||||| ||  
 TCC CC AG CGCTTCT GA  
 A \_ C\_ C

GAM1586 SPTBN4 3' AGTCCCCATGGCCGCCT 47386 CAGT AA A  
 AGGCGGCT GTG GA CT  
 ||||| ||| |||  
 TCCGCCGG TAC CT GA  
 — CC \_

GAM1586 ZNF200 3' GTAGTTCTGAATTCCCAAGCTG 12909 CAGT\_ GA  
 CCT AGGCGGCT GT AGAACTAC  
 ||||| || |||||  
 TCCGTCGA TA TCTTGATG  
 ACCCT AG

GAM1586 BTN2A1 3' GTAATTCTCAGTGTGTGAGCTG 54342 \_ TG GA C  
 CCT AGGCGGCTCA G T AGAA TAC  
 ||||| ||| |||  
 TCCGTCGAGT T G TCTT ATG  
 G GT AC A

GAM1586 CFP1 3' TAGCTCCGTCAAGCTGCCT 58771 CAGTG A\_ A  
 AGGCGGCT TGA GA CTA  
 ||||| ||| |||  
 TCCGTCGA ACT CT GAT  
 — GC C

GAM1586 FENS-1 3' TGGGAGTCACACAAGCCGCCT 40445 CA AGAA  
 AGGCGGCT GTGTGA CTA  
 ||||| ||||| |||  
 TCCGCCGA CAACT GGT  
 A\_ GAG\_

GAM1586 FLJ14082 3' AGTTCTTCCTAAGGCACCC 46668 CG CAG T  
 GG GCT TG GAAGAACT  
 || ||| || |||||  
 CC CGG AT CTTCTTGA  
 CA A\_ C

GAM1586 FLJ20539 5' TGGGGCCACCTGAGCCGCC 35363 T AAGAA  
 GGCGGCTCAG GTG CTA  
 ||||| ||| |||

CCGCCGAGTC CAC GGT  
 \_ CGG\_  
 GAM1586 FLJ22301 3' AGCCCTTCACGTAGCCTCCT 45756 C CAG AA  
 AGG GGCT TGTGAAG CT  
 ||| ||| ||||| ||  
 TCC CCGA GCACTTC GA  
 T T\_\_ CC  
 GAM1586 HEMGN 5' TAGAGAAAAAACTGAGCCACC 37380 C GTGAAGAA  
 T AGG GGCTCAGT CTA  
 ||| ||||| |||  
 TCC CCGAGTCA GAT  
 A AAAAAAGA  
 GAM1586 KIAA0379 3' GTAGTTCTTGCGAATGCCACC 68150 C TCAG G  
 GG GGC TGT AAGAACTAC  
 || ||| ||| |||||  
 CC CCG GCG TTCTTGATG  
 A TAA\_\_ \_  
 GAM1586 KIAA0494 3' TCTCACACTGACCACC 28750 C C A  
 GG GG TCAGTGTGA GA  
 || ||| ||||| ||  
 CC CC AGTCACACT CT  
 A \_ \_  
 GAM1586 LACE1 3' CTTACATTAAACCACCT 91837 C CTC  
 AGG GG AGTGTGAAG  
 ||| || |||||  
 TCC CC TTACACTTC  
 A AAA  
 GAM1586 NAPG 3' TAGTTCTTCAGGTAGCACCT 96730 CG CAG G  
 AGG GCT T TGAAGAACTA  
 ||| ||| | |||||  
 TCC CGA G ACTTCTTGAT  
 A\_ T\_\_ G  
 GAM1586 PRO2405 5' AGGAGCACATTAAGCCGCCT 37798 C AAGAA  
 AGGCGGCT AGTGTG CT  
 ||||| ||||| ||  
 TCCGCCGA TTACAC GA  
 A GAG\_  
 GAM1586 LOC121219 5' AGTCCTCAGCGAAGCCGCCT 74040 CA G A A  
 AGGCGGCT GT TGA GA CT  
 ||||| || ||| || ||  
 TCCGCCGA CG ACT CT GA  
 AG \_ C \_  
 GAM1586 LOC146990 3' CTTACACCCAGCCGCCT 83886 CA  
 AGGCGGCT GTGTGAAG  
 ||||| |||||  
 TCCGCCGA CCACTTC  
 CC  
 GAM1586 LOC148371 5' TTCCA CTGAGCCACC 78809 C T  
 GG GGCTCAGTG GAA  
 || ||||| |||



		CC CCGAGTCAC CTT		
		A _		
GAM1586	LOC152274 3'	AGTCCCTGCAGGAGCAGCCT	80498	G AG AA A
		AGGC GCTC TGTG GA CT		
		TCCG CGAG ACGT CT GA		
		A G_ CC _		
GAM1586	LOC200261 3'	AGTTGCTCCACTGAGTCACC	88653	C T AG
		GG GGCTCAGTG GA AACT		
		CC CTGAGTCAC CT TTGA		
		A _ CG		
GAM1586	LOC201562 5'	GTAGTCCGGCCCGAGCCGCT	88975	AGT GAA A
		GGCGGCTC GT GA CTAC		
		TCGCCGAG CG CT GATG		
		CC_ GC_ _		
GAM1586	LOC202347 3'	TCATGGCAGAGCCGCCT	90349	A _
		AGGCGGCTC GT GTGA		
		TCCGCCGAG CG TACT		
		A G		
GAM1586	LOC220370 3'	TCACCTCACTGAGCCACCT	92834	C _
		AGG GGCTCAGT GTGA		
		TCC CCGAGTCA CACT		
		A CTC		
GAM1586	LOC221838 5'	TTCCACTGAGCCACC	92546	C T
		GG GGCTCAGTG GAA		
		CC CCGAGTCAC CTT		
		A _		
GAM1586	LOC51716 3'	AGTTCCACACTGAGCGCCT	32786	G AA
		AGGCG CTCAGTGTG GAACT		
		TCCGC GAGTCACAC CTTGA		
		_ _		
GAM1586	LOC89919 3'	CTTCCACTGAGCCACC	60722	C T
		GG GGCTCAGTG GAAG		
		CC CCGAGTCAC CTTC		
		A _		
GAM1586	LOC91947 3'	TAGTTCTTTTATTGTAAGCCGC	67614	_ T
	T	GGCGGCT CAGTG GAAGAACTA		
		TCGCCGA GTTAC TTTCTTGAT		
		AT _		
GAM1587	APOB 3'	CCTATATTGATAAAACCAT	4604	CC GG
		GTGGTTTTA TAG GTAGG		

			TACCAAAAT GTT TATCC		
			A_ A_		
GAM1587	ATP2A3	3'	CACCCCCAAATCACG 17719	TACCTA	A
			CGTGGTTT GGGGT G		
			GCACTAAA CCCCCA C		
			C_____ C		
GAM1587	CYBB	3'	CCCACCCCTTGGAGCCAC 76355	CCT	A
			GTGGTTTTTA AGGGGT GG		
			CACCGAGGT TCCCCA CC		
			_____ C		
GAM1587	DPP4	3'	CTTCTAAGTAAAACCAC 8658	C	
			GTGGTTTTTAC TAGGGG		
			CACCAAAATG ATCTTC		
			A		
GAM1587	DRIL1	5'	CACCCCTAGCGCCG 17826	T TTTAC	A
			CG GGT CTAGGGGT G		
			GC CCG GATCCCCA C		
			_ C_____ C		
GAM1587	EFEMP1	5'	CCTACCACATGCAGATAAAACC 38154	C AGG_____	
	A		TGGTTTTTA CT GGTAGG		
			ACCAAAAT GA CCATCC		
			A CGTACA		
GAM1587	FZD10	3'	CCCACCCCCAGGAAGGCCAC 23238	A A A	
			GTGGTTTTT CCT GGGGT GG		
			CACCGGAA GGA CCCCCA CC		
			_ C C		
GAM1587	HAS3	3'	CCCACCCCTAAGTAGTCATCA 18037	T_ C	A
			TGGT TTAC TAGGGGT GG		
			ACTA GATG ATCCCCA CC		
			CT A C		
GAM1587	HYOU1	3'	CCCACCCCTAGTGGCCA 59649	TTAC	A
			TGGTT CTAGGGGT GG		
			ACCGG GATCCCCA CC		
			T_____ C		
GAM1587	KCNA6	3'	CCTAGACAGGTAAAAGCAC 9511	G AG_____	
			GTG TTTTACCT GGG		
			CAC AAAATGGA TCC		
			G CAGA		
GAM1587	KCNK2	3'	CACCCCTAGGCTCAC 26420	TTTTA	A
			GTGG CCTAGGGGT G		

CACT GGATCCCCA C  
 C\_\_\_\_\_ C  
 GAM1587 MGAT5 5' CCCACCCCTGGTAACCAC 10022 TT T A  
 GTGGT TACC AGGGGT GG  
 |||| ||| ||||| ||  
 CACCA ATGG TCCCCA CC  
 \_\_\_\_\_ C  
 GAM1587 RFX1 3' CCTACCCCCAGCAACC 11311 TTAC A  
 GGTT CT GGGGTAGG  
 |||| || |||||  
 CCAA GA CCCCATCC  
 C\_\_\_\_\_ C  
 GAM1587 SHMT2 3' CCTACCCCCAAGAGCTCAGCG 18264 \_\_\_\_\_ ACCTA  
 CGT GGTTTT GGGGTAGG  
 ||| ||||| |||||  
 GCG TCGAGA CCCCATCC  
 AC AC\_\_\_\_  
 GAM1587 SLC25A12 3' CCCAGGGAAAAAACCAC 13524 A\_ A  
 GTGGTTTT CCT GGG  
 ||||| ||| |||  
 CACCAAAA GGG CCC  
 AA A  
 GAM1587 TNFSF8 3' CCCACCCCTAGGAACCCCCAGG 6965 G TTTTA A  
 C TGG CCTAGGGGT GG  
 ||| ||||| ||  
 G ACC GGATCCCCA CC  
 G CCAA C  
 GAM1587 ZNF9 3' CCCATGTAGGAGGTAAAACCA 12771 AG\_\_\_\_  
 TGGTTTTACCT GGG  
 ||||| |||  
 ACCAAAATGGA CCC  
 GGATGTA  
 GAM1587 AP3M1 3' CCCACCCCCAGAAGTTTAC 23915 T AC A A  
 GTGG TTT CT GGGGT GG  
 ||| ||| || ||||| ||  
 CATT GAA GA CCCCCA CC  
 T \_\_\_\_\_ C C  
 GAM1587 ASE-1 5' CCTACCCCTTTGGATCCACG 23948 TTTTA T\_  
 CGTGG CC AGGGGTAGG  
 |||| || |||||  
 GCACC GG TCCCCATCC  
 TA\_\_\_\_ TT  
 GAM1587 C20orf112 3' CCCACCCCCAGATAATTACC 54641 T\_ C A A  
 GGT TTA CT GGGGT GG  
 ||| ||| || ||||| ||  
 CCA AAT GA CCCCCA CC  
 TT A C C  
 GAM1587 CDH26 3' CTTGAACCAAAGCAAAACCAC 41466 ACCTA GG  
 GTGGTTTT GG TAGG  
 ||||| || |||

CACCAAAA CC GTTC  
CGAAA AA  
GAM1587 CDK5RAP3 3' CTACCAGGCGAAAAACCAC 47282 A\_ AGG  
GTGGTTTT CCT GGTAG  
||||||| ||| |||||  
CACCAAAA GGA CCATC  
GC \_\_\_\_  
GAM1587 DKFZP566G1424 5' CCCACCCCCAGATAATTACC 84780 T\_ C A A  
GGT TTA CT GGGGT GG  
||| ||| || ||||| ||  
CCA AAT GA CCCCCA CC  
TT A C C  
GAM1587 ESM1 5' CCACCAGCAAAGACCACG 22877 AC A \_  
CGTGGTTTT CT GG GG  
||||||| || || ||  
GCACCAGAA GA CC CC  
AC \_ A  
GAM1587 FBX30 3' CCCACCCCTAGAACTGCCA 52585 TTTAC A  
TGGT CTAGGGGT GG  
||||| ||||| ||  
ACCG GATCCCCA CC  
TCAA\_ C  
GAM1587 FTSJ3 3' CCTATTCCTAAATAAAACCAGG 34454 G CC  
C TGGTTTTA TAGGGGTAGG  
| ||||| |||||  
G ACCAAAAT ATCCTTATCC  
G AA  
GAM1587 GFR 3' CCCGTAGGCAAAATCAC 24470 A G  
GTGGTTTT CCTA GGG  
||||||| ||| |||  
CACTAAAA GGAT CCC  
C G  
GAM1587 HSXIAPAF1 3' CCATCTATGACAAAACCAC 34030 ACCTAG A  
GTGGTTTT GGGT GG  
||||||| ||| ||  
CACCAAAA TCTA CC  
CAGTA\_ \_  
GAM1587 KIAA0450 5' CCCACCCCCAGAAGCCATG 27627 TAC A A  
CGTGGTTT CT GGGGT GG  
||||||| || ||||| ||  
GTACCGAA GA CCCCCA CC  
\_ C C  
GAM1587 KIAA0494 5' CACCCCTAGGTGGGA 28739 A  
TTTTACCTAGGGGT G  
||||||| ||||| |  
AGGGTGGATCCCCA C  
C  
GAM1587 KIAA0530 3' CCTTAAATAAAATCAC 70866 CC  
GTGGTTTTA TAGGG  
||||||| |||||

		CACTAAAAT ATTCC		
		AA		
GAM1587	KIAA1579	3' CTGCAAGTAAAACCCAC	36608	CTAGGG
		GTGGTTTTAC	GTAG	
		CACCAAATG	CGTC	
		AA__		
GAM1587	MGC13138	3' CCTAGGCTCCGACAAAACCCAC	53016	ACCTA _
		GTGGTTTT	GGGGT AGG	
		CACCAAAA	CCTCG TCC	
		CAG__	GA	
GAM1587	MIG2	3' CCTACCCCCAAATAAATCAGG	72424	G TACCTA
		C TGGTTT	GGGGTAGG	
		G ACTAAA	CCCCATCC	
		G TAAAC_		
GAM1587	N4BP3	3' CCCAGAATAAAACCATG	66258	C_ A
		CGTGGTTTTTA	CT GGG	
		GTACCAAAT	GA CCC	
		AA _		
GAM1587	RAI15	3' CCTACCCCCAGATTAGCACCAC	66667	T C_ A
		GTGGT TTA	CT GGGGTAGG	
		CACCA GAT	GA CCCCATCC	
		C TA C		
GAM1587	RERG	3' CCTTAGCAGAAAAACCCAC	51896	AC__
		GTGGTTTT	CTAGGG	
		CACCAAAA	GATTCC	
		AGAC		
GAM1587	RNF24	3' CTTGAGCCAAGTAAAACCA	23316	CTA GG
		TGGTTTTAC	GG TAGG	
		ACCAAATG	CC GTTC	
		AA_ GA		
GAM1587	VMP1	3' CCCATTTCTAAAAAAAACCCAC	48188	ACC_ GG A
		GTGGTTTT	TAG GT GG	
		CACCAAAA	ATC TA CC	
		AAAA TT C		
GAM1587	LOC144473	3' CCCACCCCCAAAAGCTAC	83069	ACCTA A
		GTGGTTTT	GGGGT GG	
		CATCGAAA	CCCCA CC	
		AC__ C		
GAM1587	LOC146515	5' CCCGGGAGTAAAACCCAC	77963	_ A
		GTGGTTTTAC	CT GGG	

CACCAAATG GG CCC  
A G  
GAM1587 LOC147077 3' CTCCAAGTAAAGCCACG 78250 CTA  
CGTGGTTTTAC GGGG  
||||||| |||  
GCACCGAAATG CCTC  
AA\_  
GAM1587 LOC149935 3' CCTGTCAGGTGAAAACCAC 60298 \_ AGG GT  
GTGGTTT TACCT G AGG  
||||| ||| | |||  
CACCAA GTGGA C TCC  
A \_ TG  
GAM1587 LOC152897 5' CCCACCCCTAGATATGCC 80724 TT C A  
GGT TA CTAGGGGT GG  
||| || ||||| ||  
CCG AT GATCCCCA CC  
T\_ A C  
GAM1587 LOC201911 3' CCTGAAAGGCAAAACCGCG 90260 A A\_  
CGTGGTTTT CCT GGG  
||||||| ||| |||  
GCGCCAAAA GGA TCC  
C AAG  
GAM1587 LOC219401 5' CCTGTAAATAAACACCAC 92814 \_ CC G  
GTGGT TTTA TA GGG  
||||| ||| ||| |||  
CACCA AAAT AT TCC  
C AA G  
GAM1587 LOC221454 5' CCCACCCCTAGGCCTGCAC 92301 GTTTTA A  
GTG CCTAGGGGT GG  
||| ||||| ||  
CAC GGATCCCCA CC  
GTCC\_ C  
GAM1587 LOC255030 3' CCTGGGATGAGACAAAAGCCAC 97268 A\_\_\_\_\_  
GTGGTTTT CCTAGG  
||||| |||||  
CACCGAAA GGGTCC  
ACAGAGTA  
GAM1587 LOC256537 5' CCCACCCGCTGCCAAACCACG 95225 TACC \_ A  
CGTGGTTT TAG GGGT GG  
||||| ||| ||| |||  
GCACCAA GTC CCA CC  
CC\_ G C  
GAM1587 LOC51064 3' CCTACCCCCAAGGATGCCAGG 31920 G TTTA A\_  
C TGGT CCT GGGGTAGG  
| ||| ||| |||||  
G ACCG GGA CCCCATCC  
G TA\_ AC  
GAM1587 LOC51152 3' CCCACTGACAAGACCAC 32451 ACC \_  
GTGGTTTT TAG GGG  
||||| ||| |||

			CACCAGAA GTC CCC		
			CA_ A		
GAM1587	LOC90906	5'	CCGTAAGGAAAACAC 64295	A _ G	
			GTGGTTTT CCT A GG		
			CACCAAAA GGA T CC		
			_ A G		
GAM1588	ADAM12	3'	AACCTATTTCTTAAACACTTG 12965	C C _	
			CAAGTG TT AGAA TAGGTT		
			GTTCAC AA TCTT ATCCAA		
			A T T		
GAM1588	ADD1	3'	AACCTTCAGAAGCACTCGG 26375	A A AT	
			TC AGTGCTTC GA AGGTT		
			GG TCACGAAG CT TCCAA		
			C A _		
GAM1588	ALDOA	5'	AATTCCTCTGAAGCACCGGA 3466	AA AT	
			TC GTGCTTCAGA AGGTT		
			AG CACGAAGTCT TTAA		
			GC CC		
GAM1588	BHLHB3	3'	AACCTATTCTGAAGTGGTT 47763	G	
			AA TGCTTCAGAATAGGTT		
			TT GTGAAGTCTTATCCAA		
			G		
GAM1588	CABC1	5'	AACCCACCTGCAGCACTTGG 39651	T AATA	
			TCAAGTGCT CAG GGTT		
			GGTTCACGA GTC CCAA		
			C CAC_		
GAM1588	GYPA	3'	AACCTATTCTATTGTATT 87448	TTC	
			AGTGC AGAATAGGTT		
			TTATG TCTTATCCAA		
			TTA		
GAM1588	HSD17B2	5'	CTGGCCCTGAGCACTTGA 9281	T AA_	
			TCAAGTGCT CAG TAG		
			AGTTCACGA GTC GTC		
			_ CCG		
GAM1588	LOH11CR2A	3'	AACCTATTCCCTTTCTTGA 27535	TGCTTCA	
			TCAAG GAATAGGTT		
			AGTTC CTTATCCAA		
			TTTCC_		
GAM1588	MSR1	3'	ACCCATAGGCACTTGG 56949	CAGA A	
			TCAAGTGCTT AT GGT		

		GGTTCACGGA TA CCA	
		____ C	
GAM1588	MSR1	3' ACCCATAGGCACTTGG 56957	CAGA A
		TCAAGTGCTT AT GGT	
		GGTTCACGGA TA CCA	
		____ C	
GAM1588	RAD17	3' AACCTACTCTTCTGTCATCTTG 55864	TGCTT ____
	A	TCAAG CAGAA TAGGTT	
		AGTTC GTCTT ATCCAA	
		TACT_ CTC	
GAM1588	RAD17	3' AACCTACTCTTCTGTCATCTTG 55866	TGCTT ____
	A	TCAAG CAGAA TAGGTT	
		AGTTC GTCTT ATCCAA	
		TACT_ CTC	
GAM1588	RAD17	3' AACCTACTCTTCTGTCATCTTG 55871	TGCTT ____
	A	TCAAG CAGAA TAGGTT	
		AGTTC GTCTT ATCCAA	
		TACT_ CTC	
GAM1588	RAD17	3' AACCTACTCTTCTGTCATCTTG 55869	TGCTT ____
	A	TCAAG CAGAA TAGGTT	
		AGTTC GTCTT ATCCAA	
		TACT_ CTC	
GAM1588	RAD17	3' AACCTACTCTTCTGTCATCTTG 55875	TGCTT ____
	A	TCAAG CAGAA TAGGTT	
		AGTTC GTCTT ATCCAA	
		TACT_ CTC	
GAM1588	RAD17	3' AACCTACTCTTCTGTCATCTTG 55862	TGCTT ____
	A	TCAAG CAGAA TAGGTT	
		AGTTC GTCTT ATCCAA	
		TACT_ CTC	
GAM1588	RAD17	3' AACCTACTCTTCTGTCATCTTG 11211	TGCTT ____
	A	TCAAG CAGAA TAGGTT	
		AGTTC GTCTT ATCCAA	
		TACT_ CTC	
GAM1588	RAD17	3' AACCTACTCTTCTGTCATCTTG 55873	TGCTT ____
	A	TCAAG CAGAA TAGGTT	
		AGTTC GTCTT ATCCAA	
		TACT_ CTC	
GAM1588	RRM2B	3' AACCTATTCTAAACAATTTG 67822	GCTTC
		CAAGT AGAATAGGTT	



GTTTA TCTTATCCAA  
 ACAA  
 GAM1588 SLC4A4 3' CTGTGTTAAAGTACTTGA 13636 CAGA  
 TCAAGTGCTT ATAG  
 ||||| |||  
 AGTTCATGAA TGTC  
 ATTG  
 GAM1588 ABCA5 3' AACCAAGAACGCACTTGA 37911 \_ AGAATA  
 TCAAGTGC TTC GGTT  
 ||||| || |||  
 AGTTCACG AAG CCAA  
 C AA\_\_\_\_  
 GAM1588 AGXT2L1 3' TTCTGAAGCTACCTGA 48399 A \_  
 TCA GT GCTTCAGAA  
 || || |||||  
 AGT CA CGAAGTCTT  
 C T  
 GAM1588 AK5 3' AACCTATTCTCCACACTT 23908 CTC  
 AAGTG AGAATAGGTT  
 |||| |||||  
 TTCAC TCTTATCCAA  
 ACC\_  
 GAM1588 C3IP1 3' AACCTAGAACAGCACTGA 41278 A TCAGAA  
 TCA GTGCT TAGGTT  
 || |||| |||||  
 AGT CACGA ATCCAA  
 \_ CAAG\_\_\_\_  
 GAM1588 FLJ11029 5' AACCCAGTCTCGCTAAAGCACT 60969 C\_\_\_\_ ATA  
 T AAGTGCTT AGA GGTT  
 ||||| || |||  
 TTCACGAA TCT CCAA  
 ATCGC GAC  
 GAM1588 FOLR3 3' AACCTATTCTAATAGAC 5861 G TC\_  
 GT CT AGAATAGGTT  
 || || |||||  
 CA GA TCTTATCCAA  
 \_ TAA  
 GAM1588 KIAA0451 5' ACCTATTCTGACTTG 29101 TGCT  
 CAAG TCAGAATAGGT  
 |||| |||||  
 GTTC AGTCTTATCCA  
 \_\_\_\_\_  
 GAM1588 KIAA1332 3' AACCTCAGGAGCACCTGA 71156 A A ATA  
 TCA GTGCTTC GA GGTT  
 || ||||| || |||  
 AGT CACGAGG CT CCAA  
 C A C\_\_\_\_  
 GAM1588 MGC2488 3' CTAGGCTGAAGCATCTGA 43867 AG AA  
 TCA TGCTTCAG TAG  
 || ||||| |||

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          AGT ACGAAGTC ATC
            CT   GG
GAM1588 OR2C3  3' TGTTCCTGAAGTACCTGA  75450  A
              TCA GTGCTTCAGAATA
              ||| |||||
              AGT CATGAAGTCTTGT
                C
GAM1588 PRAM-1 3' GTTGCTGAAGCAGCTGA  69382  AG  _
              TCA TGCTTCAG AAT
              ||| ||||| |||
              AGT ACGAAGTC TTG
                CG   G
GAM1588 SEC3   3' AACTGAATGAAGCATTTGA  36809      GAATA
              TCAAGTGCTTCA  GGTT
              ||||| ||| |||
              AGTTTACGAAGT  TCAA
                AAG__
GAM1588 LOC219654 3' ACCCTCTGAGCACTT  91297  T  ATA
              AAGTGCT CAGA  GGT
              ||||| ||| |||
              TTCACGA GTCT  CCA
                _  C__
GAM1588 LOC220766 5' CTACTGAAGCACTGA  90797  A  AA
              TCA GTGCTTCAG TAG
              ||| ||||| |||
              AGT CACGAAGTC ATC
                _  _
GAM1588 LOC93444 3' AACCCAGGTGAAGGCACTT  72383  _  GAATA
              AAGTGC TTCA  GGTT
              ||||| ||| |||
              TTCACG AAGT  CCAA
                G  GGACC
GAM1589 CABC1   5' GCACAAACAGACGCTC  39654  CTGGC
              GAGC  TCTGTTTGTGC
              ||| |||||
              CTCG  AGACAAACACG
                C__
GAM1589 CEACAM5 3' AACAGAGCAAGACTCCA  15153  C G
              TGGAG CT GCTCTGTT
              |||| || |||||
              ACCTC GA CGAGACAA
                A  A
GAM1589 F2R     3' AACAGAGCAAGACTCCA  8831  C G
              TGGAG CT GCTCTGTT
              |||| || |||||
              ACCTC GA CGAGACAA
                A  A
GAM1589 FGFR2   3' GACAGAGCGAGACTCCA  43377  C G
              TGGAG CT GCTCTGTT
              |||| || |||||

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			ACCTC GA CGAGACAG			
			A G			
GAM1589	FGFR2	3'	GACAGAGCGAGACTCCA	43383	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1589	FUT6	3'	GACAGAGCAAGACTCCA	3812	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1589	GCLM	5'	GGCGCAGACCAGGCTCCA	9026	C	TTGT _
			TGGAGCCTGG TCTGT		GC C	
			ACCTCGGACC AGACG		CG G	
			_ _ _ A			
GAM1589	GPC1	3'	GGCTGCAGAGCCCGGCCCA	9103	A T	TTGT
			TGG GCC GGCTCTGT		GCC	
			ACC CGG CCGAGACG		CGG	
			C C T _			
GAM1589	HPSE	3'	CAAACAGGCCAGGCTCCA	21890	T	
			TGGAGCCTGGC CTGTTTG			
			ACCTCGGACCG GACAAAC			
			-			
GAM1589	IFIT4	3'	AACAGAGCAAGACTCCA	70918	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A A			
GAM1589	KCNJ5	3'	GACAGAGCGAGACTCCA	6091	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1589	LY94	3'	GACAGAGCGAGACTCCA	16705	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1589	LZTS1	3'	ACAGAGCCTGGCCCCA	40676	A T	
			TGG GCC GGCTCTGT			
			ACC CGG CCGAGACA			
			C T			
GAM1589	MSH3	3'	AACAGAGCAAGACTCCA	10116	C G	
			TGGAG CT GCTCTGTT			

			ACCTC GA CGAGACAA		
			A A		
GAM1589	POLH	3'	AACAGAGCGAGACTCCA 21461	C G	
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1589	PRKAB1	3'	GCACACCACCAGGCTCCA 20736	CTC TT	
			TGGAGCCTGG TG TGTGC		
			ACCTCGGACC AC ACACG		
			___ C_		
GAM1589	SIGLEC6	3'	AACAGAGCGAGACTCCA 59925	C G	
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1589	SLC10A2	5'	AGCAGAGCCAGGGCCCA 4840	AG	
			TGG CCTGGCTCTGTT		
			ACC GGACCGAGACGA		
			CG		
GAM1589	SNRPN	5'	CAAGCAAAAACCAGGCTCCA 43013	CTC_	
			TGGAGCCTGG TGTTTG		
			ACCTCGGACC ACGAAC		
			AAAA		
GAM1589	SNRPN	5'	CAAGCAAAAACCAGGCTCCA 42991	CTC_	
			TGGAGCCTGG TGTTTG		
			ACCTCGGACC ACGAAC		
			AAAA		
GAM1589	SNRPN	5'	CAAGCAAAAACCAGGCTCCA 42998	CTC_	
			TGGAGCCTGG TGTTTG		
			ACCTCGGACC ACGAAC		
			AAAA		
GAM1589	SNRPN	5'	CAAGCAAAAACCAGGCTCCA 43005	CTC_	
			TGGAGCCTGG TGTTTG		
			ACCTCGGACC ACGAAC		
			AAAA		
GAM1589	TNFSF11	5'	CAGGAGCCAAAGCCGGGCTCCA 13512	CT_ G	
			TGGAGCCTGGCT GTTT TG		
			ACCTCGGGCCGA CGAG AC		
			AAC G		
GAM1589	TSNAX	3'	GGTAACAGAGCAAGACTCCA 20002	C G TTG	
			TGGAG CT GCTCTGT TGCC		

ACCTC GA CGAGACA ATGG  
 A A \_\_\_\_  
 GAM1589 UBE2L3 3' GCCTTTGCAGAGTCAAGCTCCA 12503 C TTGT  
 TGGAGC TGGCTCTGT GC  
 ||||| ||||| ||  
 ACCTCG ACTGAGACG CG  
 A TTTC  
 GAM1589 ZNF264 3' AACAGAGCGAGACTCCA 12738 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAA  
 A G  
 GAM1589 ARNTL2 3' GACAGAGCGAGACTCCA 39466 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAG  
 A G  
 GAM1589 C22orf5 3' GGATCAGAGCCAGACACCA 24344 AGC TTTGTG  
 TGG CTGGCTCTG CC  
 ||| ||||| ||  
 ACC GACCGAGAC GG  
 ACA TA\_\_\_\_  
 GAM1589 DKFZp547C176 3' GACAGAGCAAGACTCCA 67223 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAG  
 A A  
 GAM1589 DKFZp564K142 3' AACAGAGCGAGACTCCA 49522 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAA  
 A G  
 GAM1589 FADS1 3' GACAGAGCAAGACTCCA 25477 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAG  
 A A  
 GAM1589 FLJ12298 3' AACAGAGCGAGACTCCA 49664 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAA  
 A G  
 GAM1589 FLJ14117 3' AACAGAGCAAGACTCCA 42896 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAA  
 A A  
 GAM1589 FLJ14251 3' GGTAACAGAGCGAGACTCCA 45977 C G TTG  
 TGGAG CT GCTCTGT TGCC  
 ||||| || ||||| |||

ACCTC GA CGAGACA ATGG  
 A G \_\_\_\_  
 GAM1589 FLJ14327 3' AACAGAGCTAGACTCCA 46127 C  
 TGGAG CTGGCTCTGTT  
 |||| |||||  
 ACCTC GATCGAGACAA  
 A  
 GAM1589 FLJ14566 5' GGCCACAGAGCCAGCCCCA 51446 A C TT T  
 TGG GC TGGCTCTGT G GCC  
 ||| || ||||| | |||  
 ACC CG ACCGAGACA C CGG  
 C \_ \_ \_  
 GAM1589 FLJ20084 3' AACAGAGCGAGACTCCA 34511 C G  
 TGGAG CT GCTCTGTT  
 |||| || |||||  
 ACCTC GA CGAGACAA  
 A G  
 GAM1589 FLJ20306 3' GACAGAGCAAGACTCCA 34917 C G  
 TGGAG CT GCTCTGTT  
 |||| || |||||  
 ACCTC GA CGAGACAG  
 A A  
 GAM1589 FLJ20456 3' GGTAACAGAGCTAGACTCCA 35215 C TTG  
 TGGAG CTGGCTCTGT TGCC  
 |||| ||||| |||  
 ACCTC GATCGAGACA ATGG  
 A \_\_\_\_  
 GAM1589 FLJ22054 3' AACAGAGCAAGACTCCA 94391 C G  
 TGGAG CT GCTCTGTT  
 |||| || |||||  
 ACCTC GA CGAGACAA  
 A A  
 GAM1589 FLJ22393 5' AGCAGGAACCAGGCTCCA 47058 C\_  
 TGGAGCCTGG TCTGTT  
 ||||| |||||  
 ACCTCGGACC GGACGA  
 AA  
 GAM1589 FLJ23598 3' GCCAAGAGCCAGCTCCA 45522 C GTT T  
 TGGAGC TGGCTCT TG GC  
 |||| ||||| |||  
 ACCTCG ACCGAGA AC CG  
 \_ \_ \_  
 GAM1589 FLJ31168 3' GACAGAGCGAGACTCCA 58502 C G  
 TGGAG CT GCTCTGTT  
 |||| || |||||  
 ACCTC GA CGAGACAG  
 A G  
 GAM1589 GP5 3' GACAGAGCGAGACTCCA 15646 C G  
 TGGAG CT GCTCTGTT  
 |||| || |||||

			ACCTC GA CGAGACAG			
			A G			
GAM1589	GTPBP5	3'	GACAGAGCAAGACTCCA	65357	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1589	HIC	3'	AACAGAGCGAGACTCCA	67444	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A G			
GAM1589	ING1-like	3'	GACAGAGCGAGACTCCA	54156	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1589	KBRAS2	3'	AACAGAGCAAGACTCCA	34191	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A A			
GAM1589	KIAA0189	3'	CAGGAGCAGAGCCAGGCCCA	28273	A	G
			TGG GCCTGGCTCTGTTT TG			
			ACC CGGACCGAGACGAG AC			
			— G			
GAM1589	KIAA0472	3'	AGCAGAGCAAGACTCCA	71853	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACGA			
			A A			
GAM1589	KIAA0563	3'	GACAGAGCAAGACTCCA	29188	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1589	KIAA0565	3'	GACAGAGCAAGACTCCA	66890	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1589	KIAA0648	3'	CAACAGAAGCAGGCTCCA	82651		GC
			TGGAGCCTG TCTGTTTG			
			ACCTCGGAC AGACAAAC			
			GA			
GAM1589	KIAA0924	3'	AACAGAGCGAGACTCCA	29712	C G	
			TGGAG CT GCTCTGTT			

		ACCTC GA CGAGACAA			
		A G			
GAM1589	KIAA1028	3' CAGAGCACAGGCTCCA	91934	—	
		TGGAGCCTG GCTCTG			
		ACCTCGGAC CGAGAC			
		A			
GAM1589	KIAA1719	3' GGCCAGGGGCCAGGCCCA	68169	A	TTTGT
		TGG GCCTGGCTCTG	GCC		
		ACC CGGACCGGGAC	CGG		
		C			
GAM1589	KIAA1940	3' GGTCTCAGAACCAAGGCTCCA	79988	— C	TTTGT
		TGGAGCCT GG TCTG	GCC		
		ACCTCGGA CC AGAC	TGG		
		A A TC			
GAM1589	LGI2	3' CAAATCAAAGCCAGGCTC	36397	C	—
		GAGCCTGGCT TG TTTG			
		CTCGGACCGA AC AAAC			
		A T			
GAM1589	MGC10200	3' AACAGAGCGAGACTCCA	58980	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAA			
		A G			
GAM1589	MGC2705	5' GCACCAAGCCAGGCTCC	51113	C	TTT
		GGAGCCTGGCT TG GTGC			
		CCTCGGACCGA AC CACG			
		— —			
GAM1589	MGC4562	3' AACAGAGCGAGACTCCA	55908	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAA			
		A G			
GAM1589	MGC4663	3' AACAGAGCCAGACTCC	44501	C	
		GGAG CTGGCTCTGTT			
		CCTC GACCGAGACAA			
		A			
GAM1589	NPTXR	3' AACAGAGCAAGACTCCA	54171	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAA			
		A A			
GAM1589	NPTXR	3' AACAGAGCAAGACTCCA	26635	C G	
		TGGAG CT GCTCTGTT			



			ACCTC GA CGAGACAA		
			A A		
GAM1589	OR7C1	5'	AACAGAGCCAAGTCCA	82428	G C
			TGGA C TGGCTCTGTT		
			ACCT G ACCGAGACAA		
			_ A		
GAM1589	POFUT1	3'	AACAGAGCGAGACTCCA	70462	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1589	PTK6	3'	GACAGAGCGAGACTCCA	19936	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A G		
GAM1589	RASGRF2	3'	GCACGAAGCCAGGCTCC	61042	CTGT
			GGAGCCTGGCT TTGTGC		
			CCTCGGACCGA AGCACG		
			_____		
GAM1589	SC65	3'	GACAGAGCGAGACTCCA	21289	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A G		
GAM1589	SNURF	3'	CAAGCAAAAACCAGGCTCCA	19052	CTC_
			TGGAGCCTGG TGTTTG		
			ACCTCGGACC ACGAAC		
			AAAA		
GAM1589	TMG4	3'	GACAGAGCAAGACTCCA	43989	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A A		
GAM1589	WBSCR23	3'	GACAGAGCAAGACTCCA	46762	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A A		
GAM1589	WIRE	3'	GACAGAGCCAGACTCC	78305	C
			GGAG CTGGCTCTGTT		
			CCTC GACCGAGACAG		
			A		
GAM1589	WSB1	3'	AACAGAGCGAGACTCCA	56138	C G
			TGGAG CT GCTCTGTT		

			ACCTC GA CGAGACAA		
			A G		
GAM1589	WSB1	3'	AACAGAGCGAGACTCCA	56144	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1589	LOC115704	3'	CAGCCAGAGCCAGGCCCC	73541	A T
			GG GCCTGGCTCTG TTG		
			CC CGGACCGAGAC GAC		
			C C		
GAM1589	LOC124220	5'	GGCACAACCAGACGCC	59146	_ T
			GGC TCTG TTGTGCC		
			CCG AGAC AACACGG		
			C C		
GAM1589	LOC127262	3'	GACAGAGCGAGACTCCA	76110	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A G		
GAM1589	LOC129563	3'	AGCAGAGCAGGCCCCA	74878	A G
			TGG GCCTG CTCTGTT		
			ACC CGGAC GAGACGA		
			C _		
GAM1589	LOC129880	3'	AACAGAGCAAGACTCCA	74900	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A A		
GAM1589	LOC143196	3'	AACAGAGCGAGACTCCA	82903	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1589	LOC144319	3'	GGCACAAACAGGCGCCCC	83057	A CTG T
			GG GC GC CTGTTTGTGCC		
			CC CG CG GACAAACACGG		
			C _ _		
GAM1589	LOC145216	3'	GACAGAGCAAGACTCCA	83267	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A A		
GAM1589	LOC145820	3'	GACAGAGCAAGACTCCA	77514	C G
			TGGAG CT GCTCTGTT		

		ACCTC GA CGAGACAG			
		A A			
GAM1589	LOC146227 3'	GGTCAGAGCCAGACCCC	77711	AGC	TTTGT
		GG CTGGCTCTG GCC			
		CC GACCGAGAC TGG			
		CCA _____			
GAM1589	LOC146713 3'	AACAGAGCAAGACTCCA	83720	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAA			
		A A			
GAM1589	LOC147071 3'	GACAGAGCAAGACTCCA	72999	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAG			
		A A			
GAM1589	LOC147649 3'	GACAGAGCGAGACTCCA	78414	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAG			
		A G			
GAM1589	LOC148936 3'	AACAGAGCAAGACTCCA	84286	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAA			
		A A			
GAM1589	LOC149803 5'	CAGGCAGAGCAAGCTCCA	79538	CTG	
		TGGAGC GCTCTGTTTG			
		ACCTCG CGAGACGGAC			
		AA_			
GAM1589	LOC150299 3'	GACAGAGCAAGACTCCA	84970	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAG			
		A A			
GAM1589	LOC151429 3'	GACAGAGCAAGACTCCA	85353	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAG			
		A A			
GAM1589	LOC151904 3'	AACAGAGCGAGACTCCA	80382	C G	
		TGGAG CT GCTCTGTT			
		ACCTC GA CGAGACAA			
		A G			
GAM1589	LOC158292 5'	GACAGAGCGAGACTCCA	86730	C G	
		TGGAG CT GCTCTGTT			

	ACCTC GA CGAGACAG		
	A G		
GAM1589 LOC162137 5'	CAAGCAGGCCAAGCCCCA	87111	A C T
	TGG GC TGGC CTGTTTG		
	ACC CG ACCG GACGAAC		
	C A _		
GAM1589 LOC163033 5'	CGACCAGGACCAAGCCCCA	82396	A C CT T
	TGG GC TGG CTG TTG		
	ACC CG ACC GAC AGC		
	C A AG C		
GAM1589 LOC163682 3'	ACACTCAAAGCCGGGCTCCA	87020	C TT
	TGGAGCCTGGCT TG TGT		
	ACCTCGGGCCGA AC ACA		
	A TC		
GAM1589 LOC200261 3'	GCACAAACCTCTGGAGGCCCA	88655	A GGCTCT
	TGG GCCT GTTTGTGC		
	ACC CGGA CAAACACG		
	_ GGTCTC		
GAM1589 LOC201173 3'	GACAGAGCAAGACTCCA	87329	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1589 LOC201182 5'	AACAGAGCAAGACTCCA	89760	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAA		
	A A		
GAM1589 LOC219627 3'	GACAGAGCGAGACTCCA	92178	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A G		
GAM1589 LOC221543 5'	GACAGAGCAAGACTCCA	93742	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1589 LOC221943 5'	GACAGAGCAAGACTCCA	93989	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1589 LOC222160 5'	GACAGAGCAAGACTCCA	94127	C G
	TGGAG CT GCTCTGTT		

ACCTC GA CGAGACAG  
 A A  
 GAM1589 LOC253039 5' GGCTCCAAAACCAGGCTCTA 96159 CTCTG T\_  
 TGGAGCCTGG TTTG GCC  
 ||||| ||| |||  
 ATCTCGGACC AAAC CGG  
 A\_\_\_\_ CT  
 GAM1589 LOC254659 3' AAACAGAGCAAGACTCCA 95109 C G  
 TGGAG CT GCTCTGTTT  
 |||| || |||||  
 ACCTC GA CGAGACAAA  
 A A  
 GAM1589 LOC256158 5' AACATCGAGCCAGGCCCA 97639 A \_  
 TGG GCCTGGCTC TGTT  
 || ||||| |||  
 ACC CGGACCGAG ACAA  
 \_ CT  
 GAM1589 LOC256207 3' GACAGAGCAAGACTCCA 95169 C G  
 TGGAG CT GCTCTGTT  
 |||| || |||||  
 ACCTC GA CGAGACAG  
 A A  
 GAM1589 LOC257596 5' GACAGAGCAAGACTCCA 97935 C G  
 TGGAG CT GCTCTGTT  
 |||| || |||||  
 ACCTC GA CGAGACAG  
 A A  
 GAM1589 LOC56963 3' GCACAAAGCCAGGCTTCA 71455 CTGT  
 TGGAGCCTGGCT TTGTGC  
 ||||| |||||  
 ACTTCGGACCGA AACACG  
 \_\_\_\_\_  
 GAM1589 LOC91149 3' GCTGAACCAGAGCCAGACTCCA 65079 C \_ T  
 TGGAG CTGGCTCTG TTTG GC  
 |||| ||||| ||| ||  
 ACCTC GACCGAGAC AAGT CG  
 A C \_  
 GAM1589 LOC91409 3' AGGCAAGGCCAGGCCCCA 65951 A TC  
 TGG GCCTGGC TGTTT  
 || ||||| |||  
 ACC CGGACCG ACGGA  
 C GA  
 GAM1589 LOC91862 3' GGTGACAGAGCGAGACTCCA 53470 C G TGT  
 TGGAG CT GCTCTGTT GCC  
 |||| || ||||| |||  
 ACCTC GA CGAGACAG TGG  
 A G \_  
 GAM1589 LOC92482 3' AACAGAGCAAGACTCCA 69485 C G  
 TGGAG CT GCTCTGTT  
 |||| || |||||

ACCTC GA CGAGACAA  
 A A  
 GAM1590 BCL2 3' CCCAAAAGGAGAAGAACATCTG 5300 TTT CTA  
 A TCAG TTCTTCTCCTT GGG  
 |||| ||||| ||  
 AGTC AAGAAGAGGAA CCC  
 TAC AA\_  
 GAM1590 CYBB 3' CCCAAAAGAAGAAGGAAA 76354 C CTA  
 TTTTCTTCT CTT GGG  
 ||||| || ||  
 AAAGGAAGA GAA CCC  
 A AA\_  
 GAM1590 DDX6 3' CCCTAAAAAGAGAAGAA 15286 C C  
 TTCTTCTC TT TAGGG  
 ||||| || ||||  
 AAGAAGAG AA ATCCC  
 A A  
 GAM1590 NFE2 5' CCCTAGAAAATGGAAAAC 20488 TTCTCC  
 GTTTTTC TTCTAGGG  
 ||||| |||||  
 CAAAAGG AAGATCCC  
 TAA\_\_\_\_  
 GAM1590 NFIC 3' AGGAGGAAAAGAAAAA 18794 C  
 TTTTCTT TCCTTCT  
 ||||| |||||  
 AAAAAGAA AGGAGGA  
 A  
 GAM1590 PABPC4 5' AAGGAAAAGAAAAAACGA 13780 AG C  
 TC TTTTCTT TCCTT  
 || ||||| ||||  
 AG AAAAAGAA AGGAA  
 CA A  
 GAM1590 SLC4A4 3' CTTCTAGGGCAAAAGAAGAAAA 13637 \_ T\_\_\_\_\_ TCTA  
 AACTGA TTTTCTTC CCT GG  
 |||| || || ||  
 AAAAA GAAG GGG TC  
 A AAAAC||| ATCT  
 GAM1590 TBL1X 3' AGGAGAAAAAAAATGA 18926 G C  
 TCA TTTT TTCTCCT  
 || |||| |||||  
 AGT AAAAA AAGAGGA  
 A A  
 GAM1590 TPD52L2 3' TCTAGGGCCCCAGAAAGGAAAC 12368 TC T\_\_\_\_\_ TCTA  
 TGA AGTTTT TTC CCT G  
 |||| || || |  
 TCAAAG AAG GGG T  
 GA ACCCC||| ATCT  
 GAM1590 AQP9 3' CCTAGAAGCCAAACTGA 40608 TCTTCTC  
 TCAGTTTT CTTCTAGG  
 ||||| |||||

AGTCAAAA GAAGATCC  
 CC\_\_\_\_\_

GAM1590 BCoR 3' AAGGAGAAAAAAATGA 34862 G C  
 TCA TTTT TTCTCCTT  
 ||| |||| |||||  
 AGT AAAAA AAGAGGAA  
 A A

GAM1590 BTN2A1 5' CCAGCGGAGAAAAGAAAA 54340 \_ TT A  
 TTTTCT TCTCC CT GG  
 ||||| |||| ||  
 AAAAAGA AGAGG GA CC  
 AA C\_ \_

GAM1590 C19orf7 3' CCCCAAAAAGAGAAAAATGAAA 61127 \_ CTTCTA  
 AACT AGTTTTTC TTCTC GGG  
 ||||| |||| ||  
 TCAAAAAG AAGAG CCC  
 TAAA AAAAAC

GAM1590 C1orf9 5' CTGAAGAGAAGAAAAAGCGA 32635 AG C T  
 TC TTTTCTTCTC TTC AG  
 || ||||| |||| ||  
 AG AAAAGAAGAG AAG TC  
 CG \_ \_

GAM1590 C20orf108 3' CTTCTAGGGAAAAAAAAGAAA 55046 CT\_\_\_\_\_ TCTA  
 AACTGA TTTTCTT CCT GG  
 ||||| |||| ||  
 AAAAAGAA GGG TC  
 AAAAAA||| ATCT

GAM1590 CHL1 3' CCTCAAAAGAAAAACTG 21746 CTCCTTCT  
 CAGTTTTTCTT AGG  
 ||||| |||| ||  
 GTCAAAAAGAA TCC  
 AAC\_\_\_\_\_

GAM1590 DIS3 3' CTTCTAGGGAAAAAAGAAGAAA 30229 T\_\_\_\_\_ TCTA  
 AACTG TTTTCTTC CCT GG  
 ||||| |||| ||  
 AAAAAGAAG GGG TC  
 AAAAA||| ATCT

GAM1590 DKFZP564O0423 3' CTTCTAGGGAAAAAAGAAGAAA 91687 T\_\_\_\_\_ TCTA  
 AAC TTTTCTTC CCT GG  
 ||||| |||| ||  
 AAAAAGAAG GGG TC  
 AAAAA||| ATCT

GAM1590 FLJ10213 3' CTTTGAGGAGAAAAAAAC 35905 C CT  
 GTTTTT TTCTCCTT AG  
 |||| ||||| ||  
 CAAAAA AAGAGGAG TC  
 A TT

GAM1590 FLJ13231 3' CCTAGGAGTGAAAAGAAAAAC 43548 C \_  
 GTTTTTCTT TC CTTCTAGG  
 ||||| || |||||

		CAAAAAGAA AG GAGGATCC		
		A T		
GAM1590	FNBP3	5' GAAGAAGAAGAAAAAC 80152	C	
		GTTTTTCTTCT CTTC		
		CAAAAAGAAGA GAAG		
		A		
GAM1590	HEMGN	5' CCTATAGAGAAAAAACTGA 37377	C	CTTC
		TCAGTTTTT TTCTC TAGG		
		AGTCAAAAA AAGAG ATCC		
		_ AT_		
GAM1590	HEMGN	5' CTTAGAAAAAGAAAAGCTGA 37378		CTCC
		TCAGTTTTTCTT TTCTAGG		
		AGTCGAAAAGAA AAGATTC		
		A_		
GAM1590	KIAA0020	5' AAGAAGAAGAAAGAACTGA 29649	_	C
		TCAGTTTTT CTTCT CTT		
		AGTCAAGAA GAAGA GAA		
		A A		
GAM1590	KIAA0326	3' CCCAAAATGGGGAAGAAAAA 64321		TTCTA
		TTTTTCTTCTCC GGG		
		AAAAAGAAGGGG CCC		
		TAAAA		
GAM1590	KIAA1164	3' TCTAGGGGAAAGGAAGAAAAAC 69511	A	T_____ TCTA
	CGA	GTTTTTCTTC CCT G		
		CAAAAAGAAG GGG T		
		C GAAAG    ATCT		
GAM1590	KIAA1649	5' CCCCATCTAAGGAAAAAACTGA 50254		CTCCTTCTA
		TCAGTTTTTCTT GGG		
		AGTCAAAAAGGA CCC		
		ATCTAC_		
GAM1590	KR18	3' GAAGAAAAAGAAAAACTGA 52746		CTC
		TCAGTTTTTCTT CTTC		
		AGTCAAAAAGAA GAAG		
		AAA		
GAM1590	TANK	3' CCTAAAAGAAGAAAAAC 14812		CCTTC
		GTTTTTCTTCT TAGG		
		CAAAAAGAAGA ATCC		
		AA_		
GAM1590	LOC152580	3' CCCCAGGTTTAGATGAAAAACT 85776	T	CCT A
		AGTTTTTC TCT TCT GGG		



		TCAAAAAG AGA GGA CCC	
		T TTT C	
GAM1590	LOC221830 3'	CCCTTGGAGAAGAAAACT 92507	TTCT
		AGTTTTTCTTCTCC AGGG	
		TCAAAAAGAAGAGG TCCC	
		T__	
GAM1590	LOC222681 5'	CCCCAGAAGAGTCAGAAAAAAC 92851	_ T_ C A
	TGA	TCAGTTTTT CT CTC TTCT GGG	
		AGTCAAAAA GA GAG AAGA CCC	
		A CT _ C	
GAM1590	LOC254672 3'	CCAGAGAGAAGGAAAACT 94642	_ CT A
		AGTTTTTCT TTCTC TCT GG	
		TCAAAAAG AAGAG AGA CC	
		G _ _	
GAM1590	LOC257160 3'	GAAGAAGAAGAGAAACTGA 94848	C
		TCAGTTTTTCTTCT CTTC	
		AGTCAAAGAGAAGA GAAG	
		A	
GAM1590	LOC257507 5'	CCCCAGAAGAGTCAGAAAAAAC 97773	_ T_ C A
	TGA	TCAGTTTTT CT CTC TTCT GGG	
		AGTCAAAAA GA GAG AAGA CCC	
		A CT _ C	
GAM1590	LOC257625 5'	CCCCAGAAGAGTCAGAAAAAAC 97904	_ T_ C A
	TGA	TCAGTTTTT CT CTC TTCT GGG	
		AGTCAAAAA GA GAG AAGA CCC	
		A CT _ C	
GAM1590	LOC91300 5'	CCCTTTTGGAGAGAAAAAC 94595	T TTCT
		GTTTTTCT CTCC AGGG	
		CAAAAAGA GAGG TCCC	
		_ TTT_	
GAM1590	LOC91300 5'	CCCTTTTGGAGAGAAAAAC 57068	T TTCT
		GTTTTTCT CTCC AGGG	
		CAAAAAGA GAGG TCCC	
		_ TTT_	
GAM1591	RBBP9 3'	AAACTCCCCAAATTGCTATGA 70125	C AGA
		TCA AGCAATTTG AGTTTT	
		AGT TCGTTAAAC TCAAAA	
		A CCC	
GAM1591	FBXO22 3'	AAACTTCTCAGAGCT 24089	AA
		AGC TTTGAGAAGTTTT	

TCG AGACTCTTCAAAA

GAM1591 GRSF1 3' AAAACTTCTCATGGAGTGA 9138 AG ATT  
TCAC CA TGAGAAGTTTT  
|||| || |||||  
AGTG GT ACTCTTCAAAA  
AG \_

GAM1591 KIAA0992 3' AAAACTTTGGAATTGCTGTGAT 32201 GA  
ATCACAGCAATTT GAAGTTTT  
||||||| |||||  
TAGTGTCGTTAAG TTTCAAAA  
G\_

GAM1591 KIAA1729 5' AAAACTTCTCAAGTTCTGT 89122 C  
ACAG AATTTGAGAAGTTTT  
||| |||||  
TGTC TTGAACTCTTCAAAA

GAM1591 KIAA1940 3' AAAACTTATTTATTGCTGT 79972 TTGAG  
ACAGCAAT AAGTTTT  
||||| |||||  
TGTCGTTA TTCAAAA  
TTTA\_

GAM1591 MGC14156 3' AAAACTTCCCACAGGGCTG 51871 AATT A  
CAGC TG GAAGTTTT  
||| |||||  
GTCG AC CTTCAAAA  
GGAC C

GAM1591 PEG10 3' TCTCAAATTGCCTGA 30531 CA  
TCA GCAATTTGAGA  
||| |||||  
AGT CGTTAACTCT  
C\_

GAM1591 SS-56 3' GGAGCTTCAAATGGCTGTGATA 59607 A GA  
TATCACAGC ATTTGA AGTTTT  
||||||| |||||  
ATAGTGTCG TAAACT TCGAGG  
G \_

GAM1591 LOC91344 3' AAAACTGCCATTGCTGTGATG 65614 TTGAGA  
TATCACAGCAAT AGTTTT  
||||||| |||||  
GTAGTGTCGTTA TCAAAA  
CCG\_

GAM1591 LOC91689 3' CTCGGGTTCTGTGATA 52822 C  
TATCACAG AATTTGAG  
||||| |||||  
ATAGTGTC TTGGGCTC

GAM1592 ACP2 3' AGAAAGTTCTAGACTG 7851 GC TC  
CAGT CT AGAACTTTCT  
||| || |||||

GTCA GA TCTTGAAAGA

GAM1592 APTX 5' AAGAGAAAGAGATCAGGCA 34655 TCAGAA  
TGCCT CTTTCTCTT  
||||| |||||  
ACGGA GAAAGAGAA  
CTAGA\_

GAM1592 BCL7A 3' AGGCTGTCTCCTTAAGGCACTG 40637 C A\_\_ TT  
CAGTGCCTT AG AC TCT  
||||||| || || |||  
GTCACGGAA TC TG GGA  
T CTC TC

GAM1592 CLC 3' AAGAGAAAATACTGAAAGCACA 25105 A C AAC  
GG CC GTGC TTCAG TTTCTCTT  
|| ||| ||||| |||||  
GG CACG AAGTC AAAGAGAA  
A A ATA

GAM1592 CNK 3' AAGCCCTGAAGGCCTG 14517 T AA  
CAG GCCTTCAG CTT  
||| ||||| |||  
GTC CGGAAGTC GAA  
\_ CC

GAM1592 COL4A3 3' AAGTGCAGGTTCTGAGGGCACC 48549 A TCT  
GG CC GTGCCTTCAGAACTT CTT  
|| ||||| ||||| |||  
GG CACGGGAGTCTTGGA GAA  
C CGT

GAM1592 CSPG4 3' AAGAGAGACCTGGAGACAC 8570 C AAC  
GTG CTTTCTCAG TTTCTCTT  
||| ||||| |||||  
CAC GAGGTC AGAGAGAA  
A C\_\_

GAM1592 CYP1B1 3' AAGAGAAAAGAGAGAAACACTG 3651 CC AGAAC  
CAGTG TTC TTTCTCTT  
||||| ||| |||||  
GTCAC AAG AAAGAGAA  
A\_ AGAGA

GAM1592 DLG3 3' AAGAGAAAAGAGGAGGACTG 40880 G AGAAC  
CAGT CCTTC TTTCTCTT  
||||| ||||| |||||  
GTCA GGAGG AAAGAGAA  
\_ AGA\_\_

GAM1592 DLG5 5' AGGCAGACTCTGAAGGC 82909 A\_ T  
GCCTTCAGA CT TCT  
||||||| || |||  
CGGAAGTCT GA GGA  
CA C

GAM1592 FLT1 3' AAGAGAAACCGGGAGAAGGCAT 8910 AGAAC\_  
GTGCCTTC TTTCTCTT  
||||||| |||||

			TACGGAAG	AAAGAGAA		
			AGGGCC			
GAM1592	GRB10	3'	AGAGAAAATGGCACCTGG	17971	_	TTCAGAAC
			CCAG TGCC	TTTCTCT		
			GGTC ACGG	AAAGAGA		
			C TA_____			
GAM1592	LFG	3'	AAGAGAAAAGGAGCCAAGAACT	76711	GC	CAGAA _
	GG		CCAGT CTT	CTTT CTCTT		
			GGTCA GAA	GAAA GAGAA		
			A_ CCGAG	A		
GAM1592	MAN2A2	3'	AAGAGAAAGTTCATTCAC	20391	CCTTCA	
			GTG	GAAC TTTCTCTT		
			CAC	CTTGAAAGAGAA		
			TTA_____			
GAM1592	NLGN3	3'	AAGAAAAGTTCTTAAAACACT	38596	CC C	C
			AGTG TT	AGAACTTT TCTT		
			TCAC AA	TCTTGAAA AGAA		
			AA T	_		
GAM1592	NPAS1	5'	AAGGTCTCCCGAGGGCACT	59879	A_ _	
			AGTGCCTTC	GA ACTTT		
			TCACGGGAG	CT TGGAA		
			CC C			
GAM1592	PLAG1	3'	AGTGTGTTCCAAAGGCATT	10605	CA	TTT
			AGTGCCTT	GAAC CT		
			TTACGGAA	CTTG GA		
			AC	TGT		
GAM1592	PLXNA1	3'	AGAAAATGAAGGCAGTGG	72309	G	GAAC
			CCA TGCCTTCA	TTTCT		
			GGT ACGGAAGT	AAAGA		
			G	A_____		
GAM1592	PPP4R1	3'	AAGAGAAAGTACAGTAAACACT	17620	CCTTCAGA	
			AGTG	ACTTTCTCTT		
			TCAC	TGAAAGAGAA		
			AAATGACA			
GAM1592	ACYP2	3'	AAGAGAAAAATTGTAACACACT	56612	CC _	AAC
	G		CAGTG TT	CAG TTTCTCTT		
			GTCAC AA	GTT AAAGAGAA		
			AC T	AA_		
GAM1592	B3GNT6	3'	AGAAATCAGATGAAGGCAT	22503	GAAC_	
			GTGCCTTCA	TTTCT		

TACGGAAGT AAAGA  
 AGACT  
 GAM1592 BAG5 3' AAGAGAAGGGATAAAGGAC 16835 G CAGAA  
 GT CCTT CTTTCTCTT  
 || ||| |||||  
 CA GGAA GGAAGAGAA  
 \_ ATAG\_  
 GAM1592 BIVM 3' AAGAGAAAAGACTCAAGAACT 34665 GC C AAC  
 G CAGT CTT AG TTTCTCTT  
 ||| ||| || |||||  
 GTCA GAA TC AAAGAGAA  
 AA C AGA  
 GAM1592 C15orf5 3' AGAGAAAAGAAAGCAC 48195 C AGAAC  
 GTGC TTC TTTCTCT  
 ||| ||| |||||  
 CACG AAG AAAGAGA  
 A A\_\_\_\_  
 GAM1592 C20orf80 5' AAGAGAAGAAGATGAAGAAAC 65282 GC GAAC  
 GT CTTCA TTTCTCTT  
 || ||| |||||  
 CA GAAGT GAAGAGAA  
 AA AGAA  
 GAM1592 CLSTN1 3' AGTTCTGAGGACACTGG 30103 C  
 CCAGTG CTTCAGAACT  
 ||||| |||||  
 GGTCAC GGAGTCTTGA  
 A  
 GAM1592 DKFZP434P0111 3' AAGAGAAAGTTTCTGCAC 67368 CTTCA  
 GTGC GAACTTTCTCTT  
 ||| |||||  
 CACG TTTGAAAGAGAA  
 TC\_\_\_\_  
 GAM1592 DORFIN 5' AGAATTCTCTGAAGGAAC 31257 G ACT  
 GT CCTTCAGA TTCT  
 || ||||| |||  
 CA GGAAGTCT AAGA  
 A CTT  
 GAM1592 FLJ10300 5' AAGAGAAAGATGAAGACTCTG 35997 TGC GAA  
 CAG CTTCA CTTTCTCTT  
 ||| ||| |||||  
 GTC GAAGT GAAAGAGAA  
 TCA A\_\_\_\_  
 GAM1592 FLJ20373 3' AAGAGAAGAAGGAAAGGCACAG 35070 A \_AGAAC  
 G CC GTGCCTT C TTTCTCTT  
 || ||||| | |||||  
 GG CACGGAA G GAAGAGAA  
 A A GAA\_\_\_\_  
 GAM1592 FLJ23511 5' AGAGAAAAACAAGGCAT 49956 CAGAAC  
 GTGCCTT TTTCTCT  
 ||||| |||||

TACGGAA AAAGAGA  
 CAA\_\_\_\_  
 GAM1592 FLJ30681 3' AGAGAAGAAAGACCACTGG 91782 CCT AGAAC  
 CCAGTG TC TTTCTCT  
 ||||| || |||||  
 GGTCAC AG GAAGAGA  
 C\_\_ AAA\_\_  
 GAM1592 HDAC11 3' GAGCTATAGGCACTGG 45717 TC AACTTT  
 CCAGTGCCT AG CTC  
 ||||| || |||  
 GGTCACGGA TC GAG  
 TA \_\_\_\_\_  
 GAM1592 IKKE 5' AGTGAGCCCTGAAAGCTCTGG 25745 T C AA T  
 CCAG GC TTCAG CTT CT  
 ||| || |||| ||| ||  
 GGTC CG AAGTC GAG GA  
 T A CC T  
 GAM1592 KIAA0680 3' AGAGAAAATTGAAGCAT 28232 C AAC  
 GTGC TTCAG TTTCTCT  
 ||| |||| |||||  
 TACG AAGTT AAAGAGA  
 \_ A\_\_  
 GAM1592 KIAA1228 3' AGGGGGTGATTCTGAGGCACTG 65035 T \_\_ TT  
 CAGTGCCT CAGA ACT CT  
 ||||| ||| ||| ||  
 GTCACGGA GTCT TGG GA  
 \_ TAG GG  
 GAM1592 KIAA1300 5' AGGAACCCTGAAGGCA 62860 AAC  
 TGCCTTCAG TTTCT  
 ||||| ||||  
 ACGGAAGTC AAGGA  
 CC\_  
 GAM1592 KIAA1805 3' AAGAGAAAGTAGAAGCAGCA 79966 \_\_ AGA  
 TGC CTTC ACTTTCTCTT  
 ||| ||| |||||  
 ACG GAAG TGAAAGAGAA  
 AC A\_\_  
 GAM1592 LENG1 5' AAGAGAAAGCTCTGGGCATCCT 84074 \_\_ TT A  
 G CAG TGCC CAGA CTTTCTCTT  
 ||| ||| ||| |||||  
 GTC ACGG GTCT GAAAGAGAA  
 CT \_\_ C  
 GAM1592 LHX6 3' AAGAGAAAACCTCTGGGGTCA 26854 C AC  
 TG CTTCAGA TTTCTCTT  
 || ||||| |||||  
 AC GGGGTCT AAAGAGAA  
 T CA  
 GAM1592 N4BP3 3' AGCTCCAGAAGGCACTGG 66250 A\_ A  
 CCAGTGCCTTC GA CT  
 ||||| ||| ||

GGTCACGGAAG CT GA  
AC C  
GAM1592 NASP 3' AGAGGGTGAAGAACTG 67966 GC AGA  
CAGT CTTC ACTTTCT  
||||| ||| |||||  
GTCA GAAG TGGGAGA  
AA \_\_\_\_  
GAM1592 SMARCF1 3' AAAATTCTGAAGGAC 57480 G C  
GT CCTTCAGAA TTT  
|| ||||| |||  
CA GGAAGTCTT AAA  
\_ A  
GAM1592 SMARCF1 3' AAAATTCTGAAGGAC 37430 G C  
GT CCTTCAGAA TTT  
|| ||||| |||  
CA GGAAGTCTT AAA  
\_ A  
GAM1592 SMARCF1 3' AAAATTCTGAAGGAC 20034 G C  
GT CCTTCAGAA TTT  
|| ||||| |||  
CA GGAAGTCTT AAA  
\_ A  
GAM1592 TED 3' AAGAGAAAGTCCAGGGACTGG 31630 G TCA A  
CCAGT CCT GA CTTTCTCTT  
||||| ||| || |||||  
GGTCA GGA CT GAAAGAGAA  
G C\_\_ \_  
GAM1592 TGIF2 3' AGAAGGGTGCTGAAGGC 41447 AA\_  
GCCTTCAG CTTTCT  
||||| |||||  
CGGAAGTC GGAAGA  
GTG  
GAM1592 WBSCR20A 3' AAGAGAAAGAAGAGACAGCA 35958 CT AGAA  
TGC TC CTTTCTCTT  
||| || |||||  
ACG AG GAAAGAGAA  
AC AGAA  
GAM1592 LOC115273 3' AGAAAGTTCTGATGGCCAGG 73356 AGT T  
CC GCC TCAGAACTTTCT  
|| ||| |||||  
GG CGG AGTCTTGAAAGA  
AC\_ T  
GAM1592 LOC145761 5' AAGAGAAAGTGGGAAGGCATGG 83472 G AGA  
CCA TGCCTTC ACTTTCTCTT  
||| ||||| |||||  
GGT ACGGAAG TGAAAGAGAA  
\_ G\_\_  
GAM1592 LOC146179 5' AGAAAGTTTTGGGCCT 77700 T TT  
AG GCC CAGAACTTTCT  
|| ||| |||||

TC CGG GTTTTGAAAGA

GAM1592 LOC147072 3' AAGAGAAAGTGAGAAGAACTG 60407 GC AGA  
CAGT CTTC ACTTTCTCTT  
||||| |||||  
GTCA GAAG TGAAAGAGAA  
AA AG\_

GAM1592 LOC148758 5' AGAAAGTTCTGAGAAAC 78962 GCC  
GT TTCAGAACTTTCT  
|| |||||  
CA GAGTCTTGAAAGA  
AA\_

GAM1592 LOC148932 3' AGGAATCTGAAGGCACTGG 79103 AC  
CCAGTGCCTTCAGA TTTCT  
||||| |||||  
GGTCACGGAAGTCT AAGGA

GAM1592 LOC149386 5' AAGTTTTGAAAGCACT 84400 C  
AGTGC TTCAGAACTT  
||||| |||||  
TCACG AAGTTTTGAA  
A

GAM1592 LOC150139 3' AGAAAATAGAAAAAGGCGCTGG 79583 CAGAAC\_  
CCAGTGCCTT TTTCT  
||||| |||||  
GGTCGCGGAA AAAGA  
AAAGATA

GAM1592 LOC152756 3' AAGATGCAGTTCTGAAAACCTG 85871 TGCC TTC  
CAG TTCAGAACT TCTT  
||| ||||| |||||  
GTC AAGTCTTGA AGAA  
CAA\_ CGT

GAM1592 LOC162333 5' AAGAGAAAGCGATGACACTG 87114 CCT GAA  
CAGTG TCA CTTTCTCTT  
||||| ||| |||||  
GTCAC AGT GAAAGAGAA  
\_ AGC

GAM1592 LOC199221 3' AAGAGAAGCTCGAAAGCATGG 80347 G C A A T  
CCA TGC TTC GA CTT CTCTT  
||| ||| ||| ||| |||||  
GGT ACG AAG CT GAA GAGAA  
\_ A \_ C \_

GAM1592 LOC203339 3' AGAGAAAATTGGGCCTG 90542 T TCAGAAC  
CAG GCCT TTTCTCT  
||| |||||  
GTC CGGG AAAGAGA  
\_ TTA\_

GAM1592 LOC255017 3' AGAAAGAGGAACTGG 94624 G TCAGAA  
CCAGT CCT CTTTCT  
||||| ||| |||||



GGTCA GGA GAAAGA  
A \_\_\_\_\_  
GAM1592 LOC256021 3' AAGAGAAACAAAGACAACACTG 96512 CCT AGAAC  
G CCAGTG TC TTTCTCTT  
||||| || |||||  
GGTCAC AG AAAGAGAA  
AAC AAAC\_  
GAM1592 LOC90139 3' AGAATCCCGAAGGCAT 55396 A\_ ACT  
GTGCCTTC GA TTCT  
||||| || |||  
TACGGAAG CT AAGA  
CC \_\_\_\_  
GAM1593 LYPLA1 3' ATAATACAGTACTGCCACCA 20924 T A AAGTA  
TGGT G CAG TGTATTAT  
||| | ||| |||||  
ACCA C GTC ACATAATA  
\_ C ATG\_  
GAM1593 OXR1 3' ATAATACATACTTCATAGACCA 35837 GACA  
TGGTT GAAGTATGTATTAT  
|||| | |||||  
ACCAG CTTCATACATAATA  
ATA\_  
GAM1593 PRKWNK3 3' ATAATTTTGTCAACCA 61551 G  
TGGTTGACAGAA TAT  
||||| |||  
ACCAACTGTTTT ATA  
A  
GAM1593 CAPS2 3' ATAATACATATGTCATCAAC 70603 CA A  
GTTGA GA GTATGTATTAT  
|||| || |||||  
CAACT CT TATACATAATA  
A\_ G  
GAM1593 CTPS2 3' GATAATACATACTTCTGTCAAC 39086  
CA TGGTTGACAGAAGTATGTATTATC  
||||| |||||  
ACCAACTGTCTTCATACATAATAG  
GAM1593 FLJ13397 3' ATAACACATTGTCAACC 46326 GAAGT A  
GGTTGACA ATGT TTAT  
||||| ||| |||  
CCAAGTGT TACA AATA  
\_\_\_\_\_ C  
GAM1593 HOMER-2B 3' ACATTCCTCTCTGTCAAC 16719 \_ T\_  
GTTGACAGA AG ATGT  
||||| || |||  
CAACTGTCT TC TACA  
C CT  
GAM1593 KIAA1941 3' ACTACTTCTGCCAAC 74835 A T  
GTTG CAGAAGTA GT  
||| ||||| ||

			CAAC GTCTTCAT CA		
			C _		
GAM1593	LOC147080	3'	ACAACAATCTGTCAGCCA	83929	AGTA
			TGGTTGACAGA TGT		
			ACCGACTGTCT ACA		
			AACA		
GAM1593	LOC220692	3'	ATACTTCTATTAACCA	91218	C
			TGGTTGA AGAAGTAT		
			ACCAATT TCTTCATA		
			A		
GAM1593	LOC93297	3'	ACAATAAAGTCTGTCAGCCA	71949	AG_ _
			TGGTTGACAGA TAT GT		
			ACCGACTGTCT ATA CA		
			GAA A		
GAM1594	ADH1B	3'	CTTAGACATAAAGTAAAAT	72644	C CAC
			ATTT ACTTT TGTCTGAG		
			TAAA TGAAA ACAGATTC		
			A T_		
GAM1594	AHR	3'	ATCTCAGATGTTAAATAAATG	7875	CAC C T
			CATTT TTT AC GTCTGAGAT		
			GTAAA AAA TG TAGACTCTA		
			TA_ T _		
GAM1594	FDFT1	3'	TAGGAAAGTGAAATG	15518	A
			CATTTCACTTTC CTG		
			GTAAAGTGAAAG GAT		
			-		
GAM1594	JTB	3'	ATCTCAGACAGTGAAAGTGAAA	21959	
	TG		CATTTCACTTTCAGTCTGAGAT		
			GTAAAGTGAAAGTGACAGACTCTA		
GAM1594	KLF4	3'	TCCCAGACAGTGGATATG	14891	CT A
			CA TTCAGTGTCTG GA		
			GT AGGTGACAGAC CT		
			AT C		
GAM1594	PHYH	3'	ACAGTAAAAGTGAAAT	20608	C
			ATTTCACTTT ACTGT		
			TAAAGTGAAA TGACA		
			A		
GAM1594	PKD2	3'	TCCAGGTTGAAAGTGAAA	60096	CTG A
			TTTCACTTTC TCTG GA		

AAAGTGAAAGT GGAC CT  
 T\_\_ \_  
 GAM1594 WRN 3' GGGCAGTGAAAATGAAA 5098 C  
 TTTCA TTTCACTGTCT  
 ||||| |||||  
 AAAGT AAAGTGACGGG  
 A  
 GAM1594 ZNF216 3' ATCTGCACAGCAAAGTGAAA 20017 CA CTG  
 TTTCACTTT CTGT AGAT  
 ||||| ||| |||  
 AAAGTGAAA GACA TCTA  
 C\_ CG\_  
 GAM1594 CG012 5' CTCACCTCTGAAAGTGAA 83218 CT CT  
 TTCACCTTTCA GT GAG  
 ||||| || |||  
 AAGTGAAAGT CA CTC  
 CT \_  
 GAM1594 EIF2C2 3' ATCTTCTGAGAGTGAAAG 71946 G T\_  
 CTTTCACT TC GAGAT  
 ||||| || |||  
 GAAAGTGA AG TTCTA  
 G TC  
 GAM1594 FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802 ACTTTCACT  
 G CATTTC GTCTGAGAT  
 ||||| |||||  
 GTAAAG CAGACTCTA  
 AAACATTT\_  
 GAM1594 FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281 CTT  
 CATTTC TCACTGTCTGAGAT  
 ||||| |||||  
 GTAAAGT AGTGACAGACTCTA  
 C\_  
 GAM1594 KIAA0984 3' TTTGTCCAGTGAAAATGAA 65534 C TC  
 TTCA TTTCACTG TGAG  
 ||| ||||| |||  
 AAGT AAAGTGAC GTTT  
 A CT  
 GAM1594 KLHL6 3' ATCTCAGAGCAGGAAA 55299 A \_  
 TTTC CTG TCTGAGAT  
 ||| ||| |||||  
 AAAG GAC AGACTCTA  
 \_ G  
 GAM1594 NIR3 3' GCAGTGAAAGTGCAAT 66242 T  
 ATT CACTTTCACTGT  
 ||| |||||  
 TAA GTGAAAGTGACG  
 C  
 GAM1594 PORIMIN 3' ATCTCAGAGGGCCAAAGTGAA 53598 CA G  
 TTCACCTTT CT TCTGAGAT  
 ||||| || |||||

			AAGTGAAA GG AGACTCTA		
			CC G		
GAM1594	PP35	3'	ATCTCAGACTGAAA 22814	CT	
			TTTCA GTCTGAGAT		
			AAAGT CAGACTCTA		
—					
GAM1594	PRTD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148	TCAC C_	
			CATTTCACTT TGT TGAG		
			GTAAAGTGAA ACG ACTC		
			TA__ TT		
GAM1594	SEP15	3'	TCCTACAGTAAGAGTGAAA 14934	C CT	
			TTTCACTTT ACTGT GA		
			AAAGTGAGA TGACA CT		
			A TC		
GAM1594	SFXN2	3'	CTCAGGGGAAAAAAGTGAAA 73941	CACTG	
			TTTCACTTT TCTGAG		
			AAAGTGAAA GGA CTC		
			AAAGG		
GAM1594	LOC149703	3'	ATCTCAGACAGCCGTTTGGAAA 84647	ACTTTCA	
			TTTC CTGTCTGAGAT		
			AAAG GACAGACTCTA		
			GTTTGCC		
GAM1594	LOC154007	3'	ATCTCAAACCCTTTAGTGAAA 81015	TTCAC T C	
			TTTCACT GT TGAGAT		
			AAAGTGA CA ACTCTA		
			TTTCC_ A		
GAM1594	LOC155004	3'	TCATTTAAGTGAAAAGGAAA 81226	A GTC_	
			TTTC CTTTCACT TGA		
			AAAG GAAAGTGA ACT		
			_ ATTT		
GAM1594	LOC222134	5'	ACAGTGAAGTGAAATG 94136	T	
			CATTTCACTT CACTGT		
			GTAAAGTGAA GTGACA		
—					
GAM1595	A1BG	3'	CAGGGTCTCACTGTGTTGC 55413	TAT_	
			GCAACACA GGCTTTG		
			CGTTGTGT CTGGGAC		
			CACT		
GAM1595	ACPT	3'	CACCCCGCCATATGCTGC 54986	ACA TTT	
			GCA CATATGGC GTG		

			CGT GTATACCG CAC		
			C__ CCC		
GAM1595 ACPT	3'	CACCCCGCCATATGCTGC	54980	ACA	TTT
		GCA CATATGGC GTG			
		CGT GTATACCG CAC			
		C__ CCC			
GAM1595 AHCY	3'	CACAAAGCCCATGTGTTTTGC	5473	C	_
		GCAA ACATATGG CTTTGTG			
		CGTT TGTGTACC GAAACAC			
		T C			
GAM1595 BCL7A	3'	CAGGATTCCATTTGTGTTGCT	40638	T	CT G
		AGCAACACA ATGG TT TG			
		TCGTTGTGT TACC AG AC			
		T TT G			
GAM1595 CDK5R2	3'	CACAAAGCCACCGCCGCTGTT	14132	ACACATA	
		AGCA TGGCTTTGTG			
		TTGT ACCGAAACAC			
		CGCCGCC			
GAM1595 CHC1	3'	CACAAAGCATACTCTTGC	7019	CACA	G
		GCAA TATG CTTTGTG			
		CGTT ATAC GAAACAC			
		CTC_ _			
GAM1595 CIT	3'	CACAAGGCATCTGTTGCT	69741	CATATG	
		AGCAACA GCTTTGTG			
		TCGTTGT CGGAACAC			
		CTA__			
GAM1595 COL6A2	5'	CAGGGCCACAGGTGCTGC	8480	A	ATA
		GCA CAC TGGCTTTG			
		CGT GTG ACCGGGAC			
		C GAC			
GAM1595 COL6A2	5'	CAGGGCCACAGGTGCTGC	54168	A	ATA
		GCA CAC TGGCTTTG			
		CGT GTG ACCGGGAC			
		C GAC			
GAM1595 EYA1	3'	CACAGCGTTATGTGTCTGC	4952	AC	T
		GCA ACATATGGC TTGTG			
		CGT TGTGTATTG GACAC			
		C_ C			
GAM1595 FBN2	3'	CAAGGAACCATATGTG	8844	_	
		CACATATGG CTTTG			

			GTGTATACC GGAAC	
			AA	
GAM1595 FMO1	3'	CACAAATGATTGTGTTGT	8924	TATGGC
		GCAACACA TTTGTG		
		TGTTGTGT AAACAC		
		TAGT__		
GAM1595 GALNT2	3'	CACAAAGCCGTTTCGCAGCT	15594	AACACAT
		AGC ATGGCTTTGTG		
		TCG TGCCGAAACAC		
		ACGCT__		
GAM1595 GALNT2	3'	CACAAAGCCGAGTCGTGT	15593	_ A
		ACAC AT TGGCTTTGTG		
		TGTG TG GCCGAAACAC		
		C A		
GAM1595 GPR4	3'	CAGGGTCTCACTGTGTTGC	59902	TAT_
		GCAACACA GGCTTTG		
		CGTTGTGT CTGGGAC		
		CACT		
GAM1595 HNMT	3'	CACAAAGCCTGTGTTACT	22567	C TAT
		AG AACACA GGCTTTGTG		
		TC TTGTGT CCGAAACAC		
		A ____		
GAM1595 IL1RN	3'	CACAAAGCCCTTCCATGTCGC	5141	A CATAT_
		GC ACA GGCTTTGTG		
		CG TGT CCGAAACAC		
		C ACCTTC		
GAM1595 IL2RB	3'	CACAAAGTGGATGCCTGCT	6069	ACA ATG
		AGCA CAT GCTTTGTG		
		TCGT GTA TGAAACAC		
		CC_ GG_		
GAM1595 ITS2	3'	CACAAAGCCATGCACGCT	38971	AACACA
		AGC TATGGCTTTGTG		
		TCG GTACCGAAACAC		
		CAC__		
GAM1595 JRK	3'	CAGGGTCTCACTGTGTTGC	86524	TAT_
		GCAACACA GGCTTTG		
		CGTTGTGT CTGGGAC		
		CACT		
GAM1595 LANCL1	3'	CACAATTTTATATGTATGCT	20210	AC CT
		AGCA ACATATGG TTGTG		

			TCGT TGTATATT AACAC		
			A_ TT		
GAM1595 LGR6	5'	GGCCATCGTGTTGCT	84200	AT	
		AGCAACAC ATGGCT			
		TCGTTGTG TACCGG			
		C_			
GAM1595 LRRC2	3'	CAAGGCACCATGTGTTACT	44465	C	ATG
		AG AACACAT GCTTTG			
		TC TTGTGTA CGGAAC			
		A CCA			
GAM1595 MYBL2	3'	CAGGGCCATGTGCTGC	10154	ACA	
		GCA CATATGGCTTTG			
		CGT GTGTACCGGGAC			
		C_			
GAM1595 OCLN	3'	CACAAAGTTTTGGTTGCT	10314	A	TAT
		AGCAAC CA GGCTTTGTG			
		TCGTTG GT TTGAAACAC			
		_ T_			
GAM1595 OSR1	3'	CACAAAGTAATATGTG	17566	G	
		CACATAT GCTTTGTG			
		GTGTATA TGAAACAC			
		A			
GAM1595 PCDH9	5'	CACAAAGTGACAGTGCTGGCT	82794	AA_	ATATG
		AGC CAC GCTTTGTG			
		TCG GTG TGAAACAC			
		GTC ACAG_			
GAM1595 PRDM2	5'	CACAAAGCCACATCCTGC	31847	ACAC	A
		GCA AT TGGCTTTGTG			
		CGT TA ACCGAAACAC			
		CC_ C			
GAM1595 PRDM2	5'	CACAAAGCCACATCCTGC	24246	ACAC	A
		GCA AT TGGCTTTGTG			
		CGT TA ACCGAAACAC			
		CC_ C			
GAM1595 PRG4	3'	CACAAAGCTTTATCGTGTTGT	19415	_	T
		GCAACAC ATA GGCTTTGTG			
		TGTTGTG TAT TCGAAACAC			
		C T			
GAM1595 RXRB	3'	CACAAAGCACTGGCCTTGC	41757	CA_	TATG
		GCAA CA GCTTTGTG			

		CGTT GT CGAAACAC		
		CCG CA__		
GAM1595	SMARCD1	3' CACAAAGTTCCCATGTG	57429	___
		CATATGG CTTTGTG		
		GTGTACC GAAACAC		
		CTT		
GAM1595	SMARCD1	3' CACAAAGTTCCCATGTG	11811	___
		CATATGG CTTTGTG		
		GTGTACC GAAACAC		
		CTT		
GAM1595	SMURF1	3' CACGTGTGATCTGTGTTGC	92448	T G TT
		GCAACACA AT GC TGTG		
		CGTTGTGT TA TG GCAC		
		C G T_		
GAM1595	STX7	3' CACCAAGATGTGTGTTACT	13108	C GG T
		AG AACACATAT CTT GTG		
		TC TTGTGTGTA GAA CAC		
		A _ C		
GAM1595	TAF4B	3' CACAAAGCATTGTTGC	87167	CATATG
		GCAACA GCTTTGTG		
		CGTTGT CGAAACAC		
		TA___		
GAM1595	TF	3' CACAGCTCTGTGTTGC	6512	TAT T
		GCAACACA GGCT TG		
		CGTTGTGT TCGA AC		
		C_ C		
GAM1595	TLR4	5' CACAGGGCCACTGCTGCT	12317	A CATA
		AGCA CA TGGCTTTGTG		
		TCGT GT ACCGGGACAC		
		C C_		
GAM1595	TLR4	5' CACAGGGCCACTGCTGCT	56727	A CATA
		AGCA CA TGGCTTTGTG		
		TCGT GT ACCGGGACAC		
		C C_		
GAM1595	TLR4	5' CACAGGGCCACTGCTGCT	56732	A CATA
		AGCA CA TGGCTTTGTG		
		TCGT GT ACCGGGACAC		
		C C_		
GAM1595	TLR4	5' CACAGGGCCACTGCTGCT	56736	A CATA
		AGCA CA TGGCTTTGTG		



			TCGT GT ACCGGGACAC		
			C C__		
GAM1595 VIPR2	3'	CACAGTCTCCATGTGTGTC	12605	A	CT_
		GCA CACATATGG TTGTG			
		CGT GTGTGTACC GACAC			
		_ TCT			
GAM1595 ANKT	3'	CAGGGTCTCACTGTGTTGC	33024	TAT_	
		GCAACACA GGCTTTG			
		CGTTGTGT CTGGGAC			
		CACT			
GAM1595 ATP9A	3'	CACAAAGCCAGTGGCTGTT	62039	A_ ATA	
		AGCA CAC TGGCTTTGTG			
		TTGT GTG ACCGAAACAC			
		CG _			
GAM1595 CETN2	3'	CACATGTTACACCTGTGTTGC	15093	TA GCTT_	
		GCAACACA TG TGTG			
		CGTTGTGT AC ACAC			
		CC ATTGT			
GAM1595 CYLD	3'	CACAAGGTTTTATACTGCT	30883	ACAC TG	
		AGCA ATA GCTTTGTG			
		TCGT TAT TGGAACAC			
		CA__ TT			
GAM1595 DKFZP586A0522	3'	CAGGGTCTCACTGTGTTGC	25871	TAT_	
		GCAACACA GGCTTTG			
		CGTTGTGT CTGGGAC			
		CACT			
GAM1595 DKFZp762K222	3'	ACAGATGCGTGTTGCT	71116	ATATG _	
		AGCAACAC GC TTTGT			
		TCGTTGTG CG AGACA			
		_____ T			
GAM1595 FLJ10297	3'	CAGGGCTTCACTGTGTTGC	35979	TAT_	
		GCAACACA GGCTTTG			
		CGTTGTGT TCGGGAC			
		CACT			
GAM1595 FLJ10511	3'	CACATGTGTATGTGCAGCT	36204	AA G TT	
		AGC CACATATG C TGTG			
		TCG GTGTATGT G ACAC			
		AC _ T_			
GAM1595 FLJ11029	5'	CACTAGCACCTGTGTTGCT	60973	TATG TT	
		AGCAACACA GCT GTG			

TCGTTGTGT CGA CAC  
CCA\_ T\_  
GAM1595 FLJ11117 3' CACAAAGCTTGTATGTG 37073 \_  
CACATATG GCTTTGTG  
||||| |||||  
GTGTATGT CGAAACAC  
T  
GAM1595 FLJ11715 3' CAGGGTCTCCATATGTTGC 44668 C AT\_  
GCAACA AT GGCTTTG  
||||| || |||||  
CGTTGT TA CTGGGAC  
A CCT  
GAM1595 FLJ20275 3' CACAAAGGGCTTTATGTGTCAG 34819 A\_ T \_  
CT AGC ACACATA GGCT TTGTG  
||| ||||| ||| |||||  
TCG TGTGTAT TCGG AACAC  
AC T GA  
GAM1595 FLJ20413 3' CAGAGCCGCATGCACTGCT 35131 ACA A  
AGCA CAT TGGCTTTG  
|||| ||| |||||  
TCGT GTA GCCGAGAC  
CAC C  
GAM1595 FLJ20450 3' CACCTGGGACCTGTGTTGCT 35192 TAT \_ T\_  
AGCAACACA GG CTT GTG  
||||||| || ||| |||  
TCGTTGTGT CC GGG CAC  
\_ A TC  
GAM1595 FLJ20671 3' CAATTCAAATGTGTTGC 35516 A CT  
GCAACACAT TGG TTG  
||||||| ||| |||  
CGTTGTGTA ACT AAC  
A T\_  
GAM1595 FLJ23598 3' CACAAAGAGAGGCTGTGCTGC 45521 A TATGG\_  
GCA CACA CTTTGTG  
||| ||| |||||  
CGT GTGT GAAACAC  
C CGGAGA  
GAM1595 FR5B 3' CATAGGCCATACATGTTACT 19090 C CA T  
AG AACA TATGGCTT GTG  
|| ||| ||||| |||  
TC TTGT ATACCGGA TAC  
A AC \_  
GAM1595 H2AV 3' CACAGCCATATGTATTGTT 56845 C T  
AGCAA ACATATGGCT TG  
|||| ||||| ||| |||  
TTGTT TGTATACCGA AC  
A C  
GAM1595 HIC2 3' CACAAAGTCTGTACCGC 65256 AAC TAT  
GC ACA GGCTTTGTG  
|| ||| |||||

			CG TGT CTGAAACAC		
			CCA ____		
GAM1595	KIAA0140	3'	CACATGGCCATGTCTTGC	27806	CAC T
			GCAA ATATGGCT TGTG		
			CGTT TGTACCGG ACAC		
			C__ T		
GAM1595	KIAA0215	3'	CAAATTCCATATGTAATGC	28416	AC C_
			GCA ACATATGG TTTG		
			CGT TGTATACC AAAC		
			AA TT		
GAM1595	KIAA0254	3'	AGCCACCTGTGTTGCT	28595	TA
			AGCAACACA TGGCT		
			TCGTTGTGT ACCGA		
			CC		
GAM1595	KIAA0618	3'	CACAAAAACATGTGTTGT	29162	TA GC
			GCAACACA TG TTTGTG		
			TGTTGTGT AC AAACAC		
			__ AA		
GAM1595	KIAA0953	3'	AGCTTTCATAGTGTGCT	66778	A ____
			AGCAACAC TATG GCT		
			TCGTTGTG ATAC CGA		
			_ TTT		
GAM1595	KIAA1193	3'	CACAGAGCCATATACCTCGCT	67630	AACAC
			AGC ATATGGCTTTGTG		
			TCG TATACCGAGACAC		
			CTCCA		
GAM1595	KIAA1281	3'	CACAGAGTAACAAATGTTGCT	89151	CATATG
			AGCAACA GCTTTGTG		
			TCGTTGT TGAGACAC		
			AAACAA		
GAM1595	KIAA1466	5'	AGCCATATGTGCGCT	71913	AA
			AGC CACATATGGCT		
			TCG GTGTATACCGA		
			C_		
GAM1595	KIAA1821	3'	CAGGGTCTCACTGTGTTGC	71780	TAT_
			GCAACACA GGCTTTG		
			CGTTGTGT CTGGGAC		
			CACT		
GAM1595	KIF13B	3'	CACAAAGTCCGTGGTGC	30904	A ATAT
			GCA CAC GGCTTTGTG		

			CGT GTG CTGAAACAC		
			G C__		
GAM1595	KIF13B	3'	CACAAAGTCCGTGGTGC 82820	A	ATAT
			GCA CAC GGCTTTGTG		
			CGT GTG CTGAAACAC		
			G C__		
GAM1595	MGC12921	3'	CACAAAGGCCGTTATTGC 63775	CACAT	_
			GCAA ATGGC TTTGTG		
			CGTT TGCCG AAACAC		
			AT__ G		
GAM1595	MGC14836	5'	CACAAAGCTATCATCCTGC 53035	ACACAT	
			GCA ATGGCTTTGTG		
			CGT TATCGAAACAC		
			CCTAC_		
GAM1595	MGC15429	3'	CACATTGTCATGTGCAGCT 51249	AACA	TT
			AGC CATATGGC TGTG		
			TCG GTGTACTG ACAC		
			AC__ TT		
GAM1595	MGC15875	3'	CGAGGCCATAATGCT 51908	ACACA	
			AGCA TATGGCTTTG		
			TCGT ATACCGGAGC		
			A__		
GAM1595	MGC16279	5'	GAAGCCATCGTGTGCGCT 51888	A	AT
			AGC ACAC ATGGCTTT		
			TCG TGTG TACCGAAG		
			C C_		
GAM1595	MGC27434	3'	CACAATAAGTATGTGTT 58947	GGCT	
			AACACATAT TTGTG		
			TTGTGTATG AACAC		
			AAT_		
GAM1595	MGC3048	3'	CACAAAGCATGAATGTT 43899	CA	G
			AACA TATG CTTTGTG		
			TTGT GTAC GAAACAC		
			AA _		
GAM1595	MIG-6	3'	CACAAGCTGGCCTTGTTGCT 38486	TAT	__
			AGCAACACA GGCT TTGTG		
			TCGTTGTGT CCGG AACAC		
			T__ TCG		
GAM1595	MUC17	3'	CACTGCCCCATATGTGTCCCT 94271	CA	CTTT
			AG ACACATATGG GTG		

			TC TGTGTATACC CAC		
			CC CCGT		
GAM1595 MYO3B	3'		CACTCTCCCACATGTGTTGT 57301	A	CTTT
			GCAACACAT TGG GTG		
			TGTTGTGTA ACC CAC		
			C CTCT		
GAM1595 NS1-BP	3'		CACAAAGCTTTTGCATATTGC 72542	CA__	TAT
			GCAA CA GGCTTTGTG		
			CGTT GT TCGAAACAC		
			ATAC TT_		
GAM1595 OR51E2	3'		CACAGGTTTTATGTGTTCT 47791	C	TG T
			AG AACACATA GCTT GTG		
			TC TTGTGTAT TGGA CAC		
			_ TT _		
GAM1595 PRDM11	3'		CAGGTGCTCCATGTGTTGC 39581	AT	_
			GCAACACAT GGC TTTG		
			CGTTGTGTA TCG GGAC		
			CC T		
GAM1595 PRO0943	5'		CACAAAAGTGTTATATGTG 37701	___	
			CACATATGGC TTTGTG		
			GTGTATATTG AAACAC		
			TGA		
GAM1595 SULT1C2	5'		CACAACGCAGCCATATGCTG 21674	_	___
			CA CATATGGCT TTGTG		
			GT GTATACCGA AACAC		
			C CGC		
GAM1595 VEST1	3'		CACCTGCCATACATGTTGT 53685	CA	TTT
			GCAACA TATGGC GTG		
			TGTTGT ATACCG CAC		
			AC TC_		
GAM1595 ZFP100	3'		AGTCACCTGTGTTGCT 70049	TA	
			AGCAACACA TGGCT		
			TCGTTGTGT ACTGA		
			CC		
GAM1595 ZNF363	5'		AGCCATATTGTCGCT 73452	A	C
			AGC ACA ATATGGCT		
			TCG TGT TATACCGA		
			C _		
GAM1595 LOC118611	5'		CACAGAGCATTTGCGTTACT 75469	C	A TATG
			AG AAC CA GCTTTGTG		

	TC TTG GT CGAGACAC		
	A C TTA_		
GAM1595 LOC120526 3'	CAGGGCCATTGCACTGCT	74015	ACA T
	AGCA CA ATGGCTTTG		
	TCGT GT TACCGGGAC		
	CAC _		
GAM1595 LOC126669 3'	CACAAAGTTCCATATGT	75399	__
	ACATATGG CTTTGTG		
	TGTATACC GAAACAC		
	TT		
GAM1595 LOC139840 5'	CACAAGAGCCATGGGT	76266	A _
	AC TATGGCTTT GTG		
	TG GTACCGAGA CAC		
	G A		
GAM1595 LOC143465 5'	CACATGCACATATGTG	82962	_ TT
	CACATATG GC TGTG		
	GTGTATAC CG ACAC		
	A T_		
GAM1595 LOC146774 3'	CACTGACATGTGTGTGC	78094	A GCTTT
	GCA CACATATG GTG		
	CGT GTGTGTAC CAC		
	_ AGT_		
GAM1595 LOC147407 5'	CACAAAGCTATCATCCTGC	76322	ACACAT
	GCA ATGGCTTTGTG		
	CGT TATCGAAACAC		
	CCTAC_		
GAM1595 LOC151057 3'	ACAGAGCACATACTGT	85199	_ _
	ACA TATG GCTTTGT		
	TGT ATAC CGAGACA		
	C A		
GAM1595 LOC151473 3'	CACAACAACCTATGTGTT	80254	T CT_
	AACACATA GG TTGTG		
	TTGTGTAT CC AACAC		
	_ AAC		
GAM1595 LOC154739 5'	CACAAAGTTCAAATGTATGC	86227	AC A _
	GCA ACAT TGG CTTTGTG		
	CGT TGTA ACT GAAACAC		
	A_ A T		
GAM1595 LOC157507 5'	CACAGCTGTGTATGTGTGCT	81454	A _ T
	AGCA CACATAT GGCT TG		

	TCGT GTGTATG TCGA AC		
	— TG C		
GAM1595 LOC161734 3'	CACAAACATTTAGTGTGCT 87097	AT_ GC	
	AGCAACAC ATG TTTGTG		
	TCGTTGTG TAC AAACAC		
	ATT —		
GAM1595 LOC196410 3'	CACAAAAGTCATGGTG 87657 A —		
	CAC TATGGCTTT GTG		
	GTG GTACTGAAA CAC		
	— A		
GAM1595 LOC196485 3'	CACAAAAACCTGTGTTGT 87730	TAT C_	
	GCAACACA GG TTTGTG		
	TGTTGTGT CC AAACAC		
	— AA		
GAM1595 LOC196529 3'	CAGGGTCTCACTGTGTTGC 87771	TAT_	
	GCAACACA GGCTTTG		
	CGTTGTGT CTGGGAC		
	CACT		
GAM1595 LOC197003 5'	CACAAAGCTCCATGCTGT 87870 — AT		
	ACA CAT GGCTTTGTG		
	TGT GTA TCGAAACAC		
	C CC		
GAM1595 LOC202025 5'	CACAGTTGTATGGTTGCT 90281 A TG T		
	AGCAAC CATA GCT TG		
	TCGTTG GTAT TGA AC		
	— GT C		
GAM1595 LOC203276 3'	CACAAAGTTCAAGTGTATGC 90475 — ATAT		
	GCA ACAC GGCTTTGTG		
	CGT TGTG TTGAAACAC		
	A AAC_		
GAM1595 LOC203292 3'	CAGGGTTTCATATGTGTT 90509 —		
	AACACATATG GCTTTG		
	TTGTGTATAC TGGGAC		
	TT		
GAM1595 LOC203305 3'	CACAAAGTTCAAGTGTATGC 90519 — ATAT		
	GCA ACAC GGCTTTGTG		
	CGT TGTG TTGAAACAC		
	A AAC_		
GAM1595 LOC221354 3'	CACAAAAACATGTGTTGT 92409 TA GC		
	GCAACACA TG TTTGTG		

TGTGTGT AC AAACAC  
 \_ AA  
 GAM1595 LOC254243 3' CACAAAGTTCAAGTGTATGC 97404 \_ ATAT  
 GCA ACAC GGCTTTGTG  
 ||| ||| |||||  
 CGT TGTG TTGAAACAC  
 A AAC\_  
 GAM1595 LOC255870 3' CACAAGTGGCCATGTCCTGC 94657 ACAC \_  
 GCA ATATGGCT TTGTG  
 ||| ||||| ||||  
 CGT TGTACCGG AACAC  
 CC\_ TC  
 GAM1595 LOC90038 3' CACAAAGTTCAAGTGTATGC 61148 \_ ATAT  
 GCA ACAC GGCTTTGTG  
 ||| ||| |||||  
 CGT TGTG TTGAAACAC  
 A AAC\_  
 GAM1595 LOC90321 3' CACAAATGGATTGTGTGTGC 62262 A TGGC\_  
 GCA CACATA TTTGTG  
 ||| ||||| ||||  
 CGT GTGTGT AAACAC  
 \_ TAGGT  
 GAM1595 LOC90750 3' CACAAAGTTAAGATTGCT 63917 CACATA  
 AGCAA TGGCTTTGTG  
 ||||| |||||  
 TCGTT ATTGAAACAC  
 AGA\_  
 GAM1595 LOC91069 3' GAAGCCATCGTGTCACT 64778 CA AT  
 AG ACAC ATGGCTTT  
 || ||| |||||  
 TC TGTG TACCGAAG  
 AC C\_  
 GAM1595 LOC92539 3' CACAAAGCCACTGTAGC 69630 A CATA  
 GC ACA TGGCTTTGTG  
 || ||| |||||  
 CG TGT ACCGAAACAC  
 A C\_  
 GAM1596 LCP1 3' AACATCTTGAATACTCTGCCCT 9691 A T G  
 C GAG GCA AGTATTCAGGA TGTT  
 ||| ||| ||||| ||||  
 CTC CGT TCATAAGTTCT ACAA  
 C C \_  
 GAM1596 OPCML 3' AACACTCCTTTCTATTCTCTC 10342 C TATTC  
 GAGAG ATAG AGGAGTGTT  
 ||||| ||| |||||  
 CTCTC TATC TCCTCACAA  
 T TT\_  
 GAM1596 XK 3' AACACTCAAGACTATGTTCTC 40797 ATTCAG  
 GAGAGCATAGT GAGTGTT  
 ||||| |||||



CTCTTGTATCA CTCACAA  
 GAA\_\_\_\_  
 GAM1596 LOC220506 3' CCTGAATACTCTGCTC 74076 T  
 GAGCA AGTATTCAGG  
 |||| |||||  
 CTCGT TCATAAGTCC  
 C  
 GAM1596 LOC92579 3' AACACTCTGTGACCACCACACT 69836 CATA AT \_  
 C GAG GT TCA GGAGTGTT  
 || | || |||||  
 CTC CA AGT TCTCACAA  
 ACAC CC G  
 GAM1597 GPR56 3' CCACCTGCCCATGTGATGAA 19068 G T AAA A  
 TT ATCA CGTG GCAG TGG  
 || ||| ||| ||| |||  
 AA TAGT GTAC CGTC ACC  
 G \_ C\_ C  
 GAM1597 KAL1 3' TCCAGTATTATTCAAATGATCA 4017 CG AGCAGA  
 A TTGATCAT TGAA TGGA  
 ||||| ||| |||  
 AACTAGTA ACTT ACCT  
 A\_ ATTATG  
 GAM1597 FLJ14107 3' GCTTCCAGGATGATCAA 46695 G A  
 TTGATCATC TG AAGC  
 ||||| || |||  
 AACTAGTAG AC TTCG  
 G C  
 GAM1597 PRO2325 5' CCATCTGCCTCAGTCTGGGCCA 37588 AT ATCG\_ AA  
 A TTG C TGA GCAGATGG  
 || | || |||||  
 AAC G ACT CGTCTACC  
 CG GTCTG C\_  
 GAM1597 LOC119369 3' CCAAAGGCCTTCAAATGATCAA 75510 CG A AGA  
 TTGATCAT TGAA GC TGG  
 ||||| ||| || |||  
 AACTAGTA ACTT CG ACC  
 A\_ C GAA  
 GAM1598 ATP2B2 3' GCTTAAATTGCTCT 8067 TAACAG  
 AGAGCAATT AGGC  
 ||||| |||  
 TCTCGTTAAA TTCG  
 \_\_\_\_\_  
 GAM1598 AXIN1 3' AGGGCCTCTGTCAATTGT 60849 TTA  
 GCAATT ACAGAGGCCCT  
 |||| |||||  
 TGTAA TGTCTCCGGGA  
 C\_  
 GAM1598 CRP 3' GGCCATTAGAATTGC 71629 CAGA  
 GCAATTTTAA GGCC  
 ||||| |||

			CGTTAAGATT CCGG		
			A__		
GAM1598 DACH	3'	AGGACCTATGAAAATTGTCT	54968	G	AACAG C
		AGA CAATTTT AGG CCT			
		TCT GTTAAAA TCC GGA			
		_ GTA__ A			
GAM1598 FPGS	3'	AGGGCCTCTGCCTGGGACACTG	17080	A__	A_
C		GCA TTTTA CAGAGGCCCT			
		CGT AGGGT GTCTCCGGGA			
		CAC CC			
GAM1598 HLA-E	3'	GGGCCTCTGAATCTGTCTG	91025	G AT	TAA
		CAGA CA TT CAGAGGCCC			
		GTCT GT AA GTCTCCGGG			
		_ CT _			
GAM1598 HOXB3	5'	TTGTAAAATTGCTTTG	9264		
		CAGAGCAATTTTAACAG			
		GTTTCGTTAAAATTGTT			
GAM1598 HOXC5	3'	AGGGCCCCCACAGTTGCTCT	38490		TTAACAGA
		AGAGCAATT GGCCCT			
		TCTCGTTGA CCGGGA			
		CACCC__			
GAM1598 IHPK1	3'	GGGCCTCTGGTGGCTCTG	95760	AATTTTAA	
		CAGAGC CAGAGGCCC			
		GTCTCG GTCTCCGGG			
		GTG__			
GAM1598 IL22RA2	3'	CCCATGAAAATTGCTC	53690	AA GA	
		GAGCAATTTT CA GG			
		CTCGTTAAAA GT CC			
		_ AC			
GAM1598 LY64	3'	GCTTAGCAAAAATTGCTCT	18756	AACAG	
		AGAGCAATTTT AGGC			
		TCTCGTTAAAA TTCG			
		CGA__			
GAM1598 MASP1	3'	AGGGCCTCTGCATTGTTGCTC	57469	TTTAA	
		GAGCAAT CAGAGGCCCT			
		CTCGTTG GTCTCCGGGA			
		TTAC_			
GAM1598 MYO1D	3'	AGGGCCTCTGACCACCGCTCTG	71765	AATTTTAA	
		CAGAGC CAGAGGCCCT			

		GTCTCG	GTCTCCGGGA		
		CCACCA__			
GAM1598	PFKFB4	3'	AGGGCCTCTACCATCCTCTCTG 15865	CAATTTTAAC	
			CAGAG AGAGGCCCT		
			GTCTC TCTCCGGGA		
			TCCTACCA__		
GAM1598	PPP2R4	3'	GCCTCTGTTTTGCACCTG 60559	A_ TTTT	
			CAG GCAA AACAGAGGC		
			GTC CGTT TTGTCTCCG		
			CA ____		
GAM1598	RPL15	3'	TCTGTAAAACTAGTCTG 11385	GCAA	
			CAGA TTTTAACAGA		
			GTCT AAAATTGTCT		
			GATC		
GAM1598	SRD5A1	3'	TTGTTAAAATTCTCT 6461	C	
			AGAG AATTTTAACAG		
			TCTC TAAAATTGTT		
			—		
GAM1598	XYLB	3'	AGGGCCTCTCTTACTTGC 17557	TTT C	
			GCAA TAA AGAGGCCCT		
			CGTT ATT TCTCCGGGA		
			C__ C		
GAM1598	ZNF267	5'	GACCTCTGTTGCTCTG 12735	ATTTTA CC	
			CAGAGCA ACAGAGG C		
			GTCTCGT TGTCTCC G		
			AA		
GAM1598	ARTS-1	3'	CTCTTTTAAAATTGCTCTG 33184	C	
			CAGAGCAATTTTAA AGAG		
			GTCTCGTTAAAATT TCTC		
			T		
GAM1598	C1orf25	3'	GGCTCACATGTTAAAATGACCC 72536	AGCA GA__	
	TG		CAG ATTTTAACA GGCC		
			GTC TAAAATTGT TCGG		
			CCAG ACAC		
GAM1598	C22orf5	3'	AGGGCCCCCTGGGCACCGCTTCT 24339	_ AATTTTAA A	
	G		CAGA GC CAG GGCCCT		
			GTCT CG GTC CCGGGA		
			T CCACGG__ C		
GAM1598	CD109	3'	AGGAGCATACTGAAAATTGCC 56045	A AA AG_ _	
	TG		CAG GCAATTTT CAG GC CCT		

GTC CGTTAAAA GTC CG GGA  
 C \_ ATA A  
 GAM1598 FKHL18 3' AGGGCCTCTTGGGATTACTCT 79553 C\_ AC  
 G CAGAG AATTTTA AGAGGCCCT  
 |||| ||||| |||||  
 GTCTC TTAGGGT TCTCCGGGA  
 AT \_  
 GAM1598 FLJ22054 3' CCATCTGTAAAAATTACCTG 94393 AGC \_  
 CAG AATTTTAACAGA GG  
 || ||||| ||  
 GTC TTAAAATTGTCT CC  
 CA\_ A  
 GAM1598 FLJ23074 3' GCCTTAGAAAATTGCCTG 46818 A AACAA  
 CAG GCAATTTT GAGGC  
 || ||||| ||  
 GTC CGTTAAAA TTCCG  
 \_ GA\_  
 GAM1598 FLJ30473 3' GGCCTCTGCTGCCACTG 58463 A\_ ATTTTAA  
 CAG GCA CAGAGGCC  
 || || |||||  
 GTC CGT GTCTCCGG  
 AC C\_  
 GAM1598 FOXJ1 3' GGCCTCTGGGGTCTTTGCCTG 7574 A TTTTAA  
 CAG GCAA CAGAGGCC  
 || || |||||  
 GTC CGTT GTCTCCGG  
 \_ TCTGGG  
 GAM1598 KIAA0514 3' GCCTAAAATTGCACT 28086 A AACAG  
 AG GCAATTTT AGGC  
 || ||||| ||  
 TC CGTTAAAA TCCG  
 A \_  
 GAM1598 KIAA0543 3' AGAGCCCCCAGAGGCATTGTTC 68931 TTAAACAGA C  
 TG CAGAGCAAT GGC CT  
 ||||| |||  
 GTCTTGTTA CCG GA  
 CGGAGACCC A  
 GAM1598 KIAA1546 3' GGCCTCTGGATTTTGCTC 67909 TTTTAA  
 GAGCAA CAGAGGCC  
 |||| |||||  
 CTCGTT GTCTCCGG  
 TTAG\_  
 GAM1598 KRTHB2 3' AGGGCCTCTGCCCTGAACATCT 52285 GCAATTTTAA  
 G CAGA CAGAGGCCCT  
 || |||||  
 GTCT GTCTCCGGGA  
 ACAAGTCCC\_  
 GAM1598 LIPI 3' CTCATGTAAAAATCACTT 79566 CA \_  
 GAG ATTTTAACA GAG  
 || ||||| ||

TTC TAAAATTGT CTC  
 AC A  
 GAM1598 MGC15606 5' AGGACCTCTGGTCAAAATTGCC 58874 A AA\_ C  
 TG CAG GCAATTTT CAGAGG CCT  
 ||| ||||| ||||| |||  
 GTC CGTTAAAA GTCTCC GGA  
 \_ CTG A  
 GAM1598 MGC20255 3' GCCTCTGCTACGGAGCGCTTCT 53443 \_ AA \_ A  
 G CAGA GC TTT TA CAGAGGC  
 |||| | ||| || |||||  
 GTCT CG AGG AT GTCTCCG  
 T CG C C  
 GAM1598 MGC2742 5' AGGGCCTCTGTCTCCATCTCTG 43744 CAATTTTA  
 CAGAG ACAGAGGCCCT  
 |||| | |||||  
 GTCTC TGTCTCCGGGA  
 TACCTC\_  
 GAM1598 NLP\_1 3' TGTTTAAAATTGCTTTG 23710 \_  
 CAGAGCAATTTTAA CA  
 ||||| ||||| ||  
 GTTTCGTTAAAATT GT  
 T  
 GAM1598 PIK4CA 3' AGGGCCTCTGCCCCATGTGCCC 10592 A ATTTTAA  
 T AG GCA CAGAGGCCCT  
 || ||| |||||  
 TC CGT GTCTCCGGGA  
 C GTACCCC  
 GAM1598 PIK4CA 3' AGGGCCTCTGCCCCATGTGCCC 54123 A ATTTTAA  
 T AG GCA CAGAGGCCCT  
 || ||| |||||  
 TC CGT GTCTCCGGGA  
 C GTACCCC  
 GAM1598 SLC21A14 5' TTGTTCAAAATTGCTGTG 33833 G \_  
 CA AGCAATTTT AACAG  
 || ||||| |||||  
 GT TCGTTAAAA TTGTT  
 G C  
 GAM1598 TSGA14 3' GCCCACTGAAAATTGCCTG 38047 A AA A\_  
 CAG GCAATTTT CAG GGC  
 ||| ||||| ||| |||  
 GTC CGTTAAAA GTC CCG  
 \_ \_ AC  
 GAM1598 LOC124411 5' GACCTCTGTTACTCTG 74284 CAATTT CC  
 CAGAG TAACAGAGG C  
 |||| | ||||| |  
 GTCTC ATTGTCTCC G  
 \_ \_ AA  
 GAM1598 LOC139221 3' TGTTAAAATTGCACTG 75827 A  
 CAG GCAATTTTAACA  
 ||| ||||| |||||

	GTC CGTTAAAATTGT	
	A	
GAM1598 LOC144501 3'	AGGGCCTCTGTTCTCCTCT 83103	CAATTTT
	AGAG AACAGAGGCCCT	
	TCTC TTGTCTCCGGGA	
	CTC____	
GAM1598 LOC148183 3'	GGGCCCCTGTGTTCTCTG 84121	C TTTA A
	CAGAG AAT ACAG GGCCC	
	GTCTC TTG TGTC CCGGG	
	— ____ C	
GAM1598 LOC149134 5'	GGGCCTCTGTCAGCACTG 84363	A AATTTTA
	CAG GC ACAGAGGCCC	
	GTC CG TGTCTCCGGG	
	A AC____	
GAM1598 LOC149910 3'	AGGGCCTCTGCCCAGGCTCT 79528	AATTTTAA
	AGAGC CAGAGGCCCT	
	TCTCG GTCTCCGGGA	
	GACCC____	
GAM1598 LOC160156 5'	AGGGCCTCCGTTCCCTGAGCTC 82206	AATTTT A
	GAGC AAC GAGGCCCT	
	CTCG TTG CTCCGGGA	
	AGTCCC C	
GAM1598 LOC160414 5'	GCCAAAATTGTTCTG 87067	AACAGA
	CAGAGCAATTTT GGC	
	GTCTTGTTAAAA CCG	
	_____	
GAM1598 LOC162952 5'	AGGGCCTCTACACCTGCTC 82378	ATTTTAAC
	GAGCA AGAGGCCCT	
	CTCGT TCTCCGGGA	
	CCACA____	
GAM1598 LOC196214 5'	AGGGCTTATGCAAAATTGT 89615	AA G
	GCAATTTT CA AGGCCCT	
	TGTTAAAA GT TTCGGGA	
	C_ A	
GAM1598 LOC220686 3'	AGGGCCTCTGCCCCATGTGCC 92920	A ATTTTAA
T	AG GCA CAGAGGCCCT	
	TC CGT GTCTCCGGGA	
	C GTACCCC	
GAM1598 LOC257476 3'	GGGCCTCTGGTGGCTCTG 61255	AATTTTAA
	CAGAGC CAGAGGCCC	

		GTCTCG	GTCTCCGGG		
		GTG_____			
GAM1598	LOC257539	3'	GGGCCTCTGAATCTGTCTG	97703	G AT TAA
			CAGA CA TT CAGAGGCCC		
			GTCT GT AA GTCTCCGGG		
			_ CT _		
GAM1598	LOC257578	3'	GGGCCTCTGAATCTGTCTG	97823	G AT TAA
			CAGA CA TT CAGAGGCCC		
			GTCT GT AA GTCTCCGGG		
			_ CT _		
GAM1598	LOC90092	5'	GGCACCAAGTCAAAGTTACTCT	61412	C A AGAG_
		G	CAGAG AATTTT AC GCC		
			GTCTC TTGAAA TG CGG		
			A C AACCA		
GAM1599	ERH	3'	TCATATCTACTTTATAACATTC	15478	G TGCA
	A		TGAA TGTTATA GGATATGA		
			ACTT ACAATAT TCTATACT		
			_ TTCA		
GAM1599	NDRG3	3'	CCATAATATAACATTTCA	42493	GCA
			TGAAGTGTTATAT GG		
			ACTTTACAATATA CC		
			ATA		
GAM1599	NDRG3	3'	CCATAATATAACATTTCA	49294	GCA
			TGAAGTGTTATAT GG		
			ACTTTACAATATA CC		
			ATA		
GAM1599	NSD1	3'	ATATCCCAACACTCA	42399	A ATATGCA
			TGA GTGTT GGATAT		
			ACT CACAA CCTATA		
			_ C_____		
GAM1599	ABCC13	3'	TCATAAGCATTTAACACTTCA	56995	T AGGA
			TGAAGTGTTA ATGC TATGA		
			ACTTCACAAT TACG ATACT		
			T A_____		
GAM1599	FBXO32	3'	CCAGCACACGACAACACTTCA	54257	ATA_____ A
			TGAAGTGTT TGC GG		
			ACTTCACAA ACG CC		
			CAGCAC A		
GAM1599	FLJ23053	3'	TCATATCCTTAATGAACACCTC	43264	A A GC
			GA GTGTT TAT AGGATATGA		

CT CACAA GTA TCCTATACT  
 C \_ AT  
 GAM1599 FLJ23462 3' CATATCCCTTAAACTTC 45805 G TATGCA  
 GAAGT TTA GGATATG  
 ||||| ||| |||||  
 CTTCA AAT CCTATAC  
 \_ TC\_\_\_\_  
 GAM1599 MAP2K6 3' TCACTCATATAACAGCTCA 49249 AG C \_  
 TGA TGTTATATG AG GA  
 ||| ||||| || ||  
 ACT ACAATATAC TC CT  
 CG \_ A  
 GAM1599 MAP2K6 3' TCACTCATATAACAGCTCA 10874 AG C \_  
 TGA TGTTATATG AG GA  
 ||| ||||| || ||  
 ACT ACAATATAC TC CT  
 CG \_ A  
 GAM1599 SLAC2-B 3' CCTATATAGACACTTC 30511 A C  
 GAAGTGTT TATG AGG  
 ||||| ||| |||  
 CTTCACAG ATAT TCC  
 \_ A  
 GAM1599 LOC147429 3' TCACATCCTGCATAGCACTT 78364 TA A  
 AAGTGT TATGCAGGAT TGA  
 ||||| ||||| |||  
 TTCACG ATACGTCCTA ACT  
 \_ C  
 GAM1599 LOC149175 3' CACATCCTGGGAACACTTT 79207 ATATG A  
 GAAGTGTT CAGGAT TG  
 ||||| ||||| ||  
 TTTCACAA GTCCTA AC  
 GG\_\_ C  
 GAM1599 LOC169026 5' TCATATGAAAGACATACACACT 82729 TA CAGG\_\_  
 TCA TGAAGTGT TATG ATATGA  
 ||||| ||| |||||  
 ACTTCACA ATAC TATACT  
 C\_ AGAAAG  
 GAM1599 LOC84528 3' TCATATTTTGCATAGCACCCCA 50682 AA TA  
 TG GTGT TATGCAGGATATGA  
 || ||| ||||| |||||  
 AC CACG ATACGTTTTATACT  
 CC \_  
 GAM1600 ACP2 3' AGAAAGTTCTAGACTG 7851 GC TC  
 CAGT CT AGAACTTTCT  
 ||| || ||||| |||||  
 GTCA GA TCTTGAAAGA  
 \_ \_  
 GAM1600 APTX 5' AAGAGAAAGAGATCAGGCA 34655 TCAGAA  
 TGCCT CTTTCTCTT  
 |||| ||||| |||||



			ACGGA GAAAGAGAA		
			CTAGA_		
GAM1600	BCL7A	3'	AGGCTGTCTCCTTAAGGCACTG 40637	C A__	TT
			CAGTGCCTT AG AC TCT		
			GTCACGGAA TC TG GGA		
			T CTC TC		
GAM1600	CLC	3'	AAGAGAAAATACTGAAAGCACA 25105	A C	AAC
	GG		CC GTGC TTCAG TTTCTCTT		
			GG CACG AAGTC AAAGAGAA		
			A A ATA		
GAM1600	CNK	3'	AAGCCCTGAAGGCCTG 14517	T	AA
			CAG GCCTTCAG CTT		
			GTC CGGAAGTC GAA		
			_ CC		
GAM1600	COL4A3	3'	AAGTGCAGGTTCTGAGGGCACC 48549	A	TCT
	GG		CC GTGCCTTCAGAACTT CTT		
			GG CACGGGAGTCTTGGA GAA		
			C CGT		
GAM1600	CSPG4	3'	AAGAGAGACCTGGAGACAC 8570	C	AAC
			GTG CTTCAG TTTCTCTT		
			CAC GAGGTC AGAGAGAA		
			A C__		
GAM1600	CYP1B1	3'	AAGAGAAAAGAGAGAAACACTG 3651	CC	AGAAC
			CAGTG TTC TTTCTCTT		
			GTCAC AAG AAAGAGAA		
			A_ AGAGA		
GAM1600	DLG3	3'	AAGAGAAAAGAGGAGGACTG 40880	G	AGAAC
			CAGT CCTTC TTTCTCTT		
			GTCA GGAGG AAAGAGAA		
			_ AGA__		
GAM1600	DLG5	5'	AGGCAGACTCTGAAGGC 82909	A_	T
			GCCTTCAGA CT TCT		
			CGGAAGTCT GA GGA		
			CA C		
GAM1600	FLT1	3'	AAGAGAAACCGGGAGAAGGCAT 8910	AGAAC_	
			GTGCCTTC TTTCTCTT		
			TACGGAAG AAAGAGAA		
			AGGGCC		
GAM1600	GRB10	3'	AGAGAAAATGGCACCTGG 17971	_	TTCAGAAC
			CCAG TGCC TTTCTCT		

			GGTC ACGG	AAAGAGA	
			C TA_____		
GAM1600 LFG	3'	AAGAGAAAAGGAGCCAAAGAACT 76711	GC CAGAA _		
	GG	CCAGT CTT CTTT CTCTT			
		GGTCA GAA GAAA GAGAA			
		A_ CCGAG A			
GAM1600 MAN2A2	3'	AAGAGAAAAGTTCATTAC 20391	CCTTCA		
		GTG GAACTTTCTCTT			
		CAC CTTGAAAGAGAA			
		TTA_____			
GAM1600 NLGN3	3'	AAGAAAAGTTCTTAAAACACT 38596	CC C C		
		AGTG TT AGAACTTT TCTT			
		TCAC AA TCTTGAAA AGAA			
		AA T _			
GAM1600 NPAS1	5'	AAGGTCTCCCGAGGGCACT 59879	A_ _		
		AGTGCCTTC GA ACTTT			
		TCACGGGAG CT TGGAA			
		CC C			
GAM1600 PLAG1	3'	AGTGTGTTCCAAAGGCATT 10605	CA TTT		
		AGTGCCTT GAAC CT			
		TTACGGAA CTTG GA			
		AC TGT			
GAM1600 PLXNA1	3'	AGAAAATGAAGGCAGTGG 72309	G GAAC		
		CCA TGCCTTCA TTTCT			
		GGT ACGGAAGT AAAGA			
		G A_____			
GAM1600 PPP4R1	3'	AAGAGAAAAGTACAGTAAACACT 17620	CCTTCAGA		
		AGTG ACTTTCTCTT			
		TCAC TGAAAGAGAA			
		AAATGACA			
GAM1600 ACYP2	3'	AAGAGAAAAATTGTAACACACT 56612	CC _ AAC		
	G	CAGTG TT CAG TTTCTCTT			
		GTCAC AA GTT AAAGAGAA			
		AC T AA_			
GAM1600 B3GNT6	3'	AGAAATCAGATGAAGGCAT 22503	GAAC_		
		GTGCCTTCA TTTCT			
		TACGGAAGT AAAGA			
		AGACT			
GAM1600 BAG5	3'	AAGAGAAGGGATAAAGGAC 16835	G CAGAA		
		GT CCTT CTTTCTCTT			

			CA GGAA GGAAGAGAA		
			_ ATAG_		
GAM1600	BIVM	3'	AAGAGAAAAGACTCAAGAACT	34665	GC C AAC
	G		CAGT CTT AG TTTCTCTT		
			GTCA GAA TC AAAGAGAA		
			AA C AGA		
GAM1600	C15orf5	3'	AGAGAAAAGAAAGCAC	48195	C AGAAC
			GTGC TTC TTTCTCT		
			CACG AAG AAAGAGA		
			A A__		
GAM1600	C20orf80	5'	AAGAGAAGAAGATGAAGAAAC	65282	GC GAAC
			GT CTTCA TTTCTCTT		
			CA GAAGT GAAGAGAA		
			AA AGAA		
GAM1600	CLSTN1	3'	AGTTCTGAGGACACTGG	30103	C
			CCAGTG CTTCAGAACT		
			GGTCAC GGAGTCTTGA		
			A		
GAM1600	DKFZP434P0111	3'	AAGAGAAAGTTTCTGCAC	67368	CTTCA
			GTGC GAACTTTCTCTT		
			CACG TTTGAAAGAGAA		
			TC__		
GAM1600	DORFIN	5'	AGAATTCTCTGAAGGAAC	31257	G ACT
			GT CCTTCAGA TTCT		
			CA GGAAGTCT AAGA		
			A CTT		
GAM1600	FLJ10300	5'	AAGAGAAAGATGAAGACTCTG	35997	TGC GAA
			CAG CTTCA CTTTCTCTT		
			GTC GAAGT GAAAGAGAA		
			TCA A__		
GAM1600	FLJ20373	3'	AAGAGAAGAAGGAAAGGCACAG	35070	A _AGAAC
	G		CC GTGCCTT C TTTCTCTT		
			GG CACGGAA G GAAGAGAA		
			A A GAA__		
GAM1600	FLJ23511	5'	AGAGAAAACAAGGCAT	49956	CAGAAC
			GTGCCTT TTTCTCT		
			TACGGAA AAAGAGA		
			CAA__		
GAM1600	FLJ30681	3'	AGAGAAGAAAGACCACTGG	91782	CCT AGAAC
			CCAGTG TC TTTCTCT		

GGTCAC AG GAAGAGA  
C\_\_ AAA\_\_

GAM1600 HDAC11 3' GAGCTATAGGCACTGG 45717 TC AACTTT  
CCAGTGCCT AG CTC  
||||||| || |||  
GGTCACGGA TC GAG  
TA \_\_\_\_\_

GAM1600 IKKE 5' AGTGAGCCCTGAAAGCTCTGG 25745 T C AA T  
CCAG GC TTCAG CTT CT  
|||| ||||| ||| ||  
GGTC CG AAGTC GAG GA  
T A CC T

GAM1600 KIAA0680 3' AGAGAAAATTGAAGCAT 28232 C AAC  
GTGC TTCAG TTTCTCT  
|||| ||||| |||||  
TACG AAGTT AAAGAGA  
\_ A\_\_

GAM1600 KIAA1228 3' AGGGGGTGATTCTGAGGCACTG 65035 T \_\_\_\_ TT  
CAGTGCCT CAGA ACT CT  
||||||| |||| ||| ||  
GTCACGGA GTCT TGG GA  
\_ TAG GG

GAM1600 KIAA1300 5' AGGAACCCTGAAGGCA 62860 AAC  
TGCCTTCAG TTTCT  
||||||| |||||  
ACGGAAGTC AAGGA  
CC\_

GAM1600 KIAA1805 3' AAGAGAAAGTAGAAGCAGCA 79966 \_\_\_\_ AGA  
TGC CTTC ACTTTCTCTT  
||| |||| |||||  
ACG GAAG TGAAAGAGAA  
AC A\_\_

GAM1600 LENG1 5' AAGAGAAAGCTCTGGGCATCCT 84074 \_\_\_\_ TT A  
G CAG TGCC CAGA CTTTCTCTT  
||| |||| |||| |||||  
GTC ACGG GTCT GAAAGAGAA  
CT \_\_\_\_ C

GAM1600 LHX6 3' AAGAGAAAACCTCTGGGGTCA 26854 C AC  
TG CTTCAGA TTTCTCTT  
|| ||||| |||||  
AC GGGGTCT AAAGAGAA  
T CA

GAM1600 N4BP3 3' AGCTCCAGAAGGCACTGG 66250 A\_ A  
CCAGTGCCTTC GA CT  
||||||| |||  
GGTCACGGAAG CT GA  
AC C

GAM1600 NASP 3' AGAGGGTGAAGAACTG 67966 GC AGA  
CAGT CTTC ACTTTCT  
|||| |||| |||||

GTCA GAAG TGGGAGA  
 AA \_\_\_\_  
 GAM1600 SMARCF1 3' AAAATTCTGAAGGAC 57480 G C  
 GT CCTTCAGAA TTT  
 || ||||| ||  
 CA GGAAGTCTT AAA  
 \_ A  
 GAM1600 SMARCF1 3' AAAATTCTGAAGGAC 20034 G C  
 GT CCTTCAGAA TTT  
 || ||||| ||  
 CA GGAAGTCTT AAA  
 \_ A  
 GAM1600 SMARCF1 3' AAAATTCTGAAGGAC 37430 G C  
 GT CCTTCAGAA TTT  
 || ||||| ||  
 CA GGAAGTCTT AAA  
 \_ A  
 GAM1600 TED 3' AAGAGAAAGTCCAGGGACTGG 31630 G TCA A  
 CCAGT CCT GA CTTTCTCTT  
 ||||| || |||||  
 GGTCA GGA CT GAAAGAGAA  
 G C\_\_ \_  
 GAM1600 TGIF2 3' AGAAGGGTGCTGAAGGC 41447 AA\_  
 GCCTTCAG CTTTCT  
 ||||| |||||  
 CGGAAGTC GGAAGA  
 GTG  
 GAM1600 WBSCR20A 3' AAGAGAAAGAAGAGACAGCA 35958 CT AGAA  
 TGC TC CTTTCTCTT  
 ||| || |||||  
 ACG AG GAAAGAGAA  
 AC AGAA  
 GAM1600 LOC115273 3' AGAAAGTTCTGATGGCCAGG 73356 AGT T  
 CC GCC TCAGAACTTTCT  
 || ||| |||||  
 GG CGG AGTCTTGAAAGA  
 AC\_ T  
 GAM1600 LOC145761 5' AAGAGAAAGTGGGAAGGCATGG 83472 G AGA  
 CCA TGCCTTC ACTTTCTCTT  
 ||| ||||| |||||  
 GGT ACGGAAG TGAAAGAGAA  
 \_ G\_\_  
 GAM1600 LOC146179 5' AGAAAGTTTTGGGCCT 77700 T TT  
 AG GCC CAGAACTTTCT  
 || ||| |||||  
 TC CGG GTTTTGAAAGA  
 \_ \_  
 GAM1600 LOC147072 3' AAGAGAAAGTGAGAAGAACTG 60407 GC AGA  
 CAGT CTTC ACTTTCTCTT  
 ||||| |||||

GTCA GAAG TGAAAGAGAA  
 AA AG\_  
 GAM1600 LOC148758 5' AGAAAGTTCTGAGAAAC 78962 GCC  
 GT TTCAGAACTTTCT  
 || |||||  
 CA GAGTCTTGAAAGA  
 AA\_  
 GAM1600 LOC148932 3' AGGAATCTGAAGGCACTGG 79103 AC  
 CCAGTGCCTTCAGA TTTCT  
 ||||| ||||  
 GGTCACGGAAGTCT AAGGA  
  
 GAM1600 LOC149386 5' AAGTTTTGAAAGCACT 84400 C  
 AGTGC TTCAGAACTT  
 |||| |||||  
 TCACG AAGTTTTGAA  
 A  
 GAM1600 LOC150139 3' AGAAAATAGAAAAAGGCGCTGG 79583 CAGAAC\_  
 CCAGTGCCTT TTTCT  
 ||||| ||||  
 GGTCGCGGAA AAAGA  
 AAAGATA  
 GAM1600 LOC152756 3' AAGATGCAGTTCTGAAAACCTG 85871 TGCC TTC  
 CAG TTCAGAACT TCTT  
 || ||||| ||||  
 GTC AAGTCTTGA AGAA  
 CAA\_ CGT  
 GAM1600 LOC162333 5' AAGAGAAAGCGATGACACTG 87114 CCT GAA  
 CAGTG TCA CTTTCTCTT  
 |||| || |||||  
 GTCAC AGT GAAAGAGAA  
 AGC  
 GAM1600 LOC199221 3' AAGAGAAGCTCGAAAGCATGG 80347 G C A A T  
 CCA TGC TTC GA CTT CTCTT  
 || || || || || ||||  
 GGT ACG AAG CT GAA GAGAA  
 \_ A \_ C \_  
 GAM1600 LOC203339 3' AGAGAAAATTGGGCCTG 90542 T TCAGAAC  
 CAG GCCT TTTCTCT  
 || || |||||  
 GTC CGGG AAAGAGA  
 \_ TTA\_  
 GAM1600 LOC255017 3' AGAAAGAGGAACTGG 94624 G TCAGAA  
 CCAGT CCT CTTTCT  
 |||| || |||||  
 GGTCA GGA GAAAGA  
 A \_\_\_\_\_  
 GAM1600 LOC256021 3' AAGAGAAACAAAGACAACACTG 96512 CCT AGAAC  
 G CCAGTG TC TTTCTCTT  
 |||| || |||||

		GGTCAC AG AAAGAGAA	
		AAC AAAC_	
GAM1600	LOC90139	3' AGAATCCCGAAGGCAT 55396	A_ ACT
		GTGCCTTC GA TTCT	
		TACGGAAG CT AAGA	
		CC _	
GAM1601	ABCB1	5' CCAGAACATTCTCCTGGAA 6247	CTGT CT
		TTCC GG ATGTTCTGG	
		AAGG CC TACAAGACC	
		TCCT T_	
GAM1601	AGT	3' CCAGAACACAGTGCCTGGCA 3454	_ TA_
		TGT GGC TGTTCCTGG	
		ACG CCG ACAAGACC	
		GT TGAC	
GAM1601	ALDOB	3' CCAGAATACCCACCCAAGAA 68087	CCT_ CTA
		TTC GTGG TGTTCCTGG	
		AAG CACC ATAAGACC	
		AACC C_	
GAM1601	ARL4	3' CCAGAACACAGTTGTGGGAA 19198	T TG A
		TTCCC G GCT TGTTCCTGG	
		AAGGG T TGA ACAAGACC	
		_GT C	
GAM1601	B3GAT1	3' CCAGAACAAAGGACAGAGAA 37827	C GG A
		TTC CTGT CT TGTTCCTGG	
		AAG GACA GA ACAAGACC	
		A G_ A	
GAM1601	B3GAT1	3' CCAGAACAAAGGACAGAGAA 53972	C GG A
		TTC CTGT CT TGTTCCTGG	
		AAG GACA GA ACAAGACC	
		A G_ A	
GAM1601	CD79B	3' CCAGAAGAGCCACAGG 5271	ATG
		CCTGTGGCT TTCTGG	
		GGACACCGA AAGACC	
		G_	
GAM1601	CD79B	3' CCAGAAGAGCCACAGG 41207	ATG
		CCTGTGGCT TTCTGG	
		GGACACCGA AAGACC	
		G_	
GAM1601	CDH3	3' CCAAACGTCAGGCCACAG 8380	_ C
		CTGTGGCT ATGTT TGG	

			GACACCGG TGCAA ACC		
			AC _		
GAM1601 COL5A1	5'	GCCAGAACAGCCGCCACAA 3634	CC TA_____ III		
		AGAA C TGTGGC TGTCTGG C			
		G ACACCG ACAAGACC G			
		AA CCGCCG III			
GAM1601 CRIM1	3'	CCAGAACAAAGGCAG 33173 GG A			
		CTGT CT TGTCTGG			
		GACG GA ACAAGACC			
		_ A			
GAM1601 DIAPH2	3'	CCAAAACAAGTCTAGCAGGGAA 22063 _ A C			
		TTCCCTGT GGCT TGTT TGG			
		AAGGGACG CTGA ACAA ACC			
		AT _ A			
GAM1601 DMD	3'	AGAAAATATAGTCACAGG 14414 _			
		CCTGTGGCTATGT TCT			
		GGACACTGATATA AGA			
		AA			
GAM1601 ED1	3'	TTGGAACAATCACAGGGAA 7376 CTA TG			
		TTCCCTGTGG TGTT C G			
		AAGGGACACT ACAAG T			
		A_ GT			
GAM1601 EXTL3	3'	CCAAAACATGCCGCAGGGAG 7528 T C			
		TTCCCTGTGGC ATGTT TGG			
		GAGGGACGCCG TACAA ACC			
		_ A			
GAM1601 FCRH3	3'	CCAGAGTGGCCCACAGG 53630 _ GT			
		CCTGTGG CTAT TCTGG			
		GGACACC GGTG AGACC			
		C _			
GAM1601 FECH	3'	CGTGGTGCCACAGGGAA 3753 _			
		TTCCCTGTGGC TATG			
		AAGGGACACCG GTGC			
		TG			
GAM1601 FGFR1	3'	CCAGAACATACAAGGA 41619 C GGCT			
		TCC TGT ATGTTCTGG			
		AGG ACA TACAAGACC			
		A _			
GAM1601 GATA4	3'	CCAGAACAACAAGTGGGAA 9004 T GGCTA			
		TTCCC GT TGTTCTGG			



AAGGG CA ACAAGACC  
 T ACA\_\_  
 GAM1601 GNRH1 5' CCATCACCAGCCACAGAGA 5883 C AT TC  
 TC CTGTGGCT GT TGG  
 || ||||| || |||  
 AG GACACCGA CA ACC  
 A C\_ CT  
 GAM1601 HAMP 3' CCAGAACATAGGTCTTGGAA 40991 CTGT \_  
 TTCC GGC TATGTTCTGG  
 ||| ||| |||||  
 AAGG CTG ATACAAGACC  
 TT\_\_ G  
 GAM1601 IPP 3' TAGTTTGAGCCACAGAGAA 19729 C ATGTT  
 TTC CTGTGGCT CTG  
 ||| ||||| |||  
 AAG GACACCGA GAT  
 A GTTT\_  
 GAM1601 ITGB1 3' CCAGTGTGGCCAGGGAA 53369 T GTT  
 TTCCCTG GGCTAT CTGG  
 ||||| ||||| |||  
 AAGGGAC CCGGTG GACC  
 \_ T\_\_  
 GAM1601 KCNQ1 3' CCAGCTGCTGAGCCGCAGAGAA 4021 C AT T\_  
 TTC CTGTGGCT GT CTGG  
 ||| ||||| || |||  
 AAG GACGCCGA CG GACC  
 A GT TC  
 GAM1601 KDR 3' CAGAATACCACAAAGAA 9591 CC CTA  
 TTC TGTGG TGTTCCTG  
 ||| |||| |||||  
 AAG ACACC ATAAGAC  
 AA \_  
 GAM1601 LEP 3' CCAGGGGCCCACAGGGAA 4047 \_ ATGT  
 TTCCCTGTGG CT TCTGG  
 ||||| || |||||  
 AAGGGACACC GG GGACC  
 C \_  
 GAM1601 MKI67 3' CCAGTGACCAGCCACAGGAGA 10041 \_ AT \_  
 TC CCTGTGGCT GTT CTGG  
 || ||||| || |||  
 AG GGACACCGA CAG GACC  
 A C\_ T  
 GAM1601 NEFH 3' CCGGAACAGCCAAAG 40780 G AT  
 CT TGGCT GTTCTGG  
 || |||| |||||  
 GA ACCGA CAAGGCC  
 A \_  
 GAM1601 NXF2 5' CCAGAACATCACCAAG 35136 G CT  
 CT TGG ATGTTCTGG  
 || ||| |||||

			GA ACC TACAAGACC		
			_ AC		
GAM1601 PDE6D	3'	CCAGCATACACACAGGGAA	10489	GC	TT
		TTCCCTGTG TATG CTGG			
		AAGGGACAC ATAC GACC			
		AC _			
GAM1601 PHEMX	5'	CCAGCTGGAAACCACAGGGAG	57359	CTATGTT	
		TTCCCTGTGG CTGG			
		GAGGGACACC GACC			
		AAAGGTC			
GAM1601 PHEMX	5'	CCAGCTGGAAACCACAGGGAG	57364	CTATGTT	
		TTCCCTGTGG CTGG			
		GAGGGACACC GACC			
		AAAGGTC			
GAM1601 PODXL	3'	CCAGAATGACACAAAGGA	18230	C_	GCTAT
		TCC TGTG GTTCTGG			
		AGG ACAC TAAGACC			
		AA AG_			
GAM1601 PRODH	3'	CTGGGACAGCCACTGGAA	32925	CT	AT TG
		TTCC GTGGCT GTTC G			
		AAGG CACCGA CAGG C			
		T_ _ GT			
GAM1601 RANBP2L1	3'	CCAGAATAAAACCACCAGGAA	17313	CT	CTA
		TTCC GTGG TGTTCCTGG			
		AAGG CACC ATAAGACC			
		AC AAA			
GAM1601 REGL	3'	CCAGAACATGAATTCAGG	21486	TGGC	
		CCTG TATGTTCTGG			
		GGAC GTACAAGACC			
		TTAA			
GAM1601 SLC19A1	5'	CCAGAATGCATCCAGAGGGAA	11755	G	CTA
		TTCCCT TGG TGTTCCTGG			
		AAGGGA ACC GTAAGACC			
		G TAC			
GAM1601 ST14	3'	CCAGAACATACACTGTGAA	41765	CCT	GC
		TTC GTG TATGTTCTGG			
		AAG CAC ATACAAGACC			
		TGT _			
GAM1601 TBL2	3'	CCAGAACAACCTAGAGAA	52182	C	T CTA
		TTC CTG GG TGTTCCTGG			

			AAG GAT CC ACAAGACC		
			A _ A__		
GAM1601 TBL2	3'	CCAGAACACCTAGAGAA	24926	C T CTA	
		TTC CTG GG TGTTCTGG			
		AAG GAT CC ACAAGACC			
		A _ A__			
GAM1601 TCFL4	3'	CCAGGATAAGACCACAGGGAA	63461	_ A	
		TTCCCTGTGG CT TGTTCTGG			
		AAGGGACACC GA ATAGGACC			
		A _			
GAM1601 TFAP4	3'	CCGGGGCAGCCACAGGGAG	12237	AT	
		TTCCCTGTGGCT GTTCTGG			
		GAGGGACACCGA CGGGGCC			
		—			
GAM1601 UBE2L6	3'	CCAGGGGGAGCCACGG	14873	ATG	
		CTGTGGCT TTCTGG			
		GGCACCGA GGGACC			
		GG_			
GAM1601 UBQLN3	3'	CAAAACATAGTGAG	33926	CTGTG C	
		TTCC GCTATGTT TG			
		GAGG TGATACAA AC			
		— A			
GAM1601 UMOD	3'	CCAGTGCTCCAGCCACAG	12548	AT_ T	
		CTGTGGCT GT CTGG			
		GACACCGA CG GACC			
		CCT T			
GAM1601 WBSCR5	3'	CCAGAACAGGGCAGAG	41856	G G A	
		CT TG CT TGTTCTGG			
		GA AC GG ACAAGACC			
		G G _			
GAM1601 WBSCR5	3'	CCAGAACAGGGCAGAG	50610	G G A	
		CT TG CT TGTTCTGG			
		GA AC GG ACAAGACC			
		G G _			
GAM1601 WBSCR5	3'	CCAGAACAGGGCAGAG	26256	G G A	
		CT TG CT TGTTCTGG			
		GA AC GG ACAAGACC			
		G G _			
GAM1601 ZNF134	3'	CAGTTTAAGCCACAGGGAA	12846	A TT	
		TTCCCTGTGGCT TG CTG			

AAGGGACACCGA AT GAC  
 \_ TT  
 GAM1601 ZNF36 3' CCTTCGTAGCCACAAGG 93960 C TTCT  
 CC TGTGGCTATG GG  
 || ||||| ||  
 GG ACACCGATGC CC  
 A TT\_  
 GAM1601 ABCA9 5' CAGAACATGCAGAGA 54410 C GGCT  
 TC CTGT ATGTTCTG  
 || ||| |||||  
 AG GACG TACAAGAC  
 A \_  
 GAM1601 ADAMTSL1 3' CCTCAAATAGCACAGGGAA 57686 G GTTCT  
 TTCCCTGTG CTAT GG  
 ||||| ||| ||  
 AAGGGACAC GATA CC  
 \_ AACT\_  
 GAM1601 BAIAP1 3' CCAGAACGGCAGCAGG 16449 G AT  
 CCTGT GCT GTTCTGG  
 |||| ||| |||||  
 GGACG CGG CAAGACC  
 A \_  
 GAM1601 BCKDK 3' CCAGAACTTGGAGCAGGGAA 59793 GG T  
 TTCCCTGT CTA GTTCTGG  
 ||||| ||| |||||  
 AAGGGACG GGT CAAGACC  
 A\_ T  
 GAM1601 C11orf25 3' CCAAATTAGGGCCACAG 48639 AT\_ C  
 CTGTGGCT GTT TGG  
 ||||| ||| |||  
 GACACCGG TAA ACC  
 GAT \_  
 GAM1601 C20orf112 3' CCAGTGCTGCCACAGGGA 54640 TAT T  
 TCCCTGTGGC GT CTGG  
 ||||| || |||  
 AGGGACACCG CG GACC  
 T\_ T  
 GAM1601 C6orf26 3' CCAAAACACAGAGCAGG 47509 GG A C  
 CCTGT CT TGTT TGG  
 |||| ||| ||| |||  
 GGACG GA ACAA ACC  
 A\_ C A  
 GAM1601 CGGBP1 5' CTGGCACCACAGGGAA 13362 CTA CT  
 TTCCCTGTGG TGTT G  
 ||||| ||| |  
 AAGGGACACC ACGG C  
 \_ T\_  
 GAM1601 DKFZP566G1424 5' CCAGTGCTGCCACAGGGA 84779 TAT T  
 TCCCTGTGGC GT CTGG  
 ||||| ||| |||

AGGGACACCG CG GACC  
 T\_\_ T  
 GAM1601 DKFZp586l021 5' CCAGACGTCACCACAGGGA 50088 CT T  
 TCCCTGTGG ATGT CTGG  
 ||||| ||| |||  
 AGGGACACC TGCA GACC  
 AC \_  
 GAM1601 DKFZP727M111 5' CCAATCTGGTCACAGGGAA 31407 T TC  
 TTCCCTGTGGCTA GT TGG  
 ||||| ||| |||  
 AAGGGACACTGGT TA ACC  
 C \_  
 GAM1601 ELF4 3' CCGTGGATCAGCCACAGGGA 7431 AT \_  
 TCCCTGTGGCT GTTC TGG  
 ||||| ||| |||  
 AGGGACACCGA TAGG GCC  
 C\_ T  
 GAM1601 ERG-1 3' CCAGGATGCCAAAGG 41842 G TAT  
 CCT TGGC GTTCTGG  
 ||| ||| |||||  
 GGA ACCG TAGGACC  
 A \_  
 GAM1601 FLJ00058 5' CCAGAAATGCCAGCAGGGAA 78765 \_ TATG  
 TTCCCTG TGGC TTCTGG  
 ||||| ||| |||||  
 AAGGGAC ACCG AAGACC  
 G TA\_\_  
 GAM1601 FLJ12816 3' CCAGAACAGGACGACAGTGAA 41932 C GGCTA  
 TTC CTGT TGTTCTGG  
 ||| ||| |||||  
 AAG GACA ACAAGACC  
 T GCAGG  
 GAM1601 FLJ13315 3' CCAGAACATAATACA 46568 GC  
 TGTG TATGTTCTGG  
 ||| |||||  
 ACAT ATACAAGACC  
 A\_  
 GAM1601 FLJ20010 3' CCAGAACGATTGGAACAGG 38716 GG \_  
 CCTGT CTA TGTTCTGG  
 |||| ||| |||||  
 GGACA GGT GCAAGACC  
 A\_ TA  
 GAM1601 FLJ22369 5' ATGGCGCGACAGGGAA 49918 \_ \_  
 TTCCCTGT G GCTAT  
 ||||| ||| |||||  
 AAGGGACA C CGGTA  
 G G  
 GAM1601 FLJ23563 3' CCAGAATGCTACAAAAGAA 67593 CC\_ TAT  
 TTC TGTGGC GTTCTGG  
 ||| ||||| |||||

AAG ACATCG TAAGACC  
 AAA \_\_\_\_  
 GAM1601 FLJ32332 3' CACAGCACACAGGGAA 58299 \_ A  
 TTCCCTGTG GCT TG  
 ||||| ||| ||  
 AAGGGACAC CGA AC  
 A C  
 GAM1601 GRIN3A 3' CCAAGTGAAGCAGCCACAGGGA 55968 ATG \_\_\_\_  
 TCCCTGTGGCT TTC TGG  
 ||||| ||| |||  
 AGGGACACCGA AAG ACC  
 CG\_ TGA  
 GAM1601 HSPC166 3' CCAGAACACATGGAGGGAA 26366 G GCTA  
 TTCCCT TG TGTTCTGG  
 ||||| || |||||  
 AAGGGA GT ACAAGACC  
 G AC\_\_  
 GAM1601 HSPC251 3' CCAGGCTAGAGCCACAGAGA 33249 C A TT  
 TC CTGTGGCT TG CTGG  
 || ||||| || ||||  
 AG GACACCGA AT GACC  
 A G CG  
 GAM1601 IGF2AS 3' CCAGGGTGCAACAGAGAA 33095 C G TAT TT  
 TTC CTGT GC G CTGG  
 || |||| || | ||||  
 AAG GACA CG T GACC  
 A A \_\_ GG  
 GAM1601 ILF3 3' CCAAAACACGCTGGGAA 15722 T GCTA C  
 TTCCC GTG TGTT TGG  
 ||||| ||| |||||  
 AAGGG CGC ACAA ACC  
 T \_\_\_\_ A  
 GAM1601 KIAA0040 3' CCAAAGTTTCCAGCAGGGAA 27780 \_ CT GTTC  
 TTCCCTG TGG AT TGG  
 ||||| ||| || |||  
 AAGGGAC ACC TG ACC  
 G TT AA\_\_  
 GAM1601 KIAA0254 3' CAGACAGTCACAGGGAA 28596 ATGT  
 TTCCCTGTGGCT TCTG  
 ||||| ||||| |||||  
 AAGGGACACTGA AGAC  
 C\_\_  
 GAM1601 KIAA0336 3' CCAGAATAAAACCACCAGGAA 27589 CT CTA  
 TTCC GTGG TGTTCTGG  
 ||| |||| |||||  
 AAGG CACC ATAAGACC  
 AC AAA  
 GAM1601 KIAA0494 3' CCAGAACACATTTGGG 28740 T\_ GCTA  
 CCC GTG TGTTCTGG  
 ||| ||| |||||

			GGG TAC ACAAGACC		
			TT ____		
GAM1601	KIAA0537	3'	CCAGAACAGCCTACAGGGGA	29244	_ AT
			TTCCCTGT GGCT GTTCTGG		
			AGGGGACA CCGA CAAGACC		
			T ____		
GAM1601	KIAA0774	5'	CGGGATGCCACAAGGAA	91752	C TAT TG
			TTCC TGTGGC GTTC G		
			AAGG ACACCG TAGG C		
			A ____ GT		
GAM1601	KIAA0828	3'	CCATGAAAGCCACAGAGGA	81194	_ ATG _
			TCC CTGTGGCT TTC TGG		
			AGG GACACCGA AAG ACC		
			A ____ T		
GAM1601	KIAA1118	3'	CCAGAGGCCACAGGGA	69606	_ ATGT
			TCCCTGTGG CT TCTGG		
			AGGGACACC GG AGACC		
			C ____		
GAM1601	KIAA1742	3'	CAGATCCACAGGGAG	77657	CTATGT
			TTCCCTGTGG TCTG		
			GAGGGACACC AGAC		
			T ____		
GAM1601	KIAA1944	5'	CCAACCTAGCCACAGGGA	75558	T TC
			TCCCTGTGGCTA GT TGG		
			AGGGACACCGAT CA ACC		
			C ____		
GAM1601	KIAA1981	3'	CGGAACAGCACAAGGAA	88342	C G AT TG
			TTCC TGTG CT GTTC G		
			AAGG ACAC GA CAAG C		
			A _ _ GT		
GAM1601	NXPH3	3'	ACGGAGCCACAGAGAG	65747	C A
			TTC CTGTGGCT TGT		
			GAG GACACCGA GCA		
			A G		
GAM1601	PP5395	3'	TCAGGATAGCACAGGGAA	72110	G AT
			TTCCCTGTG CT GTTCTGG		
			AAGGGACAC GA TAGGACT		
			- -		
GAM1601	PRDM7	3'	CCAGAAGGGCCACAGAGAA	53788	C ATG
			TTC CTGTGGCT TTCTGG		

			AAG GACACCGG AAGACC		
			A G__		
GAM1601 PRDM9	3'	CCAGAAAGGGCCACAGAGAA	39575	C	ATG
		TTC CTGTGGCT TTCTGG			
		AAG GACACCGG AAGACC			
		A G__			
GAM1601 PXR2b	3'	ATATAGCCCAAGGAA	33337	C T	
		TTCC TG GGCTATGT			
		AAGG AC CCGATATA			
		A _			
GAM1601 RAB33B	3'	CCAGCTTAGCCACAAAGAA	48490	CC	TGTT
		TTC TGTGGCTA CTGG			
		AAG ACACCGAT GACC			
		AA TC__			
GAM1601 SH120	3'	CCAGAACATGAGAGGGAG	94606		GTGGC
		TTCCCT TATGTTCTGG			
		GAGGGA GTACAAGACC			
		GA__			
GAM1601 SH120	3'	CCAGAACATGAGAGGGAG	32920		GTGGC
		TTCCCT TATGTTCTGG			
		GAGGGA GTACAAGACC			
		GA__			
GAM1601 SLC2A12	3'	CCAGAACACACAGTGTGGA	59078	__	GCTA
		TCC CTGTG TGTTCTGG			
		AGG GACAC ACAAGACC			
		TGT ____			
GAM1601 SP329	3'	CCAGAGTGCTCCACAGGGA	47924		CTA GT
		TCCCTGTGG T TCTGG			
		AGGGACACC G AGACC			
		TC_ TG			
GAM1601 SSH2	3'	TCAGTAAGCCACAGGGAA	62213	_	ATGTT
		TTCCCTGTGG CT CTGG			
		AAGGGACACC GA GACT			
		C AT__			
GAM1601 SYTL4	5'	CCAGTCAGCCACAGGGAA	54939		ATGTT
		TTCCCTGTGGCT CTGG			
		AAGGGACACCGA GACC			
		CT__			
GAM1601 TNRC4	3'	CCAGTCAGCCACAGAGA	23221	C	ATGTT
		TC CTGTGGCT CTGG			



			AG GACACCGA GACC		
			A CT__		
GAM1601	UBE3B	3'	CCAGACTGTCTAGCACAGGGAA 76919	G _ GT	
			TTCCCTGTG CT AT TCTGG		
			AAGGGACAC GA TG AGACC		
			_ C TC		
GAM1601	VPS4A	3'	CCTTGCAGCCACAGAGA 25102 C AT TCT		
			TC CTGTGGCT GT GG		
			AG GACACCGA CG CC		
			A _ TT_		
GAM1601	XYLT1	5'	CCAACAGCAGCCACGGGA 77847 T A_ TC		
			TTCCC GTGGCT TGT TGG		
			AAGGG CACCGA ACA ACC		
			_ CG _		
GAM1601	ZFP100	3'	CCAGAAAGCCAAAAAGAA 70050 CCTG ATG		
			TTC TGGCT TTCTGG		
			AAG ACCGA AAGACC		
			AAAA _		
GAM1601	ZNF213	5'	CAGCTACCACAGGGGA 65091 C TGTT		
			TTCCCTGTGG TA CTG		
			AGGGGACACC AT GAC		
			_ C__		
GAM1601	LOC112609	3'	CCAGTGTGGCACAGGGAA 72837 G GTT		
			TTCCCTGTG CTAT CTGG		
			AAGGGACAC GGTG GACC		
			_ T_		
GAM1601	LOC115073	5'	CCAGGCGTCAAACACAGGGA 73204 CT__ T		
			TCCCTGTGG ATGT CTGG		
			AGGGACACC TGCG GACC		
			AAAC _		
GAM1601	LOC122962	5'	CCAGACAGTGGCCACTGAGAA 75587 CCT GT		
			TTC GTGGCTAT TCTGG		
			AAG CACCGGTG AGACC		
			AGT AC		
GAM1601	LOC124044	3'	CCAGAACACTCAGAGGGA 76025 G CTA		
			TCCCT TGG TGTTCTGG		
			AGGGA ACT ACAAGACC		
			G C_		
GAM1601	LOC143308	5'	CCAAATTTGGCCACAG 82936 T C		
			CTGTGGCTA GTT TGG		

GACACCGGT TAA ACC  
 T \_  
 GAM1601 LOC145314 3' CCAGAACACATCACCTGAG 77086 CCT CTA  
 TTC GTGG TGTTCTGG  
 ||| ||| |||||  
 GAG CACT ACAAGACC  
 TC\_ AC\_  
 GAM1601 LOC146420 3' CCAGAACCAGTTACAG 83667 AT  
 CTGTGGCT GTTCTGG  
 ||||| |||||  
 GACATTGA CAAGACC  
 C\_  
 GAM1601 LOC146445 3' CCAGAGCCACCACAGGGA 83678 CTAT  
 TCCCTGTGG GTTCTGG  
 ||||| |||||  
 AGGGACACC CGAGACC  
 AC\_  
 GAM1601 LOC147178 3' CCAGCCAGCCACGGAGAA 61323 C ATGTT  
 TTC CTGTGGCT CTGG  
 ||| ||||| |||  
 AAG GGCACCGA GACC  
 A CC\_  
 GAM1601 LOC148529 5' CACAGCCACAGGAGAA 84166 \_ A  
 TTC CCTGTGGCT TG  
 ||| ||||| ||  
 AAG GGACACCGA AC  
 A C  
 GAM1601 LOC148930 5' CCAGGGGCAGACCACGGGGAA 79093 CTA \_  
 TTCCCTGTGG TGTTCTGG  
 ||||| ||||| |||  
 AAGGGGCACC ACGGG ACC  
 AG\_ G  
 GAM1601 LOC149950 5' CCAGAACATGATCTCAGG 79551 T GC  
 CCTG G TATGTTCTGG  
 |||| | |||||  
 GGAC C GTACAAGACC  
 T TA  
 GAM1601 LOC150378 5' CCAGAAACAAGCCACGGGAA 79742 T ATG  
 TTCCC GTGGCT TTCTGG  
 |||| ||||| |||||  
 AAGGG CACCGA AAGACC  
 \_ ACA  
 GAM1601 LOC150951 5' CCAGGGCCACACAGGGAA 85167 GCTAT  
 TTCCCTGTG GTTCTGG  
 ||||| |||||  
 AAGGGACAC CGGGACC  
 AC\_  
 GAM1601 LOC151429 3' CCAGGAGACCACAGGGA 85347 \_ ATGT  
 TCCCTGTGG CT TCTGG  
 ||||| || |||||

AGGGACACC GA GGACC  
 A \_\_\_\_  
 GAM1601 LOC158434 3' CCAGAATAAACCACTGGGAA 86819 T CTA  
 TTCCC GTGG TGTTCTGG  
 ||||| ||| |||||  
 AAGGG CACC ATAAGACC  
 T AA\_  
 GAM1601 LOC170106 5' CCAAGGCAGTCAGCCACAGG 82571 A\_\_ TC  
 CCTGTGGCT TGT TGG  
 ||||| ||| |||  
 GGACACCGA ACG ACC  
 CTG GA  
 GAM1601 LOC196446 3' CGGAAAGCCACAGAGAA 87708 C ATG TG  
 TTC CTGTGGCT TTC G  
 ||| ||||| ||| |  
 AAG GACACCGA AAG C  
 A \_\_\_\_ GT  
 GAM1601 LOC197136 3' CCAGAACACTCAGAGGGA 89728 G CTA  
 TCCCT TGG TGTTCTGG  
 ||||| ||| |||||  
 AGGGA ACT ACAAGACC  
 G C\_  
 GAM1601 LOC197342 3' CCAGGAGAAGCCACAGGGGA 87993 ATG  
 TTCCCTGTGGCT TTCTGG  
 ||||| |||||  
 AGGGGACACCGA AGGACC  
 AG\_  
 GAM1601 LOC200734 3' CCATCCGCAGCCACAGGGGA 88860 A TTC  
 TTCCCTGTGGCT TG TGG  
 ||||| ||||| |||  
 AGGGGACACCGA GC ACC  
 C CT\_  
 GAM1601 LOC201102 3' CCTGACCAGCCACAGGAGA 88090 \_ AT CT  
 TC CCTGTGGCT GTT GG  
 || ||||| ||| ||  
 AG GGACACCGA CAG CC  
 A C\_ T\_  
 GAM1601 LOC201283 3' CCAGAACACAGTCGTGAGGA 60413 CT A  
 TCC GTGGCT TGTTCTGG  
 ||| ||||| |||||  
 AGG TGCTGA ACAAGACC  
 AG C  
 GAM1601 LOC202915 3' CCACACGCCAGCCACAGGGGA 90388 A\_ TC  
 TTCCCTGTGGCT TGT TGG  
 ||||| ||| |||  
 AGGGGACACCGA GCA ACC  
 CC C\_  
 GAM1601 LOC204965 5' CAGAGTGCACAGAGAA 90647 C G TATG  
 TTC CTGTG C TTCTG  
 ||| ||||| | |||||

AAG GACAC G GAGAC  
 A \_ T\_\_\_\_  
 GAM1601 LOC205418 3' CACAGCCAGCAGGGAA 90681 \_ A  
 TTCCCTG TGGCT TG  
 ||||| ||||| ||  
 AAGGGAC ACCGA AC  
 G C  
 GAM1601 LOC220692 3' CCAGAATAAAACCACCAGGAA 91220 CT CTA  
 TTCC GTGG TGTTCCTGG  
 ||| ||| |||||  
 AAGG CACC ATAAGACC  
 AC AAA  
 GAM1601 LOC222631 5' CCAGAACACAGCTGGAA 92838 CTGT A  
 TTCC GGCT TGTTCCTGG  
 ||| ||| |||||  
 AAGG TCGA ACAAGACC  
 \_ C  
 GAM1601 LOC253039 3' CCAAATACATCTACAGGGAA 96153 CT TC\_  
 TTCCCTGTGG ATGT TGG  
 ||||| ||| |||  
 AAGGGACATC TACA ACC  
 \_ TAA  
 GAM1601 LOC253841 5' CCAGAATGTAGCCACAG 96342  
 CTGTGGCTATGTTCTGG  
 |||||  
 GACACCGATGTAAGACC  
  
 GAM1601 LOC254028 3' CCAGAACAGAAGCACCAAGAA 96539 CC TG A\_  
 TTC TG GCT TGTTCCTGG  
 ||| ||| |||||  
 AAG AC CGA ACAAGACC  
 A\_ CA AG  
 GAM1601 LOC257449 3' CAGATCCACAGGGAG 62718 CTATGT  
 TTCCCTGTGG TCTG  
 ||||| |||  
 GAGGGACACC AGAC  
 T\_\_\_\_  
 GAM1601 LOC89231 3' GGACAGCACAGGGAA 92733 G AT  
 TTCCCTGTG CT GTTC  
 ||||| ||| |||  
 AAGGGACAC GA CAGG  
 \_ \_  
 GAM1601 LOC90550 3' CCAGAACACAAATCAGAGGGA 73090 G CTA\_  
 TCCCT TGG TGTTCCTGG  
 ||||| ||| |||||  
 AGGGA ACT ACAAGACC  
 G AAAC  
 GAM1601 LOC91373 3' CCAGCAAGGCCACAG 65834 A TT  
 CTGTGGCT TG CTGG  
 ||||| ||| |||

			GACACCGG AC GACC		
			A _		
GAM1601	LOC91445	3'	CCAGAACCTGCCACAGG	60547	TAT
			CCTGTGGC GTTCTGG		
			GGACACCG CAAGACC		
			TC_		
GAM1602	ABCC3	3'	GGCATCAAGGTGCTGA	39159	A CAATCA
			TCAGCACC TTGA GCC		
			AGTCGTGG AACT CGG		
			_ A _		
GAM1602	ATP1B2	3'	GGCTGGAGTGCAATGGTGC	8054	A A_
			GCACCATTG CA TCAGCC		
			CGTGGTAAC GT GGTCGG		
			_ GA		
GAM1602	IFNAR2	3'	GCTGGAGCGCAATGGTGT	6043	ACAA
			GCACCATTG TCAGC		
			TGTGGTAAC GGTCG		
			GCGA		
GAM1602	IL24	3'	GCTGACCTTGCTGATGGTG	22445	GA _
			CACCATT CAA TCAGC		
			GTGGTAG GTT AGTCG		
			TC CC		
GAM1602	OSM	3'	GGCTGACTCATGGCCGGGCTGA	40076	A_ T CAA
			TCAGC CCAT GA TCAGCC		
			AGTCG GGTA CT AGTCGG		
			GGCC _ C_		
GAM1602	POU2AF1	3'	GGCTGGAGTACAATGGTGC	20657	_ AA
			GCACCATTG AC TCAGCC		
			CGTGGTAAC TG GGTCGG		
			A A_		
GAM1602	SLC4A10	5'	CGGGCTGAGTGTAAGACACTGA	41911	CACCATTG A
			TCAG ACA TCAGCCCG		
			AGTC TGT AGTCGGGC		
			ACAGAA_ G		
GAM1602	TNFRSF10B	3'	GGCTGGAGTGCAATGGTGC	13876	A A_
			GCACCATTG CA TCAGCC		
			CGTGGTAAC GT GGTCGG		
			_ GA		
GAM1602	24432	5'	GGGGGTCACACGGTGCTGA	43310	AT_ AATCAG
			TCAGCACC TGAC CCC		

AGTCGTGG ACTG GGG  
 CAC G\_\_\_\_  
 GAM1602 BTN3A1 3' TTGTTAATAATGCTGA 22931 CC  
 TCAGCA ATTGACAA  
 ||||| |||||  
 AGTCGT TAATTGTT  
 AA  
 GAM1602 CECR1 3' GGCTGGAGTACAATGGTGC 33818 \_ AA  
 GCACCATTG AC TCAGCC  
 ||||| || |||||  
 CGTGGTAAC TG GGTCGG  
 A A\_  
 GAM1602 DKFZP434C212 3' GGCTGGAGTGCAATGGTGC 68916 A A\_  
 GCACCATTG CA TCAGCC  
 ||||| || |||||  
 CGTGGTAAC GT GGTCGG  
 \_ GA  
 GAM1602 DKFZP564I052 5' GGCTATTTGGCTGTCAATGGTG 66713 AT \_\_\_\_  
 TTGA TCAGCACCATTGACA CA GCC  
 ||||| || |||||  
 AGTTGTGGTAACTGT GT CGG  
 CG TTAT  
 GAM1602 FLJ11000 3' GGCTGATTTGCCAAATGC 36962 CCA A \_  
 GCA TTG CAA TCAGCC  
 || || || |||||  
 CGT AAC GTT AGTCGG  
 A\_\_ C T  
 GAM1602 GREB1 3' GGCTGGAGTGCAATGGTGC 27883 A A\_  
 GCACCATTG CA TCAGCC  
 ||||| || |||||  
 CGTGGTAAC GT GGTCGG  
 \_ GA  
 GAM1602 HSMPP8 3' GGCTGGAGTGCAATGGTGC 93481 A A\_  
 GCACCATTG CA TCAGCC  
 ||||| || |||||  
 CGTGGTAAC GT GGTCGG  
 \_ GA  
 GAM1602 HZFW1 3' CGGAAAGGAACCAATGGTGCT 47459 ACAA AGC\_  
 AGCACCATTG TC CCG  
 ||||| || |||||  
 TCGTGGTAAC AG GGC  
 CA\_\_ GAAA  
 GAM1602 KIAA0210 5' GGCTGGAGTATAATGGTGC 28482 \_ AA  
 GCACCATTG AC TCAGCC  
 ||||| || |||||  
 CGTGGTAAT TG GGTCGG  
 A A\_  
 GAM1602 KIAA0495 3' GGCTGGAGTGCAATGGTGC 62596 A A\_  
 GCACCATTG CA TCAGCC  
 ||||| || |||||

		CGTGGTAAC GT GGTCCG	
		_ GA	
GAM1602 KIAA0895	3'	GGCTTAAATAATGGTGCT 92725	ACAATC
		AGCACCATTG AGCC	
		TCGTGGTAAT TCGG	
		AAAT__	
GAM1602 MGC10818	3'	GGCTGGAGTACAATGGTGC 47542	_ AA
		GCACCATTG AC TCAGCC	
		CGTGGTAAC TG GGTCCG	
		A A_	
GAM1602 MGC21675	3'	GGCTGGAGTGCAATGGTGC 53486	A A_
		GCACCATTG CA TCAGCC	
		CGTGGTAAC GT GGTCCG	
		_ GA	
GAM1602 MGC2474	3'	GGCTGGAGTGCAATGGTGC 43728	A A_
		GCACCATTG CA TCAGCC	
		CGTGGTAAC GT GGTCCG	
		_ GA	
GAM1602 STAF65(gamma)	3'	GGCTGGAGTGCAATGGTGC 29441	A A_
		GCACCATTG CA TCAGCC	
		CGTGGTAAC GT GGTCCG	
		_ GA	
GAM1602 LOC144248	5'	GGCTGGAGTGCAATGGTGT 76742	A A_
		GCACCATTG CA TCAGCC	
		TGTGGTAAC GT GGTCCG	
		_ GA	
GAM1602 LOC147660	3'	GGCTAGAGTGCAATGGTGC 78396	A A _
		GCACCATTG CA TC AGCC	
		CGTGGTAAC GT AG TCGG	
		_ G A	
GAM1602 LOC149566	3'	GCTGATTGTCACAGGCT 84491	ACCAT
		AGC TGACAATCAGC	
		TCG ACTGTTAGTCG	
		GAC__	
GAM1602 LOC150197	3'	CGGGCTGACTGTGGCCTGC 79596	_ TGACAA
		GCA CCAT TCAGCCCG	
		CGT GGTG AGTCGGGC	
		CC TC__	
GAM1602 LOC163682	5'	GCTGCCCCTGTCCATGGTGCTG 87037	T AT__
A		TCAGCACCAT GACA CAGC	

	AGTCGTGGTA CTGT GTCG	
	C CCCC	
GAM1602 LOC169611 3'	CGGGCTGGAATGCAATGGCGC 82762	A ACAA
	GC CCATTG TCAGCCCG	
	CG GGTAAC GGTCGGGC	
	C GTAA	
GAM1602 LOC220776 3'	GGCCCATCGTGACAATGGTGC 68394	A ATCA__
	GCACCATTG CA GCC	
	CGTGGTAAC GT CGG	
	A GCTACC	
GAM1602 LOC221608 3'	TTGTTAATAATGCTGA 92190	CC
	TCAGCA ATTGACAA	
	AGTCGT TAATTGTT	
	AA	
GAM1602 LOC254351 3'	GGCTGGAGTGCAATGGTGT 94998	A A_
	GCACCATTG CA TCAGCC	
	TGTGGTAAC GT GGTCGG	
	_ GA	
GAM1602 LOC257095 5'	GGCTGACCATCAGGGCTGG 96941	A AT CAA
	TCAGC CC TGA TCAGCC	
	GGTCG GG ACT AGTCGG	
	_ _ ACC	
GAM1602 LOC89231 3'	GGCTGGAGTGCAATGGTGT 92734	A A_
	GCACCATTG CA TCAGCC	
	TGTGGTAAC GT GGTCGG	
	_ GA	
GAM1602 LOC89932 3'	GGCTGGAGTACAATGGTGC 60811	_ AA
	GCACCATTG AC TCAGCC	
	CGTGGTAAC TG GGTCGG	
	A A_	
GAM1602 LOC91661 3'	GGCTGGAATGCAATGGTGC 56404	ACAA
	GCACCATTG TCAGCC	
	CGTGGTAAC GGTCGG	
	GTAA	
GAM1602 LOC92578 5'	CGGGCTGACCCATGGTACTGA 69826	C TGACAA
	TCAG ACCAT TCAGCCCG	
	AGTC TGGTA AGTCGGGC	
	A CCC__	
GAM1602 LOC92841 3'	GGCTGGAGTGCAATGGTGC 70717	A A_
	GCACCATTG CA TCAGCC	



CGTGGTAAC GT GGTCCG  
 \_ GA  
 GAM1603 CTNNA1 3' CACTCAGTAAAACATAATGT 65917 C GA  
 ACATTA TGT TACTGAGTG  
 ||||| ||| |||||  
 TGTAAT ACA ATGACTCAC  
 \_ AA  
 GAM1603 IGFBP3 3' AGGCATCACAAGTAATGTCA 5186 \_ A\_  
 TGACATTACT GTGAT CT  
 ||||| ||| ||  
 ACTGTAATGA CACTA GA  
 A CG  
 GAM1603 IL2 5' CACTACTCACAGTAACCTCA 64646 CA TACTG  
 TGA TTACTGTGA AGTG  
 ||| ||||| |||  
 ACT AATGACACT TCAC  
 CC CA\_  
 GAM1603 MASP2 3' CCAGTGTAATGTCA 21738 TGTGAT A  
 TGACATTAC ACTG G  
 ||||| ||| |  
 ACTGTAATG TGAC C  
 \_ C  
 GAM1603 VANG2 3' CACTCAGTATTCCAATG 71646 TAC TG  
 CAT TG ATACTGAGTG  
 ||| || |||||  
 GTA AC TATGACTCAC  
 \_ CT  
 GAM1603 DKFZP434J193 3' CACTCAGGTAACAACATGTCA 71000 TAC GATA  
 TGACAT TGT CTGAGTG  
 ||||| ||| |||||  
 ACTGTA ACA GACTCAC  
 CA\_ ATG\_  
 GAM1603 EIF5 3' CACTCAGCATACTCAGTGTCA 8759 ACT ATA  
 TGACATT GTG CTGAGTG  
 ||||| ||| |||||  
 ACTGTGA CAT GACTCAC  
 CT\_ AC\_  
 GAM1603 FLJ14327 3' ATTCACCACACTAATGTCA 46130 C ATAC  
 TGACATTA TGTG TGAGT  
 ||||| ||| |||  
 ACTGTAAT ACAC ACTTA  
 C C\_  
 GAM1603 KIAA0319 3' CACTCAACAAGCCAGTGATGCC 29032 A TGATAC  
 A TG CATTACTG TGAGTG  
 || ||||| |||  
 AC GTAGTGAC ACTCAC  
 C CGAACA  
 GAM1603 MGC12538 5' TATCACAGAATATCA 51246 C A  
 TGA ATT CTGTGATA  
 ||| ||| |||||

			ACT TAA GACACTAT		
			A _		
GAM1603	PIP3-E	3'	CACTCCAGTCACAAACAATGTC 66799	AC_	ACT
	A		TGACATT TGTGAT GAGTG		
			ACTGTAA ACACTG CTCAC		
			CAA AC_		
GAM1603	RNP24	3'	CTTGGTCATAATAATGTCA 22356	C	TA TG
			TGACATTA TGTGA C AG		
			ACTGTAAT ATACT G TC		
			A __ GT		
GAM1603	LOC162333	5'	CAGTTATCACAGAATGCCA 87124	A A	_
			TG CATT CTGTGATA CTG		
			AC GTAA GACACTAT GAC		
			C _ T		
GAM1603	LOC202460	5'	CACTCAGTAGTTGTAAGACCA 89179	ACA	TGTGA
			TG TTAC TACTGAGTG		
			AC AATG ATGACTCAC		
			CAG TTG__		
GAM1603	LOC255975	5'	CACTCAGTACCCATAG 95881	A_	
			CTGTG TACTGAGTG		
			GATAC ATGACTCAC		
			CC		
GAM1604	ADH1B	3'	CTTAGACATAAAGTAAAAT 72644	C	CAC
			ATTT ACTTT TGTCTGAG		
			TAAA TGAAA ACAGATTC		
			A T__		
GAM1604	AHR	3'	ATCTCAGATGTAAAATAAATG 7875	CAC	C T
			CATTT TTT AC GTCTGAGAT		
			GTAAA AAA TG TAGACTCTA		
			TA_ T _		
GAM1604	FDFT1	3'	TAGGAAAGTGAAATG 15518	A	
			CATTTCACTTTC CTG		
			GTAAAGTGAAAG GAT		
			-		
GAM1604	JTB	3'	ATCTCAGACAGTGAAAGTGAAA 21959		
	TG		CATTTCACTTTCACTGTCTGAGAT		
			GTAAAGTGAAAGTGACAGACTCTA		
GAM1604	KLF4	3'	TCCCAGACAGTGATATG 14891	CT	A
			CA TTCACTGTCTG GA		

			GT AGGTGACAGAC CT		
			AT C		
GAM1604	PHYH	3'	ACAGTAAAAGTGAAAT 20608	C	
			ATTTCACTTT ACTGT		
			TAAAGTGAAA TGACA		
			A		
GAM1604	PKD2	3'	TCCAGGTTGAAAAGTGAAA 60096	CTG A	
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T__ _		
GAM1604	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1604	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA CTG	
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1604	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT CT	
			TTCACTTTCA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1604	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G T_	
			CTTTCACT TC GAGAT		
			GAAAGTGA AG TTCTA		
			G TC		
GAM1604	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT 45802	ACTTTCACT	
	G		CATTTT GTCTGAGAT		
			GTAAAG CAGACTCTA		
			AAACATTT_		
GAM1604	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281	CTT	
			CATTTCA TCACTGTCTGAGAT		
			GTAAAGT AGTGACAGACTCTA		
			C_		
GAM1604	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C TC	
			TTCA TTTCACTG TGAG		
			AAGT AAAGTGAC GTTT		
			A CT		
GAM1604	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A _	
			TTTC CTG TCTGAGAT		

		AAAG GAC AGACTCTA		
		— G		
GAM1604 NIR3	3'	GCAGTGAAAAGTGCAAT	66242	T
		ATT CACTTTTCACTGT		
		TAA GTGAAAAGTGACG		
		C		
GAM1604 PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA	53598	CA G
		TTCAC TTT CT TCTGAGAT		
		AAGTGAAA GG AGACTCTA		
		CC G		
GAM1604 PP35	3'	ATCTCAGACTGAAA	22814	CT
		TTTCA GTCTGAGAT		
		AAAGT CAGACTCTA		
		—		
GAM1604 PRD-NY3	3'	CTCATTGCAATAAGTGAAATG	48148	TCAC C_
		CATTTCAC TTT TGT TGAG		
		GTAAAGTGAA ACG ACTC		
		TA_ TT		
GAM1604 SEP15	3'	TCCTACAGTAAGAGTGAAA	14934	C CT
		TTTCACTTT ACTGT GA		
		AAAGTGAGA TGACA CT		
		A TC		
GAM1604 SFXN2	3'	CTCAGGGGAAAAAAGTGAAA	73941	CACTG
		TTTCACTTT TCTGAG		
		AAAGTGAAA GGA CTC		
		AAAGG		
GAM1604 LOC149703	3'	ATCTCAGACAGCCGTTTGAAA	84647	ACTTTCA
		TTTC CTGTCTGAGAT		
		AAAG GACAGACTCTA		
		GTTTGCC		
GAM1604 LOC154007	3'	ATCTCAAACCTTTAGTGAAA	81015	TTCAC T C
		TTTCACT GT TGAGAT		
		AAAGTGA CA ACTCTA		
		TTTCC_ A		
GAM1604 LOC155004	3'	TCATTTAAGTGAAAAGGAAA	81226	A GTC_
		TTTC CTTTCACT TGA		
		AAAG GAAAGTGA ACT		
		_ ATTT		
GAM1604 LOC222134	5'	ACAGTGAAGTGAAATG	94136	T
		CATTTCAC TTT CACTGT		

GTAAAGTGAA GTGACA

GAM1605 CALU 3' GATCCCTTTGCTCTA 6887 TGTTCAT  
TAGAGCAAA GGATC  
||||||| ||||  
ATCTCGTTT CCTAG  
C\_\_\_\_\_

GAM1605 CCND2 3' GGAATCCTGGATTTTGGCCCT 8296 A TGT \_  
AG GCAAA TTCAGGAT CC  
|| |||| | ||||| ||  
TC CGTTT AGGTCCTA GG  
C T\_ A

GAM1605 CTLA4 5' GGATCCTGAAAGGTTTTGCTCT 17808 \_ G  
AC GTAGAGCAAA T TTCAGGATCC  
||||||| | ||||| |||||  
CATCTCGTTT G AAAGTCCTAGG  
T G

GAM1605 CYP1A1 3' GGATCCTGCCTGCCCTAC 4945 A\_ AATGTTT  
GTAG GCA CAGGATCC  
||| ||| |||||  
CATC CGT GTCCTAGG  
CC CC\_\_\_\_\_

GAM1605 ETF1 3' CCTGAAGCTGATGCTTCAC 16394 AG AAT  
GT AGCA GTTTCAGG  
|| |||| | |||||  
CA TCGT CGAAGTCC  
CT AGT

GAM1605 HDAC4 3' GGGATCCTGCCACCTGCCCT 20115 A AA TTT  
AG GCA TG CAGGATCCC  
|| ||| || | |||||  
TC CGT AC GTCCTAGGG  
C CC C\_

GAM1605 PIGA 3' GAAACACATTGCTCTAC 40004 A\_  
GTAGAGCAA TGTTTC  
||||||| |||||  
CATCTCGTT ACAAAG  
AC

GAM1605 PIGA 3' GAAACACATTGCTCTAC 40013 A\_  
GTAGAGCAA TGTTTC  
||||||| |||||  
CATCTCGTT ACAAAG  
AC

GAM1605 PIGA 3' GAAACACATTGCTCTAC 10552 A\_  
GTAGAGCAA TGTTTC  
||||||| |||||  
CATCTCGTT ACAAAG  
AC

GAM1605 PLCB2 3' GGGATCCTGGCCCCACTCTGC 15894 CAAA TT\_  
GTAGAG TG TCAGGATCCC  
||||| || | ||||| |||||

CGTCTC AC GGTCTAGGG  
 \_\_\_\_\_ CCC  
 GAM1605 STK6 3' GGAACACGTGCTCTAC 13187 AA  
 GTAGAGCA TGTTTC  
 ||||| |||||  
 CATCTCGT ACAAGG  
 GC  
 GAM1605 TMOD2 5' GGGATCCTGGCCCCGCTCCAC 27251 A AAATGTT  
 GT GAGC TCAGGATCCC  
 || ||| |||||  
 CA CTCG GGTCTAGGG  
 C CCCC\_\_\_\_  
 GAM1605 DKFZP434K1421 3' GGAAAATTTGCTCCAC 49553 A G  
 GT GAGCAAAT TTTC  
 || ||||| |||||  
 CA CTCGTTTA AAGG  
 C A  
 GAM1605 DKFZP434N178 5' GGGATCCTTGCTCTCTGCCCT 71908 A AATGTTTC  
 GC GTAG GCA AGGATCCC  
 ||| ||| |||||  
 CGTC CGT TCCTAGGG  
 C CTCTCCGT  
 GAM1605 EST-YD1 3' GACCTCGACATTTGCTC 41080 TC A  
 GAGCAAATGTT AGG TC  
 ||||| ||| ||  
 CTCGTTTACAG TCC AG  
 C\_ \_  
 GAM1605 FLJ11026 5' GGATCACCAGTTTGCTCCAC 36993 A GTTTCAG  
 GT GAGCAAAT GATCC  
 || ||||| |||||  
 CA CTCGTTTG CTAGG  
 C ACCA\_\_\_\_  
 GAM1605 FLJ13769 3' GACCCTGAAACACTCAGC 46609 A CAAA A  
 GT GAG TGTTTCAGG TC  
 || ||| ||||| ||  
 CG CTC ACAAAGTCC AG  
 A \_\_\_\_\_ C  
 GAM1605 FLJ20294 3' GGATCCTGCTGCACCCCTCCAC 34879 A CAAA TT  
 GT GAG TGT CAGGATCC  
 || ||| ||| |||||  
 CA CTC ACG GTCCTAGG  
 C CCC\_ TC  
 GAM1605 FLJ21918 3' GATCCCAATGTTCTAC 46289 AA TTCA  
 GTAGAGCA TG GGATC  
 ||||| || |||||  
 CATCTTGT AC CCTAG  
 A\_ \_\_\_\_\_  
 GAM1605 GAB1 3' GAAACATTTGTTCCAC 8977 A  
 GT GAGCAAATGTTTC  
 || ||||| |||||

	CA CTTGTTTACAAAG	
	C	
GAM1605 HSMPP8	3' TCTAAAACATTTGCTT 93486	C
	GAGCAAATGTTT AGG	
	TTCGTTTACAAA TCT	
	A	
GAM1605 KIAA0143	3' GAAACACAACTTTGCTCTAC 64785	_____
	GTAGAGCAAA TGTTTC	
	CATCTCGTTT ACAAAG	
	CAAAC	
GAM1605 KIAA0759	3' GATCCTGGGCCAGCCCCTCCAC 67323	A CAAA TT
	GT GAG TG TCAGGATC	
	CA CTC AC GGTCTAG	
	C CCCG CG	
GAM1605 KIAA1211	3' GTCCAAAACATTTACTCTAC 68896	C CA
	GTAGAG AAATGTTT GGAT	
	CATCTC TTTACAAA CCTG	
	A A_	
GAM1605 KIAA1373	3' GGGATCCTGATTAATGCTCTA 70948	AATGTT
	TAGAGCA TCAGGATCCC	
	ATCTCGT AGTCCTAGGG	
	AATT_	
GAM1605 KIAA1511	3' GGGCACTGAAACATTTGT 70169	GA
	GCAAATGTTTCAG TCC	
	TGTTTACAAAGTC GGG	
	AC	
GAM1605 KIAA1586	5' GATCATGCCATTGTGCTCTAC 92330	_ TTT G
	GTAGAGCA AATG CA GATC	
	CATCTCGT TTAC GT CTAG	
	G C_ A	
GAM1605 MGC9753	5' GGGATCCTGCCCCCGCCCTGC 53056	A AAATGTTT
	GTAG GC CAGGATCCC	
	CGTC CG GTCCTAGGG	
	C CCCCC_	
GAM1605 NFKBIE	3' GGACCCTGAAACACCGTTGTTT 15851	A_ A
	GAGCAA TGTTTCAGG TCC	
	TTTGTT ACAAAGTCC AGG	
	GCC C	
GAM1605 LOC123435	5' GGGACCCTGGGATTTTGCTCT 74208	T TT A
	AGAGCAAA GT CAGG TCCC	

TCTCGTTT TA GTCC AGGG  
 \_ GG C  
 GAM1605 LOC136895 5' GGACCCTATTTGCTCTGC 57170 GTTTC A  
 GTAGAGCAAAT AGG TCC  
 ||||| ||| ||  
 CGTCTCGTTTA TCC AGG  
 \_ C  
 GAM1605 LOC144248 5' GGAATCCACCCTTATTTGCTCT 76741 TTTCA \_  
 AGAGCAAATG GGAT CC  
 ||||| ||| ||  
 TCTCGTTTAT CCTA GG  
 TCCCA A  
 GAM1605 LOC148189 5' GGATCCGCACCGCCCTAC 78716 A AAA TTCA  
 GTAG GC TGT GGATCC  
 ||| || ||| |||||  
 CATC CG ACG CCTAGG  
 C CC\_ \_  
 GAM1605 LOC149711 5' ATCCACTATCTGCTCTAC 84670 A TTTCA  
 GTAGAGCA ATG GGAT  
 ||||| ||| |||  
 CATCTCGT TAT CCTA  
 C CA\_ \_  
 GAM1605 LOC165693 3' GACCCTGAAACAGCTC 82597 AAA A  
 GAGC TGTTTCAGG TC  
 ||| ||||| ||  
 CTCG ACAAAGTCC AG  
 \_ C  
 GAM1605 LOC253985 5' ATCCACCATGCTCTAC 96482 AAT TTCA  
 GTAGAGCA GT GGAT  
 ||||| || |||  
 CATCTCGT CA CCTA  
 AC\_ \_  
 GAM1605 LOC256568 3' GATCAGACACATTGCTCTAC 94843 A T AG  
 GTAGAGCAA TGT TC GATC  
 ||||| ||| || |||  
 CATCTCGTT ACA AG CTAG  
 \_ C A\_  
 GAM1605 LOC91266 5' CCTGAAACATGTTC 65412 AA  
 GAGCA TGTTTCAGG  
 |||| |||||  
 CTTGT ACAAAGTCC  
 \_  
 GAM1606 CDH10 3' TAGTTCTCCCTTAAGCAACCT 22058 CG CAGTGT A  
 AGG GCT GA GAACTA  
 ||| ||| || |||||  
 TCC CGA CTCTTGAT  
 AA ATTCC\_ \_  
 GAM1606 DACH 3' TAGTTCTTCCATAACCACT 54971 C CTCA T  
 AGG GG GTG GAAGAACTA  
 ||| || ||| |||||



TCC CC TAC CTTCTTGAT  
 A AA\_\_ \_  
 GAM1606 HPS1 3' TCTTCCAGAGCTGCCT 3969 AG T  
 AGGCGGCTC TG GAAGA  
 ||||| || ||||  
 TCCGTCGAG AC CTTCT

— —  
 GAM1606 PCK1 5' TCTTCAGGCTGCCT 52264 CAGTG  
 AGGCGGCT TGAAGA  
 ||||| ||||  
 TCCGTCGG ACTTCT

— —  
 GAM1606 RORB 5' AGCTCTTCGCCGACCACCT 22606 C C AGT A  
 AGG GG TC GTGAAGA CT  
 ||| || ||||| ||  
 TCC CC AG CGCTTCT GA  
 A \_ C\_ C

GAM1606 SPTBN4 3' AGTCCCCATGGCCGCCT 47386 CAGT AA A  
 AGGCGGCT GTG GA CT  
 ||||| ||| |||  
 TCCGCCGG TAC CT GA  
 — CC \_

GAM1606 ZNF200 3' GTAGTTCTGAATTCCCAAGCTG 12909 CAGT\_ GA  
 CCT AGGCGGCT GT AGAACTAC  
 ||||| || |||||  
 TCCGTCGA TA TCTTGATG  
 ACCCT AG

GAM1606 BTN2A1 3' GTAATTCTCAGTGTGTGAGCTG 54342 \_ TG GA C  
 CCT AGGCGGCTCA G T AGAA TAC  
 ||||| ||| ||| |||  
 TCCGTCGAGT T G TCTT ATG  
 G GT AC A

GAM1606 CFP1 3' TAGCTCCGTCAAGCTGCCT 58771 CAGTG A\_ A  
 AGGCGGCT TGA GA CTA  
 ||||| ||| ||| |||  
 TCCGTCGA ACT CT GAT  
 — GC C

GAM1606 FENS-1 3' TGGGAGTCACACAAGCCGCCT 40445 CA AGAA  
 AGGCGGCT GTGTGA CTA  
 ||||| ||||| |||  
 TCCGCCGA CAACT GGT  
 A\_ GAG\_

GAM1606 FLJ14082 3' AGTTCTTCCTAAGGCACCC 46668 CG CAG T  
 GG GCT TG GAAGAACT  
 || ||| || |||||  
 CC CGG AT CTTCTTGA  
 CA A\_ C

GAM1606 FLJ20539 5' TGGGGCCACCTGAGCCGCC 35363 T AAGAA  
 GGCGGCTCAG GTG CTA  
 ||||| ||| |||

CCGCCGAGTC CAC GGT  
 \_ CGG\_  
 GAM1606 FLJ22301 3' AGCCCTTCACGTAGCCTCCT 45756 C CAG AA  
 AGG GGCT TGTGAAG CT  
 ||| ||| ||||| ||  
 TCC CCGA GCACTTC GA  
 T T\_\_ CC  
 GAM1606 HEMGN 5' TAGAGAAAAAACTGAGCCACC 37380 C GTGAAGAA  
 T AGG GGCTCAGT CTA  
 ||| ||||| |||  
 TCC CCGAGTCA GAT  
 A AAAAAAGA  
 GAM1606 KIAA0379 3' GTAGTTCTTGCGAATGCCACC 68150 C TCAG G  
 GG GGC TGT AAGAACTAC  
 || ||| ||| |||||  
 CC CCG GCG TTCTTGATG  
 A TAA\_ \_  
 GAM1606 KIAA0494 3' TCTCACACTGACCACC 28750 C C A  
 GG GG TCAGTGTGA GA  
 || ||| ||||| ||  
 CC CC AGTCACACT CT  
 A \_ \_  
 GAM1606 LACE1 3' CTTACATTAAACCACCT 91837 C CTC  
 AGG GG AGTGTGAAG  
 ||| || |||||  
 TCC CC TTACACTTC  
 A AAA  
 GAM1606 NAPG 3' TAGTTCTTCAGGTAGCACCT 96730 CG CAG G  
 AGG GCT T TGAAGAACTA  
 ||| ||| | |||||  
 TCC CGA G ACTTCTTGAT  
 A\_ T\_\_ G  
 GAM1606 PRO2405 5' AGGAGCACATTAAGCCGCCT 37798 C AAGAA  
 AGGCGGCT AGTGTG CT  
 ||||| ||||| ||  
 TCCGCCGA TTACAC GA  
 A GAG\_  
 GAM1606 LOC121219 5' AGTCCTCAGCGAAGCCGCCT 74040 CA G A A  
 AGGCGGCT GT TGA GA CT  
 ||||| || ||| || ||  
 TCCGCCGA CG ACT CT GA  
 AG \_ C \_  
 GAM1606 LOC146990 3' CTTACACCCAGCCGCCT 83886 CA  
 AGGCGGCT GTGTGAAG  
 ||||| |||||  
 TCCGCCGA CCACTTC  
 CC  
 GAM1606 LOC148371 5' TTCCA CTGAGCCACC 78809 C T  
 GG GGCTCAGTG GAA  
 || ||||| |||

		CC CCGAGTCAC CTT			
		A _			
GAM1606	LOC152274 3'	AGTCCCTGCAGGAGCAGCCT	80498	G	AG AA A
		AGGC GCTC TGTG GA CT			
		TCCG CGAG ACGT CT GA			
		A G_ CC _			
GAM1606	LOC200261 3'	AGTTGCTCCACTGAGTCACC	88653	C	T AG
		GG GGCTCAGTG GA AACT			
		CC CTGAGTCAC CT TTGA			
		A _ CG			
GAM1606	LOC201562 5'	GTAGTCCGGCCCGAGCCGCT	88975		AGT GAA A
		GGCGGCTC GT GA CTAC			
		TCGCCGAG CG CT GATG			
		CC_ GC_ _			
GAM1606	LOC202347 3'	TCATGGCAGAGCCGCCT	90349	A	_
		AGGCGGCTC GT GTGA			
		TCCGCCGAG CG TACT			
		A G			
GAM1606	LOC220370 3'	TCACCTCACTGAGCCACCT	92834	C	___
		AGG GGCTCAGT GTGA			
		TCC CCGAGTCA CACT			
		A CTC			
GAM1606	LOC221838 5'	TTCCACTGAGCCACC	92546	C	T
		GG GGCTCAGTG GAA			
		CC CCGAGTCAC CTT			
		A _			
GAM1606	LOC51716 3'	AGTTCCACACTGAGCGCCT	32786	G	AA
		AGGCG CTCAGTGTG GAACT			
		TCCGC GAGTCACAC CTTGA			
		_ _			
GAM1606	LOC89919 3'	CTTCCACTGAGCCACC	60722	C	T
		GG GGCTCAGTG GAAG			
		CC CCGAGTCAC CTTC			
		A _			
GAM1606	LOC91947 3'	TAGTTCTTTTATTGTAAGCCGC	67614	___	T
	T	GGCGGCT CAGTG GAAGAACTA			
		TCGCCGA GTTAC TTTCTTGAT			
		AT _			
GAM1607	ADAM17 3'	ATGCCTGTAATCCCAGCACTTG	41553	_ A	A
		CA GT GCTGGGATTACAG CAT			

			GT CA CGACCCTAATGTC GTA		
			T _ C		
GAM1607	ADAM17	3'	ATGCCTGTAATCCCAGCACTTG 12081	_ A	A
			CA GT GCTGGGATTACAG CAT		
			GT CA CGACCCTAATGTC GTA		
			T _ C		
GAM1607	ADAT1	3'	CTGTAATCCTAGCTACT 23898		
			AGTAGCTGGGATTACAG		
			TCATCGATCCTAATGTC		
GAM1607	AICDA	3'	CTGTAATCCCAGCACT 40326	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
GAM1607	AK1	3'	ATGCCTGTAATCCCAGCACT 4879	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			_ C		
GAM1607	ALDH3A2	3'	ATGCCTGTAATCCCAGCACT 69270	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			_ C		
GAM1607	ALDH3B1	3'	ATGCCTGTAATCCCAGCTACT 91520		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1607	ALDH3B1	3'	CTGTAATCCCAGCACT 91524	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
GAM1607	ALDH8A1	3'	ATGCCTATAATCCCAGCACT 42607	A	C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			_ A C		
GAM1607	ANKH	3'	ATGCCTGTAATCCCAACACT 53987	AGC	A
			AGT TGGGATTACAG CAT		
			TCA ACCCTAATGTC GTA		
			CA_ C		
GAM1607	ANKH	3'	CTGTAATCCCAGCTACT 53989		
			AGTAGCTGGGATTACAG		

TCATCGACCCTAATGTC

GAM1607 ARHGEF6 3' CTGTGGTCCCAGCTACTCA 68202 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTGGTGTGTC  
C

GAM1607 ATM 3' CTGTAATCCCAGCACT 56295 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 ATM 3' CTATAATCCCAGCACT 56303 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC

GAM1607 ATM 3' CTGTAATCCCAGCACT 3511 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 ATP1A2 3' ATGCCTGTAATCCCAGCACT 5521 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

GAM1607 ATP1A2 3' CTGTAATCTCAGCTACTCA 5524 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACTCTAATGTC  
C

GAM1607 BAAT 3' ATGTCTCCCCAGCTGC 8112 ATTAC  
GTAGCTGGG AGACAT  
||||| |||||  
CGTCGACCC TCTGTA  
CC\_\_

GAM1607 BHMT2 3' CTGCAATCCCAGCACT 34309 A A  
AGT GCTGGGATT CAG  
||| ||||| |||  
TCA CGACCCTAA GTC

GAM1607 BRCA1 3' CTGTAATCCCAGCTACT 23585  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCACT 23592 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCTACT 23593  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCACT 23559 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCTACT 23560  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCACT 23568 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCTACT 23569  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCACT 23576 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCTACT 23577  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCACT 23584 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCACT 23518 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCTACT 23519  
AGTAGCTGGGATTACAG  
|||||||

TCATCGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCACT 23527 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 BRCA1 3' CTGTAATCCCAGCTACT 23528  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCACT 23535 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 BRCA1 3' CTGTAATCCCAGCTACT 23536  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCACT 23543 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 BRCA1 3' CTGTAATCCCAGCTACT 23544  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1607 BRCA1 3' CTGTAATCCCAGCACT 23551 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 BRCA1 3' CTGTAATCCCAGCTACT 23552  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1607 BRCA2 3' ATGCCTGTAATCCCAACACTTT 3548 TAGC\_ A  
G CAG TGGGATTACAG CAT  
||| |||||  
GTT ACCCTAATGTC GTA  
TCACA C

GAM1607 C1orf1 3' CTGTAATCCCAACACT 6859 AGC  
AGT TGGGATTACAG  
||| |||||

			TCA ACCCTAATGTC			
			CA_			
GAM1607	C5R1	3'	CTGTAATCCCAGAACT 8204 AG			
			AGT CTGGGATTACAG			
			TCA GACCCTAATGTC			
			A_			
GAM1607	CARKL	3'	ATGCCTGTAATCCCAGCTACT 25183		A	
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1607	CASP10	3'	ATGCCTGTAATCCCAGTACTCT 52098	TA_	A	
	G		CAG GCTGGGATTACAG CAT			
			GTC TGACCCTAATGTC GTA			
			TCA C			
GAM1607	CASP10	3'	ATGCCTGTAATCCCAGTACTCT 52116	TA_	A	
	G		CAG GCTGGGATTACAG CAT			
			GTC TGACCCTAATGTC GTA			
			TCA C			
GAM1607	CASP6	3'	ATGCCTGCAATCCCAGCTACTT 52200	_	A A	
	G		CA GTAGCTGGGATT CAG CAT			
			GT CATCGACCCTAA GTC GTA			
			T C C			
GAM1607	CASP6	3'	CTGTAATCCCAGCACT 52203	A		
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			-			
GAM1607	CASP6	3'	ATGCCTGCAATCCCAGCTACTT 6907	_	A A	
	G		CA GTAGCTGGGATT CAG CAT			
			GT CATCGACCCTAA GTC GTA			
			T C C			
GAM1607	CASP6	3'	CTGTAATCCCAGCACT 6910	A		
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			-			
GAM1607	CASP8	3'	ATGTCTATAATCCCAGCACT 6913	A	C	
			AGT GCTGGGATTAGACAT			
			TCA CGACCCTAAT TCTGTA			
			A			
GAM1607	CASP8	3'	ATGTCTATAATCCCAGCACT 52919	A	C	
			AGT GCTGGGATTAGACAT			



				TCA CGACCCTAAT TCTGTA		
				— A		
GAM1607	CASP8	3'	ATGTCTATAATCCCAGCACT	52930	A	C
			AGT GCTGGGATTA AGACAT			
			TCA CGACCCTAAT TCTGTA			
			— A			
GAM1607	CASP8	3'	ATGTCTATAATCCCAGCACT	52942	A	C
			AGT GCTGGGATTA AGACAT			
			TCA CGACCCTAAT TCTGTA			
			— A			
GAM1607	CD68	3'	ATGCCTGTAATCCCAGCACT	59797	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1607	CHRNA5	3'	CTGTAATCCCAGCACT	59755	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	CHST5	3'	ATGCCTGTAATCCCAGCATTTT	24022	TA_	A
	G		CAG GCTGGGATTACAG CAT			
			GTT CGACCCTAATGTC GTA			
			TTA C			
GAM1607	CHST5	3'	CTGTAATCCCAGCTACTTA	24025	C	
			A AGTAGCTGGGATTACAG			
			A TCATCGACCCTAATGTC			
			T			
GAM1607	CNGB1	3'	ATGCCTATAATCCCAGTGCT	7110	G	C A
			AGTA CTGGGATTA AG CAT			
			TCGT GACCCTAAT TC GTA			
			— A C			
GAM1607	COG7	3'	CTGTAATCCCAGCACT	67622	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	COL16A1	3'	CTGTAATCCTAGCTATT	8500		
			AGTAGCTGGGATTACAG			
			TTATCGATCCTAATGTC			
			—			
GAM1607	COPA	3'	CTGTAATCCCAGCACT	15187	A	
			AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

GAM1607 CORO2A 3' ATGCCTGTAATCCCAGCACTCT 53400 TA\_ A  
G CAG GCTGGGATTACAG CAT  
||| |||||  
GTC CGACCCTAATGTC GTA  
TCA C

GAM1607 CORO2A 3' ATGCCTGTAATCCCAGCACTCT 12644 TA\_ A  
G CAG GCTGGGATTACAG CAT  
||| |||||  
GTC CGACCCTAATGTC GTA  
TCA C

GAM1607 CPT2 3' ATGCCTGTAATCCCAGCATTTT 3641 TA\_ A  
G CAG GCTGGGATTACAG CAT  
||| |||||  
GTT CGACCCTAATGTC GTA  
TTA C

GAM1607 CRACC 3' CTGTAATCCCAGCACT 41005 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 CTMP 3' CTGTAATCCCAGCACTTTA 53876 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||  
AT TCA CGACCCTAATGTC  
T \_

GAM1607 CTMP 3' CTGTAGTCCCAGCTACTCA 53877 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTGATGTC  
C

GAM1607 CTNNB1 3' TCTGTAATGGTACTG 8581 G GGG  
CAGTA CT ATTACAGA  
|||| || |||||  
GTCAT GG TAATGTCT

GAM1607 CTSS 3' ATGCCTGTAATCCCAGCTACTT 14540 \_ A  
G CA GTAGCTGGGATTACAG CAT  
|| |||||  
GT CATCGACCCTAATGTC GTA  
T C

GAM1607 CTSS 3' CTGTAATCCCAGTACTTG 14542 C G  
A AGTA CTGGGATTACAG  
| ||| |||||  
G TCAT GACCCTAATGTC  
T \_

GAM1607 CYP4F3 3' CTGTAATCCCAGCACTTTA 6115 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||

			AT TCA CGACCCTAATGTC		
			T _		
GAM1607	DAPP1	3'	ATGCCTGTAATCCCAGGACT 26917	AG	A
			AGT CTGGGATTACAG CAT		
			TCA GACCCTAATGTC GTA		
			G_ C		
GAM1607	DAPP1	3'	TGTAATCCCAGCTACTCA 26920	C	
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1607	DBT	3'	CTGTAATCCCAGCACT 8610	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			_		
GAM1607	DCLRE1C	3'	ATGCCTGTAATCCCAGCTAC 42524		A
			GTAGCTGGGATTACAG CAT		
			CATCGACCCTAATGTC GTA		
			C		
GAM1607	DDOST	3'	ATGCCTGTAATCCCAGCACT 17816	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			_ C		
GAM1607	DFFA	3'	CTGTAATCCCAGCACTG 15302	A	
			CAGT GCTGGGATTACAG		
			GTCA CGACCCTAATGTC		
			_		
GAM1607	DHFR	3'	ATGCCTGTAGTCCCAGCTACTC 5799	C	A
	A		A AGTAGCTGGGATTACAG CAT		
			A TCATCGACCCTGATGTC GTA		
			C C		
GAM1607	DHFR	3'	CTGTAATCCCAGCGCT 5803	A	
			AGT GCTGGGATTACAG		
			TCG CGACCCTAATGTC		
			_		
GAM1607	DMC1	3'	CTGTAATCCCAGCACT 22972	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			_		
GAM1607	DNASE2	3'	ATGCCTGTAGTCCCAGCCACTG 7263	A	A
			CAGT GCTGGGATTACAG CAT		

			GTCA CGACCCTGATGTC GTA	
			C C	
GAM1607 DSC1	3'	CTGTAATCCCAGCTACTCA	17059	C
		A AGTAGCTGGGATTACAG		
		A TCATCGACCCTAATGTC		
		C		
GAM1607 DSC1	3'	CTGTAATCCCAGCTACTCA	44328	C
		A AGTAGCTGGGATTACAG		
		A TCATCGACCCTAATGTC		
		C		
GAM1607 DVL3	3'	GTCTGTAATCCCAGCACT	15373	A
		AGT GCTGGGATTACAGAC		
		TCA CGACCCTAATGTCTG		
		—		
GAM1607 DYRK1A	3'	ATGTCTGTAACCAATAATGTA	7349	G GCTG A
		TACA TA GG TTACAGACAT		
		ATGT AT CC AATGTCTGTA		
		A AA__ _		
GAM1607 DYRK1A	3'	ATGTCTGTAACCAATAATGTA	55198	G GCTG A
		TACA TA GG TTACAGACAT		
		ATGT AT CC AATGTCTGTA		
		A AA__ _		
GAM1607 DYRK1A	3'	ATGTCTGTAACCAATAATGTA	55240	G GCTG A
		TACA TA GG TTACAGACAT		
		ATGT AT CC AATGTCTGTA		
		A AA__ _		
GAM1607 EFG2	5'	CTGTAATCCCAGCACT	50476	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607 EGFL5	3'	CTGTAATCCCAGCACT	86618	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607 EHHADH	3'	CTGTAATCCCAGCACT	8750	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607 F2R	3'	CTGTAATCCCAGCACT	8837	A
		AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1607 F2RL3 3' CTGCAATCCCAGCACT 14178 A A  
AGT GCTGGGATT CAG  
||| ||||| |||  
TCA CGACCCTAA GTC

GAM1607 F2RL3 3' CTGTAATCCCAGCACTTTA 14179 C A  
TA AGT GCTGGGATTACAG  
|| ||| ||||| |||||  
AT TCA CGACCCTAATGTC

GAM1607 F2RL3 3' TGTAATCCCAGCTACTCA 14197 C  
A AGTAGCTGGGATTACA  
| ||||| ||||| |||||  
A TCATCGACCCTAATGT  
C

GAM1607 FANCD2 3' CTGTAATCCCAGCACT 52355 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

GAM1607 FCMD 3' CTATAGTCCCAGCTAC 22091 C  
GTAGCTGGGATTA AG  
||| ||||| ||  
CATCGACCCTGAT TC  
A

GAM1607 FGFR1 3' CTGTAATCCCAGCACTTTA 43621 C A  
TA AGT GCTGGGATTACAG  
|| ||| ||||| |||||  
AT TCA CGACCCTAATGTC  
T \_

GAM1607 FGFR1 3' CTGTAATCCCAGCACTTTA 43614 C A  
TA AGT GCTGGGATTACAG  
|| ||| ||||| |||||  
AT TCA CGACCCTAATGTC  
T \_

GAM1607 FGFR2 3' ATGCCTGTAATCCCAGCACT 43376 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| ||||| |||  
TCA CGACCCTAATGTC GTA

GAM1607 FGFR2 3' ATGCCTGTAATCCCAGCACT 43382 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| ||||| |||  
TCA CGACCCTAATGTC GTA

GAM1607 FKRP 3' CTGTAATCCCAGCACT 44185 A  
AGT GCTGGGATTACAG  
||| ||||| |||||

TCA CGACCCTAATGTC

GAM1607 FLRT2 5' GTCTGTAATCCCAGCGCTCTGT 25064 TA\_  
ACAG GCTGGGATTACAGAC  
||||| |||||||||  
TGTC CGACCCTAATGTCTG  
TCG

GAM1607 FUT6 3' CTGTAATCCCAGCACT 3811 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

GAM1607 GALNT7 3' CTGTAATCCCAGCTACTTG 54018 \_  
CA GTAGCTGGGATTACAG  
|| |||||||||  
GT CATCGACCCTAATGTC  
T

GAM1607 GNE 3' CTGTAATCCCAGCACT 18478 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

GAM1607 GP2 3' ATGCCTGTAATCCCAGC 7680 A  
GCTGGGATTACAG CAT  
||||||| |||  
CGACCCTAATGTC GTA  
C

GAM1607 GP6 3' ATGTCTGTAATCCTAGCACTGT 33030 A  
G TACAGT GCTGGGATTACAGACAT  
||||| |||||||||  
GTGTCA CGATCCTAATGTCTGTA

GAM1607 GPRK7 3' TCTATAATCCCAGTTAC 57629 C  
GTAGCTGGGATTA AGA  
||||||| |||  
CATTGACCCTAAT TCT  
A

GAM1607 GRAF 3' CTATAATCCCAGCACT 30556 A C  
AGT GCTGGGATTA AG  
||| ||||||| ||  
TCA CGACCCTAAT TC

GAM1607 GRM6 3' CTGTAATCCCAGCACT 5934 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

GAM1607 HFE 3' CTGTAATCCCAGGGTGCTG 4651 G\_  
CAGTA C TGGGATTACAG  
||||| | |||||||

			GTCGT G ACCCTAATGTC		
			G G		
GAM1607 HIP1	3'	ATGCCTGTAATCCCAGAACT	18055	AG	A
		AGT CTGGGATTACAG CAT			
		TCA GACCCTAATGTC GTA			
		A_ C			
GAM1607 HIP1	3'	CTGTAATCCCAGCACT	18059	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607 HIP1	3'	GTAATCCCAGCTACTCA	18065	C	
		A AGTAGCTGGGATTAC			
		A TCATCGACCCTAATG			
		C			
GAM1607 HLA-E	3'	ATGCCTGTAATCCCAGCACT	91021	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		— C			
GAM1607 HUNK	3'	CTGTAATCCCAGCACT	27449	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607 IAPP	3'	GTGCCTGTAATCCCAGCTACTC	4696	C	A
A		A AGTAGCTGGGATTACAG CAT			
		A TCATCGACCCTAATGTC GTG			
		C C			
GAM1607 ICA1	3'	TGCAGTCCCAGCTACTCA	42257	C	A
		A AGTAGCTGGGATT CA			
		A TCATCGACCCTGA GT			
		C C			
GAM1607 ICMT	3'	CTGTAATCCCAAAGTGCTG	24812	GC_	
		CAGTA TGGGATTACAG			
		GTCGT ACCCTAATGTC			
		GAA			
GAM1607 IFIT4	3'	ATGCCTGTAATCCCAGCACT	70920	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		— C			
GAM1607 IFNAR1	3'	CTGTAATCCCAGCACT	5284	A	
		AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

—  
GAM1607 IL10 3' CTGTAATCCCAGCACT 5127 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 IL12RB2 3' ATGCCTGTAATCCCAGCACT 7768 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

— C  
GAM1607 IL17R 3' CTGTAATCCCAGCAC 26776 A  
GT GCTGGGATTACAG  
|| |||||  
CA CGACCCTAATGTC

—  
GAM1607 IL1R1 3' CTATAATCCCAGCACT 6057 A C  
AGT GCTGGGATTA AG  
||| |||||  
TCA CGACCCTAAT TC

— A  
GAM1607 IL1R1 3' CTGTAATCCCAGCTAC 6058  
GTAGCTGGGATTACAG  
|||||||  
CATCGACCCTAATGTC

GAM1607 IL4R 5' ATGCCTATAATCCCAGCACT 4699 A C A  
AGT GCTGGGATTA AG CAT  
||| ||||| ||  
TCA CGACCCTAAT TC GTA

— A C  
GAM1607 IPP 3' ATGCCTATAATCCCAGCACT 19724 A C A  
AGT GCTGGGATTA AG CAT  
||| ||||| ||  
TCA CGACCCTAAT TC GTA

— A C  
GAM1607 IRAK1 3' CTGTAATCCCAGCACT 7808 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 ITGAL 3' CTGTAATCCCAGCACT 9391 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 ITGAL 3' CTGTAGTCCCAGCTACTCA 9392 C  
A AGTAGCTGGGATTACAG  
| |||||



			A TCATCGACCCTGATGTC		
			C		
GAM1607	JRK	3'	CTGTAATCCCAGCACTG 86526	A	
			CAGT GCTGGGATTACAG		
			GTCA CGACCCTAATGTC		
			—		
GAM1607	KAI1	3'	CTGTAATCCCAGCACT 9499	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	KCNA7	3'	ATGCCTGTGATCCCAGCTACTC 49049	C	A
	A		A AGTAGCTGGGATTACAG CAT		
			A TCATCGACCCTAGTGTC GTA		
			C C		
GAM1607	KNSL1	3'	ATGCCTGTAATCCCAGCACT 15747	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			C		
GAM1607	LAMP2	3'	CTGTAATCCCAGCACT 25712	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	LDLR	3'	CTGTAATCCCAGCACT 4986	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	LDLR	3'	CTGTAATCCCAGCACT 4985	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	LEP	3'	CTGTAATCCCAGCACT 4048	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	LRR2	3'	CTATAATCCCAGCACT 44467	A	C
			AGT GCTGGGATTAG		
			TCA CGACCCTAAT TC		
			A		
GAM1607	LRR2	3'	CTATAATCCCAGCACT 44468	A	C
			AGT GCTGGGATTAG		

				TCA CGACCCTAAT TC			
				— A			
GAM1607	LRR2	3'	CTGTAATCCCAGCACT	44469	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1607	LRR2	3'	GTAATCCCAGCTACTCA	44477	C		
			A AGTAGCTGGGATTAC				
			A TCATCGACCCTAATG				
			C				
GAM1607	LUZP1	3'	ATGCCTGTAATCGCAGCTACTC	53296	C	G	A
	A		A AGTAGCTG GATTACAG CAT				
			A TCATCGAC CTAATGTC GTA				
			C G C				
GAM1607	LUZP1	3'	CTGTAATCCCAGCACT	53299	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1607	MAFF	3'	TCTGTAATCCCAGCACT	24654	A		
			AGT GCTGGGATTACAGA				
			TCA CGACCCTAATGTCT				
			—				
GAM1607	MCM4	3'	CTGTAATCCCAGCACT	61903	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1607	MIR16	3'	ATGCCTGTATTCCCAGCTACTC	33563	C	T	A
	A		A AGTAGCTGGGA TACAG CAT				
			A TCATCGACCCT ATGTC GTA				
			C T C				
GAM1607	MOG	3'	CTGTAATCCCAGCACT	10102	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1607	MSH3	3'	ATGCCTGTAATCCCAGCACT	10118	A	A	
			AGT GCTGGGATTACAG CAT				
			TCA CGACCCTAATGTC GTA				
			C				
			—				
GAM1607	MTMR8	3'	CTGTAATCCCAGCACT	31292	A		
			AGT GCTGGGATTACAG				

TCA CGACCCTAATGTC

—  
GAM1607 MTNR1A 3' CTGTAATCCCAGCTACT 19889  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1607 NFKBIL2 3' CTGTAATCCCAACACT 25525 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1607 NPHP1 3' CTGTAATCCCAACACT 62479 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1607 NPHS1 3' CTATAATCCCAGCACT 16190 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC  
— A

GAM1607 NT5C2 3' ATGCCTGTAATCCCATCATCTA 24237 C\_\_\_ A  
CT AGTAG TGGGATTACAG CAT  
||||| ||||| |||  
TCATC ACCCTAATGTC GTA  
TACT C

GAM1607 NT5C2 3' CTGTAATCCCAGCACT 24238 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 OASL 3' CTGTAATCCCAGAACT 13578 AG  
AGT CTGGGATTACAG  
||| |||||  
TCA GACCCTAATGTC  
A\_

GAM1607 OPTN 3' ATGCCTGTAATCCCAGCACT 41767 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
— C

GAM1607 P2RX7 3' GTCTGTAATCCCAGCGCT 10374 A  
AGT GCTGGGATTACAGAC  
||| |||||  
TCG CGACCCTAATGTCTG

—  
GAM1607 PA2G4 3' CTGTAATCCCAGCACT 71299 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

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      -
GAM1607 PCDH11X 3' CTGTAATCCCAGCACT    52007    A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1607 PCDH11X 3' CTGTAATCCCAGCACT    52008    A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1607 PCDH11Y 3' CTGTAATCCCAGCACT    52060    A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1607 PCDH11Y 3' CTGTAATCCCAGCACT    52066    A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1607 PDE4C  3' ATGCCTATAATCCCAGCACT  6230    A      C A
      AGT GCTGGGATTAG CAT
      ||| ||||| || |||
      TCA CGACCCTAAT TC GTA
      -      A C
GAM1607 PDE4C  3' TGCCTGTAATCCCGGTACT  6238    G      A
      AGTA CTGGGATTACAG CA
      |||| ||||| ||
      TCAT GGCCCTAATGTC GT
      -      C
GAM1607 PIK3R2 3' ATGCCTGTAATCCCAGCACT  17256   A      A
      AGT GCTGGGATTACAG CAT
      ||| ||||| |||
      TCA CGACCCTAATGTC GTA
      -      C
GAM1607 PKD2   3' CTGTAATCCCAGCACT    60092   A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1607 PLA2G2D 3' ATGCCTGTAATCCCAACACT  24786   AGC      A
      AGT TGGGATTACAG CAT
      ||| ||||| |||
      TCA ACCCTAATGTC GTA
      CA_      C
GAM1607 POLK   3' CTGTAATCCCAGCTACT    32566
      AGTAGCTGGGATTACAG
      |||||
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TCATCGACCCTAATGTC

GAM1607 PSD	5'	CTGCAATCCCAGCACT	10927	A	A
		AGT GCTGGGATT CAG			
		TCA CGACCCTAA GTC			
		— C			
GAM1607 PSMB2	3'	ATGCCTGTAATCCCAGCACT	10947	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		— C			
GAM1607 PSMB9	3'	CTATAATCCCAGCACT	10960	A	C
		AGT GCTGGGATTA AG			
		TCA CGACCCTAAT TC			
		— A			
GAM1607 PSMD5	3'	CTATAATCTCAGCTACTCA	17303	C	C
		A AGTAGCTGGGATTA AG			
		A TCATCGACTCTAAT TC			
		C A			
GAM1607 PTAFR	3'	CTGTAATCCCAGCACT	6294	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607 PTAFR	3'	CTGTAGTCCCAGCTACTCA	6295	C	
		A AGTAGCTGGGATTACAG			
		A TCATCGACCCTGATGTC			
		C			
GAM1607 RAB3B	3'	CTGTAATCCCAGCACT	11185	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607 RAB7L1	3'	CTGTAATCCCAGCACT	14107	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607 RAB7L1	3'	TGCCTGTAATCCCAGC	14110		A
		GCTGGGATTACAG CA			
		CGACCCTAATGTC GT			
		C			
GAM1607 RAD51L1	5'	CTGTAATCCCAGCGCT	56060	A	
		AGT GCTGGGATTACAG			

TCG CGACCCTAATGTC

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      -
GAM1607 RBBP5  3' ATGCCTGTAATCCCAGCTAC 17332      A
                  GTAGCTGGGATTACAG CAT
                  |||||
                  CATCGACCCTAATGTC GTA
                        C
GAM1607 RBBP5  3' CTGTAATCCCAGCACT 17334      A
                  AGT GCTGGGATTACAG
                  ||| |||||
                  TCA CGACCCTAATGTC

      -
GAM1607 RBBP9  3' ATGCCTGTAATCCCAGCACTGT 70128      A      A
      G                  TACAGT GCTGGGATTACAG CAT
                  ||||| |||||
                  GTGTCA CGACCCTAATGTC GTA
                        C
GAM1607 RBL1   3' ATGCCTATAATCCCAGCTACTT 11260      _      C A
      G                  CA GTAGCTGGGATTA AG CAT
                  || ||||| || |||
                  GT CATCGACCCTAAT TC GTA
                  T      A C
GAM1607 RBM3   3' CTGTAATCCCAGTGACT 70487      A
                  AGT GCTGGGATTACAG
                  ||| |||||
                  TCA TGACCCTAATGTC
                        G
GAM1607 RECQL5 3' ATGTCTGTATTGGCTACTGT 14924      TG GAT
                  ACAGTAGC G TACAGACAT
                  ||||| | |||||
                  TGTCATCG T ATGTCTGTA
                        GT _
GAM1607 RFC2   3' CTGTAATCCCAACACT 11304      AGC
                  AGT TGGGATTACAG
                  ||| |||||
                  TCA ACCCTAATGTC
                  CA_
GAM1607 RPN1   5' ATGCCTGTAATCCCAGCTACT 11389      A
                  AGTAGCTGGGATTACAG CAT
                  ||||| |||||
                  TCATCGACCCTAATGTC GTA
                        C
GAM1607 SCD    3' ATGTCTGTTTATTAATACTG 17346      C GATT
                  CAGTAG TGG ACAGACAT
                  ||||| ||| |||||
                  GTCATC ATT TGTCTGTA
                  A ATT_
GAM1607 SCN2B  3' CTGTAATCCCAGCACT 15938      A
                  AGT GCTGGGATTACAG
                  ||| |||||
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TCA CGACCCTAATGTC

GAM1607 SIM2 3' CTGTAATCCCAGCACT 23783 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 SLC14A1 3' CTGTAATCCCAGCACT 31839 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 SLC14A2 3' CTGTAATCCCAGCACT 23132 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 SLC26A4 3' ATGCCTGTAATCCCAGCACT 4783 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
C

GAM1607 SLC28A2 3' CTGTAATCCCAGCGCT 14869 A  
AGT GCTGGGATTACAG  
||| |||||  
TCG CGACCCTAATGTC

GAM1607 SLC2A3 3' CTGTAATCCCAGCACT 22660 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 SLC2A6 3' CTGTAATCCCAGCACT 34157 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 SLC31A1 3' ATGCCTGTAATCCCAGCACT 8511 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
C

GAM1607 SLC31A1 3' TGTAATCCCAGCTACTCA 8515 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1607 SMG1 3' CTGTAATCCCAGCACT 30651 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

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      -
GAM1607 SRGAP1  5' ATGCCTGTAGTCTCAGCTACTC 72259  C      A
      A      A AGTAGCTGGGATTACAG CAT
      | |||||
      A TCATCGACTCTGATGTC GTA
      C      C
GAM1607 STAT3  3' CTGTAATCCCAGCACT 57713 A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1607 STAT3  3' CTGTAATCCCAGCACT 11998 A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1607 SULT1A2 3' ATGTCTGCAATCCCAGCGATTT 72215 TA_ A
      G      CAG GCTGGGATT CAGACAT
      ||| ||||| |||||
      GTT CGACCCTAA GTCTGTA
      TAG      C
GAM1607 SULT1A3 3' ATGTCTGCAATCCCAGCGATTT 12052 TA_ A
      G      CAG GCTGGGATT CAGACAT
      ||| ||||| |||||
      GTT CGACCCTAA GTCTGTA
      TAG      C
GAM1607 SULT2A1 3' ATGCCTGTAATCCCAGCACT 71751 A      A
      AGT GCTGGGATTACAG CAT
      ||| ||||| |||||
      TCA CGACCCTAATGTC GTA
      C
GAM1607 SULT2A1 3' ATGTCTGTAATCCCAGCACT 71752 A
      AGT GCTGGGATTACAGACAT
      ||| ||||| |||||
      TCA CGACCCTAATGTCTGTA

      -
GAM1607 SUV39H2 3' CTGTAGTCCCAGCTACTCA 45136 C
      A AGTAGCTGGGATTACAG
      | |||||
      A TCATCGACCCTGATGTC
      C
GAM1607 SWAP70 3' CTGTAATCCCAGCACT 71348 A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1607 TBX6 3' CTGTAATCCCAACTACTTG 54964 _ C
      CA GTAG TGGGATTACAG
      || ||| |||||
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			GT CATC ACCCTAATGTC			
			T A			
GAM1607	TCF7	3'	CTGTAATCCCAGCACT	12161	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	TCTA	3'	CTGTAATCCCAACACT	42238	AGC	
			AGT TGGGATTACAG			
			TCA ACCCTAATGTC			
			CA_			
GAM1607	TEM7	3'	CTGTAATCCCAGCACT	39884	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	TKTL1	5'	ATGTCTGTCTTTCAGCCAC	24296	A	GG TT
			GT GCTG A ACAGACAT			
			CA CGAC T TGTCTGTA			
			C TTC_			
GAM1607	TM7SF3	3'	CTGTAATCCCAATACTG	59666	GC	
			CAGTA TGGGATTACAG			
			GTCAT ACCCTAATGTC			
			A_			
GAM1607	TNFRSF10A	3'	ATGCCTGTAATCCCAGCACT	13886	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1607	TNFRSF10D	3'	ATGCCTGTAATCCCAGCACT	13860	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1607	TNFSF15	3'	CTGTAATCCCAACACT	17592	AGC	
			AGT TGGGATTACAG			
			TCA ACCCTAATGTC			
			CA_			
GAM1607	TRIM14	3'	CTGTAATCCCAGCGCT	52635	A	
			AGT GCTGGGATTACAG			
			TCG CGACCCTAATGTC			
			—			
GAM1607	TRIM14	3'	ATGCCTGTAATCCCAGCTACT	28851		A
			AGTAGCTGGGATTACAG CAT			

			TCATCGACCCTAATGTC GTA		
			C		
GAM1607	TRIM9	5'	ATGCCTGTAATCCCAGCTA 30752		A
			TAGCTGGGATTACAG CAT		
			ATCGACCCTAATGTC GTA		
			C		
GAM1607	TRPM8	3'	TGTAATCCCAGCTACTCA 43987	C	
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1607	TSN	3'	CTGTAATCCCAGCACACTG 16106	A_	
			CAGT GCTGGGATTACAG		
			GTCA CGACCCTAATGTC		
			CA		
GAM1607	TSN	3'	TGCCTGTAATTCAGT 16111	G A	
			GCTGG ATTACAG CA		
			TGACT TAATGTC GT		
			— C		
GAM1607	TSNAX	3'	CTGTAATCCCAGCACT 19998	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	TTF2	3'	TGCCTGTAATCCCGACACT 13176	AGC A	
			AGT TGGGATTACAG CA		
			TCA GCCCTAATGTC GT		
			CA_ C		
GAM1607	UBE2G2	3'	CTGCAATCCCAGCACT 64855	A A	
			AGT GCTGGGATT CAG		
			TCA CGACCCTAA GTC		
			— C		
GAM1607	UBE2G2	3'	CTGTAGTCTCAGCTACTCA 64856	C	
			A AGTAGCTGGGATTACAG		
			A TCATCGACTCTGATGTC		
			C		
GAM1607	UC28	3'	ATGCCTGTAATCCCAGCTACT 41288		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1607	UC28	3'	CTGTAATCCCAGCACT 41290	A	
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

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      -
GAM1607 UPK1B  3' ATGCCTGTAATCCCAGCACT  22715  A      A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      -      C
GAM1607 USP14  3' CTGTAATCCCAGCACT    17658  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1607 VDR    3' TGTAATCCCAGCTACTCA   4574  C
      A AGTAGCTGGGATTACA
      | |||||
      A TCATCGACCCTAATGT
      C
GAM1607 VHL    3' ATGCCTGTAATCCCAGC    5058      A
      GCTGGGATTACAG CAT
      ||||| |||
      CGACCCTAATGTC GTA
      C
GAM1607 VHL    3' ATGCCTGTAATCCCAGCACT  5059  A      A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      -      C
GAM1607 VHL    3' ATGCCTGTAATCCTAGCTACTC 5060  C      A
      A
      A AGTAGCTGGGATTACAG CAT
      | |||||
      A TCATCGATCCTAATGTC GTA
      C      C
GAM1607 VHL    3' CTGTAATCCCAGCACT    5069  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1607 VHL    3' TCTGTAATCCTAGCTACT   5090
      AGTAGCTGGGATTACAGA
      |||||
      TCATCGATCCTAATGTCT

GAM1607 VPS41  3' ATGCCTGTAATCCCAGCTACT 26921      A
      AGTAGCTGGGATTACAG CAT
      |||||
      TCATCGACCCTAATGTC GTA
      C
GAM1607 WIG1   3' CTGTAATCCCAGCACT    94466  A
      AGT GCTGGGATTACAG
      ||| |||||
```

TCA CGACCCTAATGTC

GAM1607 WSX1 3' CTGTAATCCCAGCACT 16732 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 ZNF136 3' CTGTAATCCCAGCACT 59888 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 ZNF137 3' CTGTAATCCCAGCACT 12862 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 ZNF14 3' ATGCCTCTAATCCCAGCTACTC 40713 C C A  
A AGTAGCTGGGATTA AG CAT  
| ||||| || |||  
A TCATCGACCCTAAT TC GTA  
C C C

GAM1607 ZNF36 3' CTGTAATCCCAGCACT 93962 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 ZNF74 3' ATGTCCCTGTGGTCCCAGCTAC 12790 C  
TCA A AGTAGCTGGGATTACA GACAT  
| ||||| |||||  
A TCATCGACCCTGGTGT CTGTA  
C CC

GAM1607 ZNF74 3' CTGTAATCTTAACACTGTG 12795 AGC  
TACAGT TGGGATTACAG  
|||| |||||  
GTGTCA ATTCTAATGTC  
CA\_

GAM1607 AF020591 3' ATGCCTGTAATCCCAGCACTCT 27135 TA\_ A  
G CAG GCTGGGATTACAG CAT  
||| ||||| |||  
GTC CGACCCTAATGTC GTA  
TCA C

GAM1607 AF020591 3' CTGTAATCCCAGCACT 27139 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 AF020591 3' CTGTAGTCCCAGCTACTCA 27140 C  
A AGTAGCTGGGATTACAG  
| |||||

			A TCATCGACCCTGATGTC		
			C		
GAM1607 AKAP11	3'	CTGTAATCCCAGAACTCTG	57831	TAG_	
		CAG CTGGGATTACAG			
		GTC GACCCTAATGTC			
		TCAA			
GAM1607 AKR1D1	3'	ATGCCTATAATCCCAGCACT	19972	A	C A
		AGT GCTGGGATTA AG CAT			
		TCA CGACCCTAAT TC GTA			
		— A C			
GAM1607 AKR1D1	3'	TGTAATCCCAGCTACTCA	19978	C	
		A AGTAGCTGGGATTACA			
		A TCATCGACCCTAATGT			
		C			
GAM1607 APOF	3'	CTGTAATCCCAGCACTGTG	7909	A	
		TACAGT GCTGGGATTACAG			
		GTGTCA CGACCCTAATGTC			
		—			
GAM1607 APXL2	3'	CTGTAATCCCAGCACT	75189	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607 ARNTL2	3'	ATGCCTGTAATCCCAGCACT	39454	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		— C			
GAM1607 ARNTL2	3'	CTGTAATCCCAACTGCT	39462	C	
		AGTAG TGGGATTACAG			
		TCGTC ACCCTAATGTC			
		A			
GAM1607 ARNTL2	3'	CTGTAATCCCAGTACT	39463	G	
		AGTA CTGGGATTACAG			
		TCAT GACCCTAATGTC			
		—			
GAM1607 BANP	3'	ATGCCTGTAATCCCAGC	66214	A	
		GCTGGGATTACAG CAT			
		CGACCCTAATGTC GTA			
		C			
GAM1607 BFAR	3'	CTGTAATCCCAGCTACTTG	60771	_	
		CA GTAGCTGGGATTACAG			

			GT CATCGACCCTAATGTC			
			T			
GAM1607	BIA2	3'	CTGTAATCCCAGCACT	71281	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	BIRC1	3'	CTGTAATCCCAGCACT	15788	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	BLOV1	3'	ATGCCTGTAATCCCAGCTACT	76277		A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1607	BLOV1	3'	CTGTAATCCCAGCACT	76280	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	BLOV1	3'	CTGTAATCCCAGCTACTTG	76281		—
			CA GTAGCTGGGATTACAG			
			GT CATCGACCCTAATGTC			
			T			
GAM1607	BNIP-S	3'	GTCTGTAATCCCAGCACT	56274	A	
			AGT GCTGGGATTACAGAC			
			TCA CGACCCTAATGTCTG			
			—			
GAM1607	C13orf1	3'	CTGTAATCCCAGCACT	39969	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	C1orf24	3'	CTATAATCCCAGCACT	53714	A	C
			AGT GCTGGGATTA AG			
			TCA CGACCCTAAT TC			
			A			
			—			
GAM1607	C1QTNF2	3'	ATGCCTATAATCCCAGGACT	49124	AG	C A
			AGT CTGGGATTA AG CAT			
			TCA GACCCTAAT TC GTA			
			G_ A C			
GAM1607	C20orf108	3'	CTGTAATCCCAGCACT	55045	A	
			AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

GAM1607 C20orf12 3' ATGCCTGTAATCCCAGTTACT 36321 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATTGACCCTAATGTC GTA

C

GAM1607 C20orf12 3' CTGTAATCCCAGCACT 36322 A  
AGT GCTGGGATTACAG  
|||  
TCA CGACCCTAATGTC

GAM1607 C20orf130 3' GTGGCTGTCCCAGCCAC 61758 A TTA A  
GT GCTGGGA CAG CAT  
|| |||  
CA CGACCCT GTC GTG  
C G

GAM1607 C20orf142 3' CTGTAATCCCAGCTACT 74775  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1607 C20orf175 3' CTGTAATCCCAACACT 55064 AGC  
AGT TGGGATTACAG  
|||  
TCA ACCCTAATGTC  
CA\_

GAM1607 C20orf177 3' ATGCCTGTAATCCCAGCTACT 62143 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1607 C20orf177 3' CTGTAATCCCAGCACT 62146 A  
AGT GCTGGGATTACAG  
|||  
TCA CGACCCTAATGTC

GAM1607 C20orf183 3' CTGTAATCCCAGCACT 47803 A  
AGT GCTGGGATTACAG  
|||  
TCA CGACCCTAATGTC

GAM1607 C20orf29 3' CTGTAATCCCAGCACT 37126 A  
AGT GCTGGGATTACAG  
|||  
TCA CGACCCTAATGTC

GAM1607 C21orf108 3' CTATAATCCCAGCACT 88720 A C  
AGT GCTGGGATTA AG  
|||

			TCA CGACCCTAAT TC		
			— A		
GAM1607	C22orf19	3'	GTCTGTAATCCCAGCACT 13429	A	
			AGT GCTGGGATTACAGAC		
			TCA CGACCCTAATGTCTG		
			—		
GAM1607	C22orf20	3'	ATGCCTGTAATCCCAGCTATT 47425		A
			AGTAGCTGGGATTACAG CAT		
			TTATCGACCCTAATGTC GTA		
			C		
GAM1607	C2F	3'	CTGTAATCCCAGCACT 20928	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	C6orf10	5'	CTGTAATCCCATCATTTGCT 22289		C___
			AGTAG TGGGATTACAG		
			TCGTT ACCCTAATGTC		
			TACT		
GAM1607	C6orf5	3'	CTGTAATCCCAGCACT 31346	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	C6orf5	3'	CTGTAATCCCAGCACT 31347	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	C8orf2	3'	CTGTAATCCCAGCACT 23163	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	C9orf5	3'	TCTGTAATCCCAGCACT 49284	A	
			AGT GCTGGGATTACAGA		
			TCA CGACCCTAATGTCT		
			—		
GAM1607	CALN1	3'	CTATAATCCCAGCACT 48866	A	C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			A		
GAM1607	CAMKK2	5'	CTGTAATCCCAGCACT 21582	A	
			AGT GCTGGGATTACAG		



TCA CGACCCTAATGTC

GAM1607 CBCIP2 3' CTGTAATCCCAGCACT 51590 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 cerk 3' CTGTAATCCCAGCACT 42846 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 CFLAR 3' CTGTAATCCCAGCACT 13929 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 CG012 5' ATGCCTATATTCTAGCTACTCA 83214 C TAC A  
A AGTAGCTGGGAT AG CAT  
| ||||| || |||  
A TCATCGATCTTA TC GTA  
C TA\_ C

GAM1607 CG012 5' ATGCCTGTAATCCCAACACT 83215 AGC A  
AGT TGGGATTACAG CAT  
||| ||||| |||  
TCA ACCCTAATGTC GTA  
CA\_ C

GAM1607 CG012 5' CTGTAATCCCAGCTATTCGGCT 83219  
G CAGT AGCTGGGATTACAG  
||| |||||  
GTCG TCGACCCTAATGTC  
GCTTA

GAM1607 CGI-203 3' TGTAATCCCAGCTACTCA 39904 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1607 CHRFAM7A 3' ATGCTTGTAATCCCAGCTACTC 95017 C GA  
A A AGTAGCTGGGATTACA CAT  
| ||||| |||  
A TCATCGACCCTAATGT GTA  
C TC

GAM1607 CLDN15 3' ATGCCTGTAATCCCAGCACT 56558 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

GAM1607 CNNM4 3' TCTGTTGTCAACTGCTGTA 39484 CTGG T  
TACAGTAG GAT ACAGA  
||| ||| |||

			ATGTCGTC CTG TGTCT		
			AA__ T		
GAM1607	COE2	3'	ATGCCTGTAATCCCAGCTACTT 64247 _		A
	G		CA GTAGCTGGGATTACAG CAT		
			GT CATCGACCCTAATGTC GTA		
			T C		
GAM1607	COE2	3'	CTGTAATCCCAGCACT 64251 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	CPR2	3'	CTGTAATCCCAGCACT 48095 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	CPR2	3'	CTGTAATCCCAGCTACTCA 48096 C		
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTAATGTC		
			C		
GAM1607	CSAD	3'	CTGTAATCCCAGCACT 32028 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	D21S2056E	3'	ATGCCTGTAATCCCAGCTACT 13467		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1607	D21S2056E	3'	CTGTAATCCCAGCACT 13470 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	DCOHN	3'	CTGTAATCCCTGCACT 49600 A T		
			AGT GC GGGATTACAG		
			TCA CG CCCTAATGTC		
			— T		
GAM1607	DDX34	3'	CTGTAATCCCAGCACT 27982 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	DEGS	3'	ATGCCTGTAATCCCAGCTACAT 58613 _		A
	G		CA GTAGCTGGGATTACAG CAT		

			GT CATCGACCCTAATGTC GTA		
			A C		
GAM1607	DEGS	3'	ATGCCTATAATCCCAGCACT 13409	A	C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1607	DEGS	3'	ATGCCTGTAATCCCAGCTACAT 13410	—	A
	G		CA GTAGCTGGGATTACAG CAT		
			GT CATCGACCCTAATGTC GTA		
			A C		
GAM1607	DIS3	3'	ATGCCTGTAATCCCAGCTACTT 30227	—	A
	G		CA GTAGCTGGGATTACAG CAT		
			GT CATCGACCCTAATGTC GTA		
			T C		
GAM1607	DKFZP434B168	3'	CTGTAATCCCAGCACT 31253	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	DKFZP434C171	3'	CTGTAATCCCAGCACT 31553	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	DKFZP434C1715	3'	CTGTAATCCCAGCAC 86148	A	
			GT GCTGGGATTACAG		
			CA CGACCCTAATGTC		
			—		
GAM1607	DKFZp434E0519	3'	CTATAATCCCAGCACT 49986	A	C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1607	DKFZp434E2220	5'	TGTAATCCCAGCTACTCA 34304	C	
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1607	DKFZP434F091	3'	TGTAATCCCAACTACTCA 31284	C	C
			A AGTAG TGGGATTACA		
			A TCATC ACCCTAATGT		
			C A		
GAM1607	DKFZp434G171	3'	ATGCCTGTAATCCCAGCACT 79431	A	A
			AGT GCTGGGATTACAG CAT		

TCA CGACCCTAATGTC GTA  
 — C  
 GAM1607 DKFZp434G171 3' TGTAATCCCAGCTACTCA 79440 C  
 A AGTAGCTGGGATTACA  
 | |||||  
 A TCATCGACCCTAATGT  
 C  
 GAM1607 DKFZP434I1735 3' CTGTAATCCCAGCTACT 87801  
 AGTAGCTGGGATTACAG  
 |||||  
 TCATCGACCCTAATGTC  
  
 GAM1607 DKFZP434L187 5' CTGTAATCCCAGCTACT 68804  
 AGTAGCTGGGATTACAG  
 |||||  
 TCATCGACCCTAATGTC  
  
 GAM1607 DKFZP434N1511 3' ATGCCTGTAATCCCAGCACT 91415 A A  
 AGT GCTGGGATTACAG CAT  
 ||| |||||  
 TCA CGACCCTAATGTC GTA  
 — C  
 GAM1607 DKFZP434N161 3' GTCTGTAATCCCAGCACT 78522 A  
 AGT GCTGGGATTACAGAC  
 ||| |||||  
 TCA CGACCCTAATGTCTG  
 —  
 GAM1607 DKFZp547C176 3' CTGTAATCCCAGCACT 67222 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 DKFZp547I094 3' CTGTAATCCCAGCACT 49639 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 DKFZp547I094 3' CTGTAGTCACAGCTACT 49640 G  
 AGTAGCTG GATTACAG  
 ||||| |||||  
 TCATCGAC CTGATGTC  
 A  
 GAM1607 DKFZP564B1023 3' ATGCCTGTAATCCCAGCTACT 48536 A  
 AGTAGCTGGGATTACAG CAT  
 ||||| |||||  
 TCATCGACCCTAATGTC GTA  
 C  
 GAM1607 DKFZP564B1023 3' CTGTAATCCCAGCACT 48538 A  
 AGT GCTGGGATTACAG  
 ||| |||||

TCA CGACCCTAATGTC

—  
GAM1607 DKFZP564I052 3' CTGTAATCCCAGCACT 66707 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 DKFZP564M182 3' CTGTAATCCCAGCACT 78033 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 DKFZP564M182 3' CTGTAATCCCAGCTACT 78034  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1607 DKFZp566H0824 3' CTGTAATCCCAGCACTTTA 34050 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||  
AT TCA CGACCCTAATGTC  
T —

GAM1607 DKFZP586C1324 3' ATGCCTGTAATCCCAGCACT 69796 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

— C  
GAM1607 DKFZP586M1120 3' CTGTAATCCCAGCACT 48457 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 DKFZP667O116 3' TGCCTATAATCCCGGCACT 94287 A C A  
AGT GCTGGGATTA AG CA  
||| ||||| || ||  
TCA CGGCCCTAAT TC GT

— A C  
GAM1607 DKFZP761E2110 3' ATGCCTGTAATCCCAGCAC 48224 A A  
GT GCTGGGATTACAG CAT  
|| ||||| |||  
CA CGACCCTAATGTC GTA

— C  
GAM1607 DKFZP761G1913 3' ATGCCTGTAATCCCAGCACT 48909 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

— C  
GAM1607 DKFZP761G1913 3' CTGTAATCCCAGCTACTTG 48913 —  
CA GTAGCTGGGATTACAG  
|| ||||| |||||

			GT CATCGACCCTAATGTC			
			T			
GAM1607	DKFZp761J139	5'	CTGTAATCCCAGCACT	50108	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	DRF1	3'	CTATAATCCCAGCACT	47030	A	C
			AGT GCTGGGATTA AG			
			TCA CGACCCTAAT TC			
			— A			
GAM1607	DRF1	3'	CTGTAATCCCAGCACT	47032	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	DRF1	3'	TGTAATCCCAGCTACTCA	47038	C	
			A AGTAGCTGGGATTACA			
			A TCATCGACCCTAATGT			
			C			
GAM1607	FADS1	3'	ATGCCTGTAATCCCAACACT	25473	AGC	A
			AGT TGGGATTACAG CAT			
			TCA ACCCTAATGTC GTA			
			CA_ C			
GAM1607	FADS1	3'	CTGTAATCCCAGCTAC	25476		
			GTAGCTGGGATTACAG			
			CATCGACCCTAATGTC			
			—			
GAM1607	FBXO27	3'	ATGCCTGTAATCCCAGCACT	74504	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1607	FBXO27	3'	CTGTAATCCCTGCACT	74508	A	T
			AGT GC GGGATTACAG			
			TCA CG CCCTAATGTC			
			— T			
GAM1607	FBXO6	3'	CTGTAATCCCAGCACT	37383	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	FBXO9	3'	ATGCCTATAATCCCAGCACT	53100	A	C A
			AGT GCTGGGATTA AG CAT			

			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1607	FBXO9	3'	CTATAATCCCAATACT 53102 GC C		
			AGTA TGGGATTA AG		
			TCAT ACCCTAAT TC		
			A_ A		
GAM1607	FKBP14	3'	ATGCCTGTAATCCCAGCACT 35622 A A		
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1607	FKBP14	3'	ATGCCTGTAATCCCAGCACT 35623 A A		
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1607	FKSG17	3'	CTGTAATCCCAGTTACTCA 49329 C		
			A AGTAGCTGGGATTACAG		
			A TCATTGACCCTAATGTC		
			C		
GAM1607	FLJ00060	3'	ATGTCTGTAATCCCAGCACTCT 61091 TA_		
	G		CAG GCTGGGATTACAGACAT		
			GTC CGACCCTAATGTCTGTA		
			TCA		
GAM1607	FLJ10008	3'	GTCTGTAATCCCAGCACT 35729 A		
			AGT GCTGGGATTACAGAC		
			TCA CGACCCTAATGTCTG		
			—		
GAM1607	FLJ10043	3'	CTGTAATCCCAGCACT 35758 A		
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	FLJ10043	3'	CTGTAATCCCAGCTACT 35759		
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
			—		
GAM1607	FLJ10058	3'	ATGCCTGTAATCCCAGCACT 35782 A A		
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1607	FLJ10244	3'	ATGCCTGTAATCCCAGCTGCT 35940 A		
			AGTAGCTGGGATTACAG CAT		

			TCGTCGACCCTAATGTC	GTA	
			C		
GAM1607	FLJ10460	3'	CTGTAATCCCAACACT	36127	AGC
			AGT TGGGATTACAG		
			TCA ACCCTAATGTC		
			CA_		
GAM1607	FLJ10460	3'	CTGTAATCCCAGCACT	36128	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	FLJ10460	3'	CTGTAATCCCAGCTACTTG	36129	—
			CA GTAGCTGGGATTACAG		
			GT CATCGACCCTAATGTC		
			T		
GAM1607	FLJ10547	3'	CTGTAATCCCAGCACT	36267	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	FLJ10607	3'	CTGTAATCCCAGCACT	77113	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	FLJ10607	3'	CTGTAATCCCAGCTACTCA	77114	C
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTAATGTC		
			C		
GAM1607	FLJ10613	3'	GTCTGTAATCCCAGCACT	38825	A
			AGT GCTGGGATTACAGAC		
			TCA CGACCCTAATGTCTG		
			—		
GAM1607	FLJ10650	3'	CTGTAATCCCAGCACT	36382	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	FLJ10704	3'	ATGCCTGTAATCCCAGCTACT	36449	A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1607	FLJ10781	3'	CTGTAATCCCAGCACT	36631	A
			AGT GCTGGGATTACAG		



TCA CGACCCTAATGTC

—  
GAM1607 FLJ10781 3' TGTAATCCCAGCTACTCA 36638 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1607 FLJ10803 3' CTGTAATCCCAGCACT 36664 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 FLJ10826 3' ATGCCTGTAATCCCAGCTACT 36700 A  
AGTAGCTGGGATTACAG CAT  
||||| |||  
TCATCGACCCTAATGTC GTA  
C

GAM1607 FLJ10830 3' ATGCCTGTAGTCCCAGCCACTC 36717 C A A  
A A AGT GCTGGGATTACAG CAT  
| ||| ||||| |||  
A TCA CGACCCTGATGTC GTA  
C C C

GAM1607 FLJ10830 3' ATGCCTGTAGTTCCAGCTACTC 36718 C A  
A A AGTAGCTGGGATTACAG CAT  
| ||||| |||  
A TCATCGACCTTGATGTC GTA  
C C

GAM1607 FLJ10989 3' CTGTAATCCCAGCACT 36949 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 FLJ10997 3' TGCCTGACCACCTACTGTA 36957 C GATTA A  
TACAGTAG TGG CAG CA  
||||| ||| |||  
ATGTCATC ACC GTC GT  
C A C

GAM1607 FLJ11029 3' CTGTAATCCCAGCACT 60975 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 FLJ11036 3' CTGCGGTTCCAGCTACTCA 36998 C TA  
A AGTAGCTGGGAT CAG  
| ||||| |||  
A TCATCGACCTTG GTC  
C GC

GAM1607 FLJ11042 3' ATGCCTGTAATCCCAGCACT 37004 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||

			TCA CGACCCTAATGTC GTA			
			- C			
GAM1607	FLJ11126	3'	ATGCCTATAATCCCAGCAC	37083	A	C A
			GT GCTGGGATTA AG CAT			
			CA CGACCCTAAT TC GTA			
			- A C			
GAM1607	FLJ11136	3'	CTGTAATCCCAGCACT	37093	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			-			
GAM1607	FLJ11151	3'	CTGTAATCCCAGCACT	67874	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			-			
GAM1607	FLJ11151	3'	CTGTAATCCCAGCTACT	67875		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
			-			
GAM1607	FLJ11267	3'	ATGCCTGTAATCCCAGCACT	39003	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			- C			
GAM1607	FLJ11370	3'	ATGCCTGTAATCCCAGCTACT	46370		A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			- C			
GAM1607	FLJ11637	3'	CTGTAATCCCAGCACT	46380	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			-			
GAM1607	FLJ11700	3'	CTGTAATCCCAGCACT	46038	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			-			
GAM1607	FLJ11700	3'	CTGTAATCCCAGCTACTCA	46039	C	
			A AGTAGCTGGGATTACAG			
			A TCATCGACCCTAATGTC			
			- C			
GAM1607	FLJ11710	5'	ATGCCTGTAGTCCCAGCTACTC	45825	C	A
			A AGTAGCTGGGATTACAG CAT			

			A TCATCGACCCTGATGTC GTA		
			C C		
GAM1607	FLJ11722	3'	ATGCCTGTAATCCCAGGACT 46389	AG	A
			AGT CTGGGATTACAG CAT		
			TCA GACCCTAATGTC GTA		
			G_ C		
GAM1607	FLJ11722	3'	CTGTAATCCCAGCTACT 46391		
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
GAM1607	FLJ11722	3'	TGTAATCCCAGCTACTCA 46401	C	
			A AGTAGCTGGGATTACA		
			A TCATCGACCCTAATGT		
			C		
GAM1607	FLJ11726	3'	CTGTAATCCCAGCACT 46411	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
GAM1607	FLJ11996	3'	ATGCCTGTAATCCCAGCTACT 46434		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1607	FLJ12056	3'	ATGCCTATAATCCCAACACT 46251	AGC	C A
			AGT TGGGATTA AG CAT		
			TCA ACCCTAAT TC GTA		
			CA_ A C		
GAM1607	FLJ12056	3'	ATGCCTGTAATCCCAGCTATT 46252		A
			AGTAGCTGGGATTACAG CAT		
			TTATCGACCCTAATGTC GTA		
			C		
GAM1607	FLJ12122	3'	CTGTAATCCCAGCACT 46462	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
GAM1607	FLJ12178	3'	GTCTGTAATCCCAGCACT 47103	A	
			AGT GCTGGGATTACAGAC		
			TCA CGACCCTAATGTCTG		
GAM1607	FLJ12294	3'	CTATAATCCCAGCTACT 47012		C
			AGTAGCTGGGATTA AG		

				TCATCGACCCTAAT TC			
				A			
GAM1607	FLJ12294	3'	CTGTAATCCCAGCACT	47013	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1607	FLJ12331	3'	CTATAATCCCAGCACTTTA	46478	C	A	C
			TA AGT GCTGGGATTA AG				
			AT TCA CGACCCTAAT TC				
			T — A				
GAM1607	FLJ12363	3'	CTGTAATCCCAGCACT	49679	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1607	FLJ12547	3'	CTGTAATCCCAGCACTGTG	46491	A		
			TACAGT GCTGGGATTACAG				
			GTGTCA CGACCCTAATGTC				
			—				
GAM1607	FLJ12606	3'	CTGTAATCCCAGCACT	45640	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1607	FLJ12618	3'	ATGCCTGTAATCTCAGCTACTC	45994	C		A
	A		A AGTAGCTGGGATTACAG CAT				
			A TCATCGACTCTAATGTC GTA				
			C C				
GAM1607	FLJ12660	3'	CTGTAATCCCAGCACT	47141	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1607	FLJ12660	3'	CTGTAATCCCAGCTACT	47142			
			AGTAGCTGGGATTACAG				
			TCATCGACCCTAATGTC				
			—				
GAM1607	FLJ12666	3'	CTGTAATCCCAGCACT	44767	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1607	FLJ12800	3'	CTGTAATCCCAGCACT	43232	A		
			AGT GCTGGGATTACAG				

TCA CGACCCTAATGTC

GAM1607 FLJ12949 3' ATGCCTGTAGTCCCAGCTACTC 43442 C A  
A A AGTAGCTGGGATTACAG CAT

I |||||  
A TCATCGACCCTGATGTC GTA  
C C

GAM1607 FLJ12949 3' CTGTAATCCCAGCACT 43445 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 FLJ12985 3' CTGTAATCCCAGCACT 46240 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 FLJ13117 3' ATGCCTGTAATCCCAGCACT 43539 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1607 FLJ13162 3' ATGCCTGTAATCCCAGCTACT 46550 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA

GAM1607 FLJ13162 3' CTGTAATCCCAGCACT 46556 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 FLJ13193 3' ATGCCTATAATCCCGGCTACT 49758 C A  
AGTAGCTGGGATTA AG CAT  
||||| ||  
TCATCGGCCCTAAT TC GTA  
A C

GAM1607 FLJ13193 3' CTGTAATCCCAACACTTTA 49765 C AGC  
TA AGT TGGGATTACAG  
|| ||| |||||  
AT TCA ACCCTAATGTC  
T CA\_

GAM1607 FLJ13193 3' CTGTAATCCCAGCACT 49766 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 FLJ13305 3' ATGCCTGTAATCCCAGC 90125 A  
GCTGGGATTACAG CAT  
||||| |||

[illegible]

				GTC TCGATTTTA	GTC		
				—	C		
GAM1607	FLJ13952	3'	ATGCCTGTAACCCCAGCTACT	45613		A	A
			AGTAGCTGGG TTACAG CAT				
			TCATCGACCC AATGTC GTA				
			C	C			
GAM1607	FLJ13952	3'	ATGCCTGTAATCCCAGCACT	45614		A	A
			AGT GCTGGGATTACAG CAT				
			TCA CGACCCTAATGTC GTA				
			—	C			
GAM1607	FLJ13984	3'	CTGTGGTCCCAGCTACTCA	45448	C		
			A AGTAGCTGGGATTACAG				
			A TCATCGACCCTGGTGTC				
			C				
GAM1607	FLJ14100	3'	CTGTAATCCCAGCACT	46679		A	
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1607	FLJ14107	3'	ATGCCTGTAATCCCAGCACT	46689		A	A
			AGT GCTGGGATTACAG CAT				
			TCA CGACCCTAATGTC GTA				
			—	C			
GAM1607	FLJ14117	3'	ATGCCTGTAGTCCCAGCTACTC	42901	C		A
	A		A AGTAGCTGGGATTACAG CAT				
			A TCATCGACCCTGATGTC GTA				
			C	C			
GAM1607	FLJ14117	3'	CTGTAATACCAGCTACTCA	42907	C		G
			A AGTAGCTGG ATTACAG				
			A TCATCGACC TAATGTC				
			C	A			
GAM1607	FLJ14117	3'	CTGTAATCCCAGCACT	42908		A	
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1607	FLJ14225	3'	CTGTAATCCCAGCACT	45902		A	
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			—				
GAM1607	FLJ14251	3'	CTGTAATCCCAGCACT	45970		A	
			AGT GCTGGGATTACAG				

TCA CGACCCTAATGTC

GAM1607 FLJ14326 3' ATGCCTATAATCCCAGCTACT 49799 C A  
AGTAGCTGGGATTA AG CAT  
||||||| || |||  
TCATCGACCCTAAT TC GTA  
A C

GAM1607 FLJ14326 3' ATGCCTGTAATCCCAGC 49800 A  
GCTGGGATTACAG CAT  
||||||| |||  
CGACCCTAATGTC GTA  
C

GAM1607 FLJ14327 3' ATGCCTGTAATCCCAGCACT 46129 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

GAM1607 FLJ14345 3' CTGTAATCCCAGCACT 45334 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC  
C

GAM1607 FLJ14345 3' CTGTAATCCCAGCTACT 45335  
AGTAGCTGGGATTACAG  
||||||| |||  
TCATCGACCCTAATGTC

GAM1607 FLJ14346 3' CTGTAATCCCAGCACT 46709 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

GAM1607 FLJ14346 3' CTGTAATCCCAGCACT 46710 A  
AGT GCTGGGATTACAG  
||| ||||| |||  
TCA CGACCCTAATGTC

GAM1607 FLJ14397 3' ATGCCTGTAACCCCAGCTACT 51323 A A  
AGTAGCTGGG TTACAG CAT  
|||||| |||| |||  
TCATCGACCC AATGTC GTA  
C C

GAM1607 FLJ14397 3' CTATAATCCCAGCACT 51325 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC  
A

GAM1607 FLJ14621 3' CTGTAATCCCAGCACT 51470 A  
AGT GCTGGGATTACAG  
||| ||||| |||



TCA CGACCCTAATGTC

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      -
GAM1607 FLJ14642 3' ATGCCTGTAATCCCAGCACT 51493  A      A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      C
GAM1607 FLJ14642 3' CTGTAATCCCAGCACT 51499  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1607 FLJ14888 3' ATGCCTGTAATCCCAGCACT 51679  A      A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      C
GAM1607 FLJ20004 3' ATGCCTGTAATCCCAGCACT 34312  A      A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      C
GAM1607 FLJ20004 3' CTGTAATCCCAGCACT 95292  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1607 FLJ20004 3' TGCCTGTAATCCCAGCTACT 95301      A
      AGTAGCTGGGATTACAG CA
      ||||| ||
      TCATCGACCCTAATGTC GT
      C
GAM1607 FLJ20006 3' CTGTAATCCCAGCACT 34320  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1607 FLJ20006 3' CTGTAATCCCAGCTACT 34321
      AGTAGCTGGGATTACAG
      |||||
      TCATCGACCCTAATGTC

GAM1607 FLJ20034 3' CTGTAATCCCAGCACT 34371  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      -
GAM1607 FLJ20055 3' CTGAAGTCCCAGCTACTCA 34440  C      A
      A AGTAGCTGGGATT CAG
      | ||||| |||
```

A TCATCGACCCTGA GTC  
 C A  
 GAM1607 FLJ20055 3' CTGTAATCCCAGCACTTTA 34441 C A  
 TA AGT GCTGGGATTACAG  
 || ||| |||||  
 AT TCA CGACCCTAATGTC  
 T \_  
 GAM1607 FLJ20059 3' ATGCCTGTAATCCCAGCACT 34446 A A  
 AGT GCTGGGATTACAG CAT  
 ||| |||||  
 TCA CGACCCTAATGTC GTA  
 \_ C  
 GAM1607 FLJ20071 3' ATGCCTATAATCCCAGCTACTT 34479 \_ C A  
 G CA GTAGCTGGGATTA AG CAT  
 || ||||| || |||  
 GT CATCGACCCTAAT TC GTA  
 T A C  
 GAM1607 FLJ20081 3' CTGTAATCCCAGCACT 34507 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1607 FLJ20139 3' CTGTAATCCCAACACT 34624 AGC  
 AGT TGGGATTACAG  
 ||| |||||  
 TCA ACCCTAATGTC  
 CA\_  
 GAM1607 FLJ20174 3' CTGTAATCCCAAAGTGCTG 34688 GC\_  
 CAGTA TGGGATTACAG  
 |||| |||||  
 GTCGT ACCCTAATGTC  
 GAA  
 GAM1607 FLJ20200 3' TGCCTGTAATCCCTGCACT 34729 A T A  
 AGT GC GGGATTACAG CA  
 ||| || ||||| ||  
 TCA CG CCCTAATGTC GT  
 \_ T C  
 GAM1607 FLJ20211 3' CTGTAATCCCAGCACT 34751 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1607 FLJ20280 3' CTGTAATCCCAGCACT 34849 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1607 FLJ20280 3' CTGTAATCCCTGCTACT 34850 T  
 AGTAGC GGGATTACAG  
 ||||| |||||

			TCATCG CCCTAATGTC			
			T			
GAM1607	FLJ20340	3'	ATGCCTGTAATCCCAGCATTTT 34972	TA_		A
		G	CAG GCTGGGATTACAG CAT			
			GTT CGACCCTAATGTC GTA			
			TTA C			
GAM1607	FLJ20340	3'	TGTAATCCCAGCTACTCA 34979 C			
			A AGTAGCTGGGATTACA			
			A TCATCGACCCTAATGT			
			C			
GAM1607	FLJ20359	3'	ATGCCTGTAATCCCAGCACT 35035	A		A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			- C			
GAM1607	FLJ20452	3'	ATGCCTGTAATCCCAGCACT 35196	A		A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			- C			
GAM1607	FLJ20464	3'	ATGCCTATAATCCGAGCTACT 35228	G	C	A
			AGTAGCT GGATTA AG CAT			
			TCATCGA CCTAAT TC GTA			
			G A C			
GAM1607	FLJ20464	3'	ATGCCTGTAATCCCAGCACT 35229	A		A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			- C			
GAM1607	FLJ20464	3'	ATGCCTGTAATCTCAGCTACT 35230			A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACTCTAATGTC GTA			
			C			
GAM1607	FLJ20627	3'	ATGCCTGTAATCCCAGCACT 35471	A		A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			- C			
GAM1607	FLJ20627	3'	GTCATCTCAGCTACTCA 35475 C		T	
			A AGTAGCTGGGAT AC			
			A TCATCGACTCTA TG			
			C C			
GAM1607	FLJ20695	3'	ATGCCTGTAATCCCAGCACT 35556	A		A
			AGT GCTGGGATTACAG CAT			

Accession	Gene	Position	Strand	Sequence	Start	End	RefSeq	GenBank
GAM1607	FLJ20700	3'	ATGCCTGTAATCCCAGCACT	35570	A	A		
			AGT GCTGGGATTACAG CAT					
			TCA CGACCCTAATGTC GTA					
GAM1607	FLJ20783	3'	CTGTAATCCCAGCACT	35661	A			
			AGT GCTGGGATTACAG					
			TCA CGACCCTAATGTC					
GAM1607	FLJ20825	3'	ATGCCTGTAATCCCAACTCTTG	35693	T	C		A
			CAG AG TGGGATTACAG CAT					
			GTT TC ACCCTAATGTC GTA					
			C A C					
GAM1607	FLJ20825	3'	ATGCCTGTAATCCCAGCTACT	35694		A		
			AGTAGCTGGGATTACAG CAT					
			TCATCGACCCTAATGTC GTA					
			C					
GAM1607	FLJ20825	3'	CTGTAATCCCAGCACT	35696	A			
			AGT GCTGGGATTACAG					
			TCA CGACCCTAATGTC					
GAM1607	FLJ20972	3'	ATGCCTATAATCCCAGGTACT	46722	G	C	A	
			AGTA CTGGGATTA AG CAT					
			TCAT GACCCTAAT TC GTA					
			G A C					
GAM1607	FLJ21106	3'	CTGTAATCCCAGCACT	46995	A			
			AGT GCTGGGATTACAG					
			TCA CGACCCTAATGTC					
GAM1607	FLJ21144	3'	ATGCCTGTAATCCCAGCACT	42875	A	A		
			AGT GCTGGGATTACAG CAT					
			TCA CGACCCTAATGTC GTA					
			C					
GAM1607	FLJ21162	3'	ATGCCTATAATCCCAGCACT	45892	A	C	A	
			AGT GCTGGGATTA AG CAT					
			TCA CGACCCTAAT TC GTA					
			A C					
GAM1607	FLJ21162	3'	CTATAAACCCAGCTACTCA	45894	C	A	C	
			A AGTAGCTGGG TTA AG					

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          A TCATCGACCC AAT TC
          C   A   A
GAM1607 FLJ21240 3' ATGCCTGTAATATCAGCTACTC 45837 C   GG   A
          A
          A AGTAGCTG ATTACAG CAT
          | ||||| ||||| |||
          A TCATCGAC TAATGTC GTA
          C   TA   C
GAM1607 FLJ21272 3' ATGCCTGTAATCCCAGC   46735   A
          GCTGGGATTACAG CAT
          ||||| ||||| |||
          CGACCCTAATGTC GTA
          C
GAM1607 FLJ21551 3' CTGTAATCCCAGCTAC   45628
          GTAGCTGGGATTACAG
          ||||| ||||| |||
          CATCGACCCTAATGTC

GAM1607 FLJ21657 3' CTGTAATCCCAACACT   42509   AGC
          AGT TGGGATTACAG
          ||| ||||| |||||
          TCA ACCCTAATGTC
          CA_
GAM1607 FLJ21687 3' CTGTAATCCCAGCACT   45857   A
          AGT GCTGGGATTACAG
          ||| ||||| |||||
          TCA CGACCCTAATGTC

GAM1607 FLJ21870 3' ATGCCTGTAATCCCAGCACT 43458 A   A
          AGT GCTGGGATTACAG CAT
          ||| ||||| ||||| |||
          TCA CGACCCTAATGTC GTA
          C
GAM1607 FLJ22054 3' CTGTAATCCAAGCTGC   94395   G
          GTAGCT GGATTACAG
          ||||| ||||| |||||
          CGTCGA CCTAATGTC
          A
GAM1607 FLJ22054 3' CTGTAATCCCAGCACT   94396   A
          AGT GCTGGGATTACAG
          ||| ||||| ||||| |||
          TCA CGACCCTAATGTC

GAM1607 FLJ22167 3' ATGCCTGTAATCCCAGCATTTT 44565 TA_   A
          G
          CAG GCTGGGATTACAG CAT
          ||| ||||| ||||| |||
          GTT CGACCCTAATGTC GTA
          TTA   C
GAM1607 FLJ22167 3' CTGTAATCCCAGCTACTTA 44572 C
          A AGTAGCTGGGATTACAG
          | ||||| ||||| |||||

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			A TCATCGACCCTAATGTC			
			T			
GAM1607	FLJ22313	3'	GTCTGTAATCCCAGCACT	42344	A	
			AGT GCTGGGATTACAGAC			
			TCA CGACCCTAATGTCTG			
			—			
GAM1607	FLJ22692	3'	CTGTAATCCCAGCACT	46802	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	FLJ23022	3'	TGCCTGTAATCCCTGCACT	46814	A T	A
			AGT GC GGGATTACAG CA			
			TCA CG CCCTAATGTC GT			
			— T C			
GAM1607	FLJ23042	3'	ATGCCTGTAATCCCAGCTACT	47170		A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1607	FLJ23042	3'	CTGTAATCCCAGCACT	47172	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	FLJ23120	3'	CTGTAATCCCAGCTACTCA	85148	C	
			A AGTAGCTGGGATTACAG			
			A TCATCGACCCTAATGTC			
			C			
GAM1607	FLJ23235	3'	ATGCCTGTAATCCCAGCACT	46305	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1607	FLJ23323	3'	CTGTAATCCCAAAGTGCTG	45051	GC_	
			CAGTA TGGGATTACAG			
			GTCGT ACCCTAATGTC			
			GAA			
GAM1607	FLJ23447	3'	ATGCCTGTAATCCCAGCACT	45710	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1607	FLJ23476	3'	ATGCCTGTAATCCCAACATTCT	44958	TAGC_	A
	G		CAG TGGGATTACAG CAT			

				GTC ACCCTAATGTC GTA		
				TTACA C		
GAM1607	FLJ23499	3'	ATGCCTGTAATCCCAGCACT	42816	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1607	FLJ23499	3'	ATGCCTGTAATCCCAGCACT	42817	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1607	FLJ23499	3'	CTGTAATCCCAGCTACT	42821		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
GAM1607	FLJ23537	3'	ATGCCTGCAATCCCAGCTACTT	46021	—	A A
	G		CA GTAGCTGGGATT CAG CAT			
			GT CATCGACCCTAA GTC GTA			
			T C C			
GAM1607	FLJ25012	3'	ATGCCTGTAATCCAGTACT	58088	G G	A
			AGTA CTGG ATTACAG CAT			
			TCAT GACC TAATGTC GTA			
			— — C			
GAM1607	FLJ25012	3'	CTATGGTCCCAGCTACTCA	58089	C	C
			A AGTAGCTGGGATTA AG			
			A TCATCGACCCTGGT TC			
			C A			
GAM1607	FLJ25012	3'	CTGTAATCCCAGCACT	58090	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	FLJ25179	3'	ATGCCTGTAATCCCAGCACT	58354	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1607	FLJ30046	3'	CTGCAATGTTTGCTACTGTA	58100	TG G	A
			TACAGTAGC G ATT CAG			
			ATGTCATCG T TAA GTC			
			TT G C			
GAM1607	FLJ30092	3'	CTGTAATCCCAGCACT	58689	A	
			AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

—  
GAM1607 FLJ30681 3' CTGTAATCCCAGCTACT 91786  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1607 FLJ31455 3' CTGTAATCCCAGCACT 58623 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 FLJ31737 3' CTGTAATCCCAGCACT 58694 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 FUSIP1 3' ATGCCTGTAATCTCAGCTACTC 53955 C A  
A AGTAGCTGGGATTACAG CAT  
| ||||| |||  
A TCATCGACTCTAATGTC GTA  
C C

GAM1607 FUSIP1 3' CTGTAATCCCAGCACT 53957 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 GALNT6 3' ATGCCTGTAGTCGCAGCTACTC 23290 C G A  
A AGTAGCTG GATTACAG CAT  
| ||||| ||||| |||  
A TCATCGAC CTGATGTC GTA  
C G C

GAM1607 GCN2 3' ATGCCTGTAGTCCCAGCTACT 62768 A  
AGTAGCTGGGATTACAG CAT  
||||||| |||  
TCATCGACCCTGATGTC GTA  
C

GAM1607 GLTP 3' CTGTAATCCCAGCACT 33159 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 GLTP 3' CTGTAGTTCCAGCTACTCA 33160 C  
A AGTAGCTGGGATTACAG  
| ||||| |||||  
A TCATCGACCTTGATGTC  
C

GAM1607 GP5 3' CTGTAATCCCAGCACT 15645 A  
AGT GCTGGGATTACAG  
||| |||||



TCA CGACCCTAATGTC

GAM1607 HES2 3' CTGTAATCCCAGCACT 38854 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 HSD17B7 3' TGTAGTCCCAGCTACTCA 33037 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTGATGT  
C

GAM1607 HSH2 3' ATGCCTGTAATCCCAGCTACTT 51671 \_ A  
G CA GTAGCTGGGATTACAG CAT  
|| ||||| ||  
GT CATCGACCCTAATGTC GTA  
T C

GAM1607 HSMPP8 3' CTATAATCCCAGCGCT 93474 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCG CGACCCTAAT TC  
A

GAM1607 HSPC043 3' ATGCCTGTAATCCCAGCACT 67719 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| ||  
TCA CGACCCTAATGTC GTA  
C

GAM1607 HSPC043 3' CTGTAATCCCAGCTACT 67720  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1607 ICAM4 3' CTGTAATCCCAGCACT 42353 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 ICAM4 3' CTGTAATCCCAGCACT 7749 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 IL10RB 3' ATGCCTATAATCCCAGCTACT 5275 C A  
AGTAGCTGGGATTA AG CAT  
||||||| || ||  
TCATCGACCCTAAT TC GTA  
A C

GAM1607 IMAGE:4907098 3' CTGTAATCCCAGCACT 91658 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1607 INE1 3' CTGTAATCCCAGCTCTTTGT 13374 T\_  
ACAG AGCTGGGATTACAG  
|||||  
TGTT TCGACCCTAATGTC  
TC

GAM1607 ING1-like 3' CTGTAATCCCAGCACT 54155 A  
AGT GCTGGGATTACAG  
|||  
TCA CGACCCTAATGTC

GAM1607 JAM1 3' ATGCCTGTAATCCCAGCTGCT 57915 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCGTCGACCCTAATGTC GTA  
C

GAM1607 JAM1 3' CTATAATCCCAGAGGCTG 57923 AG C  
CAGT CTGGGATTA AG  
|||||  
GTCG GACCCTAAT TC  
GA A

GAM1607 JAM1 3' ATGCCTGTAATCCCAGCTGCT 57942 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCGTCGACCCTAATGTC GTA  
C

GAM1607 JAM1 3' CTATAATCCCAGAGGCTG 57949 AG C  
CAGT CTGGGATTA AG  
|||||  
GTCG GACCCTAAT TC  
GA A

GAM1607 JAM1 3' ATGCCTGTAATCCCAGCTGCT 57887 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCGTCGACCCTAATGTC GTA  
C

GAM1607 JAM1 3' CTATAATCCCAGAGGCTG 57894 AG C  
CAGT CTGGGATTA AG  
|||||  
GTCG GACCCTAAT TC  
GA A

GAM1607 JAM1 3' ATGCCTGTAATCCCAGCTGCT 33749 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCGTCGACCCTAATGTC GTA  
C

GAM1607 JAM1 3' CTATAATCCCAGAGGCTG 33756 AG C  
CAGT CTGGGATTA AG  
|||||

			GTCG GACCCTAAT TC		
			GA A		
GAM1607 KALI	3'	CTGTAATCCCAGTACT	53592	G	
		AGTA CTGGGATTACAG			
		TCAT GACCCTAATGTC			
		—			
GAM1607 KATII	3'	CTATAATCCCAGCACT	32646	A	C
		AGT GCTGGGATTAG			
		TCA CGACCCTAAT TC			
		— A			
GAM1607 KBRAS2	3'	ATGCCTGTAATCCCAGCTAC	34192		A
		GTAGCTGGGATTACAG CAT			
		CATCGACCCTAATGTC GTA			
		C			
GAM1607 KIAA0042	3'	CTGTAATCCCAGCACT	29610	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607 KIAA0090	3'	ATGCCTGTAATCCCAGC	88438		A
		GCTGGGATTACAG CAT			
		CGACCCTAATGTC GTA			
		C			
GAM1607 KIAA0159	3'	CTGTAATCCCAGCACT	29507	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607 KIAA0159	3'	TGTAATCCCAGCTACTCA	29511	C	
		A AGTAGCTGGGATTACA			
		A TCATCGACCCTAATGT			
		C			
GAM1607 KIAA0184	3'	CTGTAATCCCAGCACT	65194	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607 KIAA0226	3'	CTGTAATCCCAGCACT	63514	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607 KIAA0226	3'	CTGTAATCCCAGCTACTTG	63515	—	
		CA GTAGCTGGGATTACAG			

[illegible]

TCA CGACCCTAATGTCT

GAM1607 KIAA0472 3' ATGCCTGTAATCCAAGATACTC 71859 C G G A  
A A AGTA CT GGATTACAG CAT

I |||| || |||||||| |||  
A TCAT GA CCTAATGTC GTA  
C A A C

GAM1607 KIAA0514 3' ATGCCTGTAATCCCAGCACT 28077 A A  
AGT GCTGGGATTACAG CAT

||| |||||||||| |||  
TCA CGACCCTAATGTC GTA  
C

GAM1607 KIAA0547 3' TGTAATCCCAGCTACTCA 28918 C  
A AGTAGCTGGGATTACA

I ||||||||||||  
A TCATCGACCCTAATGT  
C

GAM1607 KIAA0563 3' CTGTAATCCCAGCACT 29187 A  
AGT GCTGGGATTACAG

||| ||||||||||  
TCA CGACCCTAATGTC

GAM1607 KIAA0565 3' TCTGTAATTGCTATTG 66900 TGG  
CAGTAGC GATTACAGA

||||| |||||||  
GTTATCG TTAATGTCT

GAM1607 KIAA0618 3' ATGCCTGTAATCCCAGC 29161 A  
GCTGGGATTACAG CAT

|||||||||| |||  
CGACCCTAATGTC GTA  
C

GAM1607 KIAA0635 3' CTGTAATCCCAGCACT 27696 A  
AGT GCTGGGATTACAG

||| ||||||||||  
TCA CGACCCTAATGTC

GAM1607 KIAA0694 3' ATGCCTATAATCCCAATACTTT 72579 C GC C A  
A TA AGTA TGGGATTA AG CAT

|| |||| |||||| || |||  
AT TCAT ACCCTAAT TC GTA  
T A\_ A C

GAM1607 KIAA0694 3' CTGTAATCCCAGCACT 72580 A  
AGT GCTGGGATTACAG

||| ||||||||||  
TCA CGACCCTAATGTC

GAM1607 KIAA0752 3' ATGCCTGCAATCCCAGCTACT 67048 A A  
AGTAGCTGGGATT CAG CAT

|||||||||| ||| |||

TCATCGACCCTAA GTC GTA  
 C C  
 GAM1607 KIAA0794 3' ATGCCTGTAATCCCAACACT 80409 AGC A  
 AGT TGGGATTACAG CAT  
 ||| ||||| |||  
 TCA ACCCTAATGTC GTA  
 CA\_ C  
 GAM1607 KIAA0794 3' CTGTAATCCCAGCTACTCA 80411 C  
 A AGTAGCTGGGATTACAG  
 | ||||| |||||  
 A TCATCGACCCTAATGTC  
 C  
 GAM1607 KIAA0795 3' CTATAATCCCAGCACT 46590 A C  
 AGT GCTGGGATTA AG  
 ||| ||||| ||  
 TCA CGACCCTAAT TC  
 \_ A  
 GAM1607 KIAA0825 3' CTGTAATCCCAGCACT 61025 A  
 AGT GCTGGGATTACAG  
 ||| ||||| |||||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1607 KIAA0825 3' GTGCCTGCAATCCCAGCTACTC 61027 C A A  
 A A AGTAGCTGGGATT CAG CAT  
 | ||||| ||| |||  
 A TCATCGACCCTAA GTC GTG  
 C C C  
 GAM1607 KIAA0831 3' CTGTAATCCCAGCTACT 29972  
 AGTAGCTGGGATTACAG  
 ||||| |||||  
 TCATCGACCCTAATGTC  
 \_  
 GAM1607 KIAA0831 3' CTGTAATCCCGGCACT 29973 A  
 AGT GCTGGGATTACAG  
 ||| ||||| |||||  
 TCA CGGCCCTAATGTC  
 \_  
 GAM1607 KIAA0852 5' CTGTAATCCCAGCACT 30077 A  
 AGT GCTGGGATTACAG  
 ||| ||||| |||||  
 TCA CGACCCTAATGTC  
 \_  
 GAM1607 KIAA0853 3' ATGTCTGTAGTCACAGCTACTC 30537 C G  
 A A AGTAGCTG GATTACAGACAT  
 | ||||| ||||| |||||  
 A TCATCGAC CTGATGTCTGTA  
 C A  
 GAM1607 KIAA0872 3' ATGCCTGTAATCCCAGCACT 30061 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| ||||| |||

				TCA CGACCCTAATGTC GTA		
				— C		
GAM1607	KIAA0872	3'	CTGTAATCCCAGCACT	30062	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	KIAA0889	3'	ATGCCTGTAATCCCAGCACT	31129	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1607	KIAA0907	3'	CTGTAATCCCAGCACT	30173	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	KIAA0907	3'	CTGTAATCCCAGCACT	30174	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	KIAA0912	3'	CTGTAATCCCAGCACT	64409	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	KIAA0918	3'	TCTGTAAGATGGGGCTACTGT	73136		GGGA_
			ACAGTAGCT TTACAGA			
			TGTCATCGG AATGTCT			
			GGTAG			
GAM1607	KIAA0930	3'	CTGTAATCCCAGCACT	70542	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	KIAA1032	3'	ATGCCTGTAGTCCCAGCTACTC	66151	C	A
	A		A AGTAGCTGGGATTACAG CAT			
			A TCATCGACCCTGATGTC GTA			
			C C			
GAM1607	KIAA1056	3'	CTGTAATCCCAGCACT	29695	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	KIAA1056	3'	CTGTAATCCCAGCTGCT	29696		
			AGTAGCTGGGATTACAG			

TCGTCGACCCTAATGTC

GAM1607 KIAA1086 3' CTATAATCCCAGCACT 70744 A C  
AGT GCTGGGATTA AG  
||| ||||| ||  
TCA CGACCCTAAT TC

— A

GAM1607 KIAA1086 3' CTGTAATCCCAGCACT 70745 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

—

GAM1607 KIAA1130 3' ATGCCTGTAATCCCAGCACT 62412 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| ||||| |||  
TCA CGACCCTAATGTC GTA

— C

GAM1607 KIAA1130 3' ATGCCTGTAATCCCAGTGCT 62413 G A  
AGTA CTGGGATTACAG CAT  
||| ||||| ||||| |||  
TCGT GACCCTAATGTC GTA

— C

GAM1607 KIAA1130 3' TGTAATCCCAGCTACTCA 62428 C  
A AGTAGCTGGGATTACA  
| ||||| ||||| |||||  
A TCATCGACCCTAATGT

C

GAM1607 KIAA1164 3' ATGCCTGTAATCCCAGTACT 69503 G A  
AGTA CTGGGATTACAG CAT  
||| ||||| ||||| |||  
TCAT GACCCTAATGTC GTA

— C

GAM1607 KIAA1191 3' CTGTAATCCCAGCACT 39954 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

—

GAM1607 KIAA1204 3' TCTGTAATCCCAACACT 69220 AGC  
AGT TGGGATTACAGA  
||| ||||| |||||  
TCA ACCCTAATGTCT

CA\_

GAM1607 KIAA1228 3' CTGTAATCCCAGCACT 65041 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

—

GAM1607 KIAA1244 3' CTGTAATCCCAGCACT 71989 A  
AGT GCTGGGATTACAG  
||| ||||| |||||



TCA CGACCCTAATGTC

GAM1607 KIAA1244 3' CTGTAATCCCAGCTACTTA 71990 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
T

GAM1607 KIAA1253 3' ATGCCTGTGGTCCCAGCTACTG 91896 A  
CAGTAGCTGGGATTACAG CAT  
|||||  
GTCATCGACCCTGGTGTC GTA  
C

GAM1607 KIAA1271 3' CTGTAATCCCAGCACT 69542 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 KIAA1271 3' GTCTGTAATCCCAGCTATT 69551  
AGTAGCTGGGATTACAGAC  
|||||  
TTATCGACCCTAATGTCTG

GAM1607 KIAA1276 3' CTGTAATCCCATCACT 66430 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CT\_

GAM1607 KIAA1277 3' ATGCCTATAATCCCAGCACT 64450 A C A  
AGT GCTGGGATTA AG CAT  
||| ||||| || |||  
TCA CGACCCTAAT TC GTA  
A C

GAM1607 KIAA1328 3' CTGTAATCCCAGGCTTTG 61646 T \_  
CAG AGC TGGGATTACAG  
||| ||| |||||  
GTT TCG ACCCTAATGTC  
\_ G

GAM1607 KIAA1348 3' ATGCCTGTAATCCCAGCTACT 68571 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1607 KIAA1348 3' CTGTAATCCCAGCACTGTG 68575 A  
TACAGT GCTGGGATTACAG  
||||| |||||  
GTGTCA CGACCCTAATGTC

GAM1607 KIAA1364 3' ATGCCTGTAATCCCAGCACT 63586 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||

			TCA CGACCCTAATGTC GTA		
			— C		
GAM1607	KIAA1364	3'	CTGTAATCCCAGCTACTTG 63593	—	
			CA GTAGCTGGGATTACAG		
			GT CATCGACCCTAATGTC		
			T		
GAM1607	KIAA1377	3'	ATGCCTGTAATCCCAGCACT 67174	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1607	KIAA1404	3'	CTGTAATCCCAGCACT 61987	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	KIAA1423	3'	TAGTCCCAGCTACTCA 61728	C	
			A AGTAGCTGGGATTA		
			A TCATCGACCCTGAT		
			C		
GAM1607	KIAA1456	3'	ATGCCTGTAATCCCAGCACT 66988	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1607	KIAA1456	3'	ATGCCTGTAATCCCAGCCACTT 66989	— A	A
	G		CA GT GCTGGGATTACAG CAT		
			GT CA CGACCCTAATGTC GTA		
			T C C		
GAM1607	KIAA1473	3'	ATGCCTGTAATCCCAGCTACT 70663		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1607	KIAA1473	3'	CTGTAATCCCAGCACT 70667	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	KIAA1486	3'	CTGTAATCCCAGCACTCTG 67379	TA_	
			CAG GCTGGGATTACAG		
			GTC CGACCCTAATGTC		
			TCA		
GAM1607	KIAA1554	3'	CTGTAATCCCAGCTACCTG 95152	—	
			CAG TAGCTGGGATTACAG		

			GTC ATCGACCCTAATGTC		
			C		
GAM1607	KIAA1559	3'	ATGCCTGTAATCCCAGCACT	73057	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1607	KIAA1559	3'	ATGCCTGTAATCCCAGCTACTT	73058	— A
	G		CA GTAGCTGGGATTACAG CAT		
			GT CATCGACCCTAATGTC GTA		
			T C		
GAM1607	KIAA1559	3'	CTGTAATCCCAGCACT	73064	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	KIAA1586	5'	CTGTAATCCCAGCACT	92329	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	KIAA1614	3'	ATGCCTATAATCCCAGCTACTT	70117	— C A
	G		CA GTAGCTGGGATTA AG CAT		
			GT CATCGACCCTAAT TC GTA		
			T A C		
GAM1607	KIAA1614	3'	ATGCCTGTAATCCCAGAACT	70118	AG A
			AGT CTGGGATTACAG CAT		
			TCA GACCCTAATGTC GTA		
			A_ C		
GAM1607	KIAA1630	3'	ATGCCTGTAATCCCAGCACT	38030	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1607	KIAA1656	5'	CTGTAATCCCAGCACT	65794	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	KIAA1674	3'	CTGTAATCCCAGCACT	68777	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	KIAA1715	3'	ATGCCTGTAATCCTAGCTACTC	68117	C A
	A		A AGTAGCTGGGATTACAG CAT		

		A TCATCGATCCTAATGTC GTA		
		C C		
GAM1607 KIAA1735	3'	CTGTAGTCCCAGCTACTCA 87627	C	
		A AGTAGCTGGGATTACAG		
		A TCATCGACCCTGATGTC		
		C		
GAM1607 KIAA1751	3'	ATGCCTGTAATCCCAGAACT 71688	AG	A
		AGT CTGGGATTACAG CAT		
		TCA GACCCTAATGTC GTA		
		A_ C		
GAM1607 KIAA1811	5'	CTGTAATCCCAGCACT 64796	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607 KIAA1829	3'	TGTAATCCCAGCTACTCA 61958	C	
		A AGTAGCTGGGATTACA		
		A TCATCGACCCTAATGT		
		C		
GAM1607 KIAA1872	3'	ATGCCTGTAATCCCAGCACTCT 62923	TA_	A
	G	CAG GCTGGGATTACAG CAT		
		GTC CGACCCTAATGTC GTA		
		TCA C		
GAM1607 KIAA1872	3'	ATGCCTGTAATCCCAGCTACT 62924		A
		AGTAGCTGGGATTACAG CAT		
		TCATCGACCCTAATGTC GTA		
		C		
GAM1607 KIAA1872	3'	CTATAATCCCAGCACT 62929	A	C
		AGT GCTGGGATTA AG		
		TCA CGACCCTAAT TC		
		— A		
GAM1607 KIAA1872	3'	CTGTAATCCCAGACTTTG 62931	T _	
		CAG AG CTGGGATTACAG		
		GTT TC GACCCTAATGTC		
		_ A		
GAM1607 KIAA1941	3'	CTGTAATCCCAGCACT 74838	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607 KIAA1948	5'	ATGCCTATAATCCCAGCTACT 82399		C A
		AGTAGCTGGGATTA AG CAT		

			TCATCGACCCTAAT TC GTA		
			A C		
GAM1607	KIAA1951	3'	CTGTAATCCCAGCACT 73761	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	KIAA1954	3'	CTGTAATCCCAGCACT 77719	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	KIAA1958	3'	CTATAATCCCAGCACT 81902	A	C
			AGT GCTGGGATTA AG		
			TCA CGACCCTAAT TC		
			— A		
GAM1607	KIAA1979	3'	CTGTAATCCCAGCACT 88278	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	KIAA1979	3'	CTGTAATCCCAGCTACTCA 88279	C	
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTAATGTC		
			C		
GAM1607	KLHL6	3'	CTGTAATCCCAGCCCTATG 55303	GTA_	
			CA GCTGGGATTACAG		
			GT CGACCCTAATGTC		
			ATCC		
GAM1607	KLHL8	3'	CTGTAATTCCAGCTACTCA 62854	C	
			A AGTAGCTGGGATTACAG		
			A TCATCGACCTTAATGTC		
			C		
GAM1607	KR18	3'	CTGTAATCCCAGTACT 52745	G	
			AGTA CTGGGATTACAG		
			TCAT GACCCTAATGTC		
			—		
GAM1607	KREMEN	3'	ATGCCTGTAATCCCAGCACT 49404	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1607	KREMEN	3'	CTGTAATCCCAGCTACT 49406		
			AGTAGCTGGGATTACAG		

TCATCGACCCTAATGTC

GAM1607 LHPP 5' CTGTAATCCCAGCACT 42101 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LIAS 3' CTGTAATCCCAGCACTTTA 70635 C A  
TA AGT GCTGGGATTACAG  
|| ||| |||||  
AT TCA CGACCCTAATGTC

GAM1607 LIM 3' CTGTAATCCCAGCACT 21302 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LIM 3' CTGTAATCCCAGCTACTCA 21303 C  
A AGTAGCTGGGATTACAG  
| |||||  
A TCATCGACCCTAATGTC  
C

GAM1607 LRG 3' CTGTAATCCCAGCACT 53750 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LRRFIP1 3' TGCCTGTAATCTCAGTAC 16420 G A  
GTA CTGGGATTACAG CA  
||| ||||| ||  
CAT GACTCTAATGTC GT  
C

GAM1607 LRRFIP1 3' TGTAATCCCAGCCACT 16421 A  
AGT GCTGGGATTACA  
||| |||||  
TCA CGACCCTAATGT  
C

GAM1607 LSR68 3' TGCCTATAATCCCAGCTACTCA 37937 C C A  
A AGTAGCTGGGATTA AG CA  
| ||||| || ||  
A TCATCGACCCTAAT TC GT  
C A C

GAM1607 LYSAL1 3' CTGTAATCCCAGCACT 16918 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 MACF1 3' CTGTAATCCCAGCACT 52316 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

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      —
GAM1607 MAWBP  3' ATGCCTGTAATCCCAGCACT 42106  A      A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      —      C
GAM1607 MCAM   3' CTGTAATCCCAGCACT   21454  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC
      —
GAM1607 MESDC2 3' CTGTAATCCCAGTACT   72492  G
      AGTA CTGGGATTACAG
      ||| |||||
      TCAT GACCCTAATGTC
      —
GAM1607 MESDC2 3' TGTAATCCCAGCTACTCA  72503  C
      A AGTAGCTGGGATTACA
      | |||||
      A TCATCGACCCTAATGT
      C
GAM1607 METL   3' ATGCCTGTAATCCCAGCCACT 37253  A      A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      C      C
GAM1607 MGC10765 3' ATGCCTGTAATCCCAGCACT 44299  A      A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      —      C
GAM1607 MGC10765 3' CTGTAATCCCAGCTAC   44301
      GTAGCTGGGATTACAG
      |||||
      CATCGACCCTAATGTC
      —
GAM1607 MGC10771 3' ATGCCTGTAATCCCAGCACT 44451  A      A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      —      C
GAM1607 MGC10814 5' ATGCCTGTAATCCCAGCACT 51036  A      A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      —      C
GAM1607 MGC10814 3' CTGTAATCCCAGCACT   51038  A
      AGT GCTGGGATTACAG
      ||| |||||
```

TCA CGACCCTAATGTC

GAM1607 MGC10999 3' ATGCCTGTAATCCCAGCACTGT 50225 A A  
G TACAGT GCTGGGATTACAG CAT  
||||| ||||||||| |||  
GTGTCA CGACCCTAATGTC GTA

GAM1607 MGC11287 5' GTCTATAATCCCAGCACTGTG 48834 A C  
TACAGT GCTGGGATTA AGAC  
||||| ||||||||| |||  
GTGTCA CGACCCTAAT TCTG

GAM1607 MGC11386 3' CTATAATCCCAGCACT 51950 A C  
AGT GCTGGGATTA AG  
||| ||||||||| ||  
TCA CGACCCTAAT TC

GAM1607 MGC13017 3' TCTGTAATCCCAGCTACT 54694  
AGTAGCTGGGATTACAGA  
||||| ||||||||| |||  
TCATCGACCCTAATGTCT

GAM1607 MGC13053 3' CTGTAATCCCAGTACT 51131 G  
AGTA CTGGGATTACAG  
||| ||||||||| |||  
TCAT GACCCTAATGTC

GAM1607 MGC13523 3' TGCCTGTAATTTCACTA 53031 C GG A  
TAG TG ATTACAG CA  
||| || ||||||| ||  
ATC AC TAATGTC GT

GAM1607 MGC14126 3' CTGTAATCCCAGCACT 51854 A  
AGT GCTGGGATTACAG  
||| ||||||||| |||  
TCA CGACCCTAATGTC

GAM1607 MGC14817 3' CTGTAATCCCAGCACT 50336 A  
AGT GCTGGGATTACAG  
||| ||||||||| |||  
TCA CGACCCTAATGTC

GAM1607 MGC15397 3' CTGTAATCCCAGCACT 54679 A  
AGT GCTGGGATTACAG  
||| ||||||||| |||  
TCA CGACCCTAATGTC

GAM1607 MGC15631 3' ATGCCTGTAATCCCAGTGCT 51259 G A  
AGTA CTGGGATTACAG CAT  
||| ||||||||| |||



			TCGT GACCCTAATGTC GTA			
			— C			
GAM1607	MGC15631	3'	CTGTCATCCCAGCTAC 51263	T		
			GTAGCTGGGAT ACAG			
			CATCGACCCTA TGTC			
			C			
GAM1607	MGC16142	3'	ATGCCTATAATCCCAGCACT 51291	A	C A	
			AGT GCTGGGATTA AG CAT			
			TCA CGACCCTAAT TC GTA			
			— A C			
GAM1607	MGC16142	3'	ATGCCTATAATCCCAGCTACT 51292		C A	
			AGTAGCTGGGATTA AG CAT			
			TCATCGACCCTAAT TC GTA			
			A C			
GAM1607	MGC16332	3'	ATGCCTGTAATCCCAACACT 56774	AGC	A	
			AGT TGGGATTACAG CAT			
			TCA ACCCTAATGTC GTA			
			CA_ C			
GAM1607	MGC16385	3'	CTGTAATCCCAGCACT 58887	A		
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	MGC16703	3'	ATGCCTGTAATCCCAGCACT 73098	A	A	
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			C			
GAM1607	MGC20235	3'	CTGTAATCCCAGTACT 58894	G		
			AGTA CTGGGATTACAG			
			TCAT GACCCTAATGTC			
			—			
GAM1607	MGC20235	3'	CTGTAGTCCCAGCTACTCA 58895	C		
			A AGTAGCTGGGATTACAG			
			A TCATCGACCCTGATGTC			
			C			
GAM1607	MGC22805	3'	ATGCCTGTAATCCCAGCTACTT 58080	—	A	
	G		CA GTAGCTGGGATTACAG CAT			
			GT CATCGACCCTAATGTC GTA			
			T C			
GAM1607	MGC2396	3'	ATGCCTGTAATCCCAGCTACT 53460		A	
			AGTAGCTGGGATTACAG CAT			

				TCATCGACCCTAATGTC GTA		
				C		
GAM1607	MGC2562	3'	CTATAATCCCAGCACT	50437	A	C
			AGT GCTGGGATTA AG			
			TCA CGACCCTAAT TC			
			— A			
GAM1607	MGC2562	3'	CTGTAATCCCAGCACT	50438	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	MGC26641	3'	CTGTAATCCCAACTACTCA	58657	C	C
			A AGTAG TGGGATTACAG			
			A TCATC ACCCTAATGTC			
			C A			
GAM1607	MGC2731	3'	ATGCCTGTAATCCCAGCTACT	43948		A
			AGTAGCTGGGATTACAG CAT			
			TCATCGACCCTAATGTC GTA			
			C			
GAM1607	MGC29762	3'	CTGTAATCCCAGCACT	58472	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	MGC29891	3'	CTGTAATCCCAACACT	58204	AGC	
			AGT TGGGATTACAG			
			TCA ACCCTAATGTC			
			CA_			
GAM1607	MGC29891	3'	CTGTAATCCCAGCACT	58205	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	MGC29937	3'	ATGCCTGTAATCCCAGCACT	58110	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			C			
GAM1607	MGC29937	3'	ATGCCTGTAATCCCAGTTACTC	58111	C	A
			A AGTAGCTGGGATTACAG CAT			
			A TCATTGACCCTAATGTC GTA			
			C C			
GAM1607	MGC3207	3'	CTGTAATCCCAGCACT	62558	A	
			AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

GAM1607 MGC39350 3' CTGTAATCCCCAGCACT 58654 A \_  
AGT GCTGGG ATTACAG  
||| ||||| |||||  
TCA CGACCC TAATGTC

— C  
GAM1607 MGC4248 3' CTGTAATCCCAGCACT 50327 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 MGC4663 3' CTATAATCCCAGCACTTTA 44505 C A C  
TA AGT GCTGGGATTA AG  
|| ||| ||||| |||  
AT TCA CGACCCTAAT TC  
T \_ A

GAM1607 MGC5254 3' CTGTAATCCCAGCACT 50410 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 MGC5384 3' ATGCCTGTAATCCCAGCACT 48269 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| ||||| |||  
TCA CGACCCTAATGTC GTA

— C  
GAM1607 MKRN4 3' CTGTAATCCCAGCACT 47746 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 MOST2 5' ATGCCTGTAGTCCCAGCTACTC 39674 C A  
A  
A AGTAGCTGGGATTACAG CAT  
| ||||| ||||| |||  
A TCATCGACCCTGATGTC GTA  
C C

GAM1607 MOST2 5' CTGTAATCCCAGCACT 39684 A  
AGT GCTGGGATTACAG  
||| ||||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 MRP63 3' CTGTAATCCCAACACTTTA 43807 C AGC  
TA AGT TGGGATTACAG  
|| ||| ||||| |||||  
AT TCA ACCCTAATGTC  
T CA\_

GAM1607 MRPL56 3' CTGTAATCCCAACACT 51688 AGC  
AGT TGGGATTACAG  
||| ||||| |||||

			TCA ACCCTAATGTC			
			CA_			
GAM1607	MRPS10	3'	CTGTAATCCCAGCACT	36292	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	MRPS10	3'	GTGCCTGTAATCCCAGCTACTC	36298	C	A
	A		A AGTAGCTGGGATTACAG CAT			
			A TCATCGACCCTAATGTC GTG			
			C C			
GAM1607	MT-ACT48	3'	ATGCCTGTAATCCCAGCACT	24686	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1607	N4BP2	3'	CTGTAATCCCAGCACT	36403	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	NDUFC2	3'	ATGCCTGTAATCCCAGCACT	15825	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1607	NDUFC2	3'	CTGCAATCCCAGCTACTCA	15832	C	A
			A AGTAGCTGGGATT CAG			
			A TCATCGACCCTAA GTC			
			C C			
GAM1607	NMNAT	3'	CTGTAATCCCAGCACT	42956	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	NMT2	3'	CTGTAATCCCAGCACT	16664	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	NPTXR	3'	CTGTAATCCCAGCACT	54178	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	NPTXR	3'	CTGTAATCCCAGCACT	26642	A	
			AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

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      -
GAM1607 OCLM  5' ATGCCTATAATCCCAGCACT 42347  A    C A
      AGT GCTGGGATTA AG CAT
      ||| ||||| || |||
      TCA CGACCCTAAT TC GTA
      -      A C
GAM1607 ORC6L 3' ATGCCTGTAATCCCAGCTCCT 26722  T      A
      AG AGCTGGGATTACAG CAT
      || ||||| |||
      TC TCGACCCTAATGTC GTA
      C      C
GAM1607 ORC6L 3' CTGTAATCCCAGCACT 26724  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC
      -
GAM1607 PAFAH2 3' ATGCCTGTAATCCCAGCACT 4760  A      A
      AGT GCTGGGATTACAG CAT
      ||| ||||| |||
      TCA CGACCCTAATGTC GTA
      -      C
GAM1607 PAFAH2 3' CTATAATCCCAGCTACTCA 4762  C      C
      A AGTAGCTGGGATTA AG
      | ||||| ||
      A TCATCGACCCTAAT TC
      C      A
GAM1607 PB1  3' CTGTAATCCCAGCACT 37021  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC
      -
GAM1607 PDCD7 3' CTGTAATCCCAACACT 72138  AGC
      AGT TGGGATTACAG
      ||| |||||
      TCA ACCCTAATGTC
      CA_
GAM1607 phorbolin-1 3' CTGTAATCCCAGCACT 88778  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC
      -
GAM1607 PILR(ALPHA) 3' CTGTAATCCCAGCTACT 25546
      AGTAGCTGGGATTACAG
      |||||
      TCATCGACCCTAATGTC
      -
GAM1607 PIWIL2 3' CTGTAGTCCCAGCTACTCA 36055  C
      A AGTAGCTGGGATTACAG
      | |||||
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A TCATCGACCCTGATGTC
C
GAM1607 PNPASE 3' ATGCCTGTAATCCTAGCTACTC 70870 C A
A A AGTAGCTGGGATTACAG CAT
I |||||
A TCATCGATCCTAATGTC GTA
C C
GAM1607 POFUT1 3' ATGCCTGTAATCCCAGCACT 70465 A A
AGT GCTGGGATTACAG CAT
||| |||||
TCA CGACCCTAATGTC GTA
C
GAM1607 POLYDOM 3' ATGCCTGTAATTCCAGCTACTC 44424 C A
A A AGTAGCTGGGATTACAG CAT
I |||||
A TCATCGACCTTAATGTC GTA
C C
GAM1607 POLYDOM 3' CTGTAATCCCAGCACT 44425 A
AGT GCTGGGATTACAG
||| |||||
TCA CGACCCTAATGTC
C
GAM1607 PPP1R3B 3' ATGCCTGTAATCCCAGCACT 44815 A A
AGT GCTGGGATTACAG CAT
||| |||||
TCA CGACCCTAATGTC GTA
C
GAM1607 PPP1R3B 3' TGCCTGTAATCCCTGCACT 44826 A T A
AGT GC GGGATTACAG CA
||| || |||||
TCA CG CCCTAATGTC GT
C
GAM1607 PRDM14 3' ATGCCTGTGGTTCCAGCCACTC 44444 C A A
A A AGT GCTGGGATTACAG CAT
I ||| |||||
A TCA CGACCTTGGTGTC GTA
C C C
GAM1607 PRDM14 3' CTGTAATCCCAGCACT 44447 A
AGT GCTGGGATTACAG
||| |||||
TCA CGACCCTAATGTC
C
GAM1607 PRO0038 3' ATGCCTATAATCCCAACACCCT 26090 TAGC_ C A
G CAG TGGGATTA AG CAT
||| ||||| |||
GTC ACCCTAAT TC GTA
CCACA A C
GAM1607 PRO0255 3' CTGTAATCTCAGCACT 26141 A
AGT GCTGGGATTACAG
||| |||||

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TCA CGACTCTAATGTC

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      —
GAM1607 PRO0478 3' ATGCCTGTAATCCCAGCACT 26183  A      A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      —      C
GAM1607 PRO0478 5' CTGTAATCCCAGCACT 26187  A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      —
GAM1607 PRO0478 3' CTGTAATCCCAGCCTG 26188  TA
      CAG GCTGGGATTACAG
      ||| |||||
      GTC CGACCCTAATGTC

      —
GAM1607 PRO0478 5' CTGTAATCCCAGGTACT 26189  G
      AGTA CTGGGATTACAG
      ||| |||||
      TCAT GACCCTAATGTC
      G
GAM1607 PRO0478 3' TGTAATCCCAGCTACTCA 26198  C
      A AGTAGCTGGGATTACA
      | |||||
      A TCATCGACCCTAATGT
      C
GAM1607 PRO0611 3' ATGCCTGTAATCCCAGCACT 26007  A      A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      —      C
GAM1607 PRO0618 3' CTGTAATCCCAGCACTTTA 26200  C  A
      TA AGT GCTGGGATTACAG
      || ||| |||||
      AT TCA CGACCCTAATGTC
      T —
GAM1607 PRO1048 5' TCTGTAATCCCAGCACT 37525  A
      AGT GCTGGGATTACAGA
      ||| |||||
      TCA CGACCCTAATGTCT

      —
GAM1607 PRO1496 3' ATGCCTGTAATCCCAGCACT 37757  A      A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      —      C
GAM1607 PRO1580 5' ATGCCTTGTCCTCCAGCTTCT 37530  T      TAC  A
      AG AGCTGGGAT AG CAT
      || ||||| || |||
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			TC TCGACCCTG TC GTA		
			T T__ C		
GAM1607	PRO1777	3'	ATGCCTGTAATCCCAGCATTCT 37762	TA_	A
	G		CAG GCTGGGATTACAG CAT		
			GTC CGACCCTAATGTC GTA		
			TTA C		
GAM1607	PRO1853	3'	ATGCCTGTAATCCCAGCACT 37771	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1607	PRO2015	3'	CTGTAATCCCAGCACT 37557	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	PRO2198	5'	CTGTAATCCCGGCACT 37791	A	
			AGT GCTGGGATTACAG		
			TCA CGGCCCTAATGTC		
			—		
GAM1607	PRO2730	3'	CTGTAATCCCAGCACT 47415	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	PRO2859	3'	ATGCCTGTAATCCCAGCACT 37614	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1607	PRO2949	3'	ATGCCTGTAATCCCAGCACT 37619	A	A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			— C		
GAM1607	PSR	3'	CTGTAATCCCAGCACT 65180	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	PTD012	3'	ATGCCTATAATCCCAGCACT 25890	A	C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			— A C		
GAM1607	PTK6	3'	ATGCCTGTAATCCCAGCACT 19934	A	A
			AGT GCTGGGATTACAG CAT		



				TCA CGACCCTAATGTC GTA		
				— C		
GAM1607 PTRF	3'	ATGCCTGTAATCCCAGCTACT	63497		A	
		AGTAGCTGGGATTACAG CAT				
		TCATCGACCCTAATGTC GTA				
				C		
GAM1607 RAB4B	5'	ATGCCTGTAATCCCAGCACT	32372	A	A	
		AGT GCTGGGATTACAG CAT				
		TCA CGACCCTAATGTC GTA				
				C		
GAM1607 RAB4B	5'	ATGCCTGTAATCCCAGCTACT	32373		A	
		AGTAGCTGGGATTACAG CAT				
		TCATCGACCCTAATGTC GTA				
				C		
GAM1607 RHOBTB3	3'	CTGTAATCCCAGCTACT	29744			
		AGTAGCTGGGATTACAG				
		TCATCGACCCTAATGTC				
				C		
GAM1607 RNO2	5'	CTGTAATCCCAGCACT	52769	A		
		AGT GCTGGGATTACAG				
		TCA CGACCCTAATGTC				
				C		
GAM1607 RoXaN	3'	ATGCCTGTAATCCCAGC	46632		A	
		GCTGGGATTACAG CAT				
		CGACCCTAATGTC GTA				
				C		
GAM1607 RoXaN	3'	CTATAATCCCAGCACTCTG	46641	TA_	C	
		CAG GCTGGGATTA AG				
		GTC CGACCCTAAT TC				
		TCA A				
GAM1607 RoXaN	3'	TCTGTAATCCCAGCTACTCA	46659	C		
		A AGTAGCTGGGATTACAGA				
		A TCATCGACCCTAATGTCT				
				C		
GAM1607 Rpo1-2	3'	ATGCCTGTAGTTCCAGCTACTC	38697	C	A	
A		A AGTAGCTGGGATTACAG CAT				
		A TCATCGACCTTGATGTC GTA				
				C		
				C		
GAM1607 RRP4	3'	CTATAATCCCAGCACT	26563	A	C	
		AGT GCTGGGATTA AG				

				TCA CGACCCTAAT TC		
				— A		
GAM1607	SAMHD1	3'	ATGCCTGTAATCCCAGCACT	61308	A	A
			AGT GCTGGGATTACAG CAT			
			TCA CGACCCTAATGTC GTA			
			— C			
GAM1607	SC65	3'	CTGTAATCCCAGCACTG	21288	A	
			CAGT GCTGGGATTACAG			
			GTCA CGACCCTAATGTC			
			—			
GAM1607	SCIN	3'	CTGTAATCCCAGCACT	52424	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	SCYA5	3'	CTGTAATCCCAGCTACT	11450		
			AGTAGCTGGGATTACAG			
			TCATCGACCCTAATGTC			
			—			
GAM1607	SEMA3E	3'	CTGTAATCCCAGCACT	24881	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	SEMA5A	3'	ATGCCTATAATCCCAGCACT	14252	A	C A
			AGT GCTGGGATTA AG CAT			
			TCA CGACCCTAAT TC GTA			
			— A C			
GAM1607	SGKL	3'	ATGCCTATAATCCCAGCTACTT	25140	—	C A
	G		CA GTAGCTGGGATTA AG CAT			
			GT CATCGACCCTAAT TC GTA			
			T A C			
GAM1607	SGKL	3'	ATGCCTTTAGTCCCAGCTACTC	25141	C	C A
	A		A AGTAGCTGGGATTA AG CAT			
			A TCATCGACCCTGAT TC GTA			
			C T C			
GAM1607	SGKL	3'	CTGTAATCCCAGCACT	25142	A	
			AGT GCTGGGATTACAG			
			TCA CGACCCTAATGTC			
			—			
GAM1607	SLC7A11	3'	TCTGTAATCATATCTAC	26757	C G	
			GTAG TG GATTACAGA			

			CATC AT CTAATGTCT		
			T A		
GAM1607	SLC7A11	3'	TCTGTAATCCCAGCACT 26758	A	
			AGT GCTGGGATTACAGA		
			TCA CGACCCTAATGTCT		
			—		
GAM1607	SMAP-5	3'	CTGTAATCCCAGCACT 47931	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	SNAPC1	3'	ATGCCTGTAATCCCAGC 11838	A	
			GCTGGGATTACAG CAT		
			CGACCCTAATGTC GTA		
			C		
GAM1607	SPTLC2	3'	ATGCCTGTAATCCCAGCTAC 16797	A	
			GTAGCTGGGATTACAG CAT		
			CATCGACCCTAATGTC GTA		
			C		
GAM1607	SS18L1	3'	CTGTAATCCCAGCACT 65344	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	SS18L1	3'	CTGTAATCCCAGCTACT 65345		
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
			—		
GAM1607	TA-LRRP	3'	ATGCCTATAATCCCAGCACT 31068	A	C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			A C		
			—		
GAM1607	TACTILE	3'	CTGTAATCCCAGCACT 19469	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	THEA	3'	CTGTAATCCCAGCACT 66282	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	TIP47	3'	CTGTAATCCCAGCACT 19479	A	
			AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1607 TMG4 3' ATGCCTGTAATCCCAGCACT 43988 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1607 TRIAD3 3' ATGCCTATAATCCCAGGTACTC 94500 C G C A  
A  
A AGTA CTGGGATTA AG CAT  
| ||| ||||| || |||  
A TCAT GACCCTAAT TC GTA

GAM1607 TRIM38 3' CTGTAATCCCAGAACTATGT 20986 GTAG\_  
ACA CTGGGATTACAG  
||| |||||  
TGT GACCCTAATGTC  
ATCAA

GAM1607 UBF-fl 3' CTGTAATCCCAGCACT 51564 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 VPS4B 3' ATGCCTGTAATCCCAGCACT 16821 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1607 VPS4B 3' TGTAATCCCAGCTACTCA 16826 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1607 WBSCR21 3' CTGTAATCCCAGCTACT 48476  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1607 WBSCR23 3' CTGTAATCCCAGCACT 46759 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 WBSCR23 3' CTGTAATCCCAGCTACT 46760  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1607 WBSCR23 3' GTCTGTAGTCCCAGCTACTCA 46770 C  
A AGTAGCTGGGATTACAGAC  
| |||||

			A TCATCGACCCTGATGTCTG		
			C		
GAM1607	YEA	3'	ATGCCTGTAATCCCAGCTACTT 51528	—	A
	G		CA GTAGCTGGGATTACAG CAT		
			GT CATCGACCCTAATGTC GTA		
			T C		
GAM1607	YME1L1	3'	CTGTAATCCCAGCACT 57778	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	YME1L1	3'	TCTGTAATCCCAGCACT 57781	A	
			AGT GCTGGGATTACAGA		
			TCA CGACCCTAATGTCT		
			—		
GAM1607	YME1L1	3'	CTGTAATCCCAGCACT 26528	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	YME1L1	3'	TCTGTAATCCCAGCACT 26531	A	
			AGT GCTGGGATTACAGA		
			TCA CGACCCTAATGTCT		
			—		
GAM1607	ZAK	3'	CTGTAATCCCAGCACT 56125	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	ZFP106	3'	CTGTAATCCCAGCACT 42466	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	ZFP106	3'	CTGTAATCCCAGCTCT 42467	T	
			AG AGCTGGGATTACAG		
			TC TCGACCCTAATGTC		
			—		
GAM1607	ZIM3	3'	ATGCCTGTAATCCCAGTACT 53536	G	A
			AGTA CTGGGATTACAG CAT		
			TCAT GACCCTAATGTC GTA		
			— C		
GAM1607	ZNF197	3'	ATGCCTGTAATCCCAGCACT 22763	A	A
			AGT GCTGGGATTACAG CAT		

TCA CGACCCTAATGTC GTA  
 — C  
 GAM1607 ZNF197 3' GTAATCCCAGCTACTCA 22766 C  
 A AGTAGCTGGGATTAC  
 | |||||  
 A TCATCGACCCTAATG  
 C  
 GAM1607 ZNF271 3' CTGTAATCCCAACACT 95250 AGC  
 AGT TGGGATTACAG  
 ||| |||||  
 TCA ACCCTAATGTC  
 CA\_  
 GAM1607 ZNF297B 5' ATGCCTATAATCCCAACACTTT 25774 C AGC C A  
 A TA AGT TGGGATTA AG CAT  
 || ||| ||||| || |||  
 AT TCA ACCCTAAT TC GTA  
 T CA\_ A C  
 GAM1607 ZNF297B 5' CTGTAATCCCAGCACT 25781 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 ZNF297B 3' CTGTAATCCCAGCACT 25782 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 ZNF297B 3' CTGTAATCCCAGCTACT 25783  
 AGTAGCTGGGATTACAG  
 |||||  
 TCATCGACCCTAATGTC  
 —  
 GAM1607 ZNF33A 3' ATGCCTGTAATCCCAGCACT 91344 A A  
 AGT GCTGGGATTACAG CAT  
 ||| |||||  
 TCA CGACCCTAATGTC GTA  
 — C  
 GAM1607 ZNF347 3' ATGCCTGTAATCCCAACACT 50845 AGC A  
 AGT TGGGATTACAG CAT  
 ||| |||||  
 TCA ACCCTAATGTC GTA  
 CA\_ C  
 GAM1607 LOC112687 3' CTATAATCCCAGCACT 72859 A C  
 AGT GCTGGGATTA AG  
 ||| ||||| ||  
 TCA CGACCCTAAT TC  
 — A  
 GAM1607 LOC113201 3' ATGCCTATAGTCCCAGCTACT 56549 C A  
 AGTAGCTGGGATTA AG CAT  
 ||||| || |||

		TCATCGACCCTGAT TC GTA		
		A C		
GAM1607	LOC115129 5'	CTATAATCCCAGCACT 73229	A	C
		AGT GCTGGGATTACAG		
		TCA CGACCCTAAT TC		
		— A		
GAM1607	LOC115129 5'	CTGTAATCCCAGCTACT 73231		
		AGTAGCTGGGATTACAG		
		TCATCGACCCTAATGTC		
GAM1607	LOC115129 5'	CTGTAATCCCAGGTACT 73232	G	
		AGTA CTGGGATTACAG		
		TCAT GACCCTAATGTC		
		G		
GAM1607	LOC115273 3'	ATGCCTGTAATCCCAGTTACT 73357		A
		AGTAGCTGGGATTACAG CAT		
		TCATTGACCCTAATGTC GTA		
		C		
GAM1607	LOC115761 3'	ATGCCTGTAATCCCAGCACTGT 91737	A	A
	G	TACAGT GCTGGGATTACAG CAT		
		GTGTCA CGACCCTAATGTC GTA		
		— C		
GAM1607	LOC116228 3'	CTGTAATCCCAGCACT 73798	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC116349 3'	CTGTAATCCCAGCACT 73830	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC119504 5'	ATGCCTGTAATCCCAGCTACT 73989		A
		AGTAGCTGGGATTACAG CAT		
		TCATCGACCCTAATGTC GTA		
		C		
GAM1607	LOC119504 5'	CTGTAATCCCAGCACT 73990	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC122704 3'	CTGTAATCCCAGCACT 74139	A	
		AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

—  
GAM1607 LOC122704 3' TGTAATCCCAGCTACTCA 74145 C  
A AGTAGCTGGGATTACA  
| |||||||||||  
A TCATCGACCCTAATGT  
C

GAM1607 LOC122970 3' CTGTAATCCCAGTACT 74178 G  
AGTA CTGGGATTACAG  
||| |||||||||  
TCAT GACCCTAATGTC

—  
GAM1607 LOC126282 3' CTGTAATCCCAGCACT 74472 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

—  
GAM1607 LOC126282 3' CTGTAATCCCAGCACT 74473 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

—  
GAM1607 LOC127262 3' ATGCCTGTAATCCCAGC 76107 A  
GCTGGGATTACAG CAT  
||||||||| |||  
CGACCCTAATGTC GTA  
C

GAM1607 LOC127428 3' ATGCCTATAATCCCAGCGCT 74662 A C A  
AGT GCTGGGATTACAG CAT  
||| ||||||| || |||  
TCG CGACCCTAAT TC GTA  
A C

—  
GAM1607 LOC130162 3' ATGTCTGTAATCCCAGCACT 74909 A  
AGT GCTGGGATTACAGACAT  
||| |||||||||||  
TCA CGACCCTAATGTCTGTA

—  
GAM1607 LOC130535 3' ATGCCTGTAATCCCAGC 76147 A  
GCTGGGATTACAG CAT  
||||||||| |||  
CGACCCTAATGTC GTA  
C

GAM1607 LOC130535 3' CTGTAGTCCCAGCTACTCA 76151 C  
A AGTAGCTGGGATTACAG  
| |||||||||||  
A TCATCGACCCTGATGTC  
C

GAM1607 LOC130589 3' CTGTAATCCCAGCACT 57132 A  
AGT GCTGGGATTACAG  
||| |||||||||



TCA CGACCCTAATGTC

GAM1607 LOC130951 3' CTGTAATCCCAACACTTTG 57143 TAGC\_  
CAG TGGGATTACAG  
||| |||||  
GTT ACCCTAATGTC  
TCACA

GAM1607 LOC131744 3' ATGCCTGTAATCCCAGCACTGT 75868 A A  
A TACAGT GCTGGGATTACAG CAT  
||||| |||||  
ATGTCA CGACCCTAATGTC GTA

GAM1607 LOC131965 3' ATGCCTGTAATCCCAGCACT 75027 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1607 LOC131965 3' TGTAATCCCAGCTACTCA 75034 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1607 LOC132625 3' ATGCCTGTAATCCCAACACTTT 75898 TAGC\_ A  
GT ACAG TGGGATTACAG CAT  
|||| |||||  
TGTT ACCCTAATGTC GTA  
TCACA C

GAM1607 LOC132625 3' CTGTGTTCCCAGCTACTCA 75906 C T  
A AGTAGCTGGGA TACAG  
| |||||  
A TCATCGACCCT GTGTC  
C T

GAM1607 LOC133926 3' ATGCCTGTAATCCCAGCGCT 75131 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCG CGACCCTAATGTC GTA  
C

GAM1607 LOC134147 3' CTGTAATCCCAGCACT 57161 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC134147 3' GTGCCTGTAATCCCAGCTACTC 57166 C A  
A A AGTAGCTGGGATTACAG CAT  
| |||||  
A TCATCGACCCTAATGTC GTG  
C C

GAM1607 LOC137362 3' ATGCCTGTAATCCCAACACTTT 75263 TAGC\_ A  
G CAG TGGGATTACAG CAT  
||| |||||

		GTT ACCCTAATGTC GTA			
		TCACA C			
GAM1607	LOC138241 3'	CTGTAATCCCAACACT	75308	AGC	
		AGT TGGGATTACAG			
		TCA ACCCTAATGTC			
		CA_			
GAM1607	LOC138428 3'	ATGCCTGTAATCCCTGCTACT	75331	T	A
		AGTAGC GGGATTACAG CAT			
		TCATCG CCCTAATGTC GTA			
		T C			
GAM1607	LOC138428 3'	CTATAATCCCAGCACT	75335	A	C
		AGT GCTGGGATTA AG			
		TCA CGACCCTAAT TC			
		_ A			
GAM1607	LOC143310 3'	CTGTAATCCCAGCACT	76532	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		_			
GAM1607	LOC143888 3'	CTGTAATCCCAGCACT	76659	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		_			
GAM1607	LOC143943 3'	ATGCCTGTAATCCCAGCACT	82994	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		_ C			
GAM1607	LOC144289 3'	CTGTAATCCCAGCTACT	83024		
		AGTAGCTGGGATTACAG			
		TCATCGACCCTAATGTC			
		_			
GAM1607	LOC144289 3'	TCTGTAATCCCAGCACT	83029	A	
		AGT GCTGGGATTACAGA			
		TCA CGACCCTAATGTCT			
		_			
GAM1607	LOC144465 3'	TGTAATCCCAGCTACTCA	76857	C	
		A AGTAGCTGGGATTACA			
		A TCATCGACCCTAATGT			
		C			
GAM1607	LOC144465 3'	ATGCCTGTAATCCCAAACT	76852	AGC	A
		AGT TGGGATTACAG CAT			

			TCA ACCCTAATGTC GTA		
			AA_ C		
GAM1607	LOC144465	3'	ATGCCTGTAATCCCAGCTACT 76853		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1607	LOC144481	3'	ATGCCTGTAATCCCAATACT 83093	GC	A
			AGTA TGGGATTACAG CAT		
			TCAT ACCCTAATGTC GTA		
			A_ C		
GAM1607	LOC144481	3'	ATGCCTGTAATCCCAGCTACT 83094		A
			AGTAGCTGGGATTACAG CAT		
			TCATCGACCCTAATGTC GTA		
			C		
GAM1607	LOC144486	3'	CTGTAATCCCAGCACGCTG 83083	A_	
			CAGT GCTGGGATTACAG		
			GTCG CGACCCTAATGTC		
			CA		
GAM1607	LOC144524	3'	ATGCCTGTAGTCCCAGCTACTT 83121	C	A
	A		A AGTAGCTGGGATTACAG CAT		
			A TCATCGACCCTGATGTC GTA		
			T C		
GAM1607	LOC144817	3'	CTGTAATCCCAGCACT 76967	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			-		
GAM1607	LOC145216	3'	CTGTAATCCCAGCACT 83265	A	
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			-		
GAM1607	LOC145216	3'	CTGTAATCCCAGCTACTCA 83266	C	
			A AGTAGCTGGGATTACAG		
			A TCATCGACCCTAATGTC		
			C		
GAM1607	LOC145231	3'	ATGCCTATAATCCCAGCACT 83278	A	C A
			AGT GCTGGGATTA AG CAT		
			TCA CGACCCTAAT TC GTA		
			- A C		
GAM1607	LOC145231	3'	ATGCCTGTAATCCCAGCACT 83279	A	A
			AGT GCTGGGATTACAG CAT		

TCA CGACCCTAATGTC GTA  
 — C  
 GAM1607 LOC145231 3' ATGCCTGTAATCCCAGCTACTT 83280 — A  
 G CA GTAGCTGGGATTACAG CAT  
 || |||||  
 GT CATCGACCCTAATGTC GTA  
 T C  
 GAM1607 LOC145299 3' CTGTAATCCCAGCACT 83314 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 LOC145333 3' CTGTAATCCCAGCACT 83326 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 LOC145387 3' CTGTAATCCCAGCACT 83354 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 LOC145438 3' ATGCCTGTAGCCCCAGCTACTC 83334 C AT A  
 A A AGTAGCTGGG TACAG CAT  
 | ||||| |||||  
 A TCATCGACCC ATGTC GTA  
 C CG C  
 GAM1607 LOC145438 3' CTGTAATCCCAGCACT 83336 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 LOC145453 3' CTGTAATCTGAGCAC 77140 A G  
 GT GCT GGATTACAG  
 || ||| |||||  
 CA CGA TCTAATGTC  
 — G  
 GAM1607 LOC145482 3' CTGTAATCCCAGCTACT 77229  
 AGTAGCTGGGATTACAG  
 |||||  
 TCATCGACCCTAATGTC  
 —  
 GAM1607 LOC145483 3' CTGTAATCCCAACACT 77242 AGC  
 AGT TGGGATTACAG  
 ||| |||||  
 TCA ACCCTAATGTC  
 CA\_  
 GAM1607 LOC145663 3' CTGTAATCCCAGCAATTG 83413 A  
 CAGT GCTGGGATTACAG  
 |||| |||||

			GTTA CGACCCTAATGTC		
			A		
GAM1607	LOC145757 3'	ATGCCTGTAATCCCAGCACT	77454	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		— C			
GAM1607	LOC145757 3'	GTAGTCCCAGCTACTCA	77470	C	
		A AGTAGCTGGGATTAC			
		A TCATCGACCCTGATG			
		C			
GAM1607	LOC145820 3'	CTGTAATCCCAGCACT	77513	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607	LOC145824 3'	ATGCCTGTAATCCCAGCACT	77523	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		— C			
GAM1607	LOC145955 3'	ATGCCTGTAATCCCAACACT	83588	AGC	A
		AGT TGGGATTACAG CAT			
		TCA ACCCTAATGTC GTA			
		CA_ C			
GAM1607	LOC146059 3'	ATGCCTGTAATCCCAGCACT	77619	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		— C			
GAM1607	LOC146059 3'	TGTAATCCCAGCTACTCA	77623	C	
		A AGTAGCTGGGATTACA			
		A TCATCGACCCTAATGT			
		C			
GAM1607	LOC146229 3'	CTGTAATCCCAGCACTCTG	77751	TA_	
		CAG GCTGGGATTACAG			
		GTC CGACCCTAATGTC			
		TCA			
GAM1607	LOC146272 5'	CTGTAATCCCAGCACT	77787	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607	LOC146332 3'	CTGTAATCCCAACACT	77824	AGC	
		AGT TGGGATTACAG			

			TCA ACCCTAATGTC		
			CA_		
GAM1607	LOC146540	3'	ATGCCTGTAGTCCCAGCTACTC 77970	C	A
	A		A AGTAGCTGGGATTACAG CAT		
			I               III		
			A TCATCGACCCTGATGTC GTA		
			C C		
GAM1607	LOC146540	3'	CTGTAATCCCAGCACT 77974	A	
			AGT GCTGGGATTACAG		
			III		
			TCA CGACCCTAATGTC		
			—		
GAM1607	LOC146667	3'	ATGCCTGTAATCCCAGCACT 83702	A	A
			AGT GCTGGGATTACAG CAT		
			III             III		
			TCA CGACCCTAATGTC GTA		
			C		
			—		
GAM1607	LOC146669	3'	CTGTAATCCAGCACTGTG 78058	A	G
			TACAGT GCTGG ATTACAG		
			GTGTCA CGACC TAATGTC		
			— —		
GAM1607	LOC146713	3'	CTGTAATCCCAGCACT 83725	A	
			AGT GCTGGGATTACAG		
			III		
			TCA CGACCCTAATGTC		
			—		
GAM1607	LOC146723	3'	CTGTAATCCCAGCTACT 78083		
			AGTAGCTGGGATTACAG		
			TCATCGACCCTAATGTC		
			—		
GAM1607	LOC146728	3'	ATGCCTGTGGTCCCAGCTACTC 83746	C	A
	A		A AGTAGCTGGGATTACAG CAT		
			I               III		
			A TCATCGACCCTGGTGTC GTA		
			C C		
GAM1607	LOC146756	3'	CTGTAATCCCAGCACT 83776	A	
			AGT GCTGGGATTACAG		
			III		
			TCA CGACCCTAATGTC		
			—		
GAM1607	LOC146756	3'	CTGTAATCCCAGCACT 83777	A	
			AGT GCTGGGATTACAG		
			III		
			TCA CGACCCTAATGTC		
			—		
GAM1607	LOC146780	3'	ATGCCTGTAATCCCTGCACTTA 83786	C A T	A
			A AGT GC GGGATTACAG CAT		
			I     II           III		

		A TCA CG CCCTAATGTC GTA		
		T _ T C		
GAM1607	LOC146901 3'	ATGCCTATAATCCCAGCTACT 83829		C A
		AGTAGCTGGGATTA AG CAT		
		TCATCGACCCTAAT TC GTA		
		A C		
GAM1607	LOC146901 3'	CTGTAATCCCCGCACT 83839	A T	
		AGT GC GGGATTACAG		
		TCA CG CCCTAATGTC		
		_ C		
GAM1607	LOC146923 3'	CTGTAATCCCAGCACT 78192	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		_		
GAM1607	LOC146975 5'	CTATAATCCCAGCACT 78223	A C	
		AGT GCTGGGATTA AG		
		TCA CGACCCTAAT TC		
		_ A		
GAM1607	LOC147057 3'	ATGCCTGTAATCCCAGCACT 83909	A A	
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		_ C		
GAM1607	LOC147071 3'	CTGTAATCCCAGCACT 72998	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		_		
GAM1607	LOC147599 3'	ATGCCTGTAATCCCAGCACCCCT 84040	TA_ A	
	G	CAG GCTGGGATTACAG CAT		
		GTC CGACCCTAATGTC GTA		
		CCA C		
GAM1607	LOC147660 3'	CTGTAATCCCAGCAC 78392	A	
		GT GCTGGGATTACAG		
		CA CGACCCTAATGTC		
		_		
GAM1607	LOC147664 3'	ATGCCTGTAATCCCAGCTACTT 78403	_ A	
	G	CA GTAGCTGGGATTACAG CAT		
		GT CATCGACCCTAATGTC GTA		
		T C		
GAM1607	LOC147664 3'	CTGTAATCCCAACACT 78408	AGC	
		AGT TGGGATTACAG		

		TCA ACCCTAATGTC		
		CA_		
GAM1607	LOC147669 3'	CTGTAATCCCAGCACT	84061	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC147700 3'	ATGCCTGTAATCCCAGCTACT	59193	A
		AGTAGCTGGGATTACAG CAT		
		TCATCGACCCTAATGTC GTA		
		C		
GAM1607	LOC147700 3'	CTGTAATCCCAACACT	59197	AGC
		AGT TGGGATTACAG		
		TCA ACCCTAATGTC		
		CA_		
GAM1607	LOC147727 5'	CTATAATCCCAGCTACTCA	78467	C
		A AGTAGCTGGGATTA AG		
		A TCATCGACCCTAAT TC		
		C A		
GAM1607	LOC147837 3'	ATGCCTGTAATCCCAGCTACT	78512	A
		AGTAGCTGGGATTACAG CAT		
		TCATCGACCCTAATGTC GTA		
		C		
GAM1607	LOC147837 3'	CTGTAATCCCAGCACT	78515	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC147990 3'	CTGTAATCCCAGCACT	84092	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC147990 3'	CTGTAATCTCAGCTACTCA	84093	C
		A AGTAGCTGGGATTACAG		
		A TCATCGACTCTAATGTC		
		C		
GAM1607	LOC148147 3'	CTGTAATCCCAGCACT	78680	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC148198 3'	ATGCCTGTAATCCCAGCTACT	70676	A
		AGTAGCTGGGATTACAG CAT		



		TCATCGACCCTAATGTC GTA		
		C		
GAM1607	LOC148198 3'	CTGTAATCCCAGCACT 70681	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC148254 3'	TGCCTGTAATCCCTGCACT 78760	A T	A
		AGT GC GGGATTACAG CA		
		TCA CG CCCTAATGTC GT		
		— T C		
GAM1607	LOC148343 3'	TGCCTGTAATCCCCGCACT 78796	A T	A
		AGT GC GGGATTACAG CA		
		TCA CG CCCTAATGTC GT		
		— C C		
GAM1607	LOC148397 3'	ATGCCTGTAATCCTAGCTATT 78812		A
		AGTAGCTGGGATTACAG CAT		
		TTATCGATCCTAATGTC GTA		
		C		
GAM1607	LOC148397 3'	CTGTAATCCCGGCACTGTG 78817	A	
		TACAGT GCTGGGATTACAG		
		GTGTCA CGGCCCTAATGTC		
		—		
GAM1607	LOC148534 3'	ATGCCTGTAATCCCAGCACT 78894	A	A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		C		
GAM1607	LOC148734 3'	CTGTAATCCCAGCACT 78954	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC148749 3'	CTGTAATCCCAGCACT 78960	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC148758 5'	ATGCCTATAATCCCAGCTACTT 78965	—	C A
	G	CA GTAGCTGGGATTA AG CAT		
		GT CATCGACCCTAAT TC GTA		
		T A C		
GAM1607	LOC148758 5'	ATGCCTGTAATCCCAGAACT 78966	AG	A
		AGT CTGGGATTACAG CAT		

TCA GACCCTAATGTC GTA  
 A\_ C  
 GAM1607 LOC148809 3' ATGCCTATAATCCCAGCTTCT 79000 T C A  
 AG AGCTGGGATTA AG CAT  
 || ||||| || |||  
 TC TCGACCCTAAT TC GTA  
 T A C  
 GAM1607 LOC148809 5' CTGTAATCCCAGCACT 79003 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 LOC148918 5' CTGTAATCCCAGCACT 79071 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 LOC148936 3' CTGTAATCCCAGCACT 84290 A  
 AGT GCTGGGATTACAG  
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 TCA CGACCCTAATGTC  
 —  
 GAM1607 LOC148938 3' CTGTAATCCCAGCACT 84270 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 LOC149073 3' CTATAATCCCAGCACT 84324 A C  
 AGT GCTGGGATTA AG  
 ||| ||||| ||  
 TCA CGACCCTAAT TC  
 — A  
 GAM1607 LOC149073 3' GTGCCTGTAATCCCAGCTACTC 84331 C A  
 A A AGTAGCTGGGATTACAG CAT  
 | ||||| |||  
 A TCATCGACCCTAATGTC GTG  
 C C  
 GAM1607 LOC149113 3' CTGTAATCCCAGAACTTTA 79164 C AG  
 TA AGT CTGGGATTACAG  
 || ||| |||||  
 AT TCA GACCCTAATGTC  
 T A\_  
 GAM1607 LOC149113 3' CTGTAATCCCAGCACT 79165 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 LOC149194 5' CTGTAATCCCAGCTACTCA 79225 C  
 A AGTAGCTGGGATTACAG  
 | |||||

A TCATCGACCCTAATGTC  
 C  
 GAM1607 LOC149194 5' GTCTGTAATCCCAGCACT 79229 A  
 AGT GCTGGGATTACAGAC  
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 TCA CGACCCTAATGTCTG  
 —  
 GAM1607 LOC149271 3' CTGTAATCCCAGCACT 79240 A  
 AGT GCTGGGATTACAG  
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 TCA CGACCCTAATGTC  
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 GAM1607 LOC149319 3' GTCTGTAATCCCAGCACT 79301 A  
 AGT GCTGGGATTACAGAC  
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 TCA CGACCCTAATGTCTG  
 —  
 GAM1607 LOC149579 5' CTGTAATCCCAGCACT 71133 A  
 AGT GCTGGGATTACAG  
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 GAM1607 LOC149606 3' GTCTGTAGTCCCAGCTACTCA 79455 C  
 A AGTAGCTGGGATTACAGAC  
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 A TCATCGACCCTGATGTCTG  
 C  
 GAM1607 LOC149628 3' CTATAATCCCAGCTACT 79462 C  
 AGTAGCTGGGATTA AG  
 ||||| ||  
 TCATCGACCCTAAT TC  
 A  
 GAM1607 LOC149628 3' CTGTAATCCCAGCACT 79463 A  
 AGT GCTGGGATTACAG  
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 TCA CGACCCTAATGTC  
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 GAM1607 LOC149668 3' ATGCCTGTAATCCCAGCACT 84534 A A  
 AGT GCTGGGATTACAG CAT  
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 TCA CGACCCTAATGTC GTA  
 C  
 GAM1607 LOC149705 3' CTGTAATCCCAACACTTTG 84623 TAGC\_  
 CAG TGGGATTACAG  
 ||| |||||  
 GTT ACCCTAATGTC  
 TCACA  
 GAM1607 LOC149837 3' TGGAAATCCCAGCTAT 84747 A\_  
 GTAGCTGGGATT CA  
 ||||| ||

		TATCGACCCTAA GT			
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GAM1607	LOC150139 3'	ATGCCTGTAATCCCAGCTG	79584		A
		TAGCTGGGATTACAG CAT			
		GTCGACCCTAATGTC GTA			
		C			
GAM1607	LOC150185 3'	ATGCCTGTAATCCCAACACT	84905	AGC	A
		AGT TGGGATTACAG CAT			
		TCA ACCCTAATGTC GTA			
		CA_ C			
GAM1607	LOC150319 3'	ATGCCTGTAATCCCAGCACT	79647	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		_ C			
GAM1607	LOC150319 3'	ATGCCTGTAATCCCAGTTACTC	79648	C	A
	A	A AGTAGCTGGGATTACAG CAT			
		A TCATTGACCCTAATGTC GTA			
		C C			
GAM1607	LOC150343 3'	CTGTAATCCCAGCACT	79672	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		_			
GAM1607	LOC150358 3'	ATGCCTATAATCCCAGCACT	84920	A	C A
		AGT GCTGGGATTA AG CAT			
		TCA CGACCCTAAT TC GTA			
		_ A C			
GAM1607	LOC150358 3'	ATGCCTGTAATCCCAGCACT	84921	A	A
		AGT GCTGGGATTACAG CAT			
		TCA CGACCCTAATGTC GTA			
		_ C			
GAM1607	LOC150358 3'	CTGTAATCCCAGGTACTCA	84922	C G	
		A AGTA CTGGGATTACAG			
		A TCAT GACCCTAATGTC			
		C G			
GAM1607	LOC150372 3'	ATGCCTGTAATCCCAGC	79786		A
		GCTGGGATTACAG CAT			
		CGACCCTAATGTC GTA			
		C			
GAM1607	LOC150481 3'	CTGTAATCCCAGCACT	79884	A	
		AGT GCTGGGATTACAG			

TCA CGACCCTAATGTC

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      —
GAM1607 LOC150622 3' CTGTAATCCCAACACT   79958   AGC
      AGT TGGGATTACAG
      ||| |||||
      TCA ACCCTAATGTC
      CA_
GAM1607 LOC150630 3' ATGCCTATAATCCCAGCTACT 85099   C A
      AGTAGCTGGGATTA AG CAT
      ||||| |||
      TCATCGACCCTAAT TC GTA
      A C
GAM1607 LOC150630 3' ATGCCTGTAATCCCAGCACT 85100   A   A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      — C
GAM1607 LOC150889 3' ATGCCTGTAATCCCAGCACT 80024   A   A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCA CGACCCTAATGTC GTA
      — C
GAM1607 LOC150935 3' ATGCCTGTAATCCCAGCGCT 80031   A   A
      AGT GCTGGGATTACAG CAT
      ||| |||||
      TCG CGACCCTAATGTC GTA
      — C
GAM1607 LOC150998 3' CTGTGGTCCCAGCTAC   85183
      GTAGCTGGGATTACAG
      |||||
      CATCGACCCTGGTGTC

GAM1607 LOC151196 3' CTGTAACCCCAGCTACTCA 85265   C   A
      A AGTAGCTGGG TTACAG
      | |||||
      A TCATCGACCC AATGTC
      C C
GAM1607 LOC151196 3' CTGTAATCCCAGCACT   85266   A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      —
GAM1607 LOC151248 3' CTGTAATCCCAGCACT   80186   A
      AGT GCTGGGATTACAG
      ||| |||||
      TCA CGACCCTAATGTC

      —
GAM1607 LOC151248 3' TGTAATCCCAGCTACTCA 80193   C
      A AGTAGCTGGGATTACA
      | |||||
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		A TCATCGACCCTAATGT		
		C		
GAM1607	LOC151429 3'	ATGCCTGTAATCCCAGC	85344	A
		GCTGGGATTACAG CAT		
		CGACCCTAATGTC GTA		
		C		
GAM1607	LOC151429 3'	CTGTAATCCCAGCACT	85352	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC151446 3'	ATGCCTGTAATCCCAGCTACTG	85375	A
		CAGTAGCTGGGATTACAG CAT		
		GTCATCGACCCTAATGTC GTA		
		C		
GAM1607	LOC151556 3'	CTGTAATCCCAGTACT	80274	G
		AGTA CTGGGATTACAG		
		TCAT GACCCTAATGTC		
		—		
GAM1607	LOC151556 3'	TGTAATCCCAGCTACTCA	80283	C
		A AGTAGCTGGGATTACA		
		A TCATCGACCCTAATGT		
		C		
GAM1607	LOC151602 3'	CTGTAATCCCAACACT	80294	AGC
		AGT TGGGATTACAG		
		TCA ACCCTAATGTC		
		CA_		
GAM1607	LOC151602 3'	CTGTAATCCCAGCTACTCA	80295	C
		A AGTAGCTGGGATTACAG		
		A TCATCGACCCTAATGTC		
		C		
GAM1607	LOC151614 3'	CTGTAATCCCAGCACT	80304	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC151623 3'	ATGCCTGTGGTCTCAGCTACTC	85456	C
	A	A AGTAGCTGGGATTACAG CAT		A
		A TCATCGACTCTGGTGTC GTA		
		C		
		C		
GAM1607	LOC151904 3'	CTGTAATCCCAGCACT	80390	A
		AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

GAM1607 LOC152263 3' CTGTAATCCCAGCACT 85674 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC152263 3' TCCATAATCCTAGCTGCT 85676 CA  
AGTAGCTGGGATTA GA  
||| ||||| ||  
TCGTCGATCCTAAT CT

AC  
GAM1607 LOC152316 3' ATGCCTGTAATCCCAGCACTTT 85609 C A A  
A TA AGT GCTGGGATTACAG CAT  
|| ||| ||||| |||  
AT TCA CGACCCTAATGTC GTA  
T \_ C

GAM1607 LOC152426 3' CTGTAATCCCAGCACT 85714 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC152445 3' ATGCCTGTAATCCCAACTACT 85746 C A  
AGTAG TGGGATTACAG CAT  
|||| ||||| |||  
TCATC ACCCTAATGTC GTA  
A C

GAM1607 LOC152453 3' ATGCCTGTAATCCCAGCACT 80592 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

C  
GAM1607 LOC152453 3' ATGCCTGTAATCCCAGCTACT 80593 A  
AGTAGCTGGGATTACAG CAT  
||||| ||||| |||  
TCATCGACCCTAATGTC GTA  
C

GAM1607 LOC152453 3' CTGTAATCCCAACACT 80595 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_

GAM1607 LOC152453 3' CTGTAATCCCAGCACT 80596 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC152453 3' CTGTAATCCCAGTTACTCA 80597 C  
A AGTAGCTGGGATTACAG  
| ||||| |||||

		A TCATTGACCCTAATGTC		
		C		
GAM1607	LOC152627 5'	TGTAATCCCAGCTACTCA	80632	C
		A AGTAGCTGGGATTACA		
		A TCATCGACCCTAATGT		
		C		
GAM1607	LOC152804 3'	ATGCCTGTAATCCCAGCTACT	85878	A
		AGTAGCTGGGATTACAG CAT		
		TCATCGACCCTAATGTC GTA		
		C		
GAM1607	LOC152860 3'	ATGTCTGTAATCCCAGCTACTG	80696	
		CAGTAGCTGGGATTACAGACAT		
		GTCATCGACCCTAATGTCTGTA		
GAM1607	LOC152860 3'	CTATAATCCCAGCACT	80701	A C
		AGT GCTGGGATTA AG		
		TCA CGACCCTAAT TC		
		— A		
GAM1607	LOC152926 3'	ATGCCTGTAATCCCAGCACT	80744	A A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
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GAM1607	LOC153077 3'	CTATAATCCCAGCTACTCA	85909	C C
		A AGTAGCTGGGATTA AG		
		A TCATCGACCCTAAT TC		
		C A		
GAM1607	LOC153260 3'	CTGTAATCCCAGCACT	80804	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC153561 3'	ATGCCTGTAATCCCAGCACT	80888	A A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		— C		
GAM1607	LOC153579 3'	CTGTAATCCCAGTACT	80895	G
		AGTA CTGGGATTACAG		
		TCAT GACCCTAATGTC		
		—		
GAM1607	LOC153642 3'	CTATAGTCTCAGCTACTCA	80907	C C
		A AGTAGCTGGGATTA AG		



		A TCATCGACTCTGAT TC		
		C            A		
GAM1607	LOC153642 3'	CTGTAATCCCAGGACT    80908	AG	
		AGT CTGGGATTACAG		
		TCA GACCCTAATGTC		
		G_		
GAM1607	LOC153682 3'	ATGCCTGTAATCCCAGCACT   86084	A	A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		C		
GAM1607	LOC153688 3'	ATGCCTATAATCCCAGCACT   86095	A	C A
		AGT GCTGGGATTA AG CAT		
		TCA CGACCCTAAT TC GTA		
		A C		
GAM1607	LOC154092 3'	TCTGTAATCCCAGCACT    86161	A	
		AGT GCTGGGATTACAGA		
		TCA CGACCCTAATGTCT		
		-		
GAM1607	LOC154215 3'	ATGTCTGTAATATACACACAC   81053	AGC GG_	
		GT TG ATTACAGACAT		
		CA AC TAATGTCTGTA		
		CAC ATA		
GAM1607	LOC154403 3'	CTGTAATCCCAGAACTTTA   81071	C AG	
		TA AGT CTGGGATTACAG		
		AT TCA GACCCTAATGTC		
		T A_		
GAM1607	LOC154739 5'	ATGTCTATAATTCCAGCTACTC   86225	C	C
	A	A AGTAGCTGGGATTA AGACAT		
		A TCATCGACCTTAAT TCTGTA		
		C            A		
GAM1607	LOC154791 3'	ATGCCTGTAATCCCAGCTACT   81154		A
		AGTAGCTGGGATTACAG CAT		
		TCATCGACCCTAATGTC GTA		
		C		
GAM1607	LOC154791 3'	CTGTAATCCCAGCACT    81156	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		-		
GAM1607	LOC154992 3'	CTGTAATCCCAGAACTTTA   81215	C AG	
		TA AGT CTGGGATTACAG		

		AT TCA GACCCTAATGTC		
		T A_		
GAM1607	LOC155006 3'	ATGCCTGTAATCCCAGCACT	81229	A A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		— C		
GAM1607	LOC155006 3'	ATGCCTGTAATCCCAGCACT	81230	A A
		AGT GCTGGGATTACAG CAT		
		TCA CGACCCTAATGTC GTA		
		— C		
GAM1607	LOC155006 3'	CTGTAATCCCAGCTACTTG	81237	—
		CA GTAGCTGGGATTACAG		
		GT CATCGACCCTAATGTC		
		T		
GAM1607	LOC155072 3'	CTGTAATCCCAGCACT	86375	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC155072 3'	CTGTAATCCCAGCACT	86376	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC155438 3'	CTGTAATCCCAGTACCT	86393	TA
		AG GCTGGGATTACAG		
		TC TGACCCTAATGTC		
		CA		
GAM1607	LOC157278 3'	CTGTAATCCCAGCACT	86423	A
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC157292 5'	CTGTAATCTCAGTTACTCA	86413	C
		A AGTAGCTGGGATTACAG		
		A TCATTGACTCTAATGTC		
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GAM1607	LOC157464 5'	CTGTAATCCCAGCACT	86448	A
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		TCA CGACCCTAATGTC		
		—		
GAM1607	LOC157657 3'	ATGCCTGTAATCCCACTACT	81516	C A
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			TCATC ACCCTAATGTC GTA		
			A C		
GAM1607	LOC157657	3'	CTGTAATCCCAGCACT	81518	A
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			TCA CGACCCTAATGTC		
			—		
GAM1607	LOC157660	3'	CTGTAATCCCAGCACT	86507	A
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			TCA CGACCCTAATGTC		
			—		
GAM1607	LOC158160	3'	TGTAGTCCCACTACTCA	73082	C C
			A AGTAG TGGGATTACA		
			A TCATC ACCCTGATGT		
			C A		
GAM1607	LOC158187	3'	CTGTAGTCCCAGCTAC	86691	
			GTAGCTGGGATTACAG		
			CATCGACCCTGATGTC		
			—		
GAM1607	LOC158191	3'	CTGTAATCCCAGCACT	81775	A
			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	LOC158292	5'	ATGCCTGTAATCCCAGCACT	86728	A A
			AGT GCTGGGATTACAG CAT		
			TCA CGACCCTAATGTC GTA		
			C		
			—		
GAM1607	LOC158292	5'	TGTAATCCCAGCTACTCA	86732	C
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			A TCATCGACCCTAATGT		
			C		
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			AGT GCTGGGATTACAG		
			TCA CGACCCTAATGTC		
			—		
GAM1607	LOC158819	3'	CTGTAATCCCAGCACT	86903	A
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			TCA CGACCCTAATGTC		
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GAM1607	LOC158819	5'	CTGTAATCCCAGCACT	86904	A
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TCA CGACCCTAATGTC

—  
GAM1607 LOC158819 5' ATGCCTGTAATCCCAGCTTCT 86901 T A  
AG AGCTGGGATTACAG CAT  
|| |||||  
TC TCGACCCTAATGTC GTA  
T C  
GAM1607 LOC158863 3' CTGTAATCCCAACACT 86923 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_  
GAM1607 LOC158987 3' CTGTAATCCCAACACT 86961 AGC  
AGT TGGGATTACAG  
||| |||||  
TCA ACCCTAATGTC  
CA\_  
GAM1607 LOC159036 3' ATGCCTGTAATCCCAGCACT 86969 A A  
AGT GCTGGGATTACAG CAT  
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TCA CGACCCTAATGTC GTA  
— C  
GAM1607 LOC159053 3' CTGTAATCCCAGGACT 86978 AG  
AGT CTGGGATTACAG  
||| |||||  
TCA GACCCTAATGTC  
G\_  
GAM1607 LOC161823 3' ATGCCTGTAATCCCAGCACT 82300 A A  
AGT GCTGGGATTACAG CAT  
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TCA CGACCCTAATGTC GTA  
— C  
GAM1607 LOC170395 3' CTGCAGTCCCAGCTACTCA 76368 C A  
A AGTAGCTGGGATT CAG  
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C C  
GAM1607 LOC170395 3' CTGTAATCCCAGCACT 76369 A  
AGT GCTGGGATTACAG  
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TCA CGACCCTAATGTC  
—  
GAM1607 LOC196047 5' CTGTAATCCCAGTACT 89600 G  
AGTA CTGGGATTACAG  
||| |||||  
TCAT GACCCTAATGTC  
—  
GAM1607 LOC196528 3' CTATAATCCCAGCACT 87764 A C  
AGT GCTGGGATTA AG  
||| ||||| ||

			TCA CGACCCTAAT TC		
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GAM1607	LOC197196 3'	CTGTAATCCCAGCACT	89733	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607	LOC197201 3'	ATGCCTGTAATCTCAGCTACTC	87933	C	A
	A	A AGTAGCTGGGATTACAG CAT			
		A TCATCGACTCTAATGTC GTA			
		C C			
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		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607	LOC197319 3'	CTGTAATCCCAGCACT	87969	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607	LOC197319 3'	CTGTAATCCCAGCTCCT	87970	T	
		AG AGCTGGGATTACAG			
		TC TCGACCCTAATGTC			
		C			
GAM1607	LOC199733 3'	CTGAAATCCCAGCTACTG	89849		A
		CAGTAGCTGGGATT CAG			
		GTCATCGACCCTAA GTC			
		A			
GAM1607	LOC199786 3'	CTGTAATCCCAGCACT	88380	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607	LOC200014 3'	CTGTAATCCCACCACT	88526	AGC	
		AGT TGGGATTACAG			
		TCA ACCCTAATGTC			
		CC_			
GAM1607	LOC200251 5'	CTGTAATCCCAGCTACTCA	88665	C	
		A AGTAGCTGGGATTACAG			
		A TCATCGACCCTAATGTC			
		C			
GAM1607	LOC200317 3'	CTGTAATCCCAGCTACTTG	88794	_	
		CA GTAGCTGGGATTACAG			

		GT CATCGACCCTAATGTC			
		T			
GAM1607	LOC200470 3'	CTGTAATCCCAACACT	90062	AGC	
		AGT TGGGATTACAG			
		TCA ACCCTAATGTC			
		CA_			
GAM1607	LOC200728 3'	CTGTAATCCCAGCACT	90115	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607	LOC200803 3'	ATGCCTGTAATCCTAGCTACTC	88879	C	A
	A	A AGTAGCTGGGATTACAG CAT			
		A TCATCGATCCTAATGTC GTA			
		C C			
GAM1607	LOC200803 3'	TGCCTGTAATCCCACCACT	88881	AGC	A
		AGT TGGGATTACAG CA			
		TCA ACCCTAATGTC GT			
		CC_ C			
GAM1607	LOC200918 3'	TGTAATCCCAGCTACTTA	88943	C	
		A AGTAGCTGGGATTACA			
		A TCATCGACCCTAATGT			
		T			
GAM1607	LOC200940 3'	ATGCCTGTAATCCCAGCTACTT	88950	—	A
	G	CA GTAGCTGGGATTACAG CAT			
		GT CATCGACCCTAATGTC GTA			
		T C			
GAM1607	LOC201173 3'	CTGTAATCCCAGCACT	87328	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607	LOC201182 5'	ATGCCTGTAATCCCAGCTAC	89763		A
		GTAGCTGGGATTACAG CAT			
		CATCGACCCTAATGTC GTA			
		C			
GAM1607	LOC201220 3'	CTGTAATCCCAGCACT	87349	A	
		AGT GCTGGGATTACAG			
		TCA CGACCCTAATGTC			
		—			
GAM1607	LOC201252 3'	ATGCCTGTAATCCCAACTACT	88165	C	A
		AGTAG TGGGATTACAG CAT			

		TCATC ACCCTAATGTC GTA		
		A C		
GAM1607	LOC201252 3'	CTGTAATCCCAGAACT 88168	AG	
		AGT CTGGGATTACAG		
		TCA GACCCTAATGTC		
		A_		
GAM1607	LOC201564 3'	ATGCCTGTAATCCCAGCTACTT 80435	_	A
	G	CA GTAGCTGGGATTACAG CAT		
		GT CATCGACCCTAATGTC GTA		
		T C		
GAM1607	LOC201685 3'	ATGTCTATGGTCCCAGCTACTC 90239	C	C
	A	A AGTAGCTGGGATTA AGACAT		
		A TCATCGACCCTGGT TCTGTA		
		C A		
GAM1607	LOC201685 3'	CTGTAATCCCAGCACT 90241	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		-		
GAM1607	LOC201689 3'	CTGTAATCCCAGCACT 67144	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		-		
GAM1607	LOC201868 3'	TGTAATCCCAGCTACTCA 89084	C	
		A AGTAGCTGGGATTACA		
		A TCATCGACCCTAATGT		
		C		
GAM1607	LOC201868 3'	CTGTAATCCCAGCACT 89077	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		-		
GAM1607	LOC201895 3'	CTGTAATCCCAGCACT 89087	A	
		AGT GCTGGGATTACAG		
		TCA CGACCCTAATGTC		
		-		
GAM1607	LOC201895 3'	GTGCCTGTAATCCCAGCTACTC 89091	C	A
	A	A AGTAGCTGGGATTACAG CAT		
		A TCATCGACCCTAATGTC GTG		
		C C		
GAM1607	LOC201911 3'	CTGTAATCCCAGCACT 90261	A	
		AGT GCTGGGATTACAG		

TCA CGACCCTAATGTC

—  
GAM1607 LOC202868 3' CTGTAATCCCAGCACT 90373 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

—  
GAM1607 LOC202868 3' CTGTAATCCCAGCACT 90374 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

—  
GAM1607 LOC203025 3' ATGCCTGTAATCCCAACACTTT 89249 TAGC\_ A  
G CAG TGGGATTACAG CAT  
||| ||||||||| |||  
GTT ACCCTAATGTC GTA  
TCACA C

GAM1607 LOC203246 3' CTGTAATCCCAGCACT 89304 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGACCCTAATGTC

—  
GAM1607 LOC203276 3' GTCTATAATTCCAGCTACTCA 90487 C C  
A AGTAGCTGGGATTA AGAC  
| ||||||||| |||  
A TCATCGACCTTAAT TCTG  
C A

GAM1607 LOC203305 3' GTCTATAATTCCAGCTACTCA 90531 C C  
A AGTAGCTGGGATTA AGAC  
| ||||||||| |||  
A TCATCGACCTTAAT TCTG  
C A

GAM1607 LOC203350 3' ATGCCTGTAATCCCAGCACT 90560 A A  
AGT GCTGGGATTACAG CAT  
||| ||||||||| |||  
TCA CGACCCTAATGTC GTA  
C

—  
GAM1607 LOC203350 3' ATGCCTGTAGTTGCAGCTACTC 90561 C G A  
A A AGTAGCTG GATTACAG CAT  
| ||||| ||||||| |||  
A TCATCGAC TTGATGTC GTA  
C G C

GAM1607 LOC203378 3' CTGTAATCCCGGCACT 90602 A  
AGT GCTGGGATTACAG  
||| |||||||||  
TCA CGGCCCTAATGTC

—  
GAM1607 LOC203378 3' CTGTAGTTCCAGCTACTG 90603  
CAGTAGCTGGGATTACAG  
|||||||||||



GTCATCGACCTTGATGTC

GAM1607 LOC219406 3' CTGCAATCCCAGCTACT 93559 A  
AGTAGCTGGGATT CAG  
||||||| |||  
TCATCGACCCTAA GTC

C

GAM1607 LOC219406 3' CTGTAATCCCAGCACT 93560 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC219540 3' CTGTAATCCCAGCTACTTG 93598 \_  
CA GTAGCTGGGATTACAG  
|| |||||  
GT CATCGACCCTAATGTC  
T

GAM1607 LOC219627 3' ATGCCTGTAATCCCAACACT 92175 AGC A  
AGT TGGGATTACAG CAT  
||| ||||| |||  
TCA ACCCTAATGTC GTA  
CA\_ C

GAM1607 LOC219627 3' CTGTAATCCCAGCACT 92177 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC219627 3' GTGCCTGTAATCCCAGCTACTC 92185 C A  
A  
A AGTAGCTGGGATTACAG CAT  
| ||||| |||  
A TCATCGACCCTAATGTC GTG  
C C

GAM1607 LOC219649 3' ATGCCTATAATCCCAGC 92950 C A  
GCTGGGATTA AG CAT  
|||||| |||  
CGACCCTAAT TC GTA  
A C

GAM1607 LOC219649 3' CTGTAATCCCAGCTACT 92956  
AGTAGCTGGGATTACAG  
|||||||  
TCATCGACCCTAATGTC

GAM1607 LOC219649 3' GTCTGTAATCCCAGCACT 92961 A  
AGT GCTGGGATTACAGAC  
||| |||||  
TCA CGACCCTAATGTCTG

GAM1607 LOC219672 5' ATGCCTGTAATCCCAGCACT 91328 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||

TCA CGACCCTAATGTC GTA  
 — C  
 GAM1607 LOC219673 3' CTGTAATCCCAGCACT 93031 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC

—  
 GAM1607 LOC219722 5' CTGTAATCCCAGCACT 93081 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC

—  
 GAM1607 LOC220370 3' ATGCCTGTAATCCCAACACTCT 92824 T C\_\_ A  
 G CAG AG TGGGATTACAG CAT  
 ||| || ||||| |||  
 GTC TC ACCCTAATGTC GTA  
 — ACA C

GAM1607 LOC220506 3' CTATAATCCCAGCACTTTA 74077 C A C  
 TA AGT GCTGGGATTA AG  
 || ||| ||||| ||  
 AT TCA CGACCCTAAT TC  
 T \_ A

GAM1607 LOC220662 3' CTGTAATCCCAGCTACTTG 91171 \_  
 CA GTAGCTGGGATTACAG  
 || |||||  
 GT CATCGACCCTAATGTC  
 T

GAM1607 LOC220662 3' CTGTCATCCCAGCTACTCA 91172 C T  
 A AGTAGCTGGGAT ACAG  
 | ||||| |||  
 A TCATCGACCCTA TGTC  
 C C

GAM1607 LOC220662 3' CTGTAATCCCAGCACT 91169 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC

—  
 GAM1607 LOC220662 3' CTGTAATCCCAGCACT 91170 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC

—  
 GAM1607 LOC220906 3' ATGCCTGTAATCCCAACACT 91396 AGC A  
 AGT TGGGATTACAG CAT  
 ||| ||||| |||  
 TCA ACCCTAATGTC GTA  
 CA\_ C

GAM1607 LOC221042 3' CTGTAATCCCAGCGCT 93185 A  
 AGT GCTGGGATTACAG  
 ||| |||||

TCG CGACCCTAATGTC

—  
GAM1607 LOC221178 3' ATGCCTGTAATCCCAGCACT 93527 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

— C  
GAM1607 LOC221178 3' ATGCCTGTAATCCCAGCTACTG 93528 A  
CAGTAGCTGGGATTACAG CAT  
|||||  
GTCATCGACCCTAATGTC GTA

C  
GAM1607 LOC221271 3' CTGTAATCCCAGCACT 91856 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 LOC221271 3' CTGTAATCCCAGCTACT 91857  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1607 LOC221474 3' CTGTAATCCCAGCACT 92381 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 LOC221474 3' TGTAATCCCAGCTACTCA 92389 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1607 LOC221477 3' CTGTAATCCCAGCTAC 92152  
GTAGCTGGGATTACAG  
|||||  
CATCGACCCTAATGTC

GAM1607 LOC221489 3' CTGTAATCCCAGCACT 93641 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 LOC221490 3' CTGTAATCCCAGCACT 93658 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 LOC221543 3' CTGTAATCCCAGCACT 93740 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1607 LOC221543 5' CTGTAATCCCAGCACTCTG 93741 TA\_ —  
CAG GCTGGGATTACAG  
||| |||||  
GTC CGACCCTAATGTC  
TCA

GAM1607 LOC221931 3' ATGCCTGTAATCCCAGCACT 93993 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1607 LOC221954 5' CTGTAATCCCAGCACT 94000 A C —  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC221962 3' CTGTAATCCCAGCACT 92681 A —  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC222066 3' CTGTAATCCCAGCTATT 92744 —  
AGTAGCTGGGATTACAG  
|||||  
TTATCGACCCTAATGTC

GAM1607 LOC222160 5' ATGCCTGTAATCCCAGCACT 94118 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA

GAM1607 LOC222160 3' CTGTAATCCCAGCTACT 94125 C —  
AGTAGCTGGGATTACAG  
|||||  
TCATCGACCCTAATGTC

GAM1607 LOC222182 3' CTGTAATCCCTTAGCTACTCA 94189 C —  
A AGTAGCT GGGATTACAG  
| ||||| |||||  
A TCATCGA CCCTAATGTC  
C TT

GAM1607 LOC222865 3' CTGTAATCCCAGCACT 92860 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC253612 3' CTGTAATCCCAACACT 96748 AGC —  
AGT TGGGATTACAG  
||| |||||

	TCA ACCCTAATGTC		
	CA_		
GAM1607 LOC253612 3'	GTCTGTAATCCCAGCTACT 96755		
	AGTAGCTGGGATTACAGAC		
	TCATCGACCCTAATGTCTG		
GAM1607 LOC253639 3'	ATGCCTGTAATCCCAGCTACT 95818		A
	AGTAGCTGGGATTACAG CAT		
	TCATCGACCCTAATGTC GTA		
	C		
GAM1607 LOC253927 3'	ATGCCTGTAATCCCAGCACT 95023	A	A
	AGT GCTGGGATTACAG CAT		
	TCA CGACCCTAATGTC GTA		
	C		
GAM1607 LOC254045 3'	ATGCCTGTAATCCCAATACT 96502	GC	A
	AGTA TGGGATTACAG CAT		
	TCAT ACCCTAATGTC GTA		
	A_ C		
GAM1607 LOC254045 3'	ATGCCTGTAATCCCAGCTACT 96503		A
	AGTAGCTGGGATTACAG CAT		
	TCATCGACCCTAATGTC GTA		
	C		
GAM1607 LOC254243 3'	GTCTATAATTCCAGCTACTCA 97416	C	C
	A AGTAGCTGGGATTA AGAC		
	A TCATCGACCTTAAT TCTG		
	C A		
GAM1607 LOC254249 5'	TGCTTGTCCCAGCTACTG 95449		TAC A
	CAGTAGCTGGGAT AG CA		
	GTCATCGACCCTG TC GT		
	T_ _		
GAM1607 LOC254531 5'	ATGCCTGTAATCCCAGCTACTT 94980	_	A
G	CA GTAGCTGGGATTACAG CAT		
	GT CATCGACCCTAATGTC GTA		
	T C		
GAM1607 LOC254531 5'	CTGTAATCCCAGCACT 94985	A	
	AGT GCTGGGATTACAG		
	TCA CGACCCTAATGTC		
	_		
GAM1607 LOC255042 3'	ATGCCTGTAATCCTAGCTACTC 95312	C	A
A	A AGTAGCTGGGATTACAG CAT		

			A	TCATCGATCCCTAATGTC	GTA			
		C		C				
GAM1607	LOC255042	3'	CTGTAATCCCAGCACT	95315	A			
			AGT GCTGGGATTACAG					
			TCA CGACCCTAATGTC					
			-					
GAM1607	LOC255042	3'	CTGTAATCCCAGCACT	95316	A			
			AGT GCTGGGATTACAG					
			TCA CGACCCTAATGTC					
			-					
GAM1607	LOC255177	3'	CTGTAATCCCAGCACT	96605	A			
			AGT GCTGGGATTACAG					
			TCA CGACCCTAATGTC					
			-					
GAM1607	LOC255196	3'	ATGCCTATAATCCCAGCACT	97164	A		C	A
			AGT GCTGGGATTA AG CAT					
			TCA CGACCCTAAT TC GTA					
			-					
			A C					
GAM1607	LOC255196	5'	CTGTAATCCCAGCACT	97169	A			
			AGT GCTGGGATTACAG					
			TCA CGACCCTAATGTC					
			-					
GAM1607	LOC255231	3'	CTGTAATCCCAGCACT	95373	A			
			AGT GCTGGGATTACAG					
			TCA CGACCCTAATGTC					
			-					
GAM1607	LOC255252	3'	ATGCCTATAATCCCAGCACT	95006	A		C	A
			AGT GCTGGGATTA AG CAT					
			TCA CGACCCTAAT TC GTA					
			-					
			A C					
GAM1607	LOC255326	3'	CTGTAATCCCAGACTGTG	96376	AG			
			TACAGT CTGGGATTACAG					
			GTGTCA GACCCTAATGTC					
			-					
GAM1607	LOC255328	3'	ATGTCTGTAATCCCAGCACT	96557	A			
			AGT GCTGGGATTACAGACAT					
			TCA CGACCCTAATGTCTGTA					
			-					
GAM1607	LOC255461	3'	CTGTAATCCCAGCACT	97319	A			
			AGT GCTGGGATTACAG					

TCA CGACCCTAATGTC

GAM1607 LOC255516 3' CTGTAATCCCAGCACT 97332 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC255624 3' CTGTAATCCCAGCACT 94523 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC255671 3' CTGTAATCCCAGCTGCT 97255  
AGTAGCTGGGATTACAG  
|||||  
TCGTCGACCCTAATGTC

GAM1607 LOC255671 3' TCTGTAATCCCAGCACT 97264 A  
AGT GCTGGGATTACAGA  
||| |||||  
TCA CGACCCTAATGTCT

GAM1607 LOC255937 3' ATGCCTGTAATCCCAGCTACT 95987 A  
AGTAGCTGGGATTACAG CAT  
|||||  
TCATCGACCCTAATGTC GTA  
C

GAM1607 LOC255937 3' CTGTAATCCCAGCTCT 95988 T  
AG AGCTGGGATTACAG  
|| |||||  
TC TCGACCCTAATGTC

GAM1607 LOC255971 3' CTATAATCCCAGCACT 96533 A C  
AGT GCTGGGATTA AG  
||| |||||  
TCA CGACCCTAAT TC

GAM1607 LOC256073 3' CTGTAATCCCAATGCT 96664 GC  
AGTA TGGGATTACAG  
||| |||||  
TCGT ACCCTAATGTC  
A\_

GAM1607 LOC256207 3' TCTGTAATTGCTATTG 95179 TGG  
CAGTAGC GATTACAGA  
||||| |||||  
GTTATCG TTAATGTCT

GAM1607 LOC256267 3' ATGCCTGTAATCCCAGCACT 96797 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||

TCA CGACCCTAATGTC GTA  
 — C  
 GAM1607 LOC256277 3' CTGTAATCCCAGCACT 94698 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC

—  
 GAM1607 LOC256520 3' TGTAATCCCAGCTACTCA 95981 C  
 A AGTAGCTGGGATTACA  
 | |||||  
 A TCATCGACCCTAATGT  
 C

GAM1607 LOC256980 3' TCTGTAATCCCAGCACTCTG 95223 TA\_  
 CAG GCTGGGATTACAGA  
 ||| |||||  
 GTC CGACCCTAATGTCT  
 TCA

GAM1607 LOC257354 3' ATGCCTATAATCCCAACACT 95085 AGC C A  
 AGT TGGGATTA AG CAT  
 ||| ||||| |||  
 TCA ACCCTAAT TC GTA  
 CA\_ A C

GAM1607 LOC257480 3' CTGTAATCCCAGCACT 77869 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC

—  
 GAM1607 LOC257539 3' ATGCCTGTAATCCCAGCACT 97699 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||  
 TCA CGACCCTAATGTC GTA  
 C

— C  
 GAM1607 LOC257578 3' ATGCCTGTAATCCCAGCACT 97819 A A  
 AGT GCTGGGATTACAG CAT  
 ||| ||||| |||  
 TCA CGACCCTAATGTC GTA  
 C

— C  
 GAM1607 LOC257596 3' CTGTAATCCCAGCACT 97933 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC

—  
 GAM1607 LOC257596 5' CTGTAATCCCAGCACTCTG 97934 TA\_  
 CAG GCTGGGATTACAG  
 ||| |||||  
 GTC CGACCCTAATGTC  
 TCA

GAM1607 LOC51145 3' TGTAATCCCAGCTACTCA 32400 C  
 A AGTAGCTGGGATTACA  
 | |||||



			A	TCATCGACCCTAATGT C			
GAM1607	LOC51333	3'	CTGTAATCCCAGCACT	33567	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			-				
GAM1607	LOC51333	3'	CTGTAATCCCAGCTACTG	33568			
			CAGTAGCTGGGATTACAG				
			GTCATCGACCCTAATGTC				
GAM1607	LOC51652	3'	ATGCCTATAATCCCAGTGCT	32191	G	C	A
			AGTA CTGGGATTA AG CAT				
			TCGT GACCCTAAT TC GTA				
			- A C				
GAM1607	LOC51716	3'	TGCCTGTAATCCCTGC	32795	T	A	
			GC GGGATTACAG CA				
			CG CCCTAATGTC GT				
			T C				
GAM1607	LOC51759	3'	ATGCCTGTAATCCCAGCTGCT	72812			A
			AGTAGCTGGGATTACAG CAT				
			TCGTCGACCCTAATGTC GTA				
			C				
GAM1607	LOC55974	3'	ATGCCTGTAATCCCAGATACT	38130	G		A
			AGTA CTGGGATTACAG CAT				
			TCAT GACCCTAATGTC GTA				
			A C				
GAM1607	LOC55974	3'	CTGTAATCCCAGCACT	38131	A		
			AGT GCTGGGATTACAG				
			TCA CGACCCTAATGTC				
			-				
GAM1607	LOC57118	3'	CTGTAATCCCAACACT	39867	AGC		
			AGT TGGGATTACAG				
			TCA ACCCTAATGTC				
			CA_				
GAM1607	LOC63929	3'	ATGCCTGTAATCCTGGCTACT	42041	TG		A
			AGTAGC GGATTACAG CAT				
			TCATCG CCTAATGTC GTA				
			GT C				
GAM1607	LOC64167	3'	CTGTAATCCCAGCACT	42279	A		
			AGT GCTGGGATTACAG				

TCA CGACCCTAATGTC

—  
GAM1607 LOC89890 3' CTGTAATCCCAGCTAC 60578  
GTAGCTGGGATTACAG  
|||||||  
CATCGACCCTAATGTC

GAM1607 LOC90038 3' GTCTATAATTCCAGCTACTCA 61159 C C  
A AGTAGCTGGGATTA AGAC  
| |||||  
A TCATCGACCTTAAT TCTG  
C A

GAM1607 LOC90092 3' CTGTAATCCCAGCACT 61405 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 LOC90092 3' CTGTAATCCCAGCACT 61406 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 LOC90141 3' ATGCCTACAATCCCAGCACT 61625 A AC A  
AGT GCTGGGATT AG CAT  
||| ||||| || |||  
TCA CGACCCTAA TC GTA  
CA C

—  
GAM1607 LOC90155 5' ATGCCTGTAATCCCAGCACT 61691 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA  
C

—  
GAM1607 LOC90321 3' ATGCCTATAATCTCAGCAC 62260 A C A  
GT GCTGGGATTA AG CAT  
|| ||||| || |||  
CA CGACTCTAAT TC GTA  
A C

—  
GAM1607 LOC90321 3' ATGCCTGCAATCCCAGCTACT 62261 A A  
AGTAGCTGGGATT CAG CAT  
||||||| ||| |||  
TCATCGACCCTAA GTC GTA  
C C

GAM1607 LOC90408 5' ATGCCTGTAATCCCAGCACT 62656 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

—  
GAM1607 LOC90509 3' CTGTAATCCCAGCACT 63104 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1607 LOC90538 3' TCTGTAATCCCAGCACT 63196 A  
AGT GCTGGGATTACAGA  
||| |||||  
TCA CGACCCTAATGTCT

GAM1607 LOC90580 3' ATGTCTGTAATCCCAGC 63371  
GCTGGGATTACAGACAT  
|||||||  
CGACCCTAATGTCTGTA

GAM1607 LOC90591 3' ATGCCTGTAATCCCAGCTACAT 63414 \_ A  
G CA GTAGCTGGGATTACAG CAT  
|| |||||  
GT CATCGACCCTAATGTC GTA  
A C

GAM1607 LOC90591 3' CTGTAATCCCAGCACT 63423 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC90591 3' CTGTAATCCCAGCACT 63424 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC90624 3' CTGTAATCCCGCACT 63603 A T  
AGT GC GGGATTACAG  
||| || |||||  
TCA CG CCCTAATGTC

GAM1607 LOC90639 3' CTGCAATCCCAGCACTTTA 63656 C A A  
TA AGT GCTGGGATT CAG  
|| ||| |||||  
AT TCA CGACCCTAA GTC  
T \_ C

GAM1607 LOC90777 3' CTATAATCTCAGCAC 63967 A C  
GT GCTGGGATTA AG  
|| |||||  
CA CGACTCTAAT TC

GAM1607 LOC90918 5' ATGCCTGTAATCCCAGCTACT 64350 A  
AGTAGCTGGGATTACAG CAT  
|||||||  
TCATCGACCCTAATGTC GTA  
C

GAM1607 LOC90979 3' CTGTAATCCCAGCACT 64526 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

GAM1607 LOC90982 5' ATGTCTCTTTCCAGCTCT 64537 T TTAC  
AG AGCTGGGA AGACAT  
|| ||||| |||||  
TC TCGACCTT TCTGTA

TC\_\_  
GAM1607 LOC91035 3' CTATAATCCCAGCACT 64669 A C  
AGT GCTGGGATTA AG  
||| ||||| |||  
TCA CGACCCTAAT TC

A  
GAM1607 LOC91056 3' ATGCCTGTAATCCCAGCACT 94756 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGACCCTAATGTC GTA

C  
GAM1607 LOC91250 5' CTGTAATCCCAGTTACT 65323  
AGTAGCTGGGATTACAG  
|||||  
TCATTGACCCTAATGTC

GAM1607 LOC91250 5' TCTGTAATCCCCGCACT 65330 A T  
AGT GC GGGATTACAGA  
||| || |||||  
TCA CG CCCTAATGTCT  
C

GAM1607 LOC91286 3' ATGCCTGTAATCCTAGCCACT 65451 A A  
AGT GCTGGGATTACAG CAT  
||| ||||| |||  
TCA CGATCCTAATGTC GTA  
C C

GAM1607 LOC91380 3' CTGTAATCCCAACTAC 65860 C  
GTAG TGGGATTACAG  
||| |||||  
CATC ACCCTAATGTC  
A

GAM1607 LOC91380 3' TGCCTGTAATCCCGGCACT 65864 A A  
AGT GCTGGGATTACAG CA  
||| ||||| |||  
TCA CGGCCCTAATGTC GT  
C

GAM1607 LOC91380 3' TGTAATCCCAGCTACTCA 65865 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1607 LOC91574 3' TCTGTAATCCCAGCACT 66521 A  
AGT GCTGGGATTACAGA  
||| |||||

TCA CGACCCTAATGTCT

GAM1607 LOC91664 3' CTGTAATCCCAGCACT 66872 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC91750 3' CTGTAATCCCAGCACT 67061 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC91796 5' ATGCCTGTAATCCCAGCACT 67210 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
C

GAM1607 LOC91812 3' GTGCCTGTAATCCCAGCTACTC 67242 C A  
A A AGTAGCTGGGATTACAG CAT  
| |||||  
A TCATCGACCCTAATGTC GTG  
C C

GAM1607 LOC91813 3' GTGCCTGTAATCCCAGCTACTC 67259 C A  
A A AGTAGCTGGGATTACAG CAT  
| |||||  
A TCATCGACCCTAATGTC GTG  
C C

GAM1607 LOC91963 5' CTGTAATCCCAGCTACTTG 67694 \_  
CA GTAGCTGGGATTACAG  
|| |||||  
GT CATCGACCCTAATGTC  
T

GAM1607 LOC92078 3' CTATAATCCCAGCACT 67980 A C  
AGT GCTGGGATTA AG  
||| |||||  
TCA CGACCCTAAT TC  
A

GAM1607 LOC92078 3' TGTAATCCCAACTACTCA 67990 C C  
A AGTAG TGGGATTACA  
| |||||  
A TCATC ACCCTAATGT  
C A

GAM1607 LOC92228 3' CTGTAATCCCAGCACT 68541 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

GAM1607 LOC92267 3' CTGTAATCCCAGCACT 68613 A  
AGT GCTGGGATTACAG  
||| |||||

TCA CGACCCTAATGTC

—  
GAM1607 LOC92270 5' CTGTAATCCCAGCACT 68630 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 LOC92270 5' TGTAATCCCAGCTACTCA 68637 C  
A AGTAGCTGGGATTACA  
| |||||  
A TCATCGACCCTAATGT  
C

GAM1607 LOC92283 3' ATGCCTGTAATCCCAGCACT 68744 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
C

—  
GAM1607 LOC92299 3' CTGTAATCCCAGCACT 68809 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 LOC92405 3' ATGTCTGTAATCCCAGCTACT 69192  
AGTAGCTGGGATTACAGACAT  
|||||  
TCATCGACCCTAATGTCTGTA

GAM1607 LOC92421 3' ATGCCTATAATCCCAGCACT 69212 A C A  
AGT GCTGGGATTA AG CAT  
||| ||||| ||  
TCA CGACCCTAAT TC GTA  
A C

—  
GAM1607 LOC92465 5' ATGCCTGTAATCCCAGCACT 69402 A A  
AGT GCTGGGATTACAG CAT  
||| |||||  
TCA CGACCCTAATGTC GTA  
C

—  
GAM1607 LOC92465 3' ATGTCTGTAGTCCCAGCCACTC 69403 C A  
A A AGT GCTGGGATTACAGACAT  
| ||| |||||  
A TCA CGACCCTGATGTCTGTA  
C C

GAM1607 LOC92465 3' CTGTAATCCCAGCACT 69406 A  
AGT GCTGGGATTACAG  
||| |||||  
TCA CGACCCTAATGTC

—  
GAM1607 LOC92465 5' TGTAATCCCAGCTACTCA 69415 C  
A AGTAGCTGGGATTACA  
| |||||

A TCATCGACCCTAATGT  
 C  
 GAM1607 LOC92466 3' ATGCCTGTAATCCCAGCACT 69422 A A  
 AGT GCTGGGATTACAG CAT  
 ||| |||||  
 TCA CGACCCTAATGTC GTA  
 — C  
 GAM1607 LOC92482 3' CTGTAATCCCAGCACT 69488 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 LOC92573 5' CTGTAATCCCAGCACT 69805 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 LOC92573 5' TCTGTAATCCCAGCTTCT 69811 T  
 AG AGCTGGGATTACAGA  
 || |||||  
 TC TCGACCCTAATGTCT  
 T  
 GAM1607 LOC92661 5' ATGCCTATAATCCCAGC 70078 C A  
 GCTGGGATTA AG CAT  
 ||||| || |||  
 CGACCCTAAT TC GTA  
 A C  
 GAM1607 LOC92771 3' TGTAATCCCAGCTACTCA 53078 C  
 A AGTAGCTGGGATTACA  
 | |||||  
 A TCATCGACCCTAATGT  
 C  
 GAM1607 LOC93132 5' CTGTAATCCCAGCACT 71488 A  
 AGT GCTGGGATTACAG  
 ||| |||||  
 TCA CGACCCTAATGTC  
 —  
 GAM1607 LOC93613 3' ATGCCTGTAATCCCAGCACT 72694 A A  
 AGT GCTGGGATTACAG CAT  
 ||| |||||  
 TCA CGACCCTAATGTC GTA  
 — C  
 GAM1607 LOC93613 3' CTGTAATCCCAGCTATT 72698  
 AGTAGCTGGGATTACAG  
 |||||  
 TTATCGACCCTAATGTC  
 —  
 GAM1607 LOC96597 5' CTGTAATCCCAGCTACTCA 66913 C  
 A AGTAGCTGGGATTACAG  
 | |||||

A TCATCGACCCTAATGTC  
 C  
 GAM1608 CDH10 3' TAGTTCTCCCTTAAGCAACCT 22058 CG CAGTGT A  
 AGG GCT GA GAACTA  
 ||| ||| || |||||  
 TCC CGA CT CTTGAT  
 AA ATTCC\_ \_  
 GAM1608 DACH 3' TAGTTCTTCCATAACCACCT 54971 C CTCA T  
 AGG GG GTG GAAGAACTA  
 ||| || ||| |||||  
 TCC CC TAC CTTCTTGAT  
 A AA\_ \_  
 GAM1608 HPS1 3' TCTTCCAGAGCTGCCT 3969 AG T  
 AGGCGGCTC TG GAAGA  
 ||||| || |||||  
 TCCGTCGAG AC CTTCT  
 \_ \_  
 GAM1608 PCK1 5' TCTTCAGGCTGCCT 52264 CAGTG  
 AGGCGGCT TGAAGA  
 ||||| |||||  
 TCCGTCGG ACTTCT  
 \_ \_  
 GAM1608 RORB 5' AGCTCTTCGCCGACCACCT 22606 C C AGT A  
 AGG GG TC GTGAAGA CT  
 ||| || ||||| ||  
 TCC CC AG CGCTTCT GA  
 A \_ C\_ C  
 GAM1608 SPTBN4 3' AGTCCCCATGGCCGCCT 47386 CAGT AA A  
 AGGCGGCT GTG GA CT  
 ||||| ||| |||  
 TCCGCCGG TAC CT GA  
 \_ \_ CC \_  
 GAM1608 ZNF200 3' GTAGTTCTGAATTCCCAAGCTG 12909 CAGT\_ GA  
 CCT AGGCGGCT GT AGAACTAC  
 ||||| || |||||  
 TCCGTCGA TA TCTTGATG  
 ACCCT AG  
 GAM1608 BTN2A1 3' GTAATTCTCAGTGTGTGAGCTG 54342 \_TG GA C  
 CCT AGGCGGCTCA G T AGAA TAC  
 ||||| ||| |||  
 TCCGTCGAGT T G TCTT ATG  
 G GT AC A  
 GAM1608 CFP1 3' TAGCTCCGTCAAGCTGCCT 58771 CAGTG A\_ A  
 AGGCGGCT TGA GA CTA  
 ||||| ||| |||  
 TCCGTCGA ACT CT GAT  
 \_ \_ GC C  
 GAM1608 FENS-1 3' TGGGAGTCACACAAGCCGCCT 40445 CA AGAA  
 AGGCGGCT GTGTGA CTA  
 ||||| ||||| |||



TCCGCCGA CACACT GGT  
 A\_ GAG\_  
 GAM1608 FLJ14082 3' AGTTCTTCCTAAGGCACCC 46668 CG CAG T  
 GG GCT TG GAAGAACT  
 || ||| || |||||  
 CC CGG AT CTTCTTGA  
 CA A\_ C  
 GAM1608 FLJ20539 5' TGGGGCCACCTGAGCCGCC 35363 T AAGAA  
 GGCGGCTCAG GTG CTA  
 ||||| ||| |||  
 CCGCCGAGTC CAC GGT  
 \_ CGG\_  
 GAM1608 FLJ22301 3' AGCCCTTCACGTAGCCTCCT 45756 C CAG AA  
 AGG GGCT TGTGAAG CT  
 ||| ||| ||||| ||  
 TCC CCGA GCACTTC GA  
 T T\_ CC  
 GAM1608 HEMGN 5' TAGAGAAAAAACTGAGCCACC 37380 C GTGAAGAA  
 T AGG GGCTCAGT CTA  
 ||| ||||| |||  
 TCC CCGAGTCA GAT  
 A AAAAAAGA  
 GAM1608 KIAA0379 3' GTAGTTCTTGCGAATGCCACC 68150 C TCAG G  
 GG GGC TGT AAGAACTAC  
 || ||| ||| |||||  
 CC CCG GCG TTCTTGATG  
 A TAA\_ \_  
 GAM1608 KIAA0494 3' TCTCACACTGACCACC 28750 C C A  
 GG GG TCAGTGTGA GA  
 || ||| ||||| ||  
 CC CC AGTCACACT CT  
 A \_ \_  
 GAM1608 LACE1 3' CTTACATTAAACCACCT 91837 C CTC  
 AGG GG AGTGTGAAG  
 ||| || |||||  
 TCC CC TTACACTTC  
 A AAA  
 GAM1608 NAPG 3' TAGTTCTTCAGGTAGCACCT 96730 CG CAG G  
 AGG GCT T TGAAGAACTA  
 ||| ||| | |||||  
 TCC CGA G ACTTCTTGAT  
 A\_ T\_ G  
 GAM1608 PRO2405 5' AGGAGCACATTAAGCCGCCT 37798 C AAGAA  
 AGGCGGCT AGTGTG CT  
 ||||| ||||| ||  
 TCCGCCGA TTACAC GA  
 A GAG\_  
 GAM1608 LOC121219 5' AGTCCTCAGCGAAGCCGCCT 74040 CA G A A  
 AGGCGGCT GT TGA GA CT  
 ||||| || ||| |||

		TCCGCCGA CG ACT CT GA		
		AG _ C _		
GAM1608	LOC146990 3'	CTTCACACCCAGCCGCCT 83886	CA	
		AGGCGGCT GTGTGAAG		
		TCCGCCGA CAACTTC		
		CC		
GAM1608	LOC148371 5'	TTCCACTGAGCCACC 78809	C	T
		GG GGCTCAGTG GAA		
		CC CCGAGTCAC CTT		
		A _		
GAM1608	LOC152274 3'	AGTCCCTGCAGGAGCAGCCT 80498	G	AG AA A
		AGGC GCTC TGTG GA CT		
		TCCG CGAG ACGT CT GA		
		A G_ CC _		
GAM1608	LOC200261 3'	AGTTGCTCCACTGAGTCACC 88653	C	T AG
		GG GGCTCAGTG GA AACT		
		CC CTGAGTCAC CT TTGA		
		A _ CG		
GAM1608	LOC201562 5'	GTAGTCCGGCCCGAGCCGCT 88975		AGT GAA A
		GGCGGCTC GT GA CTAC		
		TCGCCGAG CG CT GATG		
		CC_ GC_ _		
GAM1608	LOC202347 3'	TCATGGCAGAGCCGCCT 90349	A	_
		AGGCGGCTC GT GTGA		
		TCCGCCGAG CG TACT		
		A G		
GAM1608	LOC220370 3'	TCACCTCACTGAGCCACCT 92834	C	___
		AGG GGCTCAGT GTGA		
		TCC CCGAGTCA CACT		
		A CTC		
GAM1608	LOC221838 5'	TTCCACTGAGCCACC 92546	C	T
		GG GGCTCAGTG GAA		
		CC CCGAGTCAC CTT		
		A _		
GAM1608	LOC51716 3'	AGTTCCACACTGAGCGCCT 32786	G	AA
		AGGCG CTCAGTGTG GAACT		
		TCCGC GAGTCACAC CTTGA		
		_ _		
GAM1608	LOC89919 3'	CTTCCACTGAGCCACC 60722	C	T
		GG GGCTCAGTG GAAG		

CC CCGAGTCAC CTTC  
 A \_  
 GAM1608 LOC91947 3' TAGTTCCTTTTCATTGTAAGCCGC 67614 \_ T  
 T GCGGCT CAGTG GAAGAACTA  
 ||||| |||| |||||  
 TCGCCGA GTTAC TTTCTTGAT  
 AT \_  
 GAM1609 GPR87 5' GAGACAAGAAACCTGTTTCAA 43655 AT\_  
 TTGGAACAGGTTTC TCTC  
 ||||| ||||  
 AACTTTGTCCAAAG AGAG  
 AAC  
 GAM1609 IL17 3' TGGGGAAAATGAAACCCTCCCC 9334 AACA \_  
 AA TTGG GGTTCAT TCTCCA  
 ||| ||||| |||||  
 AACC CCAAAGTA AGGGGT  
 CCTC AA  
 GAM1609 SYBL1 3' ATTGGAAAATACATCTGTTCCA 18892 TTC C  
 G TTGGAACAGGT ATT TCCAAT  
 ||||| ||| |||||  
 GACCTTGTCTA TAA AGGTTA  
 CA\_ A  
 GAM1609 TPK1 3' GGAGAACCTGTCCAA 42384 A TTCAT  
 TTGGA CAGGT TCTCC  
 |||| |||| ||||  
 AACCT GTCCA AGAGG  
 \_ \_  
 GAM1609 CLIC6 3' TGGAGAACATGTTCCAA 82536 G TTCAT  
 TTGGAACA GT TCTCCA  
 ||||| || |||||  
 AACCTTGT CA AGAGGT  
 A \_  
 GAM1609 CLIPR-59 3' TGGAGAATTTCAATGCCCCGA 31374 AA GGTTC  
 TTGG CA ATTCTCCA  
 ||| || |||||  
 AGCC GT TAAGAGGT  
 CC AACTT\_  
 GAM1609 FLJ20452 3' AGAATAATGGCTTGTTCCA 35195 TC\_  
 TGGAACAGGTT ATTCT  
 ||||| ||||  
 ACCTTGTTTCGG TAAGA  
 TAA  
 GAM1609 KCNN1 3' AGAAAAACCTGTTCC 9556 CA  
 GGAACAGGTTT TTCT  
 ||||| ||||  
 CCTTGTCCAAA AAGA  
 \_  
 GAM1609 LOC152687 3' TTGGAGAATATTGCTCCCA 80644 AACA TTC  
 TGG GGT ATTCTCCA  
 ||| ||| |||||

			ACC TCG TAAGAGGTT		
			C___ TTA		
GAM1609	LOC160942	5'	ATTGGAGAACGAGAAGAATCCG	87072	ACAGG A
		A	TTGGA TTTC TTCTCCAAT		
			AGCCT AGAG AAGAGGTTA		
			AAGA_ C		
GAM1609	LOC222021	3'	GAAGGACCTGTTCGAA	94058 G	CA
			TT GAACAGGTTT TTC		
			AA CTTGTCCAGG AAG		
			G _		
GAM1609	LOC51202	3'	ATTGGAGAATGAAACCTGCTCC	33017 A	
		AA	TTGGA CAGGTTTCATTCTCCAAT		
			AACCT GTCCAAAGTAAGAGGTTA		
			C		
GAM1610	CAV2	3'	AGATGTTTCATTTTACTGTA	6941 T	_
			TACAGTA AATGAAGCA CT		
			ATGTCAT TTACTTTGT GA		
			T A		
GAM1610	CPM	3'	GAGATAGTGCCATTGTACT	59676 AA	C
			AGTATAATG GCACTA CTC		
			TCATGTTAC CGTGAT GAG		
			_ A		
GAM1610	HS2ST1	3'	AGGCTTCACCATACTGTA	24329 AA	A
			TACAGTAT TGAAGC CT		
			ATGTCATA ACTTCG GA		
			CC _		
GAM1610	HTR2C	3'	AGCTCTTCATTGCACTG	6019 A	CA
			CAGT TAATGAAG CT		
			GTCA GTTACTTC GA		
			C TC		
GAM1610	PCLO	3'	AGACAGTGCTTTAAACACT	94221 ATAA	AC
			AGT TGAAGCACT CT		
			TCA ATTTTCGTGA GA		
			CAAA CA		
GAM1610	ROCK2	3'	AGTGACCATTATACTGTG	66008	AAG
			TACAGTATAATG CACT		
			GTGTCATATTAC GTGA		
			CA_		
GAM1610	DKFZp434A171	3'	AGTGTGTTTACCATACTGTA	50010 AA	_
			TACAGTAT TGAA GCACT		

ATGTCATA ATTT TGTGA  
 CC G  
 GAM1610 EHM2 3' AGGTAATGCCTCATTTACTAGT 38911 \_ T A C  
 A TAC AGTA AATGA GCA TACCT  
 ||| ||| ||||| ||| |||||  
 ATG TCAT TTACT CGT ATGGA  
 A \_ C A  
 GAM1610 FLJ10375 3' AGGCAGTGCTTCCCACACTG 36068 ATAAT A  
 CAGT GAAGCACT CCT  
 |||| ||||| |||  
 GTCA CTTCGTGA GGA  
 CACC\_ C  
 GAM1610 FLJ10560 3' AGGTAGTACCATTGTATGTA 36275 G AAGC  
 TACA TATAATG ACTACCT  
 |||| ||||| |||||  
 ATGT ATGTTAC TGATGGA  
 \_ CA\_  
 GAM1610 FLJ13340 3' GAGGCAATGTAATATGCTGTA 54103 ATGAA CTA  
 TACAGTATA GCA CCTC  
 ||||| ||| |||  
 ATGTCGTAT TGT GGAG  
 AA\_ AAC  
 GAM1610 FLJ22029 3' GAGGCAGTACCCCACCATGTGT 46331 \_ AAGC\_ A  
 ACTGT ACAGTATA ATG ACT CCTC  
 ||||| ||| ||| |||  
 TGTCATGT TAC TGA GGAG  
 G CACCCCA C  
 GAM1610 KIAA0637 5' AGTGATCTATGCTGTA 29236 AT AG  
 TACAGTATA GA CACT  
 ||||| || |||  
 ATGTCGTAT CT GTGA  
 \_ A\_  
 GAM1610 KIAA0993 3' AGTGAGATTTATACTGTA 64138 TGAAG  
 TACAGTATAA CACT  
 ||||| |||  
 ATGTCATATT GTGA  
 TAGA\_  
 GAM1610 KIAA1309 3' GAGGTAACCTTGCATATTATATG 53117 G AA C\_  
 TA TACA TATAATG GCA TACCTC  
 ||| ||||| ||| |||||  
 ATGT ATATTAT CGT ATGGAG  
 \_ A\_ TCA  
 GAM1610 LGI2 3' AGTAGCACGATCATATTGTACT 36395 \_ A\_ \_  
 GTA TACAGTATA ATGA GC ACT  
 ||||| ||| || |||  
 ATGTCATGT TACT CG TGA  
 TA AGCA A  
 GAM1610 MGC11134 3' TGTTTCATCATCCTGTA 48902 T A  
 TACAG AT ATGAAGCA  
 |||| || |||||

		ATGTC TA TACTTTGT		
		C C		
GAM1610	MGC3279	3' AGAGTTTCATTACCTGTA	43813	TA A
		TACAG TAATGAAGC CT		
		ATGTC ATTACTTTG GA		
		C_ A		
GAM1610	PTK9	3' TAGTGCTTTATATTGC	11026	TA
		GTA ATGAAGCACTA		
		CGT TATTTTCGTGAT		
		TA		
GAM1610	TBDN100	3' GAGGCAATGTAATATGCTGTA	46952	ATGAA CTA
		TACAGTATA GCA CCTC		
		ATGTCGTAT TGT GGAG		
		AA_ AAC		
GAM1610	LOC150482	3' AGTGTGTTTACCATACTGTA	63074	AA _
		TACAGTAT TGAA GCACT		
		ATGTCATA ATTT TGTGA		
		CC G		
GAM1610	LOC151323	3' AGTGCTTCACTACAGTG	80215	A TAA
		TAC GTA TGAAGCACT		
		GTG CAT ACTTCGTGA		
		A C_		
GAM1610	LOC200276	3' GTGTTTACTATACTGTA	88712	ATG
		TACAGTATA AAGCAC		
		ATGTCATAT TTTGTG		
		CA_		
GAM1610	LOC200299	3' GCCACCATTATGCTGTA	89977	AA_
		TACAGTATAATG GC		
		ATGTCGTATTAC CG		
		CAC		
GAM1610	LOC200300	3' GCCACCATTATGCTGTA	89969	AA_
		TACAGTATAATG GC		
		ATGTCGTATTAC CG		
		CAC		
GAM1610	LOC200304	3' GCCACCATTATGCTGTA	89987	AA_
		TACAGTATAATG GC		
		ATGTCGTATTAC CG		
		CAC		
GAM1610	LOC200305	3' GCCACCATTATGCTGTA	89981	AA_
		TACAGTATAATG GC		

ATGTCGTATTAC CG  
 CAC  
 GAM1610 LOC200399 3' AGTGCTTCACTACAGTG 88806 A TAA  
 TAC GTA TGAAGCACT  
 ||| ||| |||||  
 GTG CAT ACTTCGTGA  
 A C\_\_  
 GAM1610 LOC256073 3' GAGGAATGTCCATCATACTGTA 96665 A AA CTA  
 TACAGTAT ATG GCA CCTC  
 ||||| ||| ||| |||  
 ATGTCATA TAC TGT GGAG  
 C C\_ AA\_  
 GAM1610 LOC51580 3' TGAAATATTATACTGTA 31865 AAG  
 TACAGTATAATG CA  
 ||||| ||| ||  
 ATGTCATATTAT GT  
 AAA  
 GAM1611 APXL 3' TAGAAAATCAATCTGGTG 7931 C C  
 CACCAGGTTGA TT CTA  
 ||||| ||| |||  
 GTGGTCTAACT AA GAT  
 A A  
 GAM1611 BMP1 3' GACCTGTAGGAAAAGAGGCC 20415 GAC\_  
 GGTT TTCCTACAGGTC  
 ||| |||||  
 CCGG AAGGATGTCCAG  
 AGAA  
 GAM1611 CLCN5 3' ACCTGTAGGAAACCGAC 3592 AC  
 GTTG TTCCTACAGGT  
 ||| |||||  
 CAGC AAGGATGTCCA  
 CA  
 GAM1611 CLN6 3' GACCCACAGGAAGTCACAGTGG 35405 G\_ T ACA  
 TG CACCA GT GACTTCCT GGTC  
 ||| ||| ||||| |||  
 GTGGT CA CTGAAGGA CCAG  
 GA \_ CAC  
 GAM1611 DLEC1 3' GACCTGCTGCCGGAAGTCATCC 23686 CA T TA\_\_\_\_  
 CAGTG CAC GG TGA CTTC CAGGTC  
 || ||| ||||| |||  
 GTG CC ACTGAAGG GTCCAG  
 AC T CCGTC  
 GAM1611 DLEC1 3' GACCTGCTGCCGGAAGTCATCC 23699 CA T TA\_\_\_\_  
 CAGTG CAC GG TGA CTTC CAGGTC  
 || ||| ||||| |||  
 GTG CC ACTGAAGG GTCCAG  
 AC T CCGTC  
 GAM1611 GALNT7 3' ACCTAAGCTGTGCAACCTGGTG 33801 \_ TTC AC  
 CACCAGGTTG AC CT AGGT  
 ||||| || |||

			GTGGTCCAAC TG GA TCCA		
			G TC_ A_		
GAM1611 GRM1	3'	GACCTGTCAATGTCAACCTAGT 5915	C	TTCCT	
		AC AGGTTGAC ACAGGTC			
		TG TCCAAC TG TGTCCAG			
		A TAAC_			
GAM1611 HSF2BP	3'	ACCTGTAGGTTACCT 22859	T	CTT	
		AGGT GA CCTACAGGT			
		TCCA CT GGATGTCCA			
		_ T_			
GAM1611 IGF2R	3'	GACCTATAAGAAGCCTTAATTT 6052	_	C C	
G		CAGGTTGA CTTC TA AGGTC			
		GTTTAATT GAAG AT TCCAG			
		CC A A			
GAM1611 LIMD1	3'	ACCTGTCTCTGTCAACCT 26455		TTCCT	
		AGGTTGAC ACAGGT			
		TCCAAC TG TGTCCA			
		TCTC_			
GAM1611 NKTR	3'	ACCTGTAAAACTAGTG 18197	CA	GACTTCC	
		CAC GGTT TACAGGT			
		GTG TCAA ATGTCCA			
		A_ AA_			
GAM1611 RANBP7	3'	GACCTGATCATGCAACCTGG 21114		ACTTCCTA	
		CCAGGTTG CAGGTC			
		GGTCCAAC GTCCAG			
		GTAATA_			
GAM1611 RGS19IP1	3'	ACCCGGGCGCAACCTGGTG 62506		ACTT ACA	
		CACCAGGTTG CCT GGT			
		GTGGTCCAAC GGG CCA			
		GC_ C_			
GAM1611 RNTRE	3'	GACCTGTAGAATTAAACCCGG 28035	A	C C	
		CC GGTTGA TTC TACAGGTC			
		GG CCAATT AAG ATGTCCAG			
		C T _			
GAM1611 SSPN	3'	ACCTGTAAAATACCTTG TG 17439	C	TGACTTCC	
		CAC AGGT TACAGGT			
		GTG TCCA ATGTCCA			
		T TAAA_			
GAM1611 WEE1	3'	GACCTGTAAAAAGTACTCAAGG 12653	AGGTTG	CC	
		CC ACTT TACAGGTC			



GG TGAA ATGTCCAG  
AACTCA AA  
GAM1611 CGRP-RCP 5' GACCTGTACGCCAACACGGTG 27130 AG ACTTCC  
CACC GTTG TACAGGTC  
||||| |||||  
GTGG CAAC ATGTCCAG  
CA CGC\_\_\_\_  
GAM1611 DKFZP434H132 5' ACCTGCTTCAGCCTGG 31315 CTCCTA  
CCAGGTTGA CAGGT  
||||| |||||  
GGTCCGACT GTCCA  
TC\_\_\_\_  
GAM1611 FLJ10110 3' GACCTGTAGTTTTCAACACTG 35823 \_ CTTC  
CAG GTTG CTACAGGTC  
||| ||||| |||||  
GTC CAACT GATGTCCAG  
A TTT\_  
GAM1611 FLJ10743 3' ACCTGTAGGAACCCAGCC 36546 AC  
GGTTG TTCCTACAGGT  
||||| |||||  
CCGAC AAGGATGTCCA  
CC  
GAM1611 FLJ20507 3' ACCTGTAAATGACCCTGTG 60205 CA GACTTCC  
CAC GGTT TACAGGT  
||| ||||| |||||  
GTG CCAG ATGTCCA  
TC TAA\_\_\_\_  
GAM1611 HYA22 3' ACCTGTAAGTCTGTAACCTGG 19416 \_\_\_\_ TCC  
CCAGGTT GACT TACAGGT  
||||| ||||| |||||  
GGTCCAA CTGA ATGTCCA  
TGT \_\_\_\_  
GAM1611 KCNJ9 3' ACCTGTAGAACACCCCTGTG 17150 C TTGACTTC  
CAC AGG CTACAGGT  
||| ||||| |||||  
GTG TCC GATGTCCA  
\_ CCACAA\_  
GAM1611 KIAA0275 3' ACCTGGGGGGCCATCCTGGTG 28670 T ACTT TA  
CACCAGG TG CC CAGGT  
||||| || |||||  
GTGGTCC AC GG GTCCA  
T C\_\_ GG  
GAM1611 KIAA1813 5' GACCTGTGCTTCAAGCTGGT 70298 G CTTCC  
ACCAG TTGA TACAGGTC  
||||| ||||| |||||  
TGGTC AACT GTGTCCAG  
G TC\_\_\_\_  
GAM1611 NASP 3' ACCTGTAGGAACAGTACCTGG 67965 TGAC  
CCAGGT TTCCTACAGGT  
||||| |||||

	GGTCCA AAGGATGTCCA	
	TGAC	
GAM1611 PPP1R16B 3'	ACCAGGCAAAGTCAACC 61376	___ ACA
	GGTTGACTT CCT GGT	
	CCAACTGAA GGA CCA	
	AC ____	
GAM1611 STOML1 3'	GACCCACAGAAACAGCCTG 16671	AC CTACA
	CAGGTTG TTC GGTC	
	GTCCGAC AAG CCAG	
	A_ ACAC_	
GAM1611 TM4SF11 3'	ACCTGTAAAAAGTGGGTTGATT 32034	TG TC ____
	GGT ACT CT ACAGGT	
	TTA TGG GA TGTCCA	
	GT GT AAAA	
GAM1611 LOC144584 5'	ACCTGTAGAAGACCCTG 67025	TTGA C
	CAGG CTTC TACAGGT	
	GTCC GAAG ATGTCCA	
	CA__ _	
GAM1611 LOC146485 3'	ACCTGTAGAAGACCCTG 59785	TTGA C
	CAGG CTTC TACAGGT	
	GTCC GAAG ATGTCCA	
	CA__ _	
GAM1611 LOC146712 5'	GACCTGTAGGAGTCCCCT 83717	TT T
	AGG GACT CCTACAGGTC	
	TCC CTGA GGATGTCCAG	
	C_ _	
GAM1611 LOC201252 5'	GACCTGTAAATCACCTCGG 88169	_ T CTTCC
	CC AGGT GA TACAGGTC	
	GG TCCA CT ATGTCCAG	
	C _ AA__	
GAM1611 LOC219686 3'	ACCTGTAGAAAACAAGTG 90837	CAG GACTTC
	CAC GTT CTACAGGT	
	GTG CAA GATGTCCA	
	AA_ AA__	
GAM1611 LOC222161 3'	GACCCAGGGGATCAACCTG 92796	C ACA
	CAGGTTGA TTCCT GGTC	
	GTCCAACT AGGGG CCAG	
	_ AC_	
GAM1611 LOC254860 5'	ACCTGTTGGTACAACCTGG 97463	ACTT T
	CCAGGTTG CC ACAGGT	

		GGTCCAAC GG TGTCCA	
		AT__ T	
GAM1611	LOC255104	3' GACCTGCAGAGTCAACC 95396	TC A
		GGTTGACT CT CAGGTC	
		CCAACTGA GA GTCCAG	
		__ C	
GAM1611	LOC255851	3' ACCTGTAGACTTATTACCTGG 96229	TGACTTC
		CCAGGT CTACAGGT	
		GGTCCA GATGTCCA	
		TTATTCA	
GAM1611	LOC90342	5' GCCTGAAAGCCAACCTGG 62360	A CCTA
		CCAGGTTG CTT CAGGT	
		GGTCCAAC GAA GTCCG	
		C A__	
GAM1612	ATF7	3' CCTATCAACATTACCGCCCCT 22465	A TA A A
		AG GG GTAA GTTGA TAGG	
		TC CC CATT CAACT ATCC	
		C GC A _	
GAM1612	BAX	3' CCTGGAGCCTCCACTGCCTCT 15064	AA TTGAA
		AGAGGTAGT AG TAGG	
		TCTCCGTCA TC GTCC	
		CC CGAG_	
GAM1612	EZH1	3' TCACCTTACTACCTC 8827	A T
		GAGGTAGTAA GT GA	
		CTCCATCATT CA CT	
		C _	
GAM1612	GARS	5' CTCGCAACCCTACCTACCTCT 8986	_ AA AAT
		AGAGGTAG TA GTTG AG	
		TCTCCATC AT CAAC TC	
		C CC GC_	
GAM1612	GRAF	3' CCTATCCATGCCCCCTACCTCT 30554	TAAAGT A
		AGAGGTAG TG ATAGG	
		TCTCCATC AC TATCC	
		CCCCGT C	
GAM1612	RASGRP1	3' TCCTTCTTCACTACCTC 19209	A TTGAAT
		GAGGTAGT AAG AGGA	
		CTCCATCA TTC TCCT	
		C T_____	
GAM1612	SLC8A2	3' CCCACTCGCCCTCCACTACCTC 66329	AA T_ ATA
	T	AGAGGTAGT AG TGA GG	

TCTCCATCA TC GCT CC  
 CC CC CAC  
 GAM1612 STATH 5' TTCAACTTCACTACTTCT 12029 A  
 AGAGGTAGT AAGTTGAA  
 ||||| |||||  
 TCTTCATCA TTCAACTT  
 C  
 GAM1612 TGFB1 5' CCTATTCAAGACCACC 5402 A AAAG  
 GGT GT TTGAATAGG  
 ||| || |||||  
 CCA CA AACTTATCC  
 C G\_\_  
 GAM1612 BG1 5' CTCCTACTCCCAATACTACCT 87311 AAGTT A  
 AGGTAGTA GA TAGGAG  
 ||||| || |||||  
 TCCATCAT CT ATCCTC  
 AACC\_ C  
 GAM1612 C21orf108 3' CCTTAATCTTTATCCACCTCT 88718 A\_ TTGAAT  
 AGAGGT GTAAAG AGG  
 ||||| ||||| |||  
 TCTCCA TATTTC TCC  
 CC TAAT\_\_  
 GAM1612 DKFZp434D0917 3' TCAAGTTCACCTACCTCT 91256 A G  
 AGAGGTAGT AA TTGA  
 ||||| || |||||  
 TCTCCATCA TT AACT  
 C G  
 GAM1612 DKFZP586G1122 3' CTCCCATTCAACTCCCCACCTC 61286 AGTAA A  
 GAGGT AGTTGAAT GGAG  
 ||||| ||||| |||||  
 CTCCA TCAACTTA CCTC  
 CCCC\_ C  
 GAM1612 FLJ10324 5' CTCCCTGGGGCTCTACTACCT 36028 A GAATA  
 AGGTAGTA AGTT GGAG  
 ||||| ||||| |||||  
 TCCATCAT TCGG CCTC  
 C GGTC\_  
 GAM1612 KIAA0853 3' CCTAAAATCTTACCCACCTCT 30538 A\_ AG GAA  
 AGAGGT GTAA TT TAGG  
 ||||| ||||| || |||||  
 TCTCCA CATT AA ATCC  
 CC CT A\_\_  
 GAM1612 KIAA1462 3' TCCCTCCCTTGCTACCTCT 91391 AGTT ATA  
 AGAGGTAGTAA GA GGA  
 ||||| ||||| || |||||  
 TCTCCATCGTT CT CCT  
 CC\_ C\_\_  
 GAM1612 KIAA1817 3' TCCTATTGCCACCACCGCT 68230 A A AAA TG  
 AG GGT GT GT AATAGGA  
 || ||||| || |||||

	TC CCA CA CG TTATCCT	
	G C C _ _	
GAM1612 MGC2574	3' TCCACACCCCACTGCCTCT 44054	AAA T AATA
	AGAGGTAGT GT G GGA	
	TCTCCGTCA CA C CCT	
	CCC _ A _	
GAM1612 P37NB	3' CTACAACATTCACTACCTCT 19505	A _ AA
	AGAGGTAGT AA GTTG TAG	
	TCTCCATCA TT CAAC ATC	
	C A _	
GAM1612 U5-116KD	3' CTCCCAAGAGGCTTCACTGCCT 14907	A GAATA
CT	AGAGGTAGT AAGTT GGAG	
	TCTCCGTCA TTCGG CCTC	
	C AGAAC	
GAM1612 LOC127534	3' CTCCTTACAACAACCTAACTAC 75438	AAA AAT _
CTC	GAGGTAGT GTTG AGGAG	
	CTCCATCA CAAC TCCTC	
	ATC AACAT	
GAM1612 LOC145371	3' CTCCTGAGCCTCCACTATCTC 77153	AA TTGAA
	GAGGTAGT AG TAGGAG	
	CTCTATCA TC GTCCTC	
	CC CGA _	
GAM1612 LOC152274	5' CAACTTCCTACCTCT 80500	TA
	AGAGGTAG AAGTTG	
	TCTCCATC TTCAAC	
	C _	
GAM1612 LOC200933	3' CTCCCTCCCTTCACTACCTC 90195	A TT ATA
	GAGGTAGT AAG GA GGAG	
	CTCCATCA TTC CT CCTC	
	C C _ C _	
GAM1612 LOC201182	5' CCTACCAATTGTTTTACTTCCT 89764	T _ _ AA
CT	AGAGG AGTAAA GTTG TAGG	
	TCTCC TCATTT TAAC ATCC	
	T TGT C _	
GAM1612 LOC256073	5' CCCCTTCTCTCCTACCTCT 96663	TAA TT TA
	AGAGGTAG AG GAA GG	
	TCTCCATC TC CTT CC	
	C _ T _ CC	
GAM1612 LOC64744	3' CCCCATCCTCTTTTCCTACCTC 61797	T _ TT ATA
T	AGAGGTAG AAAG GA GG	

			TCTCCATC TTTC CT CC			
			CT TC ACC			
GAM1613	CD80	3'	AGATCTGAAGGTAGCCTC 17766	A	AG	
			GA GCTGCC TCAGATCT			
			CT CGATGG AGTCTAGA			
			C A_			
GAM1613	CEACAM5	3'	CTAACTGACAGCTTCA 15159		C C	
			TGAAGCTG CAGT AG			
			ACTTCGAC GTCA TC			
			A A			
GAM1613	CX3CR1	5'	AGGGTGGCTGACTGGCAGATCC 70643	AAG	AT_	
	A		TG CTGCCAGTCAG CTCT			
			AC GACGGTCAGTC GGGA			
			CTA GGT			
GAM1613	DUSP6	5'	ATCTGGGCAGCTTCA 65962		AGT	
			TGAAGCTGCC CAGAT			
			ACTTCGACGG GTCTA			
			—			
GAM1613	FLNB	3'	AGAGAAGGGCAGCAGCTT 62170	CA	AGA	
			AAGCTGC GTC TCTCT			
			TTCGACG CGG AGAGA			
			A_ GA_			
GAM1613	HTN1	3'	AGAGGTTTGACTGGCAAATTCA 9284		GC	
			TGAA TGCCAGTCAGATCTCT			
			ACTT ACGGTCAGTTTGGAGA			
			AA			
GAM1613	ITPKB	3'	TCCGATTAGCAGCCTCA 9437	A	C A	
			TGA GCTGC AGTC GA			
			ACT CGACG TTAG CT			
			C A C			
GAM1613	MAPK1	3'	AGATTTAAAGTGGCAGCTTCA 10818		GTC_	
			TGAAGCTGCCA AGATCT			
			ACTTCGACGGT TTTAGA			
			GAAA			
GAM1613	MAT1A	3'	CTGACCAGCAGCTTTA 90832		CA	
			TGAAGCTGC GTCAG			
			ATTCGACG CAGTC			
			AC			
GAM1613	MMP19	3'	GTCTACTGGCGCCTCA 42974	A T	C	
			TGA GC GCCAGT AGAT			

			ACT CG CGGTCA TCTG		
			C _ _		
GAM1613	MMP19	3'	GTCTACTGGCGCCTCA	42980	A T C
			TGA GC GCCAGT AGAT		
			ACT CG CGGTCA TCTG		
			C _ _		
GAM1613	NAB1	3'	AGATAACTGACAGCTTTA	19906	C CAG
			TGAAGCTG CAGT ATCT		
			ATTTGAC GTCA TAGA		
			A A _		
GAM1613	NEF3	3'	ATGTGATTGGCAGCTTCA	18195	G
			TGAAGCTGCCAGTCA AT		
			ACTTCGACGGTTAGT TA		
			G		
GAM1613	NHP2L1	3'	AGAGATCTGGTTCCAGCTTT	17200	CC GT
			GAAGCTG A CAGATCTCT		
			TTTCGAC T GTCTAGAGA		
			C _ TG		
GAM1613	SCN1A	5'	GGACCTGACAGCTTCA	88852	GCCA A
			TGAAGCT GTCAG TCT		
			ACTTCGA CAGTC AGG		
			_ _ C		
GAM1613	TTC3	3'	CTGTTCTGGTAGCTCCA	12418	A T _
			TG AGCTGCCAG CAG		
			AC TCGATGGTC GTC		
			C TT		
GAM1613	ZNF202	3'	AGACTGCTCAACAGCTTCA	12911	CC_ T A
			TGAAGCTG AG CAG TCT		
			ACTTCGAC TC GTC AGA		
			AAC _ _		
GAM1613	BTN2A1	3'	AGAGACAGAAAGTGCAGCTTCA	54338	CAG AGA
			TGAAGCTGC TC TCTCT		
			ACTTCGACG AG AGAGA		
			TGA AC _		
GAM1613	CCR5	5'	AGAGATCTATTCTCCAGCTT	5146	CCAGTC
			AAGCTG AGATCTCT		
			TTGAC TCTAGAGA		
			CTCTTA		
GAM1613	DKFZP586I2223	5'	ATCTGACTGCAGCCCCA	54917	AA C
			TG GCTGC AGTCAGAT		

AC CGACG TCAGTCTA  
 CC \_  
 GAM1613 FLJ10242 3' AGAGTCCTGACAGCAGCTTCA 35933 CA AT  
 TGAAGCTGC GTCAG CTCT  
 ||||| ||| |||  
 ACTTCGACG CAGTC GAGA  
 A\_ CT  
 GAM1613 FLJ10314 3' AGATCTGACCAAGGTGTCA 36009 A GCCA  
 TGA GCT GTCAGATCT  
 ||| ||| |||||  
 ACT TGG CAGTCTAGA  
 G AAC\_  
 GAM1613 FLJ10901 3' TCTGACTGACAGCCTC 36834 A C  
 GA GCTG CAGTCAGA  
 || ||| |||||  
 CT CGAC GTCAGTCT  
 C A  
 GAM1613 FLJ11715 3' AGAGCTCACTGCAGCTTCA 44666 C CA T  
 TGAAGCTGC AGT GA CTCT  
 ||||| ||| || |||  
 ACTTCGACG TCA CT GAGA  
 \_ \_ C  
 GAM1613 FLJ13154 3' AGAAATCTTTTACAGTTTCA 44789 CC TC C  
 TGAAGCTG AG AGAT TCT  
 ||||| || ||| |||  
 ACTTTGAC TT TCTA AGA  
 A\_ TT A  
 GAM1613 FLJ13769 3' AGAGCTTTCTATCAGCTTCA 46595 CC TC AT  
 TGAAGCTG AG AG CTCT  
 ||||| || || |||  
 ACTTCGAC TC TC GAGA  
 TA TT \_  
 GAM1613 FLJ23132 3' AGAGACGGCAGGCAGCTT 96133 A AGA  
 AAGCTGCC GTC TCTCT  
 ||||| ||| |||  
 TTCGACGG CGG AGAGA  
 A C\_  
 GAM1613 FUBP3 3' ATTTGACTGACAATTCA 63731 GC C  
 TGAA TG CAGTCAGAT  
 ||| || |||||  
 ACTT AC GTCAGTTTA  
 A\_ A  
 GAM1613 HSJ1 3' ATGTGATGGCAGCTCCA 22124 A G G  
 TG AGCTGCCA TCA AT  
 || ||||| ||| ||  
 AC TCGACGGT AGT TA  
 C \_ G  
 GAM1613 KIAA0607 3' AGAGACGCGACTGGCGGCTCCA 72566 A AGA  
 TG AGCTGCCAGTC TCTCT  
 || ||||| ||| |||



		AC TCGGCGGTCAG AGAGA		
		C CGC		
GAM1613 KIAA0907	3'	AGAGATCTGACTGCTGGCT	30169	GC
		AGCT CAGTCAGATCTCT		
		TCGG GTCAGTCTAGAGA		
		TC		
GAM1613 KIAA1190	3'	AGGCTGACTGGCAGC	71095	A
		GCTGCCAGTCAG TCT		
		CGACGGTCAGTC GGA		
		—		
GAM1613 KIAA1196	3'	AGGTTGATGGCAGCTCCA	61460	A GTCA
		TG AGCTGCCA GATCT		
		AC TCGACGGT TTGGA		
		C AG__		
GAM1613 KIAA1300	3'	AGAGACACTGTGGCAGCT	62859	GT A_
		AGCTGCCA CAG TCTCT		
		TCGACGGT GTC AGAGA		
		__ AC		
GAM1613 LBP-9	3'	GGGTAACTAACAGCTTTA	27280	CC CA
		TGAAGCTG AGT GATCT		
		ATTCGAC TCA TTGGG		
		AA A_		
GAM1613 MGC14436	5'	AGAATCGATACTGAACAGCTTC	51851	C_ CA_ C
A		TGAAGCTG CAGT GAT TCT		
		ACTTCGAC GTCA CTA AGA		
		AA TAG _		
GAM1613 MGC4832	3'	AGAGCTGCCTGGTAGCTTCA	58997	T AT
		TGAAGCTGCCAG CAG CTCT		
		ACTTCGATGGTC GTC GAGA		
		C _		
GAM1613 P15-2	3'	AGATTTTCTTGGCAGCTCCA	38005	A _ TC
		TG AGCTGCCA G AGATCT		
		AC TCGACGGT C TTTAGA		
		C T TT		
GAM1613 RGS10	3'	AGCCGGGACTGGCAGCTTTA	11331	AGAT
		TGAAGCTGCCAGTC CT		
		ATTCGACGGTCAG GA		
		GGCC		
GAM1613 TBDN100	3'	AGAGATCTATTTGAAGCTTCA	46948	GC TC
		TGAAGCT CAG AGATCTCT		

	ACTTCGA GTT TCTAGAGA		
	A_ TA		
GAM1613 ZNF238	3' GGATATTGCAGCTTCA 20964	C	CAG
	TGAAGCTGC AGT ATCT		
	ACTTCGACG TTA TAGG		
	— —		
GAM1613 LOC113763	3' CTGGCTGGCAGCCCCA 56579	AA	
	TG GCTGCCAGTCAG		
	AC CGACGGTCGGTC		
	CC		
GAM1613 LOC125061	3' CTGACACTGACAGCTTCA 74390	C	—
	TGAAGCTG CA GTCAG		
	ACTTCGAC GT CAGTC		
	A CA		
GAM1613 LOC135293	3' CTGGGTGGCAGTTCA 76180	G	G
	TGAA CTGCCA TCAG		
	ACTT GACGGT GGTC		
	— G		
GAM1613 LOC146056	3' GAGAAGCAACAGCTTCA 77617	CCA	CAGA
	TGAAGCTG GT TCTC		
	ACTTCGAC CG AGAG		
	AA_ A_		
GAM1613 LOC147610	5' GAGACCTACAGCTTCA 87173	CCAGTC	A
	TGAAGCTG AG TCTC		
	ACTTCGAC TC AGAG		
	A_ C		
GAM1613 LOC149076	3' AGAGGGGTGCGGCAGCTTCA 79146	A T	GA
	TGAAGCTGCC G CA TCTCT		
	ACTTCGACGG C GT GGAGA		
	— GG		
GAM1613 LOC153196	5' CTGACTTGACAGCTTCA 85959	C	—
	TGAAGCTG CA GTCAG		
	ACTTCGAC GT CAGTC		
	A T		
GAM1613 LOC168975	5' GAGTTTCCACAGCTTCA 87279	CCAGTC	T
	TGAAGCTG AGA CTC		
	ACTTCGAC TTT GAG		
	ACC_ _		
GAM1613 LOC199953	3' CTAAGTGGCAGCTCCA 88503	A	C
	TG AGCTGCCAGT AG		

AC TCGACGGTCA TC  
 C \_  
 GAM1613 LOC201194 3' AGGTAGTGGCAGCTCCA 89774 A GTCAG  
 TG AGCTGCCA ATCT  
 || ||||| ||||  
 AC TCGACGGT TGGA  
 C GA\_\_  
 GAM1613 LOC219914 5' AGGTCTGCAGCTTCA 93324 CAGTC  
 TGAAGCTGC AGATCT  
 ||||| ||||  
 ACTTCGACG TCTGGA  
  
 GAM1613 LOC220672 3' AGACTGATGGCAGCTCG 60423 A G A  
 TGA GCTGCCA TCAG TCT  
 || ||||| |||| ||  
 GCT CGACGGT AGTC AGA  
  
 GAM1613 LOC222662 3' AGAACTGGCTACCAGCTTCA 92841 CC A  
 TGAAGCTG AGTCAG TCT  
 ||||| |||| ||  
 ACTTCGAC TCGGTC AGA  
 CA A  
 GAM1613 LOC245771 5' TCTGACTGACAGCCTC 92899 A C  
 GA GCTG CAGTCAGA  
 || ||| |||||  
 CT CGAC GTCAGTCT  
 C A  
 GAM1613 LOC257239 5' AGGTCTGCAGCTTCA 97061 CAGTC  
 TGAAGCTGC AGATCT  
 ||||| ||||  
 ACTTCGACG TCTGGA  
  
 GAM1613 LOC90522 3' GAGATCTCCAGCTGCA 63155 A CCAGTC  
 TG AGCTG AGATCTC  
 || |||| |||||  
 AC TCGAC TCTAGAG  
 G C\_\_  
 GAM1613 LOC90750 3' AGAGATCTAACCATGGGCA 63912 A\_\_ C  
 TGCC GT AGATCTCT  
 ||| || |||||  
 ACGG CA TCTAGAGA  
 GTAC A  
 GAM1614 CDH10 3' TAGTTCTCCCTTAAGCAACCT 22058 CG CAGTGT A  
 AGG GCT GA GAACTA  
 ||| || || |||||  
 TCC CGA CTCTTGAT  
 AA ATTCC\_ \_  
 GAM1614 DACH 3' TAGTTCTTCCATAACCACT 54971 C CTCA T  
 AGG GG GTG GAAGAACTA  
 ||| || ||| |||||

TCC CC TAC CTTCTTGAT  
 A AA\_\_ \_  
 GAM1614 HPS1 3' TCTTCCAGAGCTGCCT 3969 AG T  
 AGGCGGCTC TG GAAGA  
 ||||| || ||||  
 TCCGTCGAG AC CTTCT

— —  
 GAM1614 PCK1 5' TCTTCAGGCTGCCT 52264 CAGTG  
 AGGCGGCT TGAAGA  
 ||||| ||||  
 TCCGTCGG ACTTCT

— —  
 GAM1614 RORB 5' AGCTCTTCGCCGACCACCT 22606 C C AGT A  
 AGG GG TC GTGAAGA CT  
 ||| || ||||| ||  
 TCC CC AG CGCTTCT GA  
 A \_ C\_ C

GAM1614 SPTBN4 3' AGTCCCCATGGCCGCCT 47386 CAGT AA A  
 AGGCGGCT GTG GA CT  
 ||||| ||| |||  
 TCCGCCGG TAC CT GA  
 — CC \_

GAM1614 ZNF200 3' GTAGTTCTGAATTCCCAAGCTG 12909 CAGT\_ GA  
 CCT AGGCGGCT GT AGAACTAC  
 ||||| || |||||  
 TCCGTCGA TA TCTTGATG  
 ACCCT AG

GAM1614 BTN2A1 3' GTAATTCTCAGTGTGTGAGCTG 54342 \_ TG GA C  
 CCT AGGCGGCTCA G T AGAA TAC  
 ||||| ||| ||| |||  
 TCCGTCGAGT T G TCTT ATG  
 G GT AC A

GAM1614 CFP1 3' TAGCTCCGTCAAGCTGCCT 58771 CAGTG A\_ A  
 AGGCGGCT TGA GA CTA  
 ||||| ||| ||| |||  
 TCCGTCGA ACT CT GAT  
 — GC C

GAM1614 FENS-1 3' TGGGAGTCACACAAGCCGCCT 40445 CA AGAA  
 AGGCGGCT GTGTGA CTA  
 ||||| ||||| |||  
 TCCGCCGA CAACT GGT  
 A\_ GAG\_

GAM1614 FLJ14082 3' AGTTCTTCCTAAGGCACCC 46668 CG CAG T  
 GG GCT TG GAAGAACT  
 || ||| || |||||  
 CC CGG AT CTTCTTGA  
 CA A\_ C

GAM1614 FLJ20539 5' TGGGGCCACCTGAGCCGCC 35363 T AAGAA  
 GGCGGCTCAG GTG CTA  
 ||||| ||| |||

CCGCCGAGTC CAC GGT  
 \_ CGG\_  
 GAM1614 FLJ22301 3' AGCCCTTCACGTAGCCTCCT 45756 C CAG AA  
 AGG GGCT TGTGAAG CT  
 ||| ||| ||||| ||  
 TCC CCGA GCACTTC GA  
 T T\_\_ CC  
 GAM1614 HEMGN 5' TAGAGAAAAAACTGAGCCACC 37380 C GTGAAGAA  
 T AGG GGCTCAGT CTA  
 ||| ||||| |||  
 TCC CCGAGTCA GAT  
 A AAAAAAGA  
 GAM1614 KIAA0379 3' GTAGTTCTTGCGAATGCCACC 68150 C TCAG G  
 GG GGC TGT AAGAACTAC  
 || ||| ||| |||||  
 CC CCG GCG TTCTTGATG  
 A TAA\_ \_  
 GAM1614 KIAA0494 3' TCTCACACTGACCACC 28750 C C A  
 GG GG TCAGTGTGA GA  
 || || ||||| ||  
 CC CC AGTCACACT CT  
 A \_ \_  
 GAM1614 LACE1 3' CTTACATTAAACCACCT 91837 C CTC  
 AGG GG AGTGTGAAG  
 ||| || |||||  
 TCC CC TTACACTTC  
 A AAA  
 GAM1614 NAPG 3' TAGTTCTTCAGGTAGCACCT 96730 CG CAG G  
 AGG GCT T TGAAGAACTA  
 ||| ||| | |||||  
 TCC CGA G ACTTCTTGAT  
 A\_ T\_\_ G  
 GAM1614 PRO2405 5' AGGAGCACATTAAGCCGCCT 37798 C AAGAA  
 AGGCGGCT AGTGTG CT  
 ||||| ||||| ||  
 TCCGCCGA TTACAC GA  
 A GAG\_  
 GAM1614 LOC121219 5' AGTCCTCAGCGAAGCCGCCT 74040 CA G A A  
 AGGCGGCT GT TGA GA CT  
 ||||| || ||| || ||  
 TCCGCCGA CG ACT CT GA  
 AG \_ C \_  
 GAM1614 LOC146990 3' CTTACACCCAGCCGCCT 83886 CA  
 AGGCGGCT GTGTGAAG  
 ||||| |||||  
 TCCGCCGA CCACTTC  
 CC  
 GAM1614 LOC148371 5' TTCCACTGAGCCACC 78809 C T  
 GG GGCTCAGTG GAA  
 || ||||| |||

		CC CCGAGTCAC CTT		
		A _		
GAM1614	LOC152274 3'	AGTCCCTGCAGGAGCAGCCT 80498	G	AG AA A
		AGGC GCTC TGTG GA CT		
		TCCG CGAG ACGT CT GA		
		A G_ CC _		
GAM1614	LOC200261 3'	AGTTGCTCCACTGAGTCACC 88653	C	T AG
		GG GGCTCAGTG GA AACT		
		CC CTGAGTCAC CT TTGA		
		A _ CG		
GAM1614	LOC201562 5'	GTAGTCCGGCCCGAGCCGCT 88975		AGT GAA A
		GGCGGCTC GT GA CTAC		
		TCGCCGAG CG CT GATG		
		CC_ GC_ _		
GAM1614	LOC202347 3'	TCATGGCAGAGCCGCCT 90349	A	_
		AGGCGGCTC GT GTGA		
		TCCGCCGAG CG TACT		
		A G		
GAM1614	LOC220370 3'	TCACCTCACTGAGCCACCT 92834	C	___
		AGG GGCTCAGT GTGA		
		TCC CCGAGTCA CACT		
		A CTC		
GAM1614	LOC221838 5'	TTCCACTGAGCCACC 92546	C	T
		GG GGCTCAGTG GAA		
		CC CCGAGTCAC CTT		
		A _		
GAM1614	LOC51716 3'	AGTTCCACACTGAGCGCCT 32786	G	AA
		AGGCG CTCAGTGTG GAACT		
		TCCGC GAGTCACAC CTTGA		
		_ _		
GAM1614	LOC89919 3'	CTTCCACTGAGCCACC 60722	C	T
		GG GGCTCAGTG GAAG		
		CC CCGAGTCAC CTTC		
		A _		
GAM1614	LOC91947 3'	TAGTTCTTTTATTGTAAGCCGC 67614	___	T
T		GGCGGCT CAGTG GAAGAACTA		
		TCGCCGA GTTAC TTTCTTGAT		
		AT _		
GAM1615	AKAP1 3'	AGGTCGACCTCATCTGGGA 57709		TAAACA CA__
		TCCAGATG GAG ACCT		

		AGGGTCTAC	CTC	TGGA	
		TA____	CAGC		
GAM1615 ANXA9	5'	CTCTCCCACATCTGGGA	13103	AAAC	
		TCCCAGATGT	AGAG		
		AGGGTCTACA	TCTC		
		CCC_			
GAM1615 BLVRB	3'	CTCTGTCCCCATCTGGGA	5546	TAA	
		TCCCAGATG	ACAGAG		
		AGGGTCTAC	TGTCTC		
		CCC			
GAM1615 ENTPD1	5'	TGCTCTGTTCTTCTGG	8348	TGTA	
		CCAGA	AACAGAGCA		
		GGTCT	TTGTCTCGT		
		TC__			
GAM1615 FUT8	3'	GGTGCCTATATCTGAGA	15591	C	AAAC A A
		TC CAGATGT	AG GCA CC		
		AG GTCTATA	TC CGT GG		
		A	____ _		
GAM1615 MKI67	3'	GGTTGCTCTCACCTGAGA	10046	C	A TAAAC
		TC CAG TG	AGAGCAACC		
		AG GTC AC	TCTCGTTGG		
		A C	_____		
GAM1615 ORC2L	3'	TGTTGTGTTTACATCTG	20549	G	
		CAGATGTAAACA	AGCA		
		GTCTACATTTGT	TTGT		
		G			
GAM1615 SNTB1	5'	AGGTTGCTCCACCCCGGTCAGG	40702	CA	GTAAACA
A		TCC GAT	GAGCAACCT		
		AGG CTG	CTCGTTGGA		
		A_	GCCCCAC		
GAM1615 APOL4	5'	CTTTGTCTGCTGCATCTGG	47624	A__	
		CCAGATGTA	ACAGAG		
		GGTCTACGT	TGTTTC		
		CTGC			
GAM1615 CNOT7	3'	AGGCTGCTCTGTGACTG	25332	ATGTAA	A
		CAG	ACAGAGCA CCT		
		GTC	TGTCTCGT GGA		
		AG__	C		
GAM1615 DKFZP564M182	3'	TGCAGTGGCTTACATCTG	78046	A_	GA
		CAGATGTAA	CA GCA		

GTCTACATT GT CGT  
 CG GA  
 GAM1615 FLJ10081 3' AGGTCACCTGTGTTCAATCTGG 35798 GTA G CA\_  
 GA TCCCAGAT AACA AG ACCT  
 ||||| ||| || |||  
 AGGGTCTA TTGT TC TGGA  
 AC\_ G CAC  
 GAM1615 FLJ10716 3' AGGTTGTTTTTTCCACATCTG 36480 A\_ C  
 GGA TCCCAGATGT AA AGAGCAACCT  
 ||||| || |||||  
 AGGGTCTACA TT TTTTGTTGGA  
 CC T  
 GAM1615 FLJ10786 3' TTTGTCTATATCTGGGA 36643 A  
 TCCCAGATGTA ACAGA  
 ||||| |||||  
 AGGGTCTATAT TGTTT  
 C  
 GAM1615 FLJ13194 3' TTGCTGTTACATCTG 47133 ACAG  
 CAGATGTAA AGCAA  
 ||||| |||||  
 GTCTACATT TCGTT  
 G\_  
 GAM1615 FLJ13912 3' GCCTGCATTACATCTGG 42863 A\_ A  
 CCAGATGTAA CAG GC  
 ||||| ||| ||  
 GGTCTACATT GTC CG  
 AC \_  
 GAM1615 FLJ14525 3' GCCTCTGTTTCATCTGGGA 51417 T \_  
 TCCCAGATG AAACAGAG C  
 ||||| ||||| |  
 AGGGTCTAC TTTGTCTC G  
 \_ C  
 GAM1615 FLJ20070 3' GCCTTATTATACATCTGAGA 34476 C AAC\_ A  
 TC CAGATGTA AG GC  
 || ||||| || ||  
 AG GTCTACAT TC CG  
 A ATTAT \_  
 GAM1615 FLJ20188 3' GCCTAGTTCCCACATCTGG 34698 A\_ \_ A  
 CCAGATGT AAC AG GC  
 ||||| ||| || ||  
 GGTCTACA TTG TC CG  
 CCC A \_  
 GAM1615 GOLGB1 3' GCTTCTGCTTAATCTGAGA 15633 C G A \_  
 TC CAGAT TAA CAGA GC  
 || |||| ||| ||| ||  
 AG GTCTA ATT GTCT CG  
 A \_ C T  
 GAM1615 KIAA1323 3' AGGTTGCTTTTTTTAATC 63037 G C  
 GAT TAAA AGAGCAACCT  
 ||| ||| |||||



			CTA ATTT TTTCGTTGGA		
			— T		
GAM1615	KIAA1363	3'	TTGCTCCATCTGGG	69268	TAAACA
			CCCAGATG GAGCAA		
			GGGTCTAC CTCGTT		
			—————		
GAM1615	KIAA1671	3'	GCCTTTTACACCTGGGA	65678	A C A
			TCCCAG TGTAAG AG GC		
			AGGGTC ACATTT TC CG		
			C — —		
GAM1615	KIAA1855	3'	CTGCCTACATCTGGGG	92340	AA
			TCCCAGATGTA CAG		
			GGGGTCTACAT GTC		
			CC		
GAM1615	OSBPL10	3'	GTTGCTTCTTTTACATC	35049	CA
			GATGTAAA GAGCAAC		
			CTACATTT TTCGTTG		
			TC		
GAM1615	STIM2	3'	GCTATTTACATCCTGG	40476	— CAG
			CCAG ATGTAAA AGC		
			GGTC TACATTT TCG		
			C A__		
GAM1615	TRIM2	3'	TGCAGTTTTACATCTGTGA	30946	C CAGA
			TC CAGATGTAAA GCA		
			AG GTCTACATTT CGT		
			T TGA_		
GAM1615	LOC142941	5'	TTTTGTTTAATCTGAGA	82887	C G
			TC CAGAT TAAACAGAG		
			AG GTCTA ATTTGTTTT		
			A _		
GAM1615	LOC144631	5'	GGTTGCTCTCCATCGG	83164	A TAAAC
			CC GATG AGAGCAACC		
			GG CTAC TCTCGTTGG		
			_ C__		
GAM1615	LOC152829	3'	GGTCTCTGTCCATCTGGGA	80693	AA CA
			TCCCAGATGT ACAGAG ACC		
			AGGGTCTACA TGTCTC TGG		
			C_ _		
GAM1615	LOC157858	3'	GTTGCTCTGGCTGTTTGGGA	86601	TAAA
			TCCCAGATG CAGAGCAAC		

	AGGGTTTGT GTCTCGTTG	
	CG__	
GAM1615 LOC158431 3'	AGGCTGCCCTTGTTACATCT 86829	AC A A
	AGATGTAA AG GCA CCT	
	TCTACATT TC CGT GGA	
	GT C C	
GAM1615 LOC158777 3'	CTGTCAACATCTGGGA 82001	AA
	TCCCAGATGT ACAG	
	AGGGTCTACA TGTC	
	AC	
GAM1615 LOC199907 3'	GCTTCTATTTACATTTG 88467	C _
	CAGATGTAAA AGA GC	
	GTTTACATTT TCT CG	
	A T	
GAM1615 LOC200597 5'	GGGGATCCCGCACATCTGGGA 88842	AAACA GCAA
	TCCCAGATGT GA CCT	
	AGGGTCTACA CT GGG	
	CGCC_ AG__	
GAM1615 LOC221296 3'	TTGCTCTGACAAATTGG 91974	A_ AAA
	CCAG TGT CAGAGCAA	
	GGTT ACA GTCTCGTT	
	AA _	
GAM1615 LOC255565 3'	GTTGCTCTGAATGTCTGGGA 95100	AAA
	TCCCAGATGT CAGAGCAAC	
	AGGGTCTGTA GTCTCGTTG	
	A__	
GAM1615 LOC255862 3'	GGATGCCTACGTCTG 94487	AAAC A A
	CAGATGT AG GCA CC	
	GTCTGCA TC CGT GG	
	__ _ A	
GAM1615 LOC90010 3'	GTTGCTCTGAATGTCTGGGA 61085	AAA
	TCCCAGATGT CAGAGCAAC	
	AGGGTCTGTA GTCTCGTTG	
	A__	
GAM1616 COL19A1 3'	CTCATCAAACCTTTACGATTT 8510	ATAAG _
A	TGAATCGTAAAGA GA GAG	
	ATTTAGCATTTCT CT CTC	
	CAAA_ A	
GAM1616 CSN10 3'	CTCTCCTTACATTTTACATTCA 17805	C AA
	TGAAT GTAAAG TAAGGAGAG	

		ACTTA CATTTT ATTCCTCTC	
		_ AC	
GAM1616 HCS	3'	CTCTTGAATTCTTTAC 38468	A_
		GTAAAGAAT AGGAG	
		CATTTCTTA TTCTC	
		AG	
GAM1616 SLC35A1	3'	CTCCTTATTCTCCAATTCA 21178	CGTAA
		TGAAT AGAATAAGGAG	
		ACTTA TCTTATTCCTC	
		ACC_	
GAM1616 FLJ21687	3'	CTCTCCTTATTCATTAATTTCA 45856	TCG A
		TGAA TAA GAATAAGGAGAG	
		ACTT ATT CTTATTCCTCTC	
		TA_ A	
GAM1616 GRID1	3'	CTCTCCCTTCCACCTTTACGA 68496	AATAA_
		TCGTAAAG GGAGAG	
		AGCATTTC CCTCTC	
		CACCTTC	
GAM1616 KIAA0853	5'	CTCTCCTTATCCTTCACATTC 30540	C A A
		GAAT GT AAG ATAAGGAGAG	
		CTTA CA TTC TATTCCTCTC	
		_ C C	
GAM1616 NR1I3	5'	CTCTCCTTATAATAGACACTTC 17603	TC AAAGA
A		TGAA GT ATAAGGAGAG	
		ACTT CA TATTCCTCTC	
		CA GATAA	
GAM1616 PTPN3	3'	CTCAGGATTCCCTAACGATTCA 11057	AAA AAG
		TGAATCGT GAAT GAG	
		ACTTAGCA CTTA CTC	
		ATC GGA	
GAM1616 LOC146050	3'	CTCTCCTTGTCCTTAC 77637	A A
		GTAA GA TAAGGAGAG	
		CATT CT GTTCCTCTC	
		C _	
GAM1616 LOC157317	3'	CTCTTGAATTCTTTAC 81401	A_
		GTAAAGAAT AGGAG	
		CATTTCTTA TTCTC	
		AG	
GAM1616 LOC256112	5'	CTCTCCTTATTCTTTCCCTCA 96366	ATCGT
		TGA AAAGAATAAGGAGAG	

		ACT TTTCTTATTCCTCTC	
		CCCC_	
GAM1617 BCL6	5'	CACCAAGTCCTCCCCTGCCAC 8125	C A_ A
		GTG CA GGAG ACTTGGTG	
		CAC GT CCTC TGAACCAC	
		C CC C	
GAM1617 HEPH	3'	TTCTCCTTGGCAGTGA 57034 G	
		TCA TGCCAAGGAGAA	
		AGT ACGGTTCTCTT	
		G	
GAM1617 HEPH	3'	TTCTCCTTGGCAGTGA 28966 G	
		TCA TGCCAAGGAGAA	
		AGT ACGGTTCTCTT	
		G	
GAM1617 KRT16	5'	CACCTCCCTCCTTGGCAC 95196	AACTT
		GTGCCAAGGAG GGTG	
		CACGGTTCCTC CCAC	
		CCT__	
GAM1617 MTCP1	5'	CACCAAGGACTTGGTACTGA 26428	GAGAA
		TCAGTGCCAAG CTTGGTG	
		AGTCATGGTTC GAACCAC	
		AG__	
GAM1617 PCOLN3	3'	CCTGTCCCCTTGGGCACTGA 10910	_ A ACTT
		TCAGTGCC AAGG GA GG	
		AGTCACGG TTCC CT CC	
		G C GT__	
GAM1617 PTPN7	3'	CAGGCCCTCCCTGGCACTG 54557	A AA
		CAGTGCCA GGAG CTTG	
		GTCACGGT CCTC GGAC	
		C CC	
GAM1617 PTPN7	3'	CAGGCCCTCCCTGGCACTG 54546	A AA
		CAGTGCCA GGAG CTTG	
		GTCACGGT CCTC GGAC	
		C CC	
GAM1617 PTPN7	3'	CAGGCCCTCCCTGGCACTG 11064	A AA
		CAGTGCCA GGAG CTTG	
		GTCACGGT CCTC GGAC	
		C CC	
GAM1617 TBL2	3'	CCACCTGGCACTGA 52181	A AGAACT
		TCAGTGCCA GG TGG	

AGTCACGGT CC ACC

GAM1617 TBL2 3' CCACCTGGCACTGA 24925 A AGAACT  
TCAGTGCCA GG TGG  
||||||| || |||  
AGTCACGGT CC ACC

GAM1617 TRPM6 3' TGGGTTCTCCTAGACACTGA 34551 CCA  
TCAGTG AGGAGAACTTG  
||||| |||||  
AGTCAC TCCTCTTGGGT  
AGA

GAM1617 BRD4 3' CACCCCCTCGCTGGCACTGA 54273 AG AACTT  
TCAGTGCCA GAG GGTG  
||||||| ||| ||||  
AGTCACGGT CTC CCAC  
CG CC\_\_

GAM1617 C20orf106 5' CACCAAGGGCCTGGCAC 55055 A AGAA  
GTGCCA GG CTTGGTG  
||||| || |||||  
CACGGT CC GAACCAC  
\_ GG\_\_

GAM1617 CAMKK1 3' GCCCTCCTTGGCCTGA 50173 T AACTT  
TCAG GCCAAGGAG GGT  
||| ||||| |||  
AGTC CGGTTCTC CCG

GAM1617 FLJ12294 3' ACCAGCACTGGCACTGA 47005 A GAGAAC  
TCAGTGCCA G TTGGT  
||||||| | ||||  
AGTCACGGT C GACCA  
\_ AC\_\_

GAM1617 GPR88 5' ACTTGCTCCTGGCACTGA 41874 A AACTT  
TCAGTGCCA GGAG GGT  
||||||| |||| |||  
AGTCACGGT CCTC TCA  
\_ GT\_\_

GAM1617 KIAA1086 3' CAGGCGCCTCCTGGCACTGA 70743 A AA\_  
TCAGTGCCA GGAG CTTG  
||||||| |||| |||  
AGTCACGGT CCTC GGAC  
\_ CGC

GAM1617 KIAA1372 5' GTTTTCCTCAGCACTGA 91651 CA  
TCAGTGC AGGAGAAC  
||||| |||||  
AGTCACG TCCTTTTG  
AC

GAM1617 KIAA1538 5' CACCAAGTTCCTGCTCAC 71533 CCA A  
GTG AGG GAACTTGGTG  
||| ||| |||||

			CAC TCC CTTGAACCAC		
			TCG _		
GAM1617	MAP2K4	3'	CTTGGGCCTCCCTGGCACTGA 11548	A	AA T
			TCAGTGCCA GGAG CT GG		
			AGTCACGGT CCTC GG TC		
			C CG T		
GAM1617	NPTXR	3'	GCCTCTCCCCAGCACTGA 26645	CAA	ACTT
			TCAGTGC GGAGA GGT		
			AGTCACG CCTCT CCG		
			ACC _		
GAM1617	NPTXR	3'	GCCTCTCCCCAGCACTGA 54181	CAA	ACTT
			TCAGTGC GGAGA GGT		
			AGTCACG CCTCT CCG		
			ACC _		
GAM1617	SNAP29	3'	ACCAAGTTCTTCCAGCA 16536	CAA	
			TGC GGAGAACTTGGT		
			ACG CTTCTTGAACCA		
			AC_		
GAM1617	TUBAL2	3'	CACCCTGCCCTAGGCACTGA 38447	A	AGA ACTT
			TCAGTGCC AGG GGTG		
			AGTCACGG TCC CCAC		
			A CGTC_		
GAM1617	UBCE7IP5	3'	TTCCTCTTGGCACTGA 30165	GA	
			TCAGTGCCAAG GAA		
			AGTCACGGTTC CTT		
			TC		
GAM1617	LOC145622	3'	CACCACTCAACTGCCTGGCACT 77295	A	_ AACT_
	GA		TCAGTGCCA GG AG TGGTG		
			AGTCACGGT CC TC ACCAC		
			_ G AACTC		
GAM1617	LOC146268	3'	CACCAAGTGAAAGCGGACTGA 77802	G	AAGGAGA
			TCAGT CC ACTTGGTG		
			AGTCA GG TGAACCAC		
			_ CGAAAG_		
GAM1617	LOC146435	3'	CACCAAATGGAGCTTGGCACT 77896	GAGAAC	
			AGTGCCAAG TTGGTG		
			TCACGGTTC AACCAC		
			GAGGTA		
GAM1617	LOC149761	5'	CACCAAGGGCCTGGCAC 79483	A	AGAA
			GTGCCA GG CTTGGTG		

			CACGGT CC GAACCAC		
			_ GG_		
GAM1617	LOC155060	3'	GTTCTCCCAGGCACTGA	86332	AA
			TCAGTGCC GGAGAAC		
			AGTCACGG CCTCTTG		
			AC		
GAM1617	LOC220558	5'	CACCAAAGTCCTTGGCACTG	91137	GAAC
			CAGTGCCAAGGA TTGGTG		
			GTCACGGTTCCT AACCAC		
			GA_		
GAM1617	LOC222060	5'	CTAAGTCCTCCCTGGCACTGG	94106	A A
			TCAGTGCCA GGAG ACTTGG		
			GGTCACGGT CCTC TGAATC		
			C C		
GAM1618	BCLG	3'	TCTTAGGTTTACTGCTACATCC	56977	A A C TA
	A		TG ATGTAG AG AAG TGAGA		
			AC TACATC TC TTT ATTCT		
			C G A GG		
GAM1618	BCLG	3'	TCTTAGGTTTACTGCTACATCC	56983	A A C TA
	A		TG ATGTAG AG AAG TGAGA		
			AC TACATC TC TTT ATTCT		
			C G A GG		
GAM1618	BCLG	3'	TCTTAGGTTTACTGCTACATCC	47781	A A C TA
	A		TG ATGTAG AG AAG TGAGA		
			AC TACATC TC TTT ATTCT		
			C G A GG		
GAM1618	FAT2	3'	TTCTCATACCTGCCACAGCTC	7549	A_ AGAA A
			GA TGT GCA GTATGAGAA		
			CT ACA CGT CATACTCTT		
			CG CC_ C		
GAM1618	FPGS	3'	TTCCCACACCTGCCTGCGTTC	17092	AA A A A
			GAATGTAG GCA GT TG GAA		
			CTTGCGTC CGT CA AC CTT		
			_ C C C		
GAM1618	GPM6B	3'	TCTCATACTTAAACATT	67077	AGAAGC
			AATGT AAGTATGAGA		
			TTACA TTCATACTCT		
			AA_		
GAM1618	GRM1	3'	TCTCATGTTCCATATTCA	5918	A GCAAG
			TGAATGT GAA TATGAGA		

		ACTTATA CTT	GTACTCT		
		C	_____		
GAM1618	IL1RN	3'	TTCCATGTCGCCTCTGCATTCA 5145	A AAG	A
			TGAATGTAGA GC TATG GAA		
			ACTTACGTCT CG GTAC CTT		
			C CT_ _		
GAM1618	LIFR	3'	TTCTCATGTACTCTACCTTCA 9749	T	AGCAAG
			TGAA GTAGA TATGAGAA		
			ACTT CATCT GTACTCTT		
			C CAT_		
GAM1618	NRG1	3'	TTGGTATCTACTTCTACATCCA 15692	A	CAA G
			TG ATGTAGAAG GTAT AG		
			AC TACATCTTC TATG TT		
			C ATC G		
GAM1618	PCDHB9	3'	TTCATTGCCTCTACATT 38950	A	AGT
			AATGTAGA GCA ATGAG		
			TTACATCT CGT TACTT		
			C		
GAM1618	SLC22A1	3'	CTCATACTTGCCTAC 11761	AA	
			GTAG GCAAGTATGAG		
			CATC CGTTCATACTC		
			_____		
GAM1618	TTN	3'	CTTATACTCTACACTCA 55920	A	AGCAA
			TGA TGTAGA GTATGAG		
			ACT ACATCT CATATTC		
			C		
GAM1618	TTN	3'	CTTATACTCTACACTCA 55938	A	AGCAA
			TGA TGTAGA GTATGAG		
			ACT ACATCT CATATTC		
			C		
GAM1618	TTN	3'	CTTATACTCTACACTCA 55950	A	AGCAA
			TGA TGTAGA GTATGAG		
			ACT ACATCT CATATTC		
			C		
GAM1618	DIO2	3'	CTCAGTTGTAACTTCTACATT 5830		CAAGTA_
	CA		TGAATGTAGAAG TGAG		
			ACTTACATCTTC ACTC		
			AATTGTTG		
GAM1618	DIO2	3'	CTCAGTTGTAACTTCTACATT 25682		CAAGTA_
	CA		TGAATGTAGAAG TGAG		



		ACTTACATCTTC	ACTC		
		AATTGTTG			
GAM1618	DKFZP434K028	3'	GCGTGCTTCTACATCCA	93235	A A
			TG ATGTAGAAGCA GT		
			AC TACATCTTCGT CG		
			C G		
GAM1618	DKFZP566D193	3'	TTCTCATACTTCCCCACATT	85570	AGAAGC
			AATGT AAGTATGAGAA		
			TTACA TTCATACTCTT		
			CCCC__		
GAM1618	FLJ13263	3'	CTCTACACTTTTACATTCA	47091	CAA T
			TGAATGTAGAAG GTA GAG		
			ACTTACATTTTC CAT CTC		
			A__ _		
GAM1618	FLJ22965	3'	TTCCCATGATTCTCCTACATT	42055	A C GT_ A
	CA		TGAATGTAG AG AA ATG GAA		
			ACTTACATC TC TT TAC CTT		
			C _ AGT C		
GAM1618	GP5	3'	TTCTCATACTGGAGGTTACATT	15660	AAGCA
	CA		TGAATGTAG AGTATGAGAA		
			ACTTACATT TCATACTCTT		
			GGAGG		
GAM1618	GP5	3'	ACTTGCTTTACATCCA	15639	A A
			TG ATGTAGA GCAAGT		
			AC TACATTT CGTTCA		
			C _		
GAM1618	H2BFQ	3'	TCTCATACTTGCCTGTCTCAT	59360	T A__
			ATG AGA GCAAGTATGAGA		
			TAC TCT CGTTCATACTCT		
			_ GTC		
GAM1618	KCNT1	3'	CTCTGACACCTGCTTCTACATC	61832	A A AT__
	A		TGA TGTAGAAGCA GT GAG		
			ACT ACATCTTCGT CA CTC		
			_ C CAGT		
GAM1618	KIAA0232	3'	TCTCATACTGCAGTTACATTTA	72758	AA A
			TGAATGTAG GCA GTATGAGA		
			ATTTACATT CGT CATACTCT		
			GA _		
GAM1618	KIAA1028	3'	TCTTACGCTTATACATTCA	91950	G AAGTA
			TGAATGTA AAGC TGAGA		

		ACTTACAT TTCG ATTCT	
		A C_____	
GAM1618 KIAA1948	5'	TCTCATACACAACCTCATTCA 82407	T AAGCAA
		TGAATG AG GTATGAGA	
		ACTTAC TC CATACTCT	
		_ AACA_	
GAM1618 MGC:13379	3'	ACTCTTCTACACTCA 33243 A CA	
		TGA TGTAAGAAG AGT	
		ACT ACATCTTC TCA	
		C _____	
GAM1618 PDZD2	5'	CTCCTGGCATCTACATTCA 80869 A A TAT	
		TGAATGTAGA GC AG GAG	
		ACTTACATCT CG TC CTC	
		A G _____	
GAM1618 SAD1	5'	TCTCACGCCTACATTCA 64025 AAGCAA TA	
		TGAATGTAG G TGAGA	
		ACTTACATC C ACTCT	
		_____ GC	
GAM1618 LOC147054	5'	CTCCCACTGATTCTACATT 83919 GCA AT	
		AATGTAGAA AGT GAG	
		TTACATCTT TCA CTC	
		AG_ CC	
GAM1618 LOC151098	5'	TCTTCGGTCTACTTCTACAGTC 80117 A CA TAT_	
A		TGA TGTAAGAAG AG GAGA	
		ACT ACATCTTC TC TTCT	
		G A_ TGGC	
GAM1618 LOC152078	5'	CTTGAGAGTCTTCTACATTCA 80454 _____	
		TGAATGTAGAAG CAAG	
		ACTTACATCTTC GTTC	
		TGAGA	
GAM1618 LOC153516	3'	CTAACACTTGTCCCTACATTCA 56708 AA ATG	
		TGAATGTAG GCAAGT AG	
		ACTTACATC TGTTC TC	
		C_ CAA	
GAM1618 LOC157958	3'	TCTTCACATTCTACATTCA 81639 GCAAGTAT	
		TGAATGTAGAA GAGA	
		ACTTACATCTT TTCT	
		ACAC_____	
GAM1619 ABCA1	3'	AAAAATGTGGGTGTCTCCAGGC 18543 TCA	
A		TGCCTGGAGACACTT GTTTTT	

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ACGGACCTCTGTGGG TAAAAA
      TG_
GAM1619 ABCC12  5' TGAAAGTGTCCCCAGGC  52649  A
      GCCTGG GACACTTTCA
      ||||| |||||
      CGGACC CTGTGAAAGT
      C
GAM1619 ABCC12  5' TGAAAGTGTCCCCAGGC  52650  A
      GCCTGG GACACTTTCA
      ||||| |||||
      CGGACC CTGTGAAAGT
      C
GAM1619 ADH1B   3' AAAAAGTGAAGTATTCCCAG 72640  A CACT
      CTGG GA  TTCAGTTTTT
      ||| || |||||
      GACC CT  AAGTCAAAAA
      _ TATC
GAM1619 DDEF2   3' AAAAGTGAATTTCCCA  13947  A CACT
      TGG GA  TTCAGTTTT
      ||| || |||||
      ACC CT  AAGTCAAAA
      _ TT_
GAM1619 EHF     3' AACGCAAAATGTCTCTAGACA 24061  C  C CA
      TG CTGGAGACA TTT GTT
      || ||||| ||| |||
      AC GATCTCTGT AAA CAA
      A  A CG
GAM1619 GRAF     3' GGAAGAGCATCTCCAGGCA  30568  CA_
      TGCCTGGAGA CTTTC
      ||||| ||||
      ACGGACCTCT GAAGG
      ACGA
GAM1619 HMOX1    3' AACGAAAAGCACATCCAGGCA 9233  GACA CA
      TGCCTGGA CTTT GTT
      ||||| ||| |||
      ACGGACCT GAAA CAA
      ACAC AG
GAM1619 IL24     5' AAGAACCAGCTGCCTCCAGGCA 22440  A _ TTCA
      TGCCTGGAG CA CT  GTTTTT
      ||||| || || ||||
      ACGGACCTC GT GA  CAAGAA
      C C C_
GAM1619 KAL1     3' AACCAAAAATGTCTCCAG  4008  C CA
      CTGGAGACA TTT GTT
      ||||| ||| |||
      GACCTCTGT AAA CAA
      A AC
GAM1619 SON      3' CTGTAAAAACATCTCCAGGC 57193  CAC_ _
      GCCTGGAGA TTT CAG
      ||||| ||| |||

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		CGGACCTCT AAA GTC	
		ACAA T	
GAM1619 SON	3'	CTGTAAAAACATCTCCAGGC 54202	CAC_ _
		GCCTGGAGA TTT CAG	
		CGGACCTCT AAA GTC	
		ACAA T	
GAM1619 SON	3'	CTGTAAAAACATCTCCAGGC 57190	CAC_ _
		GCCTGGAGA TTT CAG	
		CGGACCTCT AAA GTC	
		ACAA T	
GAM1619 TEM6	3'	GGAACGTTTCCAGGCA 42746	AC
		TGCCTGGAGAC TTTC	
		ACGGACCTTTG AAGG	
		C_	
GAM1619 C20orf48	3'	AAAGTGGCACATGTCCAGGCA 46365	GA_____
		TGCCTGGA CACTTT	
		ACGGACCT GTGAAA	
		GTACACG	
GAM1619 FLJ20013	3'	GAACGTACCTCCAGGCA 34331	AC T
		TGCCTGGAG AC TTC	
		ACGGACCTC TG AAG	
		CA C	
GAM1619 KIAA1513	5'	AAAAGTAAAAATCACAGC 68562	C GA CAC
		G CTG GA TTTCAGTTTT	
		C GAC CT AAAGTCAAAA	
		_ A_ A_	
GAM1619 KIAA1941	3'	AAAATGTCTCTAGACA 74832	C C
		TG CTGGAGACA TTT	
		AC GATCTCTGT AAA	
		A A	
GAM1619 MIL1	3'	AAACGAAAATGTCTCTAGACA 31090	C C A
		TG CTGGAGACA TTTC GTTT	
		AC GATCTCTGT AAAG CAAA	
		A A _	
GAM1619 SAE1	3'	TGAAGGCATCTCCAGGCA 18535	CA
		TGCCTGGAGA CTTTCA	
		ACGGACCTCT GGAAGT	
		AC	
GAM1619 SETBP1	3'	AAAAGTGAACCCAG 31455	AGACAC
		CTGG TTTCAGTTTT	

			GACC	AAAGTCAAAA		
			CC	_____		
GAM1619	SLC39A3	3'	AAAATGTTTCCAGACA	57971	C	C
			TG CTGGAGACA TTT			
			AC GACCTTTGT AAA			
			A	A		
GAM1619	TRIM2	3'	AAAAACAAGACATCTCCAGGTA	30938		CA_ TCA
			TGCCTGGAGA CTT GTTTTT			
			ATGGACCTCT GAA CAAAAA			
			ACA	_____		
GAM1619	LOC144558	3'	ACCAAAATTGTCTCCAGACA	83144	C	C CA
			TG CTGGAGACA TTT GT			
			AC GACCTCTGT AAA CA			
			A	T AC		
GAM1619	LOC145387	3'	GAAAAATGTGTCCAGGCA	83355		G C_
			TGCCTGGA ACA TTTC			
			ACGGACCT TGT AAAG			
			G	AA		
GAM1619	LOC145483	3'	AACCAAAAATGTCTCCAG	77237		C CA
			CTGGAGACA TTT GTT			
			GACCTCTGT AAA CAA			
			A	AC		
GAM1619	LOC151623	3'	AACCAAAATTGTCTCCAGACA	85453	C	C CA
			TG CTGGAGACA TTT GTT			
			AC GACCTCTGT AAA CAA			
			A	T AC		
GAM1619	LOC152313	3'	AAAATGTCTCCAGACA	85656	C	C
			TG CTGGAGACA TTT			
			AC GACCTCTGT AAA			
			A	A		
GAM1619	LOC152313	5'	AAAATGTCTCCAGACA	85657	C	C
			TG CTGGAGACA TTT			
			AC GACCTCTGT AAA			
			A	A		
GAM1619	LOC157278	3'	ACCAAAATTGTCTCCAGACA	86420	C	C CA
			TG CTGGAGACA TTT GT			
			AC GACCTCTGT AAA CA			
			A	T AC		
GAM1619	LOC157376	3'	AAAAACCTCCTGTCTCCA	81428		CTTTCA
			TGGAGACA GTTTTT			

ACCTCTGT CAAAAA  
 CCTC\_\_  
 GAM1619 LOC221962 3' ACCAAAATTGTCTCCAGACA 92677 C C CA  
 TG CTGGAGACA TTT GT  
 || ||||| || ||  
 AC GACCTCTGT AAA CA  
 A T AC  
 GAM1619 LOC222681 5' AAAAACTGAAGATTCCAG 92848 ACAC  
 CTGGAG TTTCAGTTTTT  
 ||||| |||||  
 GACCTT GAAGTCAAAAA  
 A\_\_  
 GAM1619 LOC255461 3' ACCAAAATTGTCTCCAGACA 97313 C C CA  
 TG CTGGAGACA TTT GT  
 || ||||| || ||  
 AC GACCTCTGT AAA CA  
 A T AC  
 GAM1619 LOC255516 3' ACCAAAATTGTCTCCAGACA 97326 C C CA  
 TG CTGGAGACA TTT GT  
 || ||||| || ||  
 AC GACCTCTGT AAA CA  
 A T AC  
 GAM1619 LOC256950 3' AAAGTGTCTGCAGGCA 95425 G  
 TGCCTG AGACACTTT  
 ||||| |||||  
 ACGGAC TCTGTGAAA  
 G  
 GAM1619 LOC257507 5' AAAAACTGAAGATTCCAG 97770 ACAC  
 CTGGAG TTTCAGTTTTT  
 ||||| |||||  
 GACCTT GAAGTCAAAAA  
 A\_\_  
 GAM1619 LOC257625 5' AAAAACTGAAGATTCCAG 97901 ACAC  
 CTGGAG TTTCAGTTTTT  
 ||||| |||||  
 GACCTT GAAGTCAAAAA  
 A\_\_  
 GAM1620 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
 GTA GGAT GGGTTGTTT  
 ||| ||| |||||  
 CGT CCTA CCAACAAA  
 C CGTG\_  
 GAM1620 LCT 3' AACCGTAAAAATCCTT 9697 G  
 AAGGATTTTTA GGTT  
 ||||| |||||  
 TTCCTAAAAAT CCAA  
 G  
 GAM1620 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
 GTAAGGATTTTATAGGGTTGTTT  
 ||||| |||||

CATTCCTAAAAATCCCAACAAA

GAM1620 FBXO30 3' AACTAAAAAATCCTGAC 49573 A AG  
GT AGGATTTTT GTT  
|| ||||| |||  
CA TCCTAAAAA TCAA  
G AA

GAM1620 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTT  
GTAAG AGGGTTGTT  
|||| |||||  
CATTC TCCCAACAA  
AT\_\_\_\_

GAM1620 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
TAAG TTTT GGGTTGTTT  
||| ||| |||||  
GTTC AAAA CCAACAAA  
\_\_\_ C

GAM1620 SMT3H2 3' AACAACATAAAAATCCTTGC 22670 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1620 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
GTAAGGATTTTT GGGTT  
||||||| |||||  
CGTTCCTAAAAA TCCAA  
GTA

GAM1620 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
GGAT TT GGGTTGTTT  
||| || |||||  
CCTG AA CCAACAAA  
T\_ C

GAM1620 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
C GTA GGATTTTT TTGTTT  
|| ||||| |||||  
CGT CCTAAAAA AACAAA  
C GATAA

GAM1620 LOC148089 3' GGCCCTAAAAATTCCTAC 78637 A  
GTA GGATTTTTAGGGTT  
|| |||||  
CAT CTAAAAATCCCGG  
C

GAM1620 LOC154547 3' AACAAACATAAAAATCCTTGC 76050 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1620 LOC158104 3' ACAGCCAAAAATCCTTA 60313 AG  
TAAGGATTTTT GGTGT  
||||||| |||||

ATTCCTAAAAA CCGACA

GAM1620 LOC205880 5' AAACAACCATCATCCTGAC 90709 A TTTTAG  
GT AGGAT GGTGTGTT  
|| |||| |||||  
CA TCCTA CCAACAAA  
G CTA\_\_

GAM1620 LOC221561 3' AACAAACATAAAAAATCCTTGC 92130 GG  
GTAAGGATTTTGA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1620 LOC257591 3' AACAAACATAAAAAATCCTTGC 97840 GG  
GTAAGGATTTTGA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1620 LOC51145 3' AGCTAAAATCCTTAC 32393 TAG  
GTAAGGATTTT GTTGTT  
||||||| |||||  
CATTCCTAAAA TCGA

GAM1621 ABCC3 3' AGCAGAAAACCTGGCCCTGC 39149 TAG C  
GCAGG TAGTTTTT GCT  
|||| ||||| |||||  
CGTCC GTCAAAAG CGA  
CG\_ A

GAM1621 ALS2 3' AGCAAAAAAATGTCATC 40505 A CC  
GGT GTAGTTTT GCT  
||| ||||| |||||  
CTA CGTCAAAA CGA  
AA

GAM1621 CLU 3' AGAATTGCTCCTGCA 8447 T  
TGCAGG AGTAGTTTT  
||||| |||||  
ACGTCC TCGTTAAGA

GAM1621 CPM 3' AGCAAAAAAATGCCTGCA 59674 GTAG CC  
TGCAGGTA TTTT GCT  
|||||| ||||| |||||  
ACGTCCGT AAAA CGA  
AA\_ A\_

GAM1621 CXADR 5' AGCGAGAGCCGCCTACCTGCA 7191 \_TA C  
TGCAGGTA G GTTTTC GCT  
||||||| | ||||| |||||  
ACGTCCAT C CGAGAG CGA  
C GC \_

GAM1621 DIAPH2 3' AGCAGAAAACCTGTCTG 22061 TAG C  
CAGG TAGTTTTT GCT  
||| ||||| |||||



			GTCT GTCAAAAG CGA		
			_____ A		
GAM1621	FXYD6	3'	AGCAGAGGCAACTCCCGCA 41836	A T A	CC
			TGC GG AGT GTTTT GCT		
			ACG CC TCA CGGAG CGA		
			C _ A A_		
GAM1621	GUCY1A3	3'	GCACTTACTACCTGTA 63488	_	TTTCC
			TGCAGGTAGTA GT GC		
			ATGTCCATCAT CA CG		
			T _____		
GAM1621	HLCS	3'	AGCGAAACCTGTCTACCTGC 4659	_ T C	
			GCAGGTAG TAG TTTC GCT		
			CGTCCATC GTC AAAG CGA		
			T C _		
GAM1621	MBD1	3'	GGCCTGACTACTGCCCACA 31774	CA	TT_
			TG GGTAGTAGTT CC		
			AC CCGTCATCAG GG		
			AC TCC		
GAM1621	MBD1	3'	GGCCTGACTACTGCCCACA 31782	CA	TT_
			TG GGTAGTAGTT CC		
			AC CCGTCATCAG GG		
			AC TCC		
GAM1621	MBD1	3'	GGCCTGACTACTGCCCACA 31789	CA	TT_
			TG GGTAGTAGTT CC		
			AC CCGTCATCAG GG		
			AC TCC		
GAM1621	MBD1	3'	GGCCTGACTACTGCCCACA 9948	CA	TT_
			TG GGTAGTAGTT CC		
			AC CCGTCATCAG GG		
			AC TCC		
GAM1621	ORC4L	3'	CGGAAAACCTATTGTCC 62056	_	
			GG TAGTAGTTTTCCG		
			CC GTTATCAAAAGGC		
			T		
GAM1621	SPAG9	5'	AGCGAAAAACTATGCTGACC 14272	_ _	C
			GGT AGT AGTTTT CGCT		
			CCA TCG TCAAAA GCGA		
			G TA A		
GAM1621	YWHAZ	3'	AGCAAAGAAAACCTGCCTAC 12699	_	C_
			GTAG TAGTTTTT GCT		

			CATC GTCAAAAG CGA		
			C AAA		
GAM1621	ARL8	3'	AGCATTTTTACTACCAGCA	93195	A TTTTCC
			TGC GGTAGTAG GCT		
			ACG CCATCATT CGA		
			A TTTA__		
GAM1621	C1QTNF4	3'	AGCGGAAAGCGGGCACGCGCA	49132	AG A A_
			TGC GT GT GTTTTCCGCT		
			ACG CA CG CGAAAGGCGA		
			CG _ GG		
GAM1621	CECR1	3'	AGCGGTGGTGCTCTACCTGCA	33805	T TTT_
			TGCAGGTAG AGT CCGCT		
			ACGTCCATC TCG GGCGA		
			_ TGGT		
GAM1621	FLJ12568	5'	AAAATTACTTATCTGCA	46497	_
			TGCAGGTA GTAGTTTT		
			ACGTCTAT CATTAAAA		
			T		
GAM1621	FLJ31890	3'	GCAGAGCTATCTGCA	91339	AGTTT C
			TGCAGGTAGT TC GC		
			ACGTCTATCG AG CG		
			_____ A		
GAM1621	FRSB	3'	CGGATTACTCCTGCA	19091	T TTT
			TGCAGG AGTAG TCCG		
			ACGTCC TCATT AGGC		
			_____		
GAM1621	FUK	5'	AGCGGAGGAGCCACC	58971	A AG
			GGT GT TTTTCCGCT		
			CCA CG AGGAGGCGA		
			C _		
GAM1621	H2AFJ	3'	AGAACTACTACTACA	36838	CA
			TG GGTAGTAGTTTT		
			AC TCATCATCAAGA		
			AC		
GAM1621	HS6ST	3'	AGCGGAAAGTGGACCTGC	62022	AGTA
			GCAGGT GTTTTCCGCT		
			CGTCCA TGAAAGGCGA		
			GG_		
GAM1621	HS6ST1	3'	AGCGGAAAGTGGACCTGC	16658	AGTA
			GCAGGT GTTTTCCGCT		

			CGTCCA	TGAAAGGCGA		
			GG__			
GAM1621	KIAA0514	3'	GCAGAAGAACACCTG	28084	A AG	C
			CAGGT GT TTTTC GC			
			GTCCA CA AGAAG CG			
			— — A			
GAM1621	KIAA0930	3'	AGCGGAAAACTGTACTT	70537	G	
			AGGTA TAGTTTTCCGCT			
			TTCAT GTCAAAAGGCGA			
			—			
GAM1621	KIAA0995	3'	GCAGAAGATGCCTGCA	72877	AGTA	C
			TGCAGGT GTTTTC GC			
			ACGTCCG TAGAAG CG			
			— — A			
GAM1621	KIAA1128	3'	AGCAAAAATAATATCTGCA	68469	GTA	CC
			TGCAGGTA GTTTT GCT			
			ACGTCTAT TAAAA CGA			
			AA_ A_			
GAM1621	KIAA1344	3'	AGCAGGAAACTACCT	72445	AGTT	_
			AGGTAGT TTCC GCT			
			TCCATCA AAGG CGA			
			— — A			
GAM1621	KIAA1678	3'	AGCAGAAAACTATTGTC	72303	GT	C
			G AGTAGTTTTTC GCT			
			C TTATCAAAAG CGA			
			TG A			
GAM1621	KRTAP3-1	3'	AGCACTCACTACTGCCTACA	49229	C	TTTCC
			TG AGGTAGTAGT GCT			
			AC TCCGTCATCA CGA			
			A CTCA_			
GAM1621	LRBA	3'	AGCAGAAAACTGGCTGCT	22051	_	C
			GGTAGT AGTTTTTC GCT			
			TCGTCTG TCAAAAG CGA			
			G A			
GAM1621	MGC12217	3'	AGCAGAAAACTAGCTTGTA	51309	AG	C
			TGCAGGT TAGTTTTTC GCT			
			ATGTTCTG ATCAAAAG CGA			
			— — A			
GAM1621	ORC6L	3'	AGCAAAGCAGCCTACCTG	26720	TA_	CC
			CAGGTAG GTTTT GCT			

			GTCCATC CGAAA CGA		
			CGA _		
GAM1621 PELI2	3'	GCTTACTCTACCTGCA	41182	T	TTTCC
		TGCAGGTAG AGT GC			
		ACGTCCATC TCA CG			
		_ TT _			
GAM1621 PHF5A	3'	GCCTACTACTACCAGCA	51286	A	TTTCC
		TGC GG TAGTAGT GC			
		ACG CCATCATCA CG			
		A TC _			
GAM1621 REC8	3'	AGCAGAAAACAAGCTGCT	17616	A_	C
		GGTAGT GTTTTTC GCT			
		TCGTCCG CAAAAG CGA			
		AA A			
GAM1621 RINZF	5'	AGCGGAGGGTCTCCCCGCA	43696	A T	TA TT
		TGC GG AG G TTCCGCT			
		ACG CC TC T GAGGCGA			
		C C _ GG			
GAM1621 SLC12A8	5'	AGCGGAAAAGGTATCCCTCA	44895	C	TAGTAG
		TG AGG TTTTCCGCT			
		AC TCC AAAAGGCGA			
		_ CTATGG			
GAM1621 SLC1A7	5'	AGCAACTCCGACCACCTGC	21905	A _	TTCC
		GCAGGT GT AGTT GCT			
		CGTCCA CA TCAA CGA			
		C GCC _			
GAM1621 SMCR8	3'	GCACCTACTACCTGCA	58599		TTTTCC
		TGCAGGTAGTAG GC			
		ACGTCCATCATC CG			
		CA _			
GAM1621 TNRC11	5'	AACTACATTACCTGCA	17600	_	
		TGCAGGTA GTAGTT			
		ACGTCCAT CATCAA			
		TA			
GAM1621 TPD52	3'	AGAACTACTAGCTACA	17421	C G	
		TG AG TAGTAGTTTT			
		AC TC ATCATCAAGA			
		A G			
GAM1621 WBSCR20A	3'	AGCAAAAGTGTTGCCTGCA	49648	G	CC
		TGCAGGTAGTA TTTT GCT			

ACGTCCGTTGT AAAA CGA  
 G \_  
 GAM1621 LOC115051 3' AGCGGAAAGTGGACCTGC 60033 AGTA  
 GCAGGT GTTTTCCGCT  
 ||||| |||||  
 CGTCCA TGAAAGGCGA  
 GG\_  
 GAM1621 LOC126520 5' AGCGGCCTGCGCTACCTGCA 74521 A TTT  
 TGCAGGTAGT GT CCGCT  
 ||||| || |||||  
 ACGTCCATCG CG GGCGA  
 \_ TCC  
 GAM1621 LOC126603 5' GGGAAGTACTACTGCA 75395 G TT  
 TGCAG TAGTAGTT C  
 ||||| ||||| |  
 ACGTC ATCATCAA G  
 \_ GG  
 GAM1621 LOC140214 5' AGCGAGAGACTACATAC 75957 \_ TC  
 GTA GTAGTTT CGCT  
 ||| ||||| |||||  
 CAT CATCAGA GCGA  
 A GA  
 GAM1621 LOC145497 5' AGAACTACTACCTCCA 77213 C  
 TG AGGTAGTAGTTTT  
 || |||||  
 AC TCCATCATCAAGA  
 C  
 GAM1621 LOC158267 3' GCACATAGTACCTGCA 81831 G \_ TTTCC  
 TGCAGGTA TA GT GC  
 ||||| || || ||  
 ACGTCCAT AT CA CG  
 G A \_  
 GAM1621 LOC158364 5' AGCGGAAGTATTCTACCTG 81873 TAGT  
 CAGGTAG TTTCCGCT  
 ||||| |||||  
 GTCCATC GAAGGCGA  
 TTAT  
 GAM1621 LOC160711 5' AGCAAAAAGACTACATGCA 87070 G AG CC  
 TGCA GTAGT TTTT GCT  
 ||||| ||||| |||||  
 ACGT CATCA AAAA CGA  
 A GA A\_  
 GAM1621 LOC161003 3' AGCAAAAATGAGACCTGTA 59222 AGTA CC  
 TGCAGGT GTTTT GCT  
 ||||| ||||| |||||  
 ATGTCCA TAAAA CGA  
 GAG\_ A\_  
 GAM1621 LOC161734 3' AGCCTGGACTACTACATGCA 87095 G TCC  
 TGCA GTAGTAGTTT GCT  
 ||||| ||||| |||||

	ACGT CATCATCAGG CGA		
	A TC_		
GAM1621 LOC164714 3'	AGCCCCGACTACTACCTGC 87221	TTCC	
	GCAGGTAGTAGTT GCT		
	CGTCCATCATCAG CGA		
	CCC_		
GAM1621 LOC204285 3'	AGCGCTGACCAGTACCTGCA 89454	GTA TTC	
	TGCAGGTA GTT CGCT		
	ACGTCCAT CAG GCGA		
	GAC TC_		
GAM1621 LOC219920 5'	AGCAGAAGGCTATCCACCTCA 93299	C A_ C	
	TG AGGT GTAGTTTTTC GCT		
	AC TCCA TATCGGAAG CGA		
	_ CC A		
GAM1621 LOC219942 3'	TGAGAAAACCACTATCTGCA 93350	A _	
	TGCAGGTAGT GTTTTC CG		
	ACGTCTATCA CAAAAG GT		
	C A		
GAM1621 LOC221749 5'	GCGTGCTCTACCTGCA 92006	T TTTC	
	TGCAGGTAG AGT CGC		
	ACGTCCATC TCG GCG		
	_ T_		
GAM1621 LOC253613 5'	AGCGGAAGTATTCTACCTG 96190	TAGT	
	CAGGTAG TTTCCGCT		
	GTCCATC GAAGGCGA		
	TTAT		
GAM1621 LOC253698 3'	AGCAAAAGCACTACCTGCA 94888	A CC	
	TGCAGGTAGT GTTTT GCT		
	ACGTCCATCA CGAAA CGA		
	_ A_		
GAM1621 LOC91614 5'	AGCGGAGGGCCCGCCCGCA 57499	A AGTA	
	TGC GGT GTTTTCCGCT		
	ACG CCG CGGGAGGCGA		
	C CC_		
GAM1621 LOC92218 5'	AGCAGGAAACTACCCCGCA 68504	A TA C	
	TGC GG GTAGTTTTTC GCT		
	ACG CC CATCAAAGG CGA		
	C _ A		
GAM1622 CDH10 3'	TAGTTCTCCCTTAAGCAACCT 22058	CG CAGTGT A	
	AGG GCT GA GAACTA		

TCC CGA CTCTTGAT  
 AA ATTCC\_ \_  
 GAM1622 DACH 3' TAGTTCTTCCATAACCCACT 54971 C CTCA T  
 AGG GG GTG GAAGAACTA  
 ||| || ||| |||||  
 TCC CC TAC CTTCTTGAT  
 A AA\_ \_  
 GAM1622 HPS1 3' TCTTCCAGAGCTGCCT 3969 AG T  
 AGGCGGCTC TG GAAGA  
 ||||| || ||||  
 TCCGTCGAG AC CTTCT  
  
 GAM1622 PCK1 5' TCTTCAGGCTGCCT 52264 CAGTG  
 AGGCGGCT TGAAGA  
 ||||| ||||  
 TCCGTCGG ACTTCT  
  
 GAM1622 RORB 5' AGCTCTTCGCCGACCACCT 22606 C C AGT A  
 AGG GG TC GTGAAGA CT  
 ||| || ||||| ||  
 TCC CC AG CGCTTCT GA  
 A \_ C\_ C  
 GAM1622 SPTBN4 3' AGTCCCCATGGCCGCCT 47386 CAGT AA A  
 AGGCGGCT GTG GA CT  
 ||||| ||| |||  
 TCCGCCGG TAC CT GA  
 CC \_  
 GAM1622 ZNF200 3' GTAGTTCTGAATTCCCAAGCTG 12909 CAGT\_ GA  
 CCT AGGCGGCT GT AGAACTAC  
 ||||| || |||||  
 TCCGTCGA TA TCTTGATG  
 ACCCT AG  
 GAM1622 BTN2A1 3' GTAATTCTCAGTGTGTGAGCTG 54342 \_TG GA C  
 CCT AGGCGGCTCA G T AGAA TAC  
 ||||| ||| |||  
 TCCGTCGAGT T G TCTT ATG  
 G GT AC A  
 GAM1622 CFP1 3' TAGCTCCGTCAAGCTGCCT 58771 CAGTG A\_ A  
 AGGCGGCT TGA GA CTA  
 ||||| ||| |||  
 TCCGTCGA ACT CT GAT  
 GC C  
 GAM1622 FENS-1 3' TGGGAGTCACACAAGCCGCCT 40445 CA AGAA  
 AGGCGGCT GTGTGA CTA  
 ||||| ||||| |||  
 TCCGCCGA CAACT GGT  
 A\_ GAG\_  
 GAM1622 FLJ14082 3' AGTTCTTCCTAAGGCACCC 46668 CG CAG T  
 GG GCT TG GAAGAACT  
 || ||| || |||||

CC CGG AT CTTCTTGA  
 CA A\_\_ C  
 GAM1622 FLJ20539 5' TGGGGCCACCTGAGCCGCC 35363 T AAGAA  
 GGCGGCTCAG GTG CTA  
 ||||| ||| |||  
 CCGCCGAGTC CAC GGT  
 \_ CGG\_  
 GAM1622 FLJ22301 3' AGCCCTTCACGTAGCCTCCT 45756 C CAG AA  
 AGG GGCT TGTGAAG CT  
 ||| ||| ||||| ||  
 TCC CCGA GCACTTC GA  
 T T\_\_ CC  
 GAM1622 HEMGN 5' TAGAGAAAAAACTGAGCCACC 37380 C GTGAAGAA  
 T AGG GGCTCAGT CTA  
 ||| ||||| |||  
 TCC CCGAGTCA GAT  
 A AAAAAAGA  
 GAM1622 KIAA0379 3' GTAGTTCTTGCGAATGCCACC 68150 C TCAG G  
 GG GGC TGT AAGAACTAC  
 || ||| ||| |||||  
 CC CCG GCG TTCTTGATG  
 A TAA\_\_ \_  
 GAM1622 KIAA0494 3' TCTCACACTGACCACC 28750 C C A  
 GG GG TCAGTGTGA GA  
 || ||| ||||| ||  
 CC CC AGTCACACT CT  
 A \_ \_  
 GAM1622 LACE1 3' CTTACATTAAACCACCT 91837 C CTC  
 AGG GG AGTGTGAAG  
 ||| ||| |||||  
 TCC CC TTACACTTC  
 A AAA  
 GAM1622 NAPG 3' TAGTTCTTCAGGTAGCACCT 96730 CG CAG G  
 AGG GCT T TGAAGAACTA  
 ||| ||| | |||||  
 TCC CGA G ACTTCTTGAT  
 A\_ T\_\_ G  
 GAM1622 PRO2405 5' AGGAGCACATTAAGCCGCCT 37798 C AAGAA  
 AGGCGGCT AGTGTG CT  
 ||||| ||||| ||  
 TCCGCCGA TTACAC GA  
 A GAG\_  
 GAM1622 LOC121219 5' AGTCCTCAGCGAAGCCGCCT 74040 CA G A A  
 AGGCGGCT GT TGA GA CT  
 ||||| || ||| ||  
 TCCGCCGA CG ACT CT GA  
 AG \_ C \_  
 GAM1622 LOC146990 3' CTTACACCCAGCCGCCT 83886 CA  
 AGGCGGCT GTGTGAAG  
 ||||| |||||



			TCCGCCGA CACACTTC			
			CC			
GAM1622	LOC148371	5'	TTCCACTGAGCCACC	78809	C	T
			GG GGCTCAGTG GAA			
			CC CCGAGTCAC CTT			
			A _			
GAM1622	LOC152274	3'	AGTCCCTGCAGGAGCAGCCT	80498	G	AG AA A
			AGGC GCTC TGTG GA CT			
			TCCG CGAG ACGT CT GA			
			A G_ CC _			
GAM1622	LOC200261	3'	AGTTGCTCCACTGAGTCACC	88653	C	T AG
			GG GGCTCAGTG GA AACT			
			CC CTGAGTCAC CT TTGA			
			A _ CG			
GAM1622	LOC201562	5'	GTAGTCCGGCCCGAGCCGCT	88975		AGT GAA A
			GGCGGCTC GT GA CTAC			
			TCGCCGAG CG CT GATG			
			CC_ GC_ _			
GAM1622	LOC202347	3'	TCATGGCAGAGCCGCCT	90349	A	_
			AGGCGGCTC GT GTGA			
			TCCGCCGAG CG TACT			
			A G			
GAM1622	LOC220370	3'	TCACCTCACTGAGCCACCT	92834	C	___
			AGG GGCTCAGT GTGA			
			TCC CCGAGTCA CACT			
			A CTC			
GAM1622	LOC221838	5'	TTCCACTGAGCCACC	92546	C	T
			GG GGCTCAGTG GAA			
			CC CCGAGTCAC CTT			
			A _			
GAM1622	LOC51716	3'	AGTTCCACACTGAGCGCCT	32786	G	AA
			AGGCG CTCAGTGTG GAACT			
			TCCGC GAGTCACAC CTTGA			
			_ _			
GAM1622	LOC89919	3'	CTTCCACTGAGCCACC	60722	C	T
			GG GGCTCAGTG GAAG			
			CC CCGAGTCAC CTTC			
			A _			
GAM1622	LOC91947	3'	TAGTTCTTTTATTGTAAGCCGC	67614	___	T
			GGCGGCT CAGTG GAAGAACTA			
			T			

		TCGCCGA GTTAC TTTCTTGAT		
		AT _		
GAM1623	ACADS	3' GTGTTGGGCAGGTGGTGGGGCT 3412	ACAG	A_
	G	TAGCC ACTG TGTTCGATGC		
		GTCGG TGGT ACGGGTTGTG		
		GG_ GG		
GAM1623	ACP5	3' TGTTATGCTCTGTGGCTG 7857	CTGAT	TC
		TAGCCACAGA GT GATG		
		GTCGGTGTCT CG TTGT		
		_____ TA		
GAM1623	ADH1B	3' CTAAACAGTATTAGTTTGTGGC 72642	CGATGC	
	TA	TAGCCACAGACTGATGTT		
		ATCGGTGTTTGATTATGA		
		CAAATCA		
GAM1623	ANGPT1	3' GCATACTGTTGTTCTGTGGTTA 57772	CT	TTCG
		TAGCCACAGA GATG ATGC		
		ATTGGTGTCT TTGT TACG		
		TG CA_		
GAM1623	ASNS	3' GTGTTGGATGGGGACTGTGGGT 55942	G	A GA
	A	TA CCACAG CT TGTTCGATGC		
		AT GGTGTC GG GTAGGTTGTG		
		G A G_		
GAM1623	ASNS	3' GTGTTGGATGGGGACTGTGGGT 8033	G	A GA
	A	TA CCACAG CT TGTTCGATGC		
		AT GGTGTC GG GTAGGTTGTG		
		G A G_		
GAM1623	CD58	3' AGCATTAGTTTTGGCTG 8352	C	
		TAGCCA AGACTGATGTT		
		GTCGGT TTTGATTACGA		
		_____		
GAM1623	CLCN6	3' CATTGGGCATTCATGCTTA 41396	C AC	_
		A AG TGA TGTTCGATG		
		A TC ACT ACGGGTTAC		
		T GT T		
GAM1623	CLCN6	3' CATTGGGCATTCATGCTTA 41381	C AC	_
		A AG TGA TGTTCGATG		
		A TC ACT ACGGGTTAC		
		T GT T		
GAM1623	CLCN6	3' CATTGGGCATTCATGCTTA 7074	C AC	_
		A AG TGA TGTTCGATG		

			A TC ACT ACGGGTTAC		
			T GT T		
GAM1623	COX7A2L	3'	AATGTCAGTCTGTGCTG 16347	C	
			TAGC ACAGACTGATGTT		
			GTCG TGTCTGACTGTAA		
			—		
GAM1623	CSE1L	3'	GTATGGCGTTGGTTTGTG 61858	TG	CG
			CACAGAC ATGTT ATGC		
			GTGTTTG TGC GG TATG		
			GT —		
GAM1623	DDX38	3'	CGTGA CTTGGCTGTGGCTG 25750	A TG T	CG
			TAGCCACAG C A GTT ATG		
			GTCGGTGTC G T CAG TGC		
			— GT — —		
GAM1623	FAT2	3'	TGAGTGGTTTGTGGCTG 7547	ATG	
			TAGCCACAGACTG TTCG		
			GTCGGTGTTTGGT GAGT		
			—		
GAM1623	GFRA2	5'	GCATTGGATTTGGGGCTG 7660	A	_ TG
			TAGCC CAGA C ATGT		
			GTCGG GTTT G TACG		
			G A GT		
GAM1623	HLA-G	3'	GTATTGAGCATGTGATGGGCTG 9226	A	GACTG
			TAGCC CA ATGTTTCGATGC		
			GTCGG GT TACGAGTTATG		
			_ AGTG_		
GAM1623	IL13RA1	3'	TGTCTTTGGTTTGTGCTA 7780	C	TG TGTTT
			TAGC ACAGAC A GATG		
			ATCG TGTTTG T CTGT		
			_ GT T_		
GAM1623	IPF1	3'	ATTGGCGTTGTTTGTGGCTG 3980	T	T
			TAGCCACAGAC GATGT CGAT		
			GTCGGTGTTTG TTGCG GTTA		
			— —		
GAM1623	ITGAM	3'	GCGTTGGGCAACATTGCTGGCT 71840	_	AC A
	G		TAGCCA CAG TG TGTTTCGATGC		
			GTCGGT GTT AC ACGGGTTGCG		
			C _ A		
GAM1623	KCNS3	3'	GTATTGGGTGGGGTTTGTGGCT 9588	GA	TT
	A		TAGCCACAGACT TG CGATGC		

		ATCGGTGTTTGG GT GTTATG	
		G_ GG	
GAM1623 LSS	3'	GTGTCGAGTGGGCTCTGGGCTG 9821	A _ G GT
		TAGCC CAGA CT AT TCGATGC	
		GTCGG GTCT GG TG AGCTGTG	
		_ C G _	
GAM1623 NCF1	3'	GCATTGGACATCAGTGTGTCTG 81329	_____
TG		CACAGAC TGATGTTTCGATGC	
		GTGTCTG ACTACAGGTTACG	
		TGTG	
GAM1623 OGT	5'	GTGTAAGGGTTGGTCTTTGGTT 13205	C TG G CGATGC
G		TAGCCA AGAC AT TT	
		GTTGGT TCTG TG GA	
		T GT G ATGTG	
GAM1623 PHEMX	3'	GCATTGAGCAAATTGTGGT 57361	ACTGA
		GCCACAG TGTTTCGATGC	
		TGGTGTT ACGAGTTACG	
		AA_____	
GAM1623 PHEMX	3'	GCATTGAGCAAATTGTGGT 57366	ACTGA
		GCCACAG TGTTTCGATGC	
		TGGTGTT ACGAGTTACG	
		AA_____	
GAM1623 PHEMX	3'	GCATTGAGCAAATTGTGGT 57370	ACTGA
		GCCACAG TGTTTCGATGC	
		TGGTGTT ACGAGTTACG	
		AA_____	
GAM1623 PHEMX	3'	GCATTGAGCAAATTGTGGT 19121	ACTGA
		GCCACAG TGTTTCGATGC	
		TGGTGTT ACGAGTTACG	
		AA_____	
GAM1623 PPT2	3'	GTGTTGGGGAATATCTGTGGC 17670	CTGATG
		GCCACAGA TTCGATGC	
		CGGTGTCT GGGTTGTG	
		ATAAG_	
GAM1623 PPT2	3'	GTGTTGGGGAATATCTGTGGC 56966	CTGATG
		GCCACAGA TTCGATGC	
		CGGTGTCT GGGTTGTG	
		ATAAG_	
GAM1623 RASGRP1	3'	GTGTTGAGCAACATGGGGCTA 19208	A GAC A
		TAGCC CA TG TGTTTCGATGC	

		ATCGG GT AC ACGAGTTGTG		
		G _ A		
GAM1623 RIG	3'	GTGTCTTACAAGTTTGTGGCTA 21129	GA TC	
		TAGCCACAGACT TGT GATGC		
		ATCGGTGTTTGA ACA CTGTG		
		_ TT		
GAM1623 ROCK2	3'	CCTCAGTATTAGTCTGTGACTA 66009	C C TGC	
		TAG CACAGACTGATGTT GA		
		ATC GTGTCTGATTATGA CT		
		A _ CCA		
GAM1623 SEL1L	3'	GCATTTGGTTTGTGGTTA 17359	_ TG _	
		TAGCCA CAGAC A TGT		
		ATTGGT GTTTG T ACG		
		T GT T		
GAM1623 SKI	3'	GCGTCGGGTGGTGACCGTGGCT 11705	AGACTGA TT	
G		TAGCCAC TG CGATGC		
		GTCGGTG GT GCTGCG		
		CCAGTG_ GG		
GAM1623 SLC12A7	3'	GCTCTGAACGTTGGTTGGTGGC 21702	A TG AT	
TG		TAGCCAC GAC ATGTTCG GC		
		GTCGGTG TTG TGCAAGT CG		
		G GT CT		
GAM1623 SRGAP1	3'	GTATAGCCAGTGTTGGTCTGTG 72265	TG TG CG_	
GC		GCCACAGAC A TT ATGC		
		CGGTGTCTG T GA TATG		
		GT GT CCGA		
GAM1623 SRP14	3'	GCATTTGGCTAATTGGTCTGTG 11957	C TG _ TC	
CTG		AGC ACAGAC AT GT GATGC		
		TCG TGTCTG TA CG TTACG		
		_ GT AT GT		
GAM1623 C9orf5	3'	GTGTTGAATGAATCATGTGGT 49283	GAC _	
		GCCACA TGAT GTTCGATGC		
		TGGTGT ACTA TAAGTTGTG		
		_ AG		
GAM1623 CDC91L1	3'	GCAGGGCTTGTTAGATTGTGGC 54439	A _ GA	
TA		TAGCCACAG CTGAT GTTC TGC		
		ATCGGTGTT GATTG CGGG ACG		
		A TT _		
GAM1623 CPR2	3'	GCATTGGGGTAGTTTGTGCTG 48098	C ATGT	
		TAGC ACAGACTG TCGATGC		

GTCG TGTTTGAT GGTTACG  
 \_ GG\_  
 GAM1623 DCOHM 3' GCATTCATCTGTGGCTG 49603 CT  
 TAGCCACAGA GATGT  
 ||||| ||||  
 GTCGGTGTCT TTACG  
 AC  
 GAM1623 DKFZP434B044 3' AGCTCAGTTTGTGGTTA 48922 T  
 TAGCCACAGACTGA GTT  
 ||||| ||||  
 ATTGGTGTGTTGACT CGA  
 \_  
 GAM1623 DKFZP434I0714 5' GCGTTGGATAACGTGTGGT 85799 GAC A  
 GCCACA TG TGTTTCGATGC  
 |||| || |||||  
 TGGTGT GC ATAGGTTGCG  
 \_ A  
 GAM1623 DKFZP564O0463 3' GCATTGGACATCATTTTGTCTA 26280 CC C  
 TAG ACAGA TGATGTTTCGATGC  
 || |||| |||||  
 ATC TGTTT ACTACAGGTTACG  
 \_ T  
 GAM1623 DKFZP586C1324 3' GTGTTGGATTCTCTGTTGTTG 69799 C CT T  
 TAGC ACAGA GA GTTCGATGC  
 |||| |||| || |||||  
 GTTG TGTCT CT TAGGTTGTG  
 T C\_ \_  
 GAM1623 DKFZp762K222 3' GTGTTGCTCCCAGTCTGTGGTT 71120 ATGTT  
 A  
 TAGCCACAGACTG CGATGC  
 ||||| ||||  
 ATTGGTGTCTGAC GTTGTG  
 CCTC\_  
 GAM1623 EDG1 3' GTGTCGGGTGTTGGTGGGT 59330 A AG TG TT  
 GCC C AC ATG CGATGC  
 || | || |||||  
 TGG G TG TGT GCTGTG  
 \_ \_ GT GG  
 GAM1623 ELAC1 3' GTATTGAATCTGTTTGTG 90971 T GT  
 CACAGAC GAT TCGATGC  
 ||||| || |||||  
 GTGTTTG CTA AGTTATG  
 T \_  
 GAM1623 FLJ10188 3' GTGTTGAACATTACAAGGGCT 35872 ACAGAC  
 AGCC TGATGTTTCGATGC  
 ||| |||||  
 TCGG ATTACAAGTTGTG  
 GAAC\_  
 GAM1623 FLJ10422 5' CGGGATTGTTTGTGGCTG 36113 CT G  
 TAGCCACAGA GAT TTCG  
 ||||| || ||||

		GTCGGTGTTT TTA GGGC	
		TG _	
GAM1623	FLJ11286 3'	GACACGGTCTGTGGCTA 37219	A
		TAGCCACAGACTG TGTT	
		ATCGGTGTCTGGC ACAG	
		-	
GAM1623	FLJ12287 5'	TCCCTGGTGACAGTCTGTGGCT 42318	ATGT ATGC
	G	TAGCCACAGACTG TCG	
		GTCGGTGTCTGAC GGT	
		AGT_ CCCTC	
GAM1623	FLJ12838 3'	GTGTCATTTGCAGATTTGTGGT 44969	_ ATGTTC
	TA	TAGCCACAGA CTG GATGC	
		ATTGGTGTTT GAC CTGTG	
		A GTTTA_	
GAM1623	FLJ20232 3'	GTGTCTGCTCGTCATCTGTGGC 38673	C TT_
	TG	TAGCCACAGA TGATG C GATGC	
		GTCGGTGTCT ACTGC G CTGTG	
		_ TC T	
GAM1623	FLJ20558 3'	GCATTGGGCAGTATTTCTGGCT 35397	C CTGA
	A	TAGCCA AGA TGTTGATGC	
		ATCGGT TTT ACGGGTTACG	
		C ATG_	
GAM1623	FLJ23231 3'	GTAACGGCGTCGGTCCGTGGCT 46915	A T A
	G	TAGCCAC GACTGATGT CG TGC	
		GTCGGTG CTGGCTGCG GC ATG	
		C _ A	
GAM1623	GABARAPL1 3'	TGTTGAGCATCCCTGTCT 48604	T__
		AGAC GATGTTTCGATG	
		TCTG CTACGAGTTGT	
		TCC	
GAM1623	GNA13 3'	CGGCCTTTGTTTGTGGCTG 21650	TG TGT
		TAGCCACAGAC A TCG	
		GTCGGTGTTTG T GGC	
		GT TCC	
GAM1623	GNB1L 5'	GTCCACGGTCTGTGGCTA 53812	A TTC
		TAGCCACAGACTG TG GAT	
		ATCGGTGTCTGGC AC CTG	
		_ C_	
GAM1623	GPS2 5'	GTGTCGGGCTGCTCTGTGCTG 87163	C CTGAT
		TAGC ACAGA GTTCGATGC	

		GTCG TGTCT CGGGCTGTG	
		CGT__	
GAM1623 KCNT1	3'	CATCGGATGCTGGGGCTG 61829	A ACTGA
		TAGCC CAG TGTTGATG	
		GTCGG GTC GTAGGCTAC	
		G _____	
GAM1623 KIAA0460	3'	GCGTTGAGTGTTCAAATGGTT 78889	CAGACT TG
		AGCCA GA TTCGATGC	
		TTGGT TT GAGTTGCG	
		AAACT_ GT	
GAM1623 KIAA0826	3'	GCATTGTAGCTGTTGGTTTGTG 82638	TG _ _
		CACAGAC AT GTT CGATGC	
		GTGTTTG TG CGA GTTACG	
		GT T T	
GAM1623 KIAA1068	3'	GTATTGGGTATTGGCCCCATGG 31037	CAGA_ TG TT
C		GCCA C ATG CGATGC	
		CGGT G TAT GTTATG	
		ACCCC GT GG	
GAM1623 KIAA1155	3'	GTATAAATTCAGTATGTGGCTG 62239	G TGTTG
		TAGCCACA ACTGA ATGC	
		GTCGGTGT TGA CT TATG	
		A TAAA_	
GAM1623 KIAA1511	3'	TATTTGCCATTTGTGGCTA 70170	C AT TC
		TAGCCACAGA TG GT GATG	
		ATCGGTGTTT AC CG TTAT	
		_ _ T_	
GAM1623 KIAA1635	3'	GTCAGTGTGAGTCTTGGTTG 67861	C TG C
		TAGCCA AGACTGA TT GAT	
		GTTGGT TCTGACT GA CTG	
		GT _	
GAM1623 KIAA1813	5'	CATTGGGCAGTGTGGTT 70293	GACTGA
		AGCCACA TGTTGATG	
		TTGGTGT ACGGGTTAC	
		G_____	
GAM1623 KIAA1854	3'	CATTGGATATCAGAGCTG 71740	A_
		CAG CTGATGTTGATG	
		GTC GACTATAGGTTAC	
		GA	
GAM1623 KIF13B	3'	GCGGACTAATGTCAGCTTGTGG 82823	GA _____ ATGC
CTG		CCACA CTGAT GTTCG	



			GGTGT GACTG CAGGC		
			TC TAAT G C		
GAM1623	KIF13B	3'	GCGGACTAATGTCAGCTTGTGG 30909	GA	_____ ATGC
		CTG	CCACA CTGAT GTTCG		
			GGTGT GACTG CAGGC		
			TC TAAT G C		
GAM1623	LIN-28	3'	GCATTGGGTGGTGTGTGTCTG 45148	C G	GAT TT
			TAG CACA ACT G CGATGC		
			GTC GTGT TGG T GTTACG		
			T G ____ GG		
GAM1623	LIV-1	3'	TATTGAATATTGCTGTCTG 24626	T__	
			CAGAC GATGTTCGATG		
			GTCTG TTATAAGTTAT		
			TCG		
GAM1623	LY75	3'	AACATTGCTTTGTGGTTA 9832	CT	
			TAGCCACAGA GATGTT		
			ATTGGTGTTT TTACAA		
			CG		
GAM1623	MR	5'	GTATTGAGCCTTCCTGTGCTG 48323	C	ACT T_
			TAGC ACAG GA GTTCGATGC		
			GTCG TGTC CT CGAGTTATG		
			_ ____ TC		
GAM1623	NAP1L2	3'	AGCTATTAATCTGTGGCTA 41733	C	_
			TAGCCACAGA TGAT GTT		
			ATCGGTGTCT ATTA CGA		
			A T		
GAM1623	NUDT4	3'	CCATTTGACATCAGTCTGTGGT 38866	C	C
		T	AGCCACAGACTGATGTT GATG		
			TTGGTGTCTGACTACAG TTAC		
			T CT		
GAM1623	NYD-SP12	5'	GTGTTGGCAGATGCTGTGGCTG 49225	ACTGA	T
			TAGCCACAG TGT CGATGC		
			GTCGGTGTC ACG GTTGTG		
			GTAG_ _		
GAM1623	PGR1	3'	TATGGTCTGTGGTTG 52756	G	
			TAGCCACAGACT ATG		
			GTTGGTGTCTGG TAT		
			_		
GAM1623	PMX2B	3'	GTGTCTGCGTGTGCTAGTTTGTGT 14086	C	TG T_
		CTG	TAG CACAGACTGA T C GATGC		

			GTC GTGTTTGA	CT	G	G	CTGTG		
			T		G	T	C	T	
GAM1623	PTPN9	3'	GAATGTATTAGTTTGTGGT	11077				—	
			GCCACAGACTGAT	GTTC					
			TGGTGT	TTGATTA	TAAG				
			TG						
GAM1623	SLC2A10	3'	CATCATGTTAGTCTTTGGTTG	47818		C		TC	C
			TAGCCA	AGACTGATGT	GATG				
			GTTGGT	TCTGATTGTA	CTAC				
			T		A				
GAM1623	SNRK	3'	TATTAGTTGTGTGGTTG	34770				—	
			TAGCCACA	GA	CTGATG				
			GTTGGTGT	TTGATTAT					
			G						
GAM1623	SUN1	3'	GTGTCTTGTGTGGTTTGTGCT	47159		C		G	TG
			AGC	ACAGACT	A	T	GATGC		
			TCG	TGTTTGG	T	G	CTGTG		
			—						
			—						
GAM1623	SYT12	3'	GGCATCAGTCTTTGGTTA	94734				C	
			TAGCCA	AGACTGATGTT					
			ATTGGT	TCTGACTACGG					
			T						
GAM1623	TADA3L	3'	GCACAGGAAACATTGGCCTGTG	20983				A	TG
	GCTG		AGCCACAG	C	ATGT	TC	TGC		GA
			TCGGTGT	C	TACA	GG	ACG		
			C	GT	AA	AC			
GAM1623	TEX27	3'	TCTAGAACAGCGGTTTGTGGCT	41666				A	GATGC
	G		TAGCCACAGACTG	TGTTT					
			GTCGGTGT	TTTGGC	ACAAG				
			G		ATCTG				
GAM1623	TTY2	5'	GTGTTGGATGTCAGCATGTGTG	87008				—	GA
	T		GC	CACA	CTGATGTT	CGATGC			
			TG	GTGT	GA	CTGTAGGTTGTG			
			T		AC				
GAM1623	WSB1	5'	TATTGTCTGTGGTTG	56147				T	
			TAGCCACAGAC	GATG					
			GTTGGTGT	CTG	TTAT				
			—						
GAM1623	WSB1	5'	TATTGTCTGTGGTTG	56141				T	
			TAGCCACAGAC	GATG					

GTTGGTGTCTG TTAT

GAM1623 LOC113828 5' GTCGGCTCTGTGGTTG 56587  
TAGCCACAGA CTGAT  
||||||| ||||  
GTTGGTGTCT GGCTG

C

GAM1623 LOC115330 3' TATTTATACTTTGTGGTTA 56611 CTG TTC  
TAGCCACAGA ATG GATG  
||||||| || ||||  
ATTGGTGTTT TAT TTAT

CA\_ \_

GAM1623 LOC126917 3' CATTGGACAATGTGGT 74580 GACTGA  
GCCACA TGTCGATG  
||||| |||||  
TGGTGT ACAGGTTAC

A\_ \_

GAM1623 LOC127428 3' GCAGGCTGTGTTATTTGTGGCT 74668 C TG TCGA  
G TAGCCACAGA TGA T TGC  
||||||| ||| | |||  
GTCGGTGTTT ATT G ACG

\_ GT TCGG

GAM1623 LOC138639 3' TGTTAGTTTGTGCTG 75365 C  
TAGC ACAGACTGATG  
||| |||||  
GTCG TGTTTGATTGT

GAM1623 LOC143903 3' AAACAGAGTGTTAGTCTGTGTC 76615 C TG GATGC  
TA TAG CACAGACTGA TTC  
||| ||||| |||  
ATC GTGTCTGATT GAG

T GT ACAAAG

GAM1623 LOC147660 3' GCATTGACTTGAGTTTGTG 78393 GAT T  
CACAGACT GT CGATGC  
||||||| || |||||  
GTGTTTGA CA GTTACG

GTT \_

GAM1623 LOC147920 5' GATATTGGACTGTGGTTG 78546 A TG  
TAGCCACAG C ATGTT  
||||||| | ||||  
GTTGGTGTC G TATAG

A GT

GAM1623 LOC149707 5' GTGTCAGTCTTGGTTA 79487 C TG  
TAGCCA AGACTGA T  
||||| ||||| |  
ATTGGT TCTGACT G

\_ GT

GAM1623 LOC151031 3' GCATCGGGCATCTTAACATGGC 87188 CAGACT  
GCCA GATGTTTCGATGC  
||| |||||

	CGGT CTACGGGCTACG		
	ACAATT		
GAM1623 LOC152348 3'	GGCATCAGTTTGTGCTG 85695	C	
	TAGC ACAGACTGATGTT		
	GTCG TGTTTGA		
	CTACGG		
	—		
GAM1623 LOC152687 5'	GTATTGGACAATTTGTAGCTA 80640	C	CTGA
	TAGC ACAGA TGTTTCGATGC		
	ATCG TGTTT ACAGGTTATG		
	A A		
GAM1623 LOC158287 5'	GTATCGTCCCGGCCTGTGGCTG 86723	A	ATGTT
	TAGCCACAG CTG CGATGC		
	GTCGGTGTC GGC GCTATG		
	C CCT		
GAM1623 LOC159148 5'	GTGTTGGATGTCAGCATGTGTG 87017	—	GA
T	GC CACA CTGATGTTTCGATGC		
	TG GTGT GACTGTAGGTTGTG		
	T AC		
GAM1623 LOC200227 5'	GTGTCAGTCTTGTTA 88646	C	TG
	TAGCCA AGACTGA T		
	ATTGGT TCTGACT G		
	— GT		
GAM1623 LOC200261 3'	TGTGGGTCTGTGGCTG 88660	G	
	TAGCCACAGACT ATG		
	GTCGGTGTCTGG TGT		
	G		
GAM1623 LOC201617 5'	GCTCTAATGTTAGCTGTGGTTG 90235	A	C T
	TAGCCACAG CTGATGTT GA GC		
	GTTGGTGTC GATTGTAA CT CG		
	— T —		
GAM1623 LOC253263 3'	GCATTGGACTTCCTGTGCCTG 97033	C	ACT T
	TAG CACAG GA GTTCGATGC		
	GTC GTGTC CT CAGGTTACG		
	C — T		
GAM1623 LOC51125 3'	TGAGGGTTGGCTGTGGCTG 32250	A	TG G
	TAGCCACAG C AT TTCG		
	GTCGGTGTC G TG GAGT		
	— GT G		
GAM1623 LOC85414 5'	GTTGAGCATGGGCTG 52401	A	G
	CAG CT ATGTTTCGAT		

			GTC GG TACGAGTTG			
			_ G			
GAM1623	LOC90120	5'	GTATCGTCCCGGCCTGTGGCTG 61541	A	ATGTT	
			TAGCCACAG CTG CGATGC			
			GTCGGTGTC GGC GCTATG			
			C CCT__			
GAM1624	ADH1B	3'	CTTAGACATAAAGTAAAAT 72644	C	CAC	
			ATTT ACTTT TGTCTGAG			
			TAAA TGAAA ACAGATTC			
			A T__			
GAM1624	AHR	3'	ATCTCAGATGTTAAATAAATG 7875	CAC	C T	
			CATTT TTT AC GTCTGAGAT			
			GTAAA AAA TG TAGACTCTA			
			TA_ T _			
GAM1624	FDFT1	3'	TAGGAAAGTGAAATG 15518	A		
			CATTTCACTTTC CTG			
			GTAAAGTGAAAG GAT			
			-			
GAM1624	JTB	3'	ATCTCAGACAGTGAAAGTGAAA 21959			
	TG		CATTTCACTTTCACTGTCTGAGAT			
			GTAAAGTGAAAGTGACAGACTCTA			
GAM1624	KLF4	3'	TCCCAGACAGTGGATATG 14891	CT	A	
			CA TTCACTGTCTG GA			
			GT AGGTGACAGAC CT			
			AT C			
GAM1624	PHYH	3'	ACAGTAAAAGTGAAAT 20608	C		
			ATTTCACTTT ACTGT			
			TAAAGTGAAA TGACA			
			A			
GAM1624	PKD2	3'	TCCAGGTTGAAAGTGAAA 60096	CTG	A	
			TTTCACTTTCA TCTG GA			
			AAAGTGAAAGT GGAC CT			
			T__ -			
GAM1624	WRN	3'	GGGCAGTGAAAATGAAA 5098	C		
			TTTCA TTTCACTGTCT			
			AAAGT AAAGTGACGGG			
			A			
GAM1624	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA	CTG	
			TTTCACTTT CTGT AGAT			

			AAAGTGAAA GACA TCTA	
			C_ CG_	
GAM1624	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT CT
			TTCACTTTCA GT GAG	
			AAGTGAAAGT CA CTC	
			CT _	
GAM1624	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G T_
			CTTTCACT TC GAGAT	
			GAAAGTGA AG TTCTA	
			G TC	
GAM1624	FLJ23462	3'	ATCTCAGACTTTTACAAAGAAAT 45802	ACTTTCACT
	G		CATTTC GTCTGAGAT	
			GTAAAG CAGACTCTA	
			AAACATTT_	
GAM1624	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281	CTT
			CATTTC TCACTGTCTGAGAT	
			GTAAAGT AGTGACAGACTCTA	
			C_	
GAM1624	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C TC
			TTCA TTCACTG TGAG	
			AAGT AAAGTGAC GTTT	
			A CT	
GAM1624	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A _
			TTTC CTG TCTGAGAT	
			AAAG GAC AGACTCTA	
			_ G	
GAM1624	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T
			ATT CACTTTCACTGT	
			TAA GTGAAAGTGACG	
			C	
GAM1624	PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA 53598	CA G
			TTCACTTT CT TCTGAGAT	
			AAGTGAAA GG AGACTCTA	
			CC G	
GAM1624	PP35	3'	ATCTCAGACTGAAA 22814	CT
			TTTCA GTCTGAGAT	
			AAAGT CAGACTCTA	
			_	
GAM1624	PRTD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148	TCAC C_
			CATTTCAC TT TGT TGAG	

			GTAAAGTGAA	ACG	ACTC		
			TA__	TT			
GAM1624	SEP15	3'	TCCTACAGTAAGAGTGAAA	14934		C	CT
			TTTCACTTT	ACTGT	GA		
			AAAGTGAGA	TGACA	CT		
			A	TC			
GAM1624	SFXN2	3'	CTCAGGGGAAAAAAGTGAAA	73941			CACTG
			TTTCACTTT	TCTGAG			
			AAAGTGAAA	GGA	CTC		
			AAAGG				
GAM1624	LOC149703	3'	ATCTCAGACAGCCGTTTGAAA	84647			ACTTTCA
			TTTC	CTGTCTGAGAT			
			AAAG	GACAGACTCTA			
			GTTTGCC				
GAM1624	LOC154007	3'	ATCTCAAACCCTTTAGTGAAA	81015			TTCACT C
			TTTCACT	GT TGAGAT			
			AAAGTGA	CA	ACTCTA		
			TTTCC_	A			
GAM1624	LOC155004	3'	TCATTTAAGTGAAAGGAAA	81226		A	GTC_
			TTTC	CTTTCACT	TGA		
			AAAG	GAAAGTGA	ACT		
			_	ATTT			
GAM1624	LOC222134	5'	ACAGTGAAGTGAAATG	94136			T
			CATTTCACTT	CACTGT			
			GTAAAGTGAA	GTGACA			
			-				
GAM1625	ATP11B	3'	GTTGTCTTAAGATTTAGA	80318		AA__	
			TCTAGA	AAGACAAC			
			AGATTT	TTCTGTTG			
			AGAA				
GAM1625	AXIN2	3'	TGCTGCTTTAACTTGGA	16210		C	AAA A
			TCCCAAGT	TAGA	AG	CA	
			AGGGTTCA	ATTT	TC	GT	
			A	CG_	_		
GAM1625	CEACAM5	3'	TGTGGTCGCTCCAGACTTGGA	15163			A AAAA A
			TCCCAAGTCT	GA	GAC	ACA	
			AGGGTTCAGA	CT	CTG	TGT	
			C	CG_	G		
GAM1625	CLCN5	3'	TGTTGTCTCTTTCCTAC	3596		CTA	A
			GT	GAAA	AGACAACA		

		CA CTTT TCTGTTGT	
		TC_ C	
GAM1625	CLCN7	3' TGGAGTCTTCGAGACTTGGGA	7090 A AAA AA
		TCCCAAGTCT GA AGAC CA	
		AGGGTTCAGA CT TCTG GT	
		G ____ AG	
GAM1625	CLN3	3' TTGTCTCCCACTTGGGG	3599 CTAGAAAA
		TCCCAAGT AGACAA	
		GGGGTTCA TCTGTT	
		CCC_____	
GAM1625	CLN3	3' TTGTCTCCCACTTGGGG	72255 CTAGAAAA
		TCCCAAGT AGACAA	
		GGGGTTCA TCTGTT	
		CCC_____	
GAM1625	COL13A1	5' CTTTCCTGGACTTGG	55012 AA
		CCAAGTCTAG AAAG	
		GGTTCAGGTC TTTC	
		C_	
GAM1625	COL13A1	5' CTTTCCTGGACTTGG	55015 AA
		CCAAGTCTAG AAAG	
		GGTTCAGGTC TTTC	
		C_	
GAM1625	COL13A1	5' CTTTCCTGGACTTGG	55018 AA
		CCAAGTCTAG AAAG	
		GGTTCAGGTC TTTC	
		C_	
GAM1625	COL13A1	5' CTTTCCTGGACTTGG	55021 AA
		CCAAGTCTAG AAAG	
		GGTTCAGGTC TTTC	
		C_	
GAM1625	COL13A1	5' CTTTCCTGGACTTGG	55024 AA
		CCAAGTCTAG AAAG	
		GGTTCAGGTC TTTC	
		C_	
GAM1625	COL13A1	5' CTTTCCTGGACTTGG	55027 AA
		CCAAGTCTAG AAAG	
		GGTTCAGGTC TTTC	
		C_	
GAM1625	COL13A1	5' CTTTCCTGGACTTGG	17786 AA
		CCAAGTCTAG AAAG	



GGTTCAGGTC TTTC  
C\_

GAM1625 CREB1 3' TGTTGTCTTCTTCAATACT 15204 CTA A  
AGT GAA AAGACAACA  
||| ||| |||||  
TCA CTT TTCTGTTGT  
TAA C

GAM1625 CSN1 5' TGCTTCTCTCCAGACTTGGG 8546 A AA\_ A  
CCCAAGTCT GA AAG CA  
||||||| || ||| ||  
GGGTTCAGA CT TTC GT  
C CTC \_

GAM1625 CTSS 3' TGTAATCCCAGTACTTGGGA 14546 \_ A\_ AAAAG  
TCCCAAGT CT GA ACA  
||||||| || || |||  
AGGGTTCA GA CT TGT  
T CC AA\_

GAM1625 GAD2 3' TGTTGTCTCTCTAAAC 5878 C AAA  
GT TAGA AGACAACA  
|| ||| |||||  
CA ATCT TCTGTTGT  
A C\_

GAM1625 GALNT7 3' GTTGTCTTCATCACTGGGA 54020 A CTA AA  
TCCCA GT GA AAGACAAC  
||||| || || |||||  
AGGGT CA CT TTCTGTTG  
\_ \_ AC

GAM1625 GATM 3' TCTTCTATAGACTTGAGA 7631 C GAAA  
TC CAAGTCTA AAGA  
|| ||||| |||  
AG GTTCAGAT TTCT  
A ATC\_

GAM1625 GOLGA5 3' TTGTCTTTTTCTAGACTTGGGA 17583  
TCCCAAGTCTAGAAAAAGACAA  
||||||| |||||  
AGGGTTCAGATCTTTTTCTGTT

GAM1625 HBD 3' TTTTCTGAACTTGGGA 4971 C  
TCCCAAGT TAGAAAA  
||||| |||||  
AGGGTTCA GTCTTTT  
A

GAM1625 HOXB3 5' GTTGTCTTCCTGGTGGGA 9262 AGT AAA  
TCCCA CTAG AAGACAAC  
||||| ||| |||||  
AGGGT GGTC TTCTGTTG  
\_ C\_

GAM1625 LHX3 3' TGCTATTTCTAGACATG 27379 A A A  
CA GTCTAGAAA AG CA  
|| ||||| || ||

			GT CAGATCTTT TC GT		
			A    A _		
GAM1625 LIG3	3'	TGTCTCTTCTGGACCAGGA	25667	CAA	AA
		TCC GTCTAGAA AGACA			
		AGG CAGGTCTT TCTGT			
		AC_    C_			
GAM1625 MATN3	3'	TGTTGTCTTTTAAATGTTAGTG	9940	AGTCTAG_	
		CA    AAAAAGACAACA			
		GT    TTTTCTGTTGT			
		GATTGTAA			
GAM1625 MT1G	5'	TCTTCCCTTCTCGCTTGGGA	19880	CT	A__
		TCCCAAGT AGAA AAGA			
		AGGGTTCTG TCTT TTCT			
		C_    CCC			
GAM1625 MTR	3'	TGTCATCTTTTCTTGGAT	4222	_	CA
		GTCTA GAAAAAGA ACA			
		TAGGT CTTTTTCT TGT			
		T    AC			
GAM1625 NMI	5'	TGTCTTTTCTTTTCGCGGGG	16267	AAGTCT	
		TCCC    AGAAAAAGACA			
		GGGG    TCTTTTCTGT			
		CGCTTT			
GAM1625 OGG1	3'	CTTCCTCTAGACTTGG	33676	AA	
		CCAAGTCTAGA AAG			
		GGTTCAGATCT TTC			
		CC			
GAM1625 PCTP	3'	TGTGATTCTTCCAGCTTGGGA	41101	CT__	AAG
		TCCCAAGT    AGAAA ACA			
		AGGGTTCTG TCTTT TGT			
		ACCT    AG_			
GAM1625 PIWIL1	3'	TGTTATCTTTCTGGATGAAACT	72823	_____	AA C
	TGGGA	CCAAG    TCTAGAA AGA AACA			
		GGTTC    AGGTCTT TCT TTGT			
		AAAGT    _    A			
GAM1625 PODXL	3'	TGTTAGTCTAGGCTTAGGA	18243	C	AAAA
		TCC AAGTCTAGA    GACA			
		AGG TTCGGATCT    TTGT			
		A    GA__			
GAM1625 RAD54B	3'	TGTTGTCTTTTGCCGACCAGG	56236	AA	TAGA
		CC GTC    AAAAGACAACA			

GG CAG TTTTCTGTTGT  
AC CCG\_  
GAM1625 SCGB2A1 3' TGTTGTCTTTTATGTGG 10014 AGTCTAG  
CCA AAAAAGACAACA  
||| |||||  
GGT TTTTCTGTTGT  
GTA\_\_\_\_  
GAM1625 SMOH 3' GTCCTCTAGACTTGAGG 18869 \_ AAAA  
CC CAAGTCTAGA GAC  
|| ||||| |||  
GG GTTCAGATCT CTG  
A C\_\_\_\_  
GAM1625 SRC 3' TGTCTCTCTGGGCTGCAGA 18289 CCA AAA  
TC AGTCTAGA AGACA  
|| ||||| |||||  
AG TCGGGTCT TCTGT  
ACG C\_\_\_\_  
GAM1625 TNFRSF1A 5' TGTCACCCCAAGGCACTTGGGA 6515 \_ AGAAAAA  
TCCCAAGT CT GACA  
||||| || |||||  
AGGGTTCA GG CTGT  
C AACCCCA  
GAM1625 ZNF2 5' TGTCTCTCTAGACTGGGA 40809 A AAA  
TCCCA GTCTAGA AGACA  
||||| ||||| |||||  
AGGGT CAGATCT TCTGT  
\_ C\_\_\_\_  
GAM1625 AKR1D1 3' TTGGCTTTTCTTCTTAAGTTGG 19979 CT \_ A  
GA TCCCAAGT AGAA AAAG CAA  
||||| ||||| |||||  
AGGGTTCA TCTT TTTC GTT  
AT CT G  
GAM1625 BAG3 3' TGTCTTTTGTAGCTCTGGA 15003 CA T GA  
TCC AG CTA AAAAGACA  
||| ||||| |||||  
AGG TC GAT TTTTCTGT  
TC \_ G\_  
GAM1625 C20orf130 3' TGTCTCTTCTTCCACTTGGG 61759 CTA\_\_ AAA  
G TCCCAAGT GAA GACA  
||||| ||||| |||||  
GGGGTTCA CTT CTGT  
CCTTC CTC  
GAM1625 C5orf5 3' TGTTGCCTTTTCTTAC 33472 CT A  
GT AGAAAAAG CAACA  
|| ||||| |||||  
CA TCTTTTTC GTTGT  
T\_ C  
GAM1625 CNOT8 3' TGTTTTTATTTTAGAC 16532 \_  
GTCTAGAA AAAGACA  
||||| |||||

CAGATTTT TTTTGT  
 A  
 GAM1625 DKFZP564C196 3' TGTCTTTTCTACGCCAGG 70069 AA C  
 CC GT TAGAAAAAGACA  
 || || |||||  
 GG CG ATCTTTTCTGT  
 AC C  
 GAM1625 EPN2 3' TGTTGCCTGGCCCAGGACTTGG 30333 AGAAAA A  
 GA TCCCAAGTCT AG CAACA  
 ||||| || ||||  
 AGGGTTCAGG TC GTTGT  
 ACCCGG C  
 GAM1625 ERp44 3' TTGTCTTCTCTGGACTGTGA 81700 CCA AA  
 TC AGTCTAGA AAGACAA  
 || ||||| |||||  
 AG TCAGGTCT TTCTGTT  
 TG\_ C\_  
 GAM1625 FLJ10826 3' TGTAATCCCAGCACTTGGA 36705 \_ A\_ AAAAG  
 TCCCAAGT CT GA ACA  
 ||||| || || |||  
 AGGGTTCAG GA CT TGT  
 C CC AA\_  
 GAM1625 FLJ12838 3' TTGTCTTAGTATTTAGACTCTG 44972 CA AA\_  
 GA TCC AGTCTAGA AAGACAA  
 || ||||| |||||  
 AGG TCAGATTT TTCTGTT  
 TC ATGA  
 GAM1625 FLJ13188 3' TGTTATTTTACTAGCTT 41942 AA  
 AAGTCTAGAAA GACA  
 ||||| |||||  
 TTCAGATTTT TTGT  
 A\_  
 GAM1625 FLJ14326 3' TTGTACTCCAGCTTGGA 49822 T A AAAAG  
 TCCCAAG CT GA ACAA  
 ||||| || |||||  
 AGGGTTC GA CT TGTT  
 \_ C CA\_  
 GAM1625 FLJ14775 3' TGTTGTCTTCTTCACTGAC 51606 TA\_ A  
 GTC GAA AAGACAACA  
 || || |||||  
 CAG CTT TTCTGTTGT  
 TCA C  
 GAM1625 FLJ20045 5' GTTGTCTTCAACTTAGAC 34427 AAA\_  
 GTCTAG AAGACAAC  
 ||||| |||||  
 CAGATT TTCTGTTG  
 CAAC  
 GAM1625 FLJ20559 5' TCTTCCGCTGTGTTTGGA 35399 TC AAA  
 TCCCAAG TAG AAGA  
 ||||| || |||||

AGGGTTT GTC TTCT  
 GT GCC  
 GAM1625 FLJ22002 3' TTGTCTTTTCTGGCAGCT 45782 \_\_\_\_  
 AGT CTAGAAAAAGACAA  
 ||| |||||  
 TCG GGTCTTTTCTGTT  
 AC  
 GAM1625 FLJ23420 3' TGTCATCTTTCTGGGGCCCAGG 46851 CAA \_ AA\_  
 A TCC GTCTAGAAA GACA  
 ||| ||| ||| |||  
 AGG CGGG TCTTT CTGT  
 ACC G CTA  
 GAM1625 GMEB2 5' TGCTTCCTCCAGGACTTGGGA 24741 A\_ AA A  
 TCCCAAGTCT GA AAG CA  
 ||||| || ||| ||  
 AGGGTTCAGG CT TTC GT  
 AC CC \_  
 GAM1625 GTF3C4 5' TGTCCTTTTCTGGAC 24197 \_  
 GTCTAGAAAAAG ACA  
 ||||| ||| |||  
 CAGGTCTTTTTC TGT  
 C  
 GAM1625 GTSE1 3' TTGTAACCCTAGAACTTGGGA 33142 \_ AAAAAG  
 TCCCAAGT CTAG ACAA  
 ||||| ||| |||  
 AGGGTTCA GATC TGTT  
 A CCAA\_  
 GAM1625 HAK 3' TGTCATTCTAACCTGGGA 53644 A C AAAAA  
 TCCCA GT TAG GACA  
 |||| ||| |||  
 AGGGT CA ATC CTGT  
 C \_ CTTA\_  
 GAM1625 HPCAL4 3' TCTTTTCTCTAGACTTGG 32741 \_  
 CCAAGTCTAGA AAAAGA  
 ||||| ||||| |||||  
 GGTTCAATCT TTTTCT  
 C  
 GAM1625 HSU79252 3' TGTCCTTTTCTCCTTGAGG 25247 \_ TCT \_  
 CC CAAG AGAAAAAG ACA  
 || ||| ||||| |||  
 GG GTTC TCTTTTTC TGT  
 A C\_ C  
 GAM1625 KHSRP 3' TGTTGTCTTTTCATCTG 13486 \_\_\_\_  
 TAGA AAAAGACAACA  
 ||| ||||| |||  
 GTCT TTTTCTGTTGT  
 AC  
 GAM1625 KIAA0232 3' TGTTGCCTTTTCTTAATTG 72762 GTCT A  
 CAA AGAAAAAG CAACA  
 ||| ||||| |||||

GTT TCTTTTTC GTTGT  
 AAT\_ C  
 GAM1625 KIAA0417 3' TGTCTTTCTAGATTT 71246 AA  
 AAGTCTAGAA AGACA  
 ||||| ||||  
 TTTAGATCTT TCTGT  
  
 —  
 GAM1625 KIAA0945 3' TCTTCCTAGACTTGAGG 30216 \_ AAA  
 CC CAAGTCTAG AAGA  
 || ||||| |||  
 GG GTTCAGATC TTCT  
 A C\_  
 GAM1625 KIAA1363 3' TGTCCCCCTTCTCCTTG GGG 69266 TCT AAA\_  
 TCCCAAG AGAA GACA  
 ||||| ||| |||  
 GGGGTTTCTCTT CTGT  
 C\_ CCCC  
 GAM1625 KIAA1821 3' TGTAATCCTAGCACTTG GGA 71801 \_ AAAAAG  
 TCCCAAGTCTAG ACA  
 ||||| ||| |||  
 AGGGTTCA GATC TGT  
 C CTAA\_  
 GAM1625 MGC15437 3' TGTCTTTGCCCTAGACTCTAG 51785 CCA AA\_  
 A TC AGTCTAG AAAGACA  
 || ||||| |||||  
 AG TCAGATC TTTCTGT  
 ATC CCG  
 GAM1625 PER3 3' TGTTGTCTTTATATAACTTG 33683 C GAA  
 CAAGT TA AAAGACAACA  
 ||||| || |||||  
 GTTCA AT TTTCTGTTGT  
 \_ ATA  
 GAM1625 SETBP1 3' TGCCTTTTTTTTTTCTTGG 31459 TCT A  
 CCAAG AGAAAAAG CA  
 ||||| ||||| ||  
 GGTTCTTTTTTTC GT  
 TTT C  
 GAM1625 SHAPY 3' TGTTGCCTTTTTCTAGG 57114 A  
 TCTAGAAAAAG CAACA  
 ||||| ||||| |||||  
 GGATCTTTTTC GTTGT  
 C  
 GAM1625 SLC2A10 3' TGTTGATTTTCTAGACTTCAGA 47831 CC AGA  
 TC AAGTCTAGAAAA CAACA  
 || ||||| ||||| |||||  
 AG TTCAGATCTTTT GTTGT  
 AC A\_  
 GAM1625 TIEG 3' TGTCATCTTTTCTAGAGTT 18960 G CA  
 AA TCTAGAAAAAGA ACA  
 || ||||| ||||| |||

	TT AGATCTTTTTCT TGT		
	G AC		
GAM1625 LOC118487 3'	TTGTCTTCCCTGCATTTG 73920	C AA	
	CAAGT TAG AAAGACAA		
	GTTTA GTC TTTCTGTT		
	C CC		
GAM1625 LOC130535 3'	TTGTCTCAGTTACTTGGA 76157	CTA AAA	
	TCCCAAGT GA AGACAA		
	AGGGTTCA TT TCTGTT		
	___ GAC		
GAM1625 LOC143384 3'	GTTGCTGCTAGACTTGGGG 76555	AAAA A	
	TCCCAAGTCTAG AG CAAC		
	GGGGTTCAGATC TC GTTG		
	G___ _		
GAM1625 LOC145173 3'	TTGTTAAGCAGACTTGGA 77044	AGAAAAA	
	TCCCAAGTCT GACAA		
	AGGGTTCAGA TTGTT		
	CGAA___		
GAM1625 LOC146272 5'	TTGTCTTTACCTGGAC 77797	AA	
	GTCTAG AAAGACAA		
	CAGGTC TTTCTGTT		
	CA		
GAM1625 LOC200728 3'	TGTTGTCTTTTTTCAGGAGTG 90120	AG A	
	CA TCT GAAAAAGACAACA		
	GT GGA CTTTTTCTGTTGT		
	GA _		
GAM1625 LOC221415 5'	GTTGTCCCTTCCCATTTGGG 93877	CTA AAA	
	CCCAAGT GAA GACAAC		
	GGGTTTA CTT CTGTTG		
	CC_ CC_		
GAM1625 LOC222233 5'	TGACTTCTCCTAGGCTTGAGA 94258	C AAA A	
	TC CAAGTCTAG AAG CA		
	AG GTTCGGATC TTC GT		
	A CTC A		
GAM1625 LOC257115 3'	TGTCATCTTAGCAATTTGGA 96528	___ _ AAAA	
	TCCCAAGT CTA GA GACA		
	AGGGTTTA GAT CT CTGT		
	AC T A___		
GAM1625 LOC51580 3'	TTGTCTTCTGGTGTCTGGG 31870	AG_ AA	
	CCCA T CTAGAA AGACAA		

GGGT G GGTCTT TCTGTT  
CTT \_

GAM1625 LOC90777 3' TGTCTTTATTTGGGA 63970 CTAGAA  
TCCCAAGT AAAGACA  
||||| |||||  
AGGGTTTA TTTCTGT

\_\_\_\_\_

GAM1625 LOC93190 3' GTTTGAAGTCTCTGACTTGGGA 71659 T\_ AAA\_  
TCCCAAGTC AGA AGAC  
||||| ||| |||  
AGGGTTCAG TCT TTTG  
TC GAAG

GAM1625 LOC94976 3' TGCCTTTGTTTGGCAAACCTTGG 71750 \_ A A  
G CCCAAGT CTAGA AAAG CA  
||||| |||| ||| ||  
GGGTTCA GGTTT TTTC GT  
AAC G C

GAM1626 AHR 3' AAGTAAAATGTCTTTCC 7871 GG G  
GGAAAGACAT TTA TT  
||||| ||| ||  
CCTTTCTGTA AAT AA  
A\_ G

GAM1626 ATP1B1 3' AGCACAAATCTTTCCCA 8039 CA \_  
TGGGAAAGA TG GTT  
||||| || |||  
ACCCTTTCT AC CGA  
AA A

GAM1626 CLCA3 3' AAGCAACTAAGTTTATTCCT 16989 A CAT A  
GGGAA GA GGTTAGTT CTT  
|||| || ||||| |||  
TCCTT TT TCAATCAA GAA  
A \_ C

GAM1626 EIF2B5 3' AGCAACCATGTGCCTCCCA 61529 AAG A  
TGGGA ACATGGTT GTT  
|||| ||||| |||  
ACCCT TGTACCAA CGA  
CCG \_

GAM1626 FAFL5 3' AATCAATCCTGTCTTTCCCA 64184 T A  
TGGGAAAGACA GGTT GTT  
||||| ||| |||  
ACCCTTTCTGT CTAA TAA  
C C

GAM1626 FGF2 3' AACAAATGTGTTTCCCA 8864 G G\_  
TGGGAAA ACAT GTT  
||||| ||| |||  
ACCCTTT TGTA CAA  
G AA

GAM1626 KCNJ15 5' AACACCTATCTTTCCCA 9540 CAT TA  
TGGGAAAGA GGT GTT  
||||| ||| |||



		ACCCTTTCT CCA CAA	
		AT_ _	
GAM1626 LDB3	3'	AAGCAACAAGCAGCTTTCCCA 76402	ACATG A A
		TGGGAAAG GTT GTT CTT	
		ACCCTTTC CGA CAA GAA	
		GA_ _ A C	
GAM1626 MAPK14	3'	AAGTAACAAGGTGTCTTTTCCA 7155	GGTTA
		TGGGAAAGACAT GTTACTT	
		ACCTTTTCTGTG CAATGAA	
		GAA_ _	
GAM1626 MAPK14	3'	AAGTAACAAGGTGTCTTTTCCA 57329	GGTTA
		TGGGAAAGACAT GTTACTT	
		ACCTTTTCTGTG CAATGAA	
		GAA_ _	
GAM1626 MAPK14	3'	AAGTAACAAGGTGTCTTTTCCA 57340	GGTTA
		TGGGAAAGACAT GTTACTT	
		ACCTTTTCTGTG CAATGAA	
		GAA_ _	
GAM1626 NR5A2	3'	AAGTAATTCAAATCTTCCCCA 13787	A CA TTA
		TGGG AAGA TGG GTTACTT	
		ACCC TTCT ACT TAATGAA	
		C AA _ _	
GAM1626 B3GNT5	3'	AATTAACCCACTCCTCCC 49422	AA CAT
		GGGA GA GGTTAGTT	
		CCCT CT CCAATTAA	
		C_ CAC	
GAM1626 FLJ11286	3'	AAGTACAAGTCACATCTTTCCC 37214	CA GT A T
A		TGGGAAAGA TG T GT ACTT	
		ACCCTTTCT AC A CA TGAA	
		AC TG A _	
GAM1626 FLJ13385	3'	AAGTAATAATTATGCTTTGCC 45848	G A
A		TGG AAAG CATGGTTAGTTACTT	
		ACC TTTC GTATTAATCAATGAA	
		G _	
GAM1626 FLJ14502	3'	AACACATTCTTTCCCA 62716	C _
		TGGGAAAGA ATG GTT	
		ACCCTTTCT TAC CAA	
		_ A	
GAM1626 H_GS165L15.1	3'	AACACACAGCCTTTCCCA 16924	ACA _ TA
		TGGGAAAG TG GT GTT	

		ACCCTTTC AC CA CAA		
		CG_ A _		
GAM1626 KIAA1337	3'	AGCCCCTGTCTTTCCCA	72678	T_
		TGGGAAAGACA GGTT		
		ACCCTTTCTGT CCGA		
		CC		
GAM1626 KIAA1453	3'	AGCACCATGTCTCCTCCA	46970	AA TA
		TGGG AGACATGGT GTT		
		ACCT TCTGTACCA CGA		
		CC _		
GAM1626 MGC3413	3'	TGACCATGTCCTTCCCA	51050	A
		TGGGAA GACATGGTTA		
		ACCCTT CTGTACCAGT		
		C		
GAM1626 NAG14	3'	AGTAATGAAGCCTTTCCCA	42163	GACAT A_
		TGGGAAA GGTT GTTACT		
		ACCCTTT CCGA TAATGA		
		_ AG		
GAM1626 NYD-SP25	3'	AGCAGCATGTCTTTGCCA	53185	G G A
		TGG AAAGACATG TT GTT		
		ACC TTTCTGTAC GA CGA		
		G _ _		
GAM1626 SMARCF1	3'	TAAAAATGGCTTTCCCA	57491	A GG
		TGGGAAAG CAT TTA		
		ACCCTTTC GTA AAT		
		G AA		
GAM1626 SMARCF1	3'	TAAAAATGGCTTTCCCA	37443	A GG
		TGGGAAAG CAT TTA		
		ACCCTTTC GTA AAT		
		G AA		
GAM1626 SMARCF1	3'	TAAAAATGGCTTTCCCA	20045	A GG
		TGGGAAAG CAT TTA		
		ACCCTTTC GTA AAT		
		G AA		
GAM1626 LOC152580	5'	TAACCAGAGCCACAGCTTTCCC	85779	ACA A_
A		TGGGAAAG TGGTT GTTA		
		ACCCTTTC ACCGA CAAT		
		GAC GAC		
GAM1626 LOC200261	5'	AAGTAACTTCAGTGGTGTTCCC	88651	AGA GGTT
		GGGAA CAT AGTACTT		

		CCCTT GTG TCAATGAA		
		GTG ACT_		
GAM1626	LOC221477 3'	GTACACTTCTTTCCCA	92161	CATGGTT _
		TGGGAAAGA AGT TAC		
		ACCCTTTCT TCA ATG		
		_____ C		
GAM1627	A2M 5'	CTCCAGCTCCTTCTTTCTG	3400	GCAT A A
		TAGAAAGA GGGG CTG AG		
		GTCTTTCT TCCT GAC TC		
		_____ C C		
GAM1627	ABCD1 3'	TCACCACCTCTTTCTA	3465	CA _
		TAGAAAGAG TGG GA		
		ATCTTTCTC ACC CT		
		C_ A		
GAM1627	APTX 3'	TTCCATGCCCTTCTA	34663	A A
		TAGAA G GCATGGGA		
		ATCTT C CGTACCTT		
		_C		
GAM1627	AQP1 3'	CCTTCAGTTCTGCTTGCTC	4605	TG_
		GAGCA GGAAGTGAAGG		
		CTCGT TCTTGAATTCC		
		TCG		
GAM1627	CACNA1C 5'	CCCTCAGTTCTTACATGCTC	5559	_ A
		GAGCATG GGAAGTGA GG		
		CTCGTAC TCTTGAAT CC		
		AT C		
GAM1627	CHRNA4 3'	CCCCCAGGGCTTCCCAAGCTCT	5629	A _ AA
	TTC	GAAAGAGC TGGGAA CTG GG		
		CTTTCTCG ACCCTT GAC CC		
		A CGG CC		
GAM1627	CNGA1 3'	CCCTCACTTTCATGCCATTTT	59508	GA GG AC A
		GAAA GCATG A TGA GG		
		CTTT CGTAC T ACT CC		
		AC TT C_ C		
GAM1627	GBA 3'	CCCCCAGCCCCCATGCTT	76337	AA AA
		GAGCATGGG CTG GG		
		TTCGTACCC GAC CC		
		CC CC		
GAM1627	GBF1 3'	CCTCCAGTTCTTCCTTTTT	14831	CAT A
		GAAAGAG GGGAAGT AGG		

			TTTTCTC TTCTTGAC TCC			
			C_ C			
GAM1627	GORASP1	3'	CCCTCAGTTCACACTGCT 49108	___	A	
			AGCA TGGGAACTGA GG			
			TCGT ACCCTTGA CT CC			
			CAC C			
GAM1627	GRAF	3'	CCTCCAATTCCCGTGATC 30555	G	C A	
			GA CATGGGAA TG AGG			
			CT GTGCCCTT AC TCC			
			A A C			
GAM1627	HOXB7	3'	CCCCCAGCCCCATGCTCCCTTT 15696	AA	AA AA	
	A		TAGA GAGCATGGG CTG GG			
			ATTT CTCGTACCC GAC CC			
			CC C_ CC			
GAM1627	IL1RN	3'	CTCCAGAATGGTCTTTCTA 5142	G	G GGAA A	
			TAGAAAGA CAT CTG AG			
			ATCTTTCT GTA GAC TC			
			G A_ C			
GAM1627	LRP1	3'	CCTTCAGTGAGCCCCTC 9800	CAT	A_	
			GAG GGG ACTGAAGG			
			CTC CCC TGA CTTC			
			_ GAG			
GAM1627	LZTS1	3'	CCCTCAGTTCCTTCATTTT 40687	GAGCAT	A	
			GAAA GGGA ACTGA GG			
			CTTT TCCTTGA CT CC			
			ACT_ C			
GAM1627	MAFG	5'	CCTTCAGTTCCTTCTC 70093	CAT		
			GAG GGGA ACTGAAGG			
			CTC CCCTTGA CTTC			
			TTC			
GAM1627	MUC5B	3'	CCTCCATCCCCATGCTCTGTC 66864	A	AAC A	
			GA AGAGCATGGG TG AGG			
			CT TCTCGTACCC AC TCC			
			G CT_ C			
GAM1627	PCOLN3	3'	CCCTCAGTTCCTCAAAGCT 10909	A_	A	
			AGC TGGGA ACTGA GG			
			TCG ACCCTTGA CT CC			
			AA C			
GAM1627	RBP4	3'	CCCTCAGTTCCTCATAAACCTT 59599	AGAGC_	A	
	C		GAA ATGGGA ACTGA GG			

			CTT TACCCTTGACT CC		
			CCAAAA C		
GAM1627	RGL	3'	CCTCCAATTTCTTTGGTCTTT 30732	G T	C_ A
	C		GAAAGA CA GGGAA TG AGG		
			CTTTCT GT TCCTT AC TCC		
			G T TA C		
GAM1627	SET7	3'	CCCTCAGCCCTATTCTCTTTCT 47635	C AA	A
			AGAAAGAG ATGGG CTGA GG		
			TCTTTCTC TATCC GACT CC		
			T C_ C		
GAM1627	SLC2A8	3'	CCTTCCTGTGCATGCTCCCTC 27421	AA	GAACT
			GA GAGCATGG GAAGG		
			CT CTCGTA CT TCC		
			CC GTC__		
GAM1627	SURF5	3'	CAGGCTTCCCATGCCCT 22180	A	__
			AG GCATGGGAA CTG		
			TC CGTACCCTT GAC		
			C CG		
GAM1627	TAF1C	3'	CCCTCAGTTCTCACGCCTTCCT 19058	A A A	A
	G		TAG AAG GC TGGGAACTGA GG		
			GTC TTC CG ACTCTTGACT CC		
			C _ C C		
GAM1627	TNFAIP1	3'	CTTGACCCATGTCTTTCTA 40921	G	AACTG
			TAGAAAGA CATGGG AAG		
			ATCTTTCT GTACCC TTC		
			_ AG__		
GAM1627	TNNT2	3'	CCCCAGTTCCTCGGGCCCTCCT 4524	AA A A	AA
	G		TAG AG GC TGGGAACTG GG		
			GTC TC CG GCCCTTGAC CC		
			C_ C G CC		
GAM1627	ARFGAP1	3'	CCTTCAGCCCCTGTGCTC 36589	AA	
			GAGCATGGG CTGAAGG		
			CTCGTGTCC GACTTCC		
			CC		
GAM1627	BCMP1	3'	CCTTCAGGAACACTCTTTTTA 48735	CA	GGAA
			TAGAAAGAG TG CTGAAGG		
			ATTTTCTC AC GACTTCC		
			_ AAG_		
GAM1627	CARD14	3'	TTCCCATGCCTTCCCTA 44110	A_	A
			TAG AAG GCATGGGAA		

ATC TTC CGTACCCTT  
 CC \_  
 GAM1627 CECR7 5' CCTCCAGCCCCAGCTTT 79618 A AA A  
 AGAGC TGGG CTG AGG  
 |||| ||| ||| |||  
 TTTCG ACCC GAC TCC  
 \_ CC C  
 GAM1627 DAPK2 3' AGTATGCCCATGCTCCCTCTA 26734 AA A\_\_  
 TAGA GAGCATGGG ACT  
 ||| ||||| |||  
 ATCT CTCGTACCC TGA  
 CC GTA  
 GAM1627 DDX34 3' CCTCCAGTCCCTCCTGCTTTTT 27980 T\_\_ A A  
 AAAGAGCA GGA CTG AGG  
 ||||| ||| ||| |||  
 TTTTTCGT CCCT GAC TCC  
 CCT \_ C  
 GAM1627 DKFZP434C0826 5' CTCCAGCTCCACCTTTCTG 84036 AGCATG A A  
 TAGAAAG GGA CTG AG  
 ||||| ||| ||| |||  
 GTCTTTC CCT GAC TC  
 CA\_\_ C C  
 GAM1627 DKFZP434E2135 3' TCTGCATGCTCTTTCT 47958 \_  
 AGAAAGAGCATG GGA  
 ||||| ||| ||| |||  
 TCTTTCTCGTAC TCT  
 G  
 GAM1627 DKFZP434H132 5' CTTCAGTCCCCAGGCTC 73605 A A  
 GAGC TGGG ACTGAAG  
 ||| ||| |||||  
 CTCG ACCC TGA CTTC  
 G C  
 GAM1627 EPB41L1 3' CTTTCTCGTCCCCATGCTC 70593 A T\_  
 GAGCATGGG AC GAAGG  
 ||||| || |||||  
 CTCGTACCC TG CTTTC  
 C CT  
 GAM1627 FLJ10713 3' TTCAACAGCTCTTTT 36475 A GGAAC  
 GAAAGAGC TG TGAA  
 ||||| || |||  
 TTTTCTCG AC ACTT  
 \_ A\_\_  
 GAM1627 FLJ11700 3' CAGGCAGCCCAGCCCTTTC 46037 A A AA\_\_  
 GAAAG GC TGGG CTG  
 |||| || ||| |||  
 CTTTC CG ACCC GAC  
 C \_ GACG  
 GAM1627 FLJ12287 3' CCTTCAGTTCTGGCCATTC 42313 AGA ATG  
 GAA GC GGA ACTGAAGG  
 ||| || ||||| |||

CTT CG TCTTGACTTCC  
 AC\_ G\_  
 GAM1627 FLJ14166 3' CAGTCCCCACCTCTCTC 44682 A CA  
 GA AGAG TGGGAAGT  
 || ||| |||||  
 CT TCTC ACCCTTGAC  
 C C\_  
 GAM1627 FLJ20489 3' CTCCAGCCCTGCGTTTC 35250 GA T AA A  
 GAAA GCA GGG CTG AG  
 ||| ||| ||| |||  
 CTTT CGT CCC GAC TC  
 G\_ \_ \_ C  
 GAM1627 FLJ21144 3' CCTTCAGTAAACTTTGCTTTCC 42876 AA T GA\_  
 TA TAG AGAGCA GG ACTGAAGG  
 ||| ||||| || |||||  
 ATC TTTCGT TC TGAAGTCC  
 C\_ T AAA  
 GAM1627 GRID1 3' CTTCAGTTGCCCTTTCTG 68498 AGCAT G  
 TAGAAAG GG AACTGAAG  
 ||||| || |||||  
 GTCTTTC CC TTGACTTC  
 \_ G  
 GAM1627 GTF3C2 3' CCTTAGATCCCACTCTTTCTA 7723 CA A A  
 TAGAAAGAG TGGGA CTGA GG  
 ||||| ||| ||| |||  
 ATCTTTCTC ACCCT GATT CC  
 \_ A \_  
 GAM1627 KALI 3' CCTTCCCAGACCACTCTTTCTA 53591 CA GAACT  
 TAGAAAGAG TGG GAAGG  
 ||||| ||| |||  
 ATCTTTCTC ACC CTTCC  
 \_ AGACC  
 GAM1627 KIAA0275 3' CCCAGTCCCCTCTTTCT 28674 CAT A AA  
 AGAAAGAG GGGGA CTG G  
 ||||| ||| ||| |  
 TCTTTCTC CCCT GAC C  
 \_ \_ CC  
 GAM1627 KIAA0323 3' CCTCCAGCTCAGCCCTTTCTG 63262 A A AA A  
 TAGAAAG GC TGGG CTG AGG  
 ||||| || ||| ||| |||  
 GTCTTTC CG ACTC GAC TCC  
 C \_ \_ C  
 GAM1627 KIAA0435 3' CCCCCAGGGCCGCTCTTTC 28972 ATG AA AA  
 GAAAGAGC GG CTG GG  
 ||||| || ||| |||  
 CTTTCTCG CC GAC CC  
 \_ GG CC  
 GAM1627 KIAA0552 3' CCCTCAGCCCTTATATCTCTCT 28310 A C\_ AA A  
 CT AGA AGAG ATGGG CTGA GG  
 ||| ||| ||||| ||||| |||

TCT TCTC TATTC GACT CC  
 C TA CC C  
 GAM1627 KIAA0729 3' CCCCCAACCCCCATGCTGTTTG 95703 G G AAC AA  
 TA TA AAA AGCATGGG TG GG  
 || ||| ||||| || ||  
 AT TTT TCGTACCC AC CC  
 G G CCA CC  
 GAM1627 KIAA1045 3' TGGTCCCTCATGCCCTT 71063 A \_ A  
 AAG GCATG GG ACTG  
 ||| ||||| || ||||  
 TTC CGTAC CC TGGT  
 C T C  
 GAM1627 KIAA1881 3' TTTCCATGCTCTCCTA 95347 AA  
 TAG AGAGCATGGGAA  
 ||| ||||| |||||  
 ATC TCTCGTACCTTT  
 C\_  
 GAM1627 KIAA1915 3' CCCAAATTCTGCTTTCTCTA 73278 A \_\_\_\_\_  
 TAGA AGAGCA TGGG  
 ||||| ||||| |||||  
 ATCT TTTCGT ACCC  
 C CTAA  
 GAM1627 PKNOX2 3' CCTTCAGTGCTCCACGCCCT 90877 A A A\_  
 AG GC TGGG ACTGAAGG  
 || ||||| |||||  
 TC CG ACCT TGA CTTC  
 C C CG  
 GAM1627 PRO0899 5' CAGTCCATGCTCCTTC 37694 A GA  
 GAA GAGCATGG ACTG  
 ||| ||||| |||||  
 CTT CTCGTACC TGAC  
 C \_  
 GAM1627 SEPT1 3' CCTTCAGTCGGCCTCTTGTC 53423 \_ CA GGA  
 GA AAGAG TG ACTGAAGG  
 || ||||| || |||||  
 CT TTCTC GC TGA CTTC  
 G CG \_  
 GAM1627 STK39 3' CCTTCAACCCTCCCTCTTTCTG 25076 CAT AAC  
 TAGAAAGAG GGG TGAAGG  
 ||||| ||| |||||  
 GTCTTTCTC CCC ACTTCC  
 CCT A\_  
 GAM1627 WBP4 3' CCCCCAGTCATGCACTCTTTT 23231 \_ GGA AA  
 A TAGAAAGA GCATG ACTG GG  
 ||||| ||||| ||||| ||  
 ATTTTCT CGTAC TGAC CC  
 CA \_ CC  
 GAM1627 ZNF259 3' CCTCCAGCGCTGCTCTTTCTG 72619 TGG AA A  
 TAGAAAGAGCA G CTG AGG  
 ||||| ||||| | ||| |||



GTCTTTCTCGT C GAC TCC  
 \_\_\_\_GC C  
 GAM1627 LOC122525 3' CCTCCTGCCCATGCTCT 76008 AACT A  
 AGAGCATGGG GA GG  
 ||||| ||  
 TCTCGTACCC CT CC  
 GTC\_ \_  
 GAM1627 LOC144893 5' CCCTCAGAAACCGCTCCTTC 83186 A AT GAA A  
 GAA GAGC GG CTGA GG  
 ||| ||| || ||| ||  
 CTT CTCG CC GACT CC  
 C \_ AAA C  
 GAM1627 LOC146823 3' CCTTTGTAAGTCCCATGCTCCT 83794 AA AC\_  
 CTA TAGA GAGCATGGGA TGAAGG  
 ||| ||||| |||||  
 ATCT CTCGTACCCT GTTTC  
 C\_ GAAT  
 GAM1627 LOC148930 3' CCTCTCAGCCATGCTCT 79094 GAA \_  
 AGAGCATGG CTGA AGG  
 ||||| ||| |||  
 TCTCGTACC GACT TCC  
 \_ C  
 GAM1627 LOC149950 3' CCCTCAGTTCCTCACCCCTCT 79552 CA\_ \_ A  
 AGAG TG GGAAGTGA GG  
 ||| || ||||| ||  
 TCTC AC CCTTGACT CC  
 CCC T C  
 GAM1627 LOC152245 5' CCTTCAGTTTCCAGGCCTTCCT 85600 A A A  
 A TAG AAG GC TGGGAAGTGAAGG  
 ||| ||| ||||| |||||  
 ATC TTC CG ACCTTTGACTTCC  
 C \_ G  
 GAM1627 LOC152317 3' CCTCCAGTTCTCCCCTCCCTCT 85640 AA CAT A  
 A TAGA GAG GGGAACTG AGG  
 ||| ||| ||||| |||  
 ATCT CTC CTCTTGAC TCC  
 CC CC\_ C  
 GAM1627 LOC162239 5' CTCCAGTTCTGCCTTC 82341 A A TGG A  
 GAA G GCA GAACTG AG  
 ||| ||| ||||| ||  
 CTT C CGT CTTGAC TC  
 \_ \_ \_ C  
 GAM1627 LOC221474 5' CCCTCAGCATGCTGTGCTCT 92378 GAA\_ A  
 AGAGCATGG CTGA GG  
 ||||| ||| ||  
 TCTCGTGTC GACT CC  
 GTAC C  
 GAM1627 LOC254428 3' TCCCACCTCTTTCTA 95464 CA  
 TAGAAAGAG TGGGA  
 ||||| |||||

ATCTTTCTC ACCCT  
 C\_  
 GAM1627 LOC51063 3' TTCCCATGCTCTTTGTA 31919 G  
 TA AAAGAGCATGGGAA  
 || |||||  
 AT TTTCTCGTACCCTT  
 G  
 GAM1627 LOC64150 5' CTGATCCACACTCTTTCTA 67281 CA AACTGA  
 TAGAAAGAG TGGG AG  
 ||||| ||| ||  
 ATCTTTCTC ACCT TC  
 AC AG\_\_\_\_  
 GAM1627 LOC93259 5' CCCCCAGTTCTCCATCTC 71810 C \_ AA  
 GAG ATGG GAACTG GG  
 ||| ||| ||||| ||  
 CTC TACC CTTGAC CC  
 \_ T CC  
 GAM1628 DACH 3' TGAGAATGTTTGTAATGTACA 54974 CATCC CT  
 TGTACA ACA CATTCTCA  
 ||||| ||| |||||  
 ACATGT TGT GTAAGAGT  
 AAA\_\_ TT  
 GAM1628 IL11RA 3' GGAACGTGTGTAATGTGTACA 15712 C\_ TCA  
 TGTACACAT CACAC TTCT  
 ||||| ||||| |||||  
 ACATGTGTA GTGTG AAGG  
 AT C\_  
 GAM1628 LYPLA1 3' AGAATGAGGTGGTATTACA 20922 CACAT A  
 TGTA CCAC CTCATTCT  
 ||||| ||||| |||||  
 ACAT GGTG GAGTAAGA  
 TAT\_\_ \_  
 GAM1628 NAPB 3' GAGAATGAATGTATGT 70183 CC C  
 ACAT ACA TCATTCTC  
 ||||| ||| |||||  
 TGTA TGT AGTAAGAG  
 \_ A  
 GAM1628 NRF1 3' GAATATATGTATATGTGTACA 60120 CC CTC  
 TGTACACAT ACA ATTC  
 ||||| ||| |||||  
 ACATGTGTA TGT TAAG  
 TA ATA  
 GAM1628 PRKAB1 3' AGAGGGAATGGACTGTACA 20734 CA CA AT  
 TGTACA TCCA CTC TCT  
 ||||| ||||| ||| |||  
 ACATGT AGGT GGG AGA  
 C\_ AA \_  
 GAM1628 PTGFR 3' TGAGAGAGATGTGTACA 6319 CACA  
 TGTACACATC CTCA  
 ||||| |||||

			ACATGTGTAG GAGT		
			AGA_		
GAM1628	RBBP5	3'	AGATTGGATAGATGTGTACA 17327	CACAC	T
			TGTACACATC TCA TCT		
			ACATGTGTAG GGT AGA		
			ATA__ T		
GAM1628	SAT	3'	TGAGTCATTTAAATGTGTACA 11436	CCAC__	
			TGTACACAT ACTCA		
			ACATGTGTA TGAGT		
			AATTTAC		
GAM1628	TMP21	3'	AATGGTGTATGGATGTGACA 22399	A	_ T
			TGT CACATCCA CAC CATT		
			ACA GTGTAGGT GTG GTAA		
			_ A _		
GAM1628	UBE2V1	3'	TGAAATGTGGATGCATAC 41797	CA	C_
			GTA CATCCACA TCA		
			CAT GTAGGTGT AGT		
			AC AA		
GAM1628	UBE2V1	3'	TGAAATGTGGATGCATAC 42374	CA	C_
			GTA CATCCACA TCA		
			CAT GTAGGTGT AGT		
			AC AA		
GAM1628	UBE2V1	3'	TGAAATGTGGATGCATAC 12522	CA	C_
			GTA CATCCACA TCA		
			CAT GTAGGTGT AGT		
			AC AA		
GAM1628	ZIC1	3'	AGAATGTTCTAGTAAATGTGTA 12720	CC	ACT__
	C		GTACACAT AC CATTCT		
			CATGTGTA TG GTAAGA		
			AA ATCTT		
GAM1628	AF038169	5'	TGAAAATGAGTGCTGTAGATG 25255	_ _	C
			CATC CA CACTCATT TCA		
			GTAG GT GTGAGTAA AGT		
			AT C A		
GAM1628	CDC14A	3'	AGAAGTGGATGTATATA 13391	C	ACTCA
			TGTA ACATCCAC TTCT		
			ATAT TGTAGGTG AAGA		
			A _____		
GAM1628	DKFZP564I052	3'	GATGATCATGTGATGTGTACA 66710	C	C_
			TGTACACATC ACA TCATT		

		ACATGTGTAG TGT AGTAG	
		_ ACT	
GAM1628	DKFZP761F241 3'	TGAGAATGAGTGAGGTTTCGTA 48800	ACAT A
	CA	TGTAC CC CACTCATTCTCA	
		ACATG GG GTGAGTAAGAGT	
		CTTT A	
GAM1628	FLJ11101 3'	AGAAGTGTTGAGTGTGTACA 37049	TC _ CAT
		TGTACACA CA CACT TCT	
		ACATGTGT GT GTGA AGA	
		GA T _	
GAM1628	FLJ14642 3'	AGTATGGGTGTGTACA 51492	C
		TGTACACATCCA ACT	
		ACATGTGTGGGT TGA	
		A	
GAM1628	FLJ20399 3'	GGTGGCTGTGGATGCCACA 35125	ACA CT
		TGT CATCCACA CATT	
		ACA GTAGGTGT GTGG	
		CC_ CG	
GAM1628	GFPT1 3'	GAAGATGGGATGTGTACA 9022	A C A
		TGTACACATCC CA TC TTC	
		ACATGTGTAGG GT AG AAG	
		- - -	
GAM1628	KIAA0450 3'	GAGGGCAGTGTGGATG 27640	CA
		CATCCACACT TTCTC	
		GTAGGTGTGA GGGAG	
		C_	
GAM1628	KIAA0530 3'	GATGGTATGAAAATGTGTACA 70867	C_ C T
		TGTACACAT CA AC CATT	
		ACATGTGTA GT TG GTAG	
		AAA A _	
GAM1628	KIAA0753 3'	GGGGAGTTAAATGTGTACA 28999	CCAC ATT
		TGTACACAT ACTC CTC	
		ACATGTGTA TGAG GGG	
		AAT_ _	
GAM1628	KIAA0788 3'	TGAATTAGGAATGTGTACA 71339	_ ACAC
		TGTACACAT CC TCA	
		ACATGTGTA GG AGT	
		A ATTA	
GAM1628	KIAA0855 3'	AGAATGAGCAGTGTAC 30400	ATCCACA
		GTACAC CTCATTCT	

		CATGTG	GAGTAAGA		
		AC_____			
GAM1628	KIAA0865	5'	GAGCAAGTGGAATGTGTACA	61250	_ A__
			TGTACACAT CCAC CTC		
			ACATGTGTA GGTG GAG		
			A AAC		
GAM1628	KIAA0992	3'	GGAAGTGTGGAGCACACA	32207	ACACA CAT
			TGT TCCACACT TCT		
			ACA AGGTGTGA AGG		
			CACG_ _____		
GAM1628	MGC16037	5'	TGAGGTGTAGATATGTATA	51822	C C _
			TGTACA ATC ACAC TCA		
			ATATGT TAG TGTG AGT		
			A A G		
GAM1628	OSRF	3'	TGAAAATGCACACAAATGTGTA	59525	CCACACT C
	CA		TGTACACAT CATT TCA		
			ACATGTGTA GTAA AGT		
			AACACAC A		
GAM1628	RAB3-GAP150	3'	TGAGAATCAGAGATGTGTA	24839	CACA C
			TACACATC CT ATTCTCA		
			ATGTGTAG GA TAAGAGT		
			A__ C		
GAM1628	RAP140	3'	GATGGGTAAATGTGTACA	30844	CCAC
			TGTACACAT ACTCATT		
			ACATGTGTA TGGGTAG		
			AA_		
GAM1628	TACTILE	5'	GAGTGCATGTGTACA	19471	CCA
			TGTACACAT CACTC		
			ACATGTGTA GTGAG		
			C_		
GAM1628	LOC131873	3'	GATGTATGCATATGTGTACA	75880	CCA CT
			TGTACACAT CA CATT		
			ACATGTGTA GT GTAG		
			TAC AT		
GAM1628	LOC134145	3'	AGCTGTATATGTGTACA	75144	CC _
			TGTACACAT ACA CT		
			ACATGTGTA TGT GA		
			TA C		
GAM1628	LOC145482	3'	AATGGTATGATGTGTACA	77226	CAC T
			TGTACACATC AC CATT		

ACATGTGTAG TG GTAA  
 TA\_ \_  
 GAM1628 LOC148195 3' GAAAAGGTGGATGTGTCA 84129 T A CA  
 TG ACACATCCAC CT TTC  
 || ||||| || ||  
 AC TGTGTAGGTG GA AAG  
 \_ \_ A\_  
 GAM1628 LOC152633 5' TGAGCTGTACATGTAGAGTGTA 85826 A C CT\_ TT  
 CA TGTACAC TC ACA CA CTCA  
 ||||| || || ||  
 ACATGTG AG TGT GT GAGT  
 \_ A ACAT C\_  
 GAM1628 LOC153630 5' AATGAGTGTGCGTAC 86079 ACATC  
 GTAC CACACTCATT  
 ||| |||||  
 CATG GTGTGAGTAA  
 C\_\_\_\_  
 GAM1628 LOC221662 3' AGAATGAGGGGAATGGGCA 92399 TA CA ACA  
 TG CA TCC CTCATTCT  
 || || || |||||  
 AC GT AGG GAGTAAGA  
 GG A\_ G\_  
 GAM1628 LOC254659 5' GAGAATGGAGATGCTACA 95113 CA CACAC  
 TGTA CATC TCATTCTC  
 ||| ||| |||||  
 ACAT GTAG GGTAAGAG  
 C\_ A\_\_\_\_  
 GAM1628 LOC83693 3' AGGGTGTGTGGATGGCACA 48830 ACA TC  
 TGT CATCCACAC ATTCT  
 || ||||| ||||  
 ACA GTAGGTGTG TGGGA  
 CG\_ \_  
 GAM1628 LOC90981 3' AATGGTGATGGATGTGACA 64532 A \_ T  
 TGT CACATCCA CAC CATT  
 || ||||| || |||  
 ACA GTGTAGGT GTG GTAA  
 \_ A \_  
 GAM1629 ABCD1 5' ACAATCCTTCCAGCCA 3459 A TT  
 TG CTGG AGGATTGT  
 || ||| |||||  
 AC GACC TCCTAACA  
 C T\_  
 GAM1629 CXCL16 3' ATAGGACTAACCAGCCACTG 41916 C A GA  
 CA TG CTGGTTAG TTGT  
 || || ||||| |||  
 GT AC GACCAATC GATA  
 C C AG  
 GAM1629 DDEF2 3' AACAACTCCTGCATCTGT 13948 C\_ ACT TT  
 ACA TG GG AGGATTGTT  
 ||| || || |||||

			TGT AC CC TCCTAACAA		
			CT GT_ _		
GAM1629	GDF8	3'	ACAATCCATGCCAACGGT 17925	AC	TA
			ACTG TGGT GGATTGT		
			TGGC ACCG CCTAACA		
			A_ TA		
GAM1629	GRB10	3'	AACATGTTTTTAACCATCAGTG 17968	C	T_
			CACTGA TGGTTAGGA TGTT		
			GTGACT ACCAATTTT ACAA		
			_ TGT		
GAM1629	ITK	3'	CCAACCAGTCATGTT 18676	C	A
			AACA TGACTGGTT GG		
			TTGT ACTGACCAA CC		
			_ _		
GAM1629	LANCL1	3'	ACAATAACAGTCTGTGTT 20205	T	GTTAGG
			AACAC GACTG ATTGT		
			TTGTG CTGAC TAACA		
			T AA_		
GAM1629	MAPK7	3'	AACAATCCTTTTCAGT 57379	TT	
			ACTGG AGGATTGTT		
			TGACT TCCTAACAA		
			TT		
GAM1629	MAPK7	3'	AACAATCCTTTTCAGT 57382	TT	
			ACTGG AGGATTGTT		
			TGACT TCCTAACAA		
			TT		
GAM1629	MAPK7	3'	AACAATCCTTTTCAGT 57385	TT	
			ACTGG AGGATTGTT		
			TGACT TCCTAACAA		
			TT		
GAM1629	MAPK7	3'	AACAATCCTTTTCAGT 10839	TT	
			ACTGG AGGATTGTT		
			TGACT TCCTAACAA		
			TT		
GAM1629	MEF2C	3'	AACAATCCCGGTGTGTCAG 9986	TGG	TA
			CTGAC T GGATTGTT		
			GACTG G CCTAACAA		
			TGT GC		
GAM1629	RPL15	3'	AACAATTTAGGACAGTCATGT 11383	C	GTTA
			ACA TGACTG GGATTGTT		

			TGT ACTGAC	TTTAACAA	
			—	AGGA	
GAM1629	STAC	3'	CCAATCAGTCAGTGT	11991	A
			ACACTGACTGGTT	GG	
			TGTGACTGACTAA	CC	
			—		
GAM1629	ARPP-19	3'	AACAATATCCTAATCA	21782	—
			TGGTTAGGAT	TGTT	
			ACTAATCCTA	ACAA	
			TA		
GAM1629	FLJ12700	3'	TCCAACAGTCAGTGTT	46122	GTTA
			AACACTGACTG	GGA	
			TTGTGACTGAC	CCT	
			AA—		
GAM1629	FLJ20038	3'	AATTATCAATCAGTCAG	34399	AG—
			CTGACTGGTT	GATT	
			GACTGACTAA	TTAA	
			CTA		
GAM1629	FLJ20073	3'	AACAGAGGACCAACCAGTC	34481	A A—
			GACTGGTT	GG TTGT	
			CTGACCAA	CC GACAA	
			—	AGGA	
GAM1629	FLJ23311	3'	ACAATCCTCAATCAAGTC	45177	— —
			GACT	GGTT AGGATTGT	
			CTGA	CTAA TCCTAACA	
			A	C	
GAM1629	FLJ23598	5'	ACAACCCTATCCAGTC	45519	T A
			GACTGG	TAGG TTGT	
			CTGACC	ATCC AACA	
			T	C	
GAM1629	KIAA1364	3'	AACATGAAATCAGTCAG	63585	AGGAT
			CTGACTGGTT	TGTT	
			GACTGACTAA	ACAA	
			AGT—		
GAM1629	KIAA1399	3'	TCCAATCAGTCAATG	70253	C A
			CA	TGACTGGTT GGA	
			GT	ACTGACTAA CCT	
			A	—	
GAM1629	RAB40A	5'	AACAATCGCTGAATCAGTTTC	82066	T — —
			C	GACTGGT TAG GATTGTT	



			C TTGACTA GTC CTAACAA		
			T A G		
GAM1629	TTY2	5'	CTACCAGTCATGTT	87002	C T
			AACA TGACTGGT AG		
			TTGT ACTGACCA TC		
			— —		
GAM1629	YAP1	3'	AATTCATACCAATCAGTGTT	20346	C TA
			AACACTGA TGGT GGATT		
			TTGTGACT ACCA CTAA		
			A TA		
GAM1629	LOC132793	5'	AACAATCCTGTGCCCAATC	75918	C T__
			GA TGG TAGGATTGTT		
			CT ACC GTCCTAACAA		
			A CGT		
GAM1629	LOC145858	3'	AACCATTTTAACCAGGCA	77541	A T
			TG CTGGTTAGGAT GTT		
			AC GACCAATTTTA CAA		
			G C		
GAM1629	LOC148764	5'	AACAATCCTGCAGACAAGCGTT	78979	A GA_ GT
			AAC CT CTG TAGGATTGTT		
			TTG GA GAC GTCCTAACAA		
			C ACA _		
GAM1629	LOC159148	5'	CTACCAGTCATGTT	87011	C T
			AACA TGACTGGT AG		
			TTGT ACTGACCA TC		
			— —		
GAM1629	LOC169611	3'	AATCTTGTAACCAGTCATGTT	82752	C _
			AACA TGACTGGTTA GGATT		
			TTGT ACTGACCAAT TCTAA		
			GT		
			—		
GAM1629	LOC200488	5'	AACAAGGAAGACCAGTCA	90076	AGGA
			TGACTGGTT TTGTT		
			ACTGACCAG AACAA		
			AAGG		
GAM1629	LOC253747	5'	CCTAATCAGCCAATGT	97474	C A
			ACA TG CTGGTTAGG		
			TGT AC GACTAATCC		
			A C		
GAM1629	LOC254866	3'	AACAATCCTGCTAAATCACTG	96765	C C_ T
			CA TGA TGGT AGGATTGTT		

			GT ACT ATCG TCCTAACAA		
			C AA _		
GAM1629	LOC257436	3'	AACAATAGAATCAGTCA	95679	AGG
			TGACTGGTT ATTGTT		
			ACTGACTAA TAACAA		
			GA_		
GAM1630	AAT1	3'	ACAATAGTCCCAAAGTGG	80494	C A A
			CCAGT TG GA CTATTGT		
			GGTCA AC CT GATAACA		
			A C _		
GAM1630	CRKL	3'	TTCTGCAGACTGGCAGT	17796	_
			ACTGCCAGTCTG AGAA		
			TGACGGTCAGAC TCTT		
			G		
GAM1630	ID1	3'	ACAATAGTTCTGTGGGGCTG	70030	G__
			CAGTCT AGAACTATTGT		
			GTCGGG TCTTGATAACA		
			GTG		
GAM1630	KRT16	5'	CAATGCCAGGCTGGCAG	95195	AGAAC
			CTGCCAGTCTG TATTG		
			GACGGTCGGAC GTAAC		
			C__		
GAM1630	PAPPA	5'	GGCTCCCAAAGCTGGCAG	10424	C_ A A
			CTGCCAGT TG GA CT		
			GACGGTCG AC CT GG		
			AA C C		
GAM1630	AP3M1	3'	TCTCAGATTGGCAGTT	23918	
			AACTGCCAGTCTGAGA		
			TTGACGGTTAGACTCT		
GAM1630	ARHU	3'	ACAATAGTTCTTAGCTTTG	41069	T_
			CAG CTGAGAACTATTGT		
			GTT GATTCTTGATAACA		
			TC		
GAM1630	CITED1	5'	ACAACAGCTCCAGCTGGCAG	14727	T A A A
			CTGCCAG CTG GA CT TTGT		
			GACGGTC GAC CT GA AACA		
			_ _ C C		
GAM1630	FLJ12684	5'	CAGTATCTCAGACCAAG	44587	GCCA AC
			CT GTCTGAGA TATTG		

			GA CAGACTCT ATGAC		
			AC__ _		
GAM1630	KIAA0275	3'	GGCTCCCAACCTGGCAGT 28681	TC A A	
			ACTGCCAG TG GA CT		
			TGACGGTC AC CT GG		
			CA C C		
GAM1630	KIAA0440	3'	ACAATAGTTGCAGAT 31453	AG	
			GTCTG AACTATTGT		
			TAGAC TTGATAACA		
			G_		
GAM1630	SCAMP5	3'	GTTCCCCAGCTGGCAGTT 57263	T A_	
			AACTGCCAG CTG GAAC		
			TTGACGGTC GAC CTTG		
			_ CC		
GAM1630	LOC145608	5'	TGGTCTCAGACCAG 83388	CCA A	
			CTG GTCTGAGA CTA		
			GAC CAGACTCT GGT		
			_ _		
GAM1630	LOC155376	5'	ACAAGAGATCAGCCTGGCAGTT 81331	T GAACTA	
			AACTGCCAG CTGA TTGT		
			TTGACGGTC GACT AACA		
			C AGAG_		
GAM1630	LOC201139	3'	CAATGCCAGGCTGGCAG 88129	AGAAC	
			CTGCCAGTCTG TATTG		
			GACGGTCGGAC GTAAC		
			C_		
GAM1630	LOC222233	5'	ACAAGAGATCAGCCTGGCAGTT 94248	T GAACTA	
			AACTGCCAG CTGA TTGT		
			TTGACGGTC GACT AACA		
			C AGAG_		
GAM1630	LOC253532	5'	ACAAGAGATCAGCCTGGCAGTT 96023	T GAACTA	
			AACTGCCAG CTGA TTGT		
			TTGACGGTC GACT AACA		
			C AGAG_		
GAM1630	LOC254875	5'	ACAAGAGATCAGCCTGGCAGTT 96053	T GAACTA	
			AACTGCCAG CTGA TTGT		
			TTGACGGTC GACT AACA		
			C AGAG_		
GAM1631	DMRT2	3'	CACAACAAGCAACAAGAACA 21614	CTATC_	
			TGTTC CTTGTTGTG		

			ACAAG	GAACAACAC			
			ACAAC				
GAM1631	F8	3'	CACAACAAAAATGTAACAGGG	3725	G	CC	CC
			CCC TGT TAT TTGTTGTG				
			GGG ACAA GTA AACAACAC				
			_ T_ AA				
GAM1631	GJB3	3'	TAAGAGACAGGAACACAGG	43770	C	A	_
			CC GTGTTCTC TC CTTG				
			GG CACAAGGA AG GAAT				
			A C A				
GAM1631	SH3BP2	3'	CAAGGACAGGAACACTGGT	11593	C	A	
			ACC GTGTTCTC TCCTTG				
			TGG CACAAGGA AGGAAC				
			T C				
GAM1631	TEM8	3'	CACCCAGGGATAAAAACA	49851	CC	TT	
			TGTT TATCCTTG GTG				
			ACAA ATAGGGAC CAC				
			AA C_				
GAM1631	ZNF216	3'	CACAGATAATAGGAACA	20018		CCTTG	
			TGTTCTAT TTGTG				
			ACAAGGATA GACAC				
			ATA__				
GAM1631	C20orf142	3'	AAGGAGCAGAAACACAGGT	74763	C	C	A_
			ACC GTGTT CT TCCTT				
			TGG CACAA GA AGGAA				
			A A CG				
GAM1631	C20orf59	3'	CACACGAGCAGAGAGGAACAC	41991		A	__ T
			GTGTTCTC TC CTTGT GTG				
			CACAAGGA AG GAGCA CAC				
			G AC _				
GAM1631	CLSTN2	3'	CACAACAAGGACAACAAGGACA	42126	T	A	____
	C		GTGT CCT TCCTTGTTGTG				
			CACA GGA AGGAACAACAC				
			_ ACAAC				
GAM1631	CLSTN2	3'	CACAACAAGGACAGTCACAAC	42127	_	TC	A
			GT GT CT TCCTTGTTGTG				
			CA CA GA AGGAACAACAC				
			A CT C				
GAM1631	CLSTN2	3'	CACAACAAGGACAGTCACAACA	42128	CG	TC	A
	AGG		CC TGT CT TCCTTGTTGTG				

GG ACA GA AGGAACAACAC  
AACA CT C  
GAM1631 FLJ10101 5' CGGGGAGACAGGAACACGGG 45264 A\_\_  
CCCGTGTTCCT TCCTTG  
||||||| |||||  
GGGCACAAGGA AGGGGC  
CAG  
GAM1631 HEYL 3' CACTCAGGACAGGAACAAGG 27391 G A TTT  
CC TGTTTCCT TCCT G GTG  
|| ||||| ||||| |||||  
GG ACAAGGA AGGA C CAC  
A C \_T\_  
GAM1631 INPP4B 3' TAATAAACAGGAACAC 13915 ATCC  
GTGTTTCCT TTGTTG  
||||||| |||||  
CACAAGGA AATAAT  
CA\_\_  
GAM1631 KIAA0391 3' CAAGAGACAGGAACAC 27906 A \_  
GTGTTTCCT TC CTTG  
||||||| || |||||  
CACAAGGA AG GAAC  
C A  
GAM1631 KIAA1376 3' CACAACAAGGAACAAAACA 63621 CCTA  
TGTT TCCTTGTTGTG  
|||| |||||  
ACAA AGGAACAACAC  
AACA  
GAM1631 KIAA1494 3' CACAACAAAGTAGCAC 68457 C ATCC  
GTGTT CT TTGTTGTG  
|||| || |||||  
CACGA GA AACAACAC  
T \_\_\_\_  
GAM1631 LOC147639 3' CACAATAACAGGGACAC 78378 ATCC  
GTGTTTCCT TTGTTGTG  
||||||| |||||  
CACAGGGA AATAACAC  
C\_\_  
GAM1631 LOC219529 3' ACAGGATAACAGGAACAC 92964 \_\_\_\_ T  
GTGTTTCCT ATCCT GT  
||||||| ||||| |||||  
CACAAGGA TAGGA CA  
CAA \_  
GAM1632 CBFB 3' CAGAAACTGTGATAA 8273 G  
TTAT CACAGTTTCTG  
||| |||||  
AATA GTGTCAAAGAC  
-  
GAM1632 CBFB 3' CAGAAACTGTGATAA 43140 G  
TTAT CACAGTTTCTG  
||| |||||

AATA GTGTCAAAGAC

GAM1632 CEACAM1 3' TGACACGGACTGTGCATA 8152 TC  
TATGCACAGTT TGTTA  
||||||| ||||  
ATACGTGTCAG ACAGT  
GC

GAM1632 KMO 3' TGACAGCCACTGTGCTATAATT 13458 \_ TT  
AATTAT GCACAGT CTGTTA  
||||| ||||| |||||  
TTAATA CGTGTCA GACAGT  
T CC

GAM1632 NRIP1 3' TGATGTCATGAACTGTACATA 59955 C \_ T  
TATG ACAGTTTC TG TATCA  
||| ||||| || |||||  
ATAC TGTCAAAG AC GTAGT  
A T T

GAM1632 SACM1L 3' CGGAAACTGTGCATAGTT 25821  
AATTATGCACAGTTTCTG  
||||||| |||||  
TTGATACGTGTCAAAGGC

GAM1632 TDG 3' TGATTCTTAACTGTGCATAA 12195 TCTGTT  
TTATGCACAGTT ATCA  
||||||| ||||  
AATACGTGTCAA TAGT  
TTCT\_\_

GAM1632 TEM8 3' TGATCAGGAACTGCACAAAAT 49858 A CA GTT  
T AATT TG CAGTTTCT ATCA  
||| || ||||| ||||  
TTAA AC GTCAAAGG TAGT  
A AC AC\_

GAM1632 FLJ14260 3' ATAACATTTTGTGCATAATT 46704 TTTC  
AATTATGCACAG TGTTAT  
||||||| |||||  
TTAATACGTGTT ACAATA  
TT\_\_

GAM1632 HIC 3' AACAGAAGCATAATT 67443 ACAGT  
AATTATGC TTCTGTT  
||||| |||||  
TTAATACG AAGACAA

GAM1632 HSPC129 3' TAACAGTAGCTATGCATAAT 33072 C T  
ATTATGCA AGTT CTGTTA  
||||| ||| |||||  
TAATACGT TCGA GACAAT  
A T

GAM1632 MAPK6 3' GAGACTGTACATAATT 10834 C  
AATTATG ACAGTTTC  
||||| |||||

TTAATAC TGTCAGAG  
 A  
 GAM1632 PLP1 3' TGATAACAGCTACCATGACA 5011 \_ CA TT  
 TG CA GT CTGTTATCA  
 || || || |||||  
 AC GT CA GACAATAGT  
 A AC TC  
 GAM1632 SLC21A12 3' CAGTTAAACTGTGCATA 33014 \_\_\_\_  
 TATGCACAGTTT CTG  
 ||||| ||  
 ATACGTGTCAAA GAC  
 ATT  
 GAM1632 STAB2 3' ACAGGAACTGTGCACAAT 34111 A  
 ATT TGCACAGTTTCTGT  
 || |||||  
 TAA ACGTGTCAAGGACA  
 C  
 GAM1632 LOC148479 3' GGTAGAACTGTACATAG 78875 C  
 TTATG ACAGTTTCTGTT  
 |||| |||||  
 GATAC TGTCAAAGATGG  
 A  
 GAM1632 LOC158156 3' GGAAACTGACATAATT 81727 CA  
 AATTATG CAGTTTCT  
 |||| |||||  
 TTAATAC GTCAAAGG  
 A\_  
 GAM1632 LOC170372 3' GAGACTGTACATAATT 76361 C  
 AATTATG ACAGTTTC  
 |||| |||||  
 TTAATAC TGTCAGAG  
 A  
 GAM1632 LOC257463 3' TGATAACATTCTGCCAACATAA 71072 CA\_\_ TTTC  
 TT AATTATG CAG TGTTATCA  
 |||| || |||||  
 TTAATAC GTC ACAATAGT  
 AACC TT\_  
 GAM1632 LOC89231 3' GATCACAGAAACCATA 92731 CACA T  
 TATG GTTTCTGT ATC  
 || ||||| ||  
 ATAC CAAAGACA TAG  
 \_\_\_\_ C  
 GAM1633 ARL2 3' AACCTTCACCAAACTACCCA 8021 C \_ CT  
 TGGGTAGTG TTG TG GGTT  
 ||||| || ||  
 ACCCATCAC AAC AC CCAA  
 A C TT  
 GAM1633 BACE 5' AGAAGCCACCAGCACCACCA 23974 A T GCT  
 TGGGT GTGCT GT GGTTTCT  
 |||| |||| || |||||

ACCCA CACGA CA CCGAAGA  
 C C \_\_\_\_  
 GAM1633 BACE 5' AGAAGCCACCAGCACCACCCA 57284 A T GCT  
 TGGGT GTGCT GT GGTTTCT  
 |||| |||| || |||||  
 ACCCA CACGA CA CCGAAGA  
 C C \_\_\_\_  
 GAM1633 FLJ31762 3' AAACCAGCACAAGGAGAC 58135 AGTG  
 GT CTTGTGCTGGTTT  
 || |||||  
 CA GAACACGACCAAA  
 GAG\_  
 GAM1633 KIAA1908 3' AGAAACCAGCACCCCTGCACCC 73391 A CTT  
 A TGGGT GTG GTGCTGGTTTCT  
 |||| || |||||  
 ACCCA CGT CACGACCAAAGA  
 \_ CCC  
 GAM1633 MBD2 3' AAACCATGGAACACTACC 31714 G TGTGC  
 GGGTAGT CT TGGTTT  
 |||| || |||||  
 CCCATCA GG ACCAAA  
 A T\_\_\_\_  
 GAM1633 LOC133688 3' AAACCATGGCGTAAACACCCCC 75110 TA C \_\_\_\_  
 A TGGG GTG TTGTGCT GGTTT  
 ||| || ||||| |||||  
 ACCC CAC AATGCGG CCAA  
 C\_ A TA  
 GAM1633 LOC220763 5' AGAAACCATGATGACATCACCC 73344 A C TG GC  
 A TGGGT GTG T T TGGTTTCT  
 |||| ||| | |||||  
 ACCCA TAC A A ACCAAAGA  
 C \_GT GT  
 GAM1633 LOC90632 5' AGCACAAGCACCCCCA 63645 TA  
 TGGG GTGCTTGTGCT  
 ||| |||||  
 ACCC CACGAACACGA  
 C\_  
 GAM1633 LOC91409 3' AGAGTGTTACAGGCACCACCC 65949 A CTGGT  
 A TGGGT GTGCTTGTG TTCT  
 |||| ||||| |||||  
 ACCCA CACGGACAC GAGA  
 C TTGT\_  
 GAM1634 ADH1B 3' CTTAGACATAAAGTAAAAT 72644 C CAC  
 ATTT ACTTT TGTCTGAG  
 ||| |||| |||||  
 TAAA TGAAA ACAGATTC  
 A T\_\_\_\_  
 GAM1634 AHR 3' ATCTCAGATGTTAAATAAATG 7875 CAC C T  
 CATTT TTT AC GTCTGAGAT  
 |||| ||| || |||||



			GTAAA AAA TG TAGACTCTA		
			TA_ T _		
GAM1634	FDFT1	3'	TAGGAAAGTGAAATG 15518	A	
			CATTTCACTTTC CTG		
			GTAAAGTGAAAG GAT		
			-		
GAM1634	JTB	3'	ATCTCAGACAGTGAAAGTGAAA 21959		
	TG		CATTTCACTTTCAGTGTCTGAGAT		
			GTAAAGTGAAAGTGACAGACTCTA		
GAM1634	KLF4	3'	TCCCAGACAGTGGATATG 14891	CT	A
			CA TTCAGTGTCTG GA		
			GT AGGTGACAGAC CT		
			AT C		
GAM1634	PHYH	3'	ACAGTAAAAGTGAAAT 20608	C	
			ATTTCACTTT ACTGT		
			TAAAGTGAAA TGACA		
			A		
GAM1634	PKD2	3'	TCCAGGTTGAAAGTGAAA 60096	CTG	A
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T_ _		
GAM1634	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1634	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA	CTG
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1634	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT	CT
			TTCAGTTCGA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1634	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G	T_
			CTTTCACT TC GAGAT		
			GAAAGTGA AG TTCTA		
			G TC		
GAM1634	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT 45802	ACTTTCACT	
	G		CATTTC GTCTGAGAT		

		GTAAAG	CAGACTCTA		
		AAACATTT_			
GAM1634	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281	CTT	
			CATTTCA TCACTGTCTGAGAT		
			GTAAAGT AGTGACAGACTCTA		
			C_		
GAM1634	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C	TC
			TTCA TTCACTG TGAG		
			AAGT AAAGTGAC GTTT		
			A CT		
GAM1634	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A	_
			TTTC CTG TCTGAGAT		
			AAAG GAC AGACTCTA		
			_ G		
GAM1634	NIR3	3'	GCAGTGAAAGTGCAAT 66242	T	
			ATT CACTTTCACTGT		
			TAA GTGAAAGTGACG		
			C		
GAM1634	PORIMIN	3'	ATCTCAGAGGGCCAAAGTGAA 53598	CA	G
			TTCACTTT CT TCTGAGAT		
			AAGTGAAA GG AGACTCTA		
			CC G		
GAM1634	PP35	3'	ATCTCAGACTGAAA 22814	CT	
			TTTCA GTCTGAGAT		
			AAAGT CAGACTCTA		
			—		
GAM1634	PRTD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148	TCAC	C_
			CATTTCACTT TGT TGAG		
			GTAAAGTGAA ACG ACTC		
			TA_ TT		
GAM1634	SEP15	3'	TCCTACAGTAAGAGTGAAA 14934	C	CT
			TTTCACTTT ACTGT GA		
			AAAGTGAGA TGACA CT		
			A TC		
GAM1634	SFXN2	3'	CTCAGGGGAAAAAAGTGAAA 73941	CACTG	
			TTTCACTTT TCTGAG		
			AAAGTGAAA GGA CTC		
			AAAGG		
GAM1634	LOC149703	3'	ATCTCAGACAGCCGTTTGAAA 84647	ACTTTCA	
			TTTC CTGTCTGAGAT		

			AAAG	GACAGACTCTA		
			GTTTGCC			
GAM1634	LOC154007	3'	ATCTCAAACCCCTTTAGTGAAA	81015		TTC
			TTTCACT	GT TGAGAT		
			AAAGTGA	CA ACTCTA		
			TTTCC_	A		
GAM1634	LOC155004	3'	TCATTTAAGTGAAAGGAAA	81226	A	GTC_
			TTTC CTTTCACT	TGA		
			AAAG GAAAGTGA	ACT		
			_	ATTT		
GAM1634	LOC222134	5'	ACAGTGAAGTGAAATG	94136		T
			CATTTCACTT	CACTGT		
			GTAAAGTGAA	GTGACA		
			-			
GAM1635	ADH1B	3'	CTTAGACATAAAGTAAAAT	72644	C	CAC
			ATTT ACTTT	TGTCTGAG		
			TAAA TGAAA	ACAGATTC		
			A	T_		
GAM1635	AHR	3'	ATCTCAGATGTTAAATAAATG	7875		CAC C T
			CATTT	TTT AC GTCTGAGAT		
			GTAAA	AAA TG TAGACTCTA		
			TA_	T _		
GAM1635	FDFT1	3'	TAGGAAAGTGAAATG	15518		A
			CATTTCACTTTC	CTG		
			GTAAAGTGAAAG	GAT		
			-			
GAM1635	JTB	3'	ATCTCAGACAGTGAAAGTGAAA	21959		
	TG		CATTTCACTTTCACTGTCTGAGAT			
			GTAAAGTGAAAGTGACAGACTCTA			
			-			
GAM1635	KLF4	3'	TCCCAGACAGTGGATATG	14891	CT	A
			CA	TTCAGTGTCTG GA		
			GT	AGGTGACAGAC CT		
			AT	C		
GAM1635	PHYH	3'	ACAGTAAAAGTGAAAT	20608		C
			ATTTCACTTT	ACTGT		
			TAAAGTGAAA	TGACA		
			A			
GAM1635	PKD2	3'	TCCAGGTTGAAAGTGAAA	60096		CTG A
			TTTCACTTTCA	TCTG GA		

AAAGTGAAAGT GGAC CT  
 T\_\_ \_  
 GAM1635 WRN 3' GGGCAGTGAAAATGAAA 5098 C  
 TTTCA TTTCACTGTCT  
 ||||| |||||  
 AAAGT AAAGTGACGGG  
 A  
 GAM1635 ZNF216 3' ATCTGCACAGCAAAGTGAAA 20017 CA CTG  
 TTTCACTTT CTGT AGAT  
 ||||| ||| |||  
 AAAGTGAAA GACA TCTA  
 C\_ CG\_  
 GAM1635 CG012 5' CTCACCTCTGAAAGTGAA 83218 CT CT  
 TTCACCTTTCA GT GAG  
 ||||| || |||  
 AAGTGAAAGT CA CTC  
 CT \_  
 GAM1635 EIF2C2 3' ATCTTCTGAGAGTGAAAG 71946 G T\_  
 CTTTCACT TC GAGAT  
 ||||| || |||  
 GAAAGTGA AG TTCTA  
 G TC  
 GAM1635 FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802 ACTTTCACT  
 G CATTTC GTCTGAGAT  
 ||||| |||||  
 GTAAAG CAGACTCTA  
 AAACATTT\_  
 GAM1635 FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281 CTT  
 CATTTC TCACTGTCTGAGAT  
 ||||| |||||  
 GTAAAGT AGTGACAGACTCTA  
 C\_  
 GAM1635 KIAA0984 3' TTTGTCCAGTGAAAATGAA 65534 C TC  
 TTCA TTTCACTG TGAG  
 ||| ||||| |||  
 AAGT AAAGTGAC GTTT  
 A CT  
 GAM1635 KLHL6 3' ATCTCAGAGCAGGAAA 55299 A \_  
 TTTC CTG TCTGAGAT  
 ||| ||| |||||  
 AAAG GAC AGACTCTA  
 \_ G  
 GAM1635 NIR3 3' GCAGTGAAAGTGCAAT 66242 T  
 ATT CACTTTCACTGT  
 ||| |||||  
 TAA GTGAAAGTGACG  
 C  
 GAM1635 PORIMIN 3' ATCTCAGAGGGCCAAAGTGAA 53598 CA G  
 TTCACCTTT CT TCTGAGAT  
 ||||| || |||||

			AAGTGAAA GG AGACTCTA		
			CC G		
GAM1635	PP35	3'	ATCTCAGACTGAAA 22814	CT	
			TTTCA GTCTGAGAT		
			AAAGT CAGACTCTA		
—					
GAM1635	PRTD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148	TCAC C_	
			CATTTCACTT TGT TGAG		
			GTAAAGTGAA ACG ACTC		
			TA__ TT		
GAM1635	SEP15	3'	TCCTACAGTAAGAGTGAAA 14934	C CT	
			TTTCACTTT ACTGT GA		
			AAAGTGAGA TGACA CT		
			A TC		
GAM1635	SFXN2	3'	CTCAGGGGAAAAAAGTGAAA 73941	CACTG	
			TTTCACTTT TCTGAG		
			AAAGTGAAA GGA CTC		
			AAAGG		
GAM1635	LOC149703	3'	ATCTCAGACAGCCGTTTGAAAA 84647	ACTTTCA	
			TTTC CTGTCTGAGAT		
			AAAG GACAGACTCTA		
			GTTTGCC		
GAM1635	LOC154007	3'	ATCTCAAACCCTTTAGTGAAA 81015	TTCAC T C	
			TTTCACT GT TGAGAT		
			AAAGTGA CA ACTCTA		
			TTTCC_ A		
GAM1635	LOC155004	3'	TCATTTAAGTGAAAAGGAAA 81226	A GTC_	
			TTTC CTTTCACT TGA		
			AAAG GAAAGTGA ACT		
			_ ATTT		
GAM1635	LOC222134	5'	ACAGTGAAGTGAAATG 94136	T	
			CATTTCACTT CACTGT		
			GTAAAGTGAA GTGACA		
—					
GAM1636	DYRK1A	3'	CAGAATGGAGCTATGGAC 55199	_ C	
			GTCTG AGTTCCAT CTG		
			CAGGT TCGAGGTA GAC		
			A A		
GAM1636	GOSR1	3'	GCAGGATGAATGCAAGACTG 16829	GA_ C	
			CAGTCT GTTC ATCCTGC		

GTCAGA TAAG TAGGACG  
 ACG \_  
 GAM1636 GYPA 3' CAGAATACGACAGACTGGGT 87450 A\_ TCCATC  
 ATCCAGTCTG GT CTG  
 ||||| || |||  
 TGGGTCAGAC CA GAC  
 AG TAA\_\_  
 GAM1636 HIVEP2 3' AGGATGGTGA CTGGA 22117 TGAGTT  
 TCCAGTC CCATCCT  
 ||||| |||||  
 AGGTCAG GGTAGGA  
 T\_\_\_\_  
 GAM1636 ITGA5 3' TGGAACCCAGACTCAGA 61284 C\_ A  
 TC AGTCTG GTTCCA  
 || ||||| |||||  
 AG TCAGAC CAAGGT  
 AC C  
 GAM1636 NEO1 3' CAGAATGAGCCAGCAGACTGG 10201 A\_\_ C C  
 CCAGTCTG GTTC AT CTG  
 ||||| ||| |||  
 GGTCAGAC CGAG TA GAC  
 GAC \_ A  
 GAM1636 NR1I2 5' CAGAGACCCTCAGACTGATG 13964 C TTCCA \_  
 CATC AGTCTGAG TC CTG  
 ||| ||||| |||  
 GTAG TCAGACTC AG GAC  
 \_ CC\_\_ A  
 GAM1636 PPP1R2 3' CAGGATATATAGACTG 20686 A TCC  
 CAGTCTG GT ATCCTG  
 ||||| || |||||  
 GTCAGAT TA TAGGAC  
 A \_\_\_\_  
 GAM1636 XT3 3' ATGGAAC TCAAACAGATG 39521 CA C  
 CATC GT TGAGTTCCAT  
 ||| || |||||  
 GTAG CA ACTCAAGGTA  
 A\_ A  
 GAM1636 CECR7 3' GCAGGATGGGGGAACTGGA 79623 CTGAG  
 TCCAGT TTCCATCCTGC  
 ||||| |||||  
 AGGTCA GGGGTAGGACG  
 AAG\_\_  
 GAM1636 CUL4A 3' GCAAATAACTTTGAGATTGGA 13154 \_ CC CC  
 TCCAGTCT GAGTT AT TGC  
 ||||| ||| |||  
 AGGTTAGA TTCAA TA ACG  
 GT \_ AA  
 GAM1636 DKFZp762P2111 3' GAGCTCAGACAGGATG 86356 A  
 CATCC GTCTGAGTTC  
 ||||| |||||

			GTAGG CAGACTCGAG		
			A		
GAM1636	FLJ20232	5'	GAACCCAACTGGATG 38670	C	A
			CATCCAGT TG GTTC		
			GTAGGTCA AC CAAG		
			_ C		
GAM1636	FLJ20413	3'	CAGAATAGAAAACCTCAGAC 35130	__	C C
			GTCTGAGT TC AT CTG		
			CAGACTCA AG TA GAC		
			AA A A		
GAM1636	FLJ22301	3'	GCAGGATGGAAAATCCCCTGGA 45758		TCTGAG
			TCCAG TTCCATCCTGC		
			AGGTC AAGGTAGGACG		
			CCCTAA		
GAM1636	FLJ22795	3'	GCAGCATGACTCAGACTGCATG 46943	C	TC C
			CAT CAGTCTGAGT CAT CTGC		
			GTA GTCAGACTCA GTA GACG		
			C _ C		
GAM1636	HS6ST	3'	GCAGGCCTGGCTCAGACTGGA 62028		CCAT
			TCCAGTCTGAGTT CCTGC		
			AGGTCAGACTCGG GGACG		
			TCC_		
GAM1636	KIAA0014	3'	GCAGGACTTGCGAGACTGG 27845		AGTTCCA
			CCAGTCTG TCCTGC		
			GGTCAGAC AGGACG		
			GTTC__		
GAM1636	KIAA0286	3'	CAAGATGGGCTCAGATGGATG 68320	G	T C
			CATCCA TCTGAGT CCATC TG		
			GTAGGT AGACTCG GGTAG AC		
			_ _ A		
GAM1636	KIAA0453	3'	CAGGATGGAAACCCCAGGATG 69045		AGTCTGAG
			CATCC TTCCATCCTG		
			GTAGG AAGGTAGGAC		
			ACCCCA_		
GAM1636	KIAA0998	3'	AGGGCAAAACTCAGACTGAATG 30584	C	CCA
			CAT CAGTCTGAGTT TCCT		
			GTA GTCAGACTCAA GGGA		
			A AAC		
GAM1636	KIAA1054	3'	GAGCTCAGACTAAGTG 68437	CC	
			CAT AGTCTGAGTTC		

GTG TCAGACTCGAG  
 AA  
 GAM1636 KIAA1715 3' GAATACCACAGACTGGGT 68120 A\_\_\_  
 ATCCAGTCTG GTTC  
 ||||| |||  
 TGGGTCAGAC TAAG  
 ACCA  
 GAM1636 MIG 3' CAGGATGGCAACCAGAC 10037 A \_  
 GTCTG GTT CCATCCTG  
 |||| || |||||  
 CAGAC CAA GGTAGGAC  
 \_ C  
 GAM1636 P24B 3' GCAGGACAGAATGGTGA CTGGG 23750 TGA CA  
 TG CATCCAGTC GTTC TCCTGC  
 ||||| ||| |||||  
 GTGGGTCAG TAAG AGGACG  
 TGG AC  
 GAM1636 RAN 3' CAGGATGGAACATCAG 20905 \_  
 CTGA GTTCCATCCTG  
 ||| |||||  
 GACT CAAGGTAGGAC  
 A  
 GAM1636 RNAHP 3' GATGGAACCCAAAGTGGA 23763 GTC A  
 TCCA TG GTTCCATC  
 ||| || |||||  
 AGGT AC CAAGGTAG  
 GAA C  
 GAM1636 S164 5' GCAAGATGAACTCTCAGCTTG 60780 T TTC\_\_ C  
 GA TCCAG CTGAG CATC TGC  
 |||| ||| ||| |||  
 AGGTT GACTC GTAG ACG  
 C TCAAA A  
 GAM1636 SMOC1 3' GCAGGATGGATCACCAGAC 42150 A \_  
 GTCTG GT TCCATCCTGC  
 |||| || |||||  
 CAGAC CA AGGTAGGACG  
 \_ CT  
 GAM1636 ZNF31 5' GCAGGACAGTCGGGACTGGA 64983 \_ GTTCCA  
 TCCAGTCT GA TCCTGC  
 ||||| || |||||  
 AGGTCAGG CT AGGACG  
 G GAC\_\_  
 GAM1636 ZNF317 3' CAGGATGATTGAGACCGGA 72013 A TC  
 TCC GTCTGAGT CATCCTG  
 || ||||| |||||  
 AGG CAGACTTA GTAGGAC  
 C \_  
 GAM1636 ZNF387 5' GCAGGATGTTTTTAACTGAATG 27996 C C TTC  
 CAT CAGT TGAG CATCCTGC  
 || ||| ||| |||||



		GTA GTCA ATTT GTAGGACG		
		A _ TT_		
GAM1636	LOC115051 3'	GCAGGCCTGGCTCAGACTGGA 60039	CCAT	
		TCCAGTCTGAGTT CCTGC		
		AGGTCAGACTCGG GGACG		
		TCC_		
GAM1636	LOC120856 3'	CAAGATGAAACTCAGAAGAGAT 74027	CAG C C	
		ATC TCTGAGTT CATC TG		
		TAG AGACTCAA GTAG AC		
		AGA A A		
GAM1636	LOC146957 5'	GGAACCCAGGCTGGATG 78206	A	
		CATCCAGTCTG GTTCC		
		GTAGGTCTGGAC CAAGG		
		C		
GAM1636	LOC147178 3'	CAAGATGGAACCCCGGA 61322	A_ C	
		TCTG GTTCCATC TG		
		AGGC CAAGGTAG AC		
		CC A		
GAM1636	LOC148887 3'	GCAGGCTGACCCAGCTGGATG 84238	T A TC T	
		CATCCAG CTG GT CA CCTGC		
		GTAGGTC GAC CA GT GGACG		
		_ C _ C		
GAM1636	LOC150170 5'	GCAAAATGGAACCTTTAAAAC 79591	CT__ CC	
		GT GAGTTCCAT TGC		
		CA TTCAAGGTA ACG		
		AAAT AA		
GAM1636	LOC150175 5'	GCAAAATGGAACCTTTAAAAC 79632	CT__ CC	
		GT GAGTTCCAT TGC		
		CA TTCAAGGTA ACG		
		AAAT AA		
GAM1636	LOC150215 5'	GCAAAATGGAACCTTTAAAAC 79640	CT__ CC	
		GT GAGTTCCAT TGC		
		CA TTCAAGGTA ACG		
		AAAT AA		
GAM1636	LOC150218 5'	GCAAAATGGAACCTTTAAAAC 79721	CT__ CC	
		GT GAGTTCCAT TGC		
		CA TTCAAGGTA ACG		
		AAAT AA		
GAM1636	LOC220537 3'	GCAGCATGACTCAGACTGCATG 90729	C TC C	
		CAT CAGTCTGAGT CAT CTGC		

GTA GTCAGACTCA GTA GACG  
 C \_ C  
 GAM1636 LOC245727 5' GCAGCATGACTCAGACTGCATG 91126 C TC C  
 CAT CAGTCTGAGT CAT CTGC  
 ||| ||||| ||| ||||  
 GTA GTCAGACTCA GTA GACG  
 C \_ C  
 GAM1636 LOC254431 5' CAAGATGGAACCTTGAGATT 96849 \_ C  
 AGTCT GAGTTCCATC TG  
 ||||| ||||| ||  
 TTAGA TTCAAGGTAG AC  
 G A  
 GAM1637 ABCB11 3' CATATGAGGGAAAACC 13616 TG  
 GGTTTTCCCTT GTG  
 ||||| |||  
 CCAAAGGGAG TAC  
 TA  
 GAM1637 ABR 3' TTTGGTGAGCTGAGGAAACACC 6580 \_ TGGT  
 AC GTGGT TTTCC CTT GA  
 ||||| ||| ||  
 CACCA AAAGG GAG TT  
 C AGTC||| TGGT  
 GAM1637 ABR 3' TTTGGTGAGCTGAGGAAACACC 41732 \_ TGGT  
 AC GTGGT TTTCC CTT GA  
 ||||| ||| ||  
 CACCA AAAGG GAG TT  
 C AGTC||| TGGT  
 GAM1637 ACAA1 3' CACAAAAGCAAAACCAC 7836 CC G  
 GTGGTTTT CTTT GTG  
 ||||| |||||  
 CACCAAAA GAAA CAC  
 C\_ A  
 GAM1637 ADRA1B 5' CTCTGGGAAGAAGACCACG 5447 \_ TT  
 CGTGGTTTTT CCT GG  
 ||||| ||| ||  
 GCACCAGAAG GGG TC  
 AA TC  
 GAM1637 ADRB1 3' CAAAGAGAAAAGCCACG 5467 \_C  
 CGTGGTTTTT C CTTT  
 ||||| |||||  
 GCACCGAAA G GAAAC  
 A A  
 GAM1637 APLP2 3' TCAGAGAAGACCAC 90901 CC  
 GTGGTTTTT TTTGG  
 ||||| |||||  
 CACCAGAAG AGACT  
 \_  
 GAM1637 AVPR1A 5' CCATAGAGAAAACCAGG 5537 G C T  
 C TGGTTTTT CT TGG  
 | ||||| || |||

			G ACCAAAAG GA ACC		
			G    A T		
GAM1637	CACNA1C	3'	CTCACCAAAAGGACCCTAC	5562	TTT C
			GTGG TCC TTTGGTGAG		
			CATC AGG AAACCACTC		
			CC_ A		
GAM1637	CACNA1E	3'	CTCACATGGAGAAAACCA	5566	_ TTTG
			TGGTTTTTC CC GTGAG		
			ACCAAAAG GG CACTC		
			A TA__		
GAM1637	COL19A1	3'	CTCAACAAAGGAAAACCA	8509	C G
			GTGGTTTTTC TTTG TGAG		
			CACCAAAAGG AAAC ACTC		
			_ A		
GAM1637	DNASE1	5'	CACCTATGCGAAAGCCAC	17823	CTTT_
			GTGGTTTTTC GGTG		
			CACCGAAAGG CCAC		
			CGTAT		
GAM1637	EPB41	3'	CATCCAAGAGAAACCACG	15429	CC T
			CGTGGTTTT CTT GGTG		
			GCACCAAAG GAA CTAC		
			A_ C		
GAM1637	EZH1	3'	CTCATAGAGGAGAAAACCA	8820	_ G
			TGGTTTTTC CCTTTG TGAG		
			ACCAAAAG GGAGAT ACTC		
			A _		
GAM1637	FGFR2	3'	TCACCAAAAGATCCA	43373	T CCC
			TGG TTT TTTGGTGA		
			ACC AGA AAACCACT		
			T _		
GAM1637	FGFR2	3'	TCACCAAAAGATCCA	43504	T CCC
			TGG TTT TTTGGTGA		
			ACC AGA AAACCACT		
			T _		
GAM1637	FGFR2	3'	TCACCAAAAGATCCA	43494	T CCC
			TGG TTT TTTGGTGA		
			ACC AGA AAACCACT		
			T _		
GAM1637	FGFR2	3'	TCACCAAAAGATCCA	43361	T CCC
			TGG TTT TTTGGTGA		

			ACC AGA AAACCACT		
			T ____		
GAM1637	FGFR2	3'	TCACCAAAAGATCCA	3765	T CCC
			TGG TTT TTTGGTGA		
			ACC AGA AAACCACT		
			T ____		
GAM1637	FGFR2	3'	TCACCAAAAGATCCA	43484	T CCC
			TGG TTT TTTGGTGA		
			ACC AGA AAACCACT		
			T ____		
GAM1637	GCK	5'	CCGAGGAGAACCAC	3867	CT
			GTGGTTTTCC TTGG		
			CACCAAGAGG AGCC		
			____		
GAM1637	GRLF1	3'	CACAGAAAGAAACTAC	78552	CC G
			GTGGTTTTTC TTT GTG		
			CATCAAAG AAG CAC		
			A_ A		
GAM1637	GSK3B	3'	CACAGGAAAAACCAC	9140	C TTG
			GTGGTTTT CCT GTG		
			CACCAAAA GGA CAC		
			A ____		
GAM1637	HMGNI	3'	CTAAAGAAAACCAC	17117	CC
			GTGGTTTTTC TTTGG		
			CACCAAAAG AAATC		
			____		
GAM1637	HMX1	3'	CAAAGGAAAACACTACG	38444	C
			CGTGGTTTTCC TTTG		
			GCATCAAAGG AAAC		
			____		
GAM1637	HS3ST4	3'	CTCACTGAAAAAGAAAACAC	73471	G CC_ TG
			GTG TTTTC TT GTGAG		
			CAC AAAAG AA CACTC		
			_ AAA GT		
GAM1637	IGBP1	3'	TGCCAAGGAAAACCATG	7757	CT
			CGTGGTTTTCC TTGGTG		
			GTACCAAAAGG AACCGT		
			____		
GAM1637	JPH3	3'	TCACAGAAGAACCAC	40309	TTCC G
			GTGGTT CTTT GTGA		

			CACCAA GAAG CACT		
			_____ A		
GAM1637	KCNA7	3'	CTCAGGGAAAGAGAACCAC 49051	CC	GG
			GTGGTTTTTC TTT TGAG		
			CACCAAGAG AAG ACTC		
			A_ GG		
GAM1637	LIPE	5'	CACCAAAGAAAGAGGCAC 18087	G	CC
			GTG TTTT CTTTGGTG		
			CAC GAGA GAAACCAC		
			G AA		
GAM1637	MAPK4	5'	CTCACTAGGAGAAAACAC 10828	G	_ TT
			GTG TTTTC CCT GGTGAG		
			CAC AAAAG GGA TCACTC		
			_ A _		
GAM1637	MEIS2	3'	CCAATGAGAAAAGAACCAC 39319	CC_	_
			GTGGTTTT CTT TGG		
			CACCAAGA GAG ACC		
			AAA TA		
GAM1637	NEBL	3'	CTCTTGAAAGAAAACCA 21122	CC	TG T
			TGGTTTTTC TT G GAG		
			ACCAAAAG AG T CTC		
			AA GT_		
GAM1637	OGN	5'	TATTGAGGAAAACCAC 44327	CT	TG
			GTGGTTTTTCC T GTG		
			CACCAAAAGG A TAT		
			_ GT		
GAM1637	OGN	5'	TATTGAGGAAAACCAC 52245	CT	TG
			GTGGTTTTTCC T GTG		
			CACCAAAAGG A TAT		
			_ GT		
GAM1637	OGN	5'	TATTGAGGAAAACCAC 25921	CT	TG
			GTGGTTTTTCC T GTG		
			CACCAAAAGG A TAT		
			_ GT		
GAM1637	OLFM1	3'	CTCACCGGGGAAAAACC 26554	_	TT
			GGTTTT CCCT GGTGAG		
			CCAAAA GGGG CCACTC		
			A _		
GAM1637	P2RY6	3'	CACCAACCCCAAACCATG 14739	TCCCT	
			CGTGGTTT TTGGTG		

		GTACCAAA AACCAC	
		CCCC_	
GAM1637	PCDHA9	5' CTCAGGGATAAGAAAACCAC 49013	CCT GG
		GTGGTTTTTC TT TGAG	
		CACCAAAAG AG ACTC	
		AAT GG	
GAM1637	PCDHA9	5' CTCAGGGATAAGAAAACCAC 25761	CCT GG
		GTGGTTTTTC TT TGAG	
		CACCAAAAG AG ACTC	
		AAT GG	
GAM1637	PIK3C2B	5' CATTTTGAGGAAAAACTAC 10561	C T_
		GTGGTTTT CCTT GGTG	
		CATCAAAA GGAG TTAC	
		A TT	
GAM1637	PMP22	3' CTCATTTAGAAAACCA 4325	CCTTT
		TGGTTTTTC GGTGAG	
		ACCAAAAG TTA CTCT	
		AT__	
GAM1637	PPARBP	3' TATTAAAGAAACCAC 16492	TCC
		GTGGTTT CTTTGGTG	
		CACCAAA GAAATTAT	
		_____	
GAM1637	PPP2R5C	3' CTCACCAAAAAGAAAA 10758	CC
		TTTTT TTTGGTGAG	
		AAAAG AAACCACTC	
		AA	
GAM1637	PRDX3	3' CTCACTGAGAGAAGAACCAC 73351	_C TGG
		GTGGTTTT C CTT TGAG	
		CACCAAGA G GAG ACTC	
		A A TCA	
GAM1637	RFNG	5' TGGTGAGCCCGGAAGAACCACG 88179	_ _ _ _ _ TGGT
		CGTGGTTTT CC CTT G	
		GCACCAAGA GG GAG T	
		A CCCIII TGGT	
GAM1637	SLC13A4	3' CCACAGGCAAAGAAAACCAC 24920	_____ T
		GTGGTTTTTC CCT TGG	
		CACCAAAAG GGA ACC	
		AAAC C	
GAM1637	SLC1A4	3' CCAGAGAAAACCATG 11713	CC
		CGTGGTTTTT TTTGG	

GTACCAAAAG AGACC

GAM1637 SLC25A12 3' CCAGGGAAAAAACAC 13523 CC

GTGGTTTT CTTTGG

||||||| |||||

CACCAAAA GGGACC

AA

GAM1637 TEM7 3' TTCACAAAGGATAAACACG 39898 TC G

CGTGGTTT CTTTG TGAG

||||||| ||||| |||

GCACCAAA GGAAAC ACTT

TA

GAM1637 TITF1 3' CCAAGGAACAAAAAACAC 12422 CC\_\_\_\_

GTGGTTTT CTTTGG

||||||| |||||

CACCAAAA GGAACC

AAACAA

GAM1637 TNFSF8 3' CCAGGGAAAACCAGG 6964 G TT

C TGGTTTTCCCT GG

| ||||| ||

G ACCAAAAGGGA CC

G

GAM1637 TPX1 5' TTTGGTGAGCTCTAGGAAAACC 12380 \_\_\_\_\_ TGGT

ATG

GTGGTTTTCC CTT GA

||||||| ||| ||

TACCAAAAGG GAG TT

ATCTC||| TGGT

GAM1637 UBE2V1 3' CAAAAAGAAAAACCAC 12513 CC GG

GTGGTTTT CTTT TG

||||||| ||| ||

CACCAAAA GAAA AC

A\_ A\_

GAM1637 UBE2V1 3' CAAAAAGAAAAACCAC 41788 CC GG

GTGGTTTT CTTT TG

||||||| ||| ||

CACCAAAA GAAA AC

A\_ A\_

GAM1637 UBE2V1 3' CAAAAAGAAAAACCAC 42366 CC GG

GTGGTTTT CTTT TG

||||||| ||| ||

CACCAAAA GAAA AC

A\_ A\_

GAM1637 UC28 3' TTAAAGGAAAATCAC 41293 C

GTGGTTTTCC TTTGG

||||||| |||||

CACTAAAAGG AAATT

GAM1637 ZNF136 3' CTCATCATGGAGAAAACCA 59887 \_ TT

TGGTTTTCC CC TGGTGAG

||||||| || |||||

		ACCAAAAG GG ACTACTC	
		A T_	
GAM1637	ZNF265	3' CTCACCAAAAAAGTTAACTA 18396	TCCC__
		TGGTTT TTTGGTGAG	
		ATCAAA AAACCACTC	
		TTGAAAA	
GAM1637	AF9Q34	3' CTCTGCTGGAGAAAGCCACG 50735	CC TG _
		CGTGGTTTTT TT GT GAG	
		GCACCGAAAG AG CG CTC	
		_ GT T	
GAM1637	AGTRL2	5' CACAGGAGGGAAGACCAC 17690	TG
		GTGGTTTTTCCCTT GTG	
		CACCAGAAGGGAG CAC	
		GA	
GAM1637	API5	3' CCAAGGTAAAACCAC 21687	C T
		GTGGTTTTT CCTT GG	
		CACCAAAA GGAA CC	
		T _	
GAM1637	ATP10B	3' CCAAAGAAAAGCCAC 63367	CC
		GTGGTTTTT CTTTGG	
		CACCGAAA GAAACC	
		A_	
GAM1637	C20orf122	3' CACCAAAGAAAACC 55116	CC
		GGTTTTT TTTGGTG	
		CCAAAAG AAACCAC	
		_	
GAM1637	C5orf4	3' CTTATCAAAGGCAAAAACCAC 50493	C
		GTGGTTTTT CCTTTGGTGAG	
		CACCAAAA GGAACTATTC	
		C	
GAM1637	C5orf4	3' CTTATCAAAGGCAAAAACCAC 32982	C
		GTGGTTTTT CCTTTGGTGAG	
		CACCAAAA GGAACTATTC	
		C	
GAM1637	CASPR3	3' CCAATAAGGAGAACCAC 45934	CT_
		GTGGTTTTTCC TTGG	
		CACCAAGAGG AACC	
		AAT	
GAM1637	CDH26	3' CCAAAGCAAAAACCAC 41464	CC
		GTGGTTTTT CTTTGG	



			CACCAAAA GAAACC		
			C_		
GAM1637	CENTG2	3'	TCAAAAGGAAACCAC	29881	T C
			GTGGTTT CC TTTGG		
			CACCAAA GG AAAC		
			_ A		
GAM1637	CGI-142	3'	CATATTAAGAGAAACCAC	32176	CC TG_
			GTGGTTTT CTT GTG		
			CACCAAAG GAA TAC		
			A_ TTA		
GAM1637	CMG2	3'	CCAAGAAGAAAAACCAC	54161	_ CC
			GTGGTTTT C TTTGG		
			CACCAAAA G GAACC		
			A AA		
GAM1637	DIO2	3'	TATTAAGGAAAACCA	5834	C
			TGGTTTTCC TTTGGT		
			ACCAAAGG AAATTAT		
			-		
GAM1637	DIO2	3'	TATTAAGGAAAACCA	25686	C
			TGGTTTTCC TTTGGT		
			ACCAAAGG AAATTAT		
			-		
GAM1637	ESM1	5'	CACCAGCAAAGACCACG	22876	CCCT
			CGTGGTTTT TTGGT		
			GCACCAGAA GACCAC		
			AC_		
GAM1637	FEM-2	3'	CTACCAAAGAGAAGAT	27576	C
			GTTTTC CTTTGGTGAG		
			TAGAAG GAAACCACTC		
			A		
GAM1637	FLJ10852	3'	CCAAAGGAAAACACG	38735	G C
			CGTG TTTTCC TTTGG		
			GCAC AAAAGG AAACC		
			- -		
GAM1637	FLJ11078	3'	CCGGAGGAAAAACCAT	37029	C
			GTGGTTTT CCTTTGG		
			TACCAAAA GGAGGCC		
			A		
GAM1637	FLJ12903	3'	CTCACCACGCGAAACTACG	42771	CCCTT
			CGTGGTTTT TGGTGAG		

			GCATCAAAG ACCACTC		
			CGC__		
GAM1637	FLJ14708	3'	CCACAGCGAAAAGCCAC 51540	_ C T	
			GTGGTTTT C CT TGG		
			I		
			CACCGAAA G GA ACC		
			A C C		
GAM1637	FLJ20294	3'	CCTAGGGGAGAACCACG 34873	T	
			CGTGGTTTTCCCTT GG		
			GCACCAAGAGGGGA CC		
			T		
GAM1637	FLJ20296	3'	CAGAAAAGGGAAAGCCACG 34888	GG	
			CGTGGTTTTCCCTT TG		
			GCACCGAAAGGGAAA AC		
			AG		
GAM1637	FLJ20689	3'	CAGCAGAGAAAGCCAC 35537	CC G	
			GTGGTTTTC TTTG TG		
			CACCGAAAG AGAC AC		
			_ G		
GAM1637	FLJ21087	3'	CTAAAGAAAGCCAC 91836	CC	
			GTGGTTTTC TTTGG		
			CACCGAAAG AAATC		
			_		
GAM1637	GPR105	3'	CTCTTCCAAAGAAAGACCACG 29654	CC T_	
			CGTGGTTTT CTTTGG GAG		
			GCACCAGAA GAAACC CTC		
			A_ TT		
GAM1637	HEAB	3'	CCAAAAGGAAAACCATG 22412	C	
			CGTGGTTTTCC TTTGG		
			GTACCAAAAGG AAACC		
			A		
GAM1637	HEF1	3'	CATTAAAAAAAAAACCATG 21135	CCC	
			CGTGGTTTT TTTGGTG		
			GTACCAAAA AAATTAC		
			AAA		
GAM1637	JWA	3'	CCGAAAGAAAACCAC 21139	CC	
			GTGGTTTTC TTTGG		
			CACCAAAAG AAGCC		
			A_		
GAM1637	KIAA0189	5'	CTCTGTGAAGAAAAACCACG 28274	CC GT	
			CGTGGTTTT CTTTG GAG		

		GCACCAAAA GAAGT CTC	
		A_ GT	
GAM1637 KIAA0350	3'	CCATAGAGAAAACGCAC 61171	_ C T
		GTG GTTTTC CT TGG	
		CAC CAAAAG GA ACC	
		G A T	
GAM1637 KIAA0350	3'	CCAAAGGAAGGACAAACCACG 61169	- ____
		CGTGGTTT TCC CTTTGG	
		GCACCAAA AGG GAAACC	
		C AAG	
GAM1637 KIAA0354	3'	CCAAAGGGAAACCCACG 29568	T
		CGTGG TTTCCCTTTGG	
		GCACC AAAGGGAAACC	
		C	
GAM1637 KIAA0431	3'	CCAAGGAAAACCTAC 30889	CT
		GTGGTTTTCC TTGG	
		CATCAAAAGG AACC	
		—	
GAM1637 KIAA0798	3'	CAGAGAGAAAACCACG 27719	C
		CGTGGTTTTTC CTTTG	
		GCACCAAAAG GAGAC	
		A	
GAM1637 KIAA0828	3'	CATTAAGAAGAAAGAACCAC 81192	CC ____
		GTGGTTTT CTTT GGTG	
		CACCAAGA GAAG TTAC	
		AA AA	
GAM1637 KIAA0830	3'	CAGAGGAAGAAAAACCACG 69695	C____
		CGTGGTTTT CTTTG	
		GCACCAAAA GGAGAC	
		AGAA	
GAM1637 KIAA0889	3'	CTCACCAAAAAAAAAAAATTAT 31136	CCC__
		GTGGTTTT TTTGGTGAG	
		TATTAATA AAACCACTC	
		AAAAA	
GAM1637 KIAA1054	3'	TCAAAGAAAACCATG 68447	CC
		CGTGGTTTTTC TTTGG	
		GTACCAAAAG AAAC	
		—	
GAM1637 KIAA1199	3'	CCAAGATGGGAAAGAACCAC 72513	__ __
		GTGGTTT TCCC TTTGG	

		CACCAAG AGGG GAACC	
		AA TA	
GAM1637 KIAA1203	3'	CTCACCAAAAAAACC 71637	CCC
		GGTTTT TTTGGTGAG	
		CCAAAA AAACCACTC	
		A__	
GAM1637 KIAA1336	3'	CCAAATCAGAAAATCAC 72323	CC_
		GTGGTTTTTC TTTGG	
		CACTAAAAG AAACC	
		ACT	
GAM1637 KIAA1391	3'	CTCAATATGGAGGAAAAGACCA 67261	__ _ TTGG
	C	GTGGTT TTCC CT TGAG	
		CACCAG AAGG GG ACTC	
		AA A TATA	
GAM1637 KIAA1546	3'	CTCACTTGAAAAGACCAC 67905	CCCTTT
		GTGGTTTTT GGTGAG	
		CACCAGAA TCACTC	
		AAGT__	
GAM1637 KIAA1579	3'	CTTAGAAAAGAAAACCAC 36609	CC GG
		GTGGTTTTTC TTT TGAG	
		CACCAAAAG AAA ATTC	
		__ AG	
GAM1637 KIAA1634	3'	CTCTTTGAAGAAAAACCAC 63387	CC TG T
		GTGGTTTTT CTT G GAG	
		CACCAAAA GAA T CTC	
		A_ GT T	
GAM1637 MBLR	3'	CTCACCAAGATTTCCATG 49627	TTTTCC
		CGTGG CTTTGGTGAG	
		GTACC GAAACCACTC	
		TTTA__	
GAM1637 MGC2404	3'	CATTATGAAAGAAAACCTAC 50392	CCTT_
		GTGGTTTTTC TGGTG	
		CATCAAAAG ATTAC	
		AAAGT	
GAM1637 MGC3146	3'	TCAAGGAAAACCCG 48441	T CT
		CG GGTTTTCC TTGG	
		GC CCAAAAGG AACT	
		__ __	
GAM1637 NKX2C	3'	CTCTTCGAGGAAAACCA 59219	CT T
		TGGTTTTTCC TTGG GAG	

		ACCAAAAGG AGCT CTC	
		— T	
GAM1637 NPD009	3'	CTCATGGTAGAAAACCAT 95047	— TTTG
		GTGGTTTTTC CC GTGAG	
		TACCAAAAG GG TACTC	
		AT —	
GAM1637 OBTP	5'	TCAAGGAAGACCAC 34250	CT
		GTGGTTTTTC TTGG	
		CACCAGAAGG AACT	
		—	
GAM1637 PELI1	5'	CTCACCAAAAGTGCCAC 40265	TTTCCC
		GTGGT TTTGGTGAG	
		CACCG AAACCACTC	
		TGA—	
GAM1637 PIK3C3	3'	TCAATAAGAAAACCACG 59860	CCT
		CGTGGTTTTTC TTGG	
		GCACCAAAAG AACT	
		AAT	
GAM1637 RERG	3'	CTTAGCAGAAAACCAC 51897	CCC G
		GTGGTTTT TTTG TGAG	
		CACCAAAA AGAC ATTC	
		— G	
GAM1637 SLC5A7	3'	CATTAAAGAAAACCAC 41506	CC
		GTGGTTTT CTTTGGTG	
		CACCAAAA GAAATTAC	
		A_	
GAM1637 SUCLG2	3'	CACTAAAAAGAAAACCA 65608	CC
		TGGTTTTTC TTTGGTG	
		ACCAAAAG AAATCAC	
		AA	
GAM1637 SYNJ2	3'	CTCACCAAAAAGGAGAT 61766	CC
		GTTTTTC TTTGGTGAG	
		TAGAGG AAACCACTC	
		AA	
GAM1637 ZFP100	3'	CTCACCAAGTGTAAGCCAC 70053	TCCC
		GTGGTTT TTTGGTGAG	
		CACCGAA GAACCACTC	
		TGT_	
GAM1637 ZIM3	5'	CTTTCAGAAGAAAAGACCAC 53537	CC GGT
		GTGGTTTT CTTT GAG	

	CACCAGAA GAAG TTC	
	AA ACT	
GAM1637 ZNF304	3' CTCACCAAAAGGACCTGAGCT 40314	___ C
	GGTTT TCC TTTGGTGAG	
	TCGAG AGG AAACCACTC	
	TCC A	
GAM1637 ZNF33A	3' CAAGAAAGGAAAACTAC 91345	C GG
	GTGGTTTTCC TTT TG	
	CATCAAAAGG AAA AC	
	_ GA	
GAM1637 LOC112448	3' CTCACACGGGGAAAAACCAT 72822	_ TTG
	GTGGTTTT CCCT GTGAG	
	TACCAAAA GGGG CACTC	
	A CA_	
GAM1637 LOC116411	3' CTCTGCCTAGGAAAACCA 73863	CTTT _
	TGGTTTTCC GGT GAG	
	ACCAAAAGG CCG CTC	
	AT_ T	
GAM1637 LOC129452	3' CTCATGGAGGAAAACCA 74876	CT G
	TGGTTTTCC TT GTGAG	
	ACCAAAAGG AG TACTC	
	_ G	
GAM1637 LOC137964	5' CTCTTGGGCAGGAAAACCATG 75281	C_ TG T
	CGTGGTTTTCC TT G GAG	
	GTACCAAAAGG GG T CTC	
	AC GT_	
GAM1637 LOC139171	5' CCACAAGGAAAGAACCAC 75820	C_ _
	GTGGTTTT CCTT TGG	
	CACCAAGA GGAA ACC	
	AA C	
GAM1637 LOC144667	3' CTCATTAAGGAAAACCA 83166	C
	TGGTTTTCC TTTGGTGAG	
	ACCAAAAGG AAATTACTC	
	A	
GAM1637 LOC144893	3' CACGGAAAGCAAAACCAC 83185	CCC G
	GTGGTTTT TTT GTG	
	CACCAAAA AAG CAC	
	CGA G	
GAM1637 LOC145854	3' CTAAAGAAAACCAC 77551	CC
	GTGGTTTTC TTTGG	

CACCAAAAG AAATC

GAM1637 LOC147040 5' CACTGTCTGAAGACCAC 78229 CCTT  
GTGGTTTTTC TGGTG  
||||||| ||||  
CACCAGAAG GTCAC  
TCT\_

GAM1637 LOC149830 3' CCAAAGCTAAGGAAAACC 84723 \_\_\_\_  
GGTTTTCC CTTTGG  
||||||| |||||  
CCAAAAGG GAAACC  
AATC

GAM1637 LOC150150 5' CTCATCTTAGAAACCCAC 84867 T CCTTT  
GTGG TTTC GGTGAG  
||| ||| |||||  
CACC AAAG CTA CTC  
C ATT\_

GAM1637 LOC150630 5' CTAGAAAAAGACCACG 85103 CCC  
CGTGGTTTT TTTGG  
||||||| |||||  
GCACCAGAA AGATC  
AAA

GAM1637 LOC152274 5' CTCACCAAAGGGCC 80505 TTTT  
GG CCCTTTGGTGAG  
|| |||||  
CC GGGAAACCACTC

GAM1637 LOC152641 5' TGGTGAGCTAGGGAAACCAC 80637 \_\_\_\_ TGGT  
GTGGTTTTCC CTT G  
||||||| ||| |  
CACCAAAGGG GAG T  
ATC||| TGGT

GAM1637 LOC154726 5' CTCACCAAACCAATCAC 81105 TTCCC  
GTGGTT TTTGGTGAG  
||||| |||||  
CACTAA AAACCACTC  
CC\_

GAM1637 LOC155072 3' CCAGAGGAAACCACG 86374 TC  
CGTGGTTT CCTTTGG  
||||||| |||||  
GCACCAA GGAGACC

GAM1637 LOC157867 5' CTCACCAAAGAAGATACAC 86556 \_ CC  
GTG GTTTTC TTTGGTGAG  
||| ||||| |||||  
CAC TAGAAG AAACCACTC  
A \_

GAM1637 LOC158376 3' CTGATTAGAAAAACCAC 86796 CCC G  
GTGGTTTT TTTGGT AG  
||||||| ||||| ||

	CACCAAAA AGATTA TC	
	— G	
GAM1637 LOC158956 3'	CTAAAGAAAACCAC 66642	CC
	GTGGTTTTTC TTTGG	
	CACCAAAAG AAATC	
	—	
GAM1637 LOC161734 3'	TGTTAGAAGGAAAACCA 87104	C GT
	TGGTTTTCC TTTG G	
	ACCAAAAGG AGAT T	
	A TG	
GAM1637 LOC163590 5'	TTCACAAGGAAAACCA 58866	CTTTG
	TGGTTTTCC GTGAG	
	ACCAAAAGG CACTT	
	AA—	
GAM1637 LOC163682 5'	CCGGAAAGGAAGACCAC 87031	C_
	GTGGTTTTCC TTTGG	
	CACCAGAAGG AGGCC	
	AA	
GAM1637 LOC163682 5'	CCGGAAAGGAAGACCAC 87032	C_
	GTGGTTTTCC TTTGG	
	CACCAGAAGG AGGCC	
	AA	
GAM1637 LOC166793 5'	CTCAGGAGAAAAACCAC 59227	CC GG
	GTGGTTTT CTTT TGAG	
	CACCAAAA GAGG ACTC	
	A_ —	
GAM1637 LOC195977 3'	CCAGAGCAGGAAAAACCAC 87536	_ _
	GTGGTTTT CC CTTTGG	
	CACCAAAA GG GAGACC	
	A AC	
GAM1637 LOC201911 5'	CACCAAAGAAAGGGCTA 90257	CC
	TGGTTTT CTTTGGTG	
	ATCGGGA GAAACCAC	
	AA	
GAM1637 LOC202868 3'	CCAGAGGAAACCACG 90372	TC
	CGTGGTTT CCTTTGG	
	GCACCAA GGAGACC	
	—	
GAM1637 LOC203112 3'	CAAAAAGAAAAACCAC 89280	CC GG
	GTGGTTTT CTTT TG	



		CACCAAAA GAAA AC		
		A_ A_		
GAM1637	LOC219920 5'	CAAAGGCAAACCACG	93303	TC
		CGTGGTTT CCTTTG		
		GCACCAAA GGAAAC		
		C_		
GAM1637	LOC221069 5'	CCAGGGTGGAACCAC	93200	C
		GTGGTTTTTC CTTTGG		
		CACCAAAGG GGGACC		
		T		
GAM1637	LOC222029 3'	CCAAAAGAAAACACTAC	94036	CC
		GTGGTTTTTC TTTGG		
		CATCAAAAG AAACC		
		A_		
GAM1637	LOC222962 3'	TGGTGAGCTCTGGGAAACCAC	92878	_____ TGGT
		GTGGTTTTTC CTT G		
		CACCAAAGGG GAG T		
		TCTC    TGGT		
GAM1637	LOC253272 3'	CTCACCAAAGATTTCCATG	95361	TTTTCC
		CGTGG CTTTGGTGAG		
		GTACC GAAACCACTC		
		TTTA__		
GAM1637	LOC253681 5'	CACTGTCTGAAGACCAC	95126	CCTT
		GTGGTTTTTC TGGTG		
		CACCAGAAG GTCAC		
		TCT_		
GAM1637	LOC254251 5'	CTCTACAAAGAAAACCA	95906	CC GT
		TGGTTTTTC TTTG GAG		
		ACCAAAAG AAAC CTC		
		_ AT		
GAM1637	LOC254387 5'	CTCACCAAAGCTAACC	94909	TTCC
		GGTT CTTTGGTGAG		
		CCAA GAAACCACTC		
		TC__		
GAM1637	LOC256113 5'	CTTAAGAAGAAAAACCATG	96770	CC GG
		CGTGGTTTTT CTTT TGAG		
		GTACC AAAA GAAG ATTC		
		A_ A_		
GAM1637	LOC51312 3'	TACAAGAAAGAAAACCATG	37715	CC G
		CGTGGTTTTT TTT GTG		

			GTACCAAAAG AGA CAT		
			AA A		
GAM1637	LOC51713	3'	CCGGTGGGAAAAGACCACG 32761	___	T
			CGTGGTT TTCCC TTGG		
			GCACCAG AAGGG GGCC		
			AA T		
GAM1637	LOC57795	5'	CCAAATGAGAAAGAACCAC 69322	CC	___
			GTGGTTTT CTT TGG		
			CACCAAGA GAG ACC		
			AA TAA		
GAM1637	LOC89919	3'	CCAGAGGAAAACCAGG 60719	G	C
			C TGGTTTTCC TTTGG		
			G ACCAAAAGG AGACC		
			G _		
GAM1637	LOC91050	3'	CCGAAGGAAAACAC 64744	G	C
			GTG TTTTCC TTTGG		
			CAC AAAAGG AAGCC		
			_ _		
GAM1637	LOC91291	3'	CTCACCAAAAAGGTGGAAG 65479	_	___
			TTTTC CCTT TGGTGAG		
			GAAGG GGAA ACCACTC		
			T AA		
GAM1637	LOC91960	3'	CTGAAGAGGAAAACCACG 67660	_	TG
			CGTGGTTTTCC CTT G		
			GCACCAAAAGG GAA C		
			A GT		
GAM1637	LOC93333	3'	CTTTTCAAGGAGAACCAC 72065	CT	T
			GTGGTTTTCC TTGG GAG		
			CACCAAGAGG AACT TTC		
			_ T		
GAM1638	ADARB1	3'	GCAGGTCCGACTCGACCA 31725	A	T_
			TG TCGAGTCG CCTGC		
			AC AGCTCAGC GGACG		
			C CT		
GAM1638	ALPL	5'	GCGCAGGATTGGAACATCAGT 4894	CGAG	_
			ACTGAT TCG TCCTGCGC		
			TGACTA GGT AGGACGCG		
			CAA_ T		
GAM1638	DUX4	5'	GCGCAGGACGACGGAGGCGT 72836	TGA	GA
			AC TC GTCGTCCTGCG		

			TG AG CAGCAGGACGC		
			CGG G_		
GAM1638	FBXL7	5'	GCGCAGGACGTGCGCCG	24551	A_ _
			CG GT CGTCCTGCGC		
			GC CG GCAGGACGCG		
			CG T		
GAM1638	JUND	5'	GCGCAGGAGCCGCGCCAGT	18086	AT A C_
			ACTG CG GT G TCCTGCGC		
			TGAC GC CG C AGGACGCG		
			C_ _ C G		
GAM1638	MRPL49	5'	GCGCAGGACGGGGCGGGACCAG	69570	A__ AG
			CTG TCG TCGTCCTGCGC		
			GAC GGC GGCAGGACGCG		
			CAG GG		
GAM1638	NTE	3'	GCACTGATGACTTGACCAG	21987	A C_
			CTG TCGAGTCGTC TGC		
			GAC AGTTCAGTAG ACG		
			C TC		
GAM1638	PACE4	3'	GCACAGATCTGCTTGATCA	10401	CGTC C
			TGATCGAGT CTG GC		
			ACTAGTTCG GAC CG		
			TCTA A		
GAM1638	PACE4	3'	GCACAGATCTGCTTGATCA	56346	CGTC C
			TGATCGAGT CTG GC		
			ACTAGTTCG GAC CG		
			TCTA A		
GAM1638	RRM2B	5'	GCGCAGGGAGAGTCACTCA	67827	TC G GT
			TGA GA TC CCTGCGC		
			ACT CT AG GGACGCG		
			CA G AG		
GAM1638	SYCP1	5'	GCGCAGGAACTTAAGACAGT	12071	A GAGTCG
			ACTG TC TCCTGCGC		
			TGAC AG AGGACGCG		
			_ AATTCA		
GAM1638	TNFRSF17	3'	CATTTGACTCGAGCAGT	6816	A TCC
			ACTG TCGAGTCG TG		
			TGAC AGCTCAGC AC		
			G TTT		
GAM1638	WBSCR5	3'	GCGCAGGATTAGGATAAG	26257	G GAGTC
			CT ATC GTCCTGCGC		

			GA TAG TAGGACGCG		
			A GATT_		
GAM1638	WBSCR5	3'	GCGCAGGATTTAGGATAAG	41858	G GAGTC
			CT ATC GTCCTGCGC		
			GA TAG TAGGACGCG		
			A GATT_		
GAM1638	WBSCR5	3'	GCGCAGGATTTAGGATAAG	50611	G GAGTC
			CT ATC GTCCTGCGC		
			GA TAG TAGGACGCG		
			A GATT_		
GAM1638	C1orf17	5'	GCGCAGGGGAGCGCCAG	68215	AT AG G
			CTG CG TC TCCTGCGC		
			GAC GC AG GGGACGCG		
			C_ G_ _		
GAM1638	DJ667H12.2	3'	GCACAGCATGATCAGT	38985	A C CCT
			ACTGATCG GT GT GC		
			TGACTAGT CG CA CG		
			A A _		
GAM1638	DKFZp434N035	3'	CAAGAGATCGATCAGT	50047	G G C
			ACTGATCGA TC TC TG		
			TGACTAGCT AG AG AC		
			_ _ A		
GAM1638	FLJ10483	3'	GCACAATAGTACCGATCAGT	36172	A C_ CC
			ACTGATCG GT GT TGC		
			TGACTAGC CA TA ACG		
			_ TGA AC		
GAM1638	FLJ10607	3'	GCGCAGGGGCACAATCA	77118	CGA GT
			TGAT GTC CCTGCGC		
			ACTA CGG GGACGCG		
			ACA _		
GAM1638	FLJ10748	3'	GCACAGATGACTCCACCAG	36558	ATC C C
			CTG GAGTCGTC TG GC		
			GAC CTCAGTAG AC CG		
			CAC _ A		
GAM1638	FLJ20499	5'	GCGCAGGGCTGGCAAGCAGT	35258	ATCGA _
			ACTG GTC GTCCTGCGC		
			TGAC CGG CGGGACGCG		
			GAA_ T		
GAM1638	KIAA0441	5'	GCGCAGGAGCAGAAACCGGT	28956	AG_ _
			ATCG TC G TCCTGCGC		

			TGGC AG C AGGACGCG		
			CAA A G		
GAM1638	KIAA1466	3'	GCGCAGGACCAGTGAACCAGT 71915	A_	AGTC
			ACTG TCG GTCCTGCGC		
			TGAC AGT CAGGACGCG		
			CA GAC_		
GAM1638	KIAA1649	3'	GCGCAGGACGAAGCTCG 50267	__	
			CGAGT CGTCCTGCGC		
			GCTCG GCAGGACGCG		
			AA		
GAM1638	KIAA1863	3'	GCGCAGGAGAAGGACCAG 64872	A GAG G	
			CTG TC TC TCCTGCGC		
			GAC AG AG AGGACGCG		
			C GA_ _		
GAM1638	MGC5139	5'	GCGCAGGACGTTTTGTC 74107	T T	
			GA CGAG CGTCCTGCGC		
			CT GTTT GCAGGACGCG		
			_ T		
GAM1638	PDZD2	5'	GCAAGACTCGATCAG 80872	GTCC	
			CTGATCGAGTC TGC		
			GACTAGCTCAG ACG		
			A__		
GAM1638	PRSS25	5'	GCGCAGGACGAGGAGGCAG 59022	A GAG	
			CTG TC TCGTCCTGCGC		
			GAC GG AGCAGGACGCG		
			_ AGG		
GAM1638	PRSS25	5'	GCGCAGGACGAGGAGGCAG 25113	A GAG	
			CTG TC TCGTCCTGCGC		
			GAC GG AGCAGGACGCG		
			_ AGG		
GAM1638	PSMD12	3'	GCACTCGACTCGATCAG 10999	TCC	
			CTGATCGAGTCG TGC		
			GACTAGCTCAGC ACG		
			TC_		
GAM1638	RIP5	3'	GCACAGGAACTTGATC 38126	CG C	
			GATCGAGT TCCTG GC		
			CTAGTTCA AGGAC CG		
			_ A		
GAM1638	SMOC2	5'	GCGCAGGACGCGGCCGAT 72374	A _	
			ATCG GT CGTCCTGCGC		

			TAGC CG GCAGGACGCG		
			_ GC		
GAM1638	LOC144584	5'	GCGCTCTGAGGACCCTGACCAG 67026	A A_ G CT_	
			CTG TCG GTC TC GC GC		
			GAC AGT CAG AG GC GC		
			C CC G TCT		
GAM1638	LOC149657	3'	GCGCAGGACAGGCTATTTCAG 84574	TCG _	
			CTGA AGTC GTCCTGCGC		
			GACT TCGG CAGGACGCG		
			TA_ A		
GAM1638	LOC160954	5'	CGCGAACACCGATCAGT 87076	A C CC	
			ACTGATCG GT GT TGCG		
			TGACTAGC CA CA GC GC		
			_ _ A_		
GAM1638	LOC164714	5'	CGCAGGACGGCTCCAG 87226	ATC	
			CTG GAGTCGTCCTGCG		
			GAC CTCGGCAGGACGC		
			_____		
GAM1638	LOC196489	3'	GCGCAAGACGACTTCGGGC 87736	AT _ C	
			G CGA GTCGTC TGCGC		
			C GCT CAGCAG ACGCG		
			GG T A		
GAM1638	LOC220001	5'	GCGCAGGAGCCGAGCCCAG 91635	A_ A CG	
			CTG TCG GT TCCTGCGC		
			GAC AGC CG AGGACGCG		
			CCG _ _		
GAM1638	LOC51145	3'	GCGCAGGAGCAAGCGGTCA 32396	AGTCG	
			TGATCG TCCTGCGC		
			ACTGGC AGGACGCG		
			GAACG		
GAM1638	LOC91695	5'	GCGCAGGACGAAGCTCG 66969	_	
			CGAGT CGTCCTGCGC		
			GCTCG GCAGGACGCG		
			AA		
GAM1639	ULBP2	3'	CATGGACCCAATAGCTCATTCA 47406	CACGCAAA T	
			TGAATGAGC TC CATG		
			ACTTACTCG AG GTAC		
			ATAACCC_ _		
GAM1639	BTN1A1	3'	CATGATGAACACCTGGCTCATC 8192	A CGCAAA _	
	CA		TG ATGAGCCA TC TCATG		

AC TACTCGGT AG AGTAC  
 C CCACA\_ T  
 GAM1639 PRO0386 5' TTTGCGTAGCCCATCA 37689 A A C  
 TGA TG GC ACGCAA  
 ||| || |||||  
 ACT AC CG TGC GTT  
 \_ C A  
 GAM1639 LOC256536 3' ATGAGATTTTTCTCATCA 94710 A CCACGC  
 TGA TGAG AAATCTCAT  
 ||| ||| |||||  
 ACT ACTC TTTAGAGTA  
 \_ TTT\_ \_  
 GAM1640 ASPH 3' CATCATTTTGAAAGG 50616 TA  
 CCTT TCAGGATGATG  
 ||| |||||  
 GGAA AGTTTTACTAC  
 \_  
 GAM1640 ASPH 3' CATCATTTTGAAAGG 50629 TA  
 CCTT TCAGGATGATG  
 ||| |||||  
 GGAA AGTTTTACTAC  
 \_  
 GAM1640 DDX6 5' CTGCATTGCAATAAAGG 15287 CAGGAT  
 CCTTTAT GATGCAG  
 ||||| |||||  
 GGAAATA TTACGTC  
 ACG\_ \_  
 GAM1640 TRIP15 3' CTGCAGTGTAGTAAAGGTTT 14893 CAGGATGA  
 AAACCTTTAT TGCAG  
 ||||| |||||  
 TTTGGAAATG ACGTC  
 ATGTG\_ \_  
 GAM1640 FLJ13593 3' CAGACCTGGCAAAGGTTT 45503 AT A\_  
 AAACCTTT CAGG TG  
 ||||| ||| ||  
 TTTGGAAA GTCC AC  
 CG AG  
 GAM1640 FLJ21988 3' CTGCATCATCCCCAGCCAGGT 42554 A TTATCA\_  
 CC A ACCT GGATGATGCAG  
 ||| |||||  
 C TGGA CCTACTACGTC  
 C CCGACCC  
 GAM1640 HIRIP5 5' CTGCATCAGTTTGTACAAAG 31653 AT\_ A  
 CTTT CAGG TGATGCAG  
 ||| ||| |||||  
 GAAA GTTT ACTACGTC  
 CAT G  
 GAM1640 KIAA0547 3' TGCATCATCCCAGGTTT 28917 TTATCA  
 AAACCT GGATGATGCA  
 ||||| |||||

TTTGGA CCTACTACGT  
 C\_\_\_\_  
 GAM1640 KIAA1223 3' CTGCAGTTCCCTGATAAA 71145 ATGA  
 TTTATCAGG TGCAG  
 ||||| ||||  
 AAATAGTCC ACGTC  
 CTTG  
 GAM1640 KIAA1951 3' CTGCATCACCTGGTG 73759 A  
 TATCAGG TGATGCAG  
 ||||| |||||  
 GTGGTCC ACTACGTC  
 C  
 GAM1640 PFDN1 3' CTGCATCACCTGAGCCCCATT 10511 COTTTA A  
 TG CAAA TCAGG TGATGCAG  
 ||| |||| |||||  
 GTTT AGTCC ACTACGTC  
 ACCCG C  
 GAM1640 SLC22A6 3' CATCATTAAGGTTTG 16570 ATCAG  
 CAAACCTTT GATGATG  
 ||||| |||||  
 GTTTGGAAA TTA CTAC  
 A\_\_\_\_  
 GAM1640 LOC90835 3' CATTTTCCCCAATAAAGGTCTG 64127 A CA\_ T  
 CA ACCTTTAT GGA GATG  
 || ||||| ||| ||||  
 GT TGGAAATA CCT TTAC  
 C ACC T  
 GAM1640 LOC92218 3' CTGCACTTTCTTGATAAATATT 68505 CC TGA  
 TG CAAA TTTATCAGGA TGCAG  
 ||| ||||| ||||  
 GTTT AAATAGTTCT ACGTC  
 AT TTC  
 GAM1641 PRO2900 3' TGTGCGCATCTCAATCA 37808 CC  
 TGATTGAG GCGCACG  
 ||||| |||||  
 ACTAACTC CGCGTGT  
 TA  
 GAM1642 CNGA1 3' CAACTGATAATGTGCAAA 59507 GC A  
 TTTGCACATTA TAG TTG  
 ||||| ||| |||  
 AAACGTGTAAT GTC AAC  
 A\_ \_  
 GAM1642 ESRRG 3' TGGCAGTCTTATGTGCAAA 66396 TAGCT  
 TTTGCACAT AGATTGCCA  
 ||||| |||||  
 AAACGTGTA TCTGACGGT  
 T\_\_\_\_  
 GAM1642 KCNJ3 3' GCAATAATGTGCAAA 9525 GCTAGA  
 TTTGCACATTA TTGC  
 ||||| |||



			AAACGTGTAAT	AACG	
GAM1642	SDC2	3'	GC	AAATTAATGTGTAAA	67132 CTAGA
				TTTGCACATTAG TTGC	
				AAATGTGTAATT AACG	
				A_____	
GAM1642	USP9X	3'	ATGGCCTGATGCTAATGTGTAA	16206	TAGATT
	A			TTTGCACATTAGC GCCAT	
				AAATGTGTAATCG CGGTA	
				TAGTC_	
GAM1642	AMOTL1	3'	GGCAAGTAATGTGCAAA	73650	G AGAT
				TTTGCACATTA CT TGCC	
				AAACGTGTAAT GA ACGG	
				_____	
GAM1642	BCAR3	3'	AGTAATAATGTGCAAA	13098	
				TTTGCACATTA GCT	
				AAACGTGTAAT TGA	
				AA	
GAM1642	DKFZP434B044	3'	TGACAATTAAATGTGCAGA	48930	AGCTA C
				TTTGCACATT GATTG CA	
				AGACGTGTAA TTAAC GT	
				A_____ A	
GAM1642	MGC3184	3'	ATGACATTTTCTAATGTGCAGA	48235	CT T C
				TTTGCACATTAG AGA TG CAT	
				AGACGTGTAATC TTT AC GTA	
				_____ T A	
GAM1642	PTD012	3'	ATGGCAATCTAGCTAATGTGCA	25891	
	AA			TTTGCACATTAGCTAGATTGCCAT	
				AAACGTGTAATCGATCTAACGGTA	
				_____	
GAM1643	CLCN5	5'	TGAAATACCTAAGCTGCTCCAA	3595	
				TTGGAGCAG GTTTCA	
				AACCTCGTC TAAAGT	
				GAATCCA	
GAM1643	FLRT2	5'	ATTGAAAAATGAGGTCTGC	25056	GT CTC
				GCAG TTCATT CAAT	
				CGTC GAGTAA GTTA	
				TG AAA	
GAM1643	IL17	3'	TGGGGAAAATGAAACCCTCC	9333	CA
				GGAG GGTTTCAT TCTCCA	

			CCTC CCAAAGTA AGGGGT		
			— AA		
GAM1643	NLGN1	5'	TGAAGATGCTGCTCCAA 30026	G	—
			TTGGAGCAG TTTCA		
			AACCTCGTC GAAGT		
			GTA		
GAM1643	POLG	3'	GTGATAAACCTGCTCCAA 10682		—
			TTGGAGCAGGTT TCAT		
			AACCTCGTCCAA AGTG		
			AT		
GAM1643	TPK1	3'	GGAGAACCTGTCCAA 42384	G	TTCAT
			TTGGA CAGGT TCTCC		
			AACCT GTCCA AGAGG		
			— ———		
GAM1643	C1orf8	5'	GAGAATGAAACCCTC 16832	CA	
			GAG GGTTTCATTCTC		
			CTC CCAAAGTAAGAG		
			—		
GAM1643	CLIC6	3'	TGGAGAACATGTTCCAA 82536	G	TTCAT
			TTGGAGCA GT TCTCCA		
			AACCTTGT CA AGAGGT		
			A ———		
GAM1643	CLIPR-59	3'	TGGAGAATTTCAATGCCCGA 31374	A	GGTTTC
			TTGG GCA ATTCTCCA		
			AGCC CGT TAAGAGGT		
			C AACTT_		
GAM1643	DKFZP547L112	3'	TGGAGAACTCTTGCTCCA 66532		TTTCA
			TGGAGCAGG TTCTCCA		
			ACCTCGTTC AAGAGGT		
			TC_		
GAM1643	EPS8R3	5'	GGACCACCTGCTCCAA 57404		TTCATTC
			TTGGAGCAGGT TCC		
			AACCTCGTCCA AGG		
			CC_		
GAM1643	EPS8R3	5'	GGACCACCTGCTCCAA 55701		TTCATTC
			TTGGAGCAGGT TCC		
			AACCTCGTCCA AGG		
			CC_		
GAM1643	FLJ20552	3'	AGAACAAAAGTGTCTCCAA 35389	G	CA
			TTGGAGCAG TTT TTCT		

AACCTCGTC AAA AAGA  
\_ AC  
GAM1643 FLJ22865 5' TGGAGAAACTGCTCTAA 47071 GTTTC  
TTGGAGCAG TTCTCCA  
||||||| |||||  
AATCTCGTC AAGAGGT  
AA\_\_\_\_  
GAM1643 KIAA0372 5' ATTGAAATTTGTTACCTACTCC 27663 C TT TTCTC  
AA TTGGAG AGGT CA CAAT  
||||| ||| || |||  
AACCTC TCCA GT GTTA  
A TT TTAAA  
GAM1643 PRO0132 5' ATGAAACCACTCCAA 26101 CA  
TTGGAG GGTTTCAT  
||||| |||||  
AACCTC CCAAAGTA  
A\_  
GAM1643 TEX27 3' AGAGTGGAACCCGCTGCAA 41658 G A  
TTG AGC GGTTTCATTCT  
||| ||| |||||  
AAC TCG CCAAGGTGAGA  
G C  
GAM1643 LOC149373 3' ATTGGGGTGATGATACCCACCC 79312 AGCA T \_  
CAA TTGG GGT TCATT CTCCAAT  
|||| ||| ||||| |||||  
AACC CCA AGTAG GGGGTTA  
CCAC T T  
GAM1643 LOC152687 3' TTGGAGAATATTGCTCC 80643 GTTTC  
GGAGCAG ATTCTCCAA  
||||||| |||||  
CCTCGTT TAAGAGGTT  
A\_\_\_\_  
GAM1643 LOC51202 3' ATTGGAGAATGAAACCTGCTCC 33017  
AA TTGGAGCAGGTTTCATTCTCCAAT  
|||||||  
AACCTCGTCCAAAGTAAGAGGTTA  
GAM1644 FLRT2 3' AATGACAACTTCACTCT 25052 AT\_  
AGA GGTTTGTCATT  
||| |||||  
TCT TCAAACAGTAA  
CACT  
GAM1644 GPR81 3' AATGACAGGCTGCCCCTGCCCT 50745 AA AA\_  
G CAG CAG TGGTTTGTCATT  
||| ||| |||||  
GTC GTC GTCGGACAGTAA  
CC CCC  
GAM1644 KRT10 3' ACAACTTTCTGTTCTCA 4704 C T T  
TG AGAACAGAA GGTT GT  
|| ||||| ||| ||

AC TCTTGTCTT TCAA CA

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      _ _ _
GAM1644 MLLT2  3' AATGACATTATATTCTGTTC 19840      GTT
      GAACAGAATG TGTCATT
      ||||| |||||
      CTTGTCTTAT ACAGTAA
      ATT
GAM1644 MME    5' ATTTGCCATTCTGCTGTA 23506      AA      TT
      TGCAG CAGAATGGT GT
      |||| ||||| ||
      ATGTC GTCTTACCG TA
      TT
GAM1644 MUCDHL 3' GACGACATTCTGTTCTACA 87300      C      GT
      TG AGAACAGAATG TTGTC
      || ||||| ||||
      AC TCTTGTCTTAC AGCAG
      A      _
GAM1644 MUCDHL 3' GACGACATTCTGTTCTACA 48369      C      GT
      TG AGAACAGAATG TTGTC
      || ||||| ||||
      AC TCTTGTCTTAC AGCAG
      A      _
GAM1644 SLC17A7 3' CCAACTCTGTTCTGCA 39699      A_
      TGCAGAACAGA TGG
      ||||| |||
      ACGTCTTGTCT ACC
      CA
GAM1644 AMOT   3' GTGACCCCATCTGT 55723      TTT
      ACAGAATGG GTCAT
      ||||| ||||
      TGTCTTACC CAGTG
      C_
GAM1644 CSMD1  3' ATAGGCCATCCTGTCTCA 73118      C A  A
      TG AG ACAG ATGGTTTGT
      || || || |||||
      AC TC TGTC TACCGGATA
      _ C  C
GAM1644 FLJ13204 3' ATAATGCATTCTGTACTACA 45414      C A  GT
      TG AG ACAGAATG TTGT
      || || ||||| |||
      AC TC TGTCTTAC AATA
      A A  GT
GAM1644 KIAA1467 3' GCAACCATTTTGTCTGCA 71608      A      T
      TGCAG ACAGAATGGTT GT
      |||| ||||| ||
      ACGTC TGTTTTACCAA CG
      C      _
GAM1644 KIAA1735 3' AATGACAATAATTCCTGTTC 87622      _ _  T
      GAACAG AAT GGTT GTCATT
      ||||| || |||| |||||
```

CTTGTC TTA TCAA CAGTAA  
 C A \_  
 GAM1644 LNX 3' AAACCATGCCTATTCTGCA 50916 C A\_  
 TGCAGAA AG ATGGTTT  
 ||||| || |||||  
 ACGTCTT TC TACCAAA  
 A CG  
 GAM1644 METAP2 3' AATGACTACATCCAGTTCTGCA 60165 AGAA TTT\_  
 TGCAGAAC TGG GTCATT  
 ||||| || |||||  
 ACGTCTTG ACC CAGTAA  
 \_ TACAT  
 GAM1644 RBM5 3' GGTGAACCACTTCATTCTGCA 19332 CA \_ TG  
 TGCAGAA GAA TGGTT TC  
 ||||| || ||||| ||  
 ACGTCTT CTT ACCAA GG  
 A\_ C GT  
 GAM1644 SMT3H2 3' TGAACCACTTAGCCTGCA 22676 AAC  
 TGCAG AGAATGGTTTG  
 |||| |||||  
 ACGTC TCTTACCAAGT  
 CGA  
 GAM1644 TRAF3 3' GACCATTCTGTCCGCA 59739 A A  
 TGC GA CAGAATGGTT  
 || || |||||  
 ACG CT GTCTTACCAG  
 C \_  
 GAM1644 LOC147160 5' GGTGAGCCATTCTGCTCTGCA 83968 A TG  
 TGCAGA CAGAATGGTT TC  
 ||||| ||||| ||  
 ACGTCT GTCTTACCGA GG  
 C GT  
 GAM1644 LOC147632 5' GCAGCCACTCATTCTGCA 56669 CA A T  
 TGCAGAA GA TGGTT GT  
 ||||| || ||||| ||  
 ACGTCTT CT ACCGA CG  
 A\_ C \_  
 GAM1644 LOC148195 3' ACAAAGCATTGTTCT 84123 GA G  
 AGAACA ATG TTTGT  
 ||||| || |||||  
 TCTTGT TAC AAACA  
 \_ G  
 GAM1644 LOC254431 3' AATGACAAACACTCCTGT 96848 AATG  
 ACAG GTTTGTCATT  
 |||| |||||  
 TGTC CAAACAGTAA  
 CTCA  
 GAM1644 LOC51014 3' ATGATCTACTCTGTTCGCA 65848 A A TTT  
 TGC GAACAGA TGG GTCAT  
 || ||||| || |||||

ACG CTTGTCT ATC TAGTA  
 \_ C \_  
 GAM1644 LOC90593 3' ACAACATTTGCCGTTCTGCA 63452 A\_\_ GT  
 TGCAGAAC GAATG TTGT  
 ||||| ||| |||  
 ACGTCTTG TTTAC AACA  
 CCG \_  
 GAM1645 A1BG 3' CAGGGTCTCACTGTGTTGC 55413 TAT\_  
 GCAACACA GGCTTTG  
 ||||| |||||  
 CGTTGTGT CTGGGAC  
 CACT  
 GAM1645 ACPT 3' CACCCCGCCATATGCTGC 54980 ACA TTT  
 GCA CATATGGC GTG  
 || ||||| ||  
 CGT GTATACCG CAC  
 C\_\_ CCC  
 GAM1645 ACPT 3' CACCCCGCCATATGCTGC 54986 ACA TTT  
 GCA CATATGGC GTG  
 || ||||| ||  
 CGT GTATACCG CAC  
 C\_\_ CCC  
 GAM1645 AHCY 3' CACAAAGCCCATGTGTTTTGC 5473 C \_  
 GCAA ACATATGG CTTTGTG  
 ||| ||||| |||||  
 CGTT TGTGTACC GAAACAC  
 T C  
 GAM1645 BCL7A 3' CAGGATTCCATTTGTGTTGCT 40638 T CT G  
 AGCAACACA ATGG TT TG  
 ||||| ||| |||  
 TCGTTGTGT TACC AG AC  
 T TT G  
 GAM1645 CDK5R2 3' CACAAAGCCACCGCCGCTGTT 14132 ACACATA  
 AGCA TGGCTTTGTG  
 ||| |||||  
 TTGT ACCGAAACAC  
 CGCCGCC  
 GAM1645 CHC1 3' CACAAAGCATACTCTTGC 7019 CACA G  
 GCAA TATG CTTTGTG  
 ||| ||| |||||  
 CGTT ATAC GAAACAC  
 CTC\_ \_  
 GAM1645 CIT 3' CACAAGGCATCTGTTGCT 69741 CATATG  
 AGCAACA GCTTTGTG  
 ||||| |||||  
 TCGTTGT CGGAACAC  
 CTA\_\_  
 GAM1645 COL6A2 5' CAGGGCCACAGGTGCTGC 8480 A ATA  
 GCA CAC TGGCTTTG  
 ||| ||| |||||

			CGT GTG ACCGGGAC		
			C GAC		
GAM1645 COL6A2	5'	CAGGGCCACAGGTGCTGC	54168	A	ATA
		GCA CAC TGGCTTTG			
		CGT GTG ACCGGGAC			
		C GAC			
GAM1645 EYA1	3'	CACAGCGTTATGTGTCTGC	4952	AC	T
		GCA ACATATGGC TTGTG			
		CGT TGTGTATTG GACAC			
		C_ C			
GAM1645 FBN2	3'	CAAGGAACCATATGTG	8844	—	
		CACATATGG CTTTG			
		GTGTATACC GGAAC			
		AA			
GAM1645 FMO1	3'	CACAAATGATTGTGTTGT	8924		TATGGC
		GCAACACA TTTGTG			
		TGTTGTGT AAACAC			
		TAGT_			
GAM1645 GALNT2	3'	CACAAAGCCGAGTCGTGT	15593	_	A
		ACAC AT TGGCTTTGTG			
		TGTG TG GCCGAAACAC			
		C A			
GAM1645 GALNT2	3'	CACAAAGCCGTTCGCAGCT	15594		AACACAT
		AGC ATGGCTTTGTG			
		TCG TGCCGAAACAC			
		ACGCT_			
GAM1645 GPR4	3'	CAGGGTCTCACTGTGTTGC	59902		TAT_
		GCAACACA GGCTTTG			
		CGTTGTGT CTGGGAC			
		CACT			
GAM1645 HNMT	3'	CACAAAGCCTGTGTTACT	22567	C	TAT
		AG AACACA GGCTTTGTG			
		TC TTGTGT CCGAAACAC			
		A _			
GAM1645 IL1RN	3'	CACAAAGCCCTTCCATGTCGC	5141	A	CATAT_
		GC ACA GGCTTTGTG			
		CG TGT CCGAAACAC			
		C ACCTTC			
GAM1645 IL2RB	3'	CACAAAGTGGATGCCTGCT	6069	ACA	ATG
		AGCA CAT GCTTTGTG			

			TCGT GTA TGAAACAC		
			CC_ GG_		
GAM1645	ITSN2	3'	CACAAAGCCATGCACGCT 38971	AACACA	
			AGC TATGGCTTTGTG		
			TCG GTACCGAAACAC		
			CAC__		
GAM1645	JRK	3'	CAGGGTCTCACTGTGTTGC 86524	TAT_	
			GCAACACA GGCTTTG		
			CGTTGTGT CTGGGAC		
			CACT		
GAM1645	LANCL1	3'	CACAATTTTATATGTATGCT 20210	AC	CT
			AGCA ACATATGG TTGTG		
			TCGT TGTATATT AACAC		
			A_ TT		
GAM1645	LGR6	5'	GGCCATCGTGTTGCT 84200	AT	
			AGCAACAC ATGGCT		
			TCGTTGTG TACCGG		
			C_		
GAM1645	LRRC2	3'	CAAGGCACCATGTGTTACT 44465	C	ATG
			AG AACACAT GCTTTG		
			TC TTGTGTA CGGAAC		
			A CCA		
GAM1645	MYBL2	3'	CAGGGCCATGTGCTGC 10154	ACA	
			GCA CATATGGCTTTG		
			CGT GTGTACCGGGAC		
			C_		
GAM1645	OCLN	3'	CACAAAGTTTTGGTTGCT 10314	A	TAT
			AGCAAC CA GGCTTTGTG		
			TCGTTG GT TTGAAACAC		
			_ T_		
GAM1645	OSR1	3'	CACAAAGTAATATGTG 17566	G	
			CACATAT GCTTTGTG		
			GTGTATA TGAAACAC		
			A		
GAM1645	PCDH9	5'	CACAAAGTGACAGTGCTGGCT 82794	AA_	ATATG
			AGC CAC GCTTTGTG		
			TCG GTG TGAAACAC		
			GTC ACAG_		
GAM1645	PRDM2	5'	CACAAAGCCACATCCTGC 24246	ACAC	A
			GCA AT TGGCTTTGTG		



		CGT TA ACCGAAACAC		
		CC__ C		
GAM1645 PRDM2	5'	CACAAAGCCACATCCTGC	31847	ACAC A
		GCA AT TGGCTTTGTG		
		CGT TA ACCGAAACAC		
		CC__ C		
GAM1645 PRG4	3'	CACAAAGCTTTATCGTGTTGT	19415	_ T
		GCAACAC ATA GGCTTTGTG		
		TGTTGTG TAT TCGAAACAC		
		C T		
GAM1645 RXRB	3'	CACAAAGCACTGGCCTTGC	41757	CA_ TATG
		GCAA CA GCTTTGTG		
		CGTT GT CGAAACAC		
		CCG CA__		
GAM1645 SMARCD1	3'	CACAAAGTTCCCATGTG	57429	___
		CATATGG CTTTGTG		
		GTGTACC GAAACAC		
		CTT		
GAM1645 SMARCD1	3'	CACAAAGTTCCCATGTG	11811	___
		CATATGG CTTTGTG		
		GTGTACC GAAACAC		
		CTT		
GAM1645 SMURF1	3'	CACGTGTGATCTGTGTTGC	92448	T G TT
		GCAACACA AT GC TGTG		
		CGTTGTGT TA TG GCAC		
		C G T_		
GAM1645 STX7	3'	CACCAAGATGTGTGTTACT	13108	C GG T
		AG AACACATAT CTT GTG		
		TC TTGTGTGTA GAA CAC		
		A _ C		
GAM1645 TAF4B	3'	CACAAAGCATTGTTGC	87167	CATATG
		GCAACA GCTTTGTG		
		CGTTGT CGAAACAC		
		TA__		
GAM1645 TF	3'	CACAGCTCTGTGTTGC	6512	TAT T
		GCAACACA GGCT TG		
		CGTTGTGT TCGA AC		
		C__ C		
GAM1645 TLR4	5'	CACAGGGCCACTGCTGCT	56732	A CATA
		AGCA CA TGGCTTTGTG		

		TCGT GT ACCGGGACAC		
		C C__		
GAM1645	TLR4	5' CACAGGGCCACTGCTGCT	56727	A CATA
		AGCA CA TGGCTTTGTG		
		TCGT GT ACCGGGACAC		
		C C__		
GAM1645	TLR4	5' CACAGGGCCACTGCTGCT	12317	A CATA
		AGCA CA TGGCTTTGTG		
		TCGT GT ACCGGGACAC		
		C C__		
GAM1645	TLR4	5' CACAGGGCCACTGCTGCT	56736	A CATA
		AGCA CA TGGCTTTGTG		
		TCGT GT ACCGGGACAC		
		C C__		
GAM1645	VIPR2	3' CACAGTCTCCATGTGTGTGC	12605	A CT_
		GCA CACATATGG TTGTG		
		CGT GTGTGTACC GACAC		
		_ TCT		
GAM1645	ANKT	3' CAGGGTCTCACTGTGTTGC	33024	TAT_
		GCAACACA GGCTTTG		
		CGTTGTGT CTGGGAC		
		CACT		
GAM1645	ATP9A	3' CACAAAGCCAGTGGCTGTT	62039	A_ ATA
		AGCA CAC TGGCTTTGTG		
		TTGT GTG ACCGAAACAC		
		CG _		
GAM1645	CETN2	3' CACATGTTACACCTGTGTTGC	15093	TA GCTT_
		GCAACACA TG TGTG		
		CGTTGTGT AC ACAC		
		CC ATTGT		
GAM1645	CYLD	3' CACAAGGTTTTATACTGCT	30883	ACAC TG
		AGCA ATA GCTTTGTG		
		TCGT TAT TGGAACAC		
		CA__ TT		
GAM1645	DKFZP586A0522	3' CAGGGTCTCACTGTGTTGC	25871	TAT_
		GCAACACA GGCTTTG		
		CGTTGTGT CTGGGAC		
		CACT		
GAM1645	DKFZp762K222	3' ACAGATGCGTGTTGCT	71116	ATATG _
		AGCAACAC GC TTTGT		

		TCGTTGTG	CG AGACA		
		_____ T			
GAM1645	FLJ10297	3'	CAGGGCTTCACTGTGTTGC	35979	TAT_
			GCAACACA GGCTTTG		
			CGTTGTGT TCGGGAC		
			CACT		
GAM1645	FLJ10511	3'	CACATGTGTATGTGCAGCT	36204	AA G TT
			AGC CACATATG C TGTG		
			TCG GTGTATGT G ACAC		
			AC _ T_		
GAM1645	FLJ11029	5'	CACTAGCACCTGTGTTGCT	60973	TATG TT
			AGCAACACA GCT GTG		
			TCGTTGTGT CGA CAC		
			CCA_ T_		
GAM1645	FLJ11117	3'	CACAAAGCTTGTATGTG	37073	_
			CACATATG GCTTTGTG		
			GTGTATGT CGAAACAC		
			T		
GAM1645	FLJ11715	3'	CAGGGTCTCCATATGTTGC	44668	C AT_
			GCAACA AT GGCTTTG		
			CGTTGT TA CTGGGAC		
			A CCT		
GAM1645	FLJ20275	3'	CACAAAGGGCTTTATGTGTCAG	34819	A_ T _
	CT		AGC ACACATA GGCT TTGTG		
			TCG TGTGTAT TCGG AACAC		
			AC T GA		
GAM1645	FLJ20413	3'	CAGAGCCGCATGCACTGCT	35131	ACA A
			AGCA CAT TGGCTTTG		
			TCGT GTA GCCGAGAC		
			CAC C		
GAM1645	FLJ20450	3'	CACCTGGGACCTGTGTTGCT	35192	TAT _ T_
			AGCAACACA GG CTT GTG		
			TCGTTGTGT CC GGG CAC		
			_ A TC		
GAM1645	FLJ20671	3'	CAATTCAAATGTGTTGC	35516	A CT
			GCAACACAT TGG TTG		
			CGTTGTGTA ACT AAC		
			A T_		
GAM1645	FLJ23598	3'	CACAAAGAGAGGCTGTGCTGC	45521	A TATGG_
			GCA CACA CTTTGTG		

			CGT GTGT	GAAACAC		
			C	CGGAGA		
GAM1645	FRSB	3'	CATAGGCCATACATGTTACT	19090	C CA	T
			AG AACA TATGGCTT	GTG		
			TC TTGT ATACCGGA	TAC		
			A AC	_		
GAM1645	H2AV	3'	CACAGCCATATGTATTGTT	56845	C	T
			AGCAA ACATATGGCT	TG		
			TTGTT TGTATACCGA	AC		
			A C			
GAM1645	HIC2	3'	CACAAAGTCTGTACCGC	65256	AAC TAT	
			GC ACA GGCTTTGTG			
			CG TGT CTGAAACAC			
			CCA	_		
GAM1645	KIAA0140	3'	CACATGGCCATGTCTTGC	27806	CAC	T
			GCAA ATATGGCT	TGTG		
			CGTT TGTACCGG	ACAC		
			C_	T		
GAM1645	KIAA0215	3'	CAAATTCATATGTAATGC	28416	AC	C_
			GCA ACATATGG	TTTG		
			CGT TGTATACC	AAAC		
			AA	TT		
GAM1645	KIAA0254	3'	AGCCACCTGTGTTGCT	28595	TA	
			AGCAACACA	TGGCT		
			TCGTTGTGT	ACCGA		
			CC			
GAM1645	KIAA0618	3'	CACAAAAACATGTGTTGT	29162	TA GC	
			GCAACACA	TG TTTGTG		
			TGTTGTGT	AC AAACAC		
			_	AA		
GAM1645	KIAA0953	3'	AGCTTTCATAGTGTTGCT	66778	A	_
			AGCAACAC	TATG GCT		
			TCGTTGTG	ATAC CGA		
			_	TTT		
GAM1645	KIAA1193	3'	CACAGAGCCATATACCTCGCT	67630	AACAC	
			AGC	ATATGGCTTTGTG		
			TCG	TATACCGAGACAC		
			CTCCA			
GAM1645	KIAA1281	3'	CACAGAGTAACAAATGTTGCT	89151	CATATG	
			AGCAACA	GCTTTGTG		

		TCGTTGT	TGAGACAC		
		AAACAA			
GAM1645	KIAA1466	5'	AGCCATATGTGCGCT	71913	AA
			AGC CACATATGGCT		
			TCG GTGTATACCGA		
			C_		
GAM1645	KIAA1821	3'	CAGGGTCTCACTGTGTTGC	71780	TAT_
			GCAACACA GGCTTTG		
			CGTTGTGT CTGGGAC		
			CACT		
GAM1645	KIF13B	3'	CACAAAGTCCGTGGTGC	30904	A ATAT
			GCA CAC GGCTTTGTG		
			CGT GTG CTGAAACAC		
			G C__		
GAM1645	KIF13B	3'	CACAAAGTCCGTGGTGC	82820	A ATAT
			GCA CAC GGCTTTGTG		
			CGT GTG CTGAAACAC		
			G C__		
GAM1645	MGC12921	3'	CACAAAGGCCGTTATTGC	63775	CACAT _
			GCAA ATGGC TTTGTG		
			CGTT TGCCG AAACAC		
			AT__ G		
GAM1645	MGC14836	5'	CACAAAGCTATCATCCTGC	53035	ACACAT
			GCA ATGGCTTTGTG		
			CGT TATCGAAACAC		
			CCTAC_		
GAM1645	MGC15429	3'	CACATTGTCATGTGCAGCT	51249	AACA TT
			AGC CATATGGC TGTG		
			TCG GTGTACTG ACAC		
			AC__ TT		
GAM1645	MGC15875	3'	CGAGGCCATAATGCT	51908	ACACA
			AGCA TATGGCTTTG		
			TCGT ATACCGGAGC		
			A__		
GAM1645	MGC16279	5'	GAAGCCATCGTGTGCGCT	51888	A AT
			AGC ACAC ATGGCTTT		
			TCG TGTG TACCGAAG		
			C C_		
GAM1645	MGC27434	3'	CACAATAAGTATGTGTT	58947	GGCT
			AACACATAT TTGTG		

			TTGTGTATG AACAC		
			AAT_		
GAM1645	MGC3048	3'	CACAAAGCATGAATGTT 43899	CA	G
			AACA TATG CTTTGTG		
			TTGT GTAC GAAACAC		
			AA _		
GAM1645	MIG-6	3'	CACAAGCTGGCCTTGTGTTGCT 38486	TAT	___
			AGCAACACA GGCT TTGTG		
			TCGTTGTGT CCGG AACAC		
			T_ TCG		
GAM1645	MUC17	3'	CACTGCCCCATATGTGTCCCT 94271	CA	CTTT
			AG ACACATATGG GTG		
			TC TGTGTATACC CAC		
			CC CCGT		
GAM1645	MYO3B	3'	CACTCTCCACATGTGTTGT 57301	A	CTTT
			GCAACACAT TGG GTG		
			TGTTGTGTA ACC CAC		
			C CTCT		
GAM1645	NS1-BP	3'	CACAAAGCTTTTGCATATTGC 72542	CA_	TAT
			GCAA CA GGCTTTGTG		
			CGTT GT TCGAAACAC		
			ATAC TT_		
GAM1645	OR51E2	3'	CACAGGTTTTATGTGTTCT 47791	C	TG T
			AG AACACATA GCTT GTG		
			TC TTGTGTAT TGGA CAC		
			_ TT _		
GAM1645	PRDM11	3'	CAGGTGCTCCATGTGTTGC 39581	AT	_
			GCAACACAT GGC TTTG		
			CGTTGTGTA TCG GGAC		
			CC T		
GAM1645	PRO0943	5'	CACAAAAGTGTTATATGTG 37701		___
			CACATATGGC TTTGTG		
			GTGTATATTG AAACAC		
			TGA		
GAM1645	SULT1C2	5'	CACAACGCAGCCATATGCTG 21674	_	___
			CA CATATGGCT TTGTG		
			GT GTATACCGA AACAC		
			C CGC		
GAM1645	VEST1	3'	CACCTGCCATACATGTTGT 53685	CA	TTT
			GCAACA TATGGC GTG		

			TGTTGT ATACCG CAC		
			AC TC_		
GAM1645	ZFP100	3'	AGTCACCTGTGTTGCT	70049	TA
			AGCAACACA TGGCT		
			TCGTTGTGT ACTGA		
			CC		
GAM1645	ZNF363	5'	AGCCATATTGTCGCT	73452	A C
			AGC ACA ATATGGCT		
			TCG TGT TATACCGA		
			C _		
GAM1645	LOC118611	5'	CACAGAGCATTTGCGTTACT	75469	C A TATG
			AG AAC CA GCTTTGTG		
			TC TTG GT CGAGACAC		
			A C TTA_		
GAM1645	LOC120526	3'	CAGGGCCATTGCACTGCT	74015	ACA T
			AGCA CA ATGGCTTTG		
			TCGT GT TACCGGGAC		
			CAC _		
GAM1645	LOC126669	3'	CACAAAGTTCCATATGT	75399	__
			ACATATGG CTTTGTG		
			TGTATACC GAAACAC		
			TT		
GAM1645	LOC139840	5'	CACAAGAGCCATGGGT	76266	A _
			AC TATGGCTTT GTG		
			TG GTACCGAGA CAC		
			G A		
GAM1645	LOC143465	5'	CACATGCACATATGTG	82962	_ TT
			CACATATG GC TGTG		
			GTGTATAC CG ACAC		
			A T_		
GAM1645	LOC146774	3'	CACTGACATGTGTGTGC	78094	A GCTTT
			GCA CACATATG GTG		
			CGT GTGTGTAC CAC		
			_ AGT__		
GAM1645	LOC147407	5'	CACAAAGCTATCATCCTGC	76322	ACACAT
			GCA ATGGCTTTGTG		
			CGT TATCGAAACAC		
			CCTAC_		
GAM1645	LOC151057	3'	ACAGAGCACATACTGT	85199	_ _
			ACA TATG GCTTTGT		

	TGT ATAC CGAGACA		
	C _ A		
GAM1645 LOC151473 3'	CACAACAACCTATGTGTT 80254	T CT_	
	AACACATA GG TTGTG		
	TTGTGTAT CC AACAC		
	_ AAC		
GAM1645 LOC154739 5'	CACAAAGTTCAAATGTATGC 86227	AC A _	
	GCA ACAT TGG CTTTGTG		
	CGT TGTA ACT GAAACAC		
	A_ A T		
GAM1645 LOC157507 5'	CACAGCTGTGTATGTGTGCT 81454	A _ _ T	
	AGCA CACATAT GGCT TG		
	TCGT GTGTATG TCGA AC		
	_ TG C		
GAM1645 LOC161734 3'	CACAAACATTTAGTGTGCT 87097	AT_ GC	
	AGCAACAC ATG TTTGTG		
	TCGTTGTG TAC AAACAC		
	ATT _		
GAM1645 LOC196410 3'	CACAAAAGTCATGGTG 87657	A _	
	CAC TATGGCTTT GTG		
	GTG GTACTGAAA CAC		
	_ A		
GAM1645 LOC196485 3'	CACAAAAACCTGTGTTGT 87730	TAT C_	
	GCAACACA GG TTTGTG		
	TGTTGTGT CC AAACAC		
	_ AA		
GAM1645 LOC196529 3'	CAGGGTCTCACTGTGTTGC 87771	TAT_	
	GCAACACA GGCTTTG		
	CGTTGTGT CTGGGAC		
	CACT		
GAM1645 LOC197003 5'	CACAAAGCTCCATGCTGT 87870	_ AT	
	ACA CAT GGCTTTGTG		
	TGT GTA TCGAAACAC		
	C CC		
GAM1645 LOC202025 5'	CACAGTTGTATGGTTGCT 90281	A TG T	
	AGCAAC CATA GCT TG		
	TCGTTG GTAT TGA AC		
	_ GT C		
GAM1645 LOC203276 3'	CACAAAGTTCAAGTGTATGC 90475	_ ATAT	
	GCA ACAC GGCTTTGTG		



CGT TGTG TTGAAACAC  
 A AAC\_  
 GAM1645 LOC203292 3' CAGGGTTTCATATGTGTT 90509 \_\_\_\_  
 AACACATATG GCTTTG  
 ||||| |||||  
 TTGTGTATAC TGGGAC  
 TT  
 GAM1645 LOC203305 3' CACAAAGTTCAAGTGTATGC 90519 \_ ATAT  
 GCA ACAC GGCTTTGTG  
 ||| ||| |||||  
 CGT TGTG TTGAAACAC  
 A AAC\_  
 GAM1645 LOC221354 3' CACAAAAACATGTGTTGT 92409 TA GC  
 GCAACACA TG TTTGTG  
 ||||| || |||||  
 TGTGTGT AC AAACAC  
 \_ AA  
 GAM1645 LOC254243 3' CACAAAGTTCAAGTGTATGC 97404 \_ ATAT  
 GCA ACAC GGCTTTGTG  
 ||| ||| |||||  
 CGT TGTG TTGAAACAC  
 A AAC\_  
 GAM1645 LOC255870 3' CACAACCTGGCCATGTCCTGC 94657 ACAC \_\_\_\_  
 GCA ATATGGCT TTGTG  
 ||| ||||| |||||  
 CGT TGTACCGG AACAC  
 CC\_ TC  
 GAM1645 LOC90038 3' CACAAAGTTCAAGTGTATGC 61148 \_ ATAT  
 GCA ACAC GGCTTTGTG  
 ||| ||| |||||  
 CGT TGTG TTGAAACAC  
 A AAC\_  
 GAM1645 LOC90321 3' CACAAATGGATTGTGTGTGC 62262 A TGGC\_  
 GCA CACATA TTTGTG  
 ||| ||||| |||||  
 CGT GTGTGT AAACAC  
 \_ TAGGT  
 GAM1645 LOC90750 3' CACAAAGTTAAGATTGCT 63917 CACATA  
 AGCAA TGGCTTTGTG  
 ||||| |||||  
 TCGTT ATTGAAACAC  
 AGA\_  
 GAM1645 LOC91069 3' GAAGCCATCGTGTCCT 64778 CA AT  
 AG ACAC ATGGCTTT  
 || ||| |||||  
 TC TGTG TACCGAAG  
 AC C\_  
 GAM1645 LOC92539 3' CACAAAGCCACTGTAGC 69630 A CATA  
 GC ACA TGGCTTTGTG  
 || ||| |||||

			CG TGT ACCGAAACAC		
			A C__		
GAM1646	CSNK1G2	3'	GGCCCAGCCCTGCAGGT 7170	AAC	ACTT
			ACCTGTAG CTG GGCC		
			TGGACGTC GAC CCGG		
			CC_ ____		
GAM1646	PCDH11X	3'	CAATCATATTCTACAG 27238	CC	C
			CTGTAGAA TGA TTG		
			GACATCTT ACT AAC		
			AT _		
GAM1646	SFTPA2	3'	GGTCAGGCTCTCCAGGTG 22650	T	A
			CACCTG AGA CCTGACT		
			GTGGAC TCT GGA CTGG		
			C C		
GAM1646	TBX5	5'	CCAAGTCCTATAGGTG 54888	AACCT	
			CACCTGTAG GACTTGG		
			GTGGATATC CTGAACC		
			_____		
GAM1646	TBX5	5'	CCAAGTCCTATAGGTG 3956	AACCT	
			CACCTGTAG GACTTGG		
			GTGGATATC CTGAACC		
			_____		
GAM1646	ZNF132	3'	GCCAAGTCAA ACTTCATGCAG 12826	_	CC_
			CTGTA GAA TGA CTTG GC		
			GACGT CTT ACTGAACCG		
			A CAA		
GAM1646	C9orf14	5'	GCCAAGTCCATCTAAAGTG 86676	CTG	ACCT
			CAC TAGA GACTTG GC		
			GTG ATCT CTGAACCG		
			AA_ AC_		
GAM1646	DKFZP434J037	3'	GCCCCGGTCAGGCTCTCAG 48213	T	A T
			CTG AGA CCTGACT GGC		
			GAC TCT GGA CTGG CCG		
			_ C C		
GAM1646	ELOVL2	3'	GCCTAGGTTATACAG 34959	G	ACTT
			CTGTA AACCTG GGC		
			GACAT TTGGAT CCG		
			A ____		
GAM1646	FLJ11996	3'	TTAGGTGCCTACAGGT 46447	A_	
			ACCTGTAG ACCTGA		

			TGGACATC TGGATT		
			CG		
GAM1646	FLJ13265	3'	GCCAGAACTTTACAGGTG	45926	ACCTGAC
			CACCTGTAGA TTGGC		
			GTGGACATTT GACCG		
			CAA__		
GAM1646	FLJ20038	5'	CCAAGTCAGAACTGCG	34402	AAC
			TGTAG CTGACTTGG		
			GCGTC GACTGAACC		
			AA_		
GAM1646	FLJ20972	3'	GCCAAGTCAGTTCCTGGTG	46725	TGTA C
			CACC GAAC TGACTTGGC		
			GTGG CTTG ACTGAACCG		
			TC__ _		
GAM1646	KIAA0061	3'	GCCAAGTTCTACATGTG	68292	C ACCTG
			CAC TGTAGA ACTTGGC		
			GTG ACATCT TGAACCG		
			T ____		
GAM1646	KIAA0141	3'	CGGGAGTTCAGGTTCCCAAG	28732	GTA _ GG
			CT GAACCTGA CTT CCG		
			GA CTTGGA CT GAG GGC		
			ACC T _		
GAM1646	KIAA1260	3'	GTCAGGTTGCACAGGTG	60029	AG
			CACCTGT AACCTGAC		
			GTGGACA TTGGA CTG		
			CG		
GAM1646	KIAA1301	3'	GCCTATGGGTTTACAGG	66342	A ACTT
			CCTGTAGA CCTG GGC		
			GGACATTT GGGT CCG		
			_ AT__		
GAM1646	KIAA1485	3'	GGCTGCCAGGCTCTGCAGG	89262	A ACT
			CCTGTAGA CCTG TGGCC		
			GGACGTCT GGAC GTCGG		
			C C__		
GAM1646	KIAA1546	3'	CAGGCAAACACCTACAGGT	67904	AACC_ A
			ACCTGTAG TG CTTG		
			TGGACATC AC GGAC		
			CACAA _		
GAM1646	KIAA1643	3'	CACCTCAGGTTCCCAGGTG	64548	TA CT
			CACCTG GAACCTGA TG		

			GTGGAC CTTGGACT AC		
			C_ CC		
GAM1646	MGC10981	3'	CTGAGTCGATCCCACAGGTG	51017	A_ ACC TG
			CACCTGT GA TGA CT G		
			GTGGACA CT GCTGA C		
			CC A__ GT		
GAM1646	MGC11324	3'	AGGCAGAACCTACAGGTG	51164	AAC A
			CACCTGTAG CTG CTT		
			GTGGACATC GAC GGA		
			CAA _		
GAM1646	MOST2	5'	CGGCCAAGCCTGTGCCTACGGT	39682	T A_ CTGA
	G		CACC GTAG AC CTTGGCCG		
			GTGG CATC TG GAACCGGC		
			_ CG TCC_		
GAM1646	PADI3	3'	CGGCCAAGCTCCTGC	32657	AACCT _
			GTAG GA CTTGGCCG		
			CGTC CT GAACCGGC		
			_____ C		
GAM1646	phospho1	5'	CAGAGTCCCTACAGGTG	82367	A_ _
			CACCTGTAG AC CTG		
			GTGGACATC TG GAC		
			CC A		
GAM1646	RAB3D	3'	TGGCTGCCAGGTTCTCAGG	15010	TA ACT
			CCTG GAACCTG TGGCCG		
			GGAC CTTGGAC GTCGGT		
			TC C_		
GAM1646	LOC122955	5'	GCTGTGTCAGTTCTACAG	75585	C TT
			CTGTAGAAC TGAC GGC		
			GACATCTTG ACTG TCG		
			_____		
GAM1646	LOC149386	5'	CAAGTCAGGTCCACA	84404	A A
			TGT GA CCTGACTTG		
			ACA CT GGA CTGAAC		
			C _		
GAM1646	LOC150197	5'	GCCAGGTCCTACGG	79598	AACCT
			CTGTAG GACTTGGC		
			GGCATC CTGGACCG		
			_____		
GAM1646	LOC151878	5'	CTAGTTCAGACTCTAAGG	80374	G AC C
			CCT TAGA CTGA TTGG		

GGA ATCT GACT GATC  
 \_ CA T  
 GAM1646 LOC153146 5' GCCAGAGCCTACAGGT 85929 AAC GAC  
 ACCTGTAG CT TTGGC  
 ||||| || ||||  
 TGGACATC GA GACCG  
 C\_ \_  
 GAM1646 LOC221931 3' AAGTTGCAGGTTCTTCAG 93992 T \_  
 CTG AGAACCTG ACTT  
 || ||||| |||  
 GAC TCTTGGAC TGAA  
 T GT  
 GAM1646 LOC254848 5' CGGCAGGCACAGGTTCTCCA 97090 T A\_ G  
 TG AGAACCTG CTTG CCG  
 || ||||| ||| |||  
 AC TCTTGGAC GGAC GGC  
 C AC \_  
 GAM1647 ADH1B 3' CTTAGACATAAAGTAAAAT 72644 C CAC  
 ATTT ACTTT TGTCTGAG  
 ||| |||| |||||  
 TAAA TGAAA ACAGATTC  
 A T\_  
 GAM1647 AHR 3' ATCTCAGATGTTAAATAAATG 7875 CAC C T  
 CATTT TTT AC GTCTGAGAT  
 |||| ||| || |||||  
 GTAAA AAA TG TAGACTCTA  
 TA\_ T \_  
 GAM1647 FDFT1 3' TAGGAAAGTGAAATG 15518 A  
 CATTTCACTTTC CTG  
 ||||| |||  
 GTAAAGTGAAAG GAT  
 \_  
 GAM1647 JTB 3' ATCTCAGACAGTGAAAGTGAAA 21959  
 TG CATTTCACTTTCACTGTCTGAGAT  
 ||||| ||||| |||||  
 GTAAAGTGAAAGTGACAGACTCTA  
 GAM1647 KLF4 3' TCCCAGACAGTGGATATG 14891 CT A  
 CA TTCACTGTCTG GA  
 || ||||| |||  
 GT AGGTGACAGAC CT  
 AT C  
 GAM1647 PHYH 3' ACAGTAAAAGTGAAAT 20608 C  
 ATTTCACTTT ACTGT  
 ||||| ||||  
 TAAAGTGAAA TGACA  
 A  
 GAM1647 PKD2 3' TCCAGGTTGAAAGTGAAA 60096 CTG A  
 TTTCACTTTCA TCTG GA  
 ||||| ||| ||

AAAGTGAAAGT GGAC CT  
 T\_\_ \_  
 GAM1647 WRN 3' GGGCAGTGAAAATGAAA 5098 C  
 TTTCA TTTCACTGTCT  
 ||||| |||||  
 AAAGT AAAGTGACGGG  
 A  
 GAM1647 ZNF216 3' ATCTGCACAGCAAAGTGAAA 20017 CA CTG  
 TTTCACTTT CTGT AGAT  
 ||||| ||| |||  
 AAAGTGAAA GACA TCTA  
 C\_ CG\_  
 GAM1647 CG012 5' CTCACCTCTGAAAGTGAA 83218 CT CT  
 TTCACCTTTCA GT GAG  
 ||||| || |||  
 AAGTGAAAGT CA CTC  
 CT \_  
 GAM1647 EIF2C2 3' ATCTTCTGAGAGTGAAAG 71946 G T\_  
 CTTTCACT TC GAGAT  
 ||||| || |||  
 GAAAGTGA AG TTCTA  
 G TC  
 GAM1647 FLJ23462 3' ATCTCAGACTTTACAAAGAAAT 45802 ACTTTCACT  
 G CATTTC GTCTGAGAT  
 ||||| |||||  
 GTAAAG CAGACTCTA  
 AAACATTT\_  
 GAM1647 FLJ23510 3' ATCTCAGACAGTGACTGAAATG 45281 CTT  
 CATTTC TCACTGTCTGAGAT  
 ||||| |||||  
 GTAAAGT AGTGACAGACTCTA  
 C\_  
 GAM1647 KIAA0984 3' TTTGTCCAGTGAAAATGAA 65534 C TC  
 TTCA TTTCACTG TGAG  
 ||| ||||| |||  
 AAGT AAAGTGAC GTTT  
 A CT  
 GAM1647 KLHL6 3' ATCTCAGAGCAGGAAA 55299 A \_  
 TTTC CTG TCTGAGAT  
 ||| ||| |||||  
 AAAG GAC AGACTCTA  
 \_ G  
 GAM1647 NIR3 3' GCAGTGAAAGTGCAAT 66242 T  
 ATT CACTTTCACTGT  
 ||| |||||  
 TAA GTGAAAGTGACG  
 C  
 GAM1647 PORIMIN 3' ATCTCAGAGGGCCAAAGTGAA 53598 CA G  
 TTCACCTTT CT TCTGAGAT  
 ||||| || |||||

			AAGTGAAA GG AGACTCTA		
			CC G		
GAM1647	PP35	3'	ATCTCAGACTGAAA 22814 CT		
			TTTCA GTCTGAGAT		
			AAAGT CAGACTCTA		
—					
GAM1647	PRTD-NY3	3'	CTCATTGCAATAAGTGAAATG 48148	TCAC	C_
			CATTTCACCTT TGT TGAG		
			GTAAAGTGAA ACG ACTC		
			TA__ TT		
GAM1647	SEP15	3'	TCCTACAGTAAGAGTGAAA 14934	C	CT
			TTTCACTTT ACTGT GA		
			AAAGTGAGA TGACA CT		
			A TC		
GAM1647	SFXN2	3'	CTCAGGGGAAAAAAGTGAAA 73941	CACTG	
			TTTCACTTT TCTGAG		
			AAAGTGAAA GGA CTC		
			AAAGG		
GAM1647	LOC149703	3'	ATCTCAGACAGCCGTTTGAAA 84647	ACTTTCA	
			TTTC CTGTCTGAGAT		
			AAAG GACAGACTCTA		
			GTTTGCC		
GAM1647	LOC154007	3'	ATCTCAAACCCTTTAGTGAAA 81015	TTCAC	C
			TTTCACT GT TGAGAT		
			AAAGTGA CA ACTCTA		
			TTTCC_ A		
GAM1647	LOC155004	3'	TCATTTAAGTGAAAAGGAAA 81226	A	GTC_
			TTTC CTTTCACT TGA		
			AAAG GAAAGTGA ACT		
			_ ATTT		
GAM1647	LOC222134	5'	ACAGTGAAGTGAAATG 94136	T	
			CATTTCACCTT CACTGT		
			GTAAAGTGAA GTGACA		
—					
GAM1648	ABR	3'	GTCTCCTGGCAGCCTC 6578	A	T
			GA GCTGCCAGGA GC		
			CT CGACGGTCCT TG		
			C C		
GAM1648	ABR	3'	GTCTCCTGGCAGCCTC 41730	A	T
			GA GCTGCCAGGA GC		

			CT CGACGGTCCT TG		
			C C		
GAM1648	ADCY8	5'	GCACCGGCGGCTTCT 6654	A A	
			AGAAGCTGCC GG TGC		
			TCTTCGGCGG CC ACG		
GAM1648	ATRN	3'	GTGTCCTGCAGCCTC 57802	A C	
			GA GCTGC AGGATGC		
			CT CGACG TCCTGTG		
			C _		
GAM1648	BAP1	3'	AGCGAGGTACTGCAGCTTC 16213	C GA__	
			GAAGCTGC AG TGCT		
			CTTCGACG TC GCGA		
			_ ATGGA		
GAM1648	BCL7B	3'	GCTGCTGGCAGCTTCT 8135	GAT	
			AGAAGCTGCCAG GC		
			TCTTCGACGGTC CG		
			GT_		
GAM1648	CDH5	3'	GCCCCATGGCAGCTCCT 8388	A _ AT	
			AG AGCTGCCA GG GC		
			TC TCGACGGT CC CG		
			C A C_		
GAM1648	COL18A1	3'	TGGGGTCTGGCAGCCTC 47579	A G G	
			GA GCTGCCAG AT CTA		
			CT CGACGGTC TG GGT		
			C _ G		
GAM1648	COL18A1	3'	TGGGGTCTGGCAGCCTC 55291	A G G	
			GA GCTGCCAG AT CTA		
			CT CGACGGTC TG GGT		
			C _ G		
GAM1648	COL18A1	3'	TGGGGTCTGGCAGCCTC 55295	A G G	
			GA GCTGCCAG AT CTA		
			CT CGACGGTC TG GGT		
			C _ G		
GAM1648	CREBL2	3'	ATAGTGAAATCCTGGCA 7142	__	
			TGCCAGGAT GCTAT		
			ACGGTCCTA TGATA		
			AAG		
GAM1648	CYLN2	3'	CACCCGGCAGCTTCT 12629	A A	
			AGAAGCTGCC GG TG		



TCTTCGACGG CC AC  
 C \_  
 GAM1648 DDX11 3' GCTTCCTGGCAGCTCT 47658 A T  
 AGA GCTGCCAGGA GC  
 ||| ||||| ||  
 TCT CGACGGTCCT CG  
 \_ T  
 GAM1648 ELAVL2 5' TATCCAGCAGCTTCT 15417 CA  
 AGAAGCTGC GGATG  
 ||||| ||||  
 TCTTCGACG CCTAT  
 A\_  
 GAM1648 FLNB 3' CATCCCTGGCAGCCCCT 62176 AA \_  
 AG GCTGCCAGG ATG  
 || ||||| |||  
 TC CGACGGTCC TAC  
 CC C  
 GAM1648 FOXO1A 3' ATAGCATCAAGTCTTCT 8902 CT CAG  
 AGAAG GC GATGCTAT  
 |||| || |||||  
 TCTTC TG CTACGATA  
 \_ AA\_  
 GAM1648 FUT4 3' TGTGGCCCGTGCAGCTTC 8963 CA AT  
 GAAGCTGC GG GCTATA  
 ||||| || |||||  
 CTTTCGACG CC CGGTGT  
 TG \_  
 GAM1648 GNA11 5' GCACCGGCCTGGGCAGCTTC 76100 \_ A\_  
 GAAGCTGCC AGG TGC  
 ||||| || |||  
 CTTTCGACGG TCC ACG  
 G GGCC  
 GAM1648 GRLF1 3' GTACAGCCCGGCTGGCGGCCTC 78563 A GAT\_ A  
 GA GCTGCCAG GCT TAC  
 || ||||| ||| |||  
 CT CGGCGGTC CGA ATG  
 C GGCC C  
 GAM1648 HK1 3' ATAGCATTAGCTGCTTC 3948 T CAG  
 GAAGC GC GATGCTAT  
 |||| || |||||  
 CTTTCG CG TTACGATA  
 T A\_  
 GAM1648 HK1 3' ATAGCATTAGCTGCTTC 53119 T CAG  
 GAAGC GC GATGCTAT  
 |||| || |||||  
 CTTTCG CG TTACGATA  
 T A\_  
 GAM1648 HK1 3' ATAGCATTAGCTGCTTC 53122 T CAG  
 GAAGC GC GATGCTAT  
 |||| || |||||

		CTTCG CG TTACGATA		
		T A__		
GAM1648 HK1	3'	ATAGCATTAGCTGCTTC 53126	T CAG	
		GAAGC GC GATGCTAT		
		CTTCG CG TTACGATA		
		T A__		
GAM1648 HK1	3'	ATAGCATTAGCTGCTTC 53131	T CAG	
		GAAGC GC GATGCTAT		
		CTTCG CG TTACGATA		
		T A__		
GAM1648 HMG20A	3'	GCATCACGCCTAGCAGTTTCT 36540	C ____	
		AGAAGCTGC AGG ATGC		
		TCTTTGACG TCC TACG		
		A GCAC		
GAM1648 IKBKB	3'	GTACAGCCATGGCAGCTCCT 63211	A GGAT A	
		AG AGCTGCCA GCT TAC		
		TC TCGACGGT CGA ATG		
		C AC__ C		
GAM1648 INPP5B	3'	GCATATTTGGCAGCTT 95526	_	
		AAGCTGCCAGG ATGC		
		TTCGACGGTTT TACG		
		A		
GAM1648 JPH2	3'	GCTGTCTTGGCAGCTTCT 94449	_	
		AGAAGCTGCCAGGAT GC		
		TCTTCGACGGTTCTG CG		
		T		
GAM1648 KCNJ5	3'	GTGGCATCAGCAGCTTC 6097	CAG	
		GAAGCTGC GATGCTAT		
		CTTCGACG CTACGGTG		
		A__		
GAM1648 KCNS2	3'	CATCTAACCAGCAGTTTCT 68301	CA__	
		AGAAGCTGC GGATG		
		TCTTTGACG TCTAC		
		ACCAA		
GAM1648 LARS	3'	GTACCTAACAGCTTTT 39221	CC A	
		AGAAGCTG AGG TGC		
		TTTTCGAC TCC ATG		
		AA _		
GAM1648 LHX5	3'	GCACTCAACTGGCAGCTGCT 42304	A _ _	
		AG AGCTGCCAG GA TGC		

			TC TCGACGGTC CT ACG		
			G AA C		
GAM1648	MAP3K7	3'	GCATAACATGGTAGCATCT 12099	A	GG__
			AGA GCTGCCA ATGC		
			TCT CGATGGT TACG		
			A ACAA		
GAM1648	MBD3	3'	AGTGGGCTGGCAGCTTC 14092		GA
			GAAGCTGCCAG TGCT		
			CTTCGACGGTC GTGA		
			GG		
GAM1648	MFI2	3'	GCACCTGGCAGCTTTT 52815	A	
			AGAAGCTGCCAGG TGC		
			TTTCGACGGTCC ACG		
			—		
GAM1648	MGEA5	3'	TATAGTATTGCAGC 24219	CAG	
			GCTGC GATGCTATA		
			CGACG TTATGATAT		
			—		
GAM1648	MMP15	3'	GCGGGTCCGGCAGCTTCT 10075	A	__
			AGAAGCTGCC GGAT GC		
			TCTTCGACGG CCTG CG		
			— GG		
GAM1648	OPA1	3'	GTGGCCCTTGCAGCTTC 55533	C	AT
			GAAGCTGC AGG GCTAT		
			CTTCGACG TCC CGGTG		
			T —		
GAM1648	OPA1	3'	GTGGCCCTTGCAGCTTC 55542	C	AT
			GAAGCTGC AGG GCTAT		
			CTTCGACG TCC CGGTG		
			T —		
GAM1648	OPA1	3'	GTGGCCCTTGCAGCTTC 55551	C	AT
			GAAGCTGC AGG GCTAT		
			CTTCGACG TCC CGGTG		
			T —		
GAM1648	OPA1	3'	GTGGCCCTTGCAGCTTC 55560	C	AT
			GAAGCTGC AGG GCTAT		
			CTTCGACG TCC CGGTG		
			T —		
GAM1648	OPA1	3'	GTGGCCCTTGCAGCTTC 55569	C	AT
			GAAGCTGC AGG GCTAT		

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CTTCGACG TCC CGGTG
T _
GAM1648 PCDHB4 3' GTTTTCCTACAGCTTCT 38437 CC T_
AGAAGCTG AGGA GC
||||| ||| ||
TCTTCGAC TCCT TG
A_ TT
GAM1648 PRX 3' GTAGGCCTGGCGGCCCT 40538 AA A_
AG GCTGCCAGG TGC
|| ||||| |||
TC CGCGGTCC ATG
CC GG
GAM1648 PSMD9 3' GTGTCCTGTCAGCTTC 10989 C
GAAGCTG CAGGATGC
||||| |||||
CTTCGAC GTCCTGTG
T
GAM1648 PSPHL 3' TATAGATTCGGCAGCCTTC 92909 _ A G
GAAG CTGCC GGAT CTATA
||| |||| ||| ||||
CTTC GACGG CTTA GATAT
C _ _
GAM1648 RECQL5 3' CAGCCTGGCATCTTCT 14925 C A
AGAAG TGCCAGG TG
||||| ||||| ||
TCTTC ACGGTCC AC
T G
GAM1648 RPL10 3' GTGTCCTGCAGCCCCT 20030 AA C
AG GCTGC AGGATGC
|| ||||| |||||
TC CGACG TCCTGTG
CC _
GAM1648 SHANK2 3' AGCATCCTCAGTTCT 24584 G CC
AGAA CTG AGGATGCT
||| ||| |||||
TCTT GAC TCCTACGA
_ _
GAM1648 SPAG8 3' CATCCTGGCACTCCT 24899 A C
AG AG TGCCAGGATG
|| || |||||
TC TC ACGGTCCTAC
C _
GAM1648 SPON1 5' GCCAGCCTGGCAGCCTCT 62452 A AT_
AGA GCTGCCAGG GC
||| ||||| ||
TCT CGACGGTCC CG
C GAC
GAM1648 TAF1C 3' AGCGGCCGTTGGCAGCTGCT 19057 A _ A
AG AGCTGCCA GG TGCT
|| ||||| || |||

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		TC TCGACGGT CC GCGA	
		G TG G	
GAM1648	TBCD	3' GCACTAGCTGACAGCTTTT 19992	C GA__
		AGAAGCTG CAG TGC	
		TTTTCGAC GTC ACG	
		A GATC	
GAM1648	TTC3	3' GCCTTCCTTAGCAGCTTCT 12419	C_ T_
		AGAAGCTGC AGGA GC	
		TCTTCGACG TCCT CG	
		AT TC	
GAM1648	UBE4A	3' AGCTATTCCCAGCAGCTTC 16555	CA T__
		GAAGCTGC GGA GCT	
		CTTCGACG CCT CGA	
		AC TAT	
GAM1648	WNT5A	5' GCCTCCTTGGCAGCCTCT 12668	A _ T
		AGA GCTGCCA GGA GC	
		TCT CGACGGT CCT CG	
		C T C	
GAM1648	XKRY	5' AGCAAAATCTGGCAGCT 16253	A__
		AGCTGCCAGG TGCT	
		TCGACGGTCT ACGA	
		AAA	
GAM1648	XKRY	5' AGCAAAATCTGGCAGCT 60014	A__
		AGCTGCCAGG TGCT	
		TCGACGGTCT ACGA	
		AAA	
GAM1648	ADPRTL3	3' GTATAAGGGCAGCTTTT 18503	AGG
		AGAAGCTGCC ATGC	
		TTTTCGACGG TATG	
		GAA	
GAM1648	AKAP6	3' GTATAGCATGTAGCAGCTTC 14993	CAGG
		GAAGCTGC ATGCTATAC	
		CTTCGACG TACGATATG	
		ATG_	
GAM1648	BRPF3	3' TATGGCCGGCAGCTTC 92324	AGGAT
		GAAGCTGCC GCTATA	
		CTTCGACGG CGGTAT	
		C_____	
GAM1648	C11orf11	3' GCTGTCCTGGGAGCCCCT 93254	AA G _
		AG GCT CCAGGAT GC	

			TC CGA GGTCTG CG		
			CC G T		
GAM1648	C16orf44	3'	GTACAACTTAGCAGCTTTT 45317	C A C	
			AGAAGCTGC AGG TG TAT		
			TTTTCGACG TTC AC ATG		
			A A _		
GAM1648	CASP9	3'	GGCTCTTAGCAGCTTC 6926	C T	
			GAAGCTGC AGGA GCT		
			CTTCGACG TTCT CGG		
			A _		
GAM1648	CBX6	3'	GTGTCCTGGGCAGCTTCT 26625	_	
			AGAAGCTGCC AGGATGC		
			TCTTCGACGG TCCTGTG		
			G		
GAM1648	CGI-96	3'	ATGGCCTGCAGCTTC 31659	C GAT	
			GAAGCTGC AG GCTAT		
			CTTCGACG TC CGGTA		
			_ _ _		
GAM1648	DKFZP564O0423	3'	ATAACATCCTGGGCTC 91679	A TG C	
			GA GC CCAGGATG TAT		
			CT CG GGTCTAC ATA		
			_ _ _ A		
GAM1648	DKFZP564P1916	5'	AGTAGATGTGCAGCTTC 31607	_ GGA	
			GAAGCTGC CA TGCT		
			CTTCGACG GT ATGA		
			T AG_		
GAM1648	DKFZp566D234	3'	TATAGCATCCTGAGCTGT 61865	T _	
			GC GC CAGGATGCTATA		
			TG CG GTCCTACGATAT		
			T A		
GAM1648	DKFZP761E1824	3'	GGTGTCTTCTGGCAGCTTCT 66440		
			AGAAGCTGCCAGGATGCT		
			TCTTCGACGGTCTTGTGG		
GAM1648	EFS2	5'	GCCCCGGCGGCTTCT 19621	A AT	
			AGAAGCTGCC GG GC		
			TCTTCGGCGG CC CG		
			C _		
GAM1648	FLJ10579	3'	GTGTCCTGGCAGCTTTT 36303		
			AGAAGCTGCCAGGATGC		

TTTTCGACGGTCCTGTG

GAM1648 FLJ10724 3' GTATAACATGGTAGTTCCT 36504 A GG\_\_  
AG AGCTGCCA ATGC  
|| ||||| |||  
TC TTGATGGT TATG  
C ACAA

GAM1648 FLJ10898 5' GCACTTTGCCAGCAGCTTCT 59434 \_\_ GA  
AGAAGCTGC CAG TGC  
||||||| ||| |||  
TCTTCGACG GTT ACG  
ACC TC

GAM1648 FLJ10979 3' GCATTTGCCTGGCAGCTTTT 36935 \_\_  
AGAAGCTGCCAGG ATGC  
||||||| |||  
TTTTCGACGGTCC TACG  
GTT

GAM1648 FLJ11151 3' GCATCTTCTCAGCAGCTTCT 67877 C\_\_  
AGAAGCTGC AGGATGC  
||||||| |||||  
TCTTCGACG TTCTACG  
ACTC

GAM1648 FLJ11850 3' ATAGTTCCTGGCACCT 42717 C T  
AG TGCCAGGA GCTAT  
|| ||||| |||||  
TC ACGGTCCT TGATA  
C \_

GAM1648 FLJ12150 3' GCATGGCCTGGCAGCTCT 45350 A \_\_  
AGA GCTGCCAGG ATGC  
||| ||||| |||  
TCT CGACGGTCC TACG  
\_ GG

GAM1648 FLJ14346 3' ATAGTGTGGCAGTCTCT 46707 AG GGA  
AGA CTGCCA TGCTAT  
||| ||||| |||||  
TCT GACGGT GTGATA  
CT \_

GAM1648 FLJ14708 5' AGCCCGGCGGCTTC 51539 A AT  
GAAGCTGCC GG GCT  
||||||| || |||  
CTTCGGCGG CC CGA

GAM1648 FLJ20294 3' GCTCCTGGCAGCTTT 34877 T  
GAAGCTGCCAGGA GC  
||||||| |||  
TTTCGACGGTCCT CG

GAM1648 FLJ21616 3' GTATAACTTGCAGTTTCT 44690 C G\_  
AGAAGCTGC AG ATGC  
||||||| || |||

			TCTTTGACG TC TATG		
			T AA		
GAM1648	FLJ21918	3'	CAACCTGGTAGCTTCT 46287	A	
			AGAAGCTGCCAGG TG		
			TCTTCGATGGTCC AC		
			A		
GAM1648	FLJ31168	3'	ATGGCCTTGGCAGCCTC 58500	A	AT
			GA GCTGCCAGG GCTAT		
			CT CGACGGTTC CGGTA		
			C _		
GAM1648	HMT-1	3'	GTCCTTCCCGCAGCTTCT 38901	C_	
			AGAAGCTGC AGGAT		
			TCTTCGACG TCCTG		
			CCCT		
GAM1648	HSPF2	5'	AGCCCTGTCAGCTCCT 18640	A	C AT
			AG AGCTG CAGG GCT		
			TC TCGAC GTCC CGA		
			C T _		
GAM1648	INSM2	3'	GGCGCCTATACAGCTTCT 50868	CC_	A
			AGAAGCTG AGG TGCT		
			TCTTCGAC TCC GCGG		
			ATA _		
GAM1648	KCNT1	3'	CATCCTGGCCGCCTCT 61828	A	T
			AGA GC GCCAGGATG		
			TCT CG CGGTCCTAC		
			C C		
GAM1648	KIAA0077	3'	GCATTCCACAGCTTCT 67019	CCA	
			AGAAGCTG GGATGC		
			TCTTCGAC CTTACG		
			AC_		
GAM1648	KIAA0140	3'	GGCCCCGCAGCTTCT 27814	CA	AT
			AGAAGCTGC GG GCT		
			TCTTCGACG CC CGG		
			_ C_		
GAM1648	KIAA0252	3'	TACAGCCCACAGCTTCT 62798	CCA	AT A
			AGAAGCTG GG GCT TA		
			TCTTCGAC CC CGA AT		
			A_ _ C		
GAM1648	KIAA0469	3'	GCAGCTTGGCAGCCCCT 29332	AA	A
			AG GCTGCCAGG TGC		



			TC CGACGGTTC ACG		
			CC G		
GAM1648	KIAA0774	5'	CATCCAGCAGCTTTT 91750	CA	
			AGAAGCTGC GGATG		
			TTTTCGACG CCTAC		
			A_		
GAM1648	KIAA0774	5'	GCTGTCCCGGCAGCTTT 91753	A _	
			GAAGCTGCC GGAT GC		
			TTTCGACGG CCTG CG		
			C T		
GAM1648	KIAA0830	3'	AGCATCCAAACGGCTTCT 69692	CCA	
			AGAAGCTG GGATGCT		
			TCTTCGGC CCTACGA		
			AAA		
GAM1648	KIAA0889	3'	CAACCTCAGCAGCTTCT 31130	C_ A	
			AGAAGCTGC AGG TG		
			TCTTCGACG TCC AC		
			AC A		
GAM1648	KIAA0934	3'	GCCCTGGCAGCTCCT 64221	A AT	
			AG AGCTGCCAGG GC		
			TC TCGACGGTCC CG		
			C _		
GAM1648	KIAA1190	3'	GTACAGTGCCAGCAGCTTC 71104	CA A A	
			GAAGCTGC GG TGCT TAC		
			CTTCGACG CC GTGA ATG		
			A_ _ C		
GAM1648	KIAA1404	3'	GCATGCCAGCAGCTTCT 61989	CA _	
			AGAAGCTGC GG ATGC		
			TCTTCGACG CC TACG		
			A_ G		
GAM1648	KIAA1514	3'	GCCCTGTCTTGGCAACCTCT 38818	AGC _	
			AGA TGCCAGGAT GC		
			TCT ACGGTTCTG CG		
			CCA TCC		
GAM1648	KIAA1613	3'	ATATCAGACTGCAGCTCCT 64812	A C GA C	
			AG AGCTGC AG TG TAT		
			TC TCGACG TC AC ATA		
			C _ AG T		
GAM1648	KIAA1775	3'	AGCATCCTTACAGCTT 52373	CC	
			AAGCTG AGGATGCT		

			TTCGAC TCCTACGA		
			AT		
GAM1648	KIAA1789	5'	CATGACTGGCAGCTCT	67101	A G_
			AGA GCTGCCAG ATG		
			TCT CGACGGTC TAC		
			_ AG		
GAM1648	L3MBTL	3'	GGTAAAACCAGCAGTTTC	69530	CA A__
			GAAGCTGC GG TGCT		
			CTTTGACG CC ATGG		
			A_ AAA		
GAM1648	MAGE-E1	3'	AGCACCTAGGCGGCTTCT	47942	_ A
			AGAAGCTGCC AGG TGCT		
			TCTTCGGCGG TCC ACGA		
			A C		
GAM1648	MAGEA1	3'	GCGTCCAGCAGCTTC	17160	CA
			GAAGCTGC GGATGC		
			CTTCGACG CCTGCG		
			A_		
GAM1648	MAP2K1IP1	5'	GCGCCCTCGCAGCTTC	41744	C A
			GAAGCTGC AGG TGC		
			CTTCGACG TCC GCG		
			C C		
GAM1648	MDS033	3'	GCCTGTCCTGGGAGCCCCT	37469	AA G _
			AG GCT CCAGGAT GC		
			TC CGA GGTCTCTG CG		
			CC G TC		
GAM1648	MGC12466	5'	GTCCCGCGGCAGCTTCT	52630	A__
			AGAAGCTGCC GGAT		
			TCTTCGACGG CCTG		
			CGC		
GAM1648	MGC12760	3'	ATAACATCCTGGAATAGCT	51173	_ C
			AGCTG CCAGGATG TAT		
			TCGAT GGTCCTAC ATA		
			AA A		
GAM1648	MGC2477	5'	TGGGTCCTGGCCGCCTC	44073	A T G
			GA GC GCCAGGAT CTA		
			CT CG CGGTCCTG GGT		
			C C _		
GAM1648	MGC3222	3'	GCAAGCTGACAGCTTCT	44297	C GA
			AGAAGCTG CAG TGC		

			TCTTCGAC GTC ACG		
			A GA		
GAM1648	MGC5139	5'	GCTCTGACAGCTTCT 74108	C	AT
			AGAAGCTG CAGG GC		
			TCTTCGAC GTCT CG		
			A _		
GAM1648	MRPS6	3'	GCTCACTGACAGCTTCT 50646	C	_ T
			AGAAGCTG CAG GA GC		
			TCTTCGAC GTC CT CG		
			A A _		
GAM1648	N4BP3	3'	GTGCCTGGCAGCCCT 66271	AA	A
			AG GCTGCCAGG TGC		
			TC CGACGGTCC GTG		
			CC _		
GAM1648	NAG73	3'	GCACATGCAGTAGCTTCT 50806	_	GGA
			AGAAGCTGC CA TGC		
			TCTTCGATG GT ACG		
			AC AC_		
GAM1648	NUDE1	3'	GCAAAGTCCTGCAGCTTCT 34568	C	_
			AGAAGCTGC AGGA TGC		
			TCTTCGACG TCCT ACG		
			_ GAA		
GAM1648	OAZ2	3'	GTATAGTACTAGCTGCCTC 10310	A T C	GA
			GA GC GC AG TGCTATAC		
			CT CG CG TC ATGATATG		
			C T A _		
GAM1648	phorbolin-1	5'	GTATCGCTGACTCAGCAGCTTC 88782	_	_
			GAAGCTGC CAG GATGC		
			CTTCGACG GTC CTATG		
			ACTCA G		
GAM1648	PL6	3'	GTACATCAGCTGGCAGC 22832	_	C
			GCTGCCAG GATG TAT		
			CGACGGTC CTAC ATG		
			GA _		
GAM1648	PRO1483	3'	GGCTGCTGACAGCTTCT 37722	C	GAT
			AGAAGCTG CAG GCT		
			TCTTCGAC GTC CGG		
			A GT_		
GAM1648	PTP4A1	3'	GTATAGTAGAGGACAGC 12941	_	AGGA
			GCTG CC TGCTATAC		

			CGAC GG ATGATATG		
			A AG__		
GAM1648	RAB17	3'	CAGCCTGGCAGCCTCT 42389	A	A
			AGA GCTGCCAGG TG		
			TCT CGACGGTCC AC		
			C G		
GAM1648	RAB40C	3'	GTTCTCGGCAGCTTCT 40983		_
			AGAAGCTGCC AGGAT		
			TCTTCGACGG TCTTG		
			C		
GAM1648	SFXN2	3'	AGCCCGGACAGCTTCT 73939	_	A AT
			AGAAGCTG CC GG GCT		
			TCTTCGAC GG CC CGA		
			A _ _		
GAM1648	SIAT8C	5'	GCAGCCTGGCAGCCTC 31882	A	A
			GA GCTGCCAGG TGC		
			CT CGACGGTCC ACG		
			C G		
GAM1648	SLC12A5	3'	CATCTGGCAGCTCCT 40379	A	G
			AG AGCTGCCAG ATG		
			TC TCGACGGTC TAC		
			C _		
GAM1648	SLC38A1	3'	GGCCCAGCAGCTTTT 47724		CA AT
			AGAAGCTGC GG GCT		
			TTTTCGACG CC CGG		
			A_ _		
GAM1648	SNRK	3'	GTACTTCTGGCAATTCT 34767	GC	_
			AGAA TGCCAGGA TGC		
			TCTT ACGGTCTT ATG		
			A_ C		
GAM1648	SV2	3'	GCCCTCCTGGCAGCTCCT 29309	A	T_
			AG AGCTGCCAGGA GC		
			TC TCGACGGTCCT CG		
			C CC		
GAM1648	TAS1R1	3'	GCACGGCTGGCAGCCTTC 56920	_	GA_
			GAAG CTGCCAG TGC		
			CTTC GACGGTC ACG		
			C GGC		
GAM1648	UBE2V2	3'	GCATTCTGGCAGTTCT 12525	G	
			AGAA CTGCCAGGATGC		

TCTT GACGGTCTTACG

GAM1648 USP15 3' GCATAAATACTGCGGCAGCATT 20883 \_ A\_ \_\_\_\_\_  
CT AGAA GCTGCC GG ATGC

||||| || ||||  
TCTT CGACGG TC TACG

A CG ATAAA

GAM1648 YKT6 3' CATCCTAAGCAGCTTC 21600 C\_

GAAGCTGC AGGATG

||||| |||||  
CTTCGACG TCCTAC

AA

GAM1648 LOC113523 3' AGATCATGATCAGCTTCT 73040 C\_ G G

AGAAGCTG CA GAT CT

||||| || ||| ||  
TCTTCGAC GT CTA GA

TA A \_

GAM1648 LOC115939 3' ATGGGCCTGGCAGCCTC 73662 A ATG

GA GCTGCCAGG CTAT

|| ||||| ||||  
CT CGACGGTCC GGTA

C G\_

GAM1648 LOC120224 5' AGCATCCTGAACACTTT 57092 C C\_

GAAG TG CAGGATGCT

|||| || ||||| ||||  
TTTC AC GTCCTACGA

\_ AA

GAM1648 LOC120526 3' GTAGACTAGCAGCTTTT 74016 C GA

AGAAGCTGC AG TGC

||||| || |||  
TTTTCGACG TC ATG

A AG

GAM1648 LOC122622 3' GGCCCTGGCAGCGTCT 74136 A AT

AGA GCTGCCAGG GCT

|| ||||| ||||  
TCT CGACGGTCC CGG

G \_

GAM1648 LOC122970 5' AGCCACCGGCAGCTTC 74175 A AT

GAAGCTGCC GG GCT

||||| || |||  
CTTCGACGG CC CGA

\_ AC

GAM1648 LOC125268 3' AGGTGCTGGCAGCTCCT 76068 A G G

AG AGCTGCCAG AT CT

|| ||||| || ||  
TC TCGACGGTC TG GA

C G \_

GAM1648 LOC128936 3' GCACCTTGACAGCTTCT 75789 C A

AGAAGCTGC AGG TGC

||||| ||| |||

TCTTCGACG TCC ACG  
 T \_  
 GAM1648 LOC131870 3' GCACCCTGGCAGGTTCT 75020 G A  
 AGAA CTGCCAGG TGC  
 ||| ||||| |||  
 TCTT GACGGTCC ACG  
 G C  
 GAM1648 LOC143392 3' GCATCAGGACAACAGCCTCT 82951 A \_\_\_\_ AG  
 AGA GCTG CC GATGC  
 ||| ||| || |||||  
 TCT CGAC GG CTACG  
 C AACAA A\_  
 GAM1648 LOC144278 3' AGCACCCCGCTGGCGTTCT 76767 \_ \_ CA A  
 AGAA GCT GC GG TGCT  
 ||| ||| || |||||  
 TCTT CGG CG CC ACGA  
 G T CC \_  
 GAM1648 LOC144473 5' GTATCCTGCCAACTTC 83074 C C  
 GAAG TG CAGGATGC  
 ||| || |||||  
 CTTC AC GTCCTATG  
 A C  
 GAM1648 LOC144501 3' GCTCCCAGCAGCTTCT 83109 CA T  
 AGAAGCTGC GGA GC  
 ||||| ||| ||  
 TCTTCGACG CCT CG  
 AC \_  
 GAM1648 LOC145501 3' GCACCAGGGCCGCAGCTTC 77255 \_\_\_\_ A\_ A  
 GAAGCT GCC GG TGC  
 ||||| ||| |||||  
 CTTCGA CGG CC ACG  
 CGC GA \_  
 GAM1648 LOC146515 3' ATAGTCATGGCAGCTCCT 77962 A GGAT  
 AG AGCTGCCA GCTAT  
 || ||||| |||||  
 TC TCGACGGT TGATA  
 C AC\_  
 GAM1648 LOC146562 3' GCAGCCTGGCGGCCTC 57533 A A  
 GA GCTGCCAGG TGC  
 || ||||| |||  
 CT CGGCGGTCC ACG  
 C G  
 GAM1648 LOC146802 3' GTCTTCCTGGCAACTGCT 78137 A C T\_  
 AG AG TGCCAGGA GC  
 || || ||||| ||  
 TC TC ACGGTCCT TG  
 G A TC  
 GAM1648 LOC147136 5' GCAGGCCTGGCAGCTCT 78264 A A\_  
 AGA GCTGCCAGG TGC  
 ||| ||||| |||

	TCT CGACGGTCC ACG	
	— GG	
GAM1648 LOC148166 5'	GCCCAGCTGGCAGCTTCT 78693	AT__
	AGAAGCTGCCAGG GC	
	TCTTCGACGGTCC CG	
	GACC	
GAM1648 LOC148426 5'	AGGGTCCTGGTAGCTTC 84148	G
	GAAGCTGCCAGGAT CT	
	CTTCGATGGTCCTG GA	
	G	
GAM1648 LOC148529 5'	AGCAAATGGCCAGCTTCT 84165	_ GGA
	AGAAGCTG CCA TGCT	
	TCTTCGAC GGT ACGA	
	C AA_	
GAM1648 LOC148710 5'	GCATCCCAGTAGCTTC 84196	CA
	GAAGCTGC GGATGC	
	CTTCGATG CCTACG	
	AC	
GAM1648 LOC149182 3'	GTACCTGGCAGCTTCT 84377	A
	AGAAGCTGCCAGG TGC	
	TCTTCGACGGTCC ATG	
	—	
GAM1648 LOC149194 3'	ATGGCCCTGATAGCTTCT 79223	C AT
	AGAAGCTG CAGG GCTAT	
	TCTTCGAT GTCC CGGTA	
	A _	
GAM1648 LOC149372 5'	ATAGCATCCCAGCTCCT 79319	A CCA
	AG AGCTG GGATGCTAT	
	TC TCGAC CCTACGATA	
	C _	
GAM1648 LOC149722 5'	GCACACTGCACGCAGCTTC 84601	_ GA
	GAAGCTGC CAG TGC	
	CTTCGACG GTC ACG	
	CAC AC	
GAM1648 LOC153077 3'	TATAGCATCTCTGCTTT 85915	TGCCA
	GAAGC GGATGCTATA	
	TTTCG TCTACGATAT	
	TC__	
GAM1648 LOC157285 3'	GCTCCTGCAGCTTCT 86437	C T
	AGAAGCTGC AGGA GC	

TCTTCGACG TCCT CG

GAM1648 LOC157708 3' CGTGTGGCGCTTCT 81559 T G  
AGAAGC GCCAG ATG  
||||| ||||| ||  
TCTTCG CGGTT TGC

GAM1648 LOC158061 5' TGGACCCTGAGCAGCTTCT 81672 \_ ATG  
AGAAGCTGC CAGG CTA  
||||||| ||||| ||  
TCTTCGACG GTCC GGT

GAM1648 LOC158402 5' TAGTCTGGCAGCCTC 86811 A GAT  
GA GCTGCCAG GCTA  
|| ||||| |||||  
CT CGACGGTC TGAT  
C \_

GAM1648 LOC168512 5' AGCCTCTCTGGCAGCTTTT 82713 \_ T  
AGAAGCTGCCAG GA GCT  
||||||| || |||||  
TTTTCGACGGTC CT CGA  
T C

GAM1648 LOC170394 5' GCTGTCCTGGAGCTTC 82853 G \_  
GAAGCT CCAGGAT GC  
||||| ||||| ||  
CTTCGA GGTCTG CG  
\_ T

GAM1648 LOC196485 5' AGCACCCGACTCCCAGTTTCT 87729 CCA\_\_ A  
AGAAGCTG GG TGCT  
||||||| || |||||  
TCTTTGAC CC ACGA  
CCTCAG C

GAM1648 LOC196955 5' GCTCCTGGCAGCTGCT 77383 A T  
AG AGCTGCCAGGA GC  
|| ||||| ||||| ||  
TC TCGACGGTCCT CG  
G \_

GAM1648 LOC197423 5' GCACAGTCTGCAGCTTC 77860 C A\_\_  
GAAGCTGC AGG TGC  
||||||| ||||| |||||  
CTTCGACG TCT ACG  
\_ GAC

GAM1648 LOC200205 3' AGCACTGGCAGCTTC 88624 GA  
GAAGCTGCCAG TGCT  
||||||| ||||| |||||  
CTTCGACGGTC ACGA

GAM1648 LOC200268 3' AGTGAGCCGGTAGCTTC 88675 A AT\_  
GAAGCTGCC GG GCT  
||||||| || |||||



CTTCGATGG CC TGA  
\_ GAG  
GAM1648 LOC202025 3' GCATCCTAACTGGCAGCTACT 90290 A \_\_\_\_  
AG AGCTGCCA GGATGC  
|| ||||| |||||  
TC TCGACGGT CCTACG  
A CAAT  
GAM1648 LOC203054 5' CATCCTGGCAACGTTCT 89253 GC\_  
AGAA TGCCAGGATG  
|||| |||||  
TCTT ACGGTCCTAC  
GCA  
GAM1648 LOC205418 5' AGCCCCTGGCAGCCCCT 90679 AA AT  
AG GCTGCCAGG GCT  
|| ||||| |||  
TC CGACGGTCC CGA  
CC C\_  
GAM1648 LOC221037 3' GTATAGCATATGTCACAGCT 93157 C\_\_ GG  
AGCTG CA ATGCTATAC  
|||| || |||||  
TCGAC GT TACGATATG  
ACT A\_  
GAM1648 LOC221300 3' TATAGCATAGAGTTTC 91928 GCCAGG  
GAAGCT ATGCTATA  
|||| |||||  
CTTTGA TACGATAT  
GA\_\_\_\_  
GAM1648 LOC221424 3' GCTCTGGCAGCTCCT 93628 A AT  
AG AGCTGCCAGG GC  
|| ||||| ||  
TC TCGACGGTCT CG  
C \_  
GAM1648 LOC221495 3' GCCCTCCTGCAGCTCCT 93859 A C T\_  
AG AGCTGC AGGA GC  
|| ||||| ||| ||  
TC TCGACG TCCT CG  
C \_ CC  
GAM1648 LOC222031 3' TATAGCATCCACCTGCCTCT 94030 A TGCCA  
AGA GC GGATGCTATA  
||| || |||||  
TCT CG CCTACGATAT  
C TCCA\_  
GAM1648 LOC222057 3' GCAGCTGGCAGCCTCT 92776 A GA  
AGA GCTGCCAG TGC  
||| ||||| |||  
TCT CGACGGTC ACG  
C G\_  
GAM1648 LOC222057 3' GCCTCCTGGCAGCCTCT 92779 A T  
AGA GCTGCCAGGA GC  
||| ||||| |||

		TCT CGACGGTCCT CG		
		C C		
GAM1648	LOC222068 3'	GTA	ACTCCCATGGCAGCTCCT 92711	A _ _
		AG AGCTGCCA GGA TGC		
		TC TCGACGGT CCT ATG		
		C AC CA		
GAM1648	LOC222484 5'	TGTCCTGGAGCTTCT	94342	G
		AGAAGCT CCAGGATG		
		TCTTCGA GGTCCTGT		
		—		
GAM1648	LOC222550 3'	CATCACTGGCAGCTCCT	94352	A _
		AG AGCTGCCAG GATG		
		TC TCGACGGTC CTAC		
		C A		
GAM1648	LOC223009 5'	GCATCTTGGCAGCCTCT	94377	A
		AGA GCTGCCAGGATGC		
		TCT CGACGGTTCTACG		
		C		
GAM1648	LOC223009 5'	GCTTCTTGGCAGCCTCT	94379	A T
		AGA GCTGCCAGGA GC		
		TCT CGACGGTTCT CG		
		C T		
GAM1648	LOC245803 3'	GTATCTGCAGCTTC	91671	CA
		GAAGCTGC GGATGC		
		CTTCGACG TCTATG		
		—		
GAM1648	LOC254557 5'	TGTCCTGGCAACTACT	96239	A C
		AG AG TGCCAGGATG		
		TC TC ACGGTCCTGT		
		A A		
GAM1648	LOC255000 3'	AGCGGGTGGCAGCTTCT	96829	GGA
		AGAAGCTGCCA TGCT		
		TCTTCGACGGT GCGA		
		GG_		
GAM1648	LOC255326 3'	ATAGCATGTTAGTTTCT	96372	CCA G
		AGAAGCTG G ATGCTAT		
		TCTTTGAT T TACGATA		
		_ G		
GAM1648	LOC255759 5'	GCACCTGGCAGGCTCT	97480	AG A
		AGA CTGCCAGG TGC		

			TCT GACGGTCC ACG			
			CG _			
GAM1648	LOC255975	5'	GCCTCCTGGCAGCCTCT	95895	A	T
			AGA GCTGCCAGGA GC			
			TCT CGACGGTCCT CG			
			C C			
GAM1648	LOC256158	5'	GTAGCCCTGGCAGC	97676	AT	
			GCTGCCAGG GCTAT			
			CGACGGTCC CGATG			
			—			
GAM1648	LOC51195	3'	GCTCCTGGCAGCTACT	32947	A	T
			AG AGCTGCCAGGA GC			
			TC TCGACGGTCCT CG			
			A _			
GAM1648	LOC51337	3'	GCCTCTCCTGGCAGCTTCT	33589		T__
			AGAAGCTGCCAGGA GC			
			TCTTCGACGGTCCT CG			
			CTC			
GAM1648	LOC58525	5'	GCAGGTCCTGGCAGCTC	78647	A	—
			GA GCTGCCAGGA TGC			
			CT CGACGGTCCT ACG			
			_ GG			
GAM1648	LOC90072	3'	CAACCTCAGCAGCTTCT	61290	C_ A	
			AGAAGCTGC AGG TG			
			TCTTCGACG TCC AC			
			AC A			
GAM1648	LOC91344	5'	GCTCCTGGCAGCTCT	65615	A	T
			AGA GCTGCCAGGA GC			
			TCT CGACGGTCCT CG			
			— —			
GAM1648	LOC92979	3'	GTACCCGCTGGCAGCTCCT	56437	A	— A
			AG AGCTGCCA GG TGC			
			TC TCGACGGT CC ATG			
			C CG C			
GAM1648	LOC93259	5'	GTATCCATGCTGGCAGCTTTT	71824		G CT
			AGAAGCTGCCAG ATG ATAC			
			TTTTCGACGGTC TAC TATG			
			G C_			
GAM1649	BACH1	3'	CTGTGTATGAACAAGTCTGAAG	6799	A	CA —
	CA		TG CTTCAGACT TTCA GCAG			

			AC GAAGTCTGA AAGT TGTC	
			— AC ATG	
GAM1649	CRACC	3'	GACCGAGTCTGAAGTCA 41006	AT
			TGACTTCAGACTC TC	
			ACTGAAGTCTGAG AG	
			CC	
GAM1649	AWP1	5'	GCCGCCAGGAATGAATCTGAAG 38663	C A__ A
	TC		GACTTCAGA TCATTC GC GGT	
			CTGAAGTCT AGTAAG CG CCG	
			A GAC _	
GAM1649	DKFZP727M111	5'	ACCTGCTGCACTTCCAGAGTCA 31404	CA CTCATT
			TGACTT GA CAGCAGGT	
			ACTGAG CT GTCGTCCA	
			AC TCAC__	
GAM1649	FLJ14107	3'	ACCTAGCTGAAAACCTGAAGTC 46687	ACTCA _
			GACTTCAG TTCAGC AGGT	
			CTGAAGTC AAGTCG TCCA	
			CAA__ A	
GAM1649	FXVD5	3'	ACCTGCTGGGCACCCGAAG 26340	AGACTCA
			CTTC TTCAGCAGGT	
			GAAG GGGTCGTCCA	
			CCCAC__	
GAM1649	KIAA0472	3'	ACCCACTTTTTTAAACCTGAGG 71850	ACTCATTG_ CA
	TCA		TGACTTCAG AG GGT	
			ACTGGAGTC TC CCA	
			CAAAATTTT AC	
GAM1649	KIAA0939	3'	ACCTCGCCTTGACCCTGAAGTC 62002	AC TTCA _
	A		TGACTTCAG TCA GC AGGT	
			ACTGAAGTC AGT CG TCCA	
			CC TC__ C	
GAM1649	KIAA0945	3'	CCTGCTGAGCTGCAGCCA 30209	A T ACTCA
			TG CT CAG TTCAGCAGG	
			AC GA GTC GAGTCGTCC	
			C C _____	
GAM1649	KIAA1190	3'	ACCCGCTGGGGCCTGGAGTCA 71093	A ATT A
			TGACTTCAG CTC CAGC GGT	
			ACTGAGGTC GGG GTCG CCA	
			C __ C	
GAM1649	LIMK2	3'	ACCTGCCTGTGAACTCTGAAGT 33620	C_ TCA
	CA		TGACTTCAGA TCAT GCAGGT	

		ACTGAAGTCT AGTG CGTCCA		
		CA TC_		
GAM1649	LIMK2	3' ACCTGCCTGTGAACTCTGAAGT 18722	C_	TCA
	CA	TGACTTCAGA TCAT GCAGGT		
		ACTGAAGTCT AGTG CGTCCA		
		CA TC_		
GAM1649	LOC144563	5' ACCTCAGCCAATGAGTCCAACG 76885	TTCA	CA _
	TCA	TGAC GACTCATT GC AGGT		
		ACTG CTGAGTAA CG TCCA		
		CAAC C_ AC		
GAM1649	LOC146443	5' ACCCACTTCTGTGGTTTGAAGC 77880	A	T TC_ CA
	CA	TG CTTCAGAC CAT AG GGT		
		AC GAAGTTTG GTG TC CCA		
		C _ TCT AC		
GAM1649	LOC151632	5' ACCTCAGCCAATGAGTCCAACG 85463	TTCA	CA _
	TCA	TGAC GACTCATT GC AGGT		
		ACTG CTGAGTAA CG TCCA		
		CAAC C_ AC		
GAM1649	LOC200597	5' ACCTGCTGCTTCCTGAAGCCG 88836	A	ACTCATT
		TG CTTCAG CAGCAGGT		
		GC GAAGTC GTCGTCCA		
		C CTTC_		
GAM1649	LOC200904	5' ACCTCAGCCAATGAGTCCAATG 90183	TTCA	CA _
	TCA	TGAC GACTCATT GC AGGT		
		ACTG CTGAGTAA CG TCCA		
		TAAC C_ AC		
GAM1649	LOC203083	5' ACCTCAGCCAATGAGTCCAACA 90460	CTTCA	CA _
	TCA	TGA GACTCATT GC AGGT		
		ACT CTGAGTAA CG TCCA		
		ACAAC C_ AC		
GAM1649	LOC221795	5' ACCTCAGCCAATGAGTCCAACG 92473	TTCA	CA _
	TCA	TGAC GACTCATT GC AGGT		
		ACTG CTGAGTAA CG TCCA		
		CAAC C_ AC		
GAM1649	LOC254176	5' ACCTCAGCCAATGAGTCCAACA 97337	CTTCA	CA _
	TCA	TGA GACTCATT GC AGGT		
		ACT CTGAGTAA CG TCCA		
		ACAAC C_ AC		
GAM1649	LOC256515	5' ACCTCAGCCAATGAGTCCAACG 96459	TTCA	CA _
	TCA	TGAC GACTCATT GC AGGT		

		ACTG CTGAGTAA CG TCCA		
		CAAC C_ AC		
GAM1649	LOC256594 5'	ACCTCAGCCAATGAGTCCAACG 97074	TTCA	CA _
		TCA TGAC GACTCATT GC AGGT		
		ACTG CTGAGTAA CG TCCA		
		CAAC C_ AC		
GAM1649	LOC257160 3'	ACCTGCTGTTGCTCTAAGGCCA 94845	A C	CT TT
		TG CTT AGA CA CAGCAGGT		
		AC GGA TCT GT GTCGTCCA		
		C A C_ T_		
GAM1649	LOC90750 3'	TGAATGAAGCTGAAGTCA 63925	AC	
		TGACTTCAG TCATTCA		
		ACTGAAGTC AGTAAGT		
		GA		
GAM1650	CYP46 3'	CCTCGGTCACCTGTGCTAC 21896	G	AAGCT
		GTAGCAC AG CCGAGG		
		CATCGTG TC GGCTCC		
		_ CACT_		
GAM1650	DTR 3'	TCCTGCCATTCTTCTGGTGCTA 8692	G	CTCCG_
	CT	AGTAGCAC AGAAG AGGA		
		TCATCGTG TCTTC TCCT		
		G TTACCG		
GAM1650	FZD1 3'	TCCTCAAAATGAAGTGCTATTT 13039		GAGAAGCTCC
		AAGTAGCAC GAGGA		
		TTTATCGTG CTCCT		
		AAGTAAAA_		
GAM1650	PCDHAC1 5'	CCGCGGCTCGTGCTCT 38162	T	AAGCT A
		AG AGCACGAG CCG GG		
		TC TCGTGCTC GGC CC		
		_ _ _ _ _ G		
GAM1650	PCDHAC1 5'	CCGCGGCTCGTGCTCT 49039	T	AAGCT A
		AG AGCACGAG CCG GG		
		TC TCGTGCTC GGC CC		
		_ _ _ _ _ G		
GAM1650	RNMT 3'	CCTCCCTCTCGTGCTGCT 13717		A CTCC
		AGTAGCACGAGA G GAGG		
		TCGTCGTGCTCT C CTCC		
		_ C_		
GAM1650	SLC1A2 5'	CCTCGGAGCCCCCGGAGCT 61928	A_	AGAA
		AGC CG GCTCCGAGG		

		TCG GC CGAGGCTCC	
		AG CCC_	
GAM1650 SREBF1	3'	CCTGAGGCTCCTGTGCTACTT 94437	G A TC G
		AAGTAGCAC AG AGC C AGG	
		TTCATCGTG TC TCG G TCC	
		_ C GA _	
GAM1650 TNFAIP2	3'	TCCTGTGCTCTGATGCTACTT 20834	CG A TCCG
		AAGTAGCA AGA GC AGGA	
		TTCATCGT TCT CG TCCT	
		AG _ TG_	
GAM1650 FLJ22160	3'	CCTTGCCTCTCGTGCTAC 44732	G A TCC
		GTA CACGAGA GC GAGG	
		CAT GTGCTCT CG TTCC	
		_ C _	
GAM1650 IFI30	3'	CCTCGGCACCTGCTACTT 65868	CGAGAAGCT
		AAGTAGCA CCGAGG	
		TTCATCGT GGCTCC	
		CCAC_	
GAM1650 KIAA0298	3'	GCCCTCTGTGCTACTT 76579	_ AA
		AAGTAGCAC GAG GC	
		TTCATCGTG CTC CG	
		T C_	
GAM1650 KIAA1029	3'	TCCCCGGGTCCCTGTGCTGCTA 23480	C GA C_ A
	CTT	AAGTAGCA GA AG TCCG GGA	
		TTCATCGT CT TC GGGC CCT	
		A G_ CCT C	
GAM1650 KIAA1655	3'	CCTCTCCCTCGTGCTGC 66604	AAGCTCC
		GTAGCACGAG GAGG	
		CGTCGTGCTC CTCC	
		CCT_	
GAM1650 NR6A1	3'	CCTCGGGGCCCCCAGCTAC 52869	ACGAGAA
		GTAGC GCTCCGAGG	
		CATCG CGGGGCTCC	
		ACCC_	
GAM1650 NR6A1	3'	CCTCGGGGCCCCCAGCTAC 52881	ACGAGAA
		GTAGC GCTCCGAGG	
		CATCG CGGGGCTCC	
		ACCC_	
GAM1650 NR6A1	3'	CCTCGGGGCCCCCAGCTAC 7644	ACGAGAA
		GTAGC GCTCCGAGG	

		CATCG CGGGGCTCC		
		ACCCC__		
GAM1650	LOC152283 5'	TCCCCGACCTTCCCGTGCTGCT 85687	A	CTC A
		AGTAGCACG GAAG CG GGA		
		TCGTCGTGC CTTC GC CCT		
		C CA_ C		
GAM1650	LOC158267 3'	TCCTCTCCTTCTCGTGCTGCTT 81839		CTCC
		AAGTAGCACGAGAAG GAGGA		
		TTCGTCGTGCTCTTC CTCCT		
		CT__		
GAM1650	LOC197414 3'	TCTGACTTCTCGTGCCATTT 88072	A	C C
		AAGT GCACGAGAAG TC GA		
		TTTA CGTGCTCTTC AG CT		
		C _ T		
GAM1650	LOC204965 5'	CGAGAGATCCTCGTGCTACT 90648		AAG _
		AGTAGCACGAG CTC CG		
		TCATCGTGCTC GAG GC		
		CTA A		
GAM1650	LOC51195 3'	CCTGCTCAGCTCCTCGTGCTGC 32940	A	CCG_
		GTAGCACGAG AGCT AGG		
		CGTCGTGCTC TCGA TCC		
		C CTCG		
GAM1650	LOC51637 3'	AGCTTCTCACCTACTT 59747		CAC
		AAGTAG GAGAAGCT		
		TTCATC CTCTTCGA		
		CA_		
GAM1650	LOC90768 5'	CCCCGGAGCTTCCGAAACTGC 63953	CA_ A	A
		GTAG CG GAAGCTCCG GG		
		CGTC GC CTTCGAGGC CC		
		AAA _ C		
GAM1651	CTNS 3'	GGCCTCACCCAGCGAA 17045	AA	TATTTA
		TTC CTGG TGAGGCC		
		AAG GACC ACTCCGG		
		C_ C_____		
GAM1651	HARS 3'	GGGCCCCGCACCAAGTTGGA 9175		ATTTA A
		TTCAACTGGT TG GGCCC		
		AGGTTGACCA GC CCGGG		
		C_ C		
GAM1651	KCNK5 3'	AGGGCCTCTGTTCTCCAGCTGA 13608	A	TATTTAT
	A	TTCA CTGG GAGGCCCT		



			AAGT GACC	CTCCGGGA			
			C	TCTTGT_			
GAM1651	MEIS1	3'	GCAGGAAATACCAACTGAA	9996	AC	ATGAG	
			TTCA	TGGTATTT	GC		
			AAGT	ACCATAAA	CG		
			CA	GGA__			
GAM1651	NR2E3	3'	AGGACTTTGAATGCCAG	32969	T	GC	
			CTGGTATTTA	GAG	CCT		
			GACCGTAAGT	TTC	GGA		
			_	A_			
GAM1651	DKFZP434C131	3'	AGAACCTCATGGCCCGAGCTGA	69078	A	_ TAT	CC
	A		TTCA	CT GG	TTATGAGG	CT	
			AAGT	GA CC	GGTACTCC	GA	
			C	G C_	AA		
GAM1651	DKFZP434L0718	3'	GCTAATGAATACAATTGAA	49548	CTG	GA	
			TTCAA	GTATTTAT	GGC		
			AAGTT	CATAAGTA	TCG		
			AA_	A_			
GAM1651	FLJ12078	3'	TCATAAATACCATTGAA	46454	C		
			TTCAA	TGGTATTTATGA			
			AAGTT	ACCATAAATACT			
			-				
GAM1651	KIAA1077	3'	GGTTTTTAAATACCAG	72909	T		
			CTGGTATTTA	GAGGCC			
			GACCATAAAT	TTTTGG			
			-				
GAM1651	LOC150150	3'	GGCCTTAGTCAAATGCCAGCCG	84868	AA	A_	
	AA		TTC	CTGGTATTT	TGAGGCC		
			AAG	GACCGTAAA	ATTCCGG		
			CC	CTG			
GAM1651	LOC162333	3'	AGAGCCTGCTCAAATACCGGCT	87118	A	ATG_	C
	GAA		TTCA	CTGGTATTT	AGGC	CT	
			AAGT	GGCCATAAA	TCCG	GA	
			C	CTCG	A		
GAM1651	LOC253612	3'	CCTCATAGCCAATGAA	96746	AC	ATT	
			TTCA	TGGT	TATGAGG		
			AAGT	ACCG	ATACTCC		
			A_	__			
GAM1651	LOC255527	5'	AGGGCCTCACAAACACACCCAG	96852	TA__	A	
			CTGG	TTT	TGAGGCCCT		

		GACC AAA ACTCCGGGA	
		CACAC C	
GAM1651	LOC257445 5'	AGAACCTCATGGCCCGAGCTGA 96600	A _ TAT CC
	A	TTCA CT GG TTATGAGG CT	
		AAGT GA CC GGTACTCC GA	
		C G C__ AA	
GAM1652	ALDH1A1 3'	AAAAAAGACAAATTCGGATG 5479	AGT GC
		CATCC GT TGTCTTTTTT	
		GTAGG TA ACAGAAAAAA	
		CT_ A_	
GAM1652	ANK3 3'	AAAAACCATACACTGGATG 40626	C TC
		CATCCAGTGTG TG TTTT	
		GTAGGTCACAT AC AAAA	
		_ CA	
GAM1652	ANKRA2 5'	AAGAACACACTGGAT 43524	CTG
		ATCCAGTGTG TCTT	
		TAGGTCACAC AGAA	
		A__	
GAM1652	APPL 3'	AAAAAAGATTGAACTTGATG 23921	C GTGCT
		CATC AGT GTCTTTTTTT	
		GTAG TCA TAGAAAAAA	
		T AGT__	
GAM1652	CACNB2 5'	AAAAAAGACAAACAGGGGA 5576	AG GC
		TCC TGT TGTCTTTTTT	
		AGG ACA ACAGAAAAAA	
		GG A_	
GAM1652	CEACAM5 5'	AAGGACAGCAGACCAGA 15155	CA G
		TC GT TGCTGTCTTT	
		AG CA ACGACAGGAA	
		AC G	
GAM1652	ELK4 3'	AAAAAAAACAAACATGCTGG 41418	C_ C
		CCAGTGTG TGT TTTTTT	
		GGTCGTAC ACA AAAAAA	
		AA A	
GAM1652	FGF4 3'	AAAAAAGACAAAACA 8880	GC
		TGT TGTCTTTTTT	
		ACA ACAGAAAAAA	
		AA	
GAM1652	HOXC9 3'	AAAAAAGACACACAC 61262	C
		GTGTG TGTCTTTTTT	

CACAC ACAGAAAAAAA

GAM1652 HOXD4 5' AAAAAAAGACAACACGAGA 27517 CA GC  
TC GTGT TGTCTTTTTTT  
|| ||| |||||  
AG CACA ACAGAAAAAAA  
AG \_

GAM1652 MSX1 3' AAAAAAAGACTAGCCA 10128 T \_  
TG GCT GTCTTTTTTT  
|| ||| |||||  
AC CGA CAGAAAAAAA

\_ T  
GAM1652 PPP2R5E 3' AAGAAAGACAAACACT 20719 GC  
AGTGT TGTCTTTTTTT  
|||| |||||  
TCACA ACAGAAAGAA  
A\_

GAM1652 PVRL2 3' GGAACAGCACACTGGA 11145 \_  
TCCAGTGTGCTGT CT  
||||||| ||  
AGGTCACACGACA GG  
A

GAM1652 PXF 3' AAAAAAAGGTGTTCACTG 11146 TGC GT  
CAGTG T CTTTTTT  
|||| | |||||  
GTCAC G GAAAAAAA  
TT\_TG

GAM1652 SCN3A 3' AAGGAAACACACTGGAT 22628 CTG  
ATCCAGTGTG TCTTT  
||||||| ||||  
TAGGTCACAC AGGAA  
AA\_

GAM1652 SORCS3 3' AAAAAAAGACAGTGGTTTTG 30369 TG\_  
CAG TGCTGTCTTTTTTT  
|| |||||  
GTT GTGACAGAAAAAAA  
TTG

GAM1652 TMEFF1 5' AAAAAAACATAGTACAT 13496 C  
GTGTGCTGT TTTTTTT  
||||||| |||||  
TACATGATA AAAAAAA  
C

GAM1652 DKFZp547J036 3' AAAAAAAGACATAAACTGG 50123 GTGC  
CCAGT TGTCTTTTTTT  
|||| |||||  
GGTCA ACAGAAAAAAA  
AAT\_

GAM1652 DKFZp547J036 3' AAAAAAAGACAAAACAAAAGA 50122 CAG GC  
TC TGT TGTCTTTTTTT  
|| ||| |||||

			AG ACA ACAGAAAAAAAA		
			AAA AA		
GAM1652	FAM8A1	3'	AAAAATCTGGCATACTG 32720	TC	
			CAGTGTGCTG TTTT		
			GTCATACGGT AAAAA		
			CT		
GAM1652	FLJ20004	3'	AAAAAAAAACAAGGACGTGGGA 95282	AG G _ C	
		TG	CATCC TGT CT GT TTTTTT		
			GTAGG GCA GA CA AAAAAA		
			GT G A A		
GAM1652	KIAA0373	5'	AAAAAAGACACCAGCAT 28011	GC_	
			GTGT TGTCTTTTTT		
			TACG ACAGAAAAA		
			ACC		
GAM1652	KIAA1084	3'	AAAAAAAGCACACACAC 29832	C _	
			GTGTG TGT CTTTTTTT		
			CACAC ACA GAAAAAA		
			_ C		
GAM1652	KIAA1229	3'	AAAAAAAGCTCATCACTGG 62060	TGCT T	
			CCAGTG G CTTTTTTT		
			GGTCAC C GAAAAAA		
			TACT_		
GAM1652	KIAA1493	3'	AAAAAAAGCATATACACTG 64150	C _	
			CAGTGTG TGT CTTTTTTT		
			GTCACAT ATA GAAAAAA		
			_ C		
GAM1652	KIAA1580	3'	AAAAAAAGACAGTTTATT 69440	T	
			AGTG GCTGTCTTTTTT		
			TTAT TGACAGAAAAA		
			T		
GAM1652	MEF-2	3'	AAAAGAAACACTGGAT 64372	GCTG	
			ATCCAGTGT TCTTTT		
			TAGGTCACA AGAAAA		
			A__		
GAM1652	MGC10200	3'	AAAAAAAGACTGGGTACAGATG 58978	CAG _	
			CATC TGTGCT GTCTTTTTT		
			GTAG ACATGG CAGAAAAA		
			_ GT		
GAM1652	MGC32104	3'	AAAAAAAGACACATA 58398	C	
			TGTG TGTCTTTTTT		

ATAC ACAGAAAAAAAA

—  
 GAM1652 MYT1L 5' AAAAAAAGAAAAACACAAGAT 66822 CA GCTG  
 ATC GTGT TCTTTTTTT  
 ||| ||| |||||  
 TAG CACA AGAAAAAAAA  
 AA AA\_

GAM1652 PELI2 3' AAAAAAAGATTTCAGAGTGGATG 41176 GTG CT  
 CATCCA TG GTCTTTTTTT  
 ||||| || |||||  
 GTAGGT AC TAGAAAAAAAA  
 GAG T\_

GAM1652 LOC133686 3' AAAAAAAGACATTCACTG 75117 TGC  
 CAGTG TGTCTTTTTTT  
 ||||| |||||  
 GTCAC ACAGAAAAAAAA  
 TT\_

GAM1652 LOC143465 5' AAAAAAAGACTTTCTGG 82958 TGTGCT  
 CCAG GTCTTTTTTT  
 ||| |||||  
 GGTC CAGAAAAAAAA  
 TTT\_\_

GAM1652 LOC144262 5' AAAAAAAGACAAAATATAC 76747 C\_\_  
 GTGTG TGTCTTTTTTT  
 ||||| |||||  
 CATAT ACAGAAAAAAAA  
 AAA

GAM1652 LOC145483 3' AAAAAAAGAGCAGCAGAT 77236 G \_  
 GT TGCTG TCTTTTTT  
 || ||||| |||||  
 TA ACGAC AGAAAAAAAA  
 G G

GAM1652 LOC145608 3' AAAAAAAAACAGCACTGGGAT 83379 AGT C  
 ATCC GTGCTGT TTTTTTT  
 ||| ||||| |||||  
 TAGG CACGACA AAAAAAA  
 GT\_ A

GAM1652 LOC146901 3' AAAAAAAGACAGAGAGAAACGG 83828 A GTG\_\_  
 CC GT CTGTCTTTTTTT  
 || || |||||  
 GG CA GACAGAAAAAAAA  
 \_ AAGAGA

GAM1652 LOC157697 5' GACAGCACACAGATG 81550 CA  
 CATC GTGTGCTGTC  
 ||| |||||  
 GTAG CACACGACAG  
 A\_

GAM1652 LOC254221 5' AAAAAAAGCAGAGACAC 97599 G\_ T  
 GTGT CTG CTTTTTTT  
 ||| ||| |||||

		CACA GAC GAAAAAAA	
		GA _	
GAM1653 ADAM20	5'	TTTTCAGCACTGCAGCT 13770	CA
		AGCTGC TGCTGAAGA	
		TCGACG ACGACTTTT	
		TC	
GAM1653 DDEF2	3'	ATGAACTGTTTGTATGGCAGC 13951	TGA_ AAC
		GCTGCCATGC AG TCAT	
		CGACGGTATG TC AGTA	
		TTTG A__	
GAM1653 LIPA	3'	ATGAGCTCTCAATTTTCATGGCA 4079	C__ A A
G		CTGCCATG TGA GA CTCAT	
		GACGGTAC ACT CT GAGTA	
		TTTA _ C	
GAM1653 NFE2L1	3'	AGCTCTCAGCCACAGGCAGCTT 12167	AT__ A A
		AAGCTGCC GCTGA GA CT	
		TTCGACGG CGACT CT GA	
		ACAC _ C	
GAM1653 NRCAM	3'	TGAGTTCATTATGACAGT 17209	C CTGAA
		GCTG CATG GAACTCA	
		TGAC GTAT CTTGAGT	
		A TA__	
GAM1653 PCLO	3'	TTCCTCAGCATGGCAGCTT 94229	A
		AAGCTGCCATGCTGA GAA	
		TTCGACGGTACGACT CTT	
		C	
GAM1653 PLA2G2D	3'	GTTCCCTCAGCATGGAGCT 24800	G A
		AGCT CCATGCTGA GAAC	
		TCGA GGTACGACT CTTG	
		_ C	
GAM1653 ARHGEF15	3'	TCTAGGTCATGGCAGTT 30262	_ GA
		AGCTGCCATG CT AGA	
		TTGACGGTAC GG TCT	
		T A_	
GAM1653 C21orf109	3'	ATGAGCCTGAAGACTGCATGGC 57266	TGA__ AA
A		TGCCATGC AG CTCAT	
		ACGGTACG TC GAGTA	
		TCAGAAG C_	
GAM1653 DKFZp434N074	5'	GAGTCCCTTCCTGGAGC 62648	G TGCT A_
		GCT CCA GAAG ACTC	

CGA GGT CTTC TGAG  
 \_ C \_ CC

GAM1653 DNAJA3 3' ATGAGTTCTTCTGACAGGTT 60484 G C TGCT  
 AA CTG CA GAAGAACTCAT  
 || ||| || |||||  
 TT GAC GT CTTCTTGAGTA  
 G A C \_

GAM1653 FLJ10898 5' ATGAATTCTTCACTTCAGCAGC 59419 CATGC C  
 GCTGC TGAAGAA TCAT  
 |||| ||||| ||||  
 CGACG ACTTCTT AGTA  
 ACTTC A

GAM1653 FLJ13189 3' TTCTTCAGCATAATTGCT 45988 TGCC  
 AGC ATGCTGAAGAA  
 ||| |||||  
 TCG TACGACTTCTT  
 TTAA

GAM1653 KIAA0323 3' AGTTCTTTTGGCAACT 63256 C TGCT  
 AG TGCCA GAAGAACT  
 || |||| |||||  
 TC ACGGT TTTCTTGA  
 A \_

GAM1653 KIAA0376 5' TGAGTTCCTGAGGCAGTCC 65603 A ATGCTGAA  
 A GCTGCC GAACTCA  
 | |||| |||||  
 C TGACGG CTTGAGT  
 C AGTC \_

GAM1653 KIAA1613 3' ATGAATAGAAGCATGGCACTT 64813 C GAAGAAC  
 AAG TGCCATGCT TCAT  
 ||| ||||| ||||  
 TTC ACGGTACGA AGTA  
 \_ AGATA \_

GAM1653 MAD4 3' ATGAGCTCTGCTGCGGCAGCTT 21269 AT TGA A  
 AAGCTGCC GC AGA CTCAT  
 ||||| || ||| ||||  
 TTCGACGG CG TCT GAGTA  
 \_ TCG C

GAM1653 NPD009 3' ATGAGTTCCTGAGACATGC 95045 C \_ GAA  
 GC ATG CT GAACTCAT  
 || ||| || |||||  
 CG TAC GA CTTGAGTA  
 \_ A GTC

GAM1653 PRO1584 3' ATGAGTTCCTGCAGGAGC 37724 G A TGAA  
 GCT CC TGC GAACTCAT  
 ||| || ||| |||||  
 CGA GG ACG CTTGAGTA  
 \_ \_ TC \_

GAM1653 ST7L 3' TCCTCAGCATGAAGCT 57571 GC A  
 AGCT CATGCTGA GA  
 |||| ||||| ||

			TCGA GTACGACT CT		
			A_ C		
GAM1653	STK16	5'	GAGCTCTTCGGTAGC 72117	ATGCT	A
			GCTGCC GAAGA CTC		
			CGATGG CTTCT GAG		
			_____ C		
GAM1653	LOC123242	5'	TCTTCCCACATGGCAGC 75603	CT_	
			GCTGCCATG GAAGA		
			CGACGGTAC CTTCT		
			ACC		
GAM1653	LOC124599	3'	TCCTCAGCATGACAGCTT 75655	C	A
			AAGCTG CATGCTGA GA		
			TTCGAC GTACGACT CT		
			A C		
GAM1653	LOC150383	3'	CTTCAGCAGGGCAGCT 79813	A	
			AGCTGCC TGCTGAAG		
			TCGACGG ACGACTTC		
			G		
GAM1653	LOC157292	3'	GAGAGCTACATGGCAGC 86415	CTGA	AA
			GCTGCCATG AG CTC		
			CGACGGTAC TC GAG		
			A_ GA		
GAM1653	LOC158235	3'	AGTCTGGGCATGGTAACT 86699	C	GA A
			AG TGCCATGCT AGA CT		
			TC ATGGTACGG TCT GA		
			A G_ _		
GAM1653	LOC162333	5'	ATGGGAGCAGGATGGCAGC 87121	G	AAGAA
			GCTGCCAT CTG CTCAT		
			CGACGGTA GAC GGGTA		
			G GA_		
GAM1653	LOC220394	5'	CTTCAGCAGGGCAGCTT 92822	A	
			AAGCTGCC TGCTGAAG		
			TTCGACGG ACGACTTC		
			G		
GAM1653	LOC221463	3'	GAGATAGCAGCTTGGCAGCT 92071	T	AAGAA
			AGCTGCCA GCTG CTC		
			TCGACGGT CGAC GAG		
			T GATA_		
GAM1653	LOC221692	3'	ATGAACCCTCTGACGGTGGCAG 92235	AT	A_ AC_
		CT	AGCTGCC GCTG AGA TCAT		



TCGACGG TGGC TCT AGTA  
 \_ AG CCCA  
 GAM1653 LOC253001 5' TCTTCCCACATGGCAGC 96260 CT\_  
 GCTGCCATG GAAGA  
 ||||| ||||  
 CGACGGTAC CTTCT  
 ACC  
 GAM1653 LOC51312 3' ATGAGTTCCTGCAGGAGC 37713 G A TGAA  
 GCT CC TGC GAACTCAT  
 ||| ||| |||||  
 CGA GG ACG CTTGAGTA  
 \_ \_ TC\_  
 GAM1654 CDH10 3' TAGTTCTCCCTTAAGCAACCT 22058 CG CAGTGT A  
 AGG GCT GA GAACTA  
 ||| ||| |||||  
 TCC CGA CTCTTGAT  
 AA ATTCC\_ \_  
 GAM1654 DACH 3' TAGTTCTTCCATAACCACCT 54971 C CTCA T  
 AGG GG GTG GAAGAACTA  
 ||| ||| |||||  
 TCC CC TAC CTTCTTGAT  
 A AA\_ \_  
 GAM1654 HPS1 3' TCTTCCAGAGCTGCCT 3969 AG T  
 AGGCGGCTC TG GAAGA  
 ||||| |||||  
 TCCGTCGAG AC CTTCT  
 \_ \_  
 GAM1654 PCTK1 5' TCTTCAGGCTGCCT 52264 CAGTG  
 AGGCGGCT TGAAGA  
 ||||| |||||  
 TCCGTCGG ACTTCT  
 \_ \_ \_  
 GAM1654 RORB 5' AGCTCTTCGCCGACCACCT 22606 C C AGT A  
 AGG GG TC GTGAAGA CT  
 ||| ||| ||||| ||  
 TCC CC AG CGCTTCT GA  
 A \_ C\_ C  
 GAM1654 SPTBN4 3' AGTCCCCATGGCCGCCT 47386 CAGT AA A  
 AGGCGGCT GTG GA CT  
 ||||| ||| |||  
 TCCGCCGG TAC CT GA  
 \_ \_ CC \_  
 GAM1654 ZNF200 3' GTAGTTCTGAATTCCCAAGCTG 12909 CAGT\_ GA  
 CCT AGGCGGCT GT AGAACTAC  
 ||||| |||||  
 TCCGTCGA TA TCTTGATG  
 ACCCT AG  
 GAM1654 BTN2A1 3' GTAATTCTCAGTGTGTGAGCTG 54342 \_ TG GA C  
 CCT AGGCGGCTCA G T AGAA TAC  
 ||||| ||| ||| |||

TCCGTCGAGT T G TCTT ATG  
 G GT AC A  
 GAM1654 CFP1 3' TAGCTCCGTCAAGCTGCCT 58771 CAGTG A\_ A  
 AGGCGGCT TGA GA CTA  
 ||||| || ||||  
 TCCGTCGA ACT CT GAT  
 \_\_\_\_\_ GC C  
 GAM1654 FENS-1 3' TGGGAGTCACACAAGCCGCCT 40445 CA AGAA  
 AGGCGGCT GTGTGA CTA  
 ||||| |||| ||  
 TCCGCCGA CACACT GGT  
 A\_ GAG\_  
 GAM1654 FLJ14082 3' AGTTCTTCCTAAGGCACCC 46668 CG CAG T  
 GG GCT TG GAAGAACT  
 || || || |||||  
 CC CGG AT CTTCTTGA  
 CA A\_ C  
 GAM1654 FLJ20539 5' TGGGGCCACCTGAGCCGCC 35363 T AAGAA  
 GGCGGCTCAG GTG CTA  
 ||||| || ||  
 CCGCCGAGTC CAC GGT  
 \_ CGG\_  
 GAM1654 FLJ22301 3' AGCCCTTCACGTAGCCTCCT 45756 C CAG AA  
 AGG GGCT TGTGAAG CT  
 || || ||||| ||  
 TCC CCGA GCACTTC GA  
 T T\_ CC  
 GAM1654 HEMGN 5' TAGAGAAAAAACTGAGCCACC 37380 C GTGAAGAA  
 T AGG GGCTCAGT CTA  
 || ||||| ||  
 TCC CCGAGTCA GAT  
 A AAAAAAGA  
 GAM1654 KIAA0379 3' GTAGTTCTTGCGAATGCCACC 68150 C TCAG G  
 GG GGC TGT AAGAACTAC  
 || || || |||||  
 CC CCG GCG TTCTTGATG  
 A TAA\_ \_  
 GAM1654 KIAA0494 3' TCTCACACTGACCACC 28750 C C A  
 GG GG TCAGTGTGA GA  
 || || ||||| ||  
 CC CC AGTCACACT CT  
 A \_ \_  
 GAM1654 LACE1 3' CTTACATTAAACCACCT 91837 C CTC  
 AGG GG AGTGTGAAG  
 || || |||||  
 TCC CC TTACACTTC  
 A AAA  
 GAM1654 NAPG 3' TAGTTCTTCAGGTAGCACCT 96730 CG CAG G  
 AGG GCT T TGAAGAACTA  
 || || | |||||

		TCC CGA G ACTTCTTGAT		
		A_ T__ G		
GAM1654	PRO2405	5' AGGAGCACATTAAGCCGCCT	37798	C AAGAA
		AGGCGGCT AGTGTG CT		
		TCCGCCGA TTACAC GA		
		A GAG__		
GAM1654	LOC121219	5' AGTCCTCAGCGAAGCCGCCT	74040	CA G A A
		AGGCGGCT GT TGA GA CT		
		TCCGCCGA CG ACT CT GA		
		AG _ C _		
GAM1654	LOC146990	3' CTTACACCCAGCCGCCT	83886	CA
		AGGCGGCT GTGTGAAG		
		TCCGCCGA CACACTTC		
		CC		
GAM1654	LOC148371	5' TTCCACTGAGCCACC	78809	C T
		GG GGCTCAGTG GAA		
		CC CCGAGTCAC CTT		
		A _		
GAM1654	LOC152274	3' AGTCCCTGCAGGAGCAGCCT	80498	G AG AA A
		AGGC GCTC TGTG GA CT		
		TCCG CGAG ACGT CT GA		
		A G_ CC _		
GAM1654	LOC200261	3' AGTTGCTCCACTGAGTCACC	88653	C T AG
		GG GGCTCAGTG GA AACT		
		CC CTGAGTCAC CT TTGA		
		A _ CG		
GAM1654	LOC201562	5' GTAGTCCGGCCCGAGCCGCT	88975	AGT GAA A
		GGCGGCTC GT GA CTAC		
		TCGCCGAG CG CT GATG		
		CC_ GC_ _		
GAM1654	LOC202347	3' TCATGGCAGAGCCGCCT	90349	A _
		AGGCGGCTC GT GTGA		
		TCCGCCGAG CG TACT		
		A G		
GAM1654	LOC220370	3' TCACCTCACTGAGCCACCT	92834	C _
		AGG GGCTCAGT GTGA		
		TCC CCGAGTCA CACT		
		A CTC		
GAM1654	LOC221838	5' TTCCACTGAGCCACC	92546	C T
		GG GGCTCAGTG GAA		

CC CCGAGTCAC CTT  
 A \_  
 GAM1654 LOC51716 3' AGTTCCACACTGAGCGCCT 32786 G AA  
 AGGCG CTCAGTGTG GAACT  
 ||||| ||||| |||||  
 TCCGC GAGTCACAC CTTGA

\_ \_  
 GAM1654 LOC89919 3' CTTCCACTGAGCCACC 60722 C T  
 GG GGCTCAGTG GAAG  
 || ||||| |||||  
 CC CCGAGTCAC CTTC  
 A \_

GAM1654 LOC91947 3' TAGTTCTTTTCATTGTAAGCCGC 67614 \_ T  
 T GGCGGCT CAGTG GAAGAACTA  
 ||||| ||||| |||||  
 TCGCCGA GTTAC TTTCTTGAT  
 AT \_

GAM1655 CDH10 3' TAGTTCTCCCTTAAGCAACCT 22058 CG CAGTGT A  
 AGG GCT GA GAACTA  
 ||| ||| || |||||  
 TCC CGA CT CTTGAT  
 AA ATTCC\_ \_

GAM1655 DACH 3' TAGTTCTTCCATAACCCACCT 54971 C CTCA T  
 AGG GG GTG GAAGAACTA  
 ||| || ||| |||||  
 TCC CC TAC CTTCTTGAT  
 A AA\_ \_

GAM1655 HPS1 3' TCTTCCAGAGCTGCCT 3969 AG T  
 AGGCGGCTC TG GAAGA  
 ||||| || |||||  
 TCCGTCGAG AC CTTCT

\_ \_  
 GAM1655 PCK1 5' TCTTCAGGCTGCCT 52264 CAGTG  
 AGGCGGCT TGAAGA  
 ||||| |||||  
 TCCGTCGG ACTTCT

\_ \_  
 GAM1655 RORB 5' AGCTCTTCGCCGACCACCT 22606 C C AGT A  
 AGG GG TC GTGAAGA CT  
 ||| ||| ||||| ||  
 TCC CC AG CGCTTCT GA  
 A \_ C\_ C

GAM1655 SPTBN4 3' AGTCCCCATGGCCGCCT 47386 CAGT AA A  
 AGGCGGCT GTG GA CT  
 ||||| ||| |||  
 TCCGCCGG TAC CT GA  
 \_ \_ CC \_

GAM1655 ZNF200 3' GTAGTTCTGAATTCCCAAGCTG 12909 CAGT\_ GA  
 CCT AGGCGGCT GT AGAACTAC  
 ||||| || |||||

TCCGTCGA TA TCTTGATG  
 ACCCT AG  
 GAM1655 BTN2A1 3' GTAATTCTCAGTGTGTGAGCTG 54342 \_TG GA C  
 CCT AGGCGGCTCA G T AGAA TAC  
 ||||| | | ||| |||  
 TCCGTCGAGT T G TCTT ATG  
 G GT AC A  
 GAM1655 CFP1 3' TAGCTCCGTCAAGCTGCCT 58771 CAGTG A\_ A  
 AGGCGGCT TGA GA CTA  
 ||||| || |||  
 TCCGTCGA ACT CT GAT  
 \_\_\_\_\_ GC C  
 GAM1655 FENS-1 3' TGGGAGTCACACAAGCCGCCT 40445 CA AGAA  
 AGGCGGCT GTGTGA CTA  
 ||||| ||||| |||  
 TCCGCCGA CACACT GGT  
 A\_ GAG\_  
 GAM1655 FLJ14082 3' AGTTCTTCCTAAGGCACCC 46668 CG CAG T  
 GG GCT TG GAAGAACT  
 || ||| || |||||  
 CC CGG AT CTTCTTGA  
 CA A\_ C  
 GAM1655 FLJ20539 5' TGGGGCCACCTGAGCCGCC 35363 T AAGAA  
 GGCGGCTCAG GTG CTA  
 ||||| ||| |||  
 CCGCCGAGTC CAC GGT  
 \_ CGG\_  
 GAM1655 FLJ22301 3' AGCCCTTCACGTAGCCTCCT 45756 C CAG AA  
 AGG GGCT TGTGAAG CT  
 || ||| ||||| |||  
 TCC CCGA GCACTTC GA  
 T T\_ CC  
 GAM1655 HEMGN 5' TAGAGAAAAAACTGAGCCACC 37380 C GTGAAGAA  
 T AGG GGCTCAGT CTA  
 || ||||| |||  
 TCC CCGAGTCA GAT  
 A AAAAAAGA  
 GAM1655 KIAA0379 3' GTAGTTCTTGCGAATGCCACC 68150 C TCAG G  
 GG GGC TGT AAGAACTAC  
 || ||| || |||||  
 CC CCG GCG TTCTTGATG  
 A TAA\_ \_  
 GAM1655 KIAA0494 3' TCTCACACTGACCACC 28750 C C A  
 GG GG TCAGTGTGA GA  
 || || ||||| |||  
 CC CC AGTCACACT CT  
 A \_ \_  
 GAM1655 LACE1 3' CTTCACATTAAACCACCT 91837 C CTC  
 AGG GG AGTGTGAAG  
 ||| || |||||

		TCC CC TTACACTTC		
		A AAA		
GAM1655	NAPG	3' TAGTTCTTCAGGTAGCACCT	96730	CG CAG G
		AGG GCT T TGAAGAACTA		
		TCC CGA G ACTTCTTGAT		
		A_ T__ G		
GAM1655	PRO2405	5' AGGAGCACATTAAGCCGCCT	37798	C AAGAA
		AGGCGGCT AGTGTG CT		
		TCCGCCGA TTACAC GA		
		A GAG__		
GAM1655	LOC121219	5' AGTCCTCAGCGAAGCCGCCT	74040	CA G A A
		AGGCGGCT GT TGA GA CT		
		TCCGCCGA CG ACT CT GA		
		AG _ C _		
GAM1655	LOC146990	3' CTTACACCCAGCCGCCT	83886	CA
		AGGCGGCT GTGTGAAG		
		TCCGCCGA CACTTC		
		CC		
GAM1655	LOC148371	5' TTCCACTGAGCCACC	78809	C T
		GG GGCTCAGTG GAA		
		CC CCGAGTCAC CTT		
		A _		
GAM1655	LOC152274	3' AGTCCCTGCAGGAGCAGCCT	80498	G AG AA A
		AGGC GCTC TGTG GA CT		
		TCCG CGAG ACGT CT GA		
		A G_ CC _		
GAM1655	LOC200261	3' AGTTGCTCCACTGAGTCACC	88653	C T AG
		GG GGCTCAGTG GA AACT		
		CC CTGAGTCAC CT TTGA		
		A _ CG		
GAM1655	LOC201562	5' GTAGTCCGGCCCGAGCCGCT	88975	AGT GAA A
		GGCGGCTC GT GA CTAC		
		TCGCCGAG CG CT GATG		
		CC_ GC_ _		
GAM1655	LOC202347	3' TCATGGCAGAGCCGCCT	90349	A _
		AGGCGGCTC GT GTGA		
		TCCGCCGAG CG TACT		
		A G		
GAM1655	LOC220370	3' TCACCTCACTGAGCCACCT	92834	C _
		AGG GGCTCAGT GTGA		

TCC CCGAGTCA CACT  
 A CTC  
 GAM1655 LOC221838 5' TTCCACTGAGCCACC 92546 C T  
 GG GGCTCAGTG GAA  
 || ||||| ||  
 CC CCGAGTCAC CTT  
 A \_  
 GAM1655 LOC51716 3' AGTTCCACACTGAGCGCCT 32786 G AA  
 AGGCG CTCAGTGTG GAACT  
 |||| ||||| ||||  
 TCCGC GAGTCACAC CTTGA  
 \_ \_  
 GAM1655 LOC89919 3' CTTCCACTGAGCCACC 60722 C T  
 GG GGCTCAGTG GAAG  
 || ||||| ||||  
 CC CCGAGTCAC CTTC  
 A \_  
 GAM1655 LOC91947 3' TAGTTCTTTTCATTGTAAGCCGC 67614 \_ T  
 T GGCGGCT CAGTG GAAGAACTA  
 ||||| |||| |||||  
 TCGCCGA GTTAC TTTCTTGAT  
 AT \_  
 GAM1656 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
 GTA GGAT GGGTTGTTT  
 ||| ||| |||||  
 CGT CCTA CCCAACAAA  
 C CGTG\_  
 GAM1656 LCT 3' AACCGTAAAAATCCTT 9697 G  
 AAGGATTTTTA GGTT  
 ||||| ||||  
 TTCCTAAAAAT CCAA  
 G  
 GAM1656 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
 GTAAGGATTTTATAGGGTTGTTT  
 ||||| ||||| |||||  
 CATTCTAAAAATCCCAACAAA  
 GAM1656 FBXO30 3' AACTAAAAAAATCCTGAC 49573 A AG  
 GT AGGATTTT GGTT  
 || ||||| ||||  
 CA TCCTAAAAA TCAA  
 G AA  
 GAM1656 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTT  
 GTAAG AGGGTTGTT  
 |||| |||||  
 CATTCTCCCAACAA  
 AT\_\_\_\_  
 GAM1656 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
 TAAG TTTT GGGTTGTTT  
 |||| |||| |||||

		GTTC AAAA CCCAACAAA		
		___ C		
GAM1656	SMT3H2	3' AACAAACATAAAAAATCCTTGC	22670	GG
		GTAAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1656	LOC120103	3' AACCTATGAAAAATCCTTGC	74002	A__
		GTAAAGGATTTTTT GGGTT		
		CGTTCCTAAAAA TCCAA		
		GTA		
GAM1656	LOC129831	3' AAACAACCCCAATGTCC	74889	TT A
		GGAT TT GGGTTGTTT		
		CCTG AA CCCAACAAA		
		T_ C		
GAM1656	LOC133088	5' AAACAAAATAGAAAAATCCCTG	75075	A AGGG_
	C	GTA GGATTTTTT TTGTTT		
		CGT CCTAAAAA AACAAA		
		C GATAA		
GAM1656	LOC148089	3' GGCCCTAAAAATTCCTAC	78637	A
		GTA GGATTTTTTAGGGTT		
		CAT CTTAAAAATCCCGG		
		C		
GAM1656	LOC154547	3' AACAAACATAAAAAATCCTTGC	76050	GG
		GTAAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1656	LOC158104	3' ACAGCCAAAAATCCTTA	60313	AG
		TAAGGATTTTTT GGTTGT		
		ATTCCTAAAAA CCGACA		
		—		
GAM1656	LOC205880	5' AAACAACCATCATCCTGAC	90709	A TTTTAG
		GT AGGAT GGTGTTT		
		CA TCCTA CCAACAAA		
		G CTA__		
GAM1656	LOC221561	3' AACAAACATAAAAAATCCTTGC	92130	GG
		GTAAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1656	LOC257591	3' AACAAACATAAAAAATCCTTGC	97840	GG
		GTAAAGGATTTTTTA GTTGTT		



CGTTCCTAAAAAT CAACAA  
A\_  
GAM1656 LOC51145 3' AGCTAAAATCCTTAC 32393 TAG  
GTAAGGATTTT GGTT  
||||||| |||  
CATTCCTAAAA TCGA

—  
GAM1657 ADAM19 3' CAGGAAGAAGACTGGCCATTAT 52703 C CTGAG  
G CATGA GGCT TTCTTCCTG  
||||| ||| |||||  
GTATT CCGG AAGAAGGAC  
A TCAG\_  
GAM1657 FACL5 5' CAGGAAGAACTCAGAGCCG 64186  
CGGCTCTGAGTTCTTCCTG  
|||||||  
GCCGAGACTCAAGAAGGAC

GAM1657 GNAL 5' CAGGAAAGAGAGGAGCCGTCG 9058 GAG TC  
TGACGGCTCT T TTCCTG  
||||||| | |||||  
GCTGCCGAGG A AAGGAC  
AG\_GA  
GAM1657 KAL1 3' CAGGAAGAACTTCTGTCA 4013 CTCT  
TGACGG GAGTTCTTCCTG  
||||| |||||  
ACTGTC TTCAAGAAGGAC

—  
GAM1657 MYO1E 3' CAGGAGGACAAAACCATG 17187 AC CTC AGT  
CATG GG TG TCTTCCTG  
|||| || || |||||  
GTAC CC AC AGGAGGAC  
CA AAA \_  
GAM1657 PRKAR2B 3' CAGAAAGAACTCAGATGT 10804 \_ C  
GC TCTGAGTTCTT CTG  
|| ||||| |||  
TG AGACTCAAGAA GAC  
T A  
GAM1657 PUM2 3' AGGATCAAAGCTGTCATG 31014 C GTTCT  
CATGACGGCT TGA TCCT  
||||||| ||| |||  
GTACTGTCGA ACT AGGA  
A \_  
GAM1657 SKI 3' CAGGAAGTGCAGAGCCGCA 11701 A AGTT  
TG CGGCTCTG CTCCTG  
|| ||||| |||||  
AC GCCGAGAC GAAGGAC  
\_ GT\_  
GAM1657 TEM8 3' AGGAAGATGCAACCCCATG 36326 AC CTC AGT  
CATG GG TG TCTTCCT  
|||| || || |||||

		GTAC CC AC AGAAGGA		
		C_ A__ GT_		
GAM1657	ARHGEF4	5' AGAAAAAACTCAGGGC	52207	C C
		GCTCTGAGTT TT CT		
		CGGGA CTCAA AA GA		
		A A		
GAM1657	FLJ31978	3' CAGGAAGGAACAAGCGCC	58348	T GAG
		GGC CT TTCTTCCTG		
		CCG GA AGGAAGGAC		
		C ACA		
GAM1657	HSU24186	5' AGAACTCAAAGCCGTC	25324	C
		GACGGCT TGAGTTCT		
		CTGCCGA ACTCAAGA		
		A		
GAM1657	KCNT1	3' AGCTCCAGGGCCGCCA	61825	A _
		TG CGGCTCT GAGTT		
		AC GCCGGGA CTCGA		
		C CC		
GAM1657	KIAA1867	3' CAGGAAGAACCCAAGAGCTCAT	94822	CG GA_
		ATGA GCTCT GTTCTTCCTG		
		TACT CGAGA CAAGAAGGAC		
		_ ACC		
GAM1657	KIAA1878	3' AATTCAGAGAATCGTCATG	91707	_
		CATGACGG CTCTGAGTT		
		GTACTGCT GAGACTTAA		
		AA		
GAM1657	MFN1	3' CAGGAAGAACTCATGA	35541	_
		TC TGAGTTCTTCCTG		
		AG ACTCAAGAAGGAC		
		T		
GAM1657	MIDORI	3' CAGGGCCCTTCCAGAGCCTGTC	73784	_ AGTTCT
	ATG	CATGAC GGCTCTG TCCTG		
		GTACTG CCGAGAC GGGAC		
		T CTTCCC		
GAM1657	MYH7B	3' CAGGAAGAACCTGGCTCGCATG	70530	A _ CTGA
		CATG CG GCT GTTCTTCCTG		
		GTAC GC CGG CAAGAAGGAC		
		_ T TC_		
GAM1657	RNAHP	3' AGAAAGCAGCAGCCGTCAT	23761	_ AG
		ATGACGGCT CTG TTCT		

TACTGCCGA GAC AAGA  
 C GA  
 GAM1657 SLC37A1 3' AGACGGAGCTCAGACCC 38561 C TC  
 GG TCTGAGTTCT CT  
 || ||||| ||  
 CC AGACTCGAGG GA  
 C CA  
 GAM1657 LOC116236 3' CAGGAAAAGCACAAACCTCAT 73809 C CTC A C  
 ATGA GG TG GTT TTCCTG  
 ||| || || |||||  
 TACT CC AC CGA AAGGAC  
 \_ AA\_ A A  
 GAM1657 LOC124801 3' CAGGAAGAACTCTCTTGCATG 74336 A CTCT  
 CATG CGG GAGTTCTTCCTG  
 ||| || |||||  
 GTAC GTT CTCAAGAAGGAC  
 \_ CT\_  
 GAM1657 LOC222160 5' AGGAAGAACTCACCCC 94117 CTC  
 GG TGAGTTCTTCCT  
 || |||||  
 CC ACTCAAGAAGGA  
 CC\_  
 GAM1657 LOC51094 3' CAGGAAGAATAAAGCC 32045 CTGA  
 GGCT GTTCTTCCTG  
 ||| |||||  
 CCGA TAAGAAGGAC  
 AA\_  
 GAM1657 LOC92078 3' CAGGAAGAAGAATCGACCGTC 67977 C T G\_  
 GACGG TC GA TTCTTCCTG  
 ||| || |||||  
 CTGCC AG CT AAGAAGGAC  
 \_ \_ AAG  
 GAM1658 A1BG 3' CACAGCAACCTCTACCTC 55411 A  
 GAGGTAGAGGTTGC GTG  
 ||||| |||  
 CTCCATCTCCAACG CAC  
 A  
 GAM1658 ACVR1 5' CACTGCAGCCTCCACCTC 6604 A  
 GAGGT GAGGTTGCAGTG  
 ||| |||||  
 CTCCA CTCCGACGTCAC  
 C  
 GAM1658 AHR 3' TGGCTCACTGCAACCTCTACCT 7885  
 C GAGGTAGAGGTTGCAGTGAGTCA  
 |||||  
 CTCCATCTCCAACGTCAGTCA  
 CCGT  
 GAM1658 AIM1 3' CACTGCAGCCTCTACCTC 91818  
 GAGGTAGAGGTTGCAGTG  
 |||||

CTCCATCTCCGACGTCAC

GAM1658 ALDH1B1 3' CACTGCAACCTCCGCCTC 5491 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 ALDH3B1 3' GACTCACCCCTGCC 91526 A TTGCA  
GGTAG GG GTGAGTC  
|||| || |||||  
CCGTC CC CACTCAG  
C \_\_\_\_\_

GAM1658 AP3B2 5' CGCCGCAACCTCCTCCTC 16188 TA A  
GAGG GAGGTTGC GTG  
|||| ||||| |||  
CTCC CTCCAACG CGC  
TC C

GAM1658 APPBP2 3' CACTGCAACCTCCGCCTC 21074 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 AQP6 3' GGCTCACTGCAACCTCTACCTC 7958  
GAGGTAGAGGTTGCAGTGAGTC  
|||||||||||||||  
CTCCATCTCCAACGTCACCTCGG

GAM1658 AQP6 3' GGCTCACTGCAACCTCTACCTC 53938  
GAGGTAGAGGTTGCAGTGAGTC  
|||||||||||||||  
CTCCATCTCCAACGTCACCTCGG

GAM1658 ARCN1 3' CACTGCAACCTCCGCCTC 7972 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 ATP8B2 3' GCTCACTGCAACCTCCACCTC 65227 A  
GAGGT GAGGTTGCAGTGAGT  
|||| |||||||||  
CTCCA CTCCAACGTCACCTCG  
C

GAM1658 BRIP1 3' CACTGCAACCTTCACCTC 49397 AG  
GAGGT AGGTTGCAGTG  
|||| |||||||||  
CTCCA TCCAACGTCAC  
CT

GAM1658 C7 3' CTGCAACCTCCGCCTC 5162 TA  
GAGG GAGGTTGCAG  
|||| |||||||||

			CTCC CTCCAACGTC		
			GC		
GAM1658	CAMLG	3'	CACCGCAACCTCCACCTT	8233	A A
			GAGGT GAGGTTGC GTG		
			TTCCA CTCCAACG CAC		
			C C		
GAM1658	CCNF	3'	ACTCACTGTAACTCCGCCTC	8312	TA
			GAGG GAGGTTGCAGTGAGT		
			CTCC CTCCAATGTCACTCA		
			GC		
GAM1658	CDH17	3'	CACTGCAACCTCCGCCTC	14501	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	CIAS1	5'	CACTGCAGCCTCCACCTC	16899	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1658	CLECSF12	3'	GACTCACTGCAGCTATCTC	76690	AGA
			GAGGT GGTTCAGTGAGTC		
			CTCTA TCGACGTCACTCAG		
GAM1658	COX15	3'	ACTCTGCAACCTCCACTTC	54308	A GT
			GAGGT GAGGTTGCA GAGT		
			CTTCA CTCCAACGT CTCA		
			C		
GAM1658	CRHR1	3'	TGACTCACCACGATGACGCCTC	15215	AGAG CA
			GAGGT GTTG GTGAGTCA		
			CTCCG TAGC CACTCAGT		
			CAG_ AC		
GAM1658	CRTAP	3'	CACTGCAACCTCCGCCTC	21030	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	CSNK2A2	5'	GCTCACTGCAACCTCCACCTC	8564	A
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACTCG		
			C		
GAM1658	CXCL16	3'	GGCTCACTGCAACCCCATCTC	41923	AGA
			GAGGT GGTTCAGTGAGTC		

			CTCTA CCAACGTCACCTCGG		
			CCC		
GAM1658	CYLN2	3'	CTGCAGCCTCCACCTC 12633	A	
			GAGGT GAGGTTGCAG		
			CTCCA CTCCGACGTC		
			C		
GAM1658	CYP1A2	3'	CACTGCAACCTCTGCCTC 69099		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	CYP1A2	3'	GCTCACTGCAACCTCCACCTC 69113	A	
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACCTCG		
			C		
GAM1658	CYP1A2	3'	CACTGCAACCTCTGCCTC 5680		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	CYP1A2	3'	GCTCACTGCAACCTCCACCTC 5693	A	
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACCTCG		
			C		
GAM1658	CYP2B6	3'	GGCTCACTGCAACCTCCACC 5738	A	
			GGT GAGGTTGCAGTGAGTC		
			CCA CTCCAACGTCACCTCGG		
			C		
GAM1658	CYP4F3	3'	CATTGCAACCTCCGCCTC 6112	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTTAC		
			GC		
GAM1658	CYP8B1	3'	CACTACAACCTCTGCCTC 15258	C	
			GAGGTAGAGGTTG AGTG		
			CTCCGTCTCCAAC TCAC		
			A		
GAM1658	CYP8B1	3'	CACTGCAACCTCTGCCTC 15260		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	DFFB	3'	CACTGCAACCTCCGCCTC 87378	TA	
			GAGG GAGGTTGCAGTG		

			CTCC CTCCAACGTCAC		
			GC		
GAM1658	DISC1	3'	GGCTCACTGCAACCTCTACCTC 37886		
			GAGGTAGAGGTTGCAGTGAGTC		
			CTCCATCTCCAACGTCACCTCGG		
GAM1658	DSCR3	3'	GCTCACTGCAACCTCCACCTC 20185	A	
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACCTCG		
			C		
GAM1658	EHD2	3'	GCTCACTGCAACCTCCACCTC 27496	A	
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACCTCG		
			C		
GAM1658	EPB72	3'	CACTGCAACCTCCGCCTC 14600	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	F2RL2	3'	CATTGCAACCTCTGCCTC 14620		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTTAC		
GAM1658	FANCF	3'	CAGTGCAACCTCTGCCTC 42671	G	
			GAGGTAGAGGTTGCA TG		
			CTCCGTCTCCAACGT AC		
			G		
GAM1658	FBXL11	3'	TGATAGCACAACTCTTCC 24576	T	CA GA
			GG AGAGGTTG GT GTCA		
			CC TCTCCAAC CG TAGT		
			T A_ A_		
GAM1658	FCAR	3'	GACTCACTGCAACCTTCGCCTC 55797	TA	
			GAGG GAGGTTGCAGTGAGTC		
			CTCC TTCCAACGTCACCTCAG		
			GC		
GAM1658	FCAR	3'	GACTCACTGCAACCTTCGCCTC 55813	TA	
			GAGG GAGGTTGCAGTGAGTC		
			CTCC TTCCAACGTCACCTCAG		
			GC		
GAM1658	FEZ1	3'	TGGCTCACTGCAACCTCCACCT 42582	A	
	C		GAGGT GAGGTTGCAGTGAGTCA		

			CTCCA CTCCAACGTCACCTCGGT	
			C	
GAM1658	FGF5	3'	GGCTCACTGCAACCTCCAACTC 52492	GTA
			GAG GAGGTTGCAGTGAGTC	
			CTC CTCCAACGTCACCTCGG	
			AAC	
GAM1658	FGF5	3'	GGCTCACTGCAACCTCCAACTC 15546	GTA
			GAG GAGGTTGCAGTGAGTC	
			CTC CTCCAACGTCACCTCGG	
			AAC	
GAM1658	FHL2	5'	GCTCACTGCAAGCTCTACCTC 7565	G
			GAGGTAGAG TTGCAGTGAGT	
			CTCCATCTC AACGTCACTCG	
			G	
GAM1658	FZD4	3'	CACTGCAACCTCTGCCTC 24129	
			GAGGTAGAGGTTGCAGTG	
			CTCCGTCTCCAACGTCAC	
GAM1658	G6PC	3'	CACTGCAACCTCTTCCTC 3822	T
			GAGG AGAGGTTGCAGTG	
			CTCC TCTCCAACGTCAC	
			T	
GAM1658	GHR	3'	TGACTCACTGCAATCTCCACCT 3891	A
	C		GAGGT GAGGTTGCAGTGAGTCA	
			CTCCA CTCTAACGTCACTCAGT	
			C	
GAM1658	GM2A	3'	CACTGCAACCTCCGCCTC 67774	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			GC	
GAM1658	GNE	3'	CAATGCAACCTCTGCC 18476	G
			GGTAGAGGTTGCA TG	
			CCGTCTCCAACGT AC	
			A	
GAM1658	GPR4	3'	CACTGCAGCCTCCACCTC 59901	A
			GAGGT GAGGTTGCAGTG	
			CTCCA CTCCGACGTCAC	
			C	
GAM1658	GPR56	5'	CATCGTAACCTCCACCTC 19066	A A
			GAGGT GAGGTTGC GTG	



			CTCCA CTCCAATG TAC		
			C C		
GAM1658	GPR81	3'	CACTGCAACCTCTGCCTC 50754		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	GRAF	3'	CACTGCAACCTCCGCCTC 30551	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	HTR1E	5'	CATTGCAACCTCCGCCTC 6012	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTTAC		
			GC		
GAM1658	IL11	3'	TCACTGCAAGCTCCACCTC 5334	A G	
			GAGGT GAG TTGCAGTGA		
			CTCCA CTC AACGTCACT		
			C G		
GAM1658	INHBB	5'	TGACCCGCGACCTCCGCC 9344	TA	AGT A
			GG GAGGTTGC G GTCA		
			CC CTCCAGCG C CAGT		
			GC _ C		
GAM1658	INMT	3'	GACTCACTGCAAGCTCCGCCTC 22271	TA	G
			GAGG GAG TTGCAGTGAGTC		
			CTCC CTC AACGTCACTCAG		
			GC G		
GAM1658	ITGAM	3'	CACTGCAACCTCCGCCTC 71836	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	KMO	3'	CACTGCAACCTCTGCCTC 13447		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	LANCL1	3'	ACTCACTGCATGACCCT 20206	A	_
			AG GGT TGCAGTGAGT		
			TC CCA ACGTCACTCA		
			_ GT		
GAM1658	LILRA3	3'	CACTGCAACCTCCGCCTC 95308	TA	
			GAGG GAGGTTGCAGTG		

			CTCC CTCCAACGTCAC		
			GC		
GAM1658 LNK	3'	CACTGCAACCTCCACCTT	18459	A	
		GAGGT GAGGTTGCAGTG			
		TTCCA CTCCAACGTCAC			
		C			
GAM1658 LSS	3'	CTCAACCTCTATCTC	9817	C	
		GAGGTAGAGGTTG AG			
		CTCTATCTCCAAC TC			
		—			
GAM1658 LYZ	3'	GGCTCACTGCAACCTCCACCTC	4106	A	
		GAGGT GAGGTTGCAGTGAGTC			
		CTCCA CTCCAACGTCACCTCGG			
		C			
GAM1658 MAK	3'	TACTGCAACCTCCACCTC	19767	A	
		GAGGT GAGGTTGCAGTG			
		CTCCA CTCCAACGTCAT			
		C			
GAM1658 MEF2A	5'	CACTGCAACCTCCGCCTC	18781	TA	
		GAGG GAGGTTGCAGTG			
		CTCC CTCCAACGTCAC			
		GC			
GAM1658 MEFV	3'	CACTGCAACCTCCGCCTC	4128	TA	
		GAGG GAGGTTGCAGTG			
		CTCC CTCCAACGTCAC			
		GC			
GAM1658 MEFV	3'	GCTCACTGCAACCTCCACCTC	4142	A	
		GAGGT GAGGTTGCAGTGAGT			
		CTCCA CTCCAACGTCACCTCG			
		C			
GAM1658 MHC2TA	3'	CACTGCAACCTCCGCCTC	4166	TA	
		GAGG GAGGTTGCAGTG			
		CTCC CTCCAACGTCAC			
		GC			
GAM1658 MICB	3'	CACTGCAACCTCTGCCTC	19822		
		GAGGTAGAGGTTGCAGTG			
		CTCCGTCTCCAACGTCAC			
GAM1658 MPL	3'	CACTGCAACCTCTGCCTC	18133		
		GAGGTAGAGGTTGCAGTG			

CTCCGTCTCCAACGTCAC

GAM1658 MPL 3' GCTCACTGCAACCTCCACCTC 18145 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||||||  
CTCCA CTCCAACGTCACCTCG  
C

GAM1658 MRPL49 3' CACTGCAACTTCCACCTC 69567 A  
GAGGT GAGGTTGCAGTG  
||||| |||||||||  
CTCCA CTTCAACGTCAC  
C

GAM1658 MYCL2 3' CACTGCAACCTCTGCCTC 18177  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 NDRG3 3' CACTGCAACCTCTGCC 49293  
GGTAGAGGTTGCAGTG  
||||| |||||||||  
CCGTCTCCAACGTCAC

GAM1658 NQO1 3' CACTGCAACCTCTGCCTC 6154  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 PCDHB11 3' CACTGCAACCTCTGCCTC 38411  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 PCDHB16 3' CACTGCAACCTCTGCCTC 40551  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 PCDHB9 3' CACTGCAACCTCCGCCTC 38936 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 PDCL 3' GGCTCACTGCAACCTCCACCTC 18216 A  
GAGGT GAGGTTGCAGTGAGTC  
||||| |||||||||  
CTCCA CTCCAACGTCACCTCGG  
C

GAM1658 PDE6B 3' GCTCACTGCAACCTCCACCTC 4283 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||||||

			CTCCA CTCCAACGTCACTCG	
			C	
GAM1658	PER2	3'	CACTGCAACCTCTGCCTC 43029	
			GAGGTAGAGGTTGCAGTG	
			CTCCGTCTCCAACGTCAC	
GAM1658	PIGR	3'	CACTGCAACCTCCGCCTC 72592	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			GC	
GAM1658	PIK3C2B	3'	GA CTCACTGCAAAATCTGCCTC 10567	GG
			GAGGTAGA TTGCAGTGAGTC	
			CTCCGTCT AACGTCACTCAG	
			AA	
GAM1658	PON1	3'	CACTGCAACTTCTACCTC 4802	
			GAGGTAGAGGTTGCAGTG	
			CTCCATCTTCAACGTCAC	
GAM1658	PRKWNK3	3'	TGCTGCAACCTCCCCCTC 61559	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCGT	
			CC	
GAM1658	PSMB2	3'	CACTGCAACCTCCGCCTC 10950	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			GC	
GAM1658	RAB36	3'	CAGTGCAACCTCTGCCTC 16951	G
			GAGGTAGAGGTTGCA TG	
			CTCCGTCTCCAACGT AC	
			G	
GAM1658	RHD	3'	CACTGCAACCTCCGCCTC 32298	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			GC	
GAM1658	RHD	3'	TGGCTCACTGCAACCTCTACCT 32322	
	C		GAGGTAGAGGTTGCAGTGAGTCA	
			CTCCATCTCCAACGTCACTCGGT	
GAM1658	RHD	3'	CACTGCAACCTCCGCCTC 32607	TA
			GAGG GAGGTTGCAGTG	

			CTCC CTCCAACGTCAC	
			GC	
GAM1658	RHD	3'	TGGCTCACTGCAACCTCTACCT 32631	
	C		GAGGTAGAGGTTGCAGTGAGTCA	
			CTCCATCTCCAACGTCACCTCGGT	
GAM1658	RPH3AL	3'	GGCTCACTGCAACCTCCACCTC 22751	A
			GAGGT GAGGTTGCAGTGAGTC	
			CTCCA CTCCAACGTCACCTCGG	
			C	
GAM1658	SAS	3'	CACCGCAACCTCTGCCTC 19950	A
			GAGGTAGAGGTTGC GTG	
			CTCCGTCTCCAACG CAC	
			C	
GAM1658	SEDL	3'	CACTGCAACCTCCGCCTC 27328	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			GC	
GAM1658	SEDL	3'	TGGCTCACTGCAACCTCCACCT 27366	A
	C		GAGGT GAGGTTGCAGTGAGTCA	
			CTCCA CTCCAACGTCACCTCGGT	
			C	
GAM1658	SEDL	3'	TGGCTCACTGCAACCTCCACCT 27367	A
	C		GAGGT GAGGTTGCAGTGAGTCA	
			CTCCA CTCCAACGTCACCTCGGT	
			C	
GAM1658	SEPN1	3'	TGGCTCACTGCAACCTCCACCT 66383	A
	C		GAGGT GAGGTTGCAGTGAGTCA	
			CTCCA CTCCAACGTCACCTCGGT	
			C	
GAM1658	SERPINB9	3'	CACTGCAACCTCCTCCTC 14749	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			TC	
GAM1658	SHOX	3'	GACTCACTGCAACCTCCGCCTC 22538	TA
			GAGG GAGGTTGCAGTGAGTC	
			CTCC CTCCAACGTCACCTCAG	
			GC	
GAM1658	SIL	3'	CACTGCAACCTCTGCCTC 11686	
			GAGGTAGAGGTTGCAGTG	

CTCCGTCTCCAACGTCAC

GAM1658 SLA2 3' GCTCACTGCAACCTCCATCTC 49899 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||||||  
CTCTA CTCCAACGTCACTCG  
C

GAM1658 SLC14A2 5' TGGCTCACTGCAACCTCCACCT 23143 A  
C GAGGT GAGGTTGCAGTGAGTCA  
||||| |||||||||  
CTCCA CTCCAACGTCACTCGGT  
C

GAM1658 SLC15A1 3' CACTGCAACCTCCGCCTC 17398 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 SMAC 5' CACTGCAACCTCTGCCTC 57204  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 SNAP23 3' CACTGCAACCTCCGCCTC 55459 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 SNAP23 3' CACTGCAACCTCCGCCTC 13806 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 SNX15 3' GGCTCACTGCAACCTCCACCTC 73747 A  
GAGGT GAGGTTGCAGTGAGTC  
||||| |||||||||  
CTCCA CTCCAACGTCACTCGG  
C

GAM1658 SPN 3' CACTGCAACCTCTGCCTC 11917  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 SS18 3' CACTGCAACCTCCGCCTC 18883 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 STAU 5' ACTGCAACCTCCACCTC 15994 A  
GAGGT GAGGTTGCAGT  
||||| |||||||||

CTCCA CTCCAACGTCA  
C  
GAM1658 STAU 5' GGCTCACTGCAACCTCCACCTC 16007 A  
GAGGT GAGGTTGCAGTGAGTC  
||||| |||||||||  
CTCCA CTCCAACGTCACTCGG  
C  
GAM1658 SULT2B1 5' CACTGCAACCTCCGCCTC 16023 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC  
GAM1658 TAF4 3' CGTTGCACCCCCACCTC 12091 AGA T  
GAGGT GG TGCAGTG  
||||| || |||||  
CTCCA CC ACGTTGC  
CC\_ C  
GAM1658 TAPBP 3' TACTGCAACCTCCGCCTC 12134 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAT  
GC  
GAM1658 TAT 3' GGCTCACTGCAACCTCCACCTC 4473 A  
GAGGT GAGGTTGCAGTGAGTC  
||||| |||||||||  
CTCCA CTCCAACGTCACTCGG  
C  
GAM1658 TBXA2R 3' CACTGCAACCTCCGCCTC 6483 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC  
GAM1658 TBXA2R 3' GCTCACTGCAACCTCCACCTC 6496 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||||||  
CTCCA CTCCAACGTCACTCG  
C  
GAM1658 TMC1 5' CTGCAACCTCCGCCTC 56903 TA  
GAGG GAGGTTGCAG  
||| |||||||||  
CTCC CTCCAACGTC  
GC  
GAM1658 TNFRSF10B 3' CAGTGCAACCTCCGCCTC 13867 TA G  
GAGG GAGGTTGCA TG  
||| |||||||||  
CTCC CTCCAACGT AC  
GC G  
GAM1658 TPMT 3' CACTGCAACCTCTGCCTC 4534  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||

CTCCGTCTCCAACGTCAC

GAM1658	TRIM9	5'	CACTGCAACCTCCGCCTC	30755	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	TRPM6	3'	CACTGCAACCTCTGCCTC	34535	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	TRPV1	3'	CACTGCAACCTCTGCCTC	38073	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	TRPV1	3'	CTGCAACCTCCGCCTC	38081	TA
			GAGG GAGGTTGCAG		
			CTCC CTCCAACGTC		
			GC		
GAM1658	TRPV1	3'	CACTGCAACCTCTGCCTC	54792	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	TRPV1	3'	CTGCAACCTCCGCCTC	54802	TA
			GAGG GAGGTTGCAG		
			CTCC CTCCAACGTC		
			GC		
GAM1658	TRPV1	3'	CACTGCAACCTCTGCCTC	54827	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	TRPV1	3'	CTGCAACCTCCGCCTC	54835	TA
			GAGG GAGGTTGCAG		
			CTCC CTCCAACGTC		
			GC		
GAM1658	TRPV1	3'	CACTGCAACCTCTGCCTC	54859	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	TRPV1	3'	CTGCAACCTCCGCCTC	54867	TA
			GAGG GAGGTTGCAG		



			CTCC CTCCAACGTC		
			GC		
GAM1658	TUFT1	3'	CACTGCAACCTCTGCCTC	39252	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	VENTX2	3'	CACTGCAACCTCCGCCTC	27108	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	VHL	3'	CACTGCAACCTCTGCCTC	5064	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	ZNF133	5'	ACTCACTGCAACCTCCACC	12829	A
			GGT GAGGTTGCAGTGAGT		
			CCA CTCCAACGTCACTCA		
			C		
GAM1658	ZNF264	3'	CACTGCAACCTCCGCCTC	12746	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	ZNF264	3'	CTGCAACCTCTGCCTC	12754	
			GAGGTAGAGGTTGCAG		
			CTCCGTCTCCAACGTC		
GAM1658	20D7-FC4	5'	CACTGCAGCCTCCACCTC	60896	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1658	ARHF	3'	TGGCTCACTGCAAGCTCCACCT	38751	A G
	C		GAGGT GAG TTGCAGTGAGTCA		
			CTCCA CTC AACGTCACTCGGT		
			C G		
GAM1658	ARPP-19	3'	CACTGCAACCTCTGCCTC	21791	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	ASB16	5'	CACTGCAACCTCCGCCTC	69932	TA
			GAGG GAGGTTGCAGTG		

			CTCC CTCCAACGTCAC		
			GC		
GAM1658	ASE-1	3'	CACTGCAACCTCCGCCTC	23946	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	ATP1B4	3'	GGCTCACTGCAACCTCCACCTC	23825	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCAC		
			C		
GAM1658	BA108L7.2	3'	CACTGCAACCTCTGCCTC	48259	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	BAG5	3'	GCTCACTGCAACCTCCACCTC	16845	A
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCAC		
			C		
GAM1658	BNIP-S	3'	CACTGCAACCTCCGCCTC	56257	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	BTN3A1	3'	CTGCAACCTCCACCTC	22919	A
			GAGGT GAGGTTGCAG		
			CTCCA CTCCAACGTC		
			C		
GAM1658	C1orf24	3'	CACTGCAACCTCCGCCTC	53710	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	C1QTNF6	3'	CACTGCAACCTCTGCCTC	49139	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	C20orf167	3'	TGACTCACTGCACAGCACC	53664	AGAG T
			GGT GT GCAGTGAGTCA		
			CCA CA CGTCACTCAGT		
			CGA_ _		
GAM1658	C21orf25	3'	TACTGCAACCTCCACCTC	63556	A
			GAGGT GAGGTTGCAGTG		

CTCCA CTCCAACGTCAT  
C  
GAM1658 C21orf93 3' TGACCCTCACCTCTCACCTC 59090 \_ T C TGA  
GAGGT AGAGGT G AG GTCA  
||||| ||||| | || ||||  
CTCCA TCTCCA C TC CAGT  
C \_ \_ C \_  
GAM1658 C3F 3' GCTCACCGCAACCTCCACCTC 19293 A A  
GAGGT GAGGTTGC GTGAGT  
||||| ||||| |||||  
CTCCA CTCCAACG CACTCG  
C C  
GAM1658 C9orf9 3' CACTGCAACCTCCGCCTC 38506 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC  
GAM1658 C9orf9 3' TGGCTCACTGCAACCTCCACCT 38532 A  
C GAGGT GAGGTTGCAGTGAGTCA  
||||| |||||  
CTCCA CTCCAACGTCAGTCCGGT  
C  
GAM1658 CEACAM8 3' ACTCACTGCAAGCTCCGCCTC 8420 TA G  
GAGG GAG TTGCAGTGAGT  
||| ||| |||||  
CTCC CTC AACGTCAGTCA  
GC G  
GAM1658 CENPH 3' CACTGCAACCTCTGCCTC 43271  
GAGGTAGAGGTTGCAGTG  
||||| |||||  
CTCCGTCTCCAACGTCAC  
GAM1658 CHRAC1 3' CACTGCAACCTCCGCCTC 33867 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC  
GAM1658 CLSTN2 3' ACTCACTGTGCGTCTCCTC 42120 T G T  
GAGG AGA GT GCAGTGAGT  
||| ||| ||| |||||  
CTCC TCT CG TGTCAGTCA  
\_ G \_  
GAM1658 CPSF2 3' CACCGCAACCTCTGCCTC 61574 A  
GAGGTAGAGGTTGC GTG  
||||| ||||| |||  
CTCCGTCTCCAACG CAC  
C  
GAM1658 CYP4F8 3' GACCCACCCACCTACCTT 23410 A\_ TTGCA A  
GAGGTAG GG GTG GTC  
||||| || ||| |||

			TTCCATC CC CAC CAG		
			CA _____ C		
GAM1658	DBR1	3'	CACCGCAACCTCCGCCTC	32528	TA A
			GAGG GAGGTTGC GTG		
			CTCC CTCCAACG CAC		
			GC C		
GAM1658	DKFZp434A2417	3'	CACTGCAACTTCCACCTC	66097	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTTCAACGTCAC		
			C		
GAM1658	DKFZP434C212	3'	TGGCTCACTGCAACCTCCACCT	68921	A
	C		GAGGT GAGGTTGCAGTGAGTCA		
			CTCCA CTCCAACGTCAC		
			C		
GAM1658	DKFZp434E2220	5'	CACTGCAACCTCCGCCTC	34294	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	DKFZp547H025	3'	GCTCACTGCAACCTCCACCTC	39359	A
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCAC		
			C		
GAM1658	DKFZP564O0523	3'	GGCTCACTGCAACCTCCACCTC	49518	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCAC		
			C		
GAM1658	DKFZp761J139	5'	CACTGCAACGTCCACCTC	50104	A G
			GAGGT GA GTTGCAGTG		
			CTCCA CT CAACGTCAC		
			C G		
GAM1658	DKFZp761N1114	3'	CACTGCAACCTCCGCCTC	79015	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	DKFZp762P2111	3'	CACTGCAACCTCCGCCTC	86353	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	DRIL2	3'	CAATAAACCTCTACCTC	21323	GCAG
			GAGGTAGAGGTT TG		

			CTCCATCTCCAA	AC		
			ATA_			
GAM1658	DSCR6	3'	CACTGCAACCTCCACTTC	38543	A	
			GAGGT GAGGTTGCAGTG			
			CTTCA CTCCAACGTCAC			
			C			
GAM1658	EREG	3'	GGCTCACTGCAACCTCACCTC	7507	A	
			GAGGT GAGGTTGCAGTGAGTC			
			CTCCA CTCCAACGTCAGTCGG			
			—			
GAM1658	FBP17	3'	GGCTCACTACAACCTCCACCTC	72801	A	C
			GAGGT GAGGTTG AGTGAGTC			
			CTCCA CTCCAAC TCACTCGG			
			C A			
GAM1658	FER1L4	3'	ACTGCAACCTCCACCTC	47325	A	
			GAGGT GAGGTTGCAGT			
			CTCCA CTCCAACGTCA			
			C			
GAM1658	FER1L4	3'	ACTGCAACCTCCACCTC	47327	A	
			GAGGT GAGGTTGCAGT			
			CTCCA CTCCAACGTCA			
			C			
GAM1658	FLJ00024	5'	CACTGCAACCTCTGCCTC	63753		
			GAGGTAGAGGTTGCAGTG			
			CTCCGTCTCCAACGTCAC			
GAM1658	FLJ10232	3'	CACTGCAACCTCCGCCTC	35922	TA	
			GAGG GAGGTTGCAGTG			
			CTCC CTCCAACGTCAC			
			GC			
GAM1658	FLJ10346	5'	GGCTCACTGCAAGCTCCACCTC	36047	A	G
			GAGGT GAG TTGCAGTGAGTC			
			CTCCA CTC AACGTCAGTCGG			
			C G			
GAM1658	FLJ10535	3'	CACTGCAACCTCTGCCTC	36235		
			GAGGTAGAGGTTGCAGTG			
			CTCCGTCTCCAACGTCAC			
GAM1658	FLJ10922	3'	CACTGCAACCTCCGCCTC	36871	TA	
			GAGG GAGGTTGCAGTG			

CTCC CTCCAACGTCAC  
 GC  
 GAM1658 FLJ11004 5' GGCTCACTGCAACCTCTACCTC 36971  
 GAGGTAGAGGTTGCAGTGAGTC  
 |||||  
 CTCCATCTCCAACGTCACCTCGG

GAM1658 FLJ11106 5' TCTTGCAACCTCACCTC 37056 A T  
 GAGGT GAGGTTGCAG GA  
 |||| ||||| ||  
 CTCCA CTCCAACGTT CT

GAM1658 FLJ12287 3' TGACCCCTTCACCTCTCCC 42320 T T C TGA  
 GG AGAGGT G AG GTCA  
 || ||||| | || ||||  
 CC TCTCCA C TC CAGT  
 C \_ T CC\_

GAM1658 FLJ12363 3' GCTCACTGCAACCTCCACCTC 49684 A  
 GAGGT GAGGTTGCAGTGAGT  
 |||| |  
 CTCCA CTCCAACGTCACCTCG  
 C

GAM1658 FLJ12409 3' TGACTCACTGCAACCTCCGCCT 47053 TA  
 C GAGG GAGGTTGCAGTGAGTCA  
 |||| |  
 CTCC CTCCAACGTCACCTCAGT  
 GC

GAM1658 FLJ12572 5' CACTGCAACCTCTGCCTC 43247  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC

GAM1658 FLJ12649 3' CACTGCAACCTCCGCCTC 44777 TA  
 GAGG GAGGTTGCAGTG  
 |||| |  
 CTCC CTCCAACGTCAC  
 GC

GAM1658 FLJ12668 3' TGGTCACTGCAACCTCCATCTC 46529 A G  
 GAGGT GAGGTTGCAGTGA TCA  
 |||| |  
 CTCTA CTCCAACGTCACCT GGT  
 C \_

GAM1658 FLJ12687 3' CACTGCAACCTCCGCCTC 46188 TA  
 GAGG GAGGTTGCAGTG  
 |||| |  
 CTCC CTCCAACGTCAC  
 GC

GAM1658 FLJ12747 3' CACTGCAACCTCTGCCTC 49712  
 GAGGTAGAGGTTGCAGTG  
 |||||

CTCCGTCTCCAACGTCAC

GAM1658 FLJ12973 3' CACCGCAACCTCCGCCTC 46103 TA A  
GAGG GAGGTTGC GTG  
|||| ||||||| |||  
CTCC CTCCAACG CAC  
GC C

GAM1658 FLJ13072 5' CACTGCAACCTCTGCCTC 89804  
GAGGTAGAGGTTGCAGTG  
|||||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 FLJ13197 3' GGCTCACTGCAACCTCTACCTC 44861  
GAGGTAGAGGTTGCAGTGAGTC  
|||||||||||||||||  
CTCCATCTCCAACGTCACCTCGG

GAM1658 FLJ14950 3' GGCTCACTGCAACCTCCACCTC 51726 A  
GAGGT GAGGTTGCAGTGAGTC  
|||| |||||||||||||  
CTCCA CTCCAACGTCACCTCGG  
C

GAM1658 FLJ14957 3' CACTGCAACCTCTGCCTC 51742  
GAGGTAGAGGTTGCAGTG  
|||||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 FLJ20004 3' CATTGCAACCTCCGCCTC 95291 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTTAC  
GC

GAM1658 FLJ20034 3' CACTGCAACCTCTGCCTC 34359  
GAGGTAGAGGTTGCAGTG  
|||||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 FLJ20045 3' CACTGCAACCTCTGCCTC 34416  
GAGGTAGAGGTTGCAGTG  
|||||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 FLJ20079 3' TGGCTCACCGCAACCTCCACCT 34505 A A  
C GAGGT GAGGTTGC GTGAGTCA  
|||| ||||||| |||||||  
CTCCA CTCCAACG CACTCGGT  
C C

GAM1658 FLJ20342 3' CACTGCAACCTCTGCCTC 34987  
GAGGTAGAGGTTGCAGTG  
|||||||||||||||

CTCCGTCTCCAACGTCAC

GAM1658 FLJ20344 3' CACTGCAACCTCCGCCTC 35006 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 FLJ20507 3' CACTGCAACCTCTGCCTC 35275  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 FLJ20507 3' CACTGCAACCTCTGCCTC 60210  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 FLJ20511 3' GGCTCACTGCAAGCTCCACCTC 35329 A G  
GAGGT GAG TTGCAGTGAGTC  
|||| ||| |||||||||  
CTCCA CTC AACGTCACTCGG  
C G

GAM1658 FLJ20542 3' ACTCACCCAGCCGCCACCTC 49780 AGA CA  
GAGGT GGTG GTGAGT  
|||| ||| |||||  
CTCCA CCGAC CACTCA  
CCG C\_

GAM1658 FLJ20813 3' CACTGCAACTCCACCTC 35679 A G  
GAGGT GAG TTGCAGTG  
|||| ||| |||||||  
CTCCA CTC AACGTCAC  
C \_

GAM1658 FLJ21302 3' CACTGCAACCTCCGCCTC 43212 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 FLJ22002 3' CACTGCAACCTCCGCCTC 45768 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 FLJ22531 5' GGCTCACTGCAACCTCCACCTC 45033 A  
GAGGT GAGGTTGCAGTGAGTC  
|||| |||||||||||  
CTCCA CTCCAACGTCACTCGG  
C

GAM1658 FLJ22794 3' CACTGCAACTTCCACCTC 91603 A  
GAGGT GAGGTTGCAGTG  
|||| |||||||||



			CTCCA CTTCAACGTCAC		
			C		
GAM1658	FLJ22965	3'	CACTGCAACCTCCGCCTC	42049	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	FLJ22969	3'	CACTGCAACCTCTGCCTC	68646	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	FLJ23024	3'	CACTGCAACCTCTGCCTC	46266	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	FLJ23392	3'	CACTGCAACCTCTGCCTC	45527	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	FLJ23563	3'	CACTGCAACCTCTGCCTC	67592	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	FLJ31101	3'	CACTGCAACCTCTGCCTC	35706	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	FLJ32865	3'	CACTGCAACCTCTGCCTC	58168	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	GAL3ST-4	3'	CACTGCAACCTCTGCCTC	44934	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	GMPPB	5'	GGCTCACTGCAACCTCCACCTC	95749	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCACCTCGG		
			C		
GAM1658	GNG4	3'	GCTCACTGCGACCTCCACCTC	15618	A
			GAGGT GAGGTTGCAGTGAGT		

			CTCCA CTCCAGCGTCACTCG		
			C		
GAM1658	GP5	3'	GGCCCGCAACCCCTCCTC	15655	T A AGT A
			GAGG AG GGTTGC G GTC		
			CTCC TC CCAACG C CGG		
			_ C _ _ C		
GAM1658	GREB1	3'	CACTGCAACCTCTGCCTC	27865	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	GRWD	3'	CACTGCAACCTCCGCCTC	48963	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	GTF2E1	3'	CACTGCAACCTCTGCCTC	18611	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	GTPBG3	3'	TACTGCAACCTCCACCTC	50907	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCAACGTCAT		
			C		
GAM1658	GTPBG3	3'	TGGCTCACTGCAACCTCCATCT	50914	A
	C		GAGGT GAGGTTGCAGTGAGTCA		
			CTCTA CTCCAACGTCACTCGGT		
			C		
GAM1658	H-plk	5'	GACTCACTGCAACCTCCACCTC	31809	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCACTCAG		
			C		
GAM1658	HRH4	3'	CACTGCAACCTCTGCCTC	41248	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	HSPC065	3'	CGCTGCAACCTCCTCCTC	26293	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCGC		
			TC		
GAM1658	HSPC065	3'	TGGCTCACTGCAACCTCCACCT	26331	A
	C		GAGGT GAGGTTGCAGTGAGTCA		

			CTCCA CTCCAACGTC	ACTCGGT	
			C		
GAM1658	ICK	3'	CTGCAACCTCTGCCTC	29928	
			GAGGTAGAGGTTGCAG		
			CTCCGTCTCCAACGTC		
GAM1658	JAM1	5'	CACTGCAACCTCCTCCTC	57916	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			TC		
GAM1658	JM11	3'	CACTGCAACCTCTGCCTC	53252	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	KCNMB3L	5'	ACCCACGGTGGCCTCTCCTC	26957	T TG A A
			GAGG AGAGGT C GTG GT		
			CTCC TCTCCG G CAC CA		
			— GT G C		
GAM1658	KIAA0063	3'	GGCTCACTGCAACCTCCACCTC	29636	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTC	ACTCGG	
			C		
GAM1658	KIAA0391	3'	CACTGCAACCTCTGCCTC	27909	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	KIAA0426	3'	CACTGCAACCTCCGCCTC	28255	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	KIAA0459	3'	GGCTCACTGCAACCTCCACCTC	61002	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTC	ACTCGG	
			C		
GAM1658	KIAA0469	3'	CACTGCAGCCTCCACCTC	29323	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1658	KIAA0513	3'	ACTCACTGCAACCTCCACCTC	28327	A
			GAGGT GAGGTTGCAGTGAGT		

			CTCCA CTCCAACGTC	ACTCA		
			C			
GAM1658	KIAA0513	5'	CACTGCAGCCTCCACCTC	28343	A	
			GAGGT GAGGTTGCAGTG			
			CTCCA CTCCGACGTCAC			
			C			
GAM1658	KIAA0527	3'	CACTGCAACCTCTGCCTC	95795		
			GAGGTAGAGGTTGCAGTG			
			CTCCGTCTCCAACGTCAC			
GAM1658	KIAA0544	3'	CACGCACCTCTACC	70894	T A	
			GGTAGAGGT GC GTG			
			CCATCTCCA CG CAC			
GAM1658	KIAA0544	3'	CACTGCAACCTCCGCCTC	70896	TA	
			GAGG GAGGTTGCAGTG			
			CTCC CTCCAACGTCAC			
			GC			
GAM1658	KIAA0557	3'	TGGCTCACCACAACCTCCACCT	78012	A CA	
			C GAGGT GAGGTTG GTGAGTCA			
			CTCCA CTCCAAC CACTCGGT			
			C AC			
GAM1658	KIAA0561	3'	CACTGCAACCTCCGCCTC	65875	TA	
			GAGG GAGGTTGCAGTG			
			CTCC CTCCAACGTCAC			
			GC			
GAM1658	KIAA0562	3'	CTGCAACCTCCGCCTC	28153	TA	
			GAGG GAGGTTGCAG			
			CTCC CTCCAACGTC			
			GC			
GAM1658	KIAA0563	5'	CACTGCAACCTCTGCCTC	29184		
			GAGGTAGAGGTTGCAGTG			
			CTCCGTCTCCAACGTCAC			
GAM1658	KIAA0594	3'	TACTGCAACCTCCGCCTC	64901	TA	
			GAGG GAGGTTGCAGTG			
			CTCC CTCCAACGTCAT			
			GC			
GAM1658	KIAA0599	3'	CACTGCAACCTCCGCCTC	77169	TA	
			GAGG GAGGTTGCAGTG			

		CTCC CTCCAACGTCAC	
		GC	
GAM1658	KIAA0599	3' TACTGCAACCTCCGCCTC	77189 TA
		GAGG GAGGTTGCAGTG	
		CTCC CTCCAACGTCAT	
		GC	
GAM1658	KIAA0630	3' ACCACCACCTCTACC	89386 TGCA A
		GGTAGAGGT GTG GT	
		CCATCTCCA CAC CA	
		C _ _	
GAM1658	KIAA0720	3' CACTGCAACCTCTGCCTC	62318
		GAGGTAGAGGTTGCAGTG	
		CTCCGTCTCCAACGTCAC	
GAM1658	KIAA0841	3' CACTGCAACCTCCGCCTC	71376 TA
		GAGG GAGGTTGCAGTG	
		CTCC CTCCAACGTCAC	
		GC	
GAM1658	KIAA0841	3' CACTGCAACCTCTGCCTC	71377
		GAGGTAGAGGTTGCAGTG	
		CTCCGTCTCCAACGTCAC	
GAM1658	KIAA1041	3' CACTGCAACCTCCGCCTC	30128 TA
		GAGG GAGGTTGCAGTG	
		CTCC CTCCAACGTCAC	
		GC	
GAM1658	KIAA1054	3' CACTGCAACCTCCGCCTC	68429 TA
		GAGG GAGGTTGCAGTG	
		CTCC CTCCAACGTCAC	
		GC	
GAM1658	KIAA1161	5' CACTGCAACCCCTCCTC	81736 T A
		GAGG AG GGTTGCAGTG	
		CTCC TC CCAACGTCAC	
		_ C	
GAM1658	KIAA1170	3' CACTGCAACCTCCGCCTC	69846 TA
		GAGG GAGGTTGCAGTG	
		CTCC CTCCAACGTCAC	
		GC	
GAM1658	KIAA1193	3' CACTGCAACCTCCGCCTC	67632 TA
		GAGG GAGGTTGCAGTG	

			CTCC CTCCAACGTCAC		
			GC		
GAM1658	KIAA1198	3'	CACCGCAACCTCCGCCTC 63291	TA	A
			GAGG GAGGTTGC GTG		
			CTCC CTCCAACG CAC		
			GC C		
GAM1658	KIAA1198	3'	CACTGCAACCTCCACTTC 63293	A	
			GAGGT GAGGTTGCAGTG		
			CTTCA CTCCAACGTCAC		
			C		
GAM1658	KIAA1209	3'	CACTGCAGCCTCCACCTC 60751	A	
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1658	KIAA1257	3'	CACCGCAACCTCCGCCTC 62730	TA	A
			GAGG GAGGTTGC GTG		
			CTCC CTCCAACG CAC		
			GC C		
GAM1658	KIAA1320	5'	CACTGCAACCTCTGCCTC 69297		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	KIAA1373	3'	GCTCACTGCAACCTCCACCTC 70942	A	
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCAC TCG		
			C		
GAM1658	KIAA1497	5'	CACTGCAACCTCTGCCTC 67505		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	KIAA1508	3'	CACTGCAACCTCCGCCTC 61879	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	KIAA1571	3'	GCTCACCGCAACCTCCACCTC 60955	A	A
			GAGGT GAGGTTGC GTGAGT		
			CTCCA CTCCAACG CACTCG		
			C C		
GAM1658	KIAA1615	3'	GATCACTGCAACCTCCACCTC 68713	A	G
			GAGGT GAGGTTGCAGTGA TC		

			CTCCA CTCCAACGTC	ACT AG	
			C	—	
GAM1658	KIAA1655	3'	CACTGTAACTCCACCTC	66597	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCAATGTCAC		
			C		
GAM1658	KIAA1655	3'	CATTGCAACCTCCGCCTC	66601	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTTAC		
			GC		
GAM1658	KIAA1737	3'	CACTGCAACCTCCGCCTC	67351	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	KIAA1775	3'	TGACTCACACACCTCTACTTC	52386	TGCA
			GAGGTAGAGGT GTGAGTCA		
			CTTCATCTCCA CACTCAGT		
			CA		
GAM1658	KIAA1784	3'	CACTGCAACCTCCGCCTC	65145	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	KIAA1922	5'	CACTGCAACCTCCGCCTC	73617	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	KIAA1956	3'	CACTGCAGCCTCCACCTC	78431	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1658	KIAA1971	3'	TACTGCAACCTCCACCTC	74227	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCAACGTCAT		
			C		
GAM1658	KLK7	3'	CACTGCAACCTCCGCCTC	57729	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	KLK7	3'	CACTGCAACCTCCGCCTC	17289	TA
			GAGG GAGGTTGCAGTG		

			CTCC CTCCAACGTCAC		
			GC		
GAM1658	MCLC	3'	GGCTCACTGCAACCTCCACCTC 30691	A	
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCACCTCGG		
			C		
GAM1658	MEF-2	3'	CACTGCAACCTCCGCCTC 64379	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	MGC12518	3'	TACTGCAACCTCTGCC 64083		
			GGTAGAGGTTGCAGTG		
			CCGTCTCCAACGTCAT		
GAM1658	MGC13138	3'	CACTGCAACCTCTGCCTC 53014		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	MGC14836	3'	CACTGCAACCTCCGCCTC 53037	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	MGC1842	3'	TACTACAACCTCCGCCTC 65657	TA	C
			GAGG GAGGTTG AGTG		
			CTCC CTCCAAC TCAT		
			GC A		
GAM1658	MGC2474	3'	GACTCACTGCAACTTCCACCTC 43724	A	
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTTCAACGTCACCTCAG		
			C		
GAM1658	MGC29891	3'	CACTGCAACCTCCGCCTC 58202	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	MGC3113	3'	CACTGCAGCCTCCACCTC 43840	A	
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1658	MGC3329	3'	CACTGCAACCCCCGCCTC 44015	AGA	
			GAGGT GGTTCAGTG		



			CTCCG CCAACGTCAC	
			CCC	
GAM1658	MGC5149	3'	CACTGCAACCTCTGCCTC 72286	
			GAGGTAGAGGTTGCAGTG	
			CTCCGTCTCCAACGTCAC	
GAM1658	MGC9912	3'	GGCTCACTGCAACCTCCACCTC 54722	A
			GAGGT GAGGTTGCAGTGAGTC	
			CTCCA CTCCAACGTCACTCGG	
			C	
GAM1658	MLZE	5'	CACTGCAACCTCTGCCTC 48615	
			GAGGTAGAGGTTGCAGTG	
			CTCCGTCTCCAACGTCAC	
GAM1658	MMPL1	3'	CACTGCAGCCTCCACCTC 14717	A
			GAGGT GAGGTTGCAGTG	
			CTCCA CTCCGACGTCAC	
			C	
GAM1658	moblak	3'	CACTGCATCCTCCACCTC 55488	A T
			GAGGT GAGG TGCAGTG	
			CTCCA CTCC ACGTCAC	
			C T	
GAM1658	MOCS3	3'	CACTGCAACCTCCGCCTC 27149	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			GC	
GAM1658	MRPL44	3'	GGCTCACTGCAACCTCCACCTC 43323	A
			GAGGT GAGGTTGCAGTGAGTC	
			CTCCA CTCCAACGTCACTCGG	
			C	
GAM1658	MtFMT	3'	CACTGCAACCTCCGCCTC 57649	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			GC	
GAM1658	NDP52	3'	TGACTCACTACAGCCTCTGCCT 19535	C
	C		GAGGTAGAGGTTG AGTGAGTCA	
			CTCCGTCTCCGAC TCACTCAGT	
			A	
GAM1658	NDUFB1	5'	CACTGCAACCTCTGCCTC 15815	
			GAGGTAGAGGTTGCAGTG	

CTCCGTCTCCAACGTCAC

GAM1658 NDUFC2 3' GGCTCACTGCAACCTCCACCTC 15840 A  
GAGGT GAGGTTGCAGTGAGTC  
||||| |||||||||  
CTCCA CTCCAACGTCACCTCGG  
C

GAM1658 Nup43 3' GGCTCACTGCAACCTCCACCTC 45006 A  
GAGGT GAGGTTGCAGTGAGTC  
||||| |||||||||  
CTCCA CTCCAACGTCACCTCGG  
C

GAM1658 OSBPL2 3' CACCGCAACCTCCGCCTC 57856 TA A  
GAGG GAGGTTGC GTG  
||| ||||| ||  
CTCC CTCCAACG CAC  
GC C

GAM1658 OSBPL2 3' CACCGCAACCTCCGCCTC 29205 TA A  
GAGG GAGGTTGC GTG  
||| ||||| ||  
CTCC CTCCAACG CAC  
GC C

GAM1658 PASK 5' CACTGCAACCTCTGCCTC 30713  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1658 PELI1 5' CACTGCAACCTCCTCCTC 40255 TA  
GAGG GAGGTTGCAGTG  
||| |||||||  
CTCC CTCCAACGTCAC  
TC

GAM1658 PELI1 5' CACTGCAACCTCTGCCTC 40257  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1658 PIP3-E 3' CACTGCAACCTCTGCCTC 66801  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1658 PRO0365 5' GCTCACTGCAACCTCCACCTC 26162 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||||||  
CTCCA CTCCAACGTCACCTCG  
C

GAM1658 PRO1992 5' CACTGCAACCTCTGCCTC 26054  
GAGGTAGAGGTTGCAGTG  
|||||

CTCCGTCTCCAACGTCAC

GAM1658 PRO2955 3' CACTGCAACCTCTGCCTC 37632  
GAGGTAGAGGTTGCAGTG  
|||||||  
CTCCGTCTCCAACGTCAC

GAM1658 PSTPIP2 3' CACTGCAACCTCTGCCTC 44384  
GAGGTAGAGGTTGCAGTG  
|||||||  
CTCCGTCTCCAACGTCAC

GAM1658 RAB21 3' GGCTCACTGCAAGCTCCACCTC 30390 A G  
GAGGT GAG TTGCAGTGAGTC  
|||| ||| |||||  
CTCCA CTC AACGTCACTCGG  
C G

GAM1658 RAB33B 3' CACTGCAACCTCCGCCTC 48489 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 RAI 5' CACTGCAACCTCCGCCTC 21874 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 RASAL2 3' GACCCACTCTCCTATCTC 16723 AG TTGC A  
GAGGTAG G AGTG GTC  
||||| | ||| |||  
CTCTATC C TCAC CAG  
CT \_\_\_\_ C

GAM1658 RNF20 3' ACCACCAAACCTCTACCTC 38963 GCA A  
GAGGTAGAGGTT GTG GT  
||||||| ||| ||  
CTCCATCTCCAA CAC CA  
AC\_ \_

GAM1658 RNF8 3' GCTCACTGCAACCTCCACCTC 14230 A  
GAGGT GAGGTTGCAGTGAGT  
|||| |||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1658 RNO2 5' CACTGCAACCTCCACCTT 52764 A  
GAGGT GAGGTTGCAGTG  
|||| |||||  
TTCCA CTCCAACGTCAC  
C

GAM1658 SC4MOL 3' CACTGCAACCTCTGCCTC 22151  
GAGGTAGAGGTTGCAGTG  
|||||||

CTCCGTCTCCAACGTCAC

GAM1658 SCAMP-4 3' CACTGCAACCTCTGCCTC 54391  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1658 SCAND2 3' TGA CTCACTGCAACATCTGCCT 41891 G  
C GAGGTAGA GTTGCAGTGAGTCA  
||||| |||||  
CTCCGTCT CAACGTCACTCAGT  
A

GAM1658 SCYA16 3' CACTGTAACCTCCACCTC 15956 A  
GAGGT GAGGTTGCAGTG  
|||||  
CTCCA CTCCAATGTCAC  
C

GAM1658 SCYA22 3' ACCCATCCTCTGCCTC 90935 T CA  
GAGGTAGAGG TG GT  
||||| || ||  
CTCCGTCTCC AC CA  
T C\_

GAM1658 SCYA22 3' GGCTCACTACAACCTCGACCTC 90952 A C  
GAGGT GAGGTTG AGTGAGTC  
||||| |||||  
CTCCA CTCCAAC TCACTCGG  
G A

GAM1658 SERF1B 3' CACTGCAACCTCCGCCTC 43410 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 SIRPB1 3' CACTGCAACCCCGCCTC 20244 AGA  
GAGGT GGTTCAGTG  
|||||  
CTCCG CCAACGTCAC  
CCC

GAM1658 SLC11A1 3' ACTCATTGCAACCTCCACCTT 59450 A  
GAGGT GAGGTTGCAGTGAGT  
|||||  
TTCCA CTCCAACGTTACTCA  
C

GAM1658 SLC2A10 3' CACTGCAACCTCCACTTC 47817 A  
GAGGT GAGGTTGCAGTG  
|||||  
CTTCA CTCCAACGTCAC  
C

GAM1658 SP2 3' CGCCACAACCTCTCCTC 11888 T CA  
GAGG AGAGGTTG GTG  
||||| |||

CTCC TCTCCAAC CGC  
 — AC  
 GAM1658 STAF65(gamma) 3' GACTCACTGCAACCTCTGCCTC 29436  
 GAGGTAGAGGTTGCAGTGAGTC  
 |||||  
 CTCCGTCTCCAACGTCACCTCAG

GAM1658 SUN1 3' CACTGCAGCCTCCACCTC 47155 A  
 GAGGT GAGGTTGCAGTG  
 |||||  
 CTCCA CTCCGACGTCAC  
 C

GAM1658 SYT13 3' CACTGCAACCTCCGCCTC 93451 TA  
 GAGG GAGGTTGCAGTG  
 |||||  
 CTCC CTCCAACGTCAC  
 GC

GAM1658 TOLLIP 3' TGGTTCACAACCCCCACCCTC 38690 TAGA\_ GCA GT  
 GAGG GGTT GTGA CA  
 |||||  
 CTCC CCAA CACT GT  
 CACCC — TG

GAM1658 TOR1B 3' ACTCACTGCAACCTCCGCT 27195 TA  
 GG GAGGTTGCAGTGAGT  
 |||||  
 TC CTCCAACGTCACCTCA  
 GC

GAM1658 TRIM5 3' GGTTCACTGCAACCTCCACCTC 52301 A GT  
 GAGGT GAGGTTGCAGTGA C  
 |||||  
 CTCCA CTCCAACGTCACCT G  
 C TG

GAM1658 TRIM6 3' CACTGCAACCTCTGCCTC 54135  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC

GAM1658 TU12B1-TY 3' CACTGCAACCTCTGCCTC 33371  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC

GAM1658 TUCAN 3' CACTGCAACCTCTGCCTC 30271  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC

GAM1658 UBF-fl 3' CACTGCAACCTCTGCCTC 51555  
 GAGGTAGAGGTTGCAGTG  
 |||||

CTCCGTCTCCAACGTCAC

GAM1658 USP22 3' GGCTCACTGCAACCTCCACCTC 68019 A  
GAGGT GAGGTTGCAGTGAGTC  
||||| |||||||||  
CTCCA CTCCAACGTCACCTCGG  
C

GAM1658 VDU1 3' CACTGCGAGCCTCCACCTC 30414 A  
GAGGT GAGGTTGCAGTG  
||||| |||||||||  
CTCCA CTCCGACGTCAC  
C

GAM1658 VPS33A 3' CTCACCTGCAACCTCCACCTC 43338 A  
GAGGT GAGGTTGCAGTGAG  
||||| |||||||||  
CTCCA CTCCAACGTCACCTC  
C

GAM1658 WBSCR20A 5' CACCGCAACCTCTGCCTC 49650 A  
GAGGTAGAGGTTGC GTG  
||||| |||  
CTCCGTCTCCAACG CAC  
C

GAM1658 ZTL1 3' CACTGCAACCTCTGCCTC 43911  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 LOC112724 5' GGCTCACTGCAACCTCCACCTC 56501 A  
GAGGT GAGGTTGCAGTGAGTC  
||||| |||||||||  
CTCCA CTCCAACGTCACCTCGG  
C

GAM1658 LOC113675 5' CACTGCAACCTCCGCCTC 56570 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 LOC115219 5' CACTGCAACCTCCGCCTC 73298 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 LOC116411 5' CGCTACAACCTCCACCTC 73860 A C  
GAGGT GAGGTTG AGTG  
||||| ||||| |||  
CTCCA CTCCAAC TCGC  
C A

GAM1658 LOC119392 3' TGA CTCACTGCAACCTCTGCCT 59140  
C GAGGTAGAGGTTGCAGTGAGTCA  
||||| |||||||||

CTCCGTCTCCAACGTCACTCAGT

GAM1658	LOC120114	3'	GCTCACTGCAATCTCCACCTC	75531	A
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCTAACGTCACTCG		
			C		
GAM1658	LOC120939	3'	CACTGTAACTCCACCTC	76248	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCAATGTCAC		
			C		
GAM1658	LOC121219	5'	TGACTCAGGCCCTCAACCTC	74050	A TT AG
			GAGGT GAGG GC TGAGTCA		
			CTCCA CTCC CG ACTCAGT		
			A _ G_		
GAM1658	LOC126364	3'	CACTGCAACCTCCGCCTC	75684	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	LOC126661	3'	CACTGCAACCTCCGCCTC	74545	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	LOC128077	3'	CACTGCAACCTCCGCCTC	74707	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	LOC128077	3'	CACTGCAACCTCTGCCTC	74709	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1658	LOC128387	3'	CACTGCAACCTCCACTTC	74747	A
			GAGGT GAGGTTGCAGTG		
			CTTCA CTCCAACGTCAC		
			C		
GAM1658	LOC128989	3'	CACTGCAACCTCCGCCTC	74806	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1658	LOC130813	3'	CACCGCAACCTCCGCCTC	75764	TA A
			GAGG GAGGTTGC GTG		

		CTCC CTCCAACG CAC		
		GC C		
GAM1658	LOC132625 3'	TGGCTCACTGCAACCTCCACCT 75917	A	
	C	GAGGT GAGGTTGCAGTGAGTCA		
		CTCCA CTCCAACGTCACCTCGGT		
		C		
GAM1658	LOC133686 3'	CTGCAACCTCCATCTC 75121	A	
		GAGGT GAGGTTGCAG		
		CTCTA CTCCAACGTC		
		C		
GAM1658	LOC135154 3'	ACTCACTGCAACTTCCGCC 75212	TA	
		GG GAGGTTGCAGTGAGT		
		CC CTTCAACGTCACCTCA		
		GC		
GAM1658	LOC135293 3'	CACTGCAACCTCTGCCTC 76175		
		GAGGTAGAGGTTGCAGTG		
		CTCCGTCTCCAACGTCAC		
GAM1658	LOC135763 3'	CACTGCAACCTCCGCCTC 56787	TA	
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCAC		
		GC		
GAM1658	LOC142913 5'	TGACCACTGCAGCCTCCACCTC 76419	A	A
		GAGGT GAGGTTGCAGTG GTCA		
		CTCCA CTCCGACGTCAC CAGT		
		C		
		—		
GAM1658	LOC143187 3'	TGGCTCACTGCAACCTCCACCT 59103	A	
	C	GAGGT GAGGTTGCAGTGAGTCA		
		CTCCA CTCCAACGTCACCTCGGT		
		C		
GAM1658	LOC143241 5'	CACTGCAACCTCTGCCTC 57174		
		GAGGTAGAGGTTGCAGTG		
		CTCCGTCTCCAACGTCAC		
GAM1658	LOC144248 5'	GCTCACTGCAACCTCCACCTC 76738	A	
		GAGGT GAGGTTGCAGTGAGT		
		CTCCA CTCCAACGTCACCTCG		
		C		
GAM1658	LOC144317 5'	ACTCACTGCAACCTCTTCCTC 76782	T	
		GAGG AGAGGTTGCAGTGAGT		



		CTCC TCTCCAACGTCACTCA			
		T			
GAM1658	LOC144524 5'	GCTCACTGCAACCTCCACCTC	83130	A	
		GAGGT GAGGTTGCAGTGAGT			
		CTCCA CTCCAACGTCACTCG			
		C			
GAM1658	LOC145216 3'	ACCCACTGCTTTTCCCC	83260	TA TT	A
		GG GAGG GCAGTG GT			
		CC CTTT CGTCAC CA			
		C_ T_ C			
GAM1658	LOC145268 5'	CACTGCAACCTCCACCC	77055	A A	
		G GGT GAGGTTGCAGTG			
		C CCA CTCCAACGTCAC			
		_ C			
GAM1658	LOC145725 3'	GCTCACTGCAGCCTCCACCTC	77409	A	
		GAGGT GAGGTTGCAGTGAGT			
		CTCCA CTCCGACGTCACTCG			
		C			
GAM1658	LOC145732 3'	GCTCACTGCAGCCTCCACCTC	77431	A	
		GAGGT GAGGTTGCAGTGAGT			
		CTCCA CTCCGACGTCACTCG			
		C			
GAM1658	LOC145757 5'	CACTACAACCTCTGCCTC	77457		C
		GAGGTAGAGGTTG AGTG			
		CTCCGTCTCCAAC TCAC			
		A			
GAM1658	LOC146229 3'	CTGCAACCTCCACCTC	77750	A	
		GAGGT GAGGTTGCAG			
		CTCCA CTCCAACGTC			
		C			
GAM1658	LOC146229 3'	GGCTCACTGCAACCTCCACCTC	77768	A	
		GAGGT GAGGTTGCAGTGAGTC			
		CTCCA CTCCAACGTCACTCGG			
		C			
GAM1658	LOC146784 5'	GGCTCACTGCAACCTCCACCTC	78122	A	
		GAGGT GAGGTTGCAGTGAGTC			
		CTCCA CTCCAACGTCACTCGG			
		C			
GAM1658	LOC146901 3'	CATTGCAACCTCCACCTT	83835	A	
		GAGGT GAGGTTGCAGTG			

	TTCCA CTCCAACGTTAC		
	C		
GAM1658 LOC146909 3'	CACTGCAACCTCCGCCTC	78168	TA
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1658 LOC146952 5'	GCTCACTGCAACCTCCACCTC	83869	A
	GAGGT GAGGTTGCAGTGAGT		
	CTCCA CTCCAACGTCACCTCG		
	C		
GAM1658 LOC147071 5'	CACTGCAACCTCTGCCTC	72995	
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1658 LOC147407 3'	CACTGCAACCTCCGCCTC	76324	TA
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1658 LOC147660 3'	TGACTCACAGCAACCTCCGCCT	78398	TA A
C	GAGG GAGGTTGC GTGAGTCA		
	CTCC CTCCAACG CACTCAGT		
	GC A		
GAM1658 LOC147817 3'	TGGCTCACTGCAACCTCCACCT	78509	A
C	GAGGT GAGGTTGCAGTGAGTCA		
	CTCCA CTCCAACGTCACCTCGGT		
	C		
GAM1658 LOC147990 3'	CACTACAACCTCTGCCTC	84090	C
	GAGGTAGAGGTTG AGTG		
	CTCCGTCTCCAAC TCAC		
	A		
GAM1658 LOC148137 3'	CACGGCAACCTCCACCTC	58421	A A
	GAGGT GAGGTTGC GTG		
	CTCCA CTCCAACG CAC		
	C G		
GAM1658 LOC148189 5'	GGCTCACTGCAACCTCCACCTC	78717	A
	GAGGT GAGGTTGCAGTGAGTC		
	CTCCA CTCCAACGTCACCTCGG		
	C		
GAM1658 LOC148198 3'	GCTCACTGCAACCTCCATCTC	70683	A
	GAGGT GAGGTTGCAGTGAGT		

		CTCTA CTCCAACGTCACTCG		
		C		
GAM1658	LOC148709 3'	CACTACAACCTCCGCCTC	78935	TA C
		GAGG GAGGTTG AGTG		
		CTCC CTCCAAC TCAC		
		GC A		
GAM1658	LOC148918 5'	ACTCAGCTTCTTCTACCTC	79054	TT AG
		GAGGTAGAGG GC TGAGT		
		CTCCATCTTC CG ACTCA		
		TT _		
GAM1658	LOC148918 5'	CACTGCAGCCTCCACCTC	79064	A
		GAGGT GAGGTTGCAGTG		
		CTCCA CTCCGACGTCAC		
		C		
GAM1658	LOC149506 3'	CACTGCAACCTCTGCCTC	84453	
		GAGGTAGAGGTTGCAGTG		
		CTCCGTCTCCAACGTCAC		
GAM1658	LOC149506 3'	CACTGCAACTTCCACCTC	84454	A
		GAGGT GAGGTTGCAGTG		
		CTCCA CTTCAACGTCAC		
		C		
GAM1658	LOC150397 3'	CATTGCAACCTCCGCCTC	79843	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTTAC		
		GC		
GAM1658	LOC150519 3'	CTGCAACCTGCCACCTC	79917	AG_
		GAGGT AGGTTGCAG		
		CTCCA TCCAACGTC		
		CCG		
GAM1658	LOC150696 3'	CACTGCAGCCTCCACCTC	58478	A
		GAGGT GAGGTTGCAGTG		
		CTCCA CTCCGACGTCAC		
		C		
GAM1658	LOC150960 3'	CGCTGCAACCTCCGCCTC	80058	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCGC		
		GC		
GAM1658	LOC151057 3'	CACTGCAACCTCTGCCTC	85208	
		GAGGTAGAGGTTGCAGTG		

CTCCGTCTCCAACGTCAC

GAM1658 LOC151201 3' GCTCACTGCAACCTCCACCTC 85283 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||||||  
CTCCA CTCCAACGTCACCTCG  
C

GAM1658 LOC151475 5' CACTGCAACCTCTGCCTC 85394  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 LOC151475 5' TGGCTCACTGCAACCTCCACCT 85423 A  
C GAGGT GAGGTTGCAGTGAGTCA  
||||| |||||||||  
CTCCA CTCCAACGTCACCTCGGT  
C

GAM1658 LOC151826 3' CACTGCAACCTCCGCCTC 80354 TA  
GAGG GAGGTTGCAGTG  
||| |||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 LOC151877 3' GGCTCACTACAACCACCACCTC 85508 AGA C  
GAGGT GGTTG AGTGAGTC  
|||| ||| |||||||  
CTCCA CCAAC TCACTCGG  
CCA A

GAM1658 LOC152343 3' GACTCAGTGCAACCTCCGCCTC 80565 TA G  
GAGG GAGGTTGCA TGAGTC  
||| ||||||| |||||  
CTCC CTCCAACGT ACTCAG  
GC G

GAM1658 LOC152445 3' CACTGCAACCTCTGCCTC 85749  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||  
CTCCGTCTCCAACGTCAC

GAM1658 LOC152582 5' CACCGCAACCTCTGCCTC 85789 A  
GAGGTAGAGGTTGC GTG  
||||| ||||| |||  
CTCCGTCTCCAACG CAC  
C

GAM1658 LOC152620 3' CACTACAACCTCTGCCTC 60078 C  
GAGGTAGAGGTTG AGTG  
||||| ||||| |||  
CTCCGTCTCCAAC TCAC  
A

GAM1658 LOC152719 5' CACTGCAACCTCTGCCTC 85848  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||

CTCCGTCTCCAACGTCAC

GAM1658 LOC152794 5' CTCAGTGAACCTCTACCTC 80675  
GAGGTAGAGGTTGCAGTGAG  
|||||  
CTCCATCTCCAACGTCACCTC

GAM1658 LOC152851 3' CGCTGCAACCTCCACCC 80708 A A  
G GGT GAGGTTGCAGTG  
| |||  
C CCA CTCCAACGTCGC  
\_ C

GAM1658 LOC153077 3' CACTGCAACCTCCGCCTC 85907 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 LOC153688 3' GGCTCACTGCAACCTCCACCTC 86117 A  
GAGGT GAGGTTGCAGTGAGTC  
|||| |||||  
CTCCA CTCCAACGTCACCTCGG  
C

GAM1658 LOC153883 5' CACTGCAACCTCCACC 80979 A  
GGT GAGGTTGCAGTG  
||| |||||  
CCA CTCCAACGTCAC  
C

GAM1658 LOC154075 3' CACTGCAACCTCCGCCTC 81044 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 LOC154282 5' GGCTCACTGCAACCTCCACCTC 86207 A  
GAGGT GAGGTTGCAGTGAGTC  
|||| |||||  
CTCCA CTCCAACGTCACCTCGG  
C

GAM1658 LOC154877 3' GCTCACTGCAACCTCTACCTC 86298  
GAGGTAGAGGTTGCAGTGAGT  
|||||  
CTCCATCTCCAACGTCACCTCG

GAM1658 LOC155100 5' ACCCACGGTGGCCTCTCCTC 73023 T TG A A  
GAGG AGAGGT C GTG GT  
||| |||| | |||  
CTCC TCTCCG G CAC CA  
\_ GT G C

GAM1658 LOC157247 5' GCTCACTGCAACCTCCACC 81368 A  
GGT GAGGTTGCAGTGAGT  
||| |||||

CCA CTCCAACGTCACTCG  
 C  
 GAM1658 LOC157798 5' CACTGCAACCTCCGCCTC 86548 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1658 LOC157858 5' CACTGCAACCTCTGCCTC 86584  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1658 LOC158476 3' CACTGCAACCTCCGCC 86838 TA  
 GG GAGGTTGCAGTG  
 || |||||  
 CC CTCCAACGTCAC  
 GC  
 GAM1658 LOC158668 3' CACTGCAACCTCTGCCTC 69365  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1658 LOC158865 5' CACTGCAACCTCTGCCTC 86933  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1658 LOC161829 3' CACTGCAACCTCCGCCTC 82312 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1658 LOC196047 5' CACTGCAACCTCCGCCTC 89594 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1658 LOC196264 3' CACTGCAACCTCTGCCTC 87603  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1658 LOC196411 3' CACTGCAACCTCCGCCTC 87668 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1658 LOC196529 3' GCTCACTGCAACCTCCACCTC 87775 A  
 GAGGT GAGGTTGCAGTGAGT  
 |||||

	CTCCA CTCCAACGTC	ACTCG	
	C		
GAM1658 LOC196761 3'	ACCCACAACACCTCTGCC	89550	T CA A
	GGTAGAGGT G GTG GT		
	CCGTCTCCA C CAC CA		
	_AA C		
GAM1658 LOC196957 3'	GCTCACTGCAGCCTCCACCTC	87825	A
	GAGGT GAGGTTGCAGTGAGT		
	CTCCA CTCCGACGTC	ACTCG	
	C		
GAM1658 LOC196961 3'	GCTCACTGCAGCCTCCACCTC	87846	A
	GAGGT GAGGTTGCAGTGAGT		
	CTCCA CTCCGACGTC	ACTCG	
	C		
GAM1658 LOC197138 3'	GCTCACTGCAGCCTCCACCTC	87919	A
	GAGGT GAGGTTGCAGTGAGT		
	CTCCA CTCCGACGTC	ACTCG	
	C		
GAM1658 LOC197358 3'	CTGCAACCTCCGCCTC	88033	TA
	GAGG GAGGTTGCAG		
	CTCC CTCCAACGTC		
	GC		
GAM1658 LOC199699 3'	GCTCACTGCAAGCTCCACCTC	88309	A G
	GAGGT GAG TTGCAGTGAGT		
	CTCCA CTC AACGTC	ACTCG	
	C G		
GAM1658 LOC199786 3'	CACTGCAACCTCCGCCTC	88370	TA
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1658 LOC200014 3'	CGCTGCAACCCCCACCTC	88523	AGA
	GAGGT GGTTGCAGTG		
	CTCCA CCAACGTCGC		
	CCC		
GAM1658 LOC200169 5'	CACTGCAACCTCTGCCTC	89945	
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1658 LOC200268 3'	CACTGCAACCTCTGCCTC	88678	
	GAGGTAGAGGTTGCAGTG		

CTCCGTCTCCAACGTCAC

GAM1658 LOC200310 3' CACTACAACCTCTGCCTC 65729 C  
GAGGTAGAGGTTG AGTG  
|||||||  
CTCCGTCTCCAAC TCAC

A

GAM1658 LOC200314 3' TGGCTCACTGCAACCTCCACCT 90020 A  
C GAGGT GAGGTTGCAGTGAGTCA  
|||||  
CTCCA CTCCAACGTCACTCGGT

C

GAM1658 LOC200339 3' CACTGCAACCTCTGCCTC 90033  
GAGGTAGAGGTTGCAGTG  
|||||||  
CTCCGTCTCCAACGTCAC

GAM1658 LOC200845 5' CACTGCAACCTCCGCCTC 88896 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 LOC200860 3' TGGTTCCTGCAACCTCCACCT 90178 A GT  
C GAGGT GAGGTTGCAGTGA CA  
||||| ||  
CTCCA CTCCAACGTCACT GT  
C TG

GAM1658 LOC201173 5' CACTGCAACCTCTGCCTC 87325  
GAGGTAGAGGTTGCAGTG  
|||||||  
CTCCGTCTCCAACGTCAC

GAM1658 LOC201220 5' CACTGCAACCTCTGCCTC 87345  
GAGGTAGAGGTTGCAGTG  
|||||||  
CTCCGTCTCCAACGTCAC

GAM1658 LOC201294 3' CACTGCAACCTCCGCCTC 88203 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 LOC201294 3' CACTGCAACCTCCGCCTC 88204 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 LOC201411 3' CACTGCAACCTCTGCCTC 62952  
GAGGTAGAGGTTGCAGTG  
|||||||



CTCCGTCTCCAACGTCAC

GAM1658 LOC201626 3' CACTGCAACCTCCGCC 88988 TA  
GG GAGGTTGCAGTG  
|| |||||  
CC CTCCAACGTCAC  
GC

GAM1658 LOC201627 3' ACTGCAACCTCCACCTC 89003 A  
GAGGT GAGGTTGCAGT  
|||| |||||  
CTCCA CTCCAACGTCA  
C

GAM1658 LOC201696 3' TGA CTCACTATCACTTTACCTC 63138 GTTGC  
GAGGTAGAG AGTGAGTCA  
||||| |||||  
CTCCATTTCTCACTCAGT  
ACTA\_

GAM1658 LOC202025 3' CACTGCAACCTCCGCCTC 90284 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 LOC202934 3' CACTACAACCTCTGCCTC 90404 C  
GAGGTAGAGGTTG AGTG  
||||||| |||  
CTCCGTCTCCAAC TCAC  
A

GAM1658 LOC203297 5' CACTGCAACCTCTGCCTC 75349  
GAGGTAGAGGTTGCAGTG  
|||||||  
CTCCGTCTCCAACGTCAC

GAM1658 LOC203350 3' ACTGCAACCTCCGCCTC 90557 TA  
GAGG GAGGTTGCAGT  
||| |||||  
CTCC CTCCAACGTCA  
GC

GAM1658 LOC204804 3' GCTCACTGCAACCTCGACCTC 89475 A  
GAGGT GAGGTTGCAGTGAGT  
|||| |||||  
CTCCA CTCCAACGTCACTCG  
G

GAM1658 LOC204804 3' GGCTCACTGCCACCTCCACCTC 89481 A T  
GAGGT GAGGT GCAGTGAGTC  
|||| ||| |||||  
CTCCA CTCCA CGTCACTCGG  
C C

GAM1658 LOC219735 3' CACTGCAACCTCTGCCTC 93107  
GAGGTAGAGGTTGCAGTG  
|||||||

CTCCGTCTCCAACGTCAC

GAM1658	LOC219894	3'	TGGTTC	ACTGCAAGCTCCACCT	93291	A	G	GT
		C		GAGGT GAG TTGCAGTGA CA				
				CTCCA CTC AACGTC	ACT GT			
				C G	TG			
GAM1658	LOC220662	3'	CACTGCAACCTCCACTTC		91167	A		
				GAGGT GAGGTTGCAGTG				
				CTTCA CTCCAACGTCAC				
				C				
GAM1658	LOC220662	3'	TGGTTC	ACTGCAACCTCCACCT	91185	A		GT
		C		GAGGT GAGGTTGCAGTGA CA				
				CTCCA CTCCAACGTC	ACT GT			
				C	TG			
GAM1658	LOC221035	3'	CACTACAACCTCTGCCTC		93162	C		
				GAGGTAGAGGTTG AGTG				
				CTCCGTCTCCAAC TCAC				
				A				
GAM1658	LOC221174	5'	GCTCACTGCGACCTCCACCTC		93503	A		
				GAGGT GAGGTTGCAGTGAGT				
				CTCCA CTCCAGCGTC	ACTCG			
				C				
GAM1658	LOC221271	3'	CACTGCAACCTCTGCCTC		91850			
				GAGGTAGAGGTTGCAGTG				
				CTCCGTCTCCAACGTCAC				
GAM1658	LOC221296	3'	GGCTCACTGCAACCTCCACCTC		91968	A		
				GAGGT GAGGTTGCAGTGAGTC				
				CTCCA CTCCAACGTC	ACTCGG			
				C				
GAM1658	LOC221495	3'	TGACTCACCTTCTTCTGCC		93865		TTGCA	
				GGTAGAGG GTGAGTCA				
				CCGTCTTC CACTCAGT				
				TTC__				
GAM1658	LOC221663	5'	TGGCTCACTGCAACCTCCACCT		93826	A		
		C		GAGGT GAGGTTGCAGTGAGTCA				
				CTCCA CTCCAACGTC	ACTCGGT			
				C				
GAM1658	LOC221715	5'	ACCCAAATGCCTCTACCTT		93748		TGCAG A	
				GAGGTAGAGGT TG GT				

	TTCCATCTCCG	AC CA	
	TAA__ C		
GAM1658	LOC222070 5'	CACTGCAACCTCTGCCTC	94152
		GAGGTAGAGGTTGCAGTG	
		CTCCGTCTCCAACGTCAC	
GAM1658	LOC253612 5'	CACTGCAACCTCCGCCTC	96742
		GAGG GAGGTTGCAGTG	TA
		CTCC CTCCAACGTCAC	
		GC	
GAM1658	LOC253664 3'	CATTGCAACCTCTGCCTC	94809
		GAGGTAGAGGTTGCAGTG	
		CTCCGTCTCCAACGTTAC	
GAM1658	LOC253666 5'	CACTGCAACCTCCGCCTC	95060
		GAGG GAGGTTGCAGTG	TA
		CTCC CTCCAACGTCAC	
		GC	
GAM1658	LOC253779 3'	CACTGCAACCTCCGCCTC	97144
		GAGG GAGGTTGCAGTG	TA
		CTCC CTCCAACGTCAC	
		GC	
GAM1658	LOC255497 3'	CACTGCAACCTCCGCCTC	97188
		GAGG GAGGTTGCAGTG	TA
		CTCC CTCCAACGTCAC	
		GC	
GAM1658	LOC255919 3'	CTGCAACCTCTGCCTC	95032
		GAGGTAGAGGTTGCAG	
		CTCCGTCTCCAACGTC	
GAM1658	LOC256267 3'	CACTGCAACCTCCGCCTC	96798
		GAGG GAGGTTGCAGTG	TA
		CTCC CTCCAACGTCAC	
		GC	
GAM1658	LOC256306 3'	GCTCACTGCAACCTCCACCTC	96692
		GAGGT GAGGTTGCAGTGAGT	A
		CTCCA CTCCAACGTCAC	
		C	
GAM1658	LOC51200 3'	CACCACAACCTCTGCCTC	32991
		GAGGTAGAGGTTG	CA

		CTCCGTCTCCAAC CAC		
		AC		
GAM1658	LOC51219 5'	CACCGCAACCTCCGCCTC	33112	TA A
		GAGG GAGGTTGC GTG		
		CTCC CTCCAACG CAC		
		GC C		
GAM1658	LOC51696 3'	CACTGCAACCTCTGCCTC	32543	
		GAGGTAGAGGTTGCAGTG		
		CTCCGTCTCCAACGTCAC		
GAM1658	LOC57107 3'	TGACTCACTGCAACCTCCGCCT	39846	TA
	C	GAGG GAGGTTGCAGTGAGTCA		
		CTCC CTCCAACGTCACTCAGT		
		GC		
GAM1658	LOC57146 3'	GGCTCACTGCAACCTCCAACCTC	39926	GTA
		GAG GAGGTTGCAGTGAGTC		
		CTC CTCCAACGTCACTCGG		
		AAC		
GAM1658	LOC64102 5'	GACTCACTTGCAACTCCACCTC	42173	A G _
		GAGGT GAG TTGCA GTGAGTC		
		CTCCA CTC AACGT CACTCAG		
		C _ T		
GAM1658	LOC81034 3'	GCTCACTGCAACCTCCACCTC	47853	A
		GAGGT GAGGTTGCAGTGAGT		
		CTCCA CTCCAACGTCACTCG		
		C		
GAM1658	LOC89932 3'	TGGCTCACTGCAACCTCCACCT	60822	A
	C	GAGGT GAGGTTGCAGTGAGTCA		
		CTCCA CTCCAACGTCACTCGGT		
		C		
GAM1658	LOC90288 3'	CTCACTGCAACCTCCACCTC	62090	A
		GAGGT GAGGTTGCAGTGAG		
		CTCCA CTCCAACGTCACTC		
		C		
GAM1658	LOC90333 5'	CACTGCAACCTCCACTTC	62283	A
		GAGGT GAGGTTGCAGTG		
		CTTCA CTCCAACGTCAC		
		C		
GAM1658	LOC90333 3'	CACTGCAACCTCCTCCTC	62284	TA
		GAGG GAGGTTGCAGTG		

		CTCC CTCCAACGTCAC		
		TC		
GAM1658	LOC90371	5' TGGCTCACTGCAACCTCCACCT	62505	A
	C	GAGGT GAGGTTGCAGTGAGTCA		
		CTCCA CTCCAACGTCACTCGGT		
		C		
GAM1658	LOC90408	5' TGGCTCACTGCAACCTCTACCT	62671	
	C	GAGGTAGAGGTTGCAGTGAGTCA		
		CTCCATCTCCAACGTCACTCGGT		
GAM1658	LOC90459	3' CACTGCAACCTCCGCCTC	62883	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCAC		
		GC		
GAM1658	LOC90485	3' CACTGCAACCTCCGCCTC	63008	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCAC		
		GC		
GAM1658	LOC90591	3' GCTCACTGCAAGCTCCACCTC	63433	A G
		GAGGT GAG TTGCAGTGAGT		
		CTCCA CTC AACGTCACTCG		
		C G		
GAM1658	LOC90591	3' TGTTCACTGCCACCTCCACCTC	63448	A T T
		GAGGT GAGGT GCAGTGAG CA		
		CTCCA CTCCA CGTCACTT GT		
		C C -		
GAM1658	LOC91115	3' CACTGCAACCTCCGCCTC	64927	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCAC		
		GC		
GAM1658	LOC91115	3' GGCTCACTGCAACCTCCACCTC	64946	A
		GAGGT GAGGTTGCAGTGAGTC		
		CTCCA CTCCAACGTCACTCGG		
		C		
GAM1658	LOC91291	5' GCTCACTGCAACCTCGACCTC	65481	A
		GAGGT GAGGTTGCAGTGAGT		
		CTCCA CTCCAACGTCACTCG		
		G		
GAM1658	LOC91373	3' ACTCATCCTCTGCC	65831	TTGCA
		GGTAGAGG GTGAGT		

CCGTCTCC TACTCA

GAM1658 LOC92267 3' GCTCACTGCAACCTCCACCTC 68617 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1658 LOC92303 3' ACTCACTGCAACCTCTGCC 68819  
GGTAGAGGTTGCAGTGAGT  
||||| |||||||||  
CCGTCTCCAACGTCACTCA

GAM1658 LOC92466 3' CACTGCAACCTCCGCCTC 69423 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 LOC92661 5' TGGCTCACTGCAAGCTCCACCT 70090 A G  
C GAGGT GAG TTGCAGTGAGTCA  
||||| ||| |||||||||  
CTCCA CTC AACGTCACTCGGT  
C G

GAM1658 LOC92689 3' CACTGCAACCTCCGCCTC 70219 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 LOC92697 5' CACCGCAACCTCCGCCTC 70262 TA A  
GAGG GAGGTTGC GTG  
||| ||||||| |||  
CTCC CTCCAACG CAC  
GC C

GAM1658 LOC92697 5' CGCTACAACCTCCACCTC 70264 A C  
GAGGT GAGGTTG AGTG  
||||| ||||||| |||  
CTCCA CTCCAAC TCGC  
C A

GAM1658 LOC92841 3' CACCGCAACCTCCTCCTC 70706 TA A  
GAGG GAGGTTGC GTG  
||| ||||||| |||  
CTCC CTCCAACG CAC  
TC C

GAM1658 LOC93132 5' CACTGCAACCTCCGCCTC 71485 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1658 LOC93349 3' CACTGCAACCTCTGCCTC 56453  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||

CTCCGTCTCCAACGTCAC

GAM1658 LOC93408 5' CACTGCAACCTCTGCCTC 56475  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1659 A1BG 3' CACAGCAACCTCTACCTC 55411 A  
GAGGTAGAGGTTGC GTG  
|||||  
CTCCATCTCCAACG CAC  
A

GAM1659 ACVR1 5' CACTGCAGCCTCCACCTC 6604 A  
GAGGT GAGGTTGCAGTG  
|||||  
CTCCA CTCCGACGTCAC  
C

GAM1659 AHR 3' TGGCTCACTGCAACCTCTACCT 7885  
C GAGGTAGAGGTTGCAGTGAGTCA  
|||||  
CTCCATCTCCAACGTCAGTCTCGGT

GAM1659 AIM1 3' CACTGCAGCCTCTACCTC 91818  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCATCTCCGACGTCAC

GAM1659 ALDH1B1 3' CACTGCAACCTCCGCCTC 5491 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 ALDH3B1 3' GACTCACCCCTGCC 91526 A TTGCA  
GGTAG GG GTGAGTC  
|||||  
CCGTC CC CACTCAG  
C

GAM1659 AP3B2 5' CGCCGCAACCTCCTCCTC 16188 TA A  
GAGG GAGGTTGC GTG  
|||||  
CTCC CTCCAACG CGC  
TC C

GAM1659 APPBP2 3' CACTGCAACCTCCGCCTC 21074 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 AQP6 3' GGCTCACTGCAACCTCTACCTC 7958  
GAGGTAGAGGTTGCAGTGAGTC  
|||||

CTCCATCTCCAACGTCACCTCGG

GAM1659 AQP6 3' GGCTCACTGCAACCTCTACCTC 53938  
GAGGTAGAGGTTGCAGTGAGTC  
|||||  
CTCCATCTCCAACGTCACCTCGG

GAM1659 ARCN1 3' CACTGCAACCTCCGCCTC 7972 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 ATP8B2 3' GCTCACTGCAACCTCCACCTC 65227 A  
GAGGT GAGGTTGCAGTGAGT  
|||||  
CTCCA CTCCAACGTCACCTCG  
C

GAM1659 BRIP1 3' CACTGCAACCTTCACCTC 49397 AG  
GAGGT AGGTTGCAGTG  
|||||  
CTCCA TCCAACGTCAC  
CT

GAM1659 C7 3' CTGCAACCTCCGCCTC 5162 TA  
GAGG GAGGTTGCAG  
||| |||||  
CTCC CTCCAACGTC  
GC

GAM1659 CAMLG 3' CACCGCAACCTCCACCTT 8233 A A  
GAGGT GAGGTTGC GTG  
|||||  
TTCCA CTCCAACG CAC  
C C

GAM1659 CCNF 3' ACTCACTGTAACCTCCGCCTC 8312 TA  
GAGG GAGGTTGCAGTGAGT  
||| |||||  
CTCC CTCCAATGTCACCTCA  
GC

GAM1659 CDH17 3' CACTGCAACCTCCGCCTC 14501 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 CIAS1 5' CACTGCAGCCTCCACCTC 16899 A  
GAGGT GAGGTTGCAGTG  
|||||  
CTCCA CTCCGACGTCAC  
C

GAM1659 CLECSF12 3' GACTCACTGCAGCTATCTC 76690 AGA  
GAGGT GGTTCAGTGAGTC  
|||||



CTCTA TCGACGTCACTCAG

GAM1659 COX15 3' ACTCTGCAACCTCCACTTC 54308 A GT  
GAGGT GAGGTTGCA GAGT  
||||| ||||| ||||  
CTTCA CTCCAACGT CTCA

C  
GAM1659 CRHR1 3' TGA CTCA CACGATGACGCCTC 15215 AGAG CA  
GAGGT GTTG GTGAGTCA  
||||| ||||| |||||  
CTCCG TAGC CACTCAGT  
CAG\_ AC

GAM1659 CRTAP 3' CACTGCAACCTCCGCCTC 21030 TA  
GAGG GAGGTTGCAGTG  
||||| ||||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 CSNK2A2 5' GCTCACTGCAACCTCCACCTC 8564 A  
GAGGT GAGGTTGCAGTGAGT  
||||| ||||| ||||| |||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1659 CXCL16 3' GGCTCACTGCAACCCCCATCTC 41923 AGA  
GAGGT GGTTGCAGTGAGTC  
||||| ||||| ||||| |||||  
CTCTA CCAACGTCACTCGG  
CCC

GAM1659 CYLN2 3' CTGCAGCCTCCACCTC 12633 A  
GAGGT GAGGTTGCAG  
||||| ||||| |||||  
CTCCA CTCCGACGTC  
C

GAM1659 CYP1A2 3' CACTGCAACCTCTGCCTC 69099  
GAGGTAGAGGTTGCAGTG  
||||| ||||| ||||| |||||  
CTCCGTCTCCAACGTCAC

GAM1659 CYP1A2 3' GCTCACTGCAACCTCCACCTC 69113 A  
GAGGT GAGGTTGCAGTGAGT  
||||| ||||| ||||| |||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1659 CYP1A2 3' CACTGCAACCTCTGCCTC 5680  
GAGGTAGAGGTTGCAGTG  
||||| ||||| ||||| |||||  
CTCCGTCTCCAACGTCAC

GAM1659 CYP1A2 3' GCTCACTGCAACCTCCACCTC 5693 A  
GAGGT GAGGTTGCAGTGAGT  
||||| ||||| ||||| |||||

			CTCCA CTCCAACGTCACTCG		
			C		
GAM1659	CYP2B6	3'	GGCTCACTGCAACCTCCACC	5738	A
			GGT GAGGTTGCAGTGAGTC		
			CCA CTCCAACGTCACTCGG		
			C		
GAM1659	CYP4F3	3'	CATTGCAACCTCCGCCTC	6112	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTTAC		
			GC		
GAM1659	CYP8B1	3'	CACTACAACCTCTGCCTC	15258	C
			GAGGTAGAGGTTG AGTG		
			CTCCGTCTCCAAC TCAC		
			A		
GAM1659	CYP8B1	3'	CACTGCAACCTCTGCCTC	15260	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	DFFB	3'	CACTGCAACCTCCGCCTC	87378	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	DISC1	3'	GGCTCACTGCAACCTCTACCTC	37886	
			GAGGTAGAGGTTGCAGTGAGTC		
			CTCCATCTCCAACGTCACTCGG		
GAM1659	DSCR3	3'	GCTCACTGCAACCTCCACCTC	20185	A
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACTCG		
			C		
GAM1659	EHD2	3'	GCTCACTGCAACCTCCACCTC	27496	A
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACTCG		
			C		
GAM1659	EPB72	3'	CACTGCAACCTCCGCCTC	14600	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	F2RL2	3'	CATTGCAACCTCTGCCTC	14620	
			GAGGTAGAGGTTGCAGTG		

CTCCGTCTCCAACGTTAC

GAM1659	FANCF	3'	CAGTGCAACCTCTGCCTC	42671		G
			GAGGTAGAGGTTGCA TG			
			CTCCGTCTCCAACGT AC			
			G			
GAM1659	FBXL11	3'	TGATAGCACAACCTCTTCC	24576	T	CA GA
			GG AGAGGTTG GT GTCA			
			CC TCTCCAAC CG TAGT			
			T A_ A_			
GAM1659	FCAR	3'	GACTCACTGCAACCTTCGCCTC	55797		TA
			GAGG GAGGTTGCAGTGAGTC			
			CTCC TTCCAACGTCACTCAG			
			GC			
GAM1659	FCAR	3'	GACTCACTGCAACCTTCGCCTC	55813		TA
			GAGG GAGGTTGCAGTGAGTC			
			CTCC TTCCAACGTCACTCAG			
			GC			
GAM1659	FEZ1	3'	TGGCTCACTGCAACCTCCACCT	42582		A
	C		GAGGT GAGGTTGCAGTGAGTCA			
			CTCCA CTCCAACGTCACTCGGT			
			C			
GAM1659	FGF5	3'	GGCTCACTGCAACCTCCAACCTC	52492		GTA
			GAG GAGGTTGCAGTGAGTC			
			CTC CTCCAACGTCACTCGG			
			AAC			
GAM1659	FGF5	3'	GGCTCACTGCAACCTCCAACCTC	15546		GTA
			GAG GAGGTTGCAGTGAGTC			
			CTC CTCCAACGTCACTCGG			
			AAC			
GAM1659	FHL2	5'	GCTCACTGCAAGCTCTACCTC	7565		G
			GAGGTAGAG TTGCAGTGAGT			
			CTCCATCTC AACGTCACTCG			
			G			
GAM1659	FZD4	3'	CACTGCAACCTCTGCCTC	24129		
			GAGGTAGAGGTTGCAGTG			
			CTCCGTCTCCAACGTCAC			
GAM1659	G6PC	3'	CACTGCAACCTCTTCCTC	3822		T
			GAGG AGAGGTTGCAGTG			

			CTCC TCTCCAACGTCAC		
			T		
GAM1659	GHR	3'	TGACTCACTGCAATCTCCACCT 3891	A	
	C		GAGGT GAGGTTGCAGTGAGTCA		
			CTCCA CTCTAACGTCACTCAGT		
			C		
GAM1659	GM2A	3'	CACTGCAACCTCCGCCTC 67774	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	GNE	3'	CAATGCAACCTCTGCC 18476	G	
			GGTAGAGGTTGCA TG		
			CCGTCTCCAACGT AC		
			A		
GAM1659	GPR4	3'	CACTGCAGCCTCCACCTC 59901	A	
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1659	GPR56	5'	CATCGTAACCTCCACCTC 19066	A	A
			GAGGT GAGGTTGC GTG		
			CTCCA CTCCAATG TAC		
			C C		
GAM1659	GPR81	3'	CACTGCAACCTCTGCCTC 50754		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	GRAF	3'	CACTGCAACCTCCGCCTC 30551	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	HTR1E	5'	CATTGCAACCTCCGCCTC 6012	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTTAC		
			GC		
GAM1659	IL11	3'	TCACTGCAAGCTCCACCTC 5334	A	G
			GAGGT GAG TTGCAGTGA		
			CTCCA CTC AACGTCACT		
			C G		
GAM1659	INHBB	5'	TGACCCGCGACCTCCGCC 9344	TA	AGT A
			GG GAGGTTGC G GTCA		

			CC CTCCAGCG C CAGT	
			GC ____ C	
GAM1659	INMT	3'	GACTCACTGCAAGCTCCGCCTC 22271	TA G
			GAGG GAG TTGCAGTGAGTC	
			CTCC CTC AACGTCACTCAG	
			GC G	
GAM1659	ITGAM	3'	CACTGCAACCTCCGCCTC 71836	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			GC	
GAM1659	KMO	3'	CACTGCAACCTCTGCCTC 13447	
			GAGGTAGAGGTTGCAGTG	
			CTCCGTCTCCAACGTCAC	
GAM1659	LANCL1	3'	ACTCACTGCATGACCCT 20206	A ____
			AG GGT TGCAGTGAGT	
			TC CCA ACGTCACTCA	
			_ GT	
GAM1659	LILRA3	3'	CACTGCAACCTCCGCCTC 95308	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			GC	
GAM1659	LNK	3'	CACTGCAACCTCCACCTT 18459	A
			GAGGT GAGGTTGCAGTG	
			TTCCA CTCCAACGTCAC	
			C	
GAM1659	LSS	3'	CTCAACCTCTATCTC 9817	C
			GAGGTAGAGGTTG AG	
			CTCTATCTCCAAC TC	
GAM1659	LYZ	3'	GGCTCACTGCAACCTCCACCTC 4106	A
			GAGGT GAGGTTGCAGTGAGTC	
			CTCCA CTCCAACGTCACTCGG	
			C	
GAM1659	MAK	3'	TACTGCAACCTCCACCTC 19767	A
			GAGGT GAGGTTGCAGTG	
			CTCCA CTCCAACGTCAT	
			C	
GAM1659	MEF2A	5'	CACTGCAACCTCCGCCTC 18781	TA
			GAGG GAGGTTGCAGTG	

			CTCC CTCCAACGTCAC		
			GC		
GAM1659	MEFV	3'	CACTGCAACCTCCGCCTC	4128	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	MEFV	3'	GCTCACTGCAACCTCCACCTC	4142	A
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCAC		
			C		
GAM1659	MHC2TA	3'	CACTGCAACCTCCGCCTC	4166	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	MICB	3'	CACTGCAACCTCTGCCTC	19822	
			GAGGTAGAGGTTGCAGTG		
			CTCGTCTCCAACGTCAC		
GAM1659	MPL	3'	CACTGCAACCTCTGCCTC	18133	
			GAGGTAGAGGTTGCAGTG		
			CTCGTCTCCAACGTCAC		
GAM1659	MPL	3'	GCTCACTGCAACCTCCACCTC	18145	A
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCAC		
			C		
GAM1659	MRPL49	3'	CACTGCAACTTCCACCTC	69567	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTTCAACGTCAC		
			C		
GAM1659	MYCL2	3'	CACTGCAACCTCTGCCTC	18177	
			GAGGTAGAGGTTGCAGTG		
			CTCGTCTCCAACGTCAC		
GAM1659	NDRG3	3'	CACTGCAACCTCTGCC	49293	
			GGTAGAGGTTGCAGTG		
			CCGTCTCCAACGTCAC		
GAM1659	NQO1	3'	CACTGCAACCTCTGCCTC	6154	
			GAGGTAGAGGTTGCAGTG		

CTCCGTCTCCAACGTCAC

GAM1659 PCDHB11 3' CACTGCAACCTCTGCCTC 38411  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1659 PCDHB16 3' CACTGCAACCTCTGCCTC 40551  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1659 PCDHB9 3' CACTGCAACCTCCGCCTC 38936 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 PDCL 3' GGCTCACTGCAACCTCCACCTC 18216 A  
GAGGT GAGGTTGCAGTGAGTC  
|||| |||||  
CTCCA CTCCAACGTCACTCGG  
C

GAM1659 PDE6B 3' GCTCACTGCAACCTCCACCTC 4283 A  
GAGGT GAGGTTGCAGTGAGT  
|||| |||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1659 PER2 3' CACTGCAACCTCTGCCTC 43029  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1659 PIGR 3' CACTGCAACCTCCGCCTC 72592 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 PIK3C2B 3' GACTCACTGCAAAATCTGCCTC 10567 GG  
GAGGTAGA TTGCAGTGAGTC  
|||| |||||  
CTCCGTCT AACGTCACTCAG  
AA

GAM1659 PON1 3' CACTGCAACTTCTACCTC 4802  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCATCTTCAACGTCAC

GAM1659 PRKWNK3 3' TGCTGCAACCTCCCCCTC 61559 TA  
GAGG GAGGTTGCAGTG  
||| |||||

			CTCC CTCCAACGTCGT CC		
GAM1659 PSMB2	3'	CACTGCAACCTCCGCCTC	10950	TA	
		GAGG GAGGTTGCAGTG			
		CTCC CTCCAACGTCAC			
		GC			
GAM1659 RAB36	3'	CAGTGCAACCTCTGCCTC	16951		G
		GAGGTAGAGGTTGCA TG			
		CTCCGTCTCCAACGT AC			
		G			
GAM1659 RHD	3'	CACTGCAACCTCCGCCTC	32298	TA	
		GAGG GAGGTTGCAGTG			
		CTCC CTCCAACGTCAC			
		GC			
GAM1659 RHD C	3'	TGGCTCACTGCAACCTCTACCT	32322		
		GAGGTAGAGGTTGCAGTGAGTCA			
		CTCCATCTCCAACGTCACTCGGT			
GAM1659 RHD	3'	CACTGCAACCTCCGCCTC	32607	TA	
		GAGG GAGGTTGCAGTG			
		CTCC CTCCAACGTCAC			
		GC			
GAM1659 RHD C	3'	TGGCTCACTGCAACCTCTACCT	32631		
		GAGGTAGAGGTTGCAGTGAGTCA			
		CTCCATCTCCAACGTCACTCGGT			
GAM1659 RPH3AL	3'	GGCTCACTGCAACCTCCACCTC	22751	A	
		GAGGT GAGGTTGCAGTGAGTC			
		CTCCA CTCCAACGTCACTCGG			
		C			
GAM1659 SAS	3'	CACCGCAACCTCTGCCTC	19950		A
		GAGGTAGAGGTTGC GTG			
		CTCCGTCTCCAACG CAC			
		C			
GAM1659 SEDL	3'	CACTGCAACCTCCGCCTC	27328	TA	
		GAGG GAGGTTGCAGTG			
		CTCC CTCCAACGTCAC			
		GC			
GAM1659 SEDL C	3'	TGGCTCACTGCAACCTCCACCT	27366	A	
		GAGGT GAGGTTGCAGTGAGTCA			



			CTCCA CTCCAACGTCACTCGGT	
			C	
GAM1659	SEDL	3'	TGGCTCACTGCAACCTCCACCT 27367	A
	C		GAGGT GAGGTTGCAGTGAGTCA	
			CTCCA CTCCAACGTCACTCGGT	
			C	
GAM1659	SEPN1	3'	TGGCTCACTGCAACCTCCACCT 66383	A
	C		GAGGT GAGGTTGCAGTGAGTCA	
			CTCCA CTCCAACGTCACTCGGT	
			C	
GAM1659	SERPINB9	3'	CACTGCAACCTCCTCCTC 14749	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			TC	
GAM1659	SHOX	3'	GACTCACTGCAACCTCCGCCTC 22538	TA
			GAGG GAGGTTGCAGTGAGTC	
			CTCC CTCCAACGTCACTCAG	
			GC	
GAM1659	SIL	3'	CACTGCAACCTCTGCCTC 11686	
			GAGGTAGAGGTTGCAGTG	
			CTCCGTCTCCAACGTCAC	
GAM1659	SLA2	3'	GCTCACTGCAACCTCCATCTC 49899	A
			GAGGT GAGGTTGCAGTGAGT	
			CTCTA CTCCAACGTCACTCG	
			C	
GAM1659	SLC14A2	5'	TGGCTCACTGCAACCTCCACCT 23143	A
	C		GAGGT GAGGTTGCAGTGAGTCA	
			CTCCA CTCCAACGTCACTCGGT	
			C	
GAM1659	SLC15A1	3'	CACTGCAACCTCCGCCTC 17398	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			GC	
GAM1659	SMAC	5'	CACTGCAACCTCTGCCTC 57204	
			GAGGTAGAGGTTGCAGTG	
			CTCCGTCTCCAACGTCAC	
GAM1659	SNAP23	3'	CACTGCAACCTCCGCCTC 55459	TA
			GAGG GAGGTTGCAGTG	

			CTCC CTCCAACGTCAC		
			GC		
GAM1659	SNAP23	3'	CACTGCAACCTCCGCCTC	13806	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	SNX15	3'	GGCTCACTGCAACCTCCACCTC	73747	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCAC		
			C		
GAM1659	SPN	3'	CACTGCAACCTCTGCCTC	11917	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	SS18	3'	CACTGCAACCTCCGCCTC	18883	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	STAU	5'	ACTGCAACCTCCACCTC	15994	A
			GAGGT GAGGTTGCAGT		
			CTCCA CTCCAACGTCA		
			C		
GAM1659	STAU	5'	GGCTCACTGCAACCTCCACCTC	16007	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCAC		
			C		
GAM1659	SULT2B1	5'	CACTGCAACCTCCGCCTC	16023	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	TAF4	3'	CGTTGCACCCCCACCTC	12091	AGA T
			GAGGT GG TGCAGTG		
			CTCCA CC ACGTTGC		
			CC_ C		
GAM1659	TAPBP	3'	TACTGCAACCTCCGCCTC	12134	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAT		
			GC		
GAM1659	TAT	3'	GGCTCACTGCAACCTCCACCTC	4473	A
			GAGGT GAGGTTGCAGTGAGTC		

CTCCA CTCCAACGTCACCTCGG  
C

GAM1659 TBXA2R 3' CACTGCAACCTCCGCCTC 6483 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 TBXA2R 3' GCTCACTGCAACCTCCACCTC 6496 A  
GAGGT GAGGTTGCAGTGAGT  
|||||  
CTCCA CTCCAACGTCACCTCG  
C

GAM1659 TMC1 5' CTGCAACCTCCGCCTC 56903 TA  
GAGG GAGGTTGCAG  
|||||  
CTCC CTCCAACGTC  
GC

GAM1659 TNFRSF10B 3' CAGTGCAACCTCCGCCTC 13867 TA G  
GAGG GAGGTTGCA TG  
|||||  
CTCC CTCCAACGT AC  
GC G

GAM1659 TPMT 3' CACTGCAACCTCTGCCTC 4534  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1659 TRIM9 5' CACTGCAACCTCCGCCTC 30755 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 TRPM6 3' CACTGCAACCTCTGCCTC 34535  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1659 TRPV1 3' CACTGCAACCTCTGCCTC 38073  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1659 TRPV1 3' CTGCAACCTCCGCCTC 38081 TA  
GAGG GAGGTTGCAG  
|||||  
CTCC CTCCAACGTC  
GC

GAM1659 TRPV1 3' CACTGCAACCTCTGCCTC 54792  
GAGGTAGAGGTTGCAGTG  
|||||

CTCCGTCTCCAACGTCAC

GAM1659 TRPV1 3' CTGCAACCTCCGCCTC 54802 TA  
GAGG GAGGTTGCAG  
|||| ||||||||  
CTCC CTCCAACGTC  
GC

GAM1659 TRPV1 3' CACTGCAACCTCTGCCTC 54827  
GAGGTAGAGGTTGCAGTG  
||||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 TRPV1 3' CTGCAACCTCCGCCTC 54835 TA  
GAGG GAGGTTGCAG  
|||| ||||||||  
CTCC CTCCAACGTC  
GC

GAM1659 TRPV1 3' CACTGCAACCTCTGCCTC 54859  
GAGGTAGAGGTTGCAGTG  
||||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 TRPV1 3' CTGCAACCTCCGCCTC 54867 TA  
GAGG GAGGTTGCAG  
|||| ||||||||  
CTCC CTCCAACGTC  
GC

GAM1659 TUFT1 3' CACTGCAACCTCTGCCTC 39252  
GAGGTAGAGGTTGCAGTG  
||||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 VENTX2 3' CACTGCAACCTCCGCCTC 27108 TA  
GAGG GAGGTTGCAGTG  
|||| ||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 VHL 3' CACTGCAACCTCTGCCTC 5064  
GAGGTAGAGGTTGCAGTG  
||||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 ZNF133 5' ACTCACTGCAACCTCCACC 12829 A  
GGT GAGGTTGCAGTGAGT  
||| ||||||||||  
CCA CTCCAACGTCACTCA  
C

GAM1659 ZNF264 3' CACTGCAACCTCCGCCTC 12746 TA  
GAGG GAGGTTGCAGTG  
|||| ||||||||

			CTCC CTCCAACGTCAC		
			GC		
GAM1659	ZNF264	3'	CTGCAACCTCTGCCTC	12754	
			GAGGTAGAGGTTGCAG		
			CTCCGTCTCCAACGTC		
GAM1659	20D7-FC4	5'	CACTGCAGCCTCCACCTC	60896	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1659	ARHF	3'	TGGCTCACTGCAAGCTCCACCT	38751	A G
	C		GAGGT GAG TTGCAGTGAGTCA		
			CTCCA CTC AACGTCACTCGGT		
			C G		
GAM1659	ARPP-19	3'	CACTGCAACCTCTGCCTC	21791	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	ASB16	5'	CACTGCAACCTCCGCCTC	69932	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	ASE-1	3'	CACTGCAACCTCCGCCTC	23946	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	ATP1B4	3'	GGCTCACTGCAACCTCCACCTC	23825	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCACTCGG		
			C		
GAM1659	BA108L7.2	3'	CACTGCAACCTCTGCCTC	48259	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	BAG5	3'	GCTCACTGCAACCTCCACCTC	16845	A
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACTCG		
			C		
GAM1659	BNIP-S	3'	CACTGCAACCTCCGCCTC	56257	TA
			GAGG GAGGTTGCAGTG		

CTCC CTCCAACGTCAC  
 GC  
 GAM1659 BTN3A1 3' CTGCAACCTCCACCTC 22919 A  
 GAGGT GAGGTTGCAG  
 |||| |||||  
 CTCCA CTCCAACGTC  
 C  
 GAM1659 C1orf24 3' CACTGCAACCTCCGCCTC 53710 TA  
 GAGG GAGGTTGCAGTG  
 |||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1659 C1QTNF6 3' CACTGCAACCTCTGCCTC 49139  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC  
  
 GAM1659 C20orf167 3' TGA CTCACTGCACAGCACC 53664 AGAG T  
 GGT GT GCAGTGAGTCA  
 ||| || |||||  
 CCA CA CGTCACTCAGT  
 CGA\_ \_  
 GAM1659 C21orf25 3' TACTGCAACCTCCACCTC 63556 A  
 GAGGT GAGGTTGCAGTG  
 |||| |||||  
 CTCCA CTCCAACGTCAT  
 C  
 GAM1659 C21orf93 3' TGACCCTCACCTCTCACCTC 59090 \_ T C TGA  
 GAGGT AGAGGT G AG GTCA  
 |||| ||||| || ||||  
 CTCCA TCTCCA C TC CAGT  
 C \_ \_ C \_  
 GAM1659 C3F 3' GCTCACCGCAACCTCCACCTC 19293 A A  
 GAGGT GAGGTTGC GTGAGT  
 |||| ||||| |||||  
 CTCCA CTCCAACG CACTCG  
 C C  
 GAM1659 C9orf9 3' CACTGCAACCTCCGCCTC 38506 TA  
 GAGG GAGGTTGCAGTG  
 |||| |||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1659 C9orf9 3' TGGCTCACTGCAACCTCCACCT 38532 A  
 C GAGGT GAGGTTGCAGTGAGTCA  
 |||| |||||  
 CTCCA CTCCAACGTCACTCGGT  
 C  
 GAM1659 CEACAM8 3' ACTCACTGCAAGCTCCGCCTC 8420 TA G  
 GAGG GAG TTGCAGTGAGT  
 |||| || |||||

			CTCC CTC AACGTCACTCA		
			GC G		
GAM1659	CENPH	3'	CACTGCAACCTCTGCCTC 43271		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	CHRA1	3'	CACTGCAACCTCCGCCTC 33867	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	CLSTN2	3'	ACTCACTGTGCGTCTCCTC 42120	T G T	
			GAGG AGA GT GCAGTGAGT		
			CTCC TCT CG TGCTACTCA		
			- G -		
GAM1659	CPSF2	3'	CACCGCAACCTCTGCCTC 61574	A	
			GAGGTAGAGGTTGC GTG		
			CTCCGTCTCCAACG CAC		
			C		
GAM1659	CYP4F8	3'	GACCCACCCACCTACCTT 23410	A_ TTGCA A	
			GAGGTAG GG GTG GTC		
			TTCCATC CC CAC CAG		
			CA ____ C		
GAM1659	DBR1	3'	CACCGCAACCTCCGCCTC 32528	TA A	
			GAGG GAGGTTGC GTG		
			CTCC CTCCAACG CAC		
			GC C		
GAM1659	DKFZp434A2417	3'	CACTGCAACTTCCACCTC 66097	A	
			GAGGT GAGGTTGCAGTG		
			CTCCA CTTCAACGTCAC		
			C		
GAM1659	DKFZP434C212	3'	TGGCTCACTGCAACCTCCACCT 68921	A	
	C		GAGGT GAGGTTGCAGTGAGTCA		
			CTCCA CTCCAACGTCACGCT		
			C		
GAM1659	DKFZp434E2220	5'	CACTGCAACCTCCGCCTC 34294	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	DKFZp547H025	3'	GCTCACTGCAACCTCCACCTC 39359	A	
			GAGGT GAGGTTGCAGTGAGT		

			CTCCA CTCCAACGTCACCTCG		
			C		
GAM1659	DKFZP564O0523	3'	GGCTCACTGCAACCTCCACCTC	49518	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCACCTCGG		
			C		
GAM1659	DKFZp761J139	5'	CACTGCAACGTCCACCTC	50104	A G
			GAGGT GA GTTGCAGTG		
			CTCCA CT CAACGTCAC		
			C G		
GAM1659	DKFZp761N1114	3'	CACTGCAACCTCCGCCTC	79015	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	DKFZp762P2111	3'	CACTGCAACCTCCGCCTC	86353	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	DRIL2	3'	CAATAAACCTCTACCTC	21323	GCAG
			GAGGTAGAGGTT TG		
			CTCCATCTCCAA AC		
			ATA_		
GAM1659	DSCR6	3'	CACTGCAACCTCCACTTC	38543	A
			GAGGT GAGGTTGCAGTG		
			CTTCA CTCCAACGTCAC		
			C		
GAM1659	EREG	3'	GGCTCACTGCAACCTCACCTC	7507	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCACCTCGG		
			-		
GAM1659	FBP17	3'	GGCTCACTACAACCTCCACCTC	72801	A C
			GAGGT GAGGTTG AGTGAGTC		
			CTCCA CTCCAAC TCACTCGG		
			C A		
GAM1659	FER1L4	3'	ACTGCAACCTCCACCTC	47325	A
			GAGGT GAGGTTGCAGT		
			CTCCA CTCCAACGTCA		
			C		
GAM1659	FER1L4	3'	ACTGCAACCTCCACCTC	47327	A
			GAGGT GAGGTTGCAGT		



CTCCA CTCCAACGTCA  
C  
GAM1659 FLJ00024 5' CACTGCAACCTCTGCCTC 63753  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1659 FLJ10232 3' CACTGCAACCTCCGCCTC 35922 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 FLJ10346 5' GGCTCACTGCAAGCTCCACCTC 36047 A G  
GAGGT GAG TTGCAGTGAGTC  
|||| ||| |||||  
CTCCA CTC AACGTCACTCGG  
C G

GAM1659 FLJ10535 3' CACTGCAACCTCTGCCTC 36235  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1659 FLJ10922 3' CACTGCAACCTCCGCCTC 36871 TA  
GAGG GAGGTTGCAGTG  
||| |||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 FLJ11004 5' GGCTCACTGCAACCTCTACCTC 36971  
GAGGTAGAGGTTGCAGTGAGTC  
|||||  
CTCCATCTCCAACGTCACTCGG

GAM1659 FLJ11106 5' TCTTGCAACCTCACCTC 37056 A T  
GAGGT GAGGTTGCAG GA  
|||| ||||| ||  
CTCCA CTCCAACGTT CT

GAM1659 FLJ12287 3' TGACCCCTTCACCTCTCCC 42320 T T C TGA  
GG AGAGGT G AG GTCA  
|| |||| | || |||  
CC TCTCCA C TC CAGT  
C \_ T CC\_

GAM1659 FLJ12363 3' GCTCACTGCAACCTCCACCTC 49684 A  
GAGGT GAGGTTGCAGTGAGT  
|||| |||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1659 FLJ12409 3' TGA CTCACTGCAACCTCCGCCT 47053 TA  
C GAGG GAGGTTGCAGTGAGTCA  
||| |||||

CTCC CTCCAACGTCACTCAGT  
 GC  
 GAM1659 FLJ12572 5' CACTGCAACCTCTGCCTC 43247  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC

GAM1659 FLJ12649 3' CACTGCAACCTCCGCCTC 44777 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||  
 CTCC CTCCAACGTCAC  
 GC

GAM1659 FLJ12668 3' TGGTCACTGCAACCTCCATCTC 46529 A G  
 GAGGT GAGGTTGCAGTGA TCA  
 |||| ||||| ||  
 CTCTA CTCCAACGTCACT GGT  
 C —

GAM1659 FLJ12687 3' CACTGCAACCTCCGCCTC 46188 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||  
 CTCC CTCCAACGTCAC  
 GC

GAM1659 FLJ12747 3' CACTGCAACCTCTGCCTC 49712  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC

GAM1659 FLJ12973 3' CACCGCAACCTCCGCCTC 46103 TA A  
 GAGG GAGGTTGC GTG  
 ||| ||||| ||  
 CTCC CTCCAACG CAC  
 GC C

GAM1659 FLJ13072 5' CACTGCAACCTCTGCCTC 89804  
 GAGGTAGAGGTTGCAGTG  
 |||||  
 CTCCGTCTCCAACGTCAC

GAM1659 FLJ13197 3' GGCTCACTGCAACCTCTACCTC 44861  
 GAGGTAGAGGTTGCAGTGAGTC  
 |||||  
 CTCCATCTCCAACGTCACTCGG

GAM1659 FLJ14950 3' GGCTCACTGCAACCTCCACCTC 51726 A  
 GAGGT GAGGTTGCAGTGAGTC  
 |||| |||||  
 CTCCA CTCCAACGTCACTCGG  
 C

GAM1659 FLJ14957 3' CACTGCAACCTCTGCCTC 51742  
 GAGGTAGAGGTTGCAGTG  
 |||||

CTCCGTCTCCAACGTCAC

GAM1659 FLJ20004 3' CATTGCAACCTCCGCCTC 95291 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTTAC  
GC

GAM1659 FLJ20034 3' CACTGCAACCTCTGCCTC 34359  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 FLJ20045 3' CACTGCAACCTCTGCCTC 34416  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 FLJ20079 3' TGGCTCACCGCAACCTCCACCT 34505 A A  
C GAGGT GAGGTTGC GTGAGTCA  
|||| ||||| |||||  
CTCCA CTCCAACG CACTCGGT  
C C

GAM1659 FLJ20342 3' CACTGCAACCTCTGCCTC 34987  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 FLJ20344 3' CACTGCAACCTCCGCCTC 35006 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 FLJ20507 3' CACTGCAACCTCTGCCTC 35275  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 FLJ20507 3' CACTGCAACCTCTGCCTC 60210  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 FLJ20511 3' GGCTCACTGCAAGCTCCACCTC 35329 A G  
GAGGT GAG TTGCAGTGAGTC  
|||| || |||||||||  
CTCCA CTC AACGTCACTCGG  
C G

GAM1659 FLJ20542 3' ACTCACCCAGCCGCCACCTC 49780 AGA CA  
GAGGT GGTG GTGAGT  
|||| |||| |||||

			CTCCA CCGAC CACTCA		
			CCG C_		
GAM1659	FLJ20813	3'	CACTGCAACTCCACCTC	35679	A G
			GAGGT GAG TTGCAGTG		
			CTCCA CTC AACGTCAC		
			C _		
GAM1659	FLJ21302	3'	CACTGCAACCTCCGCCTC	43212	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	FLJ22002	3'	CACTGCAACCTCCGCCTC	45768	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	FLJ22531	5'	GGCTCACTGCAACCTCCACCTC	45033	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCAC		
			C		
GAM1659	FLJ22794	3'	CACTGCAACTTCCACCTC	91603	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTTCAACGTCAC		
			C		
GAM1659	FLJ22965	3'	CACTGCAACCTCCGCCTC	42049	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	FLJ22969	3'	CACTGCAACCTCTGCCTC	68646	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	FLJ23024	3'	CACTGCAACCTCTGCCTC	46266	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	FLJ23392	3'	CACTGCAACCTCTGCCTC	45527	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	FLJ23563	3'	CACTGCAACCTCTGCCTC	67592	
			GAGGTAGAGGTTGCAGTG		

CTCCGTCTCCAACGTCAC

GAM1659 FLJ31101 3' CACTGCAACCTCTGCCTC 35706  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1659 FLJ32865 3' CACTGCAACCTCTGCCTC 58168  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1659 GAL3ST-4 3' CACTGCAACCTCTGCCTC 44934  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1659 GMPPB 5' GGCTCACTGCAACCTCCACCTC 95749 A  
GAGGT GAGGTTGCAGTGAGTC  
|||||  
CTCCA CTCCAACGTCACTCGG  
C

GAM1659 GNG4 3' GCTCACTGCGACCTCCACCTC 15618 A  
GAGGT GAGGTTGCAGTGAGT  
|||||  
CTCCA CTCCAGCGTCACTCG  
C

GAM1659 GP5 3' GGCCCGCAACCCCTCCTC 15655 T A AGT A  
GAGG AG GGTTGC G GTC  
|||||  
CTCC TC CCAACG C CGG  
\_ C \_ C

GAM1659 GREB1 3' CACTGCAACCTCTGCCTC 27865  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1659 GRWD 3' CACTGCAACCTCCGCCTC 48963 TA  
GAGG GAGGTTGCAGTG  
|||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 GTF2E1 3' CACTGCAACCTCTGCCTC 18611  
GAGGTAGAGGTTGCAGTG  
|||||  
CTCCGTCTCCAACGTCAC

GAM1659 GTPBG3 3' TACTGCAACCTCCACCTC 50907 A  
GAGGT GAGGTTGCAGTG  
|||||

			CTCCA CTCCAACGTCAT		
			C		
GAM1659	GTPBG3	3'	TGGCTCACTGCAACCTCCATCT 50914	A	
		C	GAGGT GAGGTTGCAGTGAGTCA		
			CTCTA CTCCAACGTCACTCGGT		
			C		
GAM1659	H-plk	5'	GACTCACTGCAACCTCCACCTC 31809	A	
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCACTCAG		
			C		
GAM1659	HRH4	3'	CACTGCAACCTCTGCCTC 41248		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	HSPC065	3'	CGCTGCAACCTCCTCCTC 26293	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCGC		
			TC		
GAM1659	HSPC065	3'	TGGCTCACTGCAACCTCCACCT 26331	A	
		C	GAGGT GAGGTTGCAGTGAGTCA		
			CTCCA CTCCAACGTCACTCGGT		
			C		
GAM1659	ICK	3'	CTGCAACCTCTGCCTC 29928		
			GAGGTAGAGGTTGCAG		
			CTCCGTCTCCAACGTC		
GAM1659	JAM1	5'	CACTGCAACCTCCTCCTC 57916	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			TC		
GAM1659	JM11	3'	CACTGCAACCTCTGCCTC 53252		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	KCNMB3L	5'	ACCCACGGTGGCCTCTCCTC 26957	T	TG A A
			GAGG AGAGGT C GTG GT		
			CTCC TCTCCG G CAC CA		
			_ GT G C		
GAM1659	KIAA0063	3'	GGCTCACTGCAACCTCCACCTC 29636	A	
			GAGGT GAGGTTGCAGTGAGTC		

			CTCCA CTCCAACGTC	ACTCGG	
			C		
GAM1659	KIAA0391	3'	CACTGCAACCTCTGCCTC	27909	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	KIAA0426	3'	CACTGCAACCTCCGCCTC	28255	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	KIAA0459	3'	GGCTCACTGCAACCTCCACCTC	61002	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTC	ACTCGG	
			C		
GAM1659	KIAA0469	3'	CACTGCAGCCTCCACCTC	29323	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1659	KIAA0513	3'	ACTCACTGCAACCTCCACCTC	28327	A
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTC	ACTCA	
			C		
GAM1659	KIAA0513	5'	CACTGCAGCCTCCACCTC	28343	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1659	KIAA0527	3'	CACTGCAACCTCTGCCTC	95795	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	KIAA0544	3'	CACGCACCTCTACC	70894	T A
			GGTAGAGGT GC GTG		
			CCATCTCCA CG CAC		
			— —		
GAM1659	KIAA0544	3'	CACTGCAACCTCCGCCTC	70896	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	KIAA0557	3'	TGGCTCACCACAACCTCCACCT	78012	A CA
			GAGGT GAGGTTG GTGAGTCA		

			CTCCA CTCCAAC CACTCGGT	
			C AC	
GAM1659	KIAA0561	3'	CACTGCAACCTCCGCCTC 65875	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			GC	
GAM1659	KIAA0562	3'	CTGCAACCTCCGCCTC 28153	TA
			GAGG GAGGTTGCAG	
			CTCC CTCCAACGTC	
			GC	
GAM1659	KIAA0563	5'	CACTGCAACCTCTGCCTC 29184	
			GAGGTAGAGGTTGCAGTG	
			CTCCGTCTCCAACGTCAC	
GAM1659	KIAA0594	3'	TACTGCAACCTCCGCCTC 64901	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAT	
			GC	
GAM1659	KIAA0599	3'	CACTGCAACCTCCGCCTC 77169	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			GC	
GAM1659	KIAA0599	3'	TACTGCAACCTCCGCCTC 77189	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAT	
			GC	
GAM1659	KIAA0630	3'	ACCACCACCTCTACC 89386	TGCA A
			GGTAGAGGT GTG GT	
			CCATCTCCA CAC CA	
			C _ _	
GAM1659	KIAA0720	3'	CACTGCAACCTCTGCCTC 62318	
			GAGGTAGAGGTTGCAGTG	
			CTCCGTCTCCAACGTCAC	
GAM1659	KIAA0841	3'	CACTGCAACCTCCGCCTC 71376	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAC	
			GC	
GAM1659	KIAA0841	3'	CACTGCAACCTCTGCCTC 71377	
			GAGGTAGAGGTTGCAGTG	



CTCCGTCTCCAACGTCAC

GAM1659	KIAA1041	3'	CACTGCAACCTCCGCCTC	30128	TA	
			GAGG GAGGTTGCAGTG			
			CTCC CTCCAACGTCAC			
			GC			
GAM1659	KIAA1054	3'	CACTGCAACCTCCGCCTC	68429	TA	
			GAGG GAGGTTGCAGTG			
			CTCC CTCCAACGTCAC			
			GC			
GAM1659	KIAA1161	5'	CACTGCAACCCCTCCTC	81736	T A	
			GAGG AG GGTTGCAGTG			
			CTCC TC CCAACGTCAC			
			- C			
GAM1659	KIAA1170	3'	CACTGCAACCTCCGCCTC	69846	TA	
			GAGG GAGGTTGCAGTG			
			CTCC CTCCAACGTCAC			
			GC			
GAM1659	KIAA1193	3'	CACTGCAACCTCCGCCTC	67632	TA	
			GAGG GAGGTTGCAGTG			
			CTCC CTCCAACGTCAC			
			GC			
GAM1659	KIAA1198	3'	CACCGCAACCTCCGCCTC	63291	TA	A
			GAGG GAGGTTGC GTG			
			CTCC CTCCAACG CAC			
			GC C			
GAM1659	KIAA1198	3'	CACTGCAACCTCCACTTC	63293	A	
			GAGGT GAGGTTGCAGTG			
			CTTCA CTCCAACGTCAC			
			C			
GAM1659	KIAA1209	3'	CACTGCAGCCTCCACCTC	60751	A	
			GAGGT GAGGTTGCAGTG			
			CTCCA CTCCGACGTCAC			
			C			
GAM1659	KIAA1257	3'	CACCGCAACCTCCGCCTC	62730	TA	A
			GAGG GAGGTTGC GTG			
			CTCC CTCCAACG CAC			
			GC C			
GAM1659	KIAA1320	5'	CACTGCAACCTCTGCCTC	69297		
			GAGGTAGAGGTTGCAGTG			

CTCCGTCTCCAACGTCAC

GAM1659 KIAA1373 3' GCTCACTGCAACCTCCACCTC 70942 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||||||  
CTCCA CTCCAACGTCACCTCG  
C

GAM1659 KIAA1497 5' CACTGCAACCTCTGCCTC 67505  
GAGGTAGAGGTTGCAGTG  
||||| |||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 KIAA1508 3' CACTGCAACCTCCGCCTC 61879 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 KIAA1571 3' GCTCACCGCAACCTCCACCTC 60955 A A  
GAGGT GAGGTTGC GTGAGT  
||||| ||||||| |||||  
CTCCA CTCCAACG CACTCG  
C C

GAM1659 KIAA1615 3' GATCACTGCAACCTCCACCTC 68713 A G  
GAGGT GAGGTTGCAGTGA TC  
||||| ||||||||| ||  
CTCCA CTCCAACGTCACCT AG  
C \_

GAM1659 KIAA1655 3' CACTGTAACCTCCACCTC 66597 A  
GAGGT GAGGTTGCAGTG  
||||| |||||||||  
CTCCA CTCCAATGTCAC  
C

GAM1659 KIAA1655 3' CATTGCAACCTCCGCCTC 66601 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTTAC  
GC

GAM1659 KIAA1737 3' CACTGCAACCTCCGCCTC 67351 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 KIAA1775 3' TGA CTCA CACCTCTACTTC 52386 TGCA  
GAGGTAGAGGT GTGAGTCA  
||||||| |||||||  
CTTCATCTCCA CACTCAGT  
CA\_\_

GAM1659 KIAA1784 3' CACTGCAACCTCCGCCTC 65145 TA  
GAGG GAGGTTGCAGTG  
||| |||||||||

			CTCC CTCCAACGTCAC		
			GC		
GAM1659	KIAA1922	5'	CACTGCAACCTCCGCCTC	73617	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	KIAA1956	3'	CACTGCAGCCTCCACCTC	78431	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1659	KIAA1971	3'	TACTGCAACCTCCACCTC	74227	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCAACGTCAT		
			C		
GAM1659	KLK7	3'	CACTGCAACCTCCGCCTC	57729	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	KLK7	3'	CACTGCAACCTCCGCCTC	17289	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	MCLC	3'	GGCTCACTGCAACCTCCACCTC	30691	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCACCTCGG		
			C		
GAM1659	MEF-2	3'	CACTGCAACCTCCGCCTC	64379	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	MGC12518	3'	TACTGCAACCTCTGCC	64083	
			GGTAGAGGTTGCAGTG		
			CCGTCTCCAACGTCAT		
GAM1659	MGC13138	3'	CACTGCAACCTCTGCCTC	53014	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	MGC14836	3'	CACTGCAACCTCCGCCTC	53037	TA
			GAGG GAGGTTGCAGTG		

			CTCC CTCCAACGTCAC		
			GC		
GAM1659	MGC1842	3'	TACTACAACCTCCGCCTC	65657	TA C
			GAGG GAGGTTG AGTG		
			CTCC CTCCAAC TCAT		
			GC A		
GAM1659	MGC2474	3'	GA CTCACTGCAACTTCCACCTC	43724	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTTCAACGTCACTCAG		
			C		
GAM1659	MGC29891	3'	CA CTGCAACCTCCGCCTC	58202	TA
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	MGC3113	3'	CA CTGCAGCCTCCACCTC	43840	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1659	MGC3329	3'	CA CTGCAACCCCCGCCTC	44015	AGA
			GAGGT GGTTCAGTG		
			CTCCG CCAACGTCAC		
			CCC		
GAM1659	MGC5149	3'	CA CTGCAACCTCTGCCTC	72286	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	MGC9912	3'	GGCTCACTGCAACCTCCACCTC	54722	A
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCACTCGG		
			C		
GAM1659	MLZE	5'	CA CTGCAACCTCTGCCTC	48615	
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	MMPL1	3'	CA CTGCAGCCTCCACCTC	14717	A
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1659	moblak	3'	CA CTGCATCCTCCACCTC	55488	A T
			GAGGT GAGG TGCAGTG		

			CTCCA CTCC ACGTCAC		
			C T		
GAM1659	MOCS3	3'	CACTGCAACCTCCGCCTC 27149	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	MRPL44	3'	GGCTCACTGCAACCTCCACCTC 43323	A	
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCAC		
			C		
GAM1659	MtFMT	3'	CACTGCAACCTCCGCCTC 57649	TA	
			GAGG GAGGTTGCAGTG		
			CTCC CTCCAACGTCAC		
			GC		
GAM1659	NDP52	3'	TGACTCACTACAGCCTCTGCCT 19535		C
	C		GAGGTAGAGGTTG AGTGAGTCA		
			CTCCGTCTCCGAC TCACTCAGT		
			A		
GAM1659	NDUFB1	5'	CACTGCAACCTCTGCCTC 15815		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	NDUFC2	3'	GGCTCACTGCAACCTCCACCTC 15840	A	
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCAC		
			C		
GAM1659	Nup43	3'	GGCTCACTGCAACCTCCACCTC 45006	A	
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCAC		
			C		
GAM1659	OSBPL2	3'	CACCGCAACCTCCGCCTC 57856	TA	A
			GAGG GAGGTTGC GTG		
			CTCC CTCCAACG CAC		
			GC C		
GAM1659	OSBPL2	3'	CACCGCAACCTCCGCCTC 29205	TA	A
			GAGG GAGGTTGC GTG		
			CTCC CTCCAACG CAC		
			GC C		
GAM1659	PASK	5'	CACTGCAACCTCTGCCTC 30713		
			GAGGTAGAGGTTGCAGTG		

CTCCGTCTCCAACGTCAC

GAM1659 PELI1 5' CACTGCAACCTCCTCCTC 40255 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
TC

GAM1659 PELI1 5' CACTGCAACCTCTGCCTC 40257  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 PIP3-E 3' CACTGCAACCTCTGCCTC 66801  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 PRO0365 5' GCTCACTGCAACCTCCACCTC 26162 A  
GAGGT GAGGTTGCAGTGAGT  
|||| |||||||||||  
CTCCA CTCCAACGTCACTCG  
C

GAM1659 PRO1992 5' CACTGCAACCTCTGCCTC 26054  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 PRO2955 3' CACTGCAACCTCTGCCTC 37632  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 PSTPIP2 3' CACTGCAACCTCTGCCTC 44384  
GAGGTAGAGGTTGCAGTG  
|||||||||||||  
CTCCGTCTCCAACGTCAC

GAM1659 RAB21 3' GGCTCACTGCAAGCTCCACCTC 30390 A G  
GAGGT GAG TTGCAGTGAGTC  
|||| || |||||||||  
CTCCA CTC AACGTCACTCGG  
C G

GAM1659 RAB33B 3' CACTGCAACCTCCGCCTC 48489 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 RAI 5' CACTGCAACCTCCGCCTC 21874 TA  
GAGG GAGGTTGCAGTG  
|||| |||||||||

			CTCC CTCCAACGTCAC		
			GC		
GAM1659	RASAL2	3'	GACCCACTCTCCTATCTC 16723	AG TTGC	A
			GAGGTAG G AGTG GTC		
			CTCTATC C TCAC CAG		
			CT ____ C		
GAM1659	RNF20	3'	ACCACCAAACCTCTACCTC 38963	GCA	A
			GAGGTAGAGGTT GTG GT		
			CTCCATCTCCAA CAC CA		
			AC_ _		
GAM1659	RNF8	3'	GCTCACTGCAACCTCCACCTC 14230	A	
			GAGGT GAGGTTGCAGTGAGT		
			CTCCA CTCCAACGTCACCTCG		
			C		
GAM1659	RNO2	5'	CACTGCAACCTCCACCTT 52764	A	
			GAGGT GAGGTTGCAGTG		
			TTCCA CTCCAACGTCAC		
			C		
GAM1659	SC4MOL	3'	CACTGCAACCTCTGCCTC 22151		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	SCAMP-4	3'	CACTGCAACCTCTGCCTC 54391		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	SCAND2	3'	TGACTCACTGCAACATCTGCCT 41891	G	
			C GAGGTAGA GTTGCAGTGAGTCA		
			CTCCGTCT CAACGTCACCTCAGT		
			A		
GAM1659	SCYA16	3'	CACTGTAACTCCACCTC 15956	A	
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCAATGTCAC		
			C		
GAM1659	SCYA22	3'	ACCCATCCTCTGCCTC 90935	T CA	
			GAGGTAGAGG TG GT		
			CTCCGTCTCC AC CA		
			T C_		
GAM1659	SCYA22	3'	GGCTCACTACAACCTCGACCTC 90952	A C	
			GAGGT GAGGTTG AGTGAGTC		

CTCCA CTCCAAC TCACTCGG  
G A  
GAM1659 SERF1B 3' CACTGCAACCTCCGCCTC 43410 TA  
GAGG GAGGTTGCAGTG  
||||| |||||  
CTCC CTCCAACGTCAC  
GC  
GAM1659 SIRPB1 3' CACTGCAACCCCGCCTC 20244 AGA  
GAGGT GGTTCAGTG  
||||| |||||  
CTCCG CCAACGTCAC  
CCC  
GAM1659 SLC11A1 3' ACTCATTGCAACCTCCACCTT 59450 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||  
TTCCA CTCCAACGTTACTCA  
C  
GAM1659 SLC2A10 3' CACTGCAACCTCCACTTC 47817 A  
GAGGT GAGGTTGCAGTG  
||||| |||||  
CTTCA CTCCAACGTCAC  
C  
GAM1659 SP2 3' CGCCACAACCTCTCCTC 11888 T CA  
GAGG AGAGGTTG GTG  
||||| ||||| ||  
CTCC TCTCCAAC CGC  
— AC  
GAM1659 STAF65(gamma) 3' GACTCACTGCAACCTCTGCCTC 29436  
GAGGTAGAGGTTGCAGTGAGTC  
||||| |||||  
CTCCGTCTCCAACGTCAGTCACTCAG  
  
GAM1659 SUN1 3' CACTGCAGCCTCCACCTC 47155 A  
GAGGT GAGGTTGCAGTG  
||||| |||||  
CTCCA CTCCGACGTCAC  
C  
GAM1659 SYT13 3' CACTGCAACCTCCGCCTC 93451 TA  
GAGG GAGGTTGCAGTG  
||||| |||||  
CTCC CTCCAACGTCAC  
GC  
GAM1659 TOLLIP 3' TGGTTCACAACCCCCACCCTC 38690 TAGA\_ GCA GT  
GAGG GGTT GTGA CA  
||||| ||||| ||||| ||  
CTCC CCAA CACT GT  
CACCC \_\_\_\_ TG  
GAM1659 TOR1B 3' ACTCACTGCAACCTCCGCT 27195 TA  
GG GAGGTTGCAGTGAGT  
|| |||||



			TC CTCCAACGTCACTCA		
			GC		
GAM1659	TRIM5	3'	GGTTCACCTGCAACCTCCACCTC 52301	A	GT
			GAGGT GAGGTTGCAGTGA C		
			CTCCA CTCCAACGTCACT G		
			C TG		
GAM1659	TRIM6	3'	CACTGCAACCTCTGCCTC 54135		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	TU12B1-TY	3'	CACTGCAACCTCTGCCTC 33371		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	TUCAN	3'	CACTGCAACCTCTGCCTC 30271		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	UBF-fl	3'	CACTGCAACCTCTGCCTC 51555		
			GAGGTAGAGGTTGCAGTG		
			CTCCGTCTCCAACGTCAC		
GAM1659	USP22	3'	GGCTCACTGCAACCTCCACCTC 68019	A	
			GAGGT GAGGTTGCAGTGAGTC		
			CTCCA CTCCAACGTCACTCGG		
			C		
GAM1659	VDU1	3'	CACTGCAGCCTCCACCTC 30414	A	
			GAGGT GAGGTTGCAGTG		
			CTCCA CTCCGACGTCAC		
			C		
GAM1659	VPS33A	3'	CTCACTGCAACCTCCACCTC 43338	A	
			GAGGT GAGGTTGCAGTGAG		
			CTCCA CTCCAACGTCACTC		
			C		
GAM1659	WBSCR20A	5'	CACCGCAACCTCTGCCTC 49650	A	
			GAGGTAGAGGTTGC GTG		
			CTCCGTCTCCAACG CAC		
			C		
GAM1659	ZTL1	3'	CACTGCAACCTCTGCCTC 43911		
			GAGGTAGAGGTTGCAGTG		

CTCCGTCTCCAACGTCAC

GAM1659 LOC112724 5' GGCTCACTGCAACCTCCACCTC 56501 A  
GAGGT GAGGTTGCAGTGAGTC  
||||| |||||||||  
CTCCA CTCCAACGTCACCTCGG  
C

GAM1659 LOC113675 5' CACTGCAACCTCCGCCTC 56570 TA  
GAGG GAGGTTGCAGTG  
||| |||||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 LOC115219 5' CACTGCAACCTCCGCCTC 73298 TA  
GAGG GAGGTTGCAGTG  
||| |||||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 LOC116411 5' CGCTACAACCTCCACCTC 73860 A C  
GAGGT GAGGTTG AGTG  
||||| ||||| |||  
CTCCA CTCCAAC TCGC  
C A

GAM1659 LOC119392 3' TGACTCACTGCAACCTCTGCCT 59140  
C GAGGTAGAGGTTGCAGTGAGTCA  
||||| |||||||||  
CTCCGTCTCCAACGTCACCTCAGT

GAM1659 LOC120114 3' GCTCACTGCAATCTCCACCTC 75531 A  
GAGGT GAGGTTGCAGTGAGT  
||||| |||||||||  
CTCCA CTCTAACGTCACCTCG  
C

GAM1659 LOC120939 3' CACTGTAACCTCCACCTC 76248 A  
GAGGT GAGGTTGCAGTG  
||||| |||||||  
CTCCA CTCCAATGTCAC  
C

GAM1659 LOC121219 5' TGACTCAGGCCCTCAACCTC 74050 A TT AG  
GAGGT GAGG GC TGAGTCA  
||||| ||| || |||||  
CTCCA CTCC CG ACTCAGT  
A \_ G\_

GAM1659 LOC126364 3' CACTGCAACCTCCGCCTC 75684 TA  
GAGG GAGGTTGCAGTG  
||| |||||||  
CTCC CTCCAACGTCAC  
GC

GAM1659 LOC126661 3' CACTGCAACCTCCGCCTC 74545 TA  
GAGG GAGGTTGCAGTG  
||| |||||||

	CTCC CTCCAACGTCAC		
	GC		
GAM1659 LOC128077 3'	CACTGCAACCTCCGCCTC	74707	TA
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1659 LOC128077 3'	CACTGCAACCTCTGCCTC	74709	
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1659 LOC128387 3'	CACTGCAACCTCCACTTC	74747	A
	GAGGT GAGGTTGCAGTG		
	CTTCA CTCCAACGTCAC		
	C		
GAM1659 LOC128989 3'	CACTGCAACCTCCGCCTC	74806	TA
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1659 LOC130813 3'	CACCGCAACCTCCGCCTC	75764	TA A
	GAGG GAGGTTGC GTG		
	CTCC CTCCAACG CAC		
	GC C		
GAM1659 LOC132625 3'	TGGCTCACTGCAACCTCCACCT	75917	A
C	GAGGT GAGGTTGCAGTGAGTCA		
	CTCCA CTCCAACGTCACCTCGGT		
	C		
GAM1659 LOC133686 3'	CTGCAACCTCCATCTC	75121	A
	GAGGT GAGGTTGCAG		
	CTCTA CTCCAACGTC		
	C		
GAM1659 LOC135154 3'	ACTCACTGCAACTTCCGCC	75212	TA
	GG GAGGTTGCAGTGAGT		
	CC CTTCAACGTCACTCA		
	GC		
GAM1659 LOC135293 3'	CACTGCAACCTCTGCCTC	76175	
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1659 LOC135763 3'	CACTGCAACCTCCGCCTC	56787	TA
	GAGG GAGGTTGCAGTG		

		CTCC CTCCAACGTCAC			
		GC			
GAM1659	LOC142913 5'	TGACCACTGCAGCCTCCACCTC 76419	A		A
		GAGGT GAGGTTGCAGTG GTCA			
		CTCCA CTCCGACGTCAC CAGT			
		C _			
GAM1659	LOC143187 3'	TGGCTCACTGCAACCTCCACCT 59103	A		
	C	GAGGT GAGGTTGCAGTGAGTCA			
		CTCCA CTCCAACGTCACCTCGGT			
		C			
GAM1659	LOC143241 5'	CACTGCAACCTCTGCCTC 57174			
		GAGGTAGAGGTTGCAGTG			
		CTCCGTCTCCAACGTCAC			
GAM1659	LOC144248 5'	GCTCACTGCAACCTCCACCTC 76738	A		
		GAGGT GAGGTTGCAGTGAGT			
		CTCCA CTCCAACGTCACCTCG			
		C			
GAM1659	LOC144317 5'	ACTCACTGCAACCTCTTCCTC 76782	T		
		GAGG AGAGGTTGCAGTGAGT			
		CTCC TCTCCAACGTCACCTCA			
		T			
GAM1659	LOC144524 5'	GCTCACTGCAACCTCCACCTC 83130	A		
		GAGGT GAGGTTGCAGTGAGT			
		CTCCA CTCCAACGTCACCTCG			
		C			
GAM1659	LOC145216 3'	ACCCACTGCTTTTCCCC 83260	TA	TT	A
		GG GAGG GCAGTG GT			
		CC CTTT CGTCAC CA			
		C_ T_ C			
GAM1659	LOC145268 5'	CACTGCAACCTCCACCC 77055	A	A	
		G GGT GAGGTTGCAGTG			
		C CCA CTCCAACGTCAC			
		_ C			
GAM1659	LOC145725 3'	GCTCACTGCAGCCTCCACCTC 77409	A		
		GAGGT GAGGTTGCAGTGAGT			
		CTCCA CTCCGACGTCACCTCG			
		C			
GAM1659	LOC145732 3'	GCTCACTGCAGCCTCCACCTC 77431	A		
		GAGGT GAGGTTGCAGTGAGT			

		CTCCA CTCCGACGTC	ACTCG		
		C			
GAM1659	LOC145757 5'	CACTACAACCTCTGCCTC	77457	C	
		GAGGTAGAGGTTG	AGTG		
		CTCCGTCTCCAAC	TCAC		
		A			
GAM1659	LOC146229 3'	CTGCAACCTCCACCTC	77750	A	
		GAGGT	GAGGTTGCAG		
		CTCCA	CTCCAACGTC		
		C			
GAM1659	LOC146229 3'	GGCTCACTGCAACCTCCACCTC	77768	A	
		GAGGT	GAGGTTGCAGTGAGTC		
		CTCCA	CTCCAACGTC	ACTCGG	
		C			
GAM1659	LOC146784 5'	GGCTCACTGCAACCTCCACCTC	78122	A	
		GAGGT	GAGGTTGCAGTGAGTC		
		CTCCA	CTCCAACGTC	ACTCGG	
		C			
GAM1659	LOC146901 3'	CATTGCAACCTCCACCTT	83835	A	
		GAGGT	GAGGTTGCAGTG		
		TTCCA	CTCCAACGTTAC		
		C			
GAM1659	LOC146909 3'	CACTGCAACCTCCGCCTC	78168	TA	
		GAGG	GAGGTTGCAGTG		
		CTCC	CTCCAACGTCAC		
		GC			
GAM1659	LOC146952 5'	GCTCACTGCAACCTCCACCTC	83869	A	
		GAGGT	GAGGTTGCAGTGAGT		
		CTCCA	CTCCAACGTC	ACTCG	
		C			
GAM1659	LOC147071 5'	CACTGCAACCTCTGCCTC	72995		
		GAGGTAGAGGTTGCAGTG			
		CTCCGTCTCCAACGTCAC			
GAM1659	LOC147407 3'	CACTGCAACCTCCGCCTC	76324	TA	
		GAGG	GAGGTTGCAGTG		
		CTCC	CTCCAACGTCAC		
		GC			
GAM1659	LOC147660 3'	TGACTCACAGCAACCTCCGCCT	78398	TA	A
	C	GAGG	GAGGTTGC	GTGAGTCA	

		CTCC CTCCAACG CACTCAGT		
		GC A		
GAM1659	LOC147817 3'	TGGCTCACTGCAACCTCCACCT 78509	A	
	C	GAGGT GAGGTTGCAGTGAGTCA		
		CTCCA CTCCAACGTCACCTCGGT		
		C		
GAM1659	LOC147990 3'	CACTACAACCTCTGCCTC 84090	C	
		GAGGTAGAGGTTG AGTG		
		CTCCGTCTCCAAC TCAC		
		A		
GAM1659	LOC148137 3'	CACGGCAACCTCCACCTC 58421	A	A
		GAGGT GAGGTTGC GTG		
		CTCCA CTCCAACG CAC		
		C G		
GAM1659	LOC148189 5'	GGCTCACTGCAACCTCCACCTC 78717	A	
		GAGGT GAGGTTGCAGTGAGTC		
		CTCCA CTCCAACGTCACCTCGG		
		C		
GAM1659	LOC148198 3'	GCTCACTGCAACCTCCATCTC 70683	A	
		GAGGT GAGGTTGCAGTGAGT		
		CTCTA CTCCAACGTCACCTCG		
		C		
GAM1659	LOC148709 3'	CACTACAACCTCCGCCTC 78935	TA	C
		GAGG GAGGTTG AGTG		
		CTCC CTCCAAC TCAC		
		GC A		
GAM1659	LOC148918 5'	ACTCAGCTTCTTCTACCTC 79054	TT	AG
		GAGGTAGAGG GC TGAGT		
		CTCCATCTTC CG ACTCA		
		TT _		
GAM1659	LOC148918 5'	CACTGCAGCCTCCACCTC 79064	A	
		GAGGT GAGGTTGCAGTG		
		CTCCA CTCCGACGTCAC		
		C		
GAM1659	LOC149506 3'	CACTGCAACCTCTGCCTC 84453		
		GAGGTAGAGGTTGCAGTG		
		CTCCGTCTCCAACGTCAC		
GAM1659	LOC149506 3'	CACTGCAACTTCCACCTC 84454	A	
		GAGGT GAGGTTGCAGTG		

	CTCCA CTTCAACGTCAC		
	C		
GAM1659 LOC150397 3'	CATTGCAACCTCCGCCTC	79843	TA
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	GC		
GAM1659 LOC150519 3'	CTGCAACCTGCCACCTC	79917	AG_
	GAGGT AGGTTGCAG		
	CTCCA TCCAACGTC		
	CCG		
GAM1659 LOC150696 3'	CACTGCAGCCTCCACCTC	58478	A
	GAGGT GAGGTTGCAGTG		
	CTCCA CTCCGACGTCAC		
	C		
GAM1659 LOC150960 3'	CGCTGCAACCTCCGCCTC	80058	TA
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	CTCC CTCCAACGTCGC		
	GC		
GAM1659 LOC151057 3'	CACTGCAACCTCTGCCTC	85208	
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1659 LOC151201 3'	GCTCACTGCAACCTCCACCTC	85283	A
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	CTCCA CTCCAACGTCACCTCG		
	C		
GAM1659 LOC151475 5'	CACTGCAACCTCTGCCTC	85394	
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1659 LOC151475 5'	TGGCTCACTGCAACCTCCACCT	85423	A
C	GAGGT GAGGTTGCAGTGAGTCA		
	CTCCA CTCCAACGTCACCTCGGT		
	C		
GAM1659 LOC151826 3'	CACTGCAACCTCCGCCTC	80354	TA
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1659 LOC151877 3'	GGCTCACTACAACCACCTC	85508	AGA C
	GAGGT GGTG AGTGAGTC		

	CTCCA CCAAC TCACTCGG		
	CCA A		
GAM1659 LOC152343 3'	GACTCAGTGCAACCTCCGCCTC 80565	TA	G
	GAGG GAGGTTGCA TGAGTC		
	CTCC CTCCAACGT ACTCAG		
	GC G		
GAM1659 LOC152445 3'	CACTGCAACCTCTGCCTC 85749		
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1659 LOC152582 5'	CACCGCAACCTCTGCCTC 85789	A	
	GAGGTAGAGGTTGC GTG		
	CTCCGTCTCCAACG CAC		
	C		
GAM1659 LOC152620 3'	CACTACAACCTCTGCCTC 60078	C	
	GAGGTAGAGGTTG AGTG		
	CTCCGTCTCCAAC TCAC		
	A		
GAM1659 LOC152719 5'	CACTGCAACCTCTGCCTC 85848		
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1659 LOC152794 5'	CTCACTGCAACCTCTACCTC 80675		
	GAGGTAGAGGTTGCAGTGAG		
	CTCCATCTCCAACGTCACCTC		
GAM1659 LOC152851 3'	CGCTGCAACCTCCACCC 80708	A A	
	G GGT GAGGTTGCAGTG		
	C CCA CTCCAACGTCGC		
	- C		
GAM1659 LOC153077 3'	CACTGCAACCTCCGCCTC 85907	TA	
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1659 LOC153688 3'	GGCTCACTGCAACCTCCACCTC 86117	A	
	GAGGT GAGGTTGCAGTGAGTC		
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	C		
GAM1659 LOC153883 5'	CACTGCAACCTCCACC 80979	A	
	GGT GAGGTTGCAGTG		



CCA CTCCAACGTCAC  
 C  
 GAM1659 LOC154075 3' CACTGCAACCTCCGCCTC 81044 TA  
 GAGG GAGGTTGCAGTG  
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 GAM1659 LOC154282 5' GGCTCACTGCAACCTCCACCTC 86207 A  
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 CTCCA CTCCAACGTCACCTCGG  
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 GAM1659 LOC154877 3' GCTCACTGCAACCTCTACCTC 86298  
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 GAM1659 LOC155100 5' ACCCACGGTGGCCTCTCCTC 73023 T TG A A  
 GAGG AGAGGT C GTG GT  
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 — GT G C  
 GAM1659 LOC157247 5' GCTCACTGCAACCTCCACC 81368 A  
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 CCA CTCCAACGTCACCTCG  
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 GAM1659 LOC157798 5' CACTGCAACCTCCGCCTC 86548 TA  
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 GAM1659 LOC157858 5' CACTGCAACCTCTGCCTC 86584  
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 GAM1659 LOC158476 3' CACTGCAACCTCCGCC 86838 TA  
 GG GAGGTTGCAGTG  
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 GAM1659 LOC158668 3' CACTGCAACCTCTGCCTC 69365  
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 GAM1659 LOC158865 5' CACTGCAACCTCTGCCTC 86933  
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GAM1659 LOC161829 3' CACTGCAACCTCCGCCTC 82312 TA  
GAGG GAGGTTGCAGTG  
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GC

GAM1659 LOC196047 5' CACTGCAACCTCCGCCTC 89594 TA  
GAGG GAGGTTGCAGTG  
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GC

GAM1659 LOC196264 3' CACTGCAACCTCTGCCTC 87603  
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GAM1659 LOC196411 3' CACTGCAACCTCCGCCTC 87668 TA  
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CTCC CTCCAACGTCAC  
GC

GAM1659 LOC196529 3' GCTCACTGCAACCTCCACCTC 87775 A  
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C

GAM1659 LOC196761 3' ACCCACAACACCTCTGCC 89550 T CA A  
GGTAGAGGT G GTG GT  
||||| | |||  
CCGTCTCCA C CAC CA  
\_AA C

GAM1659 LOC196957 3' GCTCACTGCAGCCTCCACCTC 87825 A  
GAGGT GAGGTTGCAGTGAGT  
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C

GAM1659 LOC196961 3' GCTCACTGCAGCCTCCACCTC 87846 A  
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C

GAM1659 LOC197138 3' GCTCACTGCAGCCTCCACCTC 87919 A  
GAGGT GAGGTTGCAGTGAGT  
|||||  
CTCCA CTCCGACGTCACCTCG  
C

GAM1659 LOC197358 3' CTGCAACCTCCGCCTC 88033 TA  
GAGG GAGGTTGCAG  
|||||

	CTCC CTCCAACGTC		
	GC		
GAM1659 LOC199699 3'	GCTCACTGCAAGCTCCACCTC 88309	A	G
	GAGGT GAG TTGCAGTGAGT		
	CTCCA CTC AACGTCACTCG		
	C G		
GAM1659 LOC199786 3'	CACTGCAACCTCCGCCTC 88370	TA	
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1659 LOC200014 3'	CGCTGCAACCCCCACCTC 88523	AGA	
	GAGGT GGTTCAGTG		
	CTCCA CCAACGTCGC		
	CCC		
GAM1659 LOC200169 5'	CACTGCAACCTCTGCCTC 89945		
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1659 LOC200268 3'	CACTGCAACCTCTGCCTC 88678		
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1659 LOC200310 3'	CACTACAACCTCTGCCTC 65729	C	
	GAGGTAGAGGTTG AGTG		
	CTCCGTCTCCAAC TCAC		
	A		
GAM1659 LOC200314 3'	TGGCTCACTGCAACCTCCACCT 90020	A	
C	GAGGT GAGGTTGCAGTGAGTCA		
	CTCCA CTCCAACGTCACTCGGT		
	C		
GAM1659 LOC200339 3'	CACTGCAACCTCTGCCTC 90033		
	GAGGTAGAGGTTGCAGTG		
	CTCCGTCTCCAACGTCAC		
GAM1659 LOC200845 5'	CACTGCAACCTCCGCCTC 88896	TA	
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1659 LOC200860 3'	TGGTTCACTGCAACCTCCACCT 90178	A	GT
C	GAGGT GAGGTTGCAGTGA CA		

	CTCCA CTCCAACGTC	ACT	GT	
	C	TG		
GAM1659	LOC201173	5'	CACTGCAACCTCTGCCTC	87325
			GAGGTAGAGGTTGCAGTG	
			CTCCGTCTCCAACGTCAC	
GAM1659	LOC201220	5'	CACTGCAACCTCTGCCTC	87345
			GAGGTAGAGGTTGCAGTG	
			CTCCGTCTCCAACGTCAC	
GAM1659	LOC201294	3'	CACTGCAACCTCCGCCTC	88203
			GAGG GAGGTTGCAGTG	TA
			CTCC CTCCAACGTCAC	
			GC	
GAM1659	LOC201294	3'	CACTGCAACCTCCGCCTC	88204
			GAGG GAGGTTGCAGTG	TA
			CTCC CTCCAACGTCAC	
			GC	
GAM1659	LOC201411	3'	CACTGCAACCTCTGCCTC	62952
			GAGGTAGAGGTTGCAGTG	
			CTCCGTCTCCAACGTCAC	
GAM1659	LOC201626	3'	CACTGCAACCTCCGCC	88988
			GG GAGGTTGCAGTG	TA
			CC CTCCAACGTCAC	
			GC	
GAM1659	LOC201627	3'	ACTGCAACCTCCACCTC	89003
			GAGGT GAGGTTGCAGT	A
			CTCCA CTCCAACGTCA	
			C	
GAM1659	LOC201696	3'	TGACTCACTATCACTTTACCTC	63138
			GAGGTAGAG AGTGAGTCA	GTTGC
			CTCCATTTC TCACTCAGT	
			ACTA_	
GAM1659	LOC202025	3'	CACTGCAACCTCCGCCTC	90284
			GAGG GAGGTTGCAGTG	TA
			CTCC CTCCAACGTCAC	
			GC	
GAM1659	LOC202934	3'	CACTACAACCTCTGCCTC	90404
			GAGGTAGAGGTTG AGTG	C

	CTCCGTCTCCAAC TCAC			
	A			
GAM1659 LOC203297 5'	CACTGCAACCTCTGCCTC 75349			
	GAGGTAGAGGTTGCAGTG			
	CTCCGTCTCCAACGTCAC			
GAM1659 LOC203350 3'	ACTGCAACCTCCGCCTC 90557	TA		
	GAGG GAGGTTGCAGT			
	CTCC CTCCAACGTCA			
	GC			
GAM1659 LOC204804 3'	GCTCACTGCAACCTCGACCTC 89475	A		
	GAGGT GAGGTTGCAGTGAGT			
	CTCCA CTCCAACGTCACTCG			
	G			
GAM1659 LOC204804 3'	GGCTCACTGCCACCTCCACCTC 89481	A	T	
	GAGGT GAGGT GCAGTGAGTC			
	CTCCA CTCCA CGTCACTCGG			
	C C			
GAM1659 LOC219735 3'	CACTGCAACCTCTGCCTC 93107			
	GAGGTAGAGGTTGCAGTG			
	CTCCGTCTCCAACGTCAC			
GAM1659 LOC219894 3'	TGGTTCACTGCAAGCTCCACCT 93291	A	G	GT
C	GAGGT GAG TTGCAGTGA CA			
	CTCCA CTC AACGTCACCT GT			
	C G TG			
GAM1659 LOC220662 3'	CACTGCAACCTCCACTTC 91167	A		
	GAGGT GAGGTTGCAGTG			
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	C			
GAM1659 LOC220662 3'	TGGTTCACTGCAACCTCCACCT 91185	A		GT
C	GAGGT GAGGTTGCAGTGA CA			
	CTCCA CTCCAACGTCACCT GT			
	C TG			
GAM1659 LOC221035 3'	CACTACAACCTCTGCCTC 93162	C		
	GAGGTAGAGGTTG AGTG			
	CTCCGTCTCCAAC TCAC			
	A			
GAM1659 LOC221174 5'	GCTCACTGCGACCTCCACCTC 93503	A		
	GAGGT GAGGTTGCAGTGAGT			

	CTCCA CTCCAGCGTCACTCG	
	C	
GAM1659 LOC221271 3'	CACTGCAACCTCTGCCTC 91850	
	GAGGTAGAGGTTGCAGTG	
	CTCCGTCTCCAACGTCAC	
GAM1659 LOC221296 3'	GGCTCACTGCAACCTCCACCTC 91968	A
	GAGGT GAGGTTGCAGTGAGTC	
	CTCCA CTCCAACGTCCTCGG	
	C	
GAM1659 LOC221495 3'	TGACTCACCTTCTTCTGCC 93865	TTGCA
	GGTAGAGG GTGAGTCA	
	CCGTCTTC CACTCAGT	
	TTC__	
GAM1659 LOC221663 5'	TGGCTCACTGCAACCTCCACCT 93826	A
C	GAGGT GAGGTTGCAGTGAGTCA	
	CTCCA CTCCAACGTCCTCGGT	
	C	
GAM1659 LOC221715 5'	ACCCAAATGCCTCTACCTT 93748	TGCAG A
	GAGGTAGAGGT TG GT	
	TTCCATCTCCG AC CA	
	TAA__ C	
GAM1659 LOC222070 5'	CACTGCAACCTCTGCCTC 94152	
	GAGGTAGAGGTTGCAGTG	
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GAM1659 LOC253612 5'	CACTGCAACCTCCGCCTC 96742	TA
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	CTCC CTCCAACGTCAC	
	GC	
GAM1659 LOC253664 3'	CATTGCAACCTCTGCCTC 94809	
	GAGGTAGAGGTTGCAGTG	
	CTCCGTCTCCAACGTTAC	
GAM1659 LOC253666 5'	CACTGCAACCTCCGCCTC 95060	TA
	GAGG GAGGTTGCAGTG	
	CTCC CTCCAACGTCAC	
	GC	
GAM1659 LOC253779 3'	CACTGCAACCTCCGCCTC 97144	TA
	GAGG GAGGTTGCAGTG	

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	GC		
GAM1659 LOC255497 3'	CACTGCAACCTCCGCCTC	97188	TA
	GAGG GAGGTTGCAGTG		
	CTCC CTCCAACGTCAC		
	GC		
GAM1659 LOC255919 3'	CTGCAACCTCTGCCTC	95032	
	GAGGTAGAGGTTGCAG		
	CTCCGTCTCCAACGTC		
GAM1659 LOC256267 3'	CACTGCAACCTCCGCCTC	96798	TA
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	CTCC CTCCAACGTCAC		
	GC		
GAM1659 LOC256306 3'	GCTCACTGCAACCTCCACCTC	96692	A
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	CTCCA CTCCAACGTCAC		
	C		
GAM1659 LOC51200 3'	CACCACAACCTCTGCCTC	32991	CA
	GAGGTAGAGGTTG GTG		
	CTCCGTCTCCAAC CAC		
	AC		
GAM1659 LOC51219 5'	CACCGCAACCTCCGCCTC	33112	TA A
	GAGG GAGGTTGC GTG		
	CTCC CTCCAACG CAC		
	GC C		
GAM1659 LOC51696 3'	CACTGCAACCTCTGCCTC	32543	
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	CTCCGTCTCCAACGTCAC		
GAM1659 LOC57107 3'	TGACTCACTGCAACCTCCGCCT	39846	TA
C	GAGG GAGGTTGCAGTGAGTCA		
	CTCC CTCCAACGTCAC		
	GC		
GAM1659 LOC57146 3'	GGCTCACTGCAACCTCCAACTC	39926	GTA
	GAG GAGGTTGCAGTGAGTC		
	CTC CTCCAACGTCAC		
	AAC		
GAM1659 LOC64102 5'	GACTCACTTGCAACTCCACCTC	42173	A G _
	GAGGT GAG TTGCA GTGAGTC		

			CTCCA CTC AACGT CACTCAG	
			C _ T	
GAM1659	LOC81034	3'	GCTCACTGCAACCTCCACCTC 47853	A
			GAGGT GAGGTTGCAGTGAGT	
			CTCCA CTCCAACGTCACTCG	
			C	
GAM1659	LOC89932	3'	TGGCTCACTGCAACCTCCACCT 60822	A
			C GAGGT GAGGTTGCAGTGAGTCA	
			CTCCA CTCCAACGTCACTCGGT	
			C	
GAM1659	LOC90288	3'	CTCACTGCAACCTCCACCTC 62090	A
			GAGGT GAGGTTGCAGTGAG	
			CTCCA CTCCAACGTCACTC	
			C	
GAM1659	LOC90333	5'	CACTGCAACCTCCACTTC 62283	A
			GAGGT GAGGTTGCAGTG	
			CTTCA CTCCAACGTCAAC	
			C	
GAM1659	LOC90333	3'	CACTGCAACCTCCTCCTC 62284	TA
			GAGG GAGGTTGCAGTG	
			CTCC CTCCAACGTCAAC	
			TC	
GAM1659	LOC90371	5'	TGGCTCACTGCAACCTCCACCT 62505	A
			C GAGGT GAGGTTGCAGTGAGTCA	
			CTCCA CTCCAACGTCACTCGGT	
			C	
GAM1659	LOC90408	5'	TGGCTCACTGCAACCTCTACCT 62671	
			C GAGGTAGAGGTTGCAGTGAGTCA	
			CTCCATCTCCAACGTCACTCGGT	
GAM1659	LOC90459	3'	CACTGCAACCTCCGCCTC 62883	TA
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			CTCC CTCCAACGTCAAC	
			GC	
GAM1659	LOC90485	3'	CACTGCAACCTCCGCCTC 63008	TA
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			CTCC CTCCAACGTCAAC	
			GC	
GAM1659	LOC90591	3'	GCTCACTGCAAGCTCCACCTC 63433	A G
			GAGGT GAG TTGCAGTGAGT	



CTCCA CTC AACGTCACCTCG  
 C G  
 GAM1659 LOC90591 3' TGTTCACTGCCACCTCCACCTC 63448 A T T  
 GAGGT GAGGT GCAGTGAG CA  
 |||| |||| |||||| ||  
 CTCCA CTCCA CGTCACTT GT  
 C C \_  
 GAM1659 LOC91115 3' CACTGCAACCTCCGCCTC 64927 TA  
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 GAM1659 LOC91115 3' GGCTCACTGCAACCTCCACCTC 64946 A  
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 CTCCA CTCCAACGTCACTCGG  
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 GAM1659 LOC91291 5' GCTCACTGCAACCTCGACCTC 65481 A  
 GAGGT GAGGTTGCAGTGAGT  
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 CTCCA CTCCAACGTCACTCG  
 G  
 GAM1659 LOC91373 3' ACTCATCCTCTGCC 65831 TTGCA  
 GGTAGAGG GTGAGT  
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 CCGTCTCC TACTCA  
 \_\_\_\_\_  
 GAM1659 LOC92267 3' GCTCACTGCAACCTCCACCTC 68617 A  
 GAGGT GAGGTTGCAGTGAGT  
 |||| |||||||||||  
 CTCCA CTCCAACGTCACTCG  
 C  
 GAM1659 LOC92303 3' ACTCACTGCAACCTCTGCC 68819  
 GGTAGAGGTTGCAGTGAGT  
 |||||||||||||  
 CCGTCTCCAACGTCACTCA  
 \_\_\_\_\_  
 GAM1659 LOC92466 3' CACTGCAACCTCCGCCTC 69423 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||||||  
 CTCC CTCCAACGTCAC  
 GC  
 GAM1659 LOC92661 5' TGGCTCACTGCAAGCTCCACCT 70090 A G  
 C GAGGT GAG TTGCAGTGAGTCA  
 |||| || |||||||||  
 CTCCA CTC AACGTCACCTCGGT  
 C G  
 GAM1659 LOC92689 3' CACTGCAACCTCCGCCTC 70219 TA  
 GAGG GAGGTTGCAGTG  
 ||| |||||||||

		CTCC CTCCAACGTCAC		
		GC		
GAM1659	LOC92697 5'	CACCGCAACCTCCGCCTC	70262	TA A
		GAGG GAGGTTGC GTG		
		CTCC CTCCAACG CAC		
		GC C		
GAM1659	LOC92697 5'	CGCTACAACCTCCACCTC	70264	A C
		GAGGT GAGGTTG AGTG		
		CTCCA CTCCAAC TCGC		
		C A		
GAM1659	LOC92841 3'	CACCGCAACCTCCTCCTC	70706	TA A
		GAGG GAGGTTGC GTG		
		CTCC CTCCAACG CAC		
		TC C		
GAM1659	LOC93132 5'	CACTGCAACCTCCGCCTC	71485	TA
		GAGG GAGGTTGCAGTG		
		CTCC CTCCAACGTCAC		
		GC		
GAM1659	LOC93349 3'	CACTGCAACCTCTGCCTC	56453	
		GAGGTAGAGGTTGCAGTG		
		CTCCGTCTCCAACGTCAC		
GAM1659	LOC93408 5'	CACTGCAACCTCTGCCTC	56475	
		GAGGTAGAGGTTGCAGTG		
		CTCCGTCTCCAACGTCAC		
GAM1660	AGL 5'	TATGAAAGATTTCAAATCCT	3451	GGCA
		AGGATTTGAGG TTCATA		
		TCCTAAACTTT AAGTAT		
		AGA_		
GAM1660	AGL 5'	TATGAAAGATTTCAAATCCT	5351	GGCA
		AGGATTTGAGG TTCATA		
		TCCTAAACTTT AAGTAT		
		AGA_		
GAM1660	AGL 5'	TATGAAAGATTTCAAATCCT	5358	GGCA
		AGGATTTGAGG TTCATA		
		TCCTAAACTTT AAGTAT		
		AGA_		
GAM1660	AGL 5'	TATGAAAGATTTCAAATCCT	5379	GGCA
		AGGATTTGAGG TTCATA		

TCCTAAACTTT AAGTAT  
 AGA\_  
 GAM1660 CD83 3' TATGAATGCCCCCAGCTGGCC 14884 AT\_\_ A  
 GG TTG GGGGCATTCATA  
 || ||| |||||  
 CC GAC CCCCCTAAGTAT  
 GGTC \_  
 GAM1660 GABRR1 3' ATGCACCTAAATCCT 8981 G G  
 AGGATT AGG GCAT  
 ||||| ||| |||  
 TCCTAAA TCC CGTA  
 \_ A  
 GAM1660 ALS2CR3 3' TATGAAGATCCCAAATCTT 30486 A GCA  
 AGGATTG GGG TTCATA  
 ||||| ||| |||||  
 TTCTAAAC CCT AAGTAT  
 \_ AG\_  
 GAM1660 KIAA0453 3' ATGACCCAAATCCTTCC 69044 T A GG  
 A AAGGATTG GGCAT  
 | ||||| || |||  
 C TTCCTAAAC CC GTA  
 C \_ A\_  
 GAM1660 MGC10986 3' AATGCCCTGCAGCCC 47560 AT \_  
 GG TTG AGGGGCATT  
 || ||| |||||  
 CC GAC TCCCCGTAA  
 C\_ G  
 GAM1660 MGC3062 3' ATGTTTCAAATCTTTA 43945 GG  
 TAAGGATTGAG GCAT  
 ||||| |||  
 ATTTCTAAACTT TGTA  
 \_  
 GAM1660 RALGPS1A 3' ATGAATCACATCCTTAT 27596 T GGGG  
 ATAAGGAT TGA CAT  
 ||||| ||| |||  
 TATTCCTA ACT GTA  
 C AA\_  
 GAM1660 Sfrmbt 3' AATGCAGCAAATCCTT 32896 AGGG  
 AAGGATTG GCATT  
 ||||| |||  
 TTCCTAAAC CGTAA  
 GA\_  
 GAM1660 VEZATIN 3' CCTTCATCAAATCCCTAT 34226 A \_  
 ATA GGATTG GGGG  
 ||| ||||| |||  
 TAT CCTAAACT TTCC  
 C AC  
 GAM1660 ZNF294 3' AATGCCCTGTACCCTTCA 70826 T ATTTG  
 A AAGG AGGGGCATT  
 | ||| |||||

A TTCC TTCCCGTAA  
 C CATG\_  
 GAM1660 LOC142779 3' ATGAGACACCCCAAGTCCTTA 76391 A GCA  
 TAAGGATTTG GGG TTCAT  
 ||||| ||| ||||  
 ATTCCTGAAC CCC GAGTA  
 \_ ACA  
 GAM1660 LOC153196 5' TATGAATGCCCACTCCCC 85978 ATTT \_  
 GG GAG GGGCATTGATA  
 || ||| |||||  
 CC CTC CCCGTAAGTAT  
 C\_\_ A  
 GAM1660 LOC222224 3' TATGAATGTCAACAAATCTCTA 94204 AG AGG  
 TA GATTTG GGCATTGATA  
 || ||||| |||||  
 AT CTAAAC CTGTAAGTAT  
 CT AA\_  
 GAM1660 LOC254938 3' ATGAAGATTTTCCCAAATCCT 97057 A CA\_  
 AGGATTTG GGGG TTCAT  
 ||||| ||| ||||  
 TCCTAAAC CCTT AAGTA  
 \_ TTAG  
 GAM1660 LOC255702 5' GGGGAACCCCCCAAATCCT 95357 A CA\_  
 AGGATTTG GGGG TTC  
 ||||| ||| |||  
 TCCTAAAC CCCC GGG  
 C AAG  
 GAM1660 LOC256112 3' ATGAATGGAGAAATCCTT 96362 GAGGGG  
 AAGGATTT CATTGAT  
 ||||| |||||  
 TTCCTAAA GTAAGTA  
 GAG\_  
 GAM1660 LOC50999 3' TATGAATACCCCTCCCTT 32103 ATTT C  
 AAGG GAGGGG ATTCATA  
 ||| ||||| |||||  
 TTCC CTCCCC TAAGTAT  
 \_ A  
 GAM1661 ANKTM1 3' CAGACCTTCAGTGAGGCTTCTA 23675 \_ GGA A  
 TAGA GCT TTAGTGAA GTCTG  
 ||| ||| ||||| |||||  
 ATCT CGG AGTGACTT CAGAC  
 T \_ C  
 GAM1661 AOA 5' AGACTCCCTCCAGCTCT 91116 TTAGTGAA  
 AGAGCTGGA AGTCT  
 ||||| |||  
 TCTCGACCT TCAGA  
 CCC\_  
 GAM1661 CIT 3' ACTTTTGTACCTAGCTCTA 69740 AT T  
 TAGAGCTGG TAC GAAAGT  
 ||||| ||| |||||

			ATCTCGATC ATG TTTTCA	
			C_ _	
GAM1661	HDAC7A	3'	CAGACTTTGCACACAGC 31207	GATTAC _
			GCTG TG AAAGTCTG	
			CGAC AC TTTCAGAC	
			AC_ G	
GAM1661	HDAC7A	3'	CAGACTTTGCACACAGC 33448	GATTAC _
			GCTG TG AAAGTCTG	
			CGAC AC TTTCAGAC	
			AC_ G	
GAM1661	MADH3	3'	CAGACCTCATGCCCAGCTCT 19736	ATTAC AA
			AGAGCTGG TGA GTCTG	
			TCTCGACC ACT CAGAC	
			CGT_ C_	
GAM1661	SALL2	3'	CAGACTTTGGGAGACCAGCTC 63858	A A G
			GAGCTGG TT CT AAAGTCTG	
			CTCGACC AG GG TTTCAGAC	
			_ A G	
GAM1661	SIL	3'	AGATACTATCCAGCTCTA 11682	TACTGAAA
			TAGAGCTGGAT GTCT	
			ATCTCGACCTA TAGA	
			TCA_	
GAM1661	TCF21	5'	CAGACCCCAACTCCAGCTC 12182	TTAC AAA
			GAGCTGGA TG GTCTG	
			CTCGACCT AC CAGAC	
			CA_ CC_	
GAM1661	TK2	3'	AGACTTTCAGCCGACTC 16058	C ATTA
			GAG TGG CTGAAAGTCT	
			CTC GCC GACTTTCAGA	
			A _	
GAM1661	DAPK2	3'	CAGACTTTTGGACCCAGCTC 26736	ATTA TG
			GAGCTGG C AAAGTCTG	
			CTCGACC G TTTCAGAC	
			CA_ GT	
GAM1661	DIO2	3'	CAGACTTAACAGACCCAGCTCT 5828	ATTA A_
	G		TAGAGCTGG CTG AAGTCTG	
			GTCTCGACC GAC TTCAGAC	
			CA_ AA	
GAM1661	DIO2	3'	CAGACTTAACAGACCCAGCTCT 25680	ATTA A_
	G		TAGAGCTGG CTG AAGTCTG	

			GTCTCGACC	GAC	TTCAGAC		
			CA__	AA			
GAM1661	FLJ10781	3'	AGATGTAATCCAAATCTA	36629	GC	TGAAA	
			TAGA TGGATTAC	GTCT			
			ATCT ACCTAATG	TAGA			
			AA	_____			
GAM1661	FLJ23142	3'	CATTAACCAGCTCTA	44726	A	C	
			TAGAGCTGG	TTA	TG		
			ATCTCGACC	AAT	AC		
			_	T			
GAM1661	KIAA0286	3'	CAGACTTCCAAAGGGTCAGCTC	68321		ATTAC	A
			TG	TAGAGCTGG	TG	AAGTCTG	
			GTCTCGACT	AC	TTCAGAC		
			GGGAA	C			
GAM1661	KIAA0779	5'	ACTTTCAGTCTAGC	85723	TTA		
			GCTGGA	CTGAAAGT			
			CGATCT	GACTTTCA			
			_____				
GAM1661	MGC10200	3'	ACTTTCAGTCTCCACCTC	58982	C	ATT	
			GAG	TGG	ACTGAAAGT		
			CTC	ACC	TGACTTTCA		
			C	CTC			
GAM1661	MGC24039	3'	CAGACTTTTTGTCTTCCAGC	58661	TT	T	
			GCTGGA	AC	GAAAGTCTG		
			CGACCT	TG	TTTTCAGAC		
			TC	T			
GAM1661	NYD-SP29	5'	ACTCCACCTCCAGCTCT	74570	TTAC	AA	
			AGAGCTGGA	TG	AGT		
			TCTCGACCT	AC	TCA		
			CC__	CC			
GAM1661	TRPM3	3'	AGGCTCAAGAATCCAGCCCTA	64907	A	A	GAA
			TAG	GCTGGATT	CT	AGTCT	
			ATC	CGACCTAA	GA	TCGGA	
			C	_	AC_		
GAM1661	LOC118611	3'	ACTTTTGGGATCCAAATC	75466	GC	A	TG
			GA	TGGATT	C	AAAGT	
			CT	ACCTAG	G	TTTCA	
			AA	_	GT		
GAM1661	LOC148696	5'	AGACCCTCCCCAGCTCTA	84185	ATTACT	AA	
			TAGAGCTGG	GA	GTCT		

		ATCTCGACC	CT CAGA		
		C_____	CC		
GAM1661	LOC157421 5'	CAGACTTTTCATCTATCAGCCCT	86443	A	ATTAC
		AG GCTGG	TGAAAGTCTG		
		TC CGACT	ACTTTCAGAC		
		C	ATCT_		
GAM1661	LOC157773 5'	CAGACTTCCAGCTCATT	CAGCT 81605	TA_	A
	C	GAGCTGGAT	CTG AAGTCTG		
		CTCGACTTA	GAC TTCAGAC		
		CTC	C		
GAM1661	LOC199786 3'	CAGACTCTGGTGCC	CAGATC 88371	G	AT GAA
		GA CTGG	TACT AGTCTG		
		CT GACC	GTGG TCAGAC		
		A	C_ TC_		
GAM1661	LOC222057 3'	CAGACTCTTCACACCC	CAGCTCT 92763	ATTAC	_
		AGAGCTGG	TGAA AGTCTG		
		TCTCGACC	ACTT TCAGAC		
		CAC__	C		
GAM1662	FBXL7 3'	AACCAAAGGTCTCACT	AGGA 24540	AAA	CCA
		TCCTGGTGG	CT GTT		
		AGGATCACT	GA CAA		
		CTG	AAC		
GAM1662	GBP1 3'	GAGTTTCCCCAGAAGA	9010	C	T
		TCT CTGG	GGAAACTC		
		AGA GACC	CCTTTGAG		
		A	_		
GAM1662	PTPRH 3'	AACTCTGGTTTCCCC	CAGGAGA 11113	T	CC
		TCTCCTGG	GGAAACT AGTT		
		AGAGGACC	CCTTTGG TCAA		
		_	TC		
GAM1662	TIMP3 3'	AACTGTGGCCCCC	CAGGAGA 4499	T	AAA TC
		TCTCCTGG	GG C CAGTT		
		AGAGGACC	CC G GTCAA		
		_	C_ GT		
GAM1662	FLJ12572 3'	CGGAAGAGAGCCCT	CACCAGGA 43250	AAA	CAG
		TCCTGGTGG	CTC TTCG		
		AGGACCACT	GAG AGGC		
		CCC	AGA		
GAM1662	MGC15416 3'	AACCCTGTCCCCC	CAGGAGA 56538	T	AA TCCA
		TCTCCTGG	GG AC GTT		

			AGAGGACC CC TG CAA		
			_ CC TCC_		
GAM1662	USP20	3'	CTGAGCCCCCACCAGGGA	21925	T AAA C
			TC CCTGGTGG CTC AG		
			AG GGACCACC GAG TC		
			_ CCC _		
GAM1662	LOC128402	3'	GACGGCCCCCACCAGGAGA	75781	AAACT A
			TCTCCTGGTGG CC GTT		
			AGAGGACCACC GG CAG		
			CC__ _		
GAM1662	LOC152674	3'	AACTGATTTCACCAAGGA	85830	_ ACTC
			TCCT GGTGGAA CAGTT		
			AGGA CCACTTT GTCAA		
			A A__		
GAM1662	LOC197044	3'	TGGAGCCCGCACCAGGAGA	87877	GAAA
			TCTCCTGGTG CTCCA		
			AGAGGACCAC GAGGT		
			GCCC		
GAM1663	B3GALT2	3'	TGCACTCTTAAACAGCAC	13684	AA G
			GTGC TTTAAGAG TGCA		
			CACG AAATTCTC ACGT		
			AC _		
GAM1663	E2F1	3'	ACATACACCTCTGTGTGTGCAC	84792	ATTTA C
	TG		CAGTGCA AGAGGTG ATGT		
			GTCACGT TCTCCAC TACA		
			GTGTG A		
GAM1663	GPR18	5'	CATTTCTTAAATACTG	17959	CA
			CAGTG ATTTAAGAGGTG		
			GTCAC TAAATTCTTTAC		
			A_		
GAM1663	INPP5A	3'	ACATGGTTTTTGAATCACA	18656	CA GTG
			CAGTG ATTTAAGAG CATGT		
			GTCAC TAAGTTTTT GTACA		
			AC G__		
GAM1663	SUV39H1	3'	CATGCACCTCCCCACTG	12067	CAATTAA
			CAGTG GAGGTGCATG		
			GTCAC CTCCACGTAC		
			CCC__		
GAM1663	BIKE	3'	ACAGAAACCTCAATTGCAC	34181	TAA GCA
			GTGCAATT GAGGT TGT		



			CACGTAA CTCCA ACA		
			___ AAG		
GAM1663	GT650	3'	CATGCACATGAATTGCCTG	53452	T AGAG
			CAG GCAATTTA GTGCATG		
			GTC CGTTAAGT CACGTAC		
			_ A__		
GAM1663	KIAA0514	3'	ACAAAGCCTAAAATTGCACT	28072	AAG GCA
			AGTGCAATTT AGGT TGT		
			TCACGTAAA TCCG ACA		
			A__ AA_		
GAM1663	KIAA1058	3'	ACATATTTTTTTTAAATCTCACT	82250	CA TGC
	G		CAGTG ATTTAAGAGG ATGT		
			GTCAC TAAATTTTTT TACA		
			TC TA_		
GAM1663	PB1	3'	CATCCTTGAATTACAC	36369	C A
			GTG AATTTAAG GGTG		
			CAC TTAAGTTC CTAC		
			A _		
GAM1663	PTK9	3'	ACATACACCCAAATTATTGCAT	11023	TTAAGA C
	T		AGTGCAAT GGTG ATGT		
			TTACGTTA CCAC TACA		
			TTAAAC A		
GAM1663	LOC112885	3'	ACATGGTGCCGAATTGCACTG	56520	AAGA TG _
			CAGTGCAATTT GG C ATGT		
			GTCACGTAAAG CC G TACA		
			___ GT G		
GAM1663	LOC220776	3'	CCTCCTAAATTGCCTG	68390	T A
			CAG GCAATTTA GAGG		
			GTC CGTTAAAT CTCC		
			_ C		
GAM1663	LOC221405	3'	TGAACCCTTAATTTGCACTG	93889	T A G
			CAGTGCAA TTAAG GGT CA		
			GTCACGTT AATTC CCA GT		
			T _ A		
GAM1663	LOC254170	3'	CATGCACCTGTTTCACTG	94926	C TTAAG
			CAGTG AAT AGGTGCATG		
			GTCAC TTG TCCACGTAC		
			T ____		
GAM1663	LOC256113	5'	ACATAATTATTTAAATTGCA	96767	AG GC
			TGCAATTTAAG GT ATGT		

		ACGTTAAATTT TA TACA	
		AT A_	
GAM1663	LOC256714	3' ACATATACTCAACTTGCACTG 96310	TTTAA G C
		CAGTGCAA GAG TG ATGT	
		GTCACGTT CTC AT TACA	
		CAA__ _ A	
GAM1664	ADAT1	3' TGTCTCTACTAAAAATGCA 23902	T__
		TGCATTTT TAGT GCA	
		ACGTAAAAATCA TGT	
		TCTC	
GAM1664	SLC2A3	3' TGTCTCTACTAAAAATGCA 22667	T__
		TGCATTTT TAGT GCA	
		ACGTAAAAATCA TGT	
		TCTC	
GAM1664	VSX1	3' CTGACAATGTCAAGATAAAATG 27465	TAG _
	CA	TGCATTTT TTG CATTGTCAG	
		ACGTAAAA AAC GTAACAGTC	
		TAG T	
GAM1664	DEGS	3' CATCTCTACTAAAAATGCA 13411	TGCAT
		TGCATTTT TAGT TG	
		ACGTAAAAATCA AC	
		TCTCT	
GAM1664	ESM1	3' CTGAAGAACTAAAAATGCA 22878	GCATTG
		TGCATTTT TAGT TCAG	
		ACGTAAAAATCAA AGTC	
		GA__	
GAM1664	FLJ20006	3' CATCGCTACTAAAAATGCA 34319	T AT
		TGCATTTT TAGT GC TG	
		ACGTAAAAATCA CG AC	
		T CT	
GAM1664	KIAA1260	3' CTGACTTAAGACAAAAATGCA 60025	A GCATT
		TGCATTTT GTT GTCAG	
		ACGTAAAA CAG CAGTC	
		_ AATT_	
GAM1664	MGC10960	3' GTGCAACTAAAAATGTAG 51009	
		CTGCATTTT TAGTTGCAT	
		GATGTAAAAATCAACGTG	
GAM1664	MGC2731	3' GTGTCTACTAAAAATACAG 43954	C T_
		CTG ATTTT TAGT GCAT	

		GAC TAAAAATCA TGTG		
		A TC		
GAM1664	MGC29762	3' CATCTCTACTAAAAATGCA	58469	TGCAT
		TGCATTTTTAGT TG		
		ACGTAAAAATCA AC		
		TCTCT		
GAM1664	LOC144481	3' CATCTCTACTAAAAATGCA	83097	TGCAT
		TGCATTTTTAGT TG		
		ACGTAAAAATCA AC		
		TCTCT		
GAM1664	LOC149319	3' TGTCTCTACTAAAAATGCA	79305	T__
		TGCATTTTTAGT GCA		
		ACGTAAAAATCA TGT		
		TCTC		
GAM1664	LOC202868	3' TGTCTCTACTAAAAATGCA	90386	T__
		TGCATTTTTAGT GCA		
		ACGTAAAAATCA TGT		
		TCTC		
GAM1664	LOC254045	3' CATCTCTACTAAAAATGCA	96506	TGCAT
		TGCATTTTTAGT TG		
		ACGTAAAAATCA AC		
		TCTCT		
GAM1665	ADH1B	3' CTTAGACATAAAGTAAAAT	72644	C CAC
		ATTT ACTTT TGTCTGAG		
		TAAA TGAAA ACAGATTC		
		A T__		
GAM1665	AHR	3' ATCTCAGATGTTAAATAAATG	7875	CAC C T
		CATTT TTT AC GTCTGAGAT		
		GTAAA AAA TG TAGACTCTA		
		TA_ T _		
GAM1665	FDFT1	3' TAGGAAAGTGAAATG	15518	A
		CATTTCACTTTC CTG		
		GTAAAGTGAAAG GAT		
		-		
GAM1665	JTB	3' ATCTCAGACAGTGAAAGTGAAA	21959	
	TG	CATTTCACTTTCACTGTCTGAGAT		
		GTAAAGTGAAAGTGACAGACTCTA		
GAM1665	KLF4	3' TCCCAGACAGTGGATATG	14891	CT A
		CA TTCAGTGTCTG GA		

			GT AGGTGACAGAC CT		
			AT C		
GAM1665	PHYH	3'	ACAGTAAAAGTGAAAT 20608	C	
			ATTTCACTTT ACTGT		
			TAAAGTGAAA TGACA		
			A		
GAM1665	PKD2	3'	TCCAGGTTGAAAAGTGAAA 60096	CTG A	
			TTTCACTTTCA TCTG GA		
			AAAGTGAAAGT GGAC CT		
			T__ _		
GAM1665	WRN	3'	GGGCAGTGAAAATGAAA 5098	C	
			TTTCA TTTCACTGTCT		
			AAAGT AAAGTGACGGG		
			A		
GAM1665	ZNF216	3'	ATCTGCACAGCAAAGTGAAA 20017	CA CTG	
			TTTCACTTT CTGT AGAT		
			AAAGTGAAA GACA TCTA		
			C_ CG_		
GAM1665	CG012	5'	CTCACTCTGAAAGTGAA 83218	CT CT	
			TTCACTTTCA GT GAG		
			AAGTGAAAGT CA CTC		
			CT _		
GAM1665	EIF2C2	3'	ATCTTCTGAGAGTGAAAG 71946	G T_	
			CTTTCACT TC GAGAT		
			GAAAGTGA AG TTCTA		
			G TC		
GAM1665	FLJ23462	3'	ATCTCAGACTTTACAAAGAAAT 45802	ACTTTCACT	
	G		CATTTT GTCTGAGAT		
			GTAAAG CAGACTCTA		
			AAACATTT_		
GAM1665	FLJ23510	3'	ATCTCAGACAGTGACTGAAATG 45281	CTT	
			CATTTCA TCACTGTCTGAGAT		
			GTAAAGT AGTGACAGACTCTA		
			C_		
GAM1665	KIAA0984	3'	TTTGTCCAGTGAAAATGAA 65534	C TC	
			TTCA TTTCACTG TGAG		
			AAGT AAAGTGAC GTTT		
			A CT		
GAM1665	KLHL6	3'	ATCTCAGAGCAGGAAA 55299	A _	
			TTTC CTG TCTGAGAT		

		AAAG GAC AGACTCTA		
		— G		
GAM1665	NIR3	3' GCAGTGAAAAGTGCAAT	66242	T
		ATT CACTTTTCACTGT		
		TAA GTGAAAAGTGACG		
		C		
GAM1665	PORIMIN	3' ATCTCAGAGGGCCAAAGTGAA	53598	CA G
		TTCAC TTT CT TCTGAGAT		
		AAGTGAAA GG AGACTCTA		
		CC G		
GAM1665	PP35	3' ATCTCAGACTGAAA	22814	CT
		TTTCA GTCTGAGAT		
		AAAGT CAGACTCTA		
		—		
GAM1665	PRTD-NY3	3' CTCATTGCAATAAGTGAAATG	48148	TCAC C_
		CATTTCACTT TGT TGAG		
		GTAAAGTGAA ACG ACTC		
		TA__ TT		
GAM1665	SEP15	3' TCCTACAGTAAGAGTGAAA	14934	C CT
		TTTCACTTT ACTGT GA		
		AAAGTGAGA TGACA CT		
		A TC		
GAM1665	SFXN2	3' CTCAGGGGAAAAAAGTGAAA	73941	CACTG
		TTTCACTTT TCTGAG		
		AAAGTGAAA GGA CTC		
		AAAGG		
GAM1665	LOC149703	3' ATCTCAGACAGCCGTTTGAAA	84647	ACTTTCA
		TTTC CTGTCTGAGAT		
		AAAG GACAGACTCTA		
		GTTTGCC		
GAM1665	LOC154007	3' ATCTCAAACCCTTTAGTGAAA	81015	TTCAC T C
		TTTCACT GT TGAGAT		
		AAAGTGA CA ACTCTA		
		TTTCC_ A		
GAM1665	LOC155004	3' TCATTTAAGTGAAAAGGAAA	81226	A GTC_
		TTTC CTTTCACT TGA		
		AAAG GAAAGTGA ACT		
		— ATTT		
GAM1665	LOC222134	5' ACAGTGAAGTGAAATG	94136	T
		CATTTCACTT CACTGT		

GTAAAGTGAA GTGACA

GAM1666 CLCN5 5' TGAAATACCTAAGCTGCTCCAA 3595  
TTGGAGCAG GTTTCA  
||||||| |||||  
AACCTCGTC TAAAGT  
GAATCCA

GAM1666 FLRT2 5' ATTGAAAAATGAGGTCTGC 25056 GT CTC  
GCAG TTCATT CAAT  
||| ||||| |||  
CGTC GAGTAA GTTA  
TG AAA

GAM1666 IL17 3' TGGGGAAAATGAAACCCTCC 9333 CA  
GGAG GGTTTCAT TCTCCA  
||| ||||| |||||  
CCTC CCAAAGTA AGGGGT  
AA

GAM1666 NLGN1 5' TGAAGATGCTGCTCCAA 30026 G  
TTGGAGCAG TTTCA  
||||||| |||||  
AACCTCGTC GAAGT  
GTA

GAM1666 POLG 3' GTGATAAACCTGCTCCAA 10682  
TTGGAGCAGGTT TCAT  
||||||| |||||  
AACCTCGTCCAA AGTG  
AT

GAM1666 TPK1 3' GGAGAACCTGTCCAA 42384 G TTCAT  
TTGGA CAGGT TCTCC  
||||| ||||| |||||  
AACCT GTCCA AGAGG

GAM1666 C1orf8 5' GAGAATGAAACCCTC 16832 CA  
GAG GGTTTCATTCTC  
||| |||||  
CTC CCAAAGTAAGAG

GAM1666 CLIC6 3' TGGAGAACATGTTCCAA 82536 G TTCAT  
TTGGAGCA GT TCTCCA  
||||||| || |||||  
AACCTTGT CA AGAGGT  
A

GAM1666 CLIPR-59 3' TGGAGAATTTCAATGCCCCGA 31374 A GGTTTC  
TTGG GCA ATTCTCCA  
||| ||| |||||  
AGCC CGT TAAGAGGT  
C AACTT\_

GAM1666 DKFZP547L112 3' TGGAGAACTCTTGCTCCA 66532 TTTCA  
TTGGAGCAGG TTCTCCA  
||||||| |||||

			ACCTCGTTC	AAGAGGT	
			TC____		
GAM1666	EPS8R3	5'	GGACCACCTGCTCCAA	55701	TTCATTC
			TTGGAGCAGGT	TCC	
			AACCTCGTCCA	AGG	
			CC_____		
GAM1666	EPS8R3	5'	GGACCACCTGCTCCAA	57404	TTCATTC
			TTGGAGCAGGT	TCC	
			AACCTCGTCCA	AGG	
			CC_____		
GAM1666	FLJ20552	3'	AGAACAAACTGCTCCAA	35389	G CA
			TTGGAGCAG TTT TTCT		
			AACCTCGTC AAA AAGA		
			_ AC		
GAM1666	FLJ22865	5'	TGGAGAAACTGCTCTAA	47071	GTTTCA
			TTGGAGCAG TTCTCCA		
			AATCTCGTC AAGAGGT		
			AA_____		
GAM1666	KIAA0372	5'	ATTGAAATTTGTTACCTACTCC	27663	C TT TTCTC
	AA		TTGGAG AGGT CA CAAT		
			AACCTC TCCA GT GTTA		
			A TT TTAAA		
GAM1666	PRO0132	5'	ATGAAACCACTCCAA	26101	CA
			TTGGAG GGTTTCAT		
			AACCTC CCAAAGTA		
			A_		
GAM1666	TEX27	3'	AGAGTGGAACCCGCTGCAA	41658	G A
			TTG AGC GGTTTCATTCT		
			AAC TCG CCAAGGTGAGA		
			G C		
GAM1666	LOC149373	3'	ATTGGGGTGATGATACCCACCC	79312	AGCA T _
	CAA		TTGG GGT TCATT CTCCAAT		
			AACC CCA AGTAG GGGGTTA		
			CCAC T T		
GAM1666	LOC152687	3'	TTGGAGAATATTGCTCC	80643	GTTTC
			GGAGCAG ATTCTCCAA		
			CCTCGTT TAAGAGGTT		
			A_____		
GAM1666	LOC51202	3'	ATTGGAGAATGAAACCTGCTCC	33017	
	AA		TTGGAGCAGGTTTCATTCTCCAAT		

AACCTCGTCCAAAGTAAGAGGTTA

GAM1667 ACADS 3' ACCACTGTGCCTCAAGTTCC 3406 AAGACA  
GGAG GGGCACAGTGGT  
|||| |||||  
CCTT TCCGTGTCACCA  
GAAC\_\_

GAM1667 AIPL1 3' ACCCCTCCCTGTCTCCCCA 59849 A A CAC T  
TGG GA GACAGGG AG GGT  
||| ||||| |||  
ACC CT CTGTCCC TC CCA  
C \_ \_ C

GAM1667 B3GAT1 5' TGCTCTGTCCTCTCCA 53979 A  
TGGAGA GACAGGGCA  
||||| |||||  
ACCTCT CTGTCTCGT  
C

GAM1667 COG5 3' TGTACCCTGCTTCCCC 20954 A A C  
GG GAAG CAGGG ACA  
|| ||| ||||| |||  
CC CTTC GTCCC TGT  
C \_ A

GAM1667 CRTAP 3' ACCTTCATCCCTGTCTTCCTCA 21028 GA CACAGT  
TG GAAGACAGGG GGT  
|| ||||| |||  
AC CTTCTGTCCC CCA  
TC TACTT\_

GAM1667 EPB72 3' ACCACAACCAGCTTCTCCA 14594 ACA GCACA  
TGGAGAAG GG GTGGT  
||||| || |||||  
ACCTCTTC CC CACCA  
GA\_ AA\_\_

GAM1667 GAB2 3' TACCACTGTCTCTGCCCCCA 24502 AGAAGA C  
TGG CAGGG ACAGTGGTA  
||| ||||| |||||  
ACC GTCTC TGTCACCAT  
CCC\_\_ C

GAM1667 GAB2 3' TACCACTGTCTCTGCCCCCA 54459 AGAAGA C  
TGG CAGGG ACAGTGGTA  
||| ||||| |||||  
ACC GTCTC TGTCACCAT  
CCC\_\_ C

GAM1667 GPD1 3' TGCCCTGTCCCTCTCCA 59672 A\_  
TGGAGA GACAGGGCA  
||||| |||||  
ACCTCT CTGTCCCGT  
CC

GAM1667 GSTT1 3' ACCATCCCCACCCTGTCTTCCA 73457 GA CACA\_  
CA TG GAAGACAGGG GTGGT  
|| ||||| |||||



			AC CTTCTGTCCC	TACCA		
			AC	ACCCC		
GAM1667	MATN1	3'	ACCACTGTGGCCTCTCCA	9916	AGACA	G
			TGGAGA	GG CACAGTGGT		
			ACCTCT	CC GTGTCACCA		
			_____	G		
GAM1667	MAZ	3'	TGCCCTGTCTTCCCA	73390	A	
			TGG GAAGACAGGGCA			
			ACC CTTCTGTCCCGT			
			—			
GAM1667	NR1D1	3'	ACCACTCTGTCTCCCCCA	41361	AGA	GGCAC
			TGG AGACAG	AGTGGT		
			ACC TCTGTC	TCACCA		
			CCC	_____		
GAM1667	OTOF	3'	CACACCCTGTCTTCCCA	16639	A	CACA
			TGG GAAGACAGGG	GTG		
			ACC CTTCTGTCCC	CAC		
			—	A_____		
GAM1667	PCTP	3'	ACCACTGTTACAGCCTTCCCC	41094	A	ACAG C
			GG GAAG	GG ACAGTGGT		
			CC CTTC	CT TGTCACCA		
			C	CGA_ _		
GAM1667	PPP2R1A	3'	CACCTCCCGTCCTCCCCA	26442	A A A	CACA
			TGG GA GAC GGG	GTG		
			ACC CT CTG CCC	CAC		
			C C _	TC_		
GAM1667	PPP2R4	3'	TGTGCCTGCCTTCCCCA	60563	A	ACA
			TGG GAAG	GGGCACA		
			ACC CTTC	TCCGTGT		
			C	CG_		
GAM1667	SH3BP2	3'	CACGCCCTGTTCCCTCCA	11595	AA	ACA
			TGGAG GACAGGGC	GTG		
			ACCTC TTGTCCCG	CAC		
			CC	_____		
GAM1667	SMAC	3'	CACTGCCCTGTCTCCCCA	57195	A A	CA
			TGG GA GACAGGGCA	GTG		
			ACC CT CTGTCCCGT	CAC		
			C _	_____		
GAM1667	SMAC	3'	CACTGCCCTGTCTCCCCA	57205	A A	CA
			TGG GA GACAGGGCA	GTG		

ACC CT CTGTCCCGT CAC  
 C \_ \_  
 GAM1667 SMAC 3' CACTGCCCTGTCTCCCCA 39111 A A CA  
 TGG GA GACAGGGCA GTG  
 ||| || ||||| |||  
 ACC CT CTGTCCCGT CAC  
 C \_ \_  
 GAM1667 UVRAG 3' TACTGTCGCCCCATCTTCTCC 12562 CA \_  
 GGAGAAGA GGGC ACAGTG  
 ||||| ||| |||||  
 CCTCTTCT CCCG TGTCAT  
 AC C  
 GAM1667 XPA 3' ACCACTGTACCCAGGTTCT 4596 GACA C  
 AGAA GGG ACAGTGGT  
 ||| || |||||  
 TCTT CCC TGTCACCA  
 GGAC A  
 GAM1667 ZNF261 3' CCATTCCCTGCCTTCTCTA 17493 A CAC  
 TGGAGAAG CAGGG AGTGG  
 ||||| ||| |||||  
 ATCTCTTC GTCCC TTACC  
 C \_  
 GAM1667 B3GNT7 3' ACCGCACCCTGCTTCTCCA 71123 A CACA  
 TGGAGAAG CAGGG GTGGT  
 ||||| ||| |||||  
 ACCTCTTC GTCCC CGCCA  
 \_ A \_  
 GAM1667 CBCIP2 3' CACCTTTCCCCTCTTCTCCA 51589 CA CACA  
 TGGAGAAGA GGG GTG  
 ||||| ||| |||  
 ACCTCTTCT CCC CAC  
 C\_ TTTC  
 GAM1667 DKFZP434P1750 3' GCCCTCCCTGTCTCCCCCA 31377 AGA CAC T  
 TGG AGACAGGG AG GGT  
 ||| ||||| |||||  
 ACC TCTGTCCC TC CCG  
 CCC \_ \_  
 GAM1667 DKFZp547I094 5' ACCCCTGTTGCCCTGCCTTCTT 49629 A \_ T  
 CA TGGAGAAG CAGGGCA CAG GGT  
 ||||| ||||| ||| |||  
 ACTTCTTC GTCCCGT GTC CCA  
 C T C  
 GAM1667 DKFZp564I1922 3' ACCACTGTTATATTACCTTCTC 31232 AC GGC\_  
 CA TGGAGAAG AG ACAGTGGT  
 ||||| || |||||  
 ACCTCTTC TT TGTCACCA  
 CA ATAT  
 GAM1667 DUSP9 3' CACCTCCCTGTTTCTCCA 7341 A CACA  
 TGGAGA GACAGGG GTG  
 ||||| ||||| |||

ACCTCT TTGTCCC CAC  
 \_ TC\_  
 GAM1667 FLJ14708 3' ACCACTGTGGGCCCTCCTTC 51538 AC \_  
 GAAG AGGGC ACAGTGGT  
 ||| ||| |||||  
 CTTC TCCCG TGTCACCA  
 C\_ GG  
 GAM1667 FLJ23120 3' ACCACTGCACCACTGTACTCCA 85143 AAG \_ CA  
 TGGAG ACAG GG CAGTGGT  
 ||| ||| || |||||  
 ACCTC TGTC CC GTCACCA  
 A\_ A AC  
 GAM1667 IMAGE:4907098 3' ACCACTGTGGTCCCCTCCA 91656 AA AGGG  
 TGGAG GAC CACAGTGGT  
 ||| ||| |||||  
 ACCTC CTG GTGTCACCA  
 CC \_  
 GAM1667 KIAA0416 3' ACCACTACCACTCCA 31462 AAGACA CAC  
 TGGAG GGG AGTGGT  
 ||| ||| |||||  
 ACCTC CCC TCACCA  
 A\_ A\_  
 GAM1667 KIAA0545 3' CCACGCTGTTCTCCA 63144 AAGACA CA  
 TGGAG GGGCA GTGG  
 ||| ||| |||  
 ACCTC CTTGT CACC  
 \_ CG  
 GAM1667 KIAA0924 3' TGCCCTGTCCTCTGCA 29724 G A  
 TG AGA GACAGGGCA  
 || ||| |||||  
 AC TCT CTGTCCCGT  
 G C  
 GAM1667 KIAA1111 3' CATCCTGCCTGCCTTCTCCA 96206 ACA CA  
 TGGAGAAG GGGCA GTG  
 ||||| ||| |||  
 ACCTCTTC TCCGT TAC  
 CG\_ CC  
 GAM1667 KIAA1184 3' TGTGCCCTCCCTCCA 42620 AA CA  
 TGGAG GA GGGCACA  
 ||| || |||||  
 ACCTC CT CCCGTGT  
 CC C\_  
 GAM1667 MGC13138 3' TACCACCATGCCTGGCTTC 53022 ACA CA  
 GAAG GGGCA GTGGTA  
 ||| ||| |||||  
 CTTC TCCGT CACCAT  
 GG\_ AC  
 GAM1667 MGC5590 5' TACCACTGTCAGCACTCTCCA 43927 AGACAGG \_  
 TGGAGA GC ACAGTGGTA  
 |||| || |||||

		ACCTCT	CG	TGTCACCAT		
		CA_____	AC			
GAM1667	moblak	3'	CCACACCTCTGTCTCCCCCA	55490	AGA	CACA
			TGG AGACAGGG GTGG			
			ACC TCTGTCTC CACC			
			CCC CA__			
GAM1667	NR6A1	3'	ACCACTGCGAACTTTCCA	52866	AAGAC	GGCA
			TGGAG AG CAGTGGT			
			ACCTT TC GTCACCA			
			_____ AAGC			
GAM1667	NR6A1	3'	ACCACTGCGAACTTTCCA	52878	AAGAC	GGCA
			TGGAG AG CAGTGGT			
			ACCTT TC GTCACCA			
			_____ AAGC			
GAM1667	NR6A1	3'	ACCACTGCGAACTTTCCA	7641	AAGAC	GGCA
			TGGAG AG CAGTGGT			
			ACCTT TC GTCACCA			
			_____ AAGC			
GAM1667	PEG10	3'	TACCACTGCCGGATGTATTCTC	30530	G G__	CA
	CA		TGGAGAA ACA GGCA GTGGTA			
			ACCTCTT TGT CCGT CACCAT			
			A AGG _			
GAM1667	STMN3	3'	TACCACTGCAGCATCCCCCACT	31902	ACA CA_____	
	TCTCCA		GGAGAAG GGG CAGTGGTA			
			CCTCTTC CCC GTCACCAT			
			ACC TACGAC			
GAM1667	LOC126964	3'	ACCACTGTGTGCGCCTCCA	74610	AAGACAGG	
			TGGAG GCACAGTGGT			
			ACCTC TGTGTCACCA			
			CGCG_____			
GAM1667	LOC145837	5'	CATCTGCCCTGTCTCTCCA	83543	A	CA
			TGGAGA GACAGGGCA GTG			
			ACCTCT CTGTCCCGT TAC			
			_ C_			
GAM1667	LOC148930	3'	GCTTTGCCCTGTGTTCTCCA	79097	G	C
			TGGAGAA ACAGGGCA AGT			
			ACCTCTT TGTCCCGT TCG			
			G T			
GAM1667	LOC150372	3'	TACCACTGTGCCCTGGCCCA	79808	AGAAGA	
			TGG CAGGGCACAGTGGTA			

	ACC GTCCCGTGTCAACCAT	
	CG_____	
GAM1667 LOC151162 5'	GCCACCCCATTCTCCA 85244	ACA CACA
	TGGAGAAG GGG GTGGT	
	ACCTCTTT CCC CACCG	
	A__ ____	
GAM1667 LOC154761 3'	ACCACACCCACTTCTCCA 81120	ACA CACA
	TGGAGAAG GGG GTGGT	
	ACCTCTTC CCC CACCA	
	A__ A__	
GAM1667 LOC199964 3'	TGCCGTGCCTTCTCCA 89891	A G
	TGGAGAAG CA GGCA	
	ACCTCTTC GT CCGT	
	C G	
GAM1667 LOC203377 5'	GCCACCCCATTCTCCA 90582	ACA CACA
	TGGAGAAG GGG GTGGT	
	ACCTCTTT CCC CACCG	
	A__ ____	
GAM1667 LOC203504 5'	ACCCCTCCCCAGTCTTCTCCA 90635	A CAC T
	TGGAGAAGAC GGG AG GGT	
	ACCTCTTCTG CCC TC CCA	
	A C__ C	
GAM1667 LOC219654 3'	CGTTGTTCCCCGTCTTCTCCA 91302	A C
	TGGAGAAGAC GGG ACAGTG	
	ACCTCTTCTG CCC TGTTC	
	C T	
GAM1667 LOC221416 3'	TGGCACCTATCTTCTCCA 93772	C CA_
	TGGAGAAGA AGGG CA	
	ACCTCTTCT TCCC GT	
	A ACG	
GAM1667 LOC221491 5'	ACCACTGTGCCAATGCCCCC 92010	AGAAGACA
A	TGG GGGCACAGTGGT	
	ACC CCGTGTACCA	
	CCCCGTAA	
GAM1667 LOC222001 3'	ACCACTAATTAAGTTTCTCCA 92903	AGGGCAC
	TGGAGAAGAC AGTGGT	
	ACCTCTTTG TCACCA	
	AATTAA_	
GAM1667 LOC255975 5'	TACCACCGGCAGCCTCTCCA 95897	AGACAGG ACA
	TGGAGA GC GTGGTA	

		ACCTCT	CG	CACCAT		
		CCGA__	GCC			
GAM1667	LOC256901	3'	ACCACTTCCCCCTTCTCCA	96619	ACA	CAC
			TGGAGAAG GGG AGTGGT			
			ACCTCTTC CCC TCACCA			
			C__ T__			
GAM1667	LOC54550	3'	ACCACTGTGCCCAGGCGCCA	77688	AGAAGACA	
			TGG GGGCACAGTGGT			
			ACC CCCGTGTCACCA			
			GCGGA__			
GAM1667	LOC93097	3'	ACCACCAGCATTTCCTCCA	71357	AA	CAGG ACA
			TGGAG GA GC GTGGT			
			ACCTC CT CG CACCA			
			__ TTA_ AC_			
GAM1667	LOC96652	3'	ACCACCTGCACCAGCTTCTCCA	65462	ACA _	CA
			TGGAGAAG GG GCA GTGGT			
			ACCTCTTC CC CGT CACCA			
			GA_ A C_			
GAM1668	ARHGEF6	3'	CAAACCTGAAGCCAGGC	68197	ACCA	
			GCCTGG CAAGTTTG			
			CGGACC GTTCAAAC			
			GAA_			
GAM1668	CNTN2	3'	GTCACAACCCAGGTGA	17411	ACCACAA _	
			TCGCCTGG GTT TGAC			
			AGTGGACC CAA ACTG			
			_____ C			
GAM1668	CORO2A	3'	AAACTGTGGTCCAGAGA	53398	GC	A
			TC CTGGACCACA GTTT			
			AG GACCTGGTGT CAAA			
			A_ _			
GAM1668	CORO2A	3'	AAACTGTGGTCCAGAGA	12642	GC	A
			TC CTGGACCACA GTTT			
			AG GACCTGGTGT CAAA			
			A_ _			
GAM1668	GRLF1	3'	AGGTCAGAAAGTGGCCCAGG	78551	A	AAG
			CCTGG CCAC TTTGACCT			
			GGACC GGTG AGACTGGA			
			C AA_			
GAM1668	LAPTM5	3'	AGGCTTGTGGTCAAGC	22199	CTG	
			GC GACCACAAGTTT			

		CG CTGGTGTTCGGA		
		AA_		
GAM1668	POU2AF1	3' AGATTTACAGTCCAGGC	20647	CAC
		GCCTGGAC AAGTTT		
		CGGACCTG TTTAGA		
		ACA		
GAM1668	PTGS1	3' GTCTCCTGTCTTATGGTCCAG	6355	C TTT__
		CTGGACCA AAG GAC		
		GACCTGGT TTC CTG		
		A TGCCT		
GAM1668	PTGS1	3' GTCTCCTGTCTTATGGTCCAG	54574	C TTT__
		CTGGACCA AAG GAC		
		GACCTGGT TTC CTG		
		A TGCCT		
GAM1668	TRIM34	5' AGGTCAAGTTGAGCCCAG	55224	ACCA G
		CTGG CAA TTTGACCT		
		GACC GTT GAACTGGA		
		CGA_ _		
GAM1668	TRIM9	5' AGGCCAGGCAAGTCCAGGC	30749	CACAA A
		GCCTGGAC GTTTG CCT		
		CGGACCTG CGGAC GGA		
		AA__ C		
GAM1668	ABLIM	5' GATATGTAACCCAGGCGG	22030	ACC A
		TCGCCTGG ACA GTT		
		GGCGGACC TGT TAG		
		CAA A		
GAM1668	AMOT	3' AGGCATCTTCATGGTCCAGGGA	55716	G C_ TT A
		TC CCTGGACCA AAG TG CCT		
		AG GGACCTGGT TTC AC GGA		
		_ AC T_ _		
GAM1668	DKFZp434D177	5' TTAGACCCAGGCGA	50056	ACCACAA
		TCGCCTGG GTTTGA		
		AGCGGACC CAGATT		
		_____		
GAM1668	DKFZp434D177	5' TTAGACCCAGGCGA	79443	ACCACAA
		TCGCCTGG GTTTGA		
		AGCGGACC CAGATT		
		_____		
GAM1668	FLJ23420	3' CAAGTGGGTCCAGGC	46845	A AG
		GCCTGGACC CA TTTG		

CGGACCTGG GT GAAC

GAM1668 HSA249128 5' GGCGCGGTCCAGGCGG 34152 ACAA  
TCGCCTGGACC GTT  
||||||| |||  
GGCGGACCTGG CGG  
CG\_\_

GAM1668 MGC15668 5' AGACCCGGTGGTCCAGACG 51277 C AA\_  
CG CTGGACCAC GTTT  
|| ||||| |||  
GC GACCTGGTG CAGA  
A GCC

GAM1668 MGC22014 3' AGGTCCCGAGTGTAACCCAGGT 64486 ACC AGTTT  
GA TCGCCTGG ACA GACCT  
||||| ||| ||||  
AGTGGACC TGT CTGGA  
CAA GAGCC

GAM1668 SDCCAG10 5' AGAGTTGTGGTCCAAAGA 19641 GCC G  
TC TGGACCACAA TTT  
|| ||||| |||  
AG ACCTGGTGTT AGA  
AA\_ G

GAM1668 LOC115442 3' AGGTCAGGGATGGTCCAG 72676 CAAG  
CTGGACCA TTTGACCT  
||||| |||||  
GACCTGGT GGA CTGGA  
AG\_\_

GAM1668 LOC129011 5' AGACCTGCGGTCCAGGC 74862 A A  
GCCTGGACC CA GTTT  
||||| || |||  
CGGACCTGG GT CAGA  
C C

GAM1668 LOC130536 5' GCAAAGTCCAGGCG 75746 CACAAG A  
CGCCTGGAC TTTG C  
||||| ||| |  
GCGGACCTG AAAC G  
C

GAM1668 LOC149108 3' AGACTTCACTGTGGTCCA 84357 \_\_\_\_  
TGGACCACA AGTTT  
||||| |||  
ACCTGGTGT TCAGA  
CACT

GAM1668 LOC221688 5' AGACTCGGGCCCAGACGA 93674 C A ACA  
TCG CTGG CC AGTTT  
||| ||| || ||||  
AGC GACC GG TCAGA  
A C GC\_

GAM1668 LOC256228 5' AGACTTGTGGTCAAAGC 96233 CTG  
GC GACCACAAGTTT  
|| ||||| |||||



		CG CTGGTGTTCAGA		
		AAA		
GAM1668	LOC257441 5'	TTAGACCCAGGCGA	95566	ACCACAA
		TGCCTGG GTTTGA		
		AGCGGACC CAGATT		
GAM1668	LOC91960 3'	AGGTGCCTCTCGTGGTCCAAGC	67657	C A TTTG
		GC TGGACCAC AG ACCT		
		CG ACCTGGTG TC TGGA		
		A C TCCG		
GAM1668	LOC92840 3'	GTCCCTCGGGTCCAGGC	56435	ACA TTT
		GCCTGGACC AG GAC		
		CGGACCTGG TC CTG		
		GC_ C_		
GAM1669	APBA2 3'	CAAAGGAGAGTCACAGAA	18556	ATTTCAT
		TTCT CTCTCCTTTG		
		AAGA GAGAGGAAAC		
		CACT_		
GAM1669	CHC1L 3'	CAAAAGAGAACTGAAATGGA	7014	TC_ C
		TCTATTCA TCTC TTTG		
		AGGTAAAGT AGAG AAAC		
		CAA A		
GAM1669	EGFR 3'	CAAAGAAGAAACGGAGGGGATG	17835	A ATC C
A		TCATTCT TTTC TCT CTTG		
		AGTAGGG GAGG AGA GAAAC		
		_ CAA A		
GAM1669	FLRT1 3'	CAAAGGAGAGAGGGAAGAA	59610	A TT A
		TTCT T C TCTCTCCTTTG		
		AAGA A G AGAGAGGAAAC		
		_ GG _		
GAM1669	HRC 5'	CAAAGGAGAGACACAGAGAA	9278	ATTCA
		TTCT TCTCTCCTTTG		
		AAGA AGAGAGGAAAC		
		GACAC_		
GAM1669	PPIL1 3'	AGATGACATAGAATGA	32141	T
		TCATTCTAT TCATCT		
		AGTAAGATA AGTAGA		
		C		
GAM1669	SNAP23 3'	AGAGAAAAATAGAATGA	55457	CA
		TCATTCTATTT TCTCT		

			AGTAAGATAAA AGAGA		
			A_		
GAM1669	SNAP23	3'	AGAGAAAAATAGAATGA 13804	CA	
			TCATTCTATTT TCTCT		
			AGTAAGATAAA AGAGA		
			A_		
GAM1669	SNX9	3'	AAATAAGTAGATGAAATCAAAT 32587	CT	_ CC
	GA		TCATT ATTTCATCT CT TTT		
			AGTAA TAAAGTAGA GA AAA		
			AC T AT		
GAM1669	TMPRSS2	3'	AGAATGAAATGAATGA 18963	T	C
			TCATTC ATTTCAT TCT		
			AGTAAG TAAAGTA AGA		
			- -		
GAM1669	TNP2	3'	CAAAGGAGAAAAATGCTAGGATG 18297	TTT	C_
	A		TCATTCTA CAT TCTCCTTTG		
			AGTAGGAT GTA AGAGGAAAC		
			C_ AA		
GAM1669	HH114	3'	GAGTGAAATAGAATGA 50688	T	
			TCATTCTATTTCA CTC		
			AGTAAGATAAAGT GAG		
			-		
GAM1669	MGC16175	3'	AAAGGAGAAAAAAATGGA 51298	CATC	
			TCTATTT TCTCCTTT		
			AGGTAAA AGAGGAAA		
			AAA_		
GAM1669	NUDT13	3'	CAAAGGAGAAGTGACAAAAGA 63213	A _	TC
			TCT TT TCA TCTCCTTTG		
			AGA AA AGT AGAGGAAAC		
			A C GA		
GAM1669	POU2F1	3'	CAAAGGAGAGAAGGGAGAA 10687	AT	A
			TTCT TTC TCTCTCCTTTG		
			AAGA GGG AGAGAGGAAAC		
			_ A		
GAM1669	LOC115110	3'	CAAAGGAGAATTCTAGAA 71711	TTTCATC	
			TTCTA TCTCCTTTG		
			AAGAT AGAGGAAAC		
			CTTA_		
GAM1669	LOC127133	3'	AGAAATGAAATAAAATGG 74636	C	C
			TCATT TATTTCAT TCT		

		GGTAA ATAAAGTA AGA		
		A A		
GAM1669	LOC158886 5'	AGAAAGAATAGAATGA	82832	CA
		TCATTCTATTT TCT		
		AGTAAGATAAG AGA		
		AA		
GAM1669	LOC158887 5'	AGAAAGAATAGAATGA	86944	CA
		TCATTCTATTT TCT		
		AGTAAGATAAG AGA		
		AA		
GAM1669	LOC201182 5'	GGTTGAGATGGAATAGAAT	89766	T_
		ATTCTATTTTCATCTC CC		
		TAAGATAAGGTAGAG GG		
		TT		
GAM1669	LOC222066 3'	CAAAGGAGAAATCACGAGAA	92740	ATTTC C
		TTCT AT TCTCCTTTG		
		AAGA TA AGAGGAAAC		
		GCAC_ A		
GAM1670	ACVR1 5'	ATGTGACCAAGAGCCTGCATTA	6602	CT
		TAATGCAGGCTCTT TCACAT		
		ATTACGTCCGAGAA AGTGTA		
		CC		
GAM1670	ARHGAP6 5'	ATGTCCGCGCAGAGCCTGCTCC	6759	AAT TCTTC_
	ACA	TGT GCAGGCTCT ACAT		
		ACA CGTCCGAGA TGTA		
		CCT CGCGCC		
GAM1670	ATP11B 3'	AGTAGGCCTGCATTACA	80314	T T
		TGTAATGCAGGC CT CT		
		ACATTACGTCCG GA GA		
		_ T		
GAM1670	CALCR 3'	ATGTGAAGAAAAAGACCTGCA	8217	_ C_
		TGCAGG CT TTCTTCACAT		
		ACGTCC GA AAGAAGTGTA		
		A AA		
GAM1670	DUSP5 3'	ATGTGAAGAAAAGCAGTAT	15350	AG C
		ATGC GCT TTCTTCACAT		
		TATG CGA AAGAAGTGTA		
		A_ A		
GAM1670	FOXO1A 3'	ATGCGAACAGACCAACCTGGCA	8904	_ C__ TC A
	TTACA	GTAATGC AGG TCT TTC CAT		

CATTACG TCC AGA AAG GTA  
 G AACC C\_ C  
 GAM1670 SYT4 3' ATGTAAAGAAAATGTATTACA 62434 GGCTC C  
 TGTAATGCA TTCTT ACAT  
 ||||| |||| ||||  
 ACATTATGT AAGAA TGTA  
 AA\_\_ A  
 GAM1670 C1orf24 3' AAGTGCCTTGCATTACA 53699 \_ T  
 TGTAATGCA GGC CTT  
 ||||| ||| |||  
 ACATTACGT CCG GAA  
 T T  
 GAM1670 FLJ10546 3' GGAAACCTGTATTACA 59478 CTC  
 TGTAATGCAGG TTCT  
 ||||| |||  
 ACATTATGTCC AAGG  
 A\_\_  
 GAM1670 FLJ22174 3' ATGTGCGGGGGAGGCCACACT 41674 A CA \_ T  
 ACA TGTA TG GGC TCTTCT CACAT  
 ||| || ||| ||||| |||||  
 ACAT AC CCG AGGGGG GTGTA  
 C AC G C  
 GAM1670 MGC2217 5' ATGTGAAGAACTCATGCA 44175 GGCTC  
 TGCA TTCTTCACAT  
 ||| |||||  
 ACGT AAGAAGTGTA  
 ACTCA  
 GAM1670 LOC149992 5' ATGCGAAGAAGAGGACTGCTCT 79556 AT G\_ A  
 ACA TGTA GCAG CTCTTCTTC CAT  
 ||| ||| ||||| |||  
 ACAT CGTC GAGAAGAAG GTA  
 CT AG C  
 GAM1670 LOC255452 5' GAAGAAGGGACCTCCA 97535 C \_  
 TG AGG CTCTTCTTC  
 || ||| |||||  
 AC TCC GGGAAGAAG  
 C A  
 GAM1671 APBB1 3' GGAGGAAGTGGTCCAGGC 6746 GTATG  
 GCCTGGACCAGT CC  
 ||||| ||  
 CGGACCTGGTCA GG  
 AGGA\_  
 GAM1671 DGAT1 3' GGATGGCGACAGCAGGCCAGAC 64543 C A A GTA  
 A TG CTGG CC GT TGCCATCC  
 || ||| || ||| |||||  
 AC GACC GG CG GCGGTAGG  
 A \_ A ACA  
 GAM1671 EDAR 3' ATGGCAACAAAATGCAGACA 42264 C GACCAG A  
 TG CTG TGT TGCCAT  
 || ||| ||| |||||

			AC GAC	ACA ACGGTA		
			A	GTAAA_ _		
GAM1671	ITGA5	3'	ACATTGGCACCTAATCCAGGCA	61275	_____	
			TGCCTGGA	CCAGTGT		
			ACGGACCT	GGTTACA		
			AATCCAC			
GAM1671	MSL3L1	3'	TATACACTAACCAGGCA	54370	ACC	
			TGCCTGG	AGTGTATG		
			ACGGACC	TCACATAT		
			AA_			
GAM1671	NGFB	5'	GGATGGCATGCTGGACCCAAGC	10220	C A_ GT	
			GC TGG	CCAGT ATGCCATCC		
			CG ACC	GGTCG TACGGTAGG		
			A CA	_		
GAM1671	PCDH11X	3'	GGATGGCAGTATGTAATCCAG	52047	CCA TG _	
			CTGGA	G TA TGCCATCC		
			GACCT	T AT ACGGTAGG		
			AA_ GT	G		
GAM1671	PCDH11X	3'	GGATGGCAGTATGTAATCCAG	52025	CCA TG _	
			CTGGA	G TA TGCCATCC		
			GACCT	T AT ACGGTAGG		
			AA_ GT	G		
GAM1671	PCDH11Y	3'	GGATGGCAGTATGTAATCCAG	52081	CCA TG _	
			CTGGA	G TA TGCCATCC		
			GACCT	T AT ACGGTAGG		
			AA_ GT	G		
GAM1671	SOCS4	3'	TATACATGATCCAGGCA	55114	CCA	
			TGCCTGGA	GTGTATG		
			ACGGACCT	TACATAT		
			AG_			
GAM1671	ABT1	3'	GGATAATGCCTAGTCCAGGCA	25376	C T GCC	
			TGCCTGGAC	AG GTAT ATCC		
			ACGGACCTG	TC CGTA TAGG		
			A _	A_		
GAM1671	CDC14B	3'	GCCTACATCCAGGCA	52854	CCAG T	
			TGCCTGGA	TGTA GC		
			ACGGACCT	ACAT CG		
			_	C		
GAM1671	FLJ10052	3'	GGCATCCACCAGCCCAGGCA	35773	ACCA T	
			TGCCTGG	GTG ATGCC		

	ACGGACC CAC TACGG	
	CGAC C	
GAM1671 FLJ14106	3' ACAGCTGGCTCCAGGCA 46863	_ _
	TGCCTGGA CCAG TGT	
	ACGGACCT GGTC ACA	
	C G	
GAM1671 FLJ20261	3' ATGGCATCAATCTAGGCA 38713	CCAG T
	TGCCTGGA TG ATGCCAT	
	ACGGATCT AC TACGGTA	
	A _ _	
GAM1671 FLJ20294	3' ATGGTGACAGATCCAGGCA 34871	CCAG A
	TGCCTGGA TGT TGCCAT	
	ACGGACCT ACA GTGGTA	
	AG _ _	
GAM1671 FLJ20309	3' GATGGTGTGCCAGTCCAGG 34922	CAGT
	CCTGGAC GTATGCCATC	
	GGACCTG CGTGTGGTAG	
	AC _	
GAM1671 GMEB2	3' GAGGCGTGGTCCAGGCA 24733	GTGTA A
	TGCCTGGACCA TGCC TC	
	ACGGACCTGGT GCGG AG	
	_____ _	
GAM1671 HPIP	3' GATGGGTCCATCCCAGGCA 40048	ACCA T G
	TGCCTGG GTG AT CCATC	
	ACGGACC TAC TG GG TAG	
	C _ _ C _	
GAM1671 KIAA0420	3' GATGGCAAGGATCCAG 63357	_ AGTGTA
	CTGGA CC TGCCATC	
	GACCT GG ACGGTAG	
	A A _ _ _	
GAM1671 KIAA0431	5' GGATGGCATAGTCAATCCA 30893	CCAGTG
	TGGA TATGCCATCC	
	ACCT ATACGGTAGG	
	AACTG _	
GAM1671 KIAA0494	3' ATACTGACTCCAGGCA 28738	C _
	TGCCTGGA CAGTGT	
	ACGGACCT GTCATA	
	CA	
GAM1671 MGC20983	5' GATGAGAAAGTGGTCCAGGCA 58923	GTGTATGC
	TGCCTGGACCA CATC	

		ACGGACCTGGT	GTAG	
		GAAAGA__		
GAM1671	PANX2	3' GATGGCACCGTCCAGGC	53426	CAGTGTA
		GCCTGGAC	TGCCATC	
		CGGACCTG	ACGGTAG	
		CC_____		
GAM1671	PDZD2	3' ATGGCCAACACTGGTACAGACA	80862	C G AT
		TG CTG ACCAGTGT	GCCAT	
		AC GAC TGGTCACA	CGGTA	
		A A AC		
GAM1671	PRO1496	3' ATGGGACCCGGTCCAGG	37758	AGT ATG
		CCTGGACC	GT CCAT	
		GGACCTGG	CA GGTA	
		CC_ G__		
GAM1671	PRO1855	3' ATGGCAACAGTCCAGGC	37546	CAG A
		GCCTGGAC	TGT TGCCAT	
		CGGACCTG	ACA ACGGTA	
		_____		
GAM1671	RoXaN	3' ATGGCATGAACCCAGG	46633	ACCA G
		CCTGG	GT TATGCCAT	
		GGACC	CA GTACGGTA	
		_____ A		
GAM1671	SERPINA1	5' GCTGTACACTGCCCAGGCA	4307	AC _
		TGCCTGG	CAGTGTAT GC	
		ACGGACC	GTCACATG CG	
		C_ T		
GAM1671	SERPINA10	5' GGATGGTGTCTAGTCCAGG	32464	C TGT
		CCTGGAC	AG ATGCCATCC	
		GGACCTG	TC TGTGGTAGG	
		A C__		
GAM1671	SLC26A10	5' ATGGGCCATCCAGGCA	56024	CCA GTATG
		TGCCTGGA	GT CCAT	
		ACGGACCT	CG GGTA	
		AC_ _____		
GAM1671	SNAP91	3' GGATAACATACACTGTAATGGG	29267	GAC CC
		CCTG	CAGTGTATG ATCC	
		GGGT	GTCACATAC TAGG	
		AAT AA		
GAM1671	LOC128954	5' ATGGACCATCCAGGCA	75790	CCAG TATG
		TGCCTGGA	TG CCAT	

ACGGACCT AC GGTA  
 \_\_\_\_\_ CA\_\_\_\_  
 GAM1671 LOC130595 5' GGCTCAGTCCAGGCA 75750 CAG TAT  
 TGCCTGGAC TG GCC  
 ||||| || ||  
 ACGGACCTG AC CGG  
 \_\_\_\_\_ T\_\_\_\_  
 GAM1671 LOC144308 3' GGACAGCACTGATCCGGGCA 83051 C A \_  
 TGCCTGGA CAGTGT TG CC  
 ||||| ||||| || ||  
 ACGGGCCT GTCACG AC GG  
 A \_ A  
 GAM1671 LOC146515 5' GACAGCATAGCAGTCCAGGC 77965 CA G CA  
 GCCTGGAC GT TATGC TC  
 ||||| || |||| ||  
 CGGACCTG CG ATACG AG  
 A \_ AC  
 GAM1671 LOC147178 3' GGAGACACTGATCCAGCA 61325 C C ATG  
 TGC TGA CAGTGT CC  
 || |||| |||| ||  
 ACG ACCT GTCACA GG  
 \_ A GA\_  
 GAM1671 LOC151720 3' ATGGCATGAACCCAGG 80337 ACCA G  
 CCTGG GT TATGCCAT  
 |||| || |||||  
 GGACC CA GTACGGTA  
 \_\_\_\_\_ A  
 GAM1671 LOC164714 5' GGACAACAAGTGGGTGGTCCAG 87236 G G GCCA\_  
 CTGGACCA T TAT TCC  
 ||||| || || ||  
 GACCTGGT G GTG AGG  
 \_ G AACAAAC  
 GAM1671 LOC253196 3' GATGGCTGCTGTGGCTCCAGGC 96884 \_ GT T  
 A TGCCTGGA CCA GTA GCCATC  
 ||||| || || |||||  
 ACGGACCT GGT CGT CGGTAG  
 C GT \_  
 GAM1671 LOC255326 3' ATGGCATGAACCCAGG 96373 ACCA G  
 CCTGG GT TATGCCAT  
 |||| || |||||  
 GGACC CA GTACGGTA  
 \_\_\_\_\_ A  
 GAM1671 LOC257354 3' GATGGCAAGGATCCAG 95090 \_ AGTGTA  
 CTGGA CC TGCCATC  
 |||| || |||||  
 GACCT GG ACGGTAG  
 A A\_\_\_\_  
 GAM1671 LOC51246 3' GGATGGCAGCTCTGGCCCAGAC 33218 C A T A  
 A TG CTGG CCAG GT TGCCATCC  
 || |||| || || |||||



			AC GACC GGTC CG ACGGTAGG		
			A C T _		
GAM1671	LOC56965	3'	GGATGAGCTGGTCCAG 39529	G G	
			CTGGACCAGT TAT CC		
			GACCTGGTCG GTA GG		
			A _		
GAM1672	FTSJ2	3'	CCAAAAAGAGATGACAAACT 25434	T	ACAA
			AGTTTT TCATCTCT TGG		
			TCAAAA AGTAGAGA ACC		
			C AAA_		
GAM1672	LDHB	5'	CCATTTTGGAGATGAAGAACT 9708		C
	GA		TCAGTTTTTTCATCTCTA AATGG		
			AGTCAAAGAAGTAGAGGT TTACC		
			T		
GAM1672	MYCL1	3'	CCATTAACAGATGGAAAACTG 18161		CTAC
	A		TCAGTTTTTTCATCT AATGG		
			AGTCAAAAAGGTAGA TTACC		
			CAA_		
GAM1672	NT5E	3'	CCACCTGTCAGATGAAAAAACT 10280		CT A_
	GA		TCAGTTTTTTCATCT ACA TGG		
			AGTCAAAAAGGTAGA TGT ACC		
			C_ CC		
GAM1672	PTGIS	3'	CCACTTCATAGATGAGAAAACT 6327		CTACAA
	GA		TCAGTTTTTTCATCT TGG		
			AGTCAAAGAGGTAGA ACC		
			TACTTC		
GAM1672	ZNF83	3'	TTGAGAGAAACAAAAACACTGA 36982	_	CA_ A
			TCAGT TTTT TCTCT CAA		
			AGTCA AAAAA AGAGA GTT		
			C CAA _		
GAM1672	KIAA0040	5'	CCATTTTGGAGATGAAGAACT 27782		C
	GA		TCAGTTTTTTCATCTCTA AATGG		
			AGTCAAAGAAGTAGAGGT TTACC		
			T		
GAM1672	KIAA1922	5'	CCTTTTAGAGATGAGAAAACTG 73623		C T
	A		TCAGTTTTTTCATCTCTA AA GG		
			AGTCAAAGAGTAGAGAT TT CC		
			T _		
GAM1672	KRTAP1-3	3'	AGAAATGAAAAAGCCGA 48237	A	C
			TC GTTTTTTCAT TCT		

			AG CGAAAAAGTA AGA		
			C     A		
GAM1672	SGP28	3'	AGTAATGAAAAAACTGA	20227	CT
			TCAGTTTTTTTCAT		
			AGTCAAAAAAGTA GA		
			AT		
GAM1672	SIAT4A	5'	TGGAGATGAAGAACTGA	11677	
			TCAGTTTTTTTCATCTCTA		
			AGTCAAAGAAGTAGAGGT		
GAM1672	LOC113146	3'	AGAGATGCAAAAAACT	72970	—
			AGTTTTTT CATCTCT		
			TCAAAAAA GTAGAGA		
			C		
GAM1672	LOC151720	5'	CCATTACAGATGAAGAACTG	80338	C C
	A		TCAGTTTTTTTCATCT TA AATGG		
			AGTCAAAGAAGTAGA AT TTACC		
			C _		
GAM1672	LOC152580	3'	CCAGGTTTAGATGAAAAACT	85775	T CT AA
			AGTTTTT CATCT AC TGG		
			TCAAAAA GTAGA TG ACC		
			_ TT G_		
GAM1672	LOC158696	3'	CCATTGTATCTTGGAATAACT	81972	T ATCTC
			AGTT TTTC TACAATGG		
			TCAA AAAG ATGTTACC		
			T GTTCT		
GAM1672	LOC253805	3'	CCATTTCCAGATGAAGAACT	96427	CTAC
	GA		TCAGTTTTTTTCATCT AATGG		
			AGTCAAAGAAGTAGA TTACC		
			CCTT		
GAM1672	LOC92078	5'	CCATTTACAGATGAGAAAACT	67979	C C
	GA		TCAGTTTTTTTCATCT TA AATGG		
			AGTCAAAGAGTAGA AT TTACC		
			C T		
GAM1673	ACP2	3'	AGAAAGTTCTAGACTG	7851	GC TC
			CAGT CT AGAACTTTCT		
			GTCA GA TCTTGAAAGA		
GAM1673	APT X	5'	AAGAGAAAGAGATCAGGCA	34655	TCAGAA
			TGCCT CTTTCTCTT		

ACGGA GAAAGAGAA  
 CTAGA\_  
 GAM1673 BCL7A 3' AGGCTGTCTCCTTAAGGCACTG 40637 C A\_\_ TT  
 CAGTGCCTT AG AC TCT  
 ||||| || || ||  
 GTCACGGAA TC TG GGA  
 T CTC TC  
 GAM1673 CLC 3' AAGAGAAAATACTGAAAGCACA 25105 A C AAC  
 GG CC GTGC TTCAG TTTCTCTT  
 || ||| ||| |||||  
 GG CACG AAGTC AAAGAGAA  
 A A ATA  
 GAM1673 CNK 3' AAGCCCTGAAGGCCTG 14517 T AA  
 CAG GCCTTCAG CTT  
 || ||||| ||  
 GTC CGGAAGTC GAA  
 \_ CC  
 GAM1673 COL4A3 3' AAGTGCAGGTTCTGAGGGCACC 48549 A TCT  
 GG CC GTGCCTTCAGAACTT CTT  
 || ||||| |||  
 GG CACGGGAGTCTTGGA GAA  
 C CGT  
 GAM1673 CSPG4 3' AAGAGAGACCTGGAGACAC 8570 C AAC  
 GTG CTTTCAG TTTCTCTT  
 || ||| |||||  
 CAC GAGGTC AGAGAGAA  
 A C\_  
 GAM1673 CYP1B1 3' AAGAGAAAAGAGAGAAACACTG 3651 CC AGAAC  
 CAGTG TTC TTTCTCTT  
 ||| || |||||  
 GTCAC AAG AAAGAGAA  
 A\_ AGAGA  
 GAM1673 DLG3 3' AAGAGAAAAGAGGAGGACTG 40880 G AGAAC  
 CAGT CCTTC TTTCTCTT  
 ||| ||| |||||  
 GTCA GGAGG AAAGAGAA  
 \_ AGA\_  
 GAM1673 DLG5 5' AGGCAGACTCTGAAGGC 82909 A\_ T  
 GCCTTCAGA CT TCT  
 ||||| || ||  
 CGGAAGTCT GA GGA  
 CA C  
 GAM1673 FLT1 3' AAGAGAAACCGGGAGAAGGCAT 8910 AGAAC\_  
 GTGCCTTC TTTCTCTT  
 ||||| |||||  
 TACGGAAG AAAGAGAA  
 AGGGCC  
 GAM1673 GRB10 3' AGAGAAAATGGCACCTGG 17971 \_ TTCAGAAC  
 CCAG TGCC TTTCTCT  
 ||| ||| |||||

			GGTC ACGG	AAAGAGA	
			C TA_____		
GAM1673 LFG	3'	AAGAGAAAAGGAGCCAAAGAACT 76711	GC CAGAA _		
	GG	CCAGT CTT CTTT CTCTT			
		GGTCA GAA GAAA GAGAA			
		A_ CCGAG A			
GAM1673 MAN2A2	3'	AAGAGAAAAGTTCATTAC 20391	CCTTCA		
		GTG GAACTTTCTCTT			
		CAC CTTGAAAGAGAA			
		TTA_____			
GAM1673 NLGN3	3'	AAGAAAAGTTCTTAAAACACT 38596	CC C C		
		AGTG TT AGAACTTT TCTT			
		TCAC AA TCTTGAAA AGAA			
		AA T _			
GAM1673 NPAS1	5'	AAGGTCTCCCGAGGGCACT 59879	A_ _		
		AGTGCCTTC GA ACTTT			
		TCACGGGAG CT TGGAA			
		CC C			
GAM1673 PLAG1	3'	AGTGTGTTCCAAAGGCATT 10605	CA TTT		
		AGTGCCTT GAAC CT			
		TTACGGAA CTTG GA			
		AC TGT			
GAM1673 PLXNA1	3'	AGAAAATGAAGGCAGTGG 72309	G GAAC		
		CCA TGCCTTCA TTTCT			
		GGT ACGGAAGT AAAGA			
		G A_____			
GAM1673 PPP4R1	3'	AAGAGAAAAGTACAGTAAACACT 17620	CCTTCAGA		
		AGTG ACTTTCTCTT			
		TCAC TGAAAGAGAA			
		AAATGACA			
GAM1673 ACYP2	3'	AAGAGAAAAATTGTAACACACT 56612	CC _ AAC		
	G	CAGTG TT CAG TTTCTCTT			
		GTCAC AA GTT AAAGAGAA			
		AC T AA_			
GAM1673 B3GNT6	3'	AGAAATCAGATGAAGGCAT 22503	GAAC_		
		GTGCCTTCA TTTCT			
		TACGGAAGT AAAGA			
		AGACT			
GAM1673 BAG5	3'	AAGAGAAGGGATAAAGGAC 16835	G CAGAA		
		GT CCTT CTTTCTCTT			

			CA GGAA GGAAGAGAA		
			_ ATAG_		
GAM1673	BIVM	3'	AAGAGAAAAGACTCAAGAACT	34665	GC C AAC
	G		CAGT CTT AG TTTCTCTT		
			GTCA GAA TC AAAGAGAA		
			AA C AGA		
GAM1673	C15orf5	3'	AGAGAAAAGAAAGCAC	48195	C AGAAC
			GTGC TTC TTTCTCT		
			CACG AAG AAAGAGA		
			A A__		
GAM1673	C20orf80	5'	AAGAGAAGAAGATGAAGAAAC	65282	GC GAAC
			GT CTTCA TTTCTCTT		
			CA GAAGT GAAGAGAA		
			AA AGAA		
GAM1673	CLSTN1	3'	AGTTCTGAGGACACTGG	30103	C
			CCAGTG CTTCAGAACT		
			GGTCAC GGAGTCTTGA		
			A		
GAM1673	DKFZP434P0111	3'	AAGAGAAAGTTTCTGCAC	67368	CTTCA
			GTGC GAACTTTCTCTT		
			CACG TTTGAAAGAGAA		
			TC__		
GAM1673	DORFIN	5'	AGAATTCTCTGAAGGAAC	31257	G ACT
			GT CCTTCAGA TTCT		
			CA GGAAGTCT AAGA		
			A CTT		
GAM1673	FLJ10300	5'	AAGAGAAAGATGAAGACTCTG	35997	TGC GAA
			CAG CTTCA CTTTCTCTT		
			GTC GAAGT GAAAGAGAA		
			TCA A__		
GAM1673	FLJ20373	3'	AAGAGAAGAAGGAAAGGCACAG	35070	A _AGAAC
	G		CC GTGCCTT C TTTCTCTT		
			GG CACGGAA G GAAGAGAA		
			A A GAA__		
GAM1673	FLJ23511	5'	AGAGAAAACAAGGCAT	49956	CAGAAC
			GTGCCTT TTTCTCT		
			TACGGAA AAAGAGA		
			CAA__		
GAM1673	FLJ30681	3'	AGAGAAGAAAGACCACTGG	91782	CCT AGAAC
			CCAGTG TC TTTCTCT		

GGTCAC AG GAAGAGA  
C\_\_ AAA\_\_

GAM1673 HDAC11 3' GAGCTATAGGCACTGG 45717 TC AACTTT  
CCAGTGCCT AG CTC  
||||||| || |||  
GGTCACGGA TC GAG  
TA \_\_\_\_\_

GAM1673 IKKE 5' AGTGAGCCCTGAAAGCTCTGG 25745 T C AA T  
CCAG GC TTCAG CTT CT  
|||| ||||| ||| ||  
GGTC CG AAGTC GAG GA  
T A CC T

GAM1673 KIAA0680 3' AGAGAAAATTGAAGCAT 28232 C AAC  
GTGC TTCAG TTTCTCT  
|||| ||||| |||||  
TACG AAGTT AAAGAGA  
\_ A\_\_

GAM1673 KIAA1228 3' AGGGGGTGATTCTGAGGCACTG 65035 T \_\_\_\_ TT  
CAGTGCCT CAGA ACT CT  
||||||| |||| ||| ||  
GTCACGGA GTCT TGG GA  
\_ TAG GG

GAM1673 KIAA1300 5' AGGAACCCTGAAGGCA 62860 AAC  
TGCCTTCAG TTTCT  
||||||| |||||  
ACGGAAGTC AAGGA  
CC\_

GAM1673 KIAA1805 3' AAGAGAAAGTAGAAGCAGCA 79966 \_\_\_\_ AGA  
TGC CTTC ACTTTCTCTT  
||| |||| |||||  
ACG GAAG TGAAAGAGAA  
AC A\_\_

GAM1673 LENG1 5' AAGAGAAAGCTCTGGGCATCCT 84074 \_\_\_\_ TT A  
G CAG TGCC CAGA CTTTCTCTT  
||| |||| ||||| |||||  
GTC ACGG GTCT GAAAGAGAA  
CT \_\_\_\_ C

GAM1673 LHX6 3' AAGAGAAAAGTCTGAGGCACTCA 26854 C AC  
TG CTTCAGA TTTCTCTT  
|| ||||| |||||  
AC GGGGTCT AAAGAGAA  
T CA

GAM1673 N4BP3 3' AGCTCCAGAAGGCACTGG 66250 A\_ A  
CCAGTGCCTTC GA CT  
||||||| |||  
GGTCACGGAAG CT GA  
AC C

GAM1673 NASP 3' AGAGGGTGAAGAACTG 67966 GC AGA  
CAGT CTTC ACTTTCT  
|||| ||||| |||||

GTCA GAAG TGGGAGA  
 AA \_\_\_\_  
 GAM1673 SMARCF1 3' AAAATTCTGAAGGAC 57480 G C  
 GT CCTTCAGAA TTT  
 || ||||| ||  
 CA GGAAGTCTT AAA  
 \_ A  
 GAM1673 SMARCF1 3' AAAATTCTGAAGGAC 20034 G C  
 GT CCTTCAGAA TTT  
 || ||||| ||  
 CA GGAAGTCTT AAA  
 \_ A  
 GAM1673 SMARCF1 3' AAAATTCTGAAGGAC 37430 G C  
 GT CCTTCAGAA TTT  
 || ||||| ||  
 CA GGAAGTCTT AAA  
 \_ A  
 GAM1673 TED 3' AAGAGAAAGTCCAGGGACTGG 31630 G TCA A  
 CCAGT CCT GA CTTTCTCTT  
 ||||| || |||||  
 GGTCA GGA CT GAAAGAGAA  
 G C\_\_ \_  
 GAM1673 TGIF2 3' AGAAGGGTGCTGAAGGC 41447 AA\_  
 GCCTTCAG CTTTCT  
 ||||| |||||  
 CGGAAGTC GGAAGA  
 GTG  
 GAM1673 WBSCR20A 3' AAGAGAAAGAAGAGACAGCA 35958 CT AGAA  
 TGC TC CTTTCTCTT  
 ||| || |||||  
 ACG AG GAAAGAGAA  
 AC AGAA  
 GAM1673 LOC115273 3' AGAAAGTTCTGATGGCCAGG 73356 AGT T  
 CC GCC TCAGAACTTTCT  
 || ||| |||||  
 GG CGG AGTCTTGAAAGA  
 AC\_ T  
 GAM1673 LOC145761 5' AAGAGAAAGTGGGAAGGCATGG 83472 G AGA  
 CCA TGCCTTC ACTTTCTCTT  
 ||| ||||| |||||  
 GGT ACGGAAG TGAAAGAGAA  
 \_ G\_\_  
 GAM1673 LOC146179 5' AGAAAGTTTTGGGCCT 77700 T TT  
 AG GCC CAGAACTTTCT  
 || ||| |||||  
 TC CGG GTTTTGAAAGA  
 \_ \_  
 GAM1673 LOC147072 3' AAGAGAAAGTGAGAAGAACTG 60407 GC AGA  
 CAGT CTTC ACTTTCTCTT  
 ||||| |||||

GTCA GAAG TGAAAGAGAA  
 AA AG\_  
 GAM1673 LOC148758 5' AGAAAGTTCTGAGAAAC 78962 GCC  
 GT TTCAGAACTTTCT  
 || |||||  
 CA GAGTCTTGAAAGA  
 AA\_  
 GAM1673 LOC148932 3' AGGAATCTGAAGGCACTGG 79103 AC  
 CCAGTGCCTTCAGA TTTCT  
 ||||| ||||  
 GGTCACGGAAGTCT AAGGA  
  
 GAM1673 LOC149386 5' AAGTTTTGAAAGCACT 84400 C  
 AGTGC TTCAGAACTT  
 |||| |||||  
 TCACG AAGTTTTGAA  
 A  
 GAM1673 LOC150139 3' AGAAAATAGAAAAAGGCGCTGG 79583 CAGAAC\_  
 CCAGTGCCTT TTTCT  
 ||||| ||||  
 GGTCGCGGAA AAAGA  
 AAAGATA  
 GAM1673 LOC152756 3' AAGATGCAGTTCTGAAAACCTG 85871 TGCC TTC  
 CAG TTCAGAACT TCTT  
 || ||||| ||||  
 GTC AAGTCTTGA AGAA  
 CAA\_ CGT  
 GAM1673 LOC162333 5' AAGAGAAAGCGATGACACTG 87114 CCT GAA  
 CAGTG TCA CTTTCTCTT  
 |||| || |||||  
 GTCAC AGT GAAAGAGAA  
 AGC  
 GAM1673 LOC199221 3' AAGAGAAGCTCGAAAGCATGG 80347 G C A A T  
 CCA TGC TTC GA CTT CTCTT  
 || || || || || ||||  
 GGT ACG AAG CT GAA GAGAA  
 A C  
 GAM1673 LOC203339 3' AGAGAAAATTGGGCCTG 90542 T TCAGAAC  
 CAG GCCT TTTCTCT  
 || || |||||  
 GTC CGGG AAAGAGA  
 TTA  
 GAM1673 LOC255017 3' AGAAAGAGGAACTGG 94624 G TCAGAA  
 CCAGT CCT CTTTCT  
 |||| || |||||  
 GGTCA GGA GAAAGA  
 A  
 GAM1673 LOC256021 3' AAGAGAAACAAAGACAACACTG 96512 CCT AGAAC  
 G  
 CCAGTG TC TTTCTCTT  
 |||| || |||||



GGTCAC AG AAAGAGAA  
AAC AAC\_  
GAM1673 LOC90139 3' AGAATCCCGAAGGCAT 55396 A\_ ACT  
GTGCCTTC GA TTCT  
||||||| || ||||  
TACGGAAG CT AAGA  
CC \_\_\_\_  
GAM1674 AQP3 3' TTCACGATCCACCCTTTC 59593 T\_ \_  
GAAA GTGG TCGTGAA  
|||| |||| |||||||  
CTTT CACC AGCACTT  
CC T  
GAM1674 ARSB 3' TCACGACTCTTGTC 3502 AATGTG  
GACAAGA GTCGTGA  
||||||| |||||||  
CTGTTCT CAGCACT  
  
GAM1674 B4GALT5 3' TTTTCACAAAAATAGTCCTTTG 16519 AAA\_ GGTC  
TCA TGACAAG TGT GTGAAAA  
||||||| || |||||||  
ACTGTTT ATA CACTTTT  
CCTG AAAA  
GAM1674 CHRNA3 3' TCGTTACCCATTTCTT 5610 T CG  
AAGAAATG GGT TGA  
||||||| || ||||  
TTCTTTAC CCA GCT  
\_ TT  
GAM1674 DRD1 3' TTACAACCACATTTCTGGCCA 5840 ACA C  
TG AGAAATGTGGT GTGA  
|| ||||||||| ||||  
AC TCTTTACACCA CATT  
CGG A  
GAM1674 FUT1 3' TCTGATCACATCCCCTGTC 3798 AGAA T  
GACA ATGTGGTCTG GA  
|||| ||||||||| ||  
CTGT TACACTAGT CT  
CCCC \_  
GAM1674 IRF1 3' GCCACATTTCTGATCA 64345 CA  
TGA AGAAATGTGGT  
||| |||||||||  
ACT TCTTTACACCG  
AG  
GAM1674 MAP3K8 5' TCACGACCACCTCATG 17791 A AAT  
CA GA GTGGTCTGTGA  
|| || |||||||||  
GT CT CACCAGCACT  
A C\_  
GAM1674 NGFR 3' TTCTGACCACACTTCCTGTC 10231 A A T  
GACA GAA TGTGGTCTG GAA  
|||| || ||||||||| |||

			CTGT CTT ACACCAGT CTT		
			C C _		
GAM1674	OLR1	3'	TTCACAACAGTTCTTGTTA 10341	ATGTG	C
			TGACAAGAA GT GTGAA		
			ATTGTTCTT CA CACTT		
			GA__ A		
GAM1674	POU4F1	3'	CACTGAAAACATTTTTGTCA 20660	A GG	_
			TGACAAGAA TGT TC GTG		
			ACTGTTTTT ACA AG CAC		
			_ AA T		
GAM1674	SMP1	3'	TTTCACATGAATAATTTTTGTC 26705	A GGTC	
	A		TGACAAGAA TGT GTGAAA		
			ACTGTTTTT ATA CACTTT		
			A AGTA		
GAM1674	ZNF264	3'	TTCTATTAACATTTCTTTTCA 12769	C	GGTCGT
			TGA AAGAAATGT GAA		
			ACT TTCTTTACA CTT		
			T ATTAT_		
GAM1674	C20orf175	3'	CGAGCTCCACGTTTCCTGCCA 55063	A A	___
			TG CA GAAATGTGG TCG		
			AC GT CTTTGCACC AGC		
			C C TCG		
GAM1674	CAPNS2	3'	TTTCACAACCCTACATTTTCT 50323	CA	___ C
	GATCA		TGA AGAAATGT GGT GTGAAA		
			ACT TCTTTATA CCA CACTTT		
			AG CATC A		
GAM1674	CLDN6	3'	TTTACACTCACATTTTATCA 41041	CA	_ C
			TGA AGAAATGTG GT GTGAA		
			ACT TTTTACAC CA CATT		
			A_ T _		
GAM1674	DKFZP564L0864	3'	GCACCAATTTCTTGCCA 72555	A	G C
			TG CAAGAAAT TGGT GT		
			AC GTTCTTTA ACCA CG		
			C _ _		
GAM1674	DKFZP566B183	3'	TTTCATAAACATTTCTTTTCA 31330	C	GGTCGT
			TGA AAGAAATGT GAAA		
			ACT TTCTTTACA CTTT		
			T AATAC_		
GAM1674	GTF2E1	3'	TACAGACCTCTTGTC A 18616	AATGT	_
			TGACAAGA GGTC GTG		

		ACTGTTCT	CCAG CAT		
		_____ A			
GAM1674	KIAA0089	3'	TTTTAATTCACATTTCTT	69967	TCG
			AAGAAATGTGG TGAAA		
			TTCTTTACACT ATTTT		
			TA_		
GAM1674	KIAA0373	5'	TTTTCAAAGTAACATTTCTT	28015	GGTCG
			AAGAAATGT TGAAAA		
			TTCTTTACA ACTTTT		
			ATGAA		
GAM1674	KIAA1813	3'	TTTTCACACTGTAAATTTCTTG	70314	__TG C
	T		ACAAGAAAT G GT GTGAAAA		
			TGTTCTTTA T CA CACTTTT		
			AA GT _		
GAM1674	KIAA1951	3'	TTCCAGGCTTCTCTTGTC	73766	AATGT GT
			TGACAAGA GGTC GAA		
			ACTGTTCT TCGG CTT		
			CT__ AC		
GAM1674	MGC4170	3'	TTCACCATTTCTTGTC	44227	TGGTC
			GACAAGAAATG GTGAA		
			CTGTTCTTTAC CACTT		
			_____		
GAM1674	NRN1	3'	CACTGCACATTTCTCCTCA	33432	CA GTC
			TGA AGAAATGTG GTG		
			ACT TCTTTACAC CAC		
			CC GT_		
GAM1674	PLA2G12	3'	TTTTCACAACCACATTT	48028	C
			AAATGTGGT GTGAAAA		
			TTTACACCA CACTTTT		
			A		
GAM1674	PPY2	3'	CACTCCACATTCCTGGCCA	40819	ACA A TC
			TG AG AATGTGG GTG		
			AC TC TTACACC CAC		
			CGG C T_		
GAM1674	ZNF31	3'	TTTGTAGACCACATTTCTGTT	64992	A _TG
	A		TGACA GAAATGTGGTC G AA		
			ATTGT CTTTACACCAG T TT		
			C A GT		
GAM1674	LOC115219	3'	CACGACAACGGGTCCTCA	73295	CAA AA G
			TGA GA TGT GTCGTG		

ACT CT GCA CAGCAC  
 C\_\_ GG A  
 GAM1674 LOC120376 5' TTCAGAGCATTCTTTCA 75986 C GG G  
 TGA AAGAAATGT TC TGAA  
 ||| ||||| || ||||  
 ACT TTCTTTACG AG ACTT  
  
 — — —  
 GAM1674 LOC133418 3' TTTCATATACATTTTTTGCCA 75094 A GTC  
 TG CAAGAAATGTG GTGAAA  
 || ||||| |||||  
 AC GTTTTTTACAT TACTTT  
 C A\_\_  
 GAM1674 LOC151199 3' TTAAAACACAGCTCTTGCCA 80174 A AA CG  
 TG CAAGA TGTGGT TGA  
 || |||| ||||| |||  
 AC GTTCT ACACCA ATT  
 C CG AA  
 GAM1674 LOC152317 5' TCACACTGACTTTTGTCA 85649 AATG C  
 TGACAAGA TGGT GTGA  
 ||||| ||||| |||  
 ACTGTTTT GTCA CACT  
 CA\_\_ —  
 GAM1674 LOC152674 3' TTCAACCCACCCTCTTGTCA 85841 AAT TCG  
 TGACAAGA GTGG TGAA  
 ||||| ||| ||||  
 ACTGTTCT CACC ACTT  
 CC\_ CA\_  
 GAM1674 LOC152845 5' CATGACCACATTTTTCA 60330 CAA  
 TGA GAAATGTGGTCGTG  
 ||| ||||| |||||  
 ACT TTTTACACCAGTAC  
  
 —  
 GAM1674 LOC154743 3' TTTAGTCCACATTGTCTTGTCA 81118 \_ TCG  
 TGACAAGA AATGTGG TGAA  
 ||||| ||||| |||||  
 ACTGTTCT TTACACC ATTT  
 G TG\_  
 GAM1674 LOC165476 5' TTCACGGCACCTTCT 87201 AT G  
 AGAA GTG TCGTGAA  
 |||| ||| |||||  
 TCTT CAC GGCACCT  
 C\_ —  
 GAM1674 LOC254266 5' TTTTCGGTCACACATCTTATCA 97356 C AA GT T  
 TGA AAGA TGTG CG GAA  
 ||| |||| |||| |||  
 ACT TTCT ACAC GC TTT  
 A AC TG T  
 GAM1674 LOC255919 3' TTTCATTCTTACATTTCTAATC 95043 CA TC  
 A TGA AGAAATGTGG GTGAAA  
 ||| ||||| |||||

ACT TCTTTACATT TACTTT  
 AA CT  
 GAM1674 LOC51754 5' CACGGCCACATCTCTGTCA 71027 A A  
 TGACA GA ATGTGGTCGTG  
 ||||| || |||||  
 ACTGT CT TACACCGGCAC  
 \_ C  
 GAM1674 LOC55862 3' ACCTCATTTCTTGCCA 37485 A T  
 TG CAAGAAATG GGT  
 || ||||| ||  
 AC GTTCTTTAC CCA  
 C T  
 GAM1674 LOC55954 3' CACGTGGTCACTTTTCTCATCA 38877 CA T GT \_  
 TGA AGAAA GTG C GTG  
 ||| ||||| ||| | |||  
 ACT TCTTT CAC G CAC  
 AC T TG TG  
 GAM1675 BAIAP3 3' CTCCAGCTCACTGTGGCCAGC 14123 AA\_ A\_  
 GC CACGG AGCTGGAG  
 || ||||| |||||  
 CG GTGTC TCGACCTC  
 ACCG AC  
 GAM1675 GPX1 5' TCTCCAGCCTTTTCCTG 5152 C \_  
 CA GGAA GCTGGAGA  
 || ||||| |||||  
 GT CCTT CGACCTCT  
 \_ TTC  
 GAM1675 LAMB2 5' CGCTCTCCGCCCGGTGTTGCG 9672 \_ AA T A  
 CGCAACAC GG GC GGAGA CG  
 ||||| || || ||||| ||  
 GCGTTGTG CC CG CCTCT GC  
 G \_ \_ C  
 GAM1675 NRXN2 5' CTCCAGCTTCTGGCG 30627 AACA  
 CGC CGGAAGCTGGAG  
 ||| |||||  
 GCG GTCTTCGACCTC  
 \_  
 GAM1675 NRXN2 5' CTCCAGCTTCTGGCG 57013 AACA  
 CGC CGGAAGCTGGAG  
 ||| |||||  
 GCG GTCTTCGACCTC  
 \_  
 GAM1675 PUM1 5' CTCCGCCCGTGTGTTGGT 27958 G AA T  
 AC CAACACGG GC GGAG  
 || ||||| || |||||  
 TG GTTGTGCC CG CCTC  
 \_ \_ \_  
 GAM1675 TSSC3 3' GTCTCCAGCCCTGC 12406 ACAC AA A  
 GCA GG GCTGGAGA C  
 ||| || ||||| |

CGT CC CGACCTCT G  
 \_\_\_\_\_ C  
 GAM1675 DKFZP434L0117 3' TCTCCAGCTGCCTTGTGT 42921 CAC A  
 ACGCAA GG AGCTGGAGA  
 ||||| || |||||  
 TGTGTT CC TCGACCTCT  
 \_\_\_\_ G  
 GAM1675 DKFZP434P211 5' CGTCCTCCAGCTCAGCCACTGC 27264 ACAC A\_\_ A  
 GCA GG AGCTGGAG ACG  
 ||| || ||||| |||  
 CGT CC TCGACCTC TGC  
 CA\_\_ GAC C  
 GAM1675 EREG 5' CGCTCTCCAGCCACTGCCGCG 7495 AACAA AA A  
 CGC CGG GCTGGAGA CG  
 ||| ||| ||||| ||  
 GCG GTC CGACCTCT GC  
 CC\_\_ AC C  
 GAM1675 FLJ10252 3' CTCTAGCTTCCTTACTGC 35949 ACAC  
 GCA GGAAGCTGGAG  
 ||| |||||  
 CGT CCTTCGATCTC  
 CATT  
 GAM1675 FLJ11743 3' CCGCTGTCTTCCGTGTCAGC 44550 A\_ \_  
 GC ACACGGAAG C TGG  
 || ||||| | |||  
 CG TGTGCCTTC G GCC  
 AC T TC  
 GAM1675 FLJ13262 5' CGTCCTCCAGCTCCCG 46157 A A  
 CGG AGCTGGAG ACG  
 ||| ||||| |||  
 GCC TCGACCTC TGC  
 C C  
 GAM1675 FLJ22756 3' TCTCCAGCCTGAGGTG 45583 AACAA AA  
 CGC CGG GCTGGAGA  
 ||| ||| |||||  
 GTG GTC CGACCTCT  
 GA\_\_ \_  
 GAM1675 KIAA1465 5' CTGCAGCTTCCGTGCCCGT 60828 CAA G  
 ACG CACGGAAGCTG AG  
 ||| ||||| |||  
 TGC GTGCCTTCGAC TC  
 CCC G  
 GAM1675 SHAPY 5' TCAGCTTCCCACGTTGC 57111 AC\_  
 GCAAC GGAAGCTGG  
 ||||| |||||  
 CGTTG CCTTCGACT  
 CAC  
 GAM1675 SIAT9 3' TTCTGGTTCCCTGCTGCG 13993 A C G TG  
 CGCA CA GGAA C GAG  
 ||||| ||| | |||

GCGT GT CCTT G CTT  
 C C \_GT  
 GAM1675 VPS39 3' TCCCCAGCTTTGTTTCAGC 62851 AAC G A  
 GC ACG AAGCTGG GA  
 || ||| ||||| ||  
 CG TGT TTCGACC CT  
 ACT \_ C  
 GAM1675 LOC150213 5' CGTCCTCCAGCTCAGCCACTGC 74856 ACAC A\_\_ A  
 GCA GG AGCTGGAG ACG  
 ||| || ||||| |||  
 CGT CC TCGACCTC TGC  
 CA\_\_ GAC C  
 GAM1675 LOC152890 5' CTCTGGAGCTTCCGCGC 80717 AACA \_\_  
 GC CGGAAGCT GGAG  
 || ||||| |||  
 CG GCCTTCGA TCTC  
 C\_\_ GG  
 GAM1675 LOC153260 5' CCCTTCCGTGTGCG 80803 A CT  
 CGCA CACGGAAG GG  
 ||| ||||| ||  
 GCGT GTGCCTTT CC  
 \_ C\_  
 GAM1675 LOC201910 5' CTCTGGAGCTTCCGCGC 89099 AACA \_\_  
 GC CGGAAGCT GGAG  
 || ||||| |||  
 CG GCCTTCGA TCTC  
 C\_\_ GG  
 GAM1675 LOC51706 3' CTCCAGCTTCCCTGGTGC 70315 A C  
 GCA CA GGAAGCTGGAG  
 ||| || ||||| |||  
 CGT GT CCTTCGACCTC  
 G C  
 GAM1675 LOC90019 5' CTTAGCTTCCTGCTGC 56762 A C  
 GCA CA GGAAGCTGGAG  
 ||| || ||||| |||  
 CGT GT CCTTCGACTTC  
 C \_  
 GAM1676 ARAF1 5' GACAGGAGCCTGGACTTTGA 63939 ACT \_  
 TCAA GGTCT GGCTCCTGTC  
 ||| |||| ||||| |||  
 AGTT TCAGG CCGAGGACAG  
 \_\_ T  
 GAM1676 BCL11B 3' TGACAGGAGGTCATTTCA 43196 TC \_  
 TGG TGGC TCCTGTCA  
 ||| |||| ||||| |||  
 ACT ACTG AGGACAGT  
 TT G  
 GAM1676 LAMC2 3' TGACAGGAGCCTGCT 38151 CT  
 GGT GGCTCCTGTCA  
 ||| ||||| |||

		TCG CCGAGGACAGT		
		T_		
GAM1676	PTGIR	3' GACAGGAGCCAGAAAATCAG	6321	___
		CTGG TCTGGCTCCTGTC		
		GACT AGACCGAGGACAG		
		AAA		
GAM1676	DKFZp586H0623	3' ACAAGAGTGTGACAGTTTGA	34065	G TG_ C
		TCAAACCTG TC GCTC TGT		
		AGTTTGAC AG TGAG ACA		
		_ TTG A		
GAM1676	HYPH	3' TGACAGATCCTAGACCA	94899	CTC
		TGGTCTGG CTGTCA		
		ACCAGATC GACAGT		
		CTA		
GAM1676	KIAA0628	3' GATTTTACCAGACCATTTT	28869	C CTCCT
		AAA TGGTCTGG GTC		
		TTT ACCAGACC TAG		
		T ATTT_		
GAM1676	KIAA0831	3' GCAACTTCCAAACCAGTTTGA	29975	C CTCC
		TCAAACCTGGT TGG TGT		
		AGTTTGACCA ACC ACG		
		A TTCA		
GAM1676	KIAA1219	3' ACAGCAGAACAGTTTGA	61361	G GCTC
		TCAAACCTG TCTG CTGT		
		AGTTTGAC AGAC GACA		
		A _		
GAM1676	KIAA1872	3' TGACAGAAGCCTGATTA	62948	T C
		TGGTC GGCT CTGTCA		
		ATTAG CCGA GACAGT		
		T A		
GAM1676	PCDH19	3' TGACCAAGAGCCAGACTAG	63709	CT_
		CTGGTCTGGCTC GTCA		
		GATCAGACCGAG CAGT		
		AAC		
GAM1676	RoXaN	3' ATAGAAGCCAGACCGCTTGA	46631	AC C
		TCAA TGGTCTGGCT CTGT		
		AGTT GCCAGACCGA GATA		
		C_ A		
GAM1676	TU12B1-TY	3' GTGACAGAAGCCTGGC	33400	T C
		GTC GGCT CTGTCAC		



CGG CCGA GACAGTG  
 T A  
 GAM1676 LOC134265 3' GTGACAGGAGCACAGA 75175 \_  
 TCTG GCTCCTGTAC  
 |||| |||||  
 AGAC CGAGGACAGTG  
 A  
 GAM1676 LOC143678 5' GACAGGAGCCAGGACCCGT 82983 T \_  
 AC GGTC TGGCTCCTGTC  
 || |||| |||||  
 TG CCAG ACCGAGGACAG  
 C G  
 GAM1676 LOC144866 5' GTGACAGGAGCTGAAGCTCAG 83206 GT \_  
 CTG CT GGCTCCTGTAC  
 ||| || |||||  
 GAC GA TCGAGGACAGTG  
 TC AG  
 GAM1676 LOC148936 5' ACAGGAGCCAAATGCTA 84287 C\_  
 TGGT TGGCTCCTGT  
 |||| |||||  
 ATCG ACCGAGGACA  
 TAA  
 GAM1676 LOC148938 5' ACAGGAGCCAAATGCTA 84266 C\_  
 TGGT TGGCTCCTGT  
 |||| |||||  
 ATCG ACCGAGGACA  
 TAA  
 GAM1676 LOC151610 3' GCAATGGCCAGACCAGTTT 80287 CC  
 AAAGTGGTCTGGCT TGT  
 ||||| ||||| |||  
 TTTGACCAGACCGG ACG  
 TA  
 GAM1676 LOC197049 3' TGACAGGAACCAGTGCC 89695 \_ C  
 GGT CTGG TCCTGTCA  
 ||| |||| |||||  
 CCG GACC AGGACAGT  
 T A  
 GAM1676 LOC221583 5' ACAGGTGGACCCAGACCAG 92141 \_ \_  
 CTGGTCTGG CT CCTGT  
 ||||| || |||||  
 GACCAGACC GG GGACA  
 CA T  
 GAM1676 LOC254742 3' TGACAAAAGGGACCAGTTT 95783 GG CC  
 AAAGTGGTCT CT TGTCA  
 ||||| || |||||  
 TTTGACCAGG GA ACAGT  
 \_ AA  
 GAM1676 LOC255223 3' GTGACAGGAACCAGTGTCCCG 96573 T\_ C  
 TGG CTGG TCCTGTAC  
 ||| |||| |||||

GCC GACC AGGACAGTG  
 CTGT A  
 GAM1676 LOC90019 5' TGACAGGAGCCAGCCCAG 56773 T  
 CTGG CTGGCTCCTGTCA  
 ||| |||||  
 GACC GACCGAGGACAGT  
 C  
 GAM1677 B3GNT3 3' CCCACCTGGTACTGTT 26517 TACTAA A  
 AACAGTATC AG TGGG  
 ||||| || |||  
 TTGTCATGG TC ACCC  
 C  
 GAM1677 CSPG3 3' AGCCCATCTGACTTAGAACTGT 15227 A CTAAA  
 T AACAGT TCTA GATGGGCT  
 ||||| ||| |||||  
 TTGTCA AGAT TTACCCGA  
 A TCAG\_  
 GAM1677 EVA1 3' AGCCCATCTCTAATGAGGACT 58572 A AC\_ A  
 AGT TCT TA AGATGGGCT  
 ||| ||| || |||||  
 TCA GGA AT TCTACCCGA  
 \_ GTA C  
 GAM1677 ID4 3' CTTTAATAGATACTGT 7754 C  
 ACAGTATCTA TAAAG  
 ||||| |||||  
 TGTCATAGAT ATTTT  
 A  
 GAM1677 RAD51C 3' TTTAGAGATACTGTT 54255 A  
 AACAGTATCT CTAAA  
 ||||| |||||  
 TTGTCATAGA GATTT  
 -  
 GAM1677 RHO 3' AGCCCATCTTCAGCAGTTGCT 5018 T A A  
 AGTA CT CT AAGATGGGCT  
 ||| || || |||||  
 TCGT GA GA TTCTACCCGA  
 T C C  
 GAM1677 STAR 3' CTCATTAGTAGACATGTT 4445 GTA AAG  
 AACA TCTACTA ATGGG  
 ||| ||||| |||||  
 TTGT AGATGAT TACTC  
 AC\_ \_  
 GAM1677 CD109 3' AGTGGTCTCAGTAGATACT 56046 AA GG  
 AGTATCTACT AGAT GCT  
 ||||| ||| |||  
 TCATAGATGA TCTG TGA  
 C\_ G\_  
 GAM1677 FLJ00024 3' AGCCCATCCCTGGGACCTGC 63747 TCTA AA  
 GTA CTA GATGGGCT  
 ||| ||| |||||

		CGT GGT CTACCCGA	
		CCAG CC	
GAM1677	FLJ20666	3' GCTTACCACAGATACTGTT 35510	ACTAAAGA
		AACAGTATCT TGGGC	
		TTGTCATAGA ATTCG	
		CACC____	
GAM1677	FLJ20666	3' GCTTACCACAGATACTGTT 37089	ACTAAAGA
		AACAGTATCT TGGGC	
		TTGTCATAGA ATTCG	
		CACC____	
GAM1677	FLJ22969	3' GGCTCAGCAGATGCTGT 68657	ACTAAAGA
		ACAGTATCT TGGGCT	
		TGTCGTAGA ACTCGG	
		CG_____	
GAM1677	GGTLA1	5' AGCCCATCTCTGTCCCATTGT 14657	ATCT TAA
		ACAGT AC AGATGGGCT	
		TGTTA TG TCTACCCGA	
		CCC_ TC_	
GAM1677	KIAA0240	3' TTTAGTAGATTCTGTT 92443 T	
		AACAG ATCTACTAAA	
		TTGTC TAGATGATTT	
		T	
GAM1677	KIAA1028	3' TTTATTAGATACTGTT 91952 C	
		AACAGTATCTA TAAA	
		TTGTCATAGAT ATTT	
		T	
GAM1677	KIAA1332	3' CATCAAAAGATACTGTT 71163	ACTAAA
		AACAGTATCT GATG	
		TTGTCATAGA CTAC	
		AAA____	
GAM1677	KIAA1497	3' ATCTTTAGTAGACACT 67503 A	
		AGT TCTACTAAAGAT	
		TCA AGATGATTTCTA	
		C	
GAM1677	KIAA1858	3' AGCCCATCTCTAGCACACCTTG 67133	TATCTA A
		CAG CTA AGATGGGCT	
		GTT GAT TCTACCCGA	
		CCACAC C	
GAM1677	p25	3' GCCCATCCAGGACACTCC 22851 C A ACTAAA	
		A AGT TCT GATGGGC	

		C TCA AGG    CTACCCG	
		C C AC_____	
GAM1677	PME-1	3' AGCCCATCTTTTCTGTGACTGT 32351	ATCTACT
		ACAGT    AAAGATGGGCT	
		TGTCA    TTTCTACCCGA	
		GTGTCT_	
GAM1677	PRO0628	3' AGCCCATCTTCTGTACTGCT 26205	TC TA
		AGTA TAC AAGATGGGCT	
		TCGT ATG TTCTACCCGA	
		C_ TC	
GAM1677	LOC122728	3' AGCCCATCTGCTGTATTACTG 74150	TC TAA
		CAGTA TAC AGATGGGCT	
		GTCAT ATG TCTACCCGA	
		T_ TCG	
GAM1677	LOC130507	3' ATCTCTAGTAAATACTGTT 74948	C A
		AACAGTAT TACTA AGAT	
		TTGTCATA ATGAT TCTA	
		A C	
GAM1677	LOC144110	3' AGCCTGGGGCAGCAGGTA CTG 76672	A AAAGA
		CAGTATCT CT TGGGCT	
		GTCATGGA GA GTCCGA	
		C CGGG_	
GAM1677	LOC145368	3' AGCCCATCTGCTGTATTACTG 77092	TC TAA
		CAGTA TAC AGATGGGCT	
		GTCAT ATG TCTACCCGA	
		T_ TCG	
GAM1677	LOC149830	3' CCCATCTCTAAGGCAGGATGCT 84724	A__ AA_
	G	CAGTATCT CT AGATGGG	
		GTCGTAGG GA TCTACCC	
		ACG ATC	
GAM1677	LOC150236	5' AGCCCATCCCCCAGTTCACT 79680	ATCT AAA_
		AGT ACT GATGGGCT	
		TCA TGA CTACCCGA	
		CT__ CCCC	
GAM1677	LOC150279	3' CCCATGAGGCTCAGATGCTGTT 79667	ACTAAAG
		AACAGTATCT ATGGG	
		TTGTCGTAGA TACCC	
		CTCGGAG	
GAM1677	LOC150423	3' AGCCCATCTCCTGTATTACTG 79863	TC TAA
		CAGTA TAC AGATGGGCT	

GTCAT ATG TCTACCCGA  
 T\_ TCC  
 GAM1677 LOC151405 5' AGATGGGCTTTAGTAAAGACTG 85334 ATC ATGGG  
 T ACAGT TACTAAAG CT  
 |||| ||||| ||  
 TGTCA ATGATTTC GA  
 GAA GGGTA  
 GAM1677 LOC151473 3' AGCCCATCTCTAGACTCTCGT 80250 \_ TA CTAA  
 AC AG TCTA AGATGGGCT  
 || || |||| |||||  
 TG TC AGAT TCTACCCGA  
 C TC C\_\_  
 GAM1677 LOC153196 5' AGCCCATCCTTGGGACCCTACT 85953 TCTA\_ A  
 AGTA CTAA GATGGGCT  
 ||| ||| |||||  
 TCAT GGTT CTACCCGA  
 CCCAG C  
 GAM1677 LOC221002 3' AGCCCATTCAGATAAAACTG 91475 \_\_\_\_ ACTAAA  
 CAGT ATCT GATGGGCT  
 ||| ||| |||||  
 GTCA TAGA TTACCCGA  
 AAA C\_\_\_\_  
 GAM1677 LOC255290 5' AGCCCATCTCTGTCCCATTGT 95607 ATCT TAA  
 ACAGT AC AGATGGGCT  
 |||| || |||||  
 TGTTA TG TCTACCCGA  
 CCC\_ TC\_  
 GAM1677 LOC91907 3' ATCTTTAGTAGACACT 67493 A  
 AGT TCTACTAAAGAT  
 ||| |||||  
 TCA AGATGATTTCTA  
 C  
 GAM1678 RBBP9 3' TGATCGCGCCACTGTACTCCA 70143 CAC CGCA  
 TGGAG GCAG CGTGATTA  
 |||| ||| |||||  
 ACCTC TGTC GCGCTAGT  
 A\_\_ ACC\_  
 GAM1678 TEM7 3' TAATCATGCCACTGTACTCCA 39895 CAC CGCA  
 TGGAG GCAG CGTGATTA  
 |||| ||| |||||  
 ACCTC TGTC GTACTAAT  
 A\_\_ ACC\_  
 GAM1678 C20orf172 3' TAATTGCGCCACTGCACTCCA 46210 CAC CGCA TG  
 TGGAG GCAG CG ATTA  
 |||| ||| || |||  
 ACCTC CGTC GC TAAT  
 A\_\_ ACC\_ GT  
 GAM1678 DKFZP434C171 3' TGATCGCGCCACTGCACTCCA 31561 CAC CGCA  
 TGGAG GCAG CGTGATTA  
 |||| ||| |||||

ACCTC CGTC GCGCTAGT  
 A\_\_ ACC\_  
 GAM1678 ET 3' TGATCGCGCCACTGCACTCCA 44223 CAC CGCA  
 TGGAG GCAG CGTGATTA  
 |||| ||| |||||  
 ACCTC CGTC GCGCTAGT  
 A\_\_ ACC\_  
 GAM1678 FLJ10374 3' GCGCCAGCGTGCTCCA 36067 A\_  
 TGGAGCACGC GCGC  
 ||||| |||  
 ACCTCGTGCG CGCG  
 AC  
 GAM1678 KIAA1297 3' CACGGCCACCACGTGCTCCA 72169 CAGC\_ A  
 TGGAGCACG GC CGTG  
 ||||| || |||  
 ACCTCGTGCG CG GCAC  
 ACCAC \_  
 GAM1678 PTPRN2 3' AATCACAGCTCCTCGCTGCGTC 55601 C CAC\_\_\_\_  
 TCCA TGGAG ACGCAGCG GTGATT  
 |||| ||||| |||||  
 ACCTC TCGGTCGC CACTAA  
 \_ TCCTCGA  
 GAM1678 PTPRN2 3' AATCACAGCTCCTCGCTGCGTC 55605 C CAC\_\_\_\_  
 TCCA TGGAG ACGCAGCG GTGATT  
 |||| ||||| |||||  
 ACCTC TCGGTCGC CACTAA  
 \_ TCCTCGA  
 GAM1678 WBSCR23 5' TGATCACGCCACTGCACTCCA 46774 CAC CGCA  
 TGGAG GCAG CGTGATTA  
 |||| ||| |||||  
 ACCTC CGTC GCACTAGT  
 A\_\_ ACC\_  
 GAM1678 LOC222160 3' CATGATTGCGCCACTGCACTCC 94121 CAC \_\_\_\_ \_  
 A TGGAG GCA GCGCA CGTG  
 |||| ||| ||||| |||  
 ACCTC CGT CGCGT GTAC  
 A\_\_ CAC TA  
 GAM1678 LOC245726 5' TAATCACTAGTAGCTGGTGCTC 74127 G \_ AC  
 CA TGGAGCAC CAGC GC GTGATTA  
 ||||| ||| || |||||  
 ACCTCGTG GTCG TG CACTAAT  
 \_ A AT  
 GAM1678 LOC255042 3' GATCGCACCAGTGTGCTCC 95318 CAGCGCAC  
 GGAGCACG GTGATT  
 ||||| |||||  
 CCTCGTGT CGCTAG  
 CACCA\_\_\_\_  
 GAM1678 LOC90538 3' CGTGCCACTGCACTCCA 63190 CAC C\_  
 TGGAG GCAG GCACG  
 |||| ||| |||||

ACCTC CGTC CGTGC  
 A\_\_ AC  
 GAM1679 DGKG 5' CCTGCAATGAGCCAGGCC 7205 CA \_\_  
 GGCC GCTCA GCAGG  
 ||| |||| ||||  
 CCGG CGAGT CGTCC  
 AC AA  
 GAM1679 POR 3' TCTCTGCTGAGCTGGGCC 94176  
 GGCCCAGCTCAGCAGGGA  
 ||||||||||||  
 CCGGGTCGAGTCGTCTCT  
  
 GAM1679 PPP1R8 5' AAAGTGTGCTGCACCGGGGCC 10720 AGCT GG  
 GGCCC CAGCA GACAGTTT  
 |||| |||| |||||  
 CCGGG GTCGT TTGTCAAA  
 CCAC \_\_  
 GAM1679 PPP1R8 5' AAAGTGTGCTGCACCGGGGCC 56739 AGCT GG  
 GGCCC CAGCA GACAGTTT  
 |||| |||| |||||  
 CCGGG GTCGT TTGTCAAA  
 CCAC \_\_  
 GAM1679 PUNC 3' TGACCCTGCTGTAGCTGGGCC 89655 \_ A  
 GGCCCAGCT CAGCAGGG CA  
 ||||||| ||||| ||  
 CCGGGTCGA GTCGTCCC GT  
 T A  
 GAM1679 PYGO2 3' AAACCAAAGCCCTGCTGAGCAG 63981 CCA ACA\_\_  
 AGCC GGC GCTCAGCAGGG GTTT  
 || ||||| ||||  
 CCG CGAGTCGTCCC CAAA  
 AGA GAAAC  
 GAM1679 FLJ12190 3' CCCTGCTGGCTGGGCC 46872 T  
 GGCCCAGC CAGCAGGG  
 ||||||| |||||  
 CCGGGTCG GTCGTCCC  
 -  
 GAM1679 KIAA1649 5' CCCTGCTGAAGTGGACC 50255 C GC  
 GG CCA TCAGCAGGG  
 || ||| |||||  
 CC GGT AGTCGTCCC  
 A GA  
 GAM1679 MGC2865 3' AAAGTGTCCCTGCCTCTGGCAC 50449 C\_ CTCA  
 C GG CCAG GCAGGGACAGTTT  
 || ||| |||||  
 CC GGTC CGTCCCTGTCAAA  
 AC TC\_\_  
 GAM1679 PHYHIP 3' TCCCTGCTGAGCTGGGTC 28614  
 GGCCCAGCTCAGCAGGGA  
 ||||||||||||

CTGGGTCGAGTCGTCCCT

GAM1679 R32184\_3 3' CCCTGCTGGCTGGGCC 53064 T  
GGCCCAGC CAGCAGGG  
||||||| |||||||  
CCGGGTCG GTCGTCCC

GAM1679 SEI1 3' AACTGAGCCTGCTGGCTGGACC 25377 C T GA  
GG CCAGC CAGCAGG CAGTT  
|| ||||| ||||||| |||||  
CC GGTCG GTCGTCC GTCAA  
A \_ GA

GAM1679 SERF2 5' AAAGTGTCCCCGCATGAG 19306 \_ A  
CTCA GC GGGACAGTTT  
|||| || |||||||||  
GAGT CG CCCTGTCAA  
A C

GAM1679 LOC200058 3' AAACCAGCCTCGCCACCAGCT 88555 CA\_\_ AG ACA  
GGGCC GGCCCAGCT GC GG GTTT  
||||||| || || |||||  
CCGGGTCGA CG CC CAAA  
CCACC CT GAC

GAM1679 LOC256667 5' AAAGTGTCCAAAACGACCTAAG 95681 CC C AGCAG  
CC GGC AG TC GGACAGTTT  
||| || || |||||||  
CCG TC AG CCTGTCAA  
AA C CAAAA

GAM1679 LOC257451 3' AAACCAAAGCCCTGCTGAGCAG 95551 CCA ACA\_\_  
AGCC GGC GCTCAGCAGGG GTTT  
||| ||||||||| |||||  
CCG CGAGTCGTCCC CAAA  
AGA GAAAC

GAM1679 LOC51308 3' CCCTGCTGAGTGGGCC 33493 G  
GGCCCA CTCAGCAGGG  
||||| |||||||||  
CCGGGT GAGTCGTCCC

GAM1680 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
GTA GGAT GGGTTGTTT  
||| ||||| |||||||  
CGT CCTA CCAACAAA  
C CGTG\_

GAM1680 LCT 3' AACCGTAAAAATCCTT 9697 G  
AAGGATTTTTA GGTT  
||||||||| |||||  
TTCCTAAAAAT CCAA  
G

GAM1680 RPL15 3' AAACAACCCCTAAAAATCCTTAC 11382  
GTAAGGATTTTTAGGGTTGTTT  
||||||||| |||||||



CATTCCTAAAAATCCCAACAAA

GAM1680 FBXO30 3' AACTAAAAAATCCTGAC 49573 A AG  
GT AGGATTTTT GTT  
|| ||||| |||  
CA TCCTAAAAA TCAA  
G AA

GAM1680 KIAA0494 3' AACCAACCCTTACTTAC 28736 GATTTT  
GTAAG AGGGTTGTT  
|||| |||||  
CATTC TCCCAACAA  
AT\_\_\_\_

GAM1680 PRO0641 5' AAACAACCCCAAAACTTG 26210 GAT A  
TAAG TTTT GGGTTGTT  
||| ||| |||||  
GTTC AAAA CCAACAAA  
\_\_\_ C

GAM1680 SMT3H2 3' AACACATAAAAAATCCTTGC 22670 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1680 LOC120103 3' AACCTATGAAAAATCCTTGC 74002 A\_\_  
GTAAGGATTTTT GGGTT  
||||||| |||||  
CGTTCCTAAAAA TCCAA  
GTA

GAM1680 LOC129831 3' AAACAACCCCAATGTCC 74889 TT A  
GGAT TT GGGTTGTT  
||| || |||||  
CCTG AA CCAACAAA  
T\_ C

GAM1680 LOC133088 5' AAACAAAATAGAAAAATCCCTG 75075 A AGGG\_  
C GTA GGATTTTT TTGTTT  
|| ||||| |||||  
CGT CCTAAAAA AACAAA  
C GATAA

GAM1680 LOC148089 3' GGCCCTAAAAATTCCTAC 78637 A  
GTA GGATTTTTAGGGTT  
|| |||||  
CAT CTAAAAATCCCGG  
C

GAM1680 LOC154547 3' AACACATAAAAAATCCTTGC 76050 GG  
GTAAGGATTTTTA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA  
A\_

GAM1680 LOC158104 3' ACAGCCAAAAATCCTTA 60313 AG  
TAAGGATTTTT GGTGT  
||||||| |||||

ATTCCTAAAAA CCGACA

GAM1680 LOC205880 5' AAACAACCATCATCCTGAC 90709 A TTTTAG  
GT AGGAT GGTGTGTT  
|| |||| |||||  
CA TCCTA CCAACAAA  
G CTA\_\_

GAM1680 LOC221561 3' AACAAACATAAAAAATCCTTGC 92130 GG  
GTAAGGATTTTGA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA

A\_  
GAM1680 LOC257591 3' AACAAACATAAAAAATCCTTGC 97840 GG  
GTAAGGATTTTGA GTTGTT  
||||||| |||||  
CGTTCCTAAAAAT CAACAA

A\_  
GAM1680 LOC51145 3' AGCTAAAATCCTTAC 32393 TAG  
GTAAGGATTTT GTTG  
||||||| |||  
CATTCCTAAAA TCGA

GAM1681 ARNT2 3' AAACAACCCGTGCATCCCTGC 29450 A TTTTA  
GTA GGAT GGGTTGTTT  
||| ||| |||||  
CGT CCTA CCCAACAAA  
C CGTG\_

GAM1681 LCT 3' AACCGTAAAAATCCTT 9697 G  
AAGGATTTTGA GTTG  
||||||| |||  
TTCCTAAAAAT CCAA  
G

GAM1681 RPL15 3' AAACAACCCTAAAAATCCTTAC 11382  
GTAAGGATTTTGTAGGGTTGTTT  
|||||||  
CATTCCTAAAAATCCCAACAAA

GAM1681 FBXO30 3' AACTAAAAAAATCCTGAC 49573 A AG  
GT AGGATTTT GTTG  
|| ||||| |||  
CA TCCTAAAAA TCAA  
G AA

GAM1681 KIAA0494 3' AACAAACCCTTACTTAC 28736 GATTTT  
GTAAG AGGGTTGTT  
|||| |||||  
CATTC TCCCAACAA  
AT\_\_

GAM1681 PRO0641 5' AAACAACCCCAAACTTG 26210 GAT A  
TAAG TTTT GGGTTGTTT  
||| ||| |||||

		GTTC AAAA CCCAACAAA		
		___ C		
GAM1681	SMT3H2	3' AACAAACATAAAAAATCCTTGC	22670	GG
		GTAAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1681	LOC120103	3' AACCTATGAAAAATCCTTGC	74002	A__
		GTAAAGGATTTTTT GGGTT		
		CGTTCCTAAAAA TCCAA		
		GTA		
GAM1681	LOC129831	3' AAACAACCCCAATGTCC	74889	TT A
		GGAT TT GGGTTGTTT		
		CCTG AA CCCAACAAA		
		T_ C		
GAM1681	LOC133088	5' AAACAAAATAGAAAAATCCCTG	75075	A AGGG_
	C	GTA GGATTTTTT TTGTTT		
		CGT CCTAAAAA AACAAA		
		C GATAA		
GAM1681	LOC148089	3' GGCCCTAAAAATTCCTAC	78637	A
		GTA GGATTTTTTAGGGTT		
		CAT CTTAAAAATCCCGG		
		C		
GAM1681	LOC154547	3' AACAAACATAAAAAATCCTTGC	76050	GG
		GTAAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1681	LOC158104	3' ACAGCCAAAAATCCTTA	60313	AG
		TAAGGATTTTTT GGTTGT		
		ATTCCTAAAAA CCGACA		
		—		
GAM1681	LOC205880	5' AAACAACCATCATCCTGAC	90709	A TTTTAG
		GT AGGAT GGTGTTT		
		CA TCCTA CCAACAAA		
		G CTA__		
GAM1681	LOC221561	3' AACAAACATAAAAAATCCTTGC	92130	GG
		GTAAAGGATTTTTTA GTTGTT		
		CGTTCCTAAAAAT CAACAA		
		A_		
GAM1681	LOC257591	3' AACAAACATAAAAAATCCTTGC	97840	GG
		GTAAAGGATTTTTTA GTTGTT		

CGTTCCTAAAAAT CAACAA  
A\_  
GAM1681 LOC51145 3' AGCTAAAATCCTTAC 32393 TAG  
GTAAGGATTTT GGTT  
||||||| |||  
CATTCTAAAA TCGA

—  
GAM1682 GRIN2A 3' AATGGTTTCTCTAATACA 5892 GA\_  
TGTA AGAAGCCATT  
||| |||||  
ACAT TCTTTGGTAA  
AATC

GAM1682 SURF4 3' AATGGCTTCAGGACATGGG 52538 TA AGAA  
CCCA TGT GAAGCCATT  
||| ||| |||||  
GGGT ACA CTTCGGTAA  
— GGA\_

GAM1682 SYT4 3' AATGGTTGTCCTGCATAT 62432 AAGA  
ATATGTAG AGCCATT  
||||| |||||  
TATACGTC TTGGTAA  
CTG\_

GAM1682 BDH 3' AATGACTTCTTTGCATAGTG 14473 \_ A C  
CAT ATGTAGA GAAG CATT  
||| ||||| ||| |||  
GTG TACGTTT CTTC GTAA  
A \_ A

GAM1682 CECR1 3' ATGGCCTCTGTATGG 33806 GTAGA A  
CCATAT AGA GCCAT  
||||| ||| |||||  
GGTATG TCT CGGTA  
— C

GAM1682 CNK2 3' GCTTTCTACATTGGGA 75963 T GA  
TCCCA ATGTAGAA AGC  
||||| ||||| |||  
AGGGT TACATCTT TCG

— —  
GAM1682 DNAJC5 3' AATGGCCTCTGGTTTCTTGGGA 61442 TATGTAGA A  
TCCCA AGA GCCATT  
||||| ||| |||||  
AGGGT TCT CGGTAA  
TCTTTGG\_ C

GAM1682 EREG 3' AATGGCTTCTTCTAGAATGT 7485 G\_  
ATAT TAGAAGAAGCCATT  
||| |||||  
TGTA ATCTTCTTCGGTAA  
AG

GAM1682 FLJ10350 3' AATGGCTTCTCCACCAACGGA 95503 CATAT A A  
TCC GT GA GAAGCCATT  
||| ||| |||||

AGG CA CT CTTCGGTAA  
 CAAC\_ C \_  
 GAM1682 FLJ22639 3' GCTTCCTCTATTTCCTTTATATG 45610 \_\_\_\_\_ A  
 CATAT GTAGA GAAGC  
 |||| |||| ||||  
 GTATA TATCT CTTCG  
 TTTCCT C  
 GAM1682 KIAA0471 3' AATGGCTTCCATTTAATACAGG 29380 CA GTAGAA  
 CC TAT GAAGCCATT  
 || ||| |||||  
 GG ATA CTTCGGTAA  
 AC ATTTAC  
 GAM1682 KIAA0478 3' AATGGCAGTTAGATATGGGA 29538 G AAGAA  
 TCCCATAT TAG GCCATT  
 ||||| || |||||  
 AGGGTATA ATT CGGTAA  
 G GA\_\_\_\_  
 GAM1682 KIAA0748 5' AATGGCTTCTGCAGCCATGGGA 28929 AT AGA  
 TCCCAT GT AGAAGCCATT  
 |||| || |||||  
 AGGGTA CG TCTTCGGTAA  
 C\_ ACG  
 GAM1682 KIAA1223 3' AATGGCTTCTGCTCCAT 71140 T A  
 ATG AG AGAAGCCATT  
 || || |||||  
 TAC TC TCTTCGGTAA  
 C G  
 GAM1682 KIAA1228 3' AATGGCTTCCATAGCCATGAGA 65034 C AT AGAA  
 TC CAT GT GAAGCCATT  
 || ||| || |||||  
 AG GTA CG CTTCGGTAA  
 A C\_ ATAC  
 GAM1682 MGC3222 3' AATGAGTTTCTTCACATG 44290 A \_  
 TATGT GAAGAAGC CATT  
 |||| ||||| ||||  
 GTACA CTTCTTTG GTAA  
 \_ A  
 GAM1682 PRO2949 3' AATGATCACATTTTACATATGA 37618 C GAAGC\_  
 GA TC CATATGTAGAA CATT  
 || ||||| ||||  
 AG GTATACATTTT GTAA  
 A AACTA  
 GAM1682 RFX4 3' TTCTTCTACATACAAGG 50665 CA\_  
 CC TATGTAGAAGAA  
 || |||||  
 GG ATACATCTTCTT  
 AAC  
 GAM1682 VEST1 5' ATGGACTACATATTGGA 53683 C AAGAAG  
 TCC ATATGTAG CCAT  
 || ||||| ||||

AGG TATACATC GGTA  
 T A\_\_\_\_  
 GAM1682 ZNF221 5' GCCTACAATTATATATGGGA 25338 AAGAA\_  
 TCCCATATGTAG GC  
 ||||| ||  
 AGGGTATATATT CG  
 AACATC  
 GAM1682 ZNF323 5' ATGGCTTCAACAGAGGA 48078 CATA AGAA  
 TCC TGT GAAGCCAT  
 ||| ||| |||||  
 AGG ACA CTTCGGTA  
 AG\_\_ A\_\_  
 GAM1682 LOC150005 5' ATGGCTTCAGCATGGA 84816 CAT AGAA  
 TCC ATGT GAAGCCAT  
 ||| ||| |||||  
 AGG TACG CTTCGGTA  
 \_\_ A\_\_  
 GAM1682 LOC157506 3' AATGGGAACTTCTACATTG 81435 T AAG  
 CA ATGTAGAAG CCATT  
 || ||||| ||||  
 GT TACATCTTC GTTAA  
 \_ AAG  
 GAM1682 LOC200933 5' AATGGCTTTACTTTACAT 90191 A\_  
 ATGTAGA GAAGCCATT  
 ||||| |||||  
 TACATTT TTTCGGTAA  
 CA  
 GAM1682 LOC201182 5' AATGGCTTCTCCCTCTTTAAGG 89762 A TGT A\_  
 CC TA AG AGAAGCCATT  
 || || || |||||  
 GG AT TC TCTTCGGTAA  
 A TTC CC  
 GAM1682 LOC220824 3' GCTTCCTCTATTCCTTTATATG 90807 \_\_\_\_\_ A  
 CATAT GTAGA GAAGC  
 |||| |||| ||||  
 GTATA TATCT CTTCG  
 TTTCCT C  
 GAM1682 LOC253724 3' AATGGCTTCTCATTATGGGA 96481 TGTA A  
 TCCCAT GA GAAGCCATT  
 ||||| || |||||  
 AGGGTAT CT CTTCGGTAA  
 TA\_\_ \_  
 GAM1682 LOC255520 3' GCTCTACCTACATATG 95859 A\_ A  
 CATATGTAG AGA GC  
 ||||| ||| ||  
 GTATACATC TCT CG  
 CA \_  
 GAM1682 LOC57105 5' AATGGCTATTCTACAT 39811 GA  
 ATGTAGAA AGCCATT  
 ||||| |||||

			TACATCTT TCGGTAA		
			A_		
GAM1683	BDP1	5'	AGTGAAACTACGGTAGCTGCC 37363	A	AGGATGATC
			GG GGCTGCC TCACT		
			CC TCGATGG AGTGA		
			G CATCAA__		
GAM1683	CDH1	3'	AGTTCTCCCACCAGCCTCC 15140	CCA	T T
			GGAGGCTG GGA GA CT		
			CCTCCGAC CCT CT GA		
			CAC _ T		
GAM1683	CLASP1	3'	GTGCACCCTGACAGTCTCC 65308	C	A ATCT
			GGAGGCTG CAGG TG CAC		
			CCTCTGAC GTCC AC GTG		
			A C ____		
GAM1683	FLNB	3'	CATCCCTGGCAGCCCC 62175	A	_
			GG GGCTGCCAGG ATG		
			CC CCGACGGTCC TAC		
			_ C		
GAM1683	IGF2	3'	CATCCTGCAGCCTCC 5217	C	
			GGAGGCTGC AGGATG		
			CCTCCGACG TCCTAC		
			_		
GAM1683	MLC1	3'	GTGAGATCAGTCAGCTCC 30783	G	CCAGGA
			GGAG CTG TGATCTCAC		
			CCTC GAC ACTAGAGTG		
			_ TG__		
GAM1683	MLC1	3'	GTGAGATCAGTCAGCTCC 57596	G	CCAGGA
			GGAG CTG TGATCTCAC		
			CCTC GAC ACTAGAGTG		
			_ TG__		
GAM1683	SLC17A5	3'	AGATCATCCTGGTTTAAATC 24889	GGCT_	
			GA GCCAGGATGATCT		
			CT TGGTCCTACTAGA		
			AAATT		
GAM1683	SLC26A4	3'	AGTGAGTGCTGACCCAACAGCC 4782	CCA	ATGAT_
	TCT		GGAGGCTG GG CTC		
			TCTCCGAC CC GAGTGA		
			AAC AGTCGT		
GAM1683	SMG1	3'	AGCGAGACCATCCTGGC 30648	A	A
			GCCAGGATG TCTC CT		

			CGGTCCTAC AGAG GA		
			C C		
GAM1683	SOD3	3'	TCACGCTGACAGCCTCC 11865	C GA	
			GGAGGCTG CAG TGA		
			CCTCCGAC GTC ACT		
			A GC		
GAM1683	TCN2	3'	TCATCCCAGCAGCCTC 4482	CA	
			GAGGCTGC GGATGA		
			CTCCGACG CCTACT		
			AC		
GAM1683	TPD52L2	3'	GTCGCACCCCAGCAGCCTCT 12366	CA A__	
			GGAGGCTGC GG TGAT		
			TCTCCGACG CC GCTG		
			AC CAC		
GAM1683	DDX34	3'	AGACCATCCCAGCCACC 27976	A CCA A	
			GG GGCTG GGATG TCT		
			CC CCGAC CCTAC AGA		
			A ____ C		
GAM1683	DKFZp761B0514	3'	TCCTCCCAGCAGCCTCC 50159	CA T	
			GGAGGCTGC GGA GA		
			CCTCCGACG CCT CT		
			AC C		
GAM1683	FIGN	5'	GTGAACCCTGGCAGCCTTC 36087	ATGATC	
			GGAGGCTGCCAGG TCAC		
			CTTCCGACGGTCC AGTG		
			CA____		
GAM1683	FLJ13848	3'	AGATTCTGCAACCTCC 45459	C TG	
			GGAGG TGCCAGGA ATCT		
			CCTCC ACGGTCCT TAGA		
			A ____		
GAM1683	FLJ20413	5'	GTGAGAGACACCAGCCTCC 35134	GCCA A A_	
			GGAGGCT GG TG TCTCAC		
			CCTCCGA CC AC AGAGTG		
			____ _ AG		
GAM1683	FLJ20967	3'	GGGTCATCCTACAGCCTCC 41963	CC	
			GGAGGCTG AGGATGATCT		
			CCTCCGAC TCCTACTGGG		
			A_		
GAM1683	KIAA0415	3'	GTGAGAAGTGACAGCCTGC 92581	G C GGATGA	
			G AGGCTG CA TCTCAC		



			C TCCGAC GT	AGAGTG	
			G A GA_____		
GAM1683	KIAA1361	3'	ATCATCACAGCAGCCTCC	62195	CAG
			GGAGGCTGC GATGAT		
			CCTCCGACG CTACTA		
			ACA		
GAM1683	KIAA1941	3'	TCACCCCGGCAGCCTC	74844	A A
			GAGGCTGCC GG TGA		
			CTCCGACGG CC ACT		
			C C		
GAM1683	MDS018	3'	TGCTCCAGCAGCCTCC	41537	CA TGATCT
			GGAGGCTGC GGA CA		
			CCTCCGACG CCT GT		
			A_ C_____		
GAM1683	OSBPL3	3'	TGAGCTAACAGTCTCC	31439	CC GATGAT
			GGAGGCTG AG CTCA		
			CCTCTGAC TC GAGT		
			AA _____		
GAM1683	PRPF8	3'	GATGGCTTGGCAACCTCC	61190	C ATG
			GGAGG TGCCAGG ATC		
			CCTCC ACGGTTC TAG		
			A GG_		
GAM1683	RBBP4	5'	GGAGCTCTTGCAGCCTCC	18825	C TGAT A
			GGAGGCTGC AGGA CTC C		
			CCTCCGACG TTCT GAG G		
			_ C__ C		
GAM1683	SERPINA1	5'	TCACCAGCAGCCTCC	4308	CA A
			GGAGGCTGC GG TGA		
			CCTCCGACG CC ACT		
			A_ _		
GAM1683	ZNF384	3'	TGGTGTCATCCAGCAGCCTCC	55988	CA CT
			GGAGGCTGC GGATGAT CA		
			CCTCCGACG CCTACTG GT		
			A_ TG		
GAM1683	LOC144524	5'	AGTGATTCTCCTGCGCAGCCTC	83120	_ T TC
			C GGAGGCTGC CAGGA GA TCACT		
			CCTCCGACG GTCCT CT AGTGA		
			C _ T_		
GAM1683	LOC145955	5'	TATCCCAGCAGCCTTC	83598	CA
			GGAGGCTGC GGATG		

CTTCCGACG CCTAT  
 AC  
 GAM1683 LOC149271 3' CATCCTAACAGCCTCC 79238 CC  
 GGAGGCTG AGGATG  
 ||||| |||||  
 CCTCCGAC TCCTAC  
 AA  
 GAM1683 LOC150946 3' TCCTCCTGGCAGCCCC 85171 A T  
 GG GGCTGCCAGGA GA  
 || ||||| ||  
 CC CCGACGGTCCT CT  
 C  
 GAM1683 LOC222681 3' TGAGATCACCACACCATCC 92855 \_ C CCA A  
 GGA GG TG GG TGATCTCA  
 ||| || || |||||  
 CCT CC AC CC ACTAGAGT  
 A \_ A \_  
 GAM1683 LOC255031 5' GGGCTCCTGGCAGCCCC 97236 A TGAT  
 GG GGCTGCCAGGA CTC  
 || ||||| ||  
 CC CCGACGGTCCT GGG  
 C  
 GAM1683 LOC255042 5' GTGACCCCATCAGCCTCC 95324 GCCAG ATC  
 GGAGGCT GATG TCAC  
 ||||| ||| |||  
 CCTCCGA CTAC AGTG  
 CCC  
 GAM1683 LOC257507 3' TGAGATCACCACACCATCC 97777 \_ C CCA A  
 GGA GG TG GG TGATCTCA  
 ||| || || |||||  
 CCT CC AC CC ACTAGAGT  
 A \_ A \_  
 GAM1683 LOC257625 3' TGAGATCACCACACCATCC 97908 \_ C CCA A  
 GGA GG TG GG TGATCTCA  
 ||| || || |||||  
 CCT CC AC CC ACTAGAGT  
 A \_ A \_  
 GAM1683 LOC51657 5' CATCCTGGCAACCCC 32225 A C  
 GG GG TGCCAGGATG  
 || |||||  
 CC CC ACGGTCCTAC  
 A  
 GAM1683 LOC90371 5' GATCATAGCAGCCTCC 62498 CAGG  
 GGAGGCTGC ATGATC  
 ||||| |||||  
 CCTCCGACG TACTAG  
 A  
 GAM1684 GATA2 3' GGCGCCCAGCAGCCTGCC 9000 A ATAAA T  
 GGCA GCTGCTG GC GCC  
 ||| ||||| |||

			CCGT CGACGAC	CG CGG		
			C	C_____		
GAM1684	GCK	3'	AGGCAGCTCCAACAGCTTGACC	3865	_____	C ATAA
			GG CAAGCTG TG	AGCTGCCT		
			CC GTTCGAC AC	TCGACGGA		
			A	A C_____		
GAM1684	GCK	3'	AGGCAGCTCCAACAGCTTGACC	53172	_____	C ATAA
			GG CAAGCTG TG	AGCTGCCT		
			CC GTTCGAC AC	TCGACGGA		
			A	A C_____		
GAM1684	GCK	3'	AGGCAGCTCCAACAGCTTGACC	53177	_____	C ATAA
			GG CAAGCTG TG	AGCTGCCT		
			CC GTTCGAC AC	TCGACGGA		
			A	A C_____		
GAM1684	GPR56	3'	AGGAGCACAGCAGCAGCTCGCC	19064	A	ATAAA G
			GGC AGCTGCTG	GCT CCT		
			CCG TCGACGAC	CGA GGA		
			C	GACA_ _		
GAM1684	HIP1	3'	GGGCACATGAACAGCTTGCC	18064		CTGATAAAGC
			GGCAAGCTG	TGCCT		
			CCGTTCGAC	ACGGG		
			AAGTAC_____			
GAM1684	LIMK1	3'	AGGTGTCCACCAGCAGCTCAGC	33642	A_	ATAAA T
			GC AGCTGCTG	GC GCCT		
			CG TCGACGAC	TG TGGA		
			AC	CACC_ _		
GAM1684	LIMK1	3'	AGGTGTCCACCAGCAGCTCAGC	9783	A_	ATAAA T
			GC AGCTGCTG	GC GCCT		
			CG TCGACGAC	TG TGGA		
			AC	CACC_ _		
GAM1684	MUC4	3'	AGGCAGCTGTGCAGCTTCACC	56319	C_	TGATAA
			GG AAGCTGC	AGCTGCCT		
			CC TTCGACG	TCGACGGA		
			AC	TG_____		
GAM1684	NTSR1	3'	AGGCAGCTCCAAGAAAGCTCC	10285	CA	GCTGATAA
			GG AGCT	AGCTGCCT		
			CC TCGA	TCGACGGA		
			_____	AAGAACC_		
GAM1684	PAX9	5'	ATCACCATGCAGCTTGCC	20558	_____	
			GGCAAGCTGC	TGAT		

			CCGTTCGACG	ACTA		
			TACC			
GAM1684	PPT2	3'	AGGCAGCTTCACCTGCGGCTGC	57227	A	TGATA
	C		GGCA GCTGC	AAGCTGCCT		
			CCGT CGGCG	TTCGACGGA		
			_	TCCAC		
GAM1684	PSEN1	3'	GCCCCATCAGCAGCTTG	23623	AAA	
			CAAGCTGCTGAT	GC		
			GTTTCGACGACTA	CG		
			CCC			
GAM1684	PSEN1	3'	GCCCCATCAGCAGCTTG	3423	AAA	
			CAAGCTGCTGAT	GC		
			GTTTCGACGACTA	CG		
			CCC			
GAM1684	PTGIS	3'	GGCAGCTCCAGCTGTT	6338	T	ATAA
			AGC GCTG	AGCTGCC		
			TTG CGAC	TCGACGG		
			T	C__		
GAM1684	SBF1	5'	AGCTACCAGCGGCTCGCC	65456	A	ATAA
			GGC AGCTGCTG	AGCT		
			CCG TCGGCGAC	TCGA		
			C	CA__		
GAM1684	SLC22A11	3'	AGGCAGCTTCCACAGCTCACT	37489	CA	C ATA
			GG AGCTG TG	AAGCTGCCT		
			TC TCGAC AC	TTCGACGGA		
			AC	_ C__		
GAM1684	UBE4A	3'	AGGCAGCTATTCCCAGCAGCTT	16557	C	AT _
	CC		GG AAGCTGCTG	AA AGCTGCCT		
			CC TTCGACGAC	TT TCGACGGA		
			_	CC A		
GAM1684	C22orf23	3'	AGGCATACTCAGCAGCCTAGC	50782	AA_	TAAAGC
			GC GCTGCTGA	TGCCT		
			CG CGACGACT	ACGGA		
			ATC	CAT__		
GAM1684	COPS7B	3'	AGGCAGCTTTAACCAGC	42690	A_	
			GCTG TAAAGCTGCCT			
			CGAC ATTTTCGACGGA			
			CA			
GAM1684	DKFZP564F013	3'	CAGCTTCAGCTTGC	94206	CTGATA	
			GCAAGCTG	AAGCTG		

CGTTCGAC TCGAC

GAM1684 DKFZP566B183 3' GGCAGCTCTATTCTTGC 31327 CTGCT A  
GCAAG GATA AGCTGCC  
||||| ||| |||||  
CGTTC TTAT TCGACGG

\_\_\_\_\_ C  
GAM1684 EFA6R 3' AGGCAGCTTCATGTGCAGCTTA 30978 \_ TG A  
GC GC AAGCTGC AT AAGCTGCCT  
|| ||||| || |||||  
CG TTCGACG TA TTCGACGGA

A TG C  
GAM1684 FLJ12899 3' GGCAACTTTATCAGTA 44763 C  
TGCTGATAAAG TGCC  
||||||| |||  
ATGACTATTTTC ACGG  
A

GAM1684 FLJ20048 3' GCAGCTACAGATTGCC 34437 G CTGATAA  
GGCAA CTG AGCTGC  
||||| ||| |||||  
CCGTT GAC TCGACG  
A A\_\_\_\_\_

GAM1684 FLJ21736 3' AGGCAGCTCCACCTGCTGCC 46225 A TGC ATAA  
GGCA GC TG AGCTGCCT  
|||| || || |||||  
CCGT CG AC TCGACGGA  
\_ TCC C\_\_\_\_\_

GAM1684 FLJ25410 5' AGGCAGCTCCTGGAAGCTCC 58153 CA G ATAA  
GG AGCT CTG AGCTGCCT  
|| ||| ||| |||||  
CC TCGA GGT TCGACGGA  
\_ A CC\_\_\_\_\_

GAM1684 FZD9 3' AGACAGCTGACTAGCAGCTGCC 13045 A ATAA C  
GGCA GCTGCTG AGCTG CT  
|||| ||||| ||||| ||  
CCGT CGACGAT TCGAC GA  
\_ CAG\_ A

GAM1684 GRO2 5' AGGCAGCTCCTTGCCAGCTCTC 59516 CA CT TAA  
C GG AGCTG GA AGCTGCCT  
|| |||| || |||||  
CC TCGAC TT TCGACGGA  
TC CG CC\_\_\_\_\_

GAM1684 HYPC 5' CAGCAGCAGCAGCTGCC 64608 A ATAAA  
GGCA GCTGCTG GCTG  
|||| ||||| |||  
CCGT CGACGAC CGAC  
\_ GA\_\_\_\_\_

GAM1684 KIAA0415 3' GGCAGCTCTACCTGCAGC 92580 TGA A  
GCTGC TA AGCTGCC  
|||| || |||||

CGACG AT TCGACGG  
 TCC C  
 GAM1684 KIAA0418 3' GGCAGCTCCCAGCCTGCT 27560 A CTGATAA  
 GGCA GCTG AGCTGCC  
 ||| ||| |||||  
 TCGT CGAC TCGACGG  
 C CC\_\_\_\_  
 GAM1684 KIAA0513 5' AGGCAGCCTCACCAGCAGCTCC 28338 CA ATAAA  
 CC GG AGCTGCTG GCTGCCT  
 || ||||| |||||  
 CC TCGACGAC CGACGGA  
 CC CACTC  
 GAM1684 KIAA1089 3' GGCAGCTCTGGAGCCAGC 68845 \_ GA A  
 GCTG CT TA AGCTGCC  
 ||| || |||||  
 CGAC GA GT TCGACGG  
 C G\_ C  
 GAM1684 KIAA1128 3' CTTTATCAGCAACTCAGC 68478 A\_ C  
 GC AG TGCTGATAAAG  
 || |||||  
 CG TC ACGACTATTTC  
 AC A  
 GAM1684 KIAA1870 5' CAGCCCAGTCAGCAGACCACC 51826 CAAG AAA  
 GG CTGCTGAT GCTG  
 || ||||| |||  
 CC GACGACTG CGAC  
 ACCA ACC  
 GAM1684 MGC11266 3' AGGCAGCTTTGTCCCAGCTCTG 44239 \_ CT  
 CC GGCA AGCTG GATAAAGCTGCCT  
 ||| ||| |||||  
 CCGT TCGAC CTGTTTCGACGGA  
 C C\_  
 GAM1684 MGC1842 3' AGGCAGCTGACGAGGCAGCTGG 65642 A GATAA  
 CC GGC AGCTGCT AGCTGCCT  
 || ||||| |||||  
 CCG TCGACGG TCGACGGA  
 G AGCAG  
 GAM1684 MGC2306 3' GGCGCCCAGCAGCCTGCC 50965 A ATAAA T  
 GGCA GCTGCTG GC GCC  
 ||| ||||| || |||  
 CCGT CGACGAC CG CGG  
 C C\_\_\_\_\_  
 GAM1684 NTT5 3' AGACAACTCTTAATATCAGCTT 25879 C A \_ C C  
 GC GCAAGCTG TG TAA AG TG CT  
 ||||| || ||| || ||  
 CGTTCGAC AT ATT TC AC GA  
 T A C A A  
 GAM1684 RASD2 5' AGGCAGCTCCCCGCAGCTCC 26684 CA TGATAA  
 GG AGCTGC AGCTGCCT  
 || ||||| |||||

			CC TCGACG	TCGACGGA		
			___ CCCC___			
GAM1684	RASD2	5'	AGGCAGCTCTCTGAGCCGTGCC	26685	A_ GCT TAA	
			GGCA GCT GA AGCTGCCT			
			CCGT CGA CT TCGACGGA			
			GC GT_ C__			
GAM1684	SYTL4	5'	AGGCAACTCTGGTAGCTCTCC	54938	CA ATAA C	
			GG AGCTGCTG AG TGCCT			
			CC TCGATGGT TC ACGGA			
			TC C__ A			
GAM1684	TIEG	5'	GCAGCCAGCAGCCTAGC	18957	AA_ ATAAA	
			GC GCTGCTG GCTGC			
			CG CGACGAC CGACG			
			ATC _____			
GAM1684	WDR7	3'	CTTTATCAACAGCTAACC	30959	CA C	
			GG AGCTG TGATAAAG			
			CC TCGAC ACTATTTC			
			AA A			
GAM1684	LOC127435	3'	CAGCCATAGCAGCTCGCC	76115	A ATAAA	
			GGC AGCTGCTG GCTG			
			CCG TCGACGAT CGAC			
			C AC__			
GAM1684	LOC146713	3'	GCAGCCCCAGCTTGCT	83727	CTGATAAA	
			GGCAAGCTG GCTGC			
			TCGTTTCGAC CGACG			
			CC _____			
GAM1684	LOC146909	3'	GCAGCTTTATTGCTT	78173	TGCT C	
			AAGC GATAAAGCTG C			
			TTCG TTATTTCGAC G			
			_____ A			
GAM1684	LOC149296	5'	GCAGCTATGGGCAGCTGCC	79259	A G AA	
			GGCA GCTGCT AT AGCTGC			
			CCGT CGACGG TA TCGACG			
			_ G _			
GAM1684	LOC150378	5'	AGGCAGCTTTCTCTCCAGCT	79737	CT T	
			AGCTG GA AAAGCTGCCT			
			TCGAC CT TTTCGACGGA			
			CT C			
GAM1684	LOC200471	5'	GCAGCAGCAGCTCACC	90052	CA GATAAA	
			GG AGCTGCT GCTGC			

CC TCGACGA CGACG  
 AC \_\_\_\_\_  
 GAM1684 LOC219649 3' AGGCAGCTCTTCCCAATCTGCC 92949 AGC CT TAA  
 GGCA TG GA AGCTGCCT  
 ||| || || |||||  
 CCGT AC CT TCGACGGA  
 CTA C\_ TC\_  
 GAM1684 LOC220082 3' GCAGCGTTAGCAGCCTTCC 93466 CAA AAA  
 GG GCTGCTGAT GCTGC  
 || ||||| |||  
 CC CGACGATTG CGACG  
 TTC \_\_\_\_\_  
 GAM1684 LOC221747 3' GCACACATCAGCAGCTCAGC 92354 A\_ AAAGC  
 GC AGCTGCTGAT TGC  
 || ||||| |||  
 CG TCGACGACTA ACG  
 AC CACAC  
 GAM1684 LOC254057 5' GGCAGACCAGCAGCTGGCC 97001 A ATAAAG  
 GGC AGCTGCTG CTGCC  
 ||| ||||| |||  
 CCG TCGACGAC GACGG  
 G CA\_\_\_\_\_  
 GAM1684 LOC254173 3' GCAGCTACGGCAGCTTCC 96842 C ATAA C  
 GG AAGCTGCTG AGCTG C  
 || ||||| |||||  
 CC TTCGACGGC TCGAC G  
 \_ A\_\_\_\_ A  
 GAM1684 LOC254556 3' CTTTTCAGCAGCCC 94615 CAA T  
 GG GCTGCTGA AAAG  
 || ||||| |||  
 CC CGACGACT TTTC  
 \_\_\_\_\_  
 GAM1684 LOC84661 3' GCAGCTTTAATTGCC 50813 GCTGCTGA  
 GGCAA TAAAGCTGC  
 ||| |||||  
 CCGTT ATTCGACG  
 A\_\_\_\_\_  
 GAM1685 CAB1 5' GCACAAACAGACGCTC 39654 CTGGC  
 GAGC TCTGTTGTGC  
 ||| |||||  
 CTCG AGACAAACACG  
 C\_\_\_\_\_  
 GAM1685 CEACAM5 3' AACAGAGCAAGACTCCA 15153 C G  
 TGGAG CT GCTCTGTT  
 ||| || |||||  
 ACCTC GA CGAGACAA  
 A A  
 GAM1685 F2R 3' AACAGAGCAAGACTCCA 8831 C G  
 TGGAG CT GCTCTGTT  
 ||| || |||||



			ACCTC GA CGAGACAA			
			A A			
GAM1685	FGFR2	3'	GACAGAGCGAGACTCCA	43377	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1685	FGFR2	3'	GACAGAGCGAGACTCCA	43383	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1685	FUT6	3'	GACAGAGCAAGACTCCA	3812	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1685	GCLM	5'	GGCGCAGACCAGGCTCCA	9026	C	TTGT _
			TGGAGCCTGG TCTGT	GC C		
			ACCTCGGACC AGACG	CG G		
			_ _ _ A			
GAM1685	GPC1	3'	GGCTGCAGAGCCCGGCCCA	9103	A T	TTGT
			TGG GCC GGCTCTGT	GCC		
			ACC CGG CCGAGACG	CGG		
			C C T _			
GAM1685	HPSE	3'	CAAACAGGCCAGGCTCCA	21890	T	
			TGGAGCCTGGC CTGTTTG			
			ACCTCGGACCG GACAAAC			
			-			
GAM1685	IFIT4	3'	AACAGAGCAAGACTCCA	70918	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A A			
GAM1685	KCNJ5	3'	GACAGAGCGAGACTCCA	6091	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1685	LY94	3'	GACAGAGCGAGACTCCA	16705	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1685	LZTS1	3'	ACAGAGCCTGGCCCCA	40676	A T	
			TGG GCC GGCTCTGT			

			ACC CGG CCGAGACA		
			C T		
GAM1685	MSH3	3'	AACAGAGCAAGACTCCA 10116	C G	
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A A		
GAM1685	POLH	3'	AACAGAGCGAGACTCCA 21461	C G	
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1685	PRKAB1	3'	GCACACCACCAGGCTCCA 20736	CTC TT	
			TGGAGCCTGG TG TGTGC		
			ACCTCGGACC AC ACACG		
			___ C_		
GAM1685	SIGLEC6	3'	AACAGAGCGAGACTCCA 59925	C G	
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1685	SLC10A2	5'	AGCAGAGCCAGGGCCCA 4840	AG	
			TGG CCTGGCTCTGTT		
			ACC GGACCGAGACGA		
			CG		
GAM1685	SNRPN	5'	CAAGCAAAAACCAGGCTCCA 42991	CTC_	
			TGGAGCCTGG TGTTTG		
			ACCTCGGACC ACGAAC		
			AAAA		
GAM1685	SNRPN	5'	CAAGCAAAAACCAGGCTCCA 42998	CTC_	
			TGGAGCCTGG TGTTTG		
			ACCTCGGACC ACGAAC		
			AAAA		
GAM1685	SNRPN	5'	CAAGCAAAAACCAGGCTCCA 43005	CTC_	
			TGGAGCCTGG TGTTTG		
			ACCTCGGACC ACGAAC		
			AAAA		
GAM1685	SNRPN	5'	CAAGCAAAAACCAGGCTCCA 43013	CTC_	
			TGGAGCCTGG TGTTTG		
			ACCTCGGACC ACGAAC		
			AAAA		
GAM1685	TNFSF11	5'	CAGGAGCCAAAGCCGGGCTCCA 13512	CT_ G	
			TGGAGCCTGGCT GTTT TG		

			ACCTCGGGCCGA	CGAG AC		
			AAC	G		
GAM1685	TSNAX	3'	GGTAACAGAGCAAGACTCCA	20002	C G	TTG
			TGGAG CT GCTCTGT	TGCC		
			ACCTC GA CGAGACA	ATGG		
			A A	___		
GAM1685	UBE2L3	3'	GCCTTTGCAGAGTCAAGCTCCA	12503	C	TTGT
			TGGAGC TGGCTCTGT	GC		
			ACCTCG ACTGAGACG	CG		
			A	TTTC		
GAM1685	ZNF264	3'	AACAGAGCGAGACTCCA	12738	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A G			
GAM1685	ARNTL2	3'	GACAGAGCGAGACTCCA	39466	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1685	C22orf5	3'	GGATCAGAGCCAGACACCA	24344	AGC	TTTGTG
			TGG CTGGCTCTG	CC		
			ACC GACCGAGAC	GG		
			ACA	TA___		
GAM1685	DKFZp547C176	3'	GACAGAGCAAGACTCCA	67223	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1685	DKFZp564K142	3'	AACAGAGCGAGACTCCA	49522	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A G			
GAM1685	FADS1	3'	GACAGAGCAAGACTCCA	25477	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1685	FLJ12298	3'	AACAGAGCGAGACTCCA	49664	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A G			
GAM1685	FLJ14117	3'	AACAGAGCAAGACTCCA	42896	C G	
			TGGAG CT GCTCTGTT			

			ACCTC GA CGAGACAA			
			A A			
GAM1685	FLJ14251	3'	GGTAACAGAGCGAGACTCCA	45977	C G	TTG
			TGGAG CT GCTCTGT TGCC			
			ACCTC GA CGAGACA ATGG			
			A G	—		
GAM1685	FLJ14327	3'	AACAGAGCTAGACTCCA	46127	C	
			TGGAG CTGGCTCTGTT			
			ACCTC GATCGAGACAA			
			A			
GAM1685	FLJ14566	5'	GGCCACAGAGCCAGCCCCA	51446	A C	TT T
			TGG GC TGGCTCTGT G GCC			
			ACC CG ACCGAGACA C CGG			
			C _	—		
GAM1685	FLJ20084	3'	AACAGAGCGAGACTCCA	34511	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A G			
GAM1685	FLJ20306	3'	GACAGAGCAAGACTCCA	34917	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1685	FLJ20456	3'	GGTAACAGAGCTAGACTCCA	35215	C	TTG
			TGGAG CTGGCTCTGT TGCC			
			ACCTC GATCGAGACA ATGG			
			A	—		
GAM1685	FLJ22054	3'	AACAGAGCAAGACTCCA	94391	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A A			
GAM1685	FLJ22393	5'	AGCAGGAACCAGGCTCCA	47058	C_	
			TGGAGCCTGG TCTGTT			
			ACCTCGGACC GGACGA			
			AA			
GAM1685	FLJ23598	3'	GCCAAGAGCCAGCTCCA	45522	C	GTT T
			TGGAGC TGGCTCT TG GC			
			ACCTCG ACCGAGA AC CG			
			—	—		
GAM1685	FLJ31168	3'	GACAGAGCGAGACTCCA	58502	C G	
			TGGAG CT GCTCTGTT			

			ACCTC GA CGAGACAG			
			A G			
GAM1685	GP5	3'	GACAGAGCGAGACTCCA	15646	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1685	GTPBP5	3'	GACAGAGCAAGACTCCA	65357	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1685	HIC	3'	AACAGAGCGAGACTCCA	67444	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A G			
GAM1685	ING1-like	3'	GACAGAGCGAGACTCCA	54156	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A G			
GAM1685	KBRAS2	3'	AACAGAGCAAGACTCCA	34191	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A A			
GAM1685	KIAA0189	3'	CAGGAGCAGAGCCAGGCCCA	28273	A	G
			TGG GCCTGGCTCTGTTT TG			
			ACC CGGACCGAGACGAG AC			
			— G			
GAM1685	KIAA0472	3'	AGCAGAGCAAGACTCCA	71853	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACGA			
			A A			
GAM1685	KIAA0563	3'	GACAGAGCAAGACTCCA	29188	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1685	KIAA0565	3'	GACAGAGCAAGACTCCA	66890	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAG			
			A A			
GAM1685	KIAA0648	3'	CAACAGAAGCAGGCTCCA	82651		GC
			TGGAGCCTG TCTGTTTG			

			ACCTCGGAC AGACAAAC			
			GA			
GAM1685	KIAA0924	3'	AACAGAGCGAGACTCCA	29712	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A G			
GAM1685	KIAA1028	3'	CAGAGCACAGGCTCCA	91934	—	
			TGGAGCCTG GCTCTG			
			ACCTCGGAC CGAGAC			
			A			
GAM1685	KIAA1719	3'	GGCCAGGGCCAGGCCCCA	68169	A	TTTGT
			TGG GCCTGGCTCTG	GCC		
			ACC CGGACCGGGAC	CGG		
			C			
GAM1685	KIAA1940	3'	GGTCTCAGAACCAAGGCTCCA	79988	— C	TTTGT
			TGGAGCCT GG TCTG	GCC		
			ACCTCGGA CC AGAC	TGG		
			A A TC			
GAM1685	LGI2	3'	CAAATCAAAGCCAGGCTC	36397	C	—
			GAGCCTGGCT TG TTTG			
			CTCGGACCGA AC AAAC			
			A T			
GAM1685	MGC10200	3'	AACAGAGCGAGACTCCA	58980	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A G			
GAM1685	MGC2705	5'	GCACCAAGCCAGGCTCC	51113	C	TTT
			GGAGCCTGGCT TG GTGC			
			CCTCGGACCGA AC CACG			
			— —			
GAM1685	MGC4562	3'	AACAGAGCGAGACTCCA	55908	C G	
			TGGAG CT GCTCTGTT			
			ACCTC GA CGAGACAA			
			A G			
GAM1685	MGC4663	3'	AACAGAGCCAGACTCC	44501	C	
			GGAG CTGGCTCTGTT			
			CCTC GACCGAGACAA			
			A			
GAM1685	NPTXR	3'	AACAGAGCAAGACTCCA	26635	C G	
			TGGAG CT GCTCTGTT			

			ACCTC GA CGAGACAA		
			A A		
GAM1685	NPTXR	3'	AACAGAGCAAGACTCCA	54171	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A A		
GAM1685	OR7C1	5'	AACAGAGCCAAGTCCA	82428	G C
			TGGA C TGGCTCTGTT		
			ACCT G ACCGAGACAA		
			_ A		
GAM1685	POFUT1	3'	AACAGAGCGAGACTCCA	70462	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1685	PTK6	3'	GACAGAGCGAGACTCCA	19936	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A G		
GAM1685	RASGRF2	3'	GCACGAAGCCAGGCTCC	61042	CTGT
			GGAGCCTGGCT TTGTGC		
			CCTCGGACCGA AGCACG		
			_____		
GAM1685	SC65	3'	GACAGAGCGAGACTCCA	21289	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A G		
GAM1685	SNURF	3'	CAAGCAAAAACCAGGCTCCA	19052	CTC_
			TGGAGCCTGG TGTTTG		
			ACCTCGGACC ACGAAC		
			AAAA		
GAM1685	TMG4	3'	GACAGAGCAAGACTCCA	43989	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A A		
GAM1685	WBSCR23	3'	GACAGAGCAAGACTCCA	46762	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A A		
GAM1685	WIRE	3'	GACAGAGCCAGACTCC	78305	C
			GGAG CTGGCTCTGTT		

			CCTC GACCGAGACAG		
			A		
GAM1685	WSB1	3'	AACAGAGCGAGACTCCA	56138	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1685	WSB1	3'	AACAGAGCGAGACTCCA	56144	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1685	LOC115704	3'	CAGCCAGAGCCAGGCCCC	73541	A T
			GG GCCTGGCTCTG TTG		
			CC CGGACCGAGAC GAC		
			C C		
GAM1685	LOC124220	5'	GGCACAACCAGACGCC	59146	_ T
			GGC TCTG TTGTGCC		
			CCG AGAC AACACGG		
			C C		
GAM1685	LOC127262	3'	GACAGAGCGAGACTCCA	76110	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAG		
			A G		
GAM1685	LOC129563	3'	AGCAGAGCAGGCCCCA	74878	A G
			TGG GCCTG CTCTGTT		
			ACC CGGAC GAGACGA		
			C _		
GAM1685	LOC129880	3'	AACAGAGCAAGACTCCA	74900	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A A		
GAM1685	LOC143196	3'	AACAGAGCGAGACTCCA	82903	C G
			TGGAG CT GCTCTGTT		
			ACCTC GA CGAGACAA		
			A G		
GAM1685	LOC144319	3'	GGCACAAACAGGCGCCCC	83057	A CTG T
			GG GC GC CTGTTTGTGCC		
			CC CG CG GACAAACACGG		
			C _ _		
GAM1685	LOC145216	3'	GACAGAGCAAGACTCCA	83267	C G
			TGGAG CT GCTCTGTT		



	ACCTC GA CGAGACAG		
	A A		
GAM1685 LOC145820 3'	GACAGAGCAAGACTCCA 77514	C G	
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1685 LOC146227 3'	GGTCAGAGCCAGACCCC 77711	AGC	TTTGT
	GG CTGGCTCTG GCC		
	CC GACCGAGAC TGG		
	CCA _____		
GAM1685 LOC146713 3'	AACAGAGCAAGACTCCA 83720	C G	
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAA		
	A A		
GAM1685 LOC147071 3'	GACAGAGCAAGACTCCA 72999	C G	
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1685 LOC147649 3'	GACAGAGCGAGACTCCA 78414	C G	
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A G		
GAM1685 LOC148936 3'	AACAGAGCAAGACTCCA 84286	C G	
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAA		
	A A		
GAM1685 LOC149803 5'	CAGGCAGAGCAAGCTCCA 79538	CTG	
	TGGAGC GCTCTGTTTG		
	ACCTCG CGAGACGGAC		
	AA_		
GAM1685 LOC150299 3'	GACAGAGCAAGACTCCA 84970	C G	
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1685 LOC151429 3'	GACAGAGCAAGACTCCA 85353	C G	
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1685 LOC151904 3'	AACAGAGCGAGACTCCA 80382	C G	
	TGGAG CT GCTCTGTT		

	ACCTC GA CGAGACAA		
	A G		
GAM1685 LOC158292 5'	GACAGAGCGAGACTCCA	86730	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A G		
GAM1685 LOC162137 5'	CAAGCAGGCCAAGCCCCA	87111	A C T
	TGG GC TGGC CTGTTTG		
	ACC CG ACCG GACGAAC		
	C A _		
GAM1685 LOC163033 5'	CGACCAGGACCAAGCCCCA	82396	A C CT T
	TGG GC TGG CTG TTG		
	ACC CG ACC GAC AGC		
	C A AG C		
GAM1685 LOC163682 3'	ACACTCAAAGCCGGGCTCCA	87020	C TT
	TGGAGCCTGGCT TG TGT		
	ACCTCGGGCCGA AC ACA		
	A TC		
GAM1685 LOC200261 3'	GCACAAACCTCTGGAGGCCCA	88655	A GGCTCT
	TGG GCCT GTTTGTGC		
	ACC CGGA CAAACACG		
	_ GGTCTC		
GAM1685 LOC201173 3'	GACAGAGCAAGACTCCA	87329	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1685 LOC201182 5'	AACAGAGCAAGACTCCA	89760	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAA		
	A A		
GAM1685 LOC219627 3'	GACAGAGCGAGACTCCA	92178	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A G		
GAM1685 LOC221543 5'	GACAGAGCAAGACTCCA	93742	C G
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1685 LOC221943 5'	GACAGAGCAAGACTCCA	93989	C G
	TGGAG CT GCTCTGTT		

	ACCTC GA CGAGACAG		
	A A		
GAM1685 LOC222160 5'	GACAGAGCAAGACTCCA 94127	C G	
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1685 LOC253039 5'	GGCTCCAAAACCAGGCTCTA 96159	CTCTG T_	
	TGGAGCCTGG TTTG GCC		
	ATCTCGGACC AAAC CGG		
	A_____ CT		
GAM1685 LOC254659 3'	AAACAGAGCAAGACTCCA 95109	C G	
	TGGAG CT GCTCTGTTT		
	ACCTC GA CGAGACAAA		
	A A		
GAM1685 LOC256158 5'	AACATCGAGCCAGGCCCA 97639	A _	
	TGG GCCTGGCTC TGTT		
	ACC CGGACCGAG ACAA		
	_ CT		
GAM1685 LOC256207 3'	GACAGAGCAAGACTCCA 95169	C G	
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1685 LOC257596 5'	GACAGAGCAAGACTCCA 97935	C G	
	TGGAG CT GCTCTGTT		
	ACCTC GA CGAGACAG		
	A A		
GAM1685 LOC56963 3'	GCACAAAGCCAGGCTTCA 71455	CTGT	
	TGGAGCCTGGCT TTGTGC		
	ACTTCGGACCGA AACACG		
	_____		
GAM1685 LOC91149 3'	GCTGAACCAGAGCCAGACTCCA 65079	C _ T	
	TGGAG CTGGCTCTG TTTG GC		
	ACCTC GACCGAGAC AAGT CG		
	A C _		
GAM1685 LOC91409 3'	AGGCAAGGCCAGGCCCCA 65951	A TC	
	TGG GCCTGGC TGTTT		
	ACC CGGACCG ACGGA		
	C GA		
GAM1685 LOC91862 3'	GGTGACAGAGCGAGACTCCA 53470	C G TGT	
	TGGAG CT GCTCTGTT GCC		

ACCTC GA CGAGACAG TGG  
 A G \_\_\_\_  
 GAM1685 LOC92482 3' AACAGAGCAAGACTCCA 69485 C G  
 TGGAG CT GCTCTGTT  
 ||||| || |||||  
 ACCTC GA CGAGACAA  
 A A  
 GAM1686 ATRN 3' CAACACTAACCCCACTCC 57796 AGATT  
 GGAGT GTTAGTGTTG  
 ||||| |||||  
 CCTCA CAATCACAAC  
 CCC\_\_  
 GAM1686 CSAGE 3' CAACACTATCCAGCCACTCTGA 86860 G AGA T\_  
 TCAG AGT TTG TAGTGTTG  
 ||||| ||||| |||||  
 AGTC TCA GAC ATCACAAC  
 \_ CC\_ CT  
 GAM1686 DPP8 3' CATGTAACATCTACTCCTGA 55233 T \_  
 TCAGGAGTAGAT GTTA GTG  
 ||||| ||||| |||||  
 AGTCCTCATCTA CAAT TAC  
 \_ G  
 GAM1686 FLJ13197 5' CAACACCAGCGCTGCACC 44847 A AT A  
 GG GTAG TGTT GTGTTG  
 || ||||| ||||| |||||  
 CC CGTC GCGA CACAAC  
 A \_ C  
 GAM1686 TRAG3 3' CAACACTATCCAGCCACTCTGA 16932 G AGA T\_  
 TCAG AGT TTG TAGTGTTG  
 ||||| ||||| |||||  
 AGTC TCA GAC ATCACAAC  
 \_ CC\_ CT  
 GAM1686 TRAG3 3' CAACACTATCCAGCCACTCTGA 67525 G AGA T\_  
 TCAG AGT TTG TAGTGTTG  
 ||||| ||||| |||||  
 AGTC TCA GAC ATCACAAC  
 \_ CC\_ CT  
 GAM1686 LOC196890 3' AACAACTGCTCCTGA 89642 A  
 TCAGGAGTAG TTGTT  
 ||||| ||||| |||||  
 AGTCCTCGTC AACAA  
 C  
 GAM1686 LOC92017 5' AACCATCCACTCCTGA 67883 A T  
 TCAGGAGT GAT GTT  
 ||||| ||||| |||||  
 AGTCCTCA CTA CAA  
 C C  
 GAM1687 ATRN 3' CAACACTAACCCCACTCC 57796 AGATT  
 GGAGT GTTAGTGTTG  
 ||||| ||||| |||||

			CCTCA CAATCACAAC		
			CCC__		
GAM1687 CSAGE	3'	CAAACTATCCAGCCACTCTGA 86860		G AGA T_	
		TCAG AGT TTG TAGTGTTG			
		AGTC TCA GAC ATCACAAC			
		_ CC_ CT			
GAM1687 DPP8	3'	CATGTAACATCTACTCCTGA 55233		T _	
		TCAGGAGTAGAT GTTA GTG			
		AGTCCTCATCTA CAAT TAC			
		_ G			
GAM1687 FLJ13197	5'	CAACACCAGCGCTGCACC 44847	A AT A		
		GG GTAG TGTT GTGTTG			
		CC CGTC GCGA CACAAC			
		A _ C			
GAM1687 TRAG3	3'	CAAACTATCCAGCCACTCTGA 67525	G AGA T_		
		TCAG AGT TTG TAGTGTTG			
		AGTC TCA GAC ATCACAAC			
		_ CC_ CT			
GAM1687 TRAG3	3'	CAAACTATCCAGCCACTCTGA 16932	G AGA T_		
		TCAG AGT TTG TAGTGTTG			
		AGTC TCA GAC ATCACAAC			
		_ CC_ CT			
GAM1687 LOC196890	3'	AACAACCTGCTCCTGA 89642	A		
		TCAGGAGTAG TTGTT			
		AGTCCTCGTC AACAA			
		C			
GAM1687 LOC92017	5'	AACCATCCACTCCTGA 67883	A T		
		TCAGGAGT GAT GTT			
		AGTCCTCA CTA CAA			
		C C			
GAM1688 ANXA9	3'	TAAAATCCCTTAATTTTCCC 13105	CTT		
		GGGA TTAAGGGATTTTA			
		CCCT AATTCCTAAAAT			
		TTT			
GAM1688 CD4	3'	TAAAATCCCTCCTTCATCCC 5228	CTTTTA		
		GGGA AGGGATTTTA			
		CCCT TCCCTAAAAT			
		ACTTCC			
GAM1688 DPYSL3	3'	AAAATCCCTCAGCCTT 7307	A TTTA		
		AGGG CT AGGGATTTT			

TTCC GA TCCCTAAAA  
 \_ C\_  
 GAM1688 MAN2A2 3' AAATCCATCCCTTAT 20390 CTTTTAAG  
 ATAAGGGA GGATTT  
 ||||| |||||  
 TATTCCCT CCTAAA  
 A\_\_\_\_\_  
 GAM1688 MNT 3' AGATCCTAAAAATCCCTTCC 39702 T C AA  
 A AAGGGA TTTT GGGATTT  
 | ||||| ||| |||||  
 C TTCCCT AAAA TCCTAGA  
 C A \_  
 GAM1688 SIM2 3' AAAATCCCTCTGGCCC 17382 A TTTA  
 GGG CT AGGGATTTT  
 ||| || |||||  
 CCC GG TCCCTAAAA  
 \_ TC\_  
 GAM1688 FLJ10483 3' CCAGAAAGTCCCTTA 36167 AA  
 TAAGGGACTTTT GG  
 ||||| ||| ||  
 ATTCCCTGAAAG CC  
 A\_  
 GAM1688 GNG4 3' ATGCCTAAATATCCCTTAT 15609 CT A G  
 ATAAGGGA TTTA GG AT  
 ||||| ||| |||  
 TATTCCCT AAAT CC TA  
 AT \_ G  
 GAM1688 KIAA0514 3' TTCCTTAAAAGTCCCTTGT 28101  
 ATAAGGGACTTTTAAGGGA  
 |||||  
 TGTTCCCTGAAAATTCCTT  
 GAM1688 KIAA1870 5' AAAATCCCCAAAAGCCTCCCT 51823 \_ AA  
 AGGGA CTTT GGGATTTT  
 |||| |||| |||||  
 TCCCT GAAAA CCCTAAAA  
 CC C\_  
 GAM1688 MED8 3' AGTCATAAAGTCCCCTAT 53520 A TAAGG  
 ATA GGGACTTT GATT  
 || ||||| |||  
 TAT CCCTGAAA CTGA  
 C TA\_\_\_\_  
 GAM1688 PJA1 5' TTTTAAAGGCCCTTAT 42327 A  
 ATAAGGG CTTTTAAGG  
 ||||| |||||  
 TATTCCC GGAAATTTT  
 C  
 GAM1688 PRRG1 3' TAAAATCCCTTTTGCTACCCC 6286 ACTTTT\_  
 GGG AAGGGATTTTA  
 ||| |||||

CCC TTCCCTAAAAT  
 CATCGTT  
 GAM1688 LOC123242 5' CCCCTAGAAGTCCCCTAT 75598 A A  
 ATA GGGACTTTTA GGG  
 ||| ||||| |||  
 TAT CCCTGAAGAT CCC  
 C C  
 GAM1688 LOC149711 3' AAAACCCCAGGTGGGTCCTT 84664 TTAA A  
 AGGGACTT GGG TTTT  
 ||||| ||| |||  
 TTCCTGGG CCC AAAA  
 TGGA C  
 GAM1688 LOC166034 5' AAAATCCCTTCTCCTTTA 87257 CTTT  
 TAAGGGA AAGGGATTTT  
 ||||| |||||  
 ATTCCT TTCCCTAAAA  
 C\_\_\_\_  
 GAM1688 LOC196955 5' CCCCTAGAAGTCCCCTAT 77372 A A  
 ATA GGGACTTTTA GGG  
 ||| ||||| |||  
 TAT CCCTGAAGAT CCC  
 C C  
 GAM1689 ARF3 3' TACTGTCACCCTGCC 8008 A A  
 GG CAGG TGACAGTG  
 || ||| |||||  
 CC GTCC ACTGTCAT  
 \_ C  
 GAM1689 CRYBA2 5' AGCGCGTGGTGCCACCCTTCC 54043 C A A GTGA A  
 GGA AGG TG CA GC CGCT  
 ||| ||| || |||  
 CCT TCC AC GT TG GCGA  
 \_ C C GG\_ C  
 GAM1689 CTGF 3' AGCGTGCTCACTGACCTGCC 8574 A ATGA  
 GG CAGG CAGTGAGCACGCT  
 || ||| |||||  
 CC GTCC GTCACCTCGTGCGA  
 \_ A\_\_\_\_  
 GAM1689 MGAT1 3' GCTCACTGCCTCCTGCC 10009 A TGA  
 GG CAGGA CAGTGAGC  
 || |||| |||||  
 CC GTCCT GTCACCTCG  
 \_ CC\_  
 GAM1689 C9orf7 3' AGCGCCCCACTGTACCCTGCC 34163 A A A AC  
 GG CAGG TGACAGTG GC GCT  
 || ||| ||||| || |||  
 CC GTCC ACTGTCAC CG CGA  
 \_ C C \_  
 GAM1689 CNNM4 3' AGCGTGAGAGGTCATCCTGCC 39471 A AGTGAG  
 GG CAGGATGAC CACGCT  
 || ||||| |||||

		CC GTCCTACTG	GTGCGA		
		— GAGA—			
GAM1689	DKFZP564D166	3'	CACCTTCATCCTGTCC	47670	CA
			GGACAGGATGA GTG		
			CCTGTCCTACT CAC		
			TC		
GAM1689	FLJ20366	3'	AGCATGCTCATGACCCTGCC	35050	A ATGACA C
			GG CAGG GTGAGCA GCT		
			CC GTCC TACTCGT CGA		
			— CAG— A		
GAM1689	KIAA1866	3'	AGCGTGCTCAGCCCCGCTGCC	60932	A GATGACAG
			GG CAG TGAGCACGCT		
			CC GTC ACTCGTGCGA		
			— GCCCG—		
GAM1689	KIAA1878	3'	GCACACTCTGTATCTCCTGTCC	91713	TG_ _ A
			GGACAGGA ACA GTG GC		
			CCTGTCCT TGT CAC CG		
			CTA CT A		
GAM1689	MGC24976	3'	GCACACTCTTCCATCCTGTCC	58115	AC_ A
			GGACAGGATG AGTG GC		
			CCTGTCCTAC TCAC CG		
			CTTC A		
GAM1689	PADI3	3'	GCTCCCACCCACCATCCTGTCC	32661	ACA_ _
			GGACAGGATG GT GAGC		
			CCTGTCCTAC CA CTCG		
			CACC CC		
GAM1689	PRO2521	3'	GCCACTACCATCCTGTC	37592	AC A
			GACAGGATG AGTG GC		
			CTGTCCTAC TCAC CG		
			CA _		
GAM1689	LOC144563	5'	AGCAAAACCGCCATCTTGTCC	76886	ACA AGCAC
			GGACAGGATG GTG GCT		
			CCTGTTCTAC CGC CGA		
			— CAAAA		
GAM1689	LOC145955	5'	GCTCACTGCCACCCTCC	83594	CA A A
			GGA GG TG CAGTGAGC		
			CCT CC AC GTCACG		
			— C C		
GAM1689	LOC147111	3'	TGCTCACTGCCCTCCTGCC	83949	A TGA
			GG CAGGA CAGTGAGCA		



CC GTCCT GTCAC TCGT  
 \_ CCC  
 GAM1689 LOC158969 3' CTCAC TGTCCCCATCC 82059 CA AT  
 GGA GG GACAGTGAG  
 ||| || |||||  
 CCT CC CTGTCACTC  
 AC C\_  
 GAM1689 LOC159765 5' GCTCAACCGTCATCCTCC 82197 CA AG\_  
 GGA GGATGAC TGAGC  
 ||| ||||| |||||  
 CCT CCTACTG ACTCG  
 \_ CCA  
 GAM1689 LOC163231 5' TGCTCACTGTCAACCCTCTCC 82445 C A  
 GGA AGG TGACAGTGAGCA  
 ||| ||| |||||  
 CCT TCC ACTGTCACTCGT  
 C C  
 GAM1689 LOC169436 5' AGCGTGCCCTGAAGCTCCTGTC 82738 TGA\_ TGA  
 C GGACAGGA CAG GCACGCT  
 ||||| ||| |||||  
 CCTGTCCT GTC CGTGCGA  
 CGAA C\_  
 GAM1690 ADAMTS8 5' TTTCTCTCTCTGATCC 22889 C G  
 GGA CAGAG AGAGAGA  
 ||| ||||| |||||  
 CCT GTCTC TCTCTT  
 A \_  
 GAM1690 APOB48R 3' CGGTGCTCTGGGAGCCAGGCC 37959 A AGA AGAG\_  
 GG CC GG AGAGCACCG  
 || || || |||||  
 CC GG CC TCTCGTGGC  
 \_ A\_ GAGGG  
 GAM1690 CACNG7 3' GCCCCTTTCCTCTGGCC 49095 A AGA  
 GG CCAGAGGAGAG GC  
 || ||||| ||  
 CC GGTCTCCTTTC CG  
 \_ CC\_  
 GAM1690 CNTN2 5' CTCTTCTCCTCCGATCC 17409 CCA G  
 GGA GAGGAGA AGAG  
 ||| ||||| |||||  
 CCT CTCCTCT TCTC  
 AGC \_  
 GAM1690 COL4A6 5' TCGGTGCTCCCTGGGCTGCTGG 8474 A AG\_ A  
 TCT GGACCAG GG AG GAGCACCGA  
 ||||| || || |||||  
 TCTGGTC TC TC CTCGTGGCT  
 G GGG C  
 GAM1690 COL6A1 3' CTCCCTCTCCTCTGTCC 8477 C A  
 GGAC AGAGGAGAG GAG  
 ||||| ||||| |||

			CCTG TCTCCTCTC CTC				
			- C				
GAM1690	EDNRA	3'	CGGGAATCTCTTCTCTGATCC	64107	C		GAGCA
			GGA CAGAGGAGAGA CCG				
			CCT GTCTCTTCTCT GGC				
			A AAG__				
GAM1690	EPO	5'	GCCCTCTCCTCCAGGCC	5854	A A_		AGA
			GG CC GAGGAGAG GC				
			CC GG CTCCTCTC CG				
			_ AC C_				
GAM1690	FAT2	3'	TCCCTCCCTCTGGTCC	7546		A A	
			GGACCAGAGG GAG GA				
			CCTGGTCTCC CTC CT				
			- C				
GAM1690	GFAP	3'	CTCCCTCCTCTGTCC	9013	C		A
			GGAC AGAGGAG GAG				
			CCTG TCTCCTC CTC				
			- C				
GAM1690	GTF2F1	3'	TCTCCTCCTCTGGCC	9157	A		A
			GG CCAGAGGAG GAGA				
			CC GGTCTCCTC CTCT				
			- -				
GAM1690	HLCS	3'	GTTTTCTCTCTTCCAGTCC	4674		CA	
			GGAC GAGGAGAGAGAGC				
			CCTG CTTCTCTCTTTTG				
			AC				
GAM1690	HNF4A	3'	GCCTTTCTCCTCCAACC	4854		ACCA	A
			GG GAGGAGAGAG GC				
			CC CTCCTCTTTC CG				
			AAC_ -				
GAM1690	HRY	5'	CTCTCTCCTTGGTCC	18637		G	
			GGACCA AGGAGAGAG				
			CCTGGT TCCTCTCTC				
			-				
GAM1690	KRT5	5'	TCGACAGCTCTCTCGCCCAGCC	4713		ACCAGA A	AC_
			GG GG GAGAGAGC CGA				
			CC CC CTCTCTCG GCT				
			GAC_ G ACA				
GAM1690	LAMP2	5'	TCAGTGCTCTTGACCCAGGTCC	9685		AGA AGA	C
			GGACC GG GAGAGCAC GA				

			CCTGG CC TTCTCGTG CT			
			AC_ AG_ A			
GAM1690 LAMP2	5'	TCAGTGCTCTTGACCCAGGTCC 25719		AGA AGA		C
		GGACC GG GAGAGCAC GA				
		CCTGG CC TTCTCGTG CT				
		AC_ AG_ A				
GAM1690 LFG	3'	CTCCTCTCCTCCGGGCC 76718	A A		A	
		GG CC GAGGAGAG GAG				
		CC GG CTCCTCTC CTC				
		G C _				
GAM1690 MAF	5'	CTCCCTCTCCTCCAGTC 18099	CA		A	
		GAC GAGGAGAG GAG				
		CTG CTCCTCTC CTC				
		AC C				
GAM1690 MAP4	3'	TGCCTCTCCCTCTGGTCC 9911		A A		
		GGACCAGAGG GAGAG GCA				
		CCTGGTCTCC CTCTC CGT				
		_ _				
GAM1690 MAP4	3'	TGCCTCTCCCTCTGGTCC 48062		A A		
		GGACCAGAGG GAGAG GCA				
		CCTGGTCTCC CTCTC CGT				
		_ _				
GAM1690 MDFI	3'	TGCCTCTCTCCTCCACCC 18774	ACCA		A	
		GG GAGGAGAGAG GCA				
		CC CTCCTCTCTC CGT				
		CAC_ _				
GAM1690 MFRP	3'	TGCCTCTCCTCTGGCC 48708	A		AGA	
		GG CCAGAGGAGAG GCA				
		CC GGTCTCCTCTC CGT				
		_ _				
GAM1690 MYO3A	3'	CGACGCTCTCTCTCGGA ACTCC 60137	CCAGAG			AC
		GGA GAGAGAGAGC CG				
		CCT CTCTCTCTCG GC				
		CAAGG_ CA				
GAM1690 NRXN2	5'	CTCTTCTCTCCTCCAGCC 57025	ACCA			_
		GG GAGGAGAGA GAG				
		CC CTCCTCTCT CTC				
		GAC_ T				
GAM1690 OTP	3'	GCCTCCCCTCCGGTCC 49500	A AGA A			
		GGACC GAGG GAG GC				

CCTGG CTCC CTC CG  
 C C\_\_ \_  
 GAM1690 PLOD3 3' GCCTCTCTCCTCCGCC 6554 ACCA A  
 GG GAGGAGAGAG GC  
 || ||||| ||  
 CC CTCCTCTCTC CG  
 GC\_\_ \_  
 GAM1690 PMM1 3' GGGCCCCTCCTCTGGCC 10669 A AGAGA A  
 GG CCAGAGGAG GC CC  
 || ||||| || ||  
 CC GGTCTCCTC CG GG  
 \_ CC\_\_ \_  
 GAM1690 PTPRA 3' CTCTCTCCCTGGTCC 11092 A  
 GGACCAG GGAGAGAG  
 ||||| |||||  
 CCTGGTC CCTCTCTC  
 \_  
 GAM1690 PTPRA 3' CTCTCTCCCTGGTCC 55082 A  
 GGACCAG GGAGAGAG  
 ||||| |||||  
 CCTGGTC CCTCTCTC  
 \_  
 GAM1690 PTPRA 3' CTCTCTCCCTGGTCC 55090 A  
 GGACCAG GGAGAGAG  
 ||||| |||||  
 CCTGGTC CCTCTCTC  
 \_  
 GAM1690 SERPINF2 3' TGTCTCCCTCCTCTGCC 6260 AC A G  
 GG CAGAGGAG GAGA CA  
 || ||||| || ||  
 CC GTCTCCTC CTCT GT  
 \_ C \_  
 GAM1690 SFRP5 3' TCGGCATAGACCCCTTCTGGT 11582 AGAGAGAGCA  
 CC GGACCAGAGG CCGA  
 ||||| ||||  
 CCTGGTCTTC GGCT  
 CCCAGATAC  
 GAM1690 SH2D1A 3' TCAGTGCAAATACTCTGGTCC 9851 GAGAGAGA C  
 GGACCAGAG GCAC GA  
 ||||| || ||  
 CCTGGTCTC CGTG CT  
 ATAAA\_\_ A  
 GAM1690 SLC25A17 5' CGGTGCTCCTTTCCTAACTCC 20996 CCAG A  
 GGA AGGAGAG GAGACCG  
 || ||||| |||||  
 CCT TCCTTTC CTCGTGGC  
 CAA\_\_ \_  
 GAM1690 SRC 3' CGGTGCTCCCTCTGTCATCC 18285 C\_\_ AGAGA  
 GGA CAGAGG GAGACCG  
 || ||||| |||||

CCT GTCTCC CTCGTGGC  
 ACT \_\_\_\_\_  
 GAM1690 ST5 3' GTGCTCTCTGGGCCTGGCTCC 18292 \_ AGGAG  
 GGA CCAG AGAGAGCAC  
 ||| ||| |||||  
 CCT GGTC TCTCTCGTG  
 C CGGG\_  
 GAM1690 ST5 3' GTGCTCTCTGGGCCTGGCTCC 57498 \_ AGGAG  
 GGA CCAG AGAGAGCAC  
 ||| ||| |||||  
 CCT GGTC TCTCTCGTG  
 C CGGG\_  
 GAM1690 TBL3 3' GCCTCTCTCCAGTCC 21266 CAGA A  
 GGAC GGAGAGAG GC  
 ||| ||||| ||  
 CCTG CCTCTCTC CG  
 A\_\_\_\_\_  
 GAM1690 TCIRG1 5' GTGCTCTCCCCAGGCTGGCC 20202 A AGGAGA  
 GG CCAG GAGAGCAC  
 || ||| |||||  
 CC GGTC CTCTCGTG  
 \_ GGACCC  
 GAM1690 TEM7 3' CTCTCTCTCCTCTAGTTC 39883 C  
 GGAC AGAGGAGAGAGAG  
 ||| |||||  
 CTTG TCTCCTCTCTCTC  
 A  
 GAM1690 TMC1 3' CTCTCTCCCCTGCTCC 56900 C A  
 GGA CAG GGAGAGAG  
 ||| ||| |||||  
 CCT GTC CCTCTCTC  
 C C  
 GAM1690 TRIM14 3' GTGCCTGGTGCTCTGGCC 28858 A GAGAG A  
 GG CCAGAG AG GCAC  
 || ||||| || |||  
 CC GGTCTC TC CGTG  
 \_ GTGG\_ \_  
 GAM1690 CCRN4L 5' TCGGTGCTCTCGGCCCCAGCC 24010 ACCAGA AGA  
 GG GG GAGAGCACCGA  
 || || |||||  
 CC CC CTCTCGTGGCT  
 GACC\_ GG\_  
 GAM1690 CHST3 3' TCATGGCTACCTCCTCTGACCC 14980 AC AGAG ACC  
 GG CAGAGGAG AGC GA  
 || ||||| ||| ||  
 CC GTCTCCTC TCG CT  
 CA CA\_ GTA  
 GAM1690 CHST3 3' TGCTCCCTCCTCTGTTCC 14982 C AGA  
 GGA CAGAGGAG GAGCA  
 ||| ||||| |||

CCT GTCTCCTC CTCGT  
 T C\_\_  
 GAM1690 DKFZP761D0211 3' CGGTGCCCTCTCCTTGCC 49352 ACCA AGA  
 GG GAGGAGAG GCACCG  
 || ||||| ||||  
 CC TTCCTCTC CGTGGC  
 G\_\_ C\_\_  
 GAM1690 DKK3 3' TCAGTGCTCTCTCCACTACCC 25134 ACCAG GA C  
 GG AG GAGAGAGCAC GA  
 || || ||||| ||  
 CC TC CTCTCTCGTG CT  
 CA\_\_ AC A  
 GAM1690 EZF-2 3' CTCTCCCTCCTCCATTCC 37099 CCA A  
 GGA GAGGAG GAGAG  
 ||| ||||| ||||  
 CCT CTCCTC CTCTC  
 TAC C  
 GAM1690 EZF-2 3' TTCTCTCTCCTGCGGCC 37105 A AG  
 GG CC AGGAGAGAGAG  
 || || ||||| ||||  
 CC GG TCCTCTCTCTT  
 \_ CG  
 GAM1690 FHX 3' CTTTCTCTCCTCAGTCC 37304 CA  
 GGAC GAGGAGAGAGAG  
 ||| ||||| ||||  
 CCTG CTCCTCTCTTTC  
 A\_  
 GAM1690 FLJ10193 3' CTCTCTCTCCTCCC 35884 ACCA  
 GG GAGGAGAGAGAG  
 || ||||| ||||  
 CC CTCCTCTCTCTC  
 \_\_\_\_\_  
 GAM1690 FLJ10901 3' GCTCTGTGCTCTGGTTC 36829 GAGAG  
 GGACCAGAG AGAGC  
 ||||| ||||  
 CTTGGTCTC TCTCG  
 GTG\_\_  
 GAM1690 FLJ11807 3' TCTCCCTCCTCTGCCCC 46354 AC A  
 GG CAGAGGAG GAGA  
 || ||||| ||||  
 CC GTCTCCTC CTCT  
 CC C  
 GAM1690 FLJ13117 3' GCCTCTCTCCTCTATCC 43543 CC A  
 GGA AGAGGAGAGAG GC  
 ||| ||||| ||||  
 CCT TCTCCTCTCTC CG  
 A\_ \_  
 GAM1690 FLN29 5' GCGTTTCTCCTCTCGTCC 21984 C GA  
 GGAC AGAGGAGAGA GC  
 ||| ||||| ||||

CCTG TCTCCTCTTT CG  
 C G\_  
 GAM1690 FREQ 3' CGATTTCCTCTCTGGTCC 26574 GGAGA A C\_  
 GGACCAGA GAG GCA CG  
 ||||| ||| ||  
 CCTGGTCT CTC CGT GC  
 \_\_\_\_\_ TTA  
 GAM1690 HINT1 5' CGAGCCTCTCCTCTGGCC 73218 A AGA AC  
 GG CCAGAGGAGAG GC CG  
 || ||||| || ||  
 CC GGTCTCCTCTC CG GC  
 \_\_\_\_\_ A\_  
 GAM1690 HSU79275 5' GCATTTCTCCTCTGGTC 66318 GA  
 GACCAGAGGAGAGA GC  
 ||||| ||  
 CTGGTCTCCTCTTT CG  
 A\_  
 GAM1690 IMP13 5' CTCTCTCTCCCGTGACCC 27731 AC GA  
 GG CA GGAGAGAGAG  
 || || |||||  
 CC GT CCTCTCTCTC  
 CA GC  
 GAM1690 IMUP 5' GCTCCTCCCCCTGCTCC 78596 C A A A  
 GGA CAG GG GAG GAGC  
 ||| || ||| |||  
 CCT GTC CC CTC CTCG  
 C \_ C \_  
 GAM1690 KIAA0275 3' GTGCCCTCTCCTCGATGCC 28687 ACCA AGA  
 GG GAGGAGAG GCAC  
 || ||||| |||  
 CC CTCCTCTC CGTG  
 GTAG C\_  
 GAM1690 KIAA0356 3' GTGCCTTTCTTGGCC 66196 A G AGA  
 GG CCA AGGAGAG GCAC  
 || ||| ||||| |||  
 CC GGT TCCTTTC CGTG  
 \_\_\_\_\_  
 GAM1690 KIAA0607 3' TGGTGCCTCCTCTGGCC 72572 A AGAGA  
 GG CCAGAGGAG GCACCG  
 || ||||| ||||  
 CC GGTCTCCTC CGTGGT  
 \_\_\_\_\_  
 GAM1690 KIAA0843 3' TCAGTGCTCTCTTGGGG 30115 AGAGGA C  
 CC GAGAGAGCAC GA  
 || ||||| ||  
 GG TTCTCTCGTG CT  
 GG\_\_\_\_\_ A  
 GAM1690 KIAA1115 3' TTCTCTCCTCTGGACC 30021 A  
 GG CCAGAGGAGAGAG  
 || ||||| |||||

CC GGTCTCCTCTCTT  
 A  
 GAM1690 KIAA1181 3' GTGCCCTGTCTCCTTTGGCC 68376 A G A  
 GG CCAGAGGAGA AG GCAC  
 || ||||| || ||||  
 CC GGTTTCCTCT TC CGTG  
 \_ G C  
 GAM1690 KIAA1199 3' CTGCTCTCTCCCTGGCC 72514 A A \_  
 GG CCAG GGAGAGAG AG  
 || ||| ||||| ||  
 CC GGTC CCTCTCTC TC  
 \_ \_ G  
 GAM1690 KIAA1271 3' TTCCCTCCCCTCTGGTCT 69555 A A  
 GGACCAGAGG GAG GAG  
 ||||| ||| |||  
 TCTGGTCTCC CTC CTT  
 C C  
 GAM1690 KIAA1364 3' CTCTCTCTCCACTGACCC 63591 AC A  
 GG CAG GGAGAGAGAG  
 || ||| |||||  
 CC GTC CCTCTCTCTC  
 CA A  
 GAM1690 KIAA1602 3' CTCTCTCTGCCCTGGTCC 64628 A \_  
 GGACCAG GG AGAGAGAG  
 ||||| || |||||  
 CCTGGTC CC TCTCTCTC  
 \_ G  
 GAM1690 KRT6IRS 3' GCTTTCCTCCTCTGCC 53089 AC A  
 GG CAGAGGAG GAGAGC  
 || ||||| |||||  
 CC GTCTCCTC CTTTCG  
 \_ \_  
 GAM1690 MGC14798 3' CTCCCTCTCCTTTAACC 54674 ACC A  
 GG AGAGGAGAG GAG  
 || ||||| |||  
 CC TTTCTCTC CTC  
 AA\_ C  
 GAM1690 MGC20235 3' GGGCCCTCTCTGGTCC 58902 GGAGA A A  
 GGACCAGA GAG GC CC  
 ||||| ||| |||  
 CCTGGTCT CTC CG GG  
 \_ \_ C \_  
 GAM1690 NCX 5' GCGGTTCTCCTCGGCC 32419 A A AGA  
 GG CC GAGGAGAG GC  
 || || ||||| ||  
 CC GG CTCCTCTT CG  
 \_ \_ GG\_  
 GAM1690 PDCD6IP 5' CTCTCTCTCCTCGGCC 82285 A A  
 GG CC GAGGAGAGAGAG  
 || || ||||| |||||



CC GG CTCCTCTCTCTC

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      - -
GAM1690 PDZ-  3' TCCCTCTCCTCTGCC    64999  AC    A
                GG CAGAGGAGAG GA
                || ||||| ||
                CC GTCTCCTCTC CT
                  - C
GAM1690 PDZ-  3' TTCCTTTCCTCTGGCC    65000  A      A
                GG CCAGAGGAGAG GAG
                || ||||| ||
                CC GGTCTCCTTTC CTT
                  - -
GAM1690 SDC3  5' TCGGTGCTCCCCCTCCCTGAAT 27766  C_ A  AGA
      CC      GGA CAG GGAG GAGCACCGA
                ||| ||| ||| |||||
                CCT GTC CCTC CTCGTGGCT
                AA _ CCC
GAM1690 SEMA7A 3' TGCAGCTCCCTCTCTGGTCC 13220      G A A_
                GGACCAGAG AG GAG GCA
                ||||| || ||| ||
                CCTGGTCTC TC CTC CGT
                  - C GA
GAM1690 SPEC1 5' CTCTCTCTCTGGTCC    39608      G
                GGACCAGAG AGAGAG
                ||||| |||||
                CCTGGTCTC TCTCTC
                  -
GAM1690 ST7L  3' GCCCTCTCTTTTCTATCC    34855  CC    A
                GGA AGAGGAGAGAG GC
                ||| ||||| ||
                CCT TCTTTTCTCTC CG
                A_ C
GAM1690 ST7L  3' GCCCTCTCTTTTCTATCC    56999  CC    A
                GGA AGAGGAGAGAG GC
                ||| ||||| ||
                CCT TCTTTTCTCTC CG
                A_ C
GAM1690 ST7L  3' GCCCTCTCTTTTCTATCC    57576  CC    A
                GGA AGAGGAGAGAG GC
                ||| ||||| ||
                CCT TCTTTTCTCTC CG
                A_ C
GAM1690 STAB2 3' GCTTCCTCCTCTGACCC    34114  AC    A G
                GG CAGAGGAG GA AGC
                || ||||| || ||
                CC GTCTCCTC CT TCG
                CA - -
GAM1690 TAF9L 5' CTCTCTCCTCTGGTCT    32003
                GGACCAGAGGAGAGAG
                ||||| |||||
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TCTGGTCTCCTCTCTC

GAM1690 TUBB5 3' GCTCCTACCTCTGACCC 20306 AC AG A  
GG CAGAGG AG GAGC  
|| ||||| || ||||  
CC GTCTCC TC CTCG  
CA A\_ \_

GAM1690 TUBB5 3' GCTCCTACCTCTGACCC 20307 AC AG A  
GG CAGAGG AG GAGC  
|| ||||| || ||||  
CC GTCTCC TC CTCG  
CA A\_ \_

GAM1690 LOC113763 3' GGTGCTCACCCTGCC 56581 AC A AGAGA  
GG CAG GG GAGCACC  
|| ||| || |||||  
CC GTC CC CTCGTGG  
\_ \_ A\_ \_

GAM1690 LOC126917 3' CTCCTCTCCTCTGACCC 74582 AC A  
GG CAGAGGAGAG GAG  
|| ||||| |||||  
CC GTCTCCTCTC CTC  
CA \_

GAM1690 LOC139770 5' GCCCCTCTCCTCGGCC 75388 A A AGA  
GG CC GAGGAGAG GC  
|| || ||||| ||  
CC GG CTCCTCTC CG  
\_ \_ CC\_

GAM1690 LOC144473 3' TTCCCTCTCCTTGGCC 83076 A G A  
GG CCA AGGAGAG GAG  
|| ||| ||||| |||||  
CC GGT TCCTCTC CTT  
\_ \_ C

GAM1690 LOC145693 3' TCTCTCTTCTCTGACCC 77354 AC  
GG CAGAGGAGAGAGA  
|| ||||| |||||  
CC GTCTCTTCTCTCT  
CA

GAM1690 LOC147299 3' TGCCTTCCTCTCCTCAGCC 78350 ACCA AG \_  
GG GAGGAGAG AG CA  
|| ||||| || ||  
CC CTCCTCTC TC GT  
GA\_ CT C

GAM1690 LOC149699 5' TCATCTCTCTTCTAATCC 79507 CC \_  
GGA AGAGGAGAGA GA  
||| ||||| |||||  
CCT TCTTCTCTCT CT  
AA A

GAM1690 LOC150527 5' GCCTCCCTCCTCTGGCC 79929 A A A  
GG CCAGAGGAG GAG GC  
|| ||||| ||||| ||

CC GGTCTCCTC CTC CG  
 \_ C \_  
 GAM1690 LOC151124 5' CGTGCCTACCTCTGGTCT 85227 AGAG A C  
 GGACCAGAGG AG GCAC G  
 ||||| |||||  
 TCTGGTCTCC TC CGTG C  
 A \_ \_ A  
 GAM1690 LOC151188 5' GCCTCTCCTTTGGCC 80160 A AGA  
 GG CCAGAGGAGAG GC  
 || ||||| ||  
 CC GGTTCCTCTC CG  
 \_ \_  
 GAM1690 LOC154877 3' CTCCCTGGCTTCTCTGCC 86293 AC \_ A  
 GG CAGAGGAG AG GAG  
 || ||||| |||||  
 CC GTCTCTTC TC CTC  
 \_ GG C  
 GAM1690 LOC158125 5' GGGCTCTCTCTAGTCC 81717 CAGAGG A  
 GGAC AGAGAGAGC CC  
 ||| ||||| ||  
 CCTG TCTCTCTCG GG  
 A \_ \_  
 GAM1690 LOC158549 3' GCCTCCCTCCCCTACTCC 86866 CC A A A  
 GGA AG GGAG GAG GC  
 ||| ||||| |||  
 CCT TC CCTC CTC CG  
 CA C C \_  
 GAM1690 LOC160646 5' CGGACTCTCTCTTCCAGCC 82226 ACCA AGCA  
 GG GAGGAGAGAG CCG  
 || ||||| |||  
 CC CTTCTCTCTC GGC  
 GAC\_ A\_  
 GAM1690 LOC165721 5' GTTCCCTCTCCTCTCACC 82603 ACC A  
 GG AGAGGAGAG GAGC  
 || ||||| |||||  
 CC TCTCCTCTC CTTG  
 AC\_ C  
 GAM1690 LOC199899 5' TCGGCTTGTCCCTCCTCTGG 89873 A G CA  
 CCAGAGGAG GA AG CCGA  
 ||||| || |||||  
 GGTCTCCTC CT TT GGCT  
 \_ G C\_  
 GAM1690 LOC220567 3' CGGTGCTCTGGGAGCCAGGCC 90737 A AGA AGAG\_  
 GG CC GG AGAGCACCG  
 || || |||||  
 CC GG CC TCTCGTGGC  
 \_ A\_ GAGGG  
 GAM1690 LOC221760 5' CGGTAACAAACCCCTGCCCTGG 93784 A A \_ AGAGAGC\_  
 CC GG CCAG GG AG ACCG  
 || |||| |||||

CC GGTC CC TC TGGC  
 \_ \_ G CCCAAACAA  
 GAM1690 LOC253430 5' CGGCGCCCCCTCCCTCGCCC 96237 ACCA A AGA A  
 GG GAGG GAG GC CCG  
 || |||| || ||||  
 CC CTCC CTC CG GGC  
 CG\_ \_ CCC C  
 GAM1690 LOC254299 3' TTCCCTCTCCTCCGGGCC 96550 A A A  
 GG CC GAGGAGAG GAG  
 || || |||| ||||  
 CC GG CTCCTCTC CTT  
 G C C  
 GAM1690 LOC254531 5' CTCTTTCTCCTCTGGCC 94984 A  
 GG CCAGAGGAGAGAGAG  
 || |||| |||| ||||  
 CC GGTCTCCTCTTTCTC  
 \_  
 GAM1690 LOC254559 3' GCATCTCTCCCCTCAGCC 96596 ACCA A \_  
 GG GAGG GAGAGA GC  
 || |||| |||| ||  
 CC CTCC CTCTCT CG  
 GA\_ C A  
 GAM1690 LOC257358 3' CTCTCTCTCCCCTCATCC 97099 CC A  
 GGA AG GGAGAGAGAG  
 || || |||| ||||  
 CCT TC CCTCTCTCTC  
 AC C  
 GAM1690 LOC257600 5' TCATCTCTCTCTGGTCC 97850 G \_  
 GGACCAGAG AGAGA GA  
 |||| |||| |||| ||  
 CCTGGTCTC TCTCT CT  
 \_ A  
 GAM1690 LOC51308 3' TGGGCCCCCTCTCCTCTGCCCC 33497 AC AGA A  
 GG CAGAGGAGAG GC CCG  
 || |||| |||| || ||||  
 CC GTCTCCTCTC CG GGT  
 CC CC\_ \_  
 GAM1690 LOC51659 3' CGGTGCTTATCCTCTAAGCC 32240 ACC GAGA  
 GG AGAGGA GAGCACCG  
 || |||| |||| ||||  
 CC TCTCCT TTCGTGGC  
 GAA A\_  
 GAM1690 LOC51659 3' CGGTGCTTATCCTCTAAGCC 94576 ACC GAGA  
 GG AGAGGA GAGCACCG  
 || |||| |||| ||||  
 CC TCTCCT TTCGTGGC  
 GAA A\_  
 GAM1690 LOC56959 5' GCCCCTCTCCTCTGCTCC 81926 C AGA  
 GGA CAGAGGAGAG GC  
 || |||| |||| || ||

			CCT GTCTCCTCTC	CG		
			C	CC_		
GAM1690	LOC90835	5'	GCGCCTCTCCTTAGTCC	64131	CA	AGA
			GGAC GAGGAGAG	GC		
			CCTG TTCCTCTC	CG		
			A_	CG_		
GAM1690	LOC90927	3'	TCAGTGCTCTCCCTCCTC	64429	A	C
			GAGGAG GAGAGCAC	GA		
			CTCCTC CTCTCGTG	CT		
			C	A		
GAM1690	LOC91149	3'	GTA CTCTCTCTTTTATC	65082	CC	A
			GA AGAGGAGAGAG	GC		
			CT TTTTCTCTCTC	TG		
			A_	A		
GAM1690	LOC91875	3'	TTCTCTCTCCTCTGTCC	67438	C	
			GGAC AGAGGAGAGAGAG			
			CCTG TCTCCTCTCTCTT			
			—			
GAM1690	LOC92303	3'	TGTTCTTCTCTCCTCTAATCC	68831	CC	—
			GGA AGAGGAGAGA	GAGCA		
			CCT TCTCCTCTCT	CTTGT		
			AA	T		
GAM1690	LOC92691	3'	CTCCCTCCTCTGGCC	56423	A	A
			GG CCAGAGGAG	GAG		
			CC GGTCTCCTC	CTC		
			—	C		
GAM1691	MAGEA12	5'	AGCACTAGCTCCTGCCACACT	18109	ATCGT	—
	C		GAGT	GTAG AGCTAGTGCT		
			CTCA	CGTC TCGATCACGA		
			CACC_	C		
GAM1691	MGC29898	3'	AGCACTAACTGTGGGTA CTCA	58926	GTG	G C
			TGAGTATC	TA AG TAGTGCT		
			ACTCATGG	GT TC ATCACGA		
			—	G A		
GAM1691	MMP24	3'	AGCACTAGCTCTCAT	21938	T	
			GTG AGAGCTAGTGCT			
			TAC TCTCGATCACGA			
			—			
GAM1691	LOC203411	5'	GCACTAGCTTTGACAT	90627	—	
			GTGT AGAGCTAGTGC			

			TACA TTTCGATCACG		
			G		
GAM1691	LOC91170	5'	GCACTAGCTAGAAACCTCA	65137	TATC GTAG
			TGAG GT AGCTAGTGC		
			ACTC CA TCGATCACG		
			____ AAGA		
GAM1692	DTNB	3'	TACTTAAACAGAGCTT	52499	ACA A C
			AAGC TC TGG TTTAAGTA		
			TTCG AG ACC AAATTCAT		
			____ _ A		
GAM1692	EIF2C1	3'	TGAAGCCATGATTACTTTA	24181	CAC
			TAAAG ATCATGGCTTTA		
			ATTTT TAGTACCGAAGT		
			AT_		
GAM1692	FLT1	3'	AGGCCATGATGGCCTTA	8912	A A
			TAA GC CATCATGGCTT		
			ATT CG GTAGTACCGGA		
			C _		
GAM1692	HTLF	3'	AAAGCCATAATGGACTT	9282	CA C
			AAG CAT ATGGCTTT		
			TTC GTA TACCGAAA		
			AG A		
GAM1692	P4HB	3'	TGAAACCATGATGTACTTT	6220	C C
			AAAG ACATCATGG TTTA		
			TTTC TGTAGTACC AAGT		
			A A		
GAM1692	PPP1R2	3'	CTATGACAAACGTGCTTTA	20690	A_____
			TAAAGCAC TCATGG		
			ATTTCTGTG AGTATC		
			CAAAC		
GAM1692	RNF28	3'	ACTCACAGGGACGATGTGCT	50860	ATGG A__
			AGCACATC CTTT AGT		
			TCGTGTAG GGG A TCA		
			CA__ CAC		
GAM1692	USH2A	5'	ACTTAAAGTACCCTGCTT	23062	CATCATG
			AAGCA GCTTTAAGT		
			TTCGT TGAAATTCA		
			CCCA__		
GAM1692	ZNF192	3'	ACTTAAAGTATTTATGCTT	20852	CATCATG
			AAGCA GCTTTAAGT		

		TTCGT	TGAAATTCA		
		ATTTA__			
GAM1692	ELL2	3'	ACTTAAAAGTTGTATGTGTTT 23869	C TG	_
			AAGCACAT A GCTTT AAGT		
			I		
			TTTGTGTA T TGAAA TTCA		
			_GT A		
GAM1692	FLJ23445	3'	TACATGACCATAATGTGTTT 89034	C CT A	
			AAGCACAT ATGG TTA GTA		
			TTTGTGTA TACC AGT CAT		
			A _ A		
GAM1692	HEI10	5'	TACCTAAAGCCTGGT 40999 T A		
			ATCA GGCTTTA GTA		
			TGGT CCGAAAT CAT		
			_ C		
GAM1692	KIAA0547	3'	ACTTAAAGCCAGGAGTTT 28906	ACA A	
			AAGC TC TGGCTTTAAGT		
			TTTG AG ACCGAAATTCA		
			_ G		
GAM1692	PRO1600	3'	ACTTAAAGGCCATATGACCTT 26032	CA C	_
			AAG CAT ATGGC TTTAAGT		
			TTC GTA TACCG AAATTCA		
			CA _ G		
GAM1692	LOC120196	3'	ACTTGTACATGTGCTTTA 75546	TCA GCTT	
			TAAAGCACA TG TAAGT		
			ATTTTCGTGT AC GTTCA		
			_ AT_		
GAM1692	LOC135307	3'	TACTTAAAGACAATGTCACTTT 75226	C_ CA G	
	A		TAAAG ACAT TG CTTTAAGTA		
			ATTTTC TGTA AC GAAATTCAT		
			AC _ A		
GAM1692	LOC257017	5'	TACTTAATTTCTTATTATGTGC 97377	A C CT_	
	CTTA		TAA GCACAT ATGG TTAAGTA		
			ATT CGTGTA TATT AATTCAT		
			C T CTTT		
GAM1692	LOC51336	5'	ACTTAGCATAATGTGC 33575	C GCT	
			GCACAT ATG TTAAGT		
			CGTGTA TAC GATTCA		
			A _		
GAM1693	ADAM12	3'	CAAAAGGGAACCCAGCT 12967	G	
			AGCTGGGT TTCTTTTGT		

TCGACCCA AGGGAAAAC

GAM1693 EMX2 3' CAAAAAGAATCAGGACTTGTA 87563 \_ GGGT  
TACAAG CT GTTCTTTTGT  
||||| || |||||||  
ATGTTC GG TAAGAAAAAC  
A AC\_

GAM1693 LTB4R 5' CAAAAAGATATCAGCATTGTA 5641 \_ GTGT  
TACAA GCTGG TCTTTTGT  
||||| ||| |||||||  
ATGTT CGACT AGAAAAAC  
A AT\_

GAM1693 CPR2 3' AGGCACACCCAGCCTGTA 48089 A T  
TACA GCTGGGTGT CTT  
||| ||||||| |||  
ATGT CGACCCACA GGA  
C C

GAM1693 MEP50 3' CAAAAATGCAGCCCAGCT 44081 GTTC  
AGCTGGGT TTTTGT  
||||| |||  
TCGACCCG AAAAAC  
ACGT

GAM1694 CENPF 3' TCTTCTAATTAACAGCTC 32966 CC  
GAGCTG AGTTAGAAGA  
||||| |||||||  
CTCGAC TTAATCTTCT  
AA

GAM1694 D10S170 3' AACCATCTCTAATAGCCAACTC 18365 C CCA A  
T AGAG TG GTTAGA GATGGTT  
||||| ||| |||||||  
TCTC AC TAATCT CTACCAA  
A CGA \_

GAM1694 SFRP4 3' AACCATCTCATTCTAACAGCT 11574 GCCA \_\_\_\_  
AGCT GTTAGA AGATGGTT  
||| ||| |||||||  
TCGA CAATCT TCTACCAA  
\_\_\_\_ TTAC

GAM1694 TYK2 5' AACCATCTTTTGATGGCA 59873 G  
TGCCA TTAGAAGATGGTT  
||||| |||||||  
ACGGT AGTTTTCTACCAA

GAM1694 WNT5A 3' CGTTTCCAAACGGCAGCTC 12664 A AGA  
GAGCTGCC GTT AGATG  
||||| ||| |||  
CTCGACGG CAA TTTGC  
\_ ACC

GAM1694 KIAA0218 3' AACCATCTCCTCTCCAGC 28616 CC TT A  
GCTG AG AG AGATGGTT  
||| || || |||||||



		CGAC TC TC TCTACCAA	
		C_ _ C	
GAM1694	LOC138835 5'	ACCATCTCCACGGCAGCTT 75952	A TAGA
		GAGCTGCC GT AGATGGT	
		TTCGACGG CA TCTACCA	
		_ CC_	
GAM1694	LOC149267 3'	ACCCTCTACCTGGCAGCTCT 56673	T AGAT
		AGAGCTGCCAG TAGA GGT	
		TCTCGACGGTC ATCT CCA	
		C C_	
GAM1694	LOC158263 5'	ACCACCCTTGGCAGCT 81842	GTT AAGA
		AGCTGCCA AG TGGT	
		TCGACGGT TC ACCA	
		_ CC_	
GAM1694	LOC162083 5'	AACCATCTGTAGTCAGCAGC 82332	CAG GA
		GCTGC TTA AGATGGTT	
		CGACG GAT TCTACCAA	
		ACT G_	
GAM1694	LOC199953 3'	CTTCCTACTGGCAGCTC 88504	TA
		GAGCTGCCAGT GAAG	
		CTCGACGGTCA CTTC	
		TC	
GAM1694	LOC222949 5'	AACCATCTCCCACCAGCTCT 94366	CCA TA A
		AGAGCTG GT GA GATGGTT	
		TCTCGAC CA CTCTACCAA	
		_ CC _	
GAM1695	ARF1 3'	TCGAAAAAGACAACCTCT 70660	ACC GTA
		AGAGGTTGT CTTT GA	
		TCTCCAACA GAAAA CT	
		_ AG_	
GAM1695	CDH15 3'	TTGTATGAAAGACAGCAACCTC 17030	ACC TG G
		GAGGTTGT CTTT TA AA	
		CTCCAACG GAAA AT TT	
		ACA GT G	
GAM1695	CNN1 3'	CTGTAGAACTCAACCTCT 7113	TACCC
		AGAGGTTG TTTTGTAG	
		TCTCCAAC AAGATGTC	
		TC_	
GAM1695	CTNNA2 3'	TCTACAAAAGCAAACCTCT 15246	G TACC
		AGAG TTG CTTTTGTAGA	

			TCTC AAC GAAAACATCT		
			A _____		
GAM1695	FBXW1B	3'	CTATAAAGTAAACCTCT 53339	G	CCT
			AGAGGTT TAC TTTGTAG		
			TCTCCAA ATG AAATATC		
			— —		
GAM1695	FBXW1B	3'	CTATAAAGTAAACCTCT 53328	G	CCT
			AGAGGTT TAC TTTGTAG		
			TCTCCAA ATG AAATATC		
			— —		
GAM1695	FBXW1B	3'	CTATAAAGTAAACCTCT 24524	G	CCT
			AGAGGTT TAC TTTGTAG		
			TCTCCAA ATG AAATATC		
			— —		
GAM1695	IL18R1	3'	CTACAAAAAGGGCGCATCT 13907	T TA	_
			AGGT G CCCTTTT GTAG		
			TCTA C GGGAAAA CATC		
			_ GC A		
GAM1695	MAFG	3'	CTGCAAAGCACAACCT 70096	ACCC	
			AGGTTGT TTTTGTAG		
			TCCAACA GAAACGTC		
			C_		
GAM1695	MTRR	3'	GAAAGATACAACCTTT 10132	CC	
			AGAGGTTGTA CTTTT		
			TTTCCAACAT GAAAG		
			A_		
GAM1695	MTRR	3'	GAAAGATACAACCTTT 43771	CC	
			AGAGGTTGTA CTTTT		
			TTTCCAACAT GAAAG		
			A_		
GAM1695	PLS1	3'	TTCTACAAAAGAGATTCT 10665	GTACC	
			AGAGGTT CTTTTGTAGAA		
			TCTTTAG GAAAACATCTT		
			A_		
GAM1695	PRDM4	3'	CTGCTCAAGGCACAACCTCT 24824	AC	TT
			AGAGGTTGT CCTT GTAG		
			TCTCCAACA GGAA CGTC		
			C_ CT		
GAM1695	SHOX	3'	CTGGAGAAGGGTAAACC 4836	G	G
			GGTT TACCCTTTT TAG		

CCAA ATGGGAAGA GTC  
 — G  
 GAM1695 SLC7A6 3' TCTGACCAGGTACAACACCT 14315 AG CTTTGTG  
 AG GTTGTACC TAGA  
 || ||||| |||  
 TC CAACATGG GTCT  
 CA ACCA\_\_  
 GAM1695 SMP1 3' CTACAACTGAGCACAACCTCT 26699 ACC \_\_  
 AGAGGTTGT CTT TTGTAG  
 ||||| || |||||  
 TCTCCAACA GAG AACATC  
 C\_\_ TC  
 GAM1695 SPON1 3' TTCAACAAAATACAATCTCT 62459 CCC A  
 AGAGGTTGTA TTTTGT GAA  
 ||||| ||||| |||  
 TCTCTAACAT AAAACA CTT  
 — A  
 GAM1695 TLR1 5' CTACAAAAGGAATCT 12313 GTAC  
 AGGTT CCTTTTGTAG  
 |||| |||||  
 TCTAA GGAAAACATC  
 —  
 GAM1695 C20orf21 3' CTACAAGCACACAACCTC 35111 ACCCT  
 GAGGTTGT TTTGTAG  
 ||||| |||||  
 CTCCAACA GAACATC  
 CAC\_\_  
 GAM1695 C20orf54 5' TCTACAAAAAGGTGCA 53009 C  
 TGTACC TTTTGTAGA  
 |||| |||||  
 ACGTGG AAAACATCT  
 A  
 GAM1695 C8orf14 5' TCTGCCTGGGCTCAACCTCT 54004 TA TTTT  
 AGAGGTTG CCC GTAGA  
 ||||| || |||||  
 TCTCCAAC GGG CGTCT  
 TC TC\_\_  
 GAM1695 CL24751 5' TTCTGTAGAAGATACCACCTCT 64690 T CC  
 AGAGGT GTA CTTTGTAGAA  
 |||| || |||||  
 TCTCCA CAT GAAGATGTCTT  
 C A\_  
 GAM1695 CSR1 3' CTGCAGAAGGGCCAACCCCT 32686 A TA  
 AG GGTG CCCTTTTGTAG  
 || |||| |||||  
 TC CCAAC GGGAAGACGTC  
 C C\_  
 GAM1695 DKFZP566M1046 5' CAGCCTGGTATAACCTCT 49534 CTT  
 AGAGGTTGTACC TTG  
 ||||| |||

TCTCCAATATGG GAC  
 TCC  
 GAM1695 DKFZP586M0622 3' TCTTATGAGAACACAACCTC 31487 ACC TTGT  
 GAGGTTGT CTT AGA  
 ||||| ||| |||  
 CTCCAACA GAG TCT  
 CAA TAT\_  
 GAM1695 FLJ14399 3' TCTACAAAAAATTAGCC 51332 TACCC  
 GGTTG TTTTGTAGA  
 |||| |||||  
 CCGAT AAAACATCT  
 TAAA\_  
 GAM1695 KIAA0455 3' TTCTAGAAAAACCAACCTCT 72471 TACCC G  
 AGAGGTTG TTTT TAGAA  
 ||||| ||| |||||  
 TCTCCAAC AAAA ATCTT  
 CA\_\_ G  
 GAM1695 KIAA0537 3' TCTACAGCACAACCTCT 29260 ACCCTT  
 AGAGGTTGT TTGTAGA  
 ||||| |||||  
 TCTCCAACA GACATCT  
 C\_\_\_\_  
 GAM1695 KIAA1161 5' CTATGAAATGAACACAACCTCT 81744 ACCC\_ TG  
 AGAGGTTGT TTT TAG  
 ||||| ||| |||  
 TCTCCAACA AAA ATC  
 CAAGT GT  
 GAM1695 LATS1 3' CTCCAAGAGGTACAACCT 60275 C T  
 GGTTGTACC TTTTG AG  
 ||||| |||| ||  
 TCAACATGG AGAAC TC  
 \_ C  
 GAM1695 LYPLA3 3' AAAAGGGTACAGCCTCT 24627  
 AGAGGTTGTACCCTTTT  
 |||||  
 TCTCCGACATGGGAAAA  
 GAM1695 MGC21621 5' TCCACAAAAGGAGGCCTC 58798 GTAC A  
 GAGGTT CCTTTTGT GA  
 |||| ||||| ||  
 CTCCGG GGAAAACA CT  
 A\_\_ C  
 GAM1695 OSBPL3 3' TAGAAAAAAATCAACCTCT 31438 TACCC G  
 AGAGGTTG TTTT TA  
 ||||| ||| ||  
 TCTCCAAC AAAA AT  
 TAAAA G  
 GAM1695 PMAIP1 3' CTACAAAAAGTGATCTCT 40890 TG ACCC  
 AGAGGT T TTTTGTAG  
 |||| | |||||

TCTCTA G AAAACATC  
 GT A\_\_\_\_  
 GAM1695 PRO1496 3' TCTACAAAAAATACAA 37761 CCC  
 TTGTA TTTTGTAGA  
 |||| |||||  
 AACAT AAAACATCT  
 AAA  
 GAM1695 PRO1855 3' TTCTGCTGGACACAACCTCT 37548 AC TTTT  
 AGAGGTTGT CC GTAGAA  
 ||||| || ||||  
 TCTCCAACA GG CGTCTT  
 CA T\_\_\_\_  
 GAM1695 SAC2 3' TCTACAAAAAATACAA 30058 CCC  
 TTGTA TTTTGTAGA  
 |||| |||||  
 AACAT AAAACATCT  
 AAA  
 GAM1695 SEMA4G 5' TCTATTGCAGCACAGCCTCT 94686 ACC TTT  
 AGAGGTTGT CT GTAGA  
 ||||| || ||||  
 TCTCCGACA GA TATCT  
 C\_\_ CGT  
 GAM1695 SPINLW1 3' TTCTACAAAGATTGTAAAACC 39873 A G C\_\_\_\_  
 CT AG GGTT TAC CTTTTGTAGAA  
 || |||| || |||||  
 TC CCAA ATG GAAAACATCTT  
 \_ A TTA  
 GAM1695 LOC128439 3' TAGGTCGGCACAGCCTCT 57354 A CT  
 AGAGGTTGT CC TTTG  
 ||||| || ||||  
 TCTCCGACA GG GGAT  
 C CT  
 GAM1695 LOC136319 3' TCTACAAAGGCCAACTCT 75260 G TACC  
 AGAG TTG CTTTTGTAGA  
 |||| || |||||  
 TCTC AAC GGAAACATCT  
 \_ C\_\_\_\_  
 GAM1695 LOC145438 5' TCCTCAGGTAGACACAGCCTCT 83344 ACCCT TA  
 AGAGGTTGT TTTG GA  
 ||||| |||| ||  
 TCTCCGACA GGAC CT  
 CAGAT TC  
 GAM1695 LOC146958 3' TCTACAAAAAATACAA 83882 CCC  
 TTGTA TTTTGTAGA  
 |||| |||||  
 AACAT AAAACATCT  
 AAA  
 GAM1695 LOC149073 5' TCTACACATACAACCT 84334 CCCTTT  
 AGGTTGTA TGTA  
 ||||| |||||

	TCCAACAT ACATCT	
	AC_____	
GAM1695 LOC158581 5'	CTGAAAAAGCACAACCTTC 86869	ACC G
	GAGGTTGT CTTTT TAG	
	CTTCAACA GAAAA GTC	
	C__ A	
GAM1695 LOC162333 5'	TTCTACAAAACCGAAAGCTCT 87146	G GTACCC
	AGAG TT TTTTGTAGAA	
	TCTC AA AAAACATCTT	
	G AGCC__	
GAM1695 LOC196746 3'	ACAAAACAGCAACAGCCTC 87510	ACCC_
	GAGGTTGT TTTTGT	
	CTCCGACA AAAACA	
	ACGAC	
GAM1695 LOC197201 3'	ATGAAAATACAACCTCT 87932	CCC TG
	AGAGGTTGTA TTT T	
	TCTCCAACAT AAA A	
	A__ GT	
GAM1695 LOC220522 3'	TCCTCAAAGGGTACAACCTTCT 60523	T TA
	AGAGGTTGTACCCTTT G GA	
	TCTTCAACATGGGAAA C CT	
	_TC	
GAM1695 LOC220766 5'	ACAAGAATCACAACCTC 90790	ACCC
	GAGGTTGT TTTTGT	
	CTCCAACA AGAACA	
	CTA_	
GAM1695 LOC253840 5'	TTCTACTGCTGCACAACCTC 96189	ACCCTTTT
	GAGGTTGT GTAGAA	
	CTCCAACA CATCTT	
	CGTCGT__	
GAM1695 LOC254556 3'	AGAGGACAACCTCT 94614	AC
	AGAGGTTGT CCTTT	
	TCTCCAACA GGAGA	
	—	
GAM1695 LOC91818 5'	TTCTAAAAGGATACAATCTCT 67273	C TG
	AGAGGTTGTA CCTTT TAGAA	
	TCTCTAACAT GGAAA ATCTT	
	A _	
GAM1696 ARHGEF12 3'	AGTAATTATGCTTCCTG 30994	T GA C
	CAG GAAGCA AAT ACT	

			GTC CTTCGT TTA TGA		
			— A_ A		
GAM1696	CHD2	3'	TGCTTTCTGTTTCACTG 7036	T	
			CAGTGAAGCAGAAA CA		
			GTCAC TTTGTCTTT GT		
			C		
GAM1696	DSC3	3'	AAAGCAACATCGTCTGCTTCAT 8671	AATCACTA	
			GTGAAGCAGA CTTT		
			TACTTCGTCT GAAA		
			GCTACAAC		
GAM1696	DSC3	3'	AAAGCAACATCGTCTGCTTCAT 44334	AATCACTA	
			GTGAAGCAGA CTTT		
			TACTTCGTCT GAAA		
			GCTACAAC		
GAM1696	EPB72	3'	GACTTCTGCTTACTG 14603	A A	
			CAGTGA GCAGAA TC		
			GTCATT CGTCTT AG		
			— C		
GAM1696	MTMR2	3'	GAAATCTTGCTTCACTG 32383	— AA	
			CAGTGAAGCA GA TC		
			GTCAC TTCGT CT AG		
			T AA		
GAM1696	NEDD4L	3'	GTGATTCTACTCAACT 30952	GA C	
			AGT AG AGAAATCAC		
			TCA TC TCTTTAGTG		
			AC A		
GAM1696	PABPC3	3'	AGAAATTTGTGCTTCAC 48276	G CA	
			GTGAAGCA AAAT CT		
			CACTTCGT TTTA GA		
			G AA		
GAM1696	PTP4A2	3'	AAAGTAGTGATGGATTCA 54414	GCAGAA	
			TGAA ATCACTACTTT		
			ACTT TAGTGATGAAA		
			AGG__		
GAM1696	PTP4A2	3'	AAAGTAGTGATGGATTCA 12979	GCAGAA	
			TGAA ATCACTACTTT		
			ACTT TAGTGATGAAA		
			AGG__		
GAM1696	RTN3	3'	AGTGGTTTCTACGTCACTG 73896	AGC	
			CAGTGA AGAAATCACT		

			GTCACT TCTTTGGTGA		
			GCA		
GAM1696	SPAG11	3'	AAAGTAGTGATTATGTCCAC 54240	AA	GA
			GTG GCA AATCACTACTTT		
			CAC TGT TTAGTGATGAAA		
			C_ A_		
GAM1696	SPAG11	3'	AAAGTAGTGATTATGTCCAC 54246	AA	GA
			GTG GCA AATCACTACTTT		
			CAC TGT TTAGTGATGAAA		
			C_ A_		
GAM1696	CHL1	3'	GGTGACTTTGCTTCACT 21749	AA	
			AGTGAAGCAGA TCACT		
			TCACTTCGTTT AGTGG		
			C_		
GAM1696	CL25084	3'	AAAGTCATGATAATTTCTGTCC 31655	AA	___ CT
			CACTG CAGTG GCAGAA ATCA ACTTT		
			GTCAC TGTCTT TAGT TGAAA		
			CC TAA AC		
GAM1696	FLJ13910	3'	TGATTCTGCTTCACTG 42931	A	
			CAGTGAAGCAGAA TCA		
			GTCACTTCGTCTT AGT		
			—		
GAM1696	FLJ20291	3'	AGTGACCCTGCTTCATTG 34865	AAA	
			CAGTGAAGCAG TCACT		
			GTTACTTCGTC AGTGA		
			CC_		
GAM1696	JAM1	3'	AAGTAGTAACTGCTACTG 57884	GA	AAATC
			CAGT AGCAG ACTACTT		
			GTCA TCGTC TGATGAA		
			___ AA___		
GAM1696	JAM1	3'	AAGTAGTAACTGCTACTG 57907	GA	AAATC
			CAGT AGCAG ACTACTT		
			GTCA TCGTC TGATGAA		
			___ AA___		
GAM1696	JAM1	3'	AAGTAGTAACTGCTACTG 57938	GA	AAATC
			CAGT AGCAG ACTACTT		
			GTCA TCGTC TGATGAA		
			___ AA___		
GAM1696	JAM1	3'	AAGTAGTAACTGCTACTG 33746	GA	AAATC
			CAGT AGCAG ACTACTT		



			GTCA TCGTC TGATGAA		
			— AA—		
GAM1696	KIAA0256	3'	AAAGTTAGATTTCTGCTTCA 64414	ACT	
			TGAAGCAGAAATC ACTTT		
			ACTTCGTCTTTAG TGAAA		
			AT_		
GAM1696	KIAA0561	3'	AAGTTTGAATTTTCAGCTTCACT 65869	A _ CT	
	G		CAGTGAAGC GAAAT CA ACTT		
			GTCACTTCG CTTTA GT TGAA		
			A A T_		
GAM1696	KIAA1034	3'	TGATTTCTGCTTCACT 62471		
			AGTGAAGCAGAAATCA		
			TCACTTCGTCTTTAGT		
GAM1696	LAGY	3'	AGCAGTGGCTTCACTG 57631	AGAAAT A	
			CAGTGAAGC CACT CT		
			GTCACTTCG GTGA GA		
			_____ C		
GAM1696	LAGY	3'	AGCAGTGGCTTCACTG 50673	AGAAAT A	
			CAGTGAAGC CACT CT		
			GTCACTTCG GTGA GA		
			_____ C		
GAM1696	LAGY	3'	AGCAGTGGCTTCACTG 57630	AGAAAT A	
			CAGTGAAGC CACT CT		
			GTCACTTCG GTGA GA		
			_____ C		
GAM1696	PCMF	3'	AGGGGTGATCTCTGCTTCCTG 73578	T A TA	
			CAG GAAGCAGA ATCAC CT		
			GTC CTTCGTCT TAGTG GA		
			_ C GG		
GAM1696	TEB4	3'	TGAAC TTATGCTTCACTG 60657	G _	
			CAGTGAAGCA AAA TCA		
			GTCACTTCGT TTT AGT		
			A CA		
GAM1696	LOC124538	5'	AAAGTAGTGA CTTCATGTATC 75647	A _ A	
			GA GCA GAA TCACTACTTT		
			CT TGT CTT AGTGATGAAA		
			A A C		
GAM1696	LOC133088	5'	AAAGTAATGATTCATGGATTCA 75076	G_ GA C	
			TGAA CA AATCA TACTTT		

ACTT GT TTAGT ATGAAA  
 AG AC A  
 GAM1696 LOC196955 5' AAGTACCTCTGCTTCCTG 77358 T AATCAC  
 CAG GAAGCAGA TACTT  
 ||| ||||| ||||  
 GTC CTTCGTCT ATGAA  
 \_ CC\_\_\_\_  
 GAM1696 LOC221830 3' AGTTGTTCTGTTCACTG 92505 G ATC  
 CAGTGAA CAGAA ACT  
 ||||| |||| ||  
 GTCAC TT GTCTT TGA  
 \_ GT\_  
 GAM1696 LOC51018 3' AAAGGATATATTTCTGCTTGAC 32124 G CACTA  
 GT AAGCAGAAAT CTTT  
 || ||||| ||||  
 CA TTCGTCTTTA GAAA  
 G TATAG  
 GAM1697 A1BG 3' GCATGAGCCACCATGCCTGGC 55420 TG CA C  
 GC GGCA GTGGCTCA GC  
 || ||| ||||| ||  
 CG CCGT CACCGAGT CG  
 GT AC A  
 GAM1697 ADAMTS4 3' GCGTGAGCCACCGTGCCTGGC 17508 TG A  
 GC GGCAC GTGGCTCACGC  
 || |||| ||||| ||  
 CG CCGTG CACCGAGTGCG  
 GT C  
 GAM1697 ADCY6 5' CGTGAGCCACCACGCCTGGC 30929 TG ACA  
 GC GGC GTGGCTCACG  
 || ||| ||||| ||  
 CG CCG CACCGAGTGC  
 GT CAC  
 GAM1697 ADCY6 5' GCGCCCGCCACCACGCCCGGCT 30931 ACA TCA  
 AGCTGGGC GTGGC CGC  
 ||||| |||| ||  
 TCGGCCCG CACCG GCG  
 CAC CCC  
 GAM1697 ADRA1A 3' GCGTGAGCCACCGTGCCCGGC 52787 A  
 GCTGGGCAC GTGGCTCACGC  
 ||||| ||||| ||  
 CGGCCCGTG CACCGAGTGCG  
 C  
 GAM1697 ALOX15 3' GCCATCATGCCAGCT 6685 CA  
 AGCTGGGCA GTGGC  
 ||||| ||||  
 TCGACCCGT TACCG  
 AC  
 GAM1697 AMFR 3' GCCCTGTGCCCGACTGA 6695 C T  
 TCAG TGGGCACAG GGC  
 ||| ||||| ||

			AGTC GCCCGTGTGTC CCG			
			A _			
GAM1697	AMFR	3'	GCCCTGTGCCCGACTGA 57245	C	T	
			TCAG TGGGCACAG GGC			
			AGTC GCCCGTGTGTC CCG			
			A _			
GAM1697	APAF1	3'	GCGTGAGCCACCGTGCCTGGC 6731	TG	A	
			GC GGCAC GTGGCTCACGC			
			CG CCGTG CACCGAGTGCG			
			GT C			
GAM1697	APAF1	3'	GCGTGAGCCACCGTGCCTGGC 25040	TG	A	
			GC GGCAC GTGGCTCACGC			
			CG CCGTG CACCGAGTGCG			
			GT C			
GAM1697	APM1	3'	GCATGAGCCACCATGCCAGTC 16593	A	CA	C
	GA		TC GCTGGGCA GTGGCTCA GC			
			AG TGACCCGT CACCGAGT CG			
			C AC A			
GAM1697	APM1	3'	GCCACTGCGCCAGCT 16594	A		
			AGCTGGGC CAGTGGC			
			TCGACCCG GTCACCG			
			C			
GAM1697	APOL1	3'	GCGCCTACCACCATGCCAGCT 13347	CA	CTCA	
			AGCTGGGCA GTGG CGC			
			TCGACCCGT CACC GCG			
			AC ATCC			
GAM1697	APPL	3'	GCGTGAGCCACCGTGCCCGGC 23927	A		
			GCTGGGCAC GTGGCTCACGC			
			CGGCCCGTG CACCGAGTGCG			
			C			
GAM1697	AQP6	3'	GCGCCTGCCACCACGCCAGCT 53928	ACA	TCA	
			AGCTGGGC GTGGC CGC			
			TCGACCCG CACCG GCG			
			CAC TCC			
GAM1697	AQP6	3'	GCGTGAGCCACCGTGCCCGGC 53929	A		
			GCTGGGCAC GTGGCTCACGC			
			CGGCCCGTG CACCGAGTGCG			
			C			
GAM1697	AQP6	3'	GCGCCTGCCACCACGCCAGCT 7952	ACA	TCA	
			AGCTGGGC GTGGC CGC			

			TCGACCCG CACCG GCG		
			CAC TCC		
GAM1697	AQP6	3'	GCGTGAGCCACCGTGCCCCGGC 7953	A	
			GCTGGGCAC GTGGCTCACGC		
			CGGCCCGTG CACCGAGTGCG		
			C		
GAM1697	ARCN1	3'	GCATGAGCCACCATGCCCAGCT 7979	CA	C
	G		CAGCTGGGCA GTGGCTCA GC		
			GTCGACCCGT CACCGAGT CG		
			AC A		
GAM1697	ATM	3'	GCATGAGCTACTATGCCCA 56304	C	C
			TGGGCA AGTGGCTCA GC		
			ACCCGT TCATCGAGT CG		
			A A		
GAM1697	ATP1B2	3'	GCATGTGCCACCATGCCCGGCT 8050	CA	T C
			AGCTGGGCA GTGGC CA GC		
			TCGGCCCGT CACCG GT CG		
			AC T A		
GAM1697	ATP6V1A1	3'	GCATGCTCCACCATGCCCAGCT 8078	CA	CT C
			AGCTGGGCA GTGG CA GC		
			TCGACCCGT CACC GT CG		
			AC TC A		
GAM1697	ATP6V1A1	3'	GCGTGAGCCACCGCGCCTGGC 8079	TG	ACA
			GC GGC GTGGCTCACGC		
			CG CCG CACCGAGTGCG		
			GT CGC		
GAM1697	ATP8B2	3'	GCGTGAGCCACCACACCCAGCT 65225	CACA	
			AGCTGGG GTGGCTCACGC		
			TCGACCC CACCGAGTGCG		
			ACAC		
GAM1697	AXL	3'	GCATGAGCCACTGCACTCA 8100	CA	C
			TGGG CAGTGGCTCA GC		
			ACTC GTCACCGAGT CG		
			AC A		
GAM1697	AXL	3'	GCATGAGCCACTGCACTCA 41597	CA	C
			TGGG CAGTGGCTCA GC		
			ACTC GTCACCGAGT CG		
			AC A		
GAM1697	C7	3'	TGAACCACCACGCCTGGCTGG 5169	TG	ACA C
			TCAGC GGC GTGG TCA		

			GGTCG CCG CACC AGT		
			GT CAC A		
GAM1697	CAMLG	3'	GCATGCACCACCACGCCAGCT 8239	ACA	CT C
			AGCTGGGC GTGG CA GC		
			TCGACCCG CACC GT CG		
			CAC AC A		
GAM1697	CASP2	3'	GCCACCGTGCCCGGCT 6899	A	
			AGCTGGGCAC GTGGC		
			TCGGCCCGTG CACCG		
			C		
GAM1697	CASP2	3'	GCGTGAGCCACTGCGCCCGGGC 6900	_	A
			GCT GGGC CAGTGGCTCACGC		
			CGG CCCG GTCACCGAGTGCG		
			G C		
GAM1697	CASP2	3'	GCCACCGTGCCCGGCT 52141	A	
			AGCTGGGCAC GTGGC		
			TCGGCCCGTG CACCG		
			C		
GAM1697	CASP2	3'	GCGTGAGCCACTGCGCCCGGGC 52142	_	A
			GCT GGGC CAGTGGCTCACGC		
			CGG CCCG GTCACCGAGTGCG		
			G C		
GAM1697	CASP2	3'	GCCACCGTGCCCGGCT 52154	A	
			AGCTGGGCAC GTGGC		
			TCGGCCCGTG CACCG		
			C		
GAM1697	CASP2	3'	GCGTGAGCCACTGCGCCCGGGC 52155	_	A
			GCT GGGC CAGTGGCTCACGC		
			CGG CCCG GTCACCGAGTGCG		
			G C		
GAM1697	CASP2	3'	GCCACCGTGCCCGGCT 52169	A	
			AGCTGGGCAC GTGGC		
			TCGGCCCGTG CACCG		
			C		
GAM1697	CASP2	3'	GCGTGAGCCACTGCGCCCGGGC 52170	_	A
			GCT GGGC CAGTGGCTCACGC		
			CGG CCCG GTCACCGAGTGCG		
			G C		
GAM1697	CASP8	3'	GCGTGAGCCACCGCGCCTGGCC 52922	A TG	ACA
	GA		TC GC GGC GTGGCTCACGC		

			AG CG CCG CACCGAGTGCG		
			C GT CGC		
GAM1697	CASP8	3'	GCGTGAGCCACCGCGCCTGGCC 52933	A TG	ACA
	GA		TC GC GGC GTGGCTCACGC		
			AG CG CCG CACCGAGTGCG		
			C GT CGC		
GAM1697	CASP8	3'	GCGTGAGCCACCGCGCCTGGCC 52947	A TG	ACA
	GA		TC GC GGC GTGGCTCACGC		
			AG CG CCG CACCGAGTGCG		
			C GT CGC		
GAM1697	CASP8	3'	GCGTGAGCCACCGCGCCTGGCC 6916	A TG	ACA
	GA		TC GC GGC GTGGCTCACGC		
			AG CG CCG CACCGAGTGCG		
			C GT CGC		
GAM1697	CBFA2T2	3'	CTGAGCCACTGTGTCCGG 17465		C
			CTGGGCACAGTGGCTCA G		
			GGCCTGTGTCACCGAGT C		
			A		
GAM1697	CDC6	3'	GCGTGAGCCACCATGCTCAGC 6983	CA	
			GCTGGGCA GTGGCTCACGC		
			C GACTCGT CACCGAGTGCG		
			AC		
GAM1697	CDH1	3'	TGAGCCACTGCACCTGCCAG 15151	_____	
			CTGGGCA CAGTGGCTCA		
			GACCCGT GTCACCGAGT		
			CCAC		
GAM1697	CHRN4	3'	GCCACCGTGCCCAGCT 5632	A	
			AGCTGGGCAC GTGGC		
			TCGACCCGTG CACCG		
			C		
GAM1697	CHST6	3'	GCATGAGCCACTGTACCTGGC 41231	TG C	C
			GC GG ACAGTGGCTCA GC		
			CG CC TGTCACCGAGT CG		
			GT A A		
GAM1697	CIAS1	5'	GCGTGAGCCACTGTGCCCGGC 16900		
			GCTGGGCACAGTGGCTCACGC		
			CGGCCCGTGTACCGAGTGCG		
GAM1697	CLECSF12	3'	GCGTGAGCCACTGCACCCAGC 76691	CA	
			GCTGGG CAGTGGCTCACGC		

		CGACCC GTCACCGAGTGCG		
		AC		
GAM1697 COX15	3'	GCATGGGCCACACGCCAGCT 54315	ACA	C
		AGCTGGGC GTGGCTCA GC		
		TCGACCCG CACCGGGT CG		
		CAC A		
GAM1697 CR1	3'	GCATGAGCCACCGCGCCTGGC 5134	TG ACA	C
		GC GGC GTGGCTCA GC		
		CG CCG CACCGAGT CG		
		GT CGC A		
GAM1697 CRTAP	3'	GCATGTGCCACACGCCCGGCT 21034	ACA	T C
		AGCTGGGC GTGGC CA GC		
		TCGGCCCG CACCG GT CG		
		CAC T A		
GAM1697 CRTAP	3'	GCGTGAGCCACCATGCCCGGC 21035	CA	
		GCTGGGCA GTGGCTCACGC		
		CGGCCCGT CACCGAGTGCG		
		AC		
GAM1697 CSRP1	3'	GCATGGGCTGTACCCAAGCTGA 14532	_ C GTG	C
		TCAGCT GGG ACA GCTCA GC		
		AGTCGA CCC TGT CGGGT CG		
		A A _ A		
GAM1697 CYP2B6	3'	GCGTGAGTCACCGTGCCCAGC 5732	A	
		GCTGGGCAC GTGGCTCACGC		
		CGACCCGTG CACTGAGTGCG		
		C		
GAM1697 CYP8B1	3'	GCATGAGCCACTGTGCCAGT 15263		C
		GCTGGGCACAGTGGCTCA GC		
		TGACCCGTGTCACCGAGT CG		
		A		
GAM1697 DDX3	3'	CCACGCACACCCGTGCCAGCC 43757	_ A_ _ _ TCAC	
TGA		AG CTGGGCAC GTG GC G		
		TC GACCCGTG CAC CG C		
		C CC A    CACT		
GAM1697 DFFB	3'	GCATGAGCCACTGCACCTGACC 87384	CT_ CA	C
TG		CAG GGG CAGTGGCTCA GC		
		GTC TCC GTCACCGAGT CG		
		CAG AC A		
GAM1697 DFFB	3'	GCATGTGCCACACGCCCGGCT 87385	ACA	T C
		AGCTGGGC GTGGC CA GC		

		TCGGCCCG CACCG GT CG	
		CAC T A	
GAM1697 DHFR	3'	GCGCGCCACCACGCCCGGCT 5806	ACA TCA
		AGCTGGGC GTGGC CGC	
		TCGGCCCG CACCG GCG	
		CAC C__	
GAM1697 DISC1	3'	GTGAGCCACCGCACCCGGC 37891	CACA
		GCTGGG GTGGCTCAC	
		CGGCC CACCGAGTG	
		ACGC	
GAM1697 DLEC1	3'	GCGCACCCAGGCCAGCTGA 23702	ACA_ ____
		TCAGCTGGGC GTG GC	
		AGTCGACCCG CAC CG	
		GACC G	
GAM1697 DNASE1L1	5'	GCATGAGCCACCACGCCAGC 22076	ACA C
		GCTGGGC GTGGCTCA GC	
		CGACCCG CACCGAGT CG	
		CAC A	
GAM1697 DSC3	3'	GCGCCCACCACCACGCCCGGCT 8676	ACA CTCA
		AGCTGGGC GTGG CGC	
		TCGGCCCG CACC GCG	
		CAC ACCC	
GAM1697 DSC3	3'	GCGCCCACCACCACGCCCGGCT 44341	ACA CTCA
		AGCTGGGC GTGG CGC	
		TCGGCCCG CACC GCG	
		CAC ACCC	
GAM1697 DSCR3	5'	CGTGAGCCACTGCCGGC 20178	GCA
		GCTGG CAGTGGCTCACG	
		CGGCC GTCACCGAGTGC	
		_____	
GAM1697 DSCR3	3'	GCCACCGTGCCCGGCT 20181	A
		AGCTGGGCAC GTGGC	
		TCGGCCCGTG CACCG	
		C	
GAM1697 EDG8	3'	GCATGCACCACCATGCCAGTT 78478	CA CT C
		AGCTGGGCA GTGG CA GC	
		TTGACCCGT CACC GT CG	
		AC AC A	
GAM1697 EHD2	3'	GCATGAGCCACCGTGCCCGGCT 27494	A C
		AGCTGGGCAC GTGGCTCA GC	



			TCGGCCCGTG CACCGAGT CG		
			C A		
GAM1697	EIF2S3	3'	GCGTGAGCCACCTTGCCCAGC 7417	CA	
			GCTGGGCA GTGGCTCACGC		
			CGACCCGT CACCGAGTGCG		
			TC		
GAM1697	EPB72	3'	GCCACCATGCCCAGCT 14604	CA	
			AGCTGGGCA GTGGC		
			TCGACCCGT CACCG		
			AC		
GAM1697	F2RL2	3'	GCGTGAGCCACTGAGCCAGC 14623	G A	
			GCTGG C CAGTGGCTCACGC		
			CGACC G GTCACCGAGTGCG		
			_ A		
GAM1697	F3	3'	GCGTGAACCACCATGCCCAGCC 67080	A CA C	
	GA		TC GCTGGGCA GTGG TCACGC		
			AG CGACCCGT CACC AGTGCG		
			C AC A		
GAM1697	FANCF	3'	GCGTGAGCCACCGCGCCTGGC 42674	TG ACA	
			GC GGC GTGGCTCACGC		
			CG CCG CACCGAGTGCG		
			GT CGC		
GAM1697	FANCF	3'	GGCCACCATGCCC GGCT 42677	CA	
			AGCTGGGCA GTGGCT		
			TCGGCCCGT CACCGG		
			AC		
GAM1697	FCAR	3'	GCATGAGCCACCACGCCTGGC 55749	TG ACA C	
			GC GGC GTGGCTCA GC		
			CG CCG CACCGAGT CG		
			GT CAC A		
GAM1697	FCAR	3'	GCATGAGCCACCACGCCTGGC 55760	TG ACA C	
			GC GGC GTGGCTCA GC		
			CG CCG CACCGAGT CG		
			GT CAC A		
GAM1697	FCAR	3'	GCATGAGCCACCACGCCTGGC 55771	TG ACA C	
			GC GGC GTGGCTCA GC		
			CG CCG CACCGAGT CG		
			GT CAC A		
GAM1697	FCAR	3'	GCATGAGCCACCACGCCTGGC 55782	TG ACA C	
			GC GGC GTGGCTCA GC		

		CG CCG CACCGAGT CG		
		GT CAC A		
GAM1697 FCAR	3'	GCGTGAGCCACCGCGCCTGGC 55800	TG ACA	
		GC GGC GTGGCTCACGC		
		CG CCG CACCGAGTGCG		
		GT CGC		
GAM1697 FCAR	3'	GCATGAGCCACCACGCCTGGC 8854	TG ACA C	
		GC GGC GTGGCTCA GC		
		CG CCG CACCGAGT CG		
		GT CAC A		
GAM1697 FUT1	3'	GCATGAGCCACTGTGCCCAGC 3788		C
		GCTGGGCACAGTGGCTCA GC		
		CGACCCGTGTCACCGAGT CG		
		A		
GAM1697 FUT1	3'	GCGCCCGCCACCACGCCCCGGCT 3790	ACA TCA	
		AGCTGGGC GTGGC CGC		
		TCGGCCCG CACCG GCG		
		CAC CCC		
GAM1697 FUT1	3'	GCGTGAGCCACCATGCCTGGC 3791	TG CA	
		GC GGCA GTGGCTCACGC		
		CG CCGT CACCGAGTGCG		
		GT AC		
GAM1697 FZD4	3'	GCGTGCTACCACGCCAGCT 24141	ACA CT_	
		AGCTGGGC GTGG CACGC		
		TCGACCCG CACC GTGCG		
		____ ATC		
GAM1697 GFAP	3'	GCCACCATGCCCAGCT 9017	CA	
		AGCTGGGCA GTGGC		
		TCGACCCGT CACCG		
		AC		
GAM1697 GM2A GA	3'	GCATGAGCCACTACACCCAGCC 67778	A CAC C	
		TC GCTGGG AGTGGCTCA GC		
		AG CGACCC TCACCGAGT CG		
		C ACA A		
GAM1697 GNE	3'	TGCACCACGCCCGGCTGA 18485	ACA CT	
		TCAGCTGGGC GTGG CA		
		AGTCGGCCCG CACC GT		
		____ AC		
GAM1697 GPR81 T	3'	GCGCCCCACCACCACGCCCGGC 50759	ACA CTCA_	
		AGCTGGGC GTGG CGC		

			TCGGCCCG CACC GCG		
			CAC ACCCC		
GAM1697	GPR81	3'	GCGTGAGCCACCGTGCCCGGC 50760	A	
			GCTGGGCAC GTGGCTCACGC		
			CGGCCCGTG CACCGAGTGCG		
			C		
GAM1697	GPRK6	3'	GCACACATGTGCCCAGC 9111	-	_____
			GCTGGGCACA GTG GC		
			CGACCCGTGT CAC CG		
			A A		
GAM1697	GRM7	5'	GCATGAGTCACCATATCCAGC 5945	CACA	C
			GCTGGG GTGGCTCA GC		
			CGACCT CACTGAGT CG		
			ATAC A		
GAM1697	HCS	3'	GCATGCGCCACCATGCCCAGCT 38470	CA	T C
			AGCTGGGCA GTGGC CA GC		
			TCGACCCGT CACCG GT CG		
			AC C A		
GAM1697	HCS	3'	GCCACCATGCCCAGCT 38472	CA	
			AGCTGGGCA GTGGC		
			TCGACCCGT CACCG		
			AC		
GAM1697	HCS	3'	GCGTGAGCCACCACGCCTGGC 38473	TG	ACA
			GC GGC GTGGCTCACGC		
			CG CCG CACCGAGTGCG		
			GT CAC		
GAM1697	HLCS	5'	GCTACCATGCCCGGCT 4667	CA	
			AGCTGGGCA GTGGC		
			TCGGCCCGT CATCG		
			AC		
GAM1697	HSD17B1	5'	GCATGAGCCACCGTGCCCAGC 4687	A	C
			GCTGGGCAC GTGGCTCA GC		
			CGACCCGTG CACCGAGT CG		
			C A		
GAM1697	HTR1D	3'	CGTGTGTCACCAGGCCCAGCT 5995	ACA	T
			AGCTGGGC GTGGC CACG		
			TCGACCCG CACTG GTGC		
			GAC T		
GAM1697	HTR1D	3'	GCATGAGCCACTGTGCCTGGC 5997	TG	C
			GC GGCACAGTGGCTCA GC		

		CG CCGTGTACCGAGT CG	
		GT A	
GAM1697	HYAL4	5' GCCATCATGCCCAGCTGA 24374	CA
		TCAGCTGGGCA GTGGC	
		AGTCGACCCGT TACCG	
		AC	
GAM1697	ICMT	3' GCGTGAGCCACCACGCCCAGC 24815	ACA
		GCTGGGC GTGGCTCACGC	
		CGACCCG CACCGAGTGCG	
		CAC	
GAM1697	IL4R	3' GCACACCCATGCCAGCTG 4702	CA_ ____
		CAGCTGGGCA GTG GC	
		GTCGACCCGT CAC CG	
		ACC A	
GAM1697	INMT	3' GCCACCATGCCCGGCT 22272	CA
		AGCTGGGCA GTGGC	
		TCGGCCCGT CACCG	
		AC	
GAM1697	INMT	3' GCGTGAGCCACCGCACCCAGC 22273	CACA
		GCTGGG GTGGCTCACGC	
		CGACCC CACCGAGTGCG	
		ACGC	
GAM1697	KCNJ16	5' CCATTGCCAGCTGA 37854	CA
		TCAGCTGGGCA GTGG	
		AGTCGACCCGT TACC	
		—	
GAM1697	LLGL1	3' GCGCCCACCACGCCCAGCT 66878	ACA CTCA
		AGCTGGGC GTGG CGC	
		TCGACCCG CACC GCG	
		CAC ACCC	
GAM1697	LYZ	3' GCGCCCGCCACCACGCCCAGCT 4101	ACA TCA
		AGCTGGGC GTGGC CGC	
		TCGGCCCG CACCG GCG	
		CAC CCC	
GAM1697	LYZ	3' GCGTGAGCCACTGCGCCCGGC 4102	A
		GCTGGGC CAGTGGCTCACGC	
		CGGCCCG GTCACCGAGTGCG	
		C	
GAM1697	MEFV	3' GCATGAGCCACCATGCCTGGC 4137	TG CA C
		GC GGCA GTGGCTCA GC	

			CG CCGT CACCGAGT CG		
			GT AC A		
GAM1697	MEFV	3'	GCATGAGCCACTGTGCCCGGC 4138	C	
			GCTGGGCACAGTGGCTCA GC		
			CGGCCCGTGTACCGAGT CG		
			A		
GAM1697	MEFV	3'	GCGCCCGCCACCATGCCCGGCT 4140	CA	TCA
			AGCTGGGCA GTGGC CGC		
			TCGGCCCGT CACCG GCG		
			AC CCC		
GAM1697	MHC2TA	3'	GCGTGAGCCACTGCACCGGGC 4175	G	CA
			GCT GG CAGTGGCTCACGC		
			CGG CC GTCACCGAGTGCG		
			G AC		
GAM1697	MLANA	3'	GCGTGAGCCACCACGCCTGGCT 18587	TG	ACA
	GG		TCAGC GGC GTGGCTCACGC		
			GGTCG CCG CACCGAGTGCG		
			GT CAC		
GAM1697	MPL	3'	GCATGAGCCACTGCGCCCGGCT 18143	A	C
	GA		TCAGCTGGGC CAGTGGCTCA GC		
			AGTCGGCCCG GTCACCGAGT CG		
			C A		
GAM1697	MYCL2	3'	GCGCCTGCCACCACGCCTAGCT 18182	ACA	TCA
			AGCTGGGC GTGGC CGC		
			TCGATCCG CACCG GCG		
			CAC TCC		
GAM1697	ORC1L	3'	GCCACCATGCCCAGCTGA 14737	CA	
			TCAGCTGGGCA GTGGC		
			AGTCGACCCGT CACCG		
			AC		
GAM1697	PAICS	3'	TGAGCCACTGTGCCTGTCT 21263	C	
			AG TGGGCACAGTGGCTCA		
			TC GTCCGTGTCACCGAGT		
			T		
GAM1697	PCDHA9	3'	GCGTGAGCCACCGCGCCTGGC 25763	TG	ACA
			GC GGC GTGGCTCACGC		
			CG CCG CACCGAGTGCG		
			GT CGC		
GAM1697	PCDHB9	3'	GCATGAGCCACCGCACCCAGC 38939	CACA	C
			GCTGGG GTGGCTCA GC		

			CGACCC CACCGAGT CG		
			ACGC A		
GAM1697	PDE6B	3'	GCATGAGCCACCACGCCCAGC 4280	ACA	C
			GCTGGGC GTGGCTCA GC		
			CGACCCG CACCGAGT CG		
			CAC A		
GAM1697	PER2	3'	GCGTGAGCCACCACGCCCAACT 43035	C	ACA
	GG		TCAG TGGGC GTGGCTCACGC		
			GGTC ACCCG CACCGAGTGCG		
			A CAC		
GAM1697	PIGR	3'	CGTGAGCCACCGCGTCCGG 72598	ACA	
			CTGGGC GTGGCTCACG		
			GGCCTG CACCGAGTGC		
			CGC		
GAM1697	PIK3C2B	3'	GCGTGAGCCACCATGCCCCGC 10570	T	CA
			GC GGGCA GTGGCTCACGC		
			CG CCCGT CACCGAGTGCG		
			C AC		
GAM1697	PIK3CD	3'	GCATGAGCCACCACGCCCGGC 17245	ACA	C
			GCTGGGC GTGGCTCA GC		
			CGGCCCG CACCGAGT CG		
			CAC A		
GAM1697	PLA2G10	5'	GCGTGAGTCACCGCGCCCGGC 13088	ACA	
			GCTGGGC GTGGCTCACGC		
			CGGCCCG CACTGAGTGCG		
			CGC		
GAM1697	PLA2G2D	3'	CCATCTGTGCCTCAGCTGA 24790	—	—
			TCAGCTG GGCACAG TGG		
			AGTCGAC CCGTGTC ACC		
			T T		
GAM1697	POU2AF1	3'	GCGTGAGCCACCGCACCCAGC 20653	CACA	
			GCTGGG GTGGCTCACGC		
			CGACCC CACCGAGTGCG		
			ACGC		
GAM1697	PPEF2	3'	GCATGAGCCACCGCACCCAGC 20671	CACA	C
			GCTGGG GTGGCTCA GC		
			CGACCC CACCGAGT CG		
			ACGC A		
GAM1697	PPID	3'	CGTGCCACCACGCCCAGCT 87431	ACA	TC
			AGCTGGGC GTGGC ACG		

			TCGACCCG CACCG TGC			
			CAC _			
GAM1697	PPID	3'	GTGAGCCACCGTGCCCGGC 87436	A		
			GCTGGGCAC GTGGCTCAC			
			CGGCCCGTG CACCGAGTG			
			C			
GAM1697	PRKR	3'	GCATGTGCCACCCACCCAACT 10882	C	CACA	T C
			AG TGGG GTGGC CA GC			
			TC ACCC CACCG GT CG			
			A ACC_ T A			
GAM1697	PSMD9	3'	GCGTGAGCCACTGCGCCCAGC 10986	A		
			GCTGGGC CAGTGGCTCACGC			
			CGACCCG GTCACCGAGTGCG			
			C			
GAM1697	PTGIS	3'	GCATGAGCCACCATGCCCGGC 6333	CA		C
			GCTGGGCA GTGGCTCA GC			
			CGGCCCGT CACCGAGT CG			
			AC A			
GAM1697	PTGIS	3'	GTGAGCCACCGCGCCCAGC 6339	ACA		
			GCTGGGC GTGGCTCAC			
			CGACCCG CACCGAGTG			
			CGC			
GAM1697	RABL2A	3'	GCATGAGCCACCGCGCCCAGC 25502	ACA		C
			GCTGGGC GTGGCTCA GC			
			CGGCCCG CACCGAGT CG			
			CGC A			
GAM1697	RABL2B	3'	GCATGAGCCACCGCGCCCAGC 23001	ACA		C
			GCTGGGC GTGGCTCA GC			
			CGGCCCG CACCGAGT CG			
			CGC A			
GAM1697	RAI3	3'	GCGTGAGCCACAGCTCCCAGC 14285	CACA		
			GCTGGG GTGGCTCACGC			
			CGACCC CACCGAGTGCG			
			TCGA			
GAM1697	RBBP9	3'	GCATGAGCCACCATGCCCGGC 70133	CA		C
			GCTGGGCA GTGGCTCA GC			
			CGGCCCGT CACCGAGT CG			
			AC A			
GAM1697	RBM8A	3'	GCCACCATGCCAGCT 17546	CA		
			AGCTGGGCA GTGGC			

		TCGACCCGT CACCG		
		AC		
GAM1697 RHD	3'	GTGAGCCACCGTGCCCAGC 32312	A	
		GCTGGGCAC GTGGCTCAC		
		CGACCCGTG CACCGAGTG		
		C		
GAM1697 RHD	3'	GTGAGCCACCGTGCCCAGC 32621	A	
		GCTGGGCAC GTGGCTCAC		
		CGACCCGTG CACCGAGTG		
		C		
GAM1697 RPP30	3'	TGAGCCACCACATGCAGCCAG 21174	__ CA__	
		CTGG GCA GTGGCTCA		
		GACC CGT CACCGAGT		
		GA ACAC		
GAM1697 SAS	3'	GCGTGAGCCACCACGCCCCGC 19954	T ACA	
		GC GGC GTGGCTCACGC		
		CG CCG CACCGAGTGCG		
		C CAC		
GAM1697 SCML2	3'	GCATGAGCCACCTGCCCAGC 20318	CA C	
		GCTGGGCA GTGGCTCA GC		
		CGACCCGT CACCGAGT CG		
		C_ A		
GAM1697 SCNN1G	3'	AGCCACCGTGCCCAGC 6429	A	
		GCTGGGCAC GTGGCT		
		CGACCCGTG CACCGA		
		C		
GAM1697 SEDL	3'	GCATGAACCACCGTGCCCGGC 27337	A C C	
		GCTGGGCAC GTGG TCA GC		
		CGGCCCGTG CACC AGT CG		
		C A A		
GAM1697 SEDL	3'	GCGTGAGCCACCGTGCCCA 27339	A	
		TGGGCAC GTGGCTCACGC		
		ACCCGTG CACCGAGTGCG		
		C		
GAM1697 SEDL	3'	GCGTGCCACCACGCCCGGCT 27340	ACA TC	
		AGCTGGGC GTGGC ACGC		
		TCGGCCCG CACCG TGCG		
		CAC _		
GAM1697 SERPINB9	3'	GCGCCCGCCACCACGCCCGGCT 14756	ACA TCA	
		AGCTGGGC GTGGC CGC		



			TCGGCCCG	CACCG	GCG		
			CAC	CCC			
GAM1697	SIGLEC11	3'	CGTGAGCCACCACAGCTGGCTG	53543		TG GCACA	
	A		TCAGC	G	GTGGCTCACG		
			AGTCG	C	CACCGAGTGC		
			GT	GACAC			
GAM1697	SIL	5'	GCGTGAGCCACCGCCCCTGA	11690	CT	ACA	
			TCAG	GGGC	GTGGCTCACGC		
			AGTC	CCCG	CACCGAGTGCG		
			—	C—			
GAM1697	SIL	3'	GCGTGAGCCACTGCCCAGCT	11691		CA	
			AGCTGGGCA	GTGGCTCACGC			
			TCGACCCGT	CACCGAGTGCG			
			—				
GAM1697	SLC17A5	3'	GCATGAGCCACTGTGCCAGC	24891		C	
			GCTGGGCACAGTGGCTCA	GC			
			CGACCCGTGTCACCGAGT	CG			
			A				
GAM1697	SLC39A1	5'	GCGCGAGCCACTGCGTCCGGCC	27052	A	A	A
	GG		TC	GCTGGGC	CAGTGGCTC	CGC	
			GG	CGGCCTG	GTCACCGAG	GCG	
			C	C	C		
GAM1697	SLC7A7	5'	AGATACTGCACTCAGCTGA	14291	CA	G	
			TCAGCTGGG	CAGTG	CT		
			AGTCGACTC	GTCAT	GA		
			AC	A			
GAM1697	SMAC	5'	GCGCCCGCCACCACGCCCGGCT	57211	ACA	TCA	
			AGCTGGGC	GTGGC	CGC		
			TCGGCCCG	CACCG	GCG		
			CAC	CCC			
GAM1697	SNAP23	3'	GCGTGAGCCACTGTGCCTGGCT	13810	TG		
	GA		TCAGC	GGCACAGTGGCTCACGC			
			AGTCG	CCGTGTCACCGAGTGCG			
			GT				
GAM1697	SNAP23	3'	GCGTGAGCCACTGTGCCTGGCT	55463	TG		
	GA		TCAGC	GGCACAGTGGCTCACGC			
			AGTCG	CCGTGTCACCGAGTGCG			
			GT				
GAM1697	SPN	3'	CCACCATGCCCAGCTG	11918	CA		
			CAGCTGGGCA	GTGG			

			GTCGACCCGT CACC		
			AC		
GAM1697	TAPBP	3'	GCGTGAGCCACCGCGCCCGGCT 12127	ACA	
	G		CAGCTGGGC GTGGCTCACGC		
			GTCGGCCCG CACCGAGTGCG		
			CGC		
GAM1697	TAT	3'	GCGTGAGCCACCATGCCCGGCT 4469	CA	
			AGCTGGGCA GTGGCTCACGC		
			TCGGCCCGT CACCGAGTGCG		
			AC		
GAM1697	TBXA2R	3'	GCGCGCCACCACGCCCGGCT 6493	ACA	TCA
			AGCTGGGC GTGGC CGC		
			TCGGCCCG CACCG GCG		
			CAC C__		
GAM1697	TBXA2R	3'	GCGTAAGCCACTGCGCCCGGC 6494	A	C
			GCTGGGC CAGTGGCT ACGC		
			CGGCCCG GTCACCGA TGCG		
			C A		
GAM1697	TDGF1	3'	GCATGTGTCACCATGCCCAGCT 12199	CA	T C
			AGCTGGGCA GTGGC CA GC		
			TCGACCCGT CACTG GT CG		
			AC T A		
GAM1697	TERF1	3'	CGTGAGCCACTGCGTCCTGC 33971	T	A
			GC GGC CAGTGGCTCACG		
			CG CCTG GTCACCGAGTGC		
			T C		
GAM1697	TERF2	3'	GCATGAGCCACCGCGCCTGGC 18947	TG	ACA C
			GC GGC GTGGCTCA GC		
			CG CCG CACCGAGT CG		
			GT CGC A		
GAM1697	TIM3	3'	GCATGCACCACCATGCCCAGCT 51344	CA	CT C
			AGCTGGGCA GTGG CA GC		
			TCGACCCGT CACC GT CG		
			AC AC A		
GAM1697	TIM3	3'	GCGTGAGCCACCACATCCAGC 51345	CACA	
			GCTGGG GTGGCTCACGC		
			CGACCT CACCGAGTGCG		
			ACAC		
GAM1697	TIMP3	3'	GCACACAAGTGCCCGAGC 4510	_	A_ ____
			GC TGGGCAC GTG GC		

		CG ACCCGTG CAC CG		
		G AA AIII		
GAM1697	TNFRSF10B 3'	GCGTGAGCCACCAGCCAGGC 13870	G ACA	
		GCT GGC GTGGCTCACGC		
		CGG CCG CACCGAGTGCG		
		A AC_		
GAM1697	TPMT 3'	GCGTGAGCCACTGCACCTGGC 4540	TG CA	
		GC GG CAGTGGCTCACGC		
		CG CC GTCACCGAGTGCG		
		GT AC		
GAM1697	UMPS 3'	GTGAGCCACTGTGCCCAGC 4554		
		GCTGGGCACAGTGGCTCAC		
		CGACCCGTGTCACCGAGTG		
GAM1697	VENTX2 3'	GCATGAGCCACTGCACCCGGC 27113	CA C	
		GCTGGG CAGTGGCTCA GC		
		CGGCCG GTCACCGAGT CG		
		AC A		
GAM1697	VIPR2 3'	GCGTGAGCCACTGCGCCCGGC 12612	A	
		GCTGGGC CAGTGGCTCACGC		
		CGGCCG GTCACCGAGTGCG		
		C		
GAM1697	WBSCR5 5'	CGTGAGCCACCGCTCCTGG 41857	CT ACA	
		TCAG GGGC GTGGCTCACG		
		GGTC CTCG CACCGAGTGC		
		_ C_		
GAM1697	WHSC1 5'	GCATGAGCCACCGTGCCT 29910	A C	
		GGGCAC GTGGCTCA GC		
		TCCGTG CACCGAGT CG		
		C A		
GAM1697	WHSC1 5'	GCATGAGCCACCGTGCCT 23663	A C	
		GGGCAC GTGGCTCA GC		
		TCCGTG CACCGAGT CG		
		C A		
GAM1697	WHSC1 5'	GCATGAGCCACCGTGCCT 55829	A C	
		GGGCAC GTGGCTCA GC		
		TCCGTG CACCGAGT CG		
		C A		
GAM1697	WHSC1 5'	GCATGAGCCACCGTGCCT 55846	A C	
		GGGCAC GTGGCTCA GC		

			TCCGTG CACCGAGT CG		
			C A		
GAM1697 XRCC2	3'	GCGTGAGCCACTGCTCGTGGCC 18324	G	_____	
A		TGG CAC AGTGGCTCACGC			
		ACC GTG TCACCGAGTGCG			
		G CTCG			
GAM1697 YES1	3'	GCGTGAGCCACCGCGCCCAGC 18353	ACA		
		GCTGGGC GTGGCTCACGC			
		CGACCCG CACCGAGTGCG			
		CGC			
GAM1697 ZNF133	5'	GCATGAGCCACTGCGCCCAGCC 12837	A	A	C
GA		TC GCTGGGC CAGTGGCTCA GC			
		AG CGACCCG GTCACCGAGT CG			
		C C A			
GAM1697 ZNF137	3'	TGAACCACTATGCCCCGGCT 12868	C	C	
		AGCTGGGCA AGTGG TCA			
		TCGGCCCCG TCACC AGT			
		A A			
GAM1697 AAK1	3'	GTGAGCCACCATGCCCAGC 29853	CA		
		GCTGGGCA GTGGCTCAC			
		CGACCCGT CACCGAGTG			
		AC			
GAM1697 AD7C-NTP	3'	GCGTGAGCCACCTACCCAGCC 27164	A	CACA	
GG		TC GCTGGG GTGGCTCACGC			
		GG CGACCC CACCGAGTGCG			
		C ACTC			
GAM1697 APOL2	3'	GCACCTGCCACCACGCCCGGCT 48047	ACA	TCAC	
		AGCTGGGC GTGGC GC			
		TCGGCCCCG CACCG CG			
		CAC TCCA			
GAM1697 APOL2	3'	GCGTGAGCCACCGCGCCTGGC 48048	TG	ACA	
		GC GGC GTGGCTCACGC			
		CG CCG CACCGAGTGCG			
		GT CGC			
GAM1697 APXL2	5'	GCGTGTGCCACCACGCCAGCT 75190	ACA	T	
		AGCTGGGC GTGGC CACGC			
		TCGACCCG CACCG GTGCG			
		CAC T			
GAM1697 ARHF	3'	GCGTGAGCCACCGTGCCCGGC 38744	A		
		GCTGGGCAC GTGGCTCACGC			

CGGCCCGTG CACCGAGTGCG  
 C  
 GAM1697 ARHGAP11A 3' GCATGAGCCACCACGCCCGGCT 28795 ACA C  
 AGCTGGGC GTGGCTCA GC  
 ||||| ||||| ||  
 TCGGCCCG CACCGAGT CG  
 CAC A  
 GAM1697 ARHGAP5 5' GCGTGAGCCACTGCACCTGGC 77076 TG CA  
 GC GG CAGTGGCTCACGC  
 || || |||||  
 CG CC GTCACCGAGTGCG  
 GT AC  
 GAM1697 ARPP-19 3' GCGTCCGCCACCATGCCCAGC 21797 CA TC  
 GCTGGGCA GTGGC ACGC  
 ||||| |||| |||  
 CGACCCGT CACCG TGCG  
 AC CC  
 GAM1697 ASB16 3' GCATGAGCCACTGCGCCTGGTT 55107 TG A C  
 G CAGC GGC CAGTGGCTCA GC  
 ||| || ||||| ||  
 GTTG CCG GTCACCGAGT CG  
 GT C A  
 GAM1697 ASE-1 3' GTGAGCCACCGCACCTGC 23952 T CACA  
 GC GGG GTGGCTCAC  
 || || |||||  
 CG CCC CACCGAGTG  
 T ACGC  
 GAM1697 ATP1B4 3' GCGTGAGCCACCGCACCCGGCT 23820 CACA  
 AGCTGGG GTGGCTCACGC  
 ||||| |||||  
 TCGGCCCG CACCGAGTGCG  
 ACGC  
 GAM1697 BA108L7.2 3' GCATGAGCCACTGTGCCCAGC 48262 C  
 GCTGGGCACAGTGGCTCA GC  
 ||||| ||||| ||  
 CGACCCGTGTCACCGAGT CG  
 A  
 GAM1697 BM-002 3' GCATGCACCACCACGCCCAGCT 33524 ACA CT C  
 AGCTGGGC GTGG CA GC  
 ||||| ||| ||  
 TCGACCCG CACC GT CG  
 CAC AC A  
 GAM1697 C11orf17 3' GCGTGAGCCACCGCGCCCGGC 40211 ACA  
 GCTGGGC GTGGCTCACGC  
 ||||| |||||  
 CGGCCCG CACCGAGTGCG  
 CGC  
 GAM1697 C20orf142 3' GCATGAGCCACCGCGCCCGGCT 74776 ACA C  
 AGCTGGGC GTGGCTCA GC  
 ||||| ||||| ||

			TCGGCCCG	CACCGAGT	CG		
			CGC	A			
GAM1697	C20orf173	3'	AGCTCAGCCTAGCTGA	55059		ACAGT	
			TCAGCTGGGC	GGCT			
			AGTCGATCCG	TCGA			
			AC__				
GAM1697	C20orf59	3'	CCACTGTGGAGCCTGA	41993	_	GGG	
			TCAGCT	CACAGTGG			
			AGTCGA	GTGTCACC			
			C	G__			
GAM1697	C22orf19	3'	GCATGAGCCACCACACCCGGC	13423		CACA	C
			GCTGGG	GTGGCTCA	GC		
			CGGCC	CACCGAGT	CG		
			ACAC	A			
GAM1697	C3F	3'	GCCACCATGCCCAGCT	19290		CA	
			AGCTGGGCA	GTGGC			
			TCGACCCGT	CACCG			
			AC				
GAM1697	C3F	3'	GCGTGAGCCACCGTGCCCGGC	19291		A	
			GCTGGGCAC	GTGGCTCACGC			
			CGGCCCGTG	CACCGAGTGCG			
			C				
GAM1697	C6orf5	3'	GCGCCTGCCACCATGCCCAGCT	31350		CA	TCA
			AGCTGGGCA	GTGGC	CGC		
			TCGACCCGT	CACCG	GCG		
			AC	TCC			
GAM1697	C6orf5	3'	GTGAGCCACCACACCCAGC	31360		CACA	
			GCTGGG	GTGGCTCAC			
			CGACCC	CACCGAGTG			
			ACAC				
GAM1697	C9orf14	5'	GCGTGAGCCACCGCGCCCGGC	86677		ACA	
			GCTGGGC	GTGGCTCACGC			
			CGGCCCG	CACCGAGTGCG			
			CGC				
GAM1697	CCRN4L	3'	GCGCCCGTCACCACGCCCAGCT	24008		ACA	TCA
			AGCTGGGC	GTGGC	CGC		
			TCGACCCG	CACTG	GCG		
			CAC	CCC			
GAM1697	CDC14B	3'	GCGTCTGCCACCACGCCCGGCT	52855		ACA	TC
			AGCTGGGC	GTGGC	ACGC		

			TCGGCCCG CACCG TGCG		
			CAC TC		
GAM1697	CDV-1	3'	GAGCCACCATGCCAGCT 48905	CA	
			AGCTGGGCA GTGGCTC		
			TCGACCCGT CACCGAG		
			AC		
GAM1697	CECR1	3'	GCATGTGCCACCACCCAGCT 33815	CACA	T C
	GA		TCAGCTGGG GTGGC CA GC		
			AGTCGACCC CACCG GT CG		
			ACAC T A		
GAM1697	CECR1	3'	TGAGCCACCACACTCAGC 33822	CACA	
			GCTGGG GTGGCTCA		
			CGACTC CACCGAGT		
			ACAC		
GAM1697	CENPH	3'	GCCGCCATGCCAGCT 43274	CA	
			AGCTGGGCA GTGGC		
			TCGACCCGT CGCCG		
			AC		
GAM1697	CIP29	3'	GCACACCTGGCCCAGCT 50404	A	_ _ _ _
			AGCTGGGC CAG TG GC		
			TCGACCCG GTC AC CG		
			_ C A		
GAM1697	CPSF2	3'	CGTGAGCCACTGCTCCTGG 61579	TG	CA
			C GG CAGTGGCTCACG		
			G CC GTCACCGAGTGC		
			GT TC		
GAM1697	CPSF2	3'	GCATGCACCACCACGCCAGCT 61587	ACA	CT C
			AGCTGGGC GTGG CA GC		
			TCGACCCG CACC GT CG		
			CAC AC A		
GAM1697	CSL4	3'	GCATGAACCACTGTGCTTGGC 32113	TG	C C
			GC GGCACAGTGG TCA GC		
			CG TCGTGTACC AGT CG		
			GT A A		
GAM1697	DBR1	3'	GCGTGAGCCACTGTGCCTGGCC 32533	A	TG
	GA		TC GC GGCACAGTGGCTCACGC		
			AG CG CCGTGTACCGAGTGCG		
			C GT		
GAM1697	DDX34	3'	GCGTGAGCCACTGCACCCGGC 27985	CA	
			GCTGGG CAGTGGCTCACGC		

	CGGCCC GTCACCGAGTGCG		
	AC		
GAM1697 DKFZp434A2417 3'	GCGTGAGCCACTGCACCTGGC	66103	TG CA
	GC GG CAGTGGCTCACGC		
	CG CC GTCACCGAGTGCG		
	GT AC		
GAM1697 DKFZP434B044 3'	GCATGAGCCACTGCGCCCGGC	48925	A C
	GCTGGGC CAGTGGCTCA GC		
	CGGCCCG GTCACCGAGT CG		
	C A		
GAM1697 DKFZP434B044 3'	GCGTGAGCTACCATGCCCGGCT	48926	CA
	AGCTGGGCA GTGGCTCACGC		
	TCGGCCCGT CATCGAGTGCG		
	AC		
GAM1697 DKFZP434C212 3'	GCGTGAACCACCCTGCCCAGC	68911	CA C
	GCTGGGCA GTGG TCACGC		
	CGACCCGT CACC AGTGCG		
	CC A		
GAM1697 DKFZP434D146 3'	GCATGAGCCACCGTGCCCAGC	31524	A C
	GCTGGGCAC GTGGCTCA GC		
	CGACCCGTG CACCGAGT CG		
	C A		
GAM1697 DKFZP434J037 3'	GCGCCCGCCACCATGCCCGGCT	48214	CA TCA
	AGCTGGGCA GTGGC CGC		
	TCGGCCCGT CACCG GCG		
	AC CCC		
GAM1697 DKFZP434J037 3'	GCGTGAGCCACCGCGCCC	48215	ACA
	GGGC GTGGCTCACGC		
	CCCG CACCGAGTGCG		
	CGC		
GAM1697 DKFZP564G092 5'	GCGTGAGCCACTGCGCCCAGC	31537	A
	GCTGGGC CAGTGGCTCACGC		
	CGACCCG GTCACCGAGTGCG		
	C		
GAM1697 DKFZp761J139 5'	GCGTGAGCCACCATAACCGGC	50110	CACA
	GCTGGG GTGGCTCACGC		
	CGGCC CACCGAGTGCG		
	ATAC		
GAM1697 DKFZp761N1114 3'	GCGTGAGCCACTGCACCCAGC	79018	CA
	GCTGGG CAGTGGCTCACGC		



CGACCC GTCACCGAGTGCG  
 AC  
 GAM1697 DKFZp761O0113 5' GCGTGAGCCACCGCGCCCGGC 37278 ACA  
 GCTGGGC GTGGCTCACGC  
 ||||| |||||  
 CGGCCCG CACCGAGTGCG  
 CGC  
 GAM1697 DSCR6 3' GCGTGAGCCACTGAGCCCGGC 38548 A  
 GCTGGGC CAGTGGCTCACGC  
 ||||| |||||  
 CGGCCCG GTCACCGAGTGCG  
 A  
 GAM1697 EREG 3' GCCACCATGCCAGCT 7500 CA  
 AGCTGGGCA GTGGC  
 ||||| ||||  
 TCGACCCGT CACCG  
 AC  
 GAM1697 EREG 3' GCGTGAGCCACCGCACGTAGC 7501 G\_\_ ACA  
 GCTG GC GTGGCTCACGC  
 ||| || |||||  
 CGAT CG CACCGAGTGCG  
 GCA C\_\_  
 GAM1697 EVI5 3' GTGAGCCACTGCACCCAGC 19007 CA  
 GCTGGG CAGTGGCTCAC  
 ||||| |||||  
 CGACCC GTCACCGAGTG  
 AC  
 GAM1697 FBP17 3' GCGTGACCAACCACGCCCGGCT 72794 ACA CT  
 AGCTGGGC GTGG CACGC  
 ||||| ||| ||||  
 TCGGCCCG CACC GTGCG  
 CAC AC  
 GAM1697 FGD3 5' GCGCCTGTGCCCGCCGA 72898 A T TG  
 TC GC GGGCACAG GC  
 || ||||| ||  
 AG CG CCCGTGTC CG  
 C \_ CG  
 GAM1697 FLB6421 3' GCATGAGCCACCGTGCTGGCT 39225 TG A C  
 AGC GGCAC GTGGCTCA GC  
 || |||| ||||| ||  
 TCG CCGTG CACCGAGT CG  
 GT C A  
 GAM1697 FLJ00060 5' GCGCCCACCACCATGCCCGGCT 61098 CA CTCA  
 AGCTGGGCA GTGG CGC  
 ||||| ||| ||  
 TCGGCCCGT CACC GCG  
 AC ACCC  
 GAM1697 FLJ10298 3' CTGAGCCACCACAGCTGG 35989 GGCACA C  
 TCAGCTG GTGGCTCA G  
 ||||| ||||| |

		GGTCGAC CACCGAGT C	
		AC_____ A	
GAM1697	FLJ10346	5' GCATGCACCACCATGCCAGCT 36043	CA CT C
		AGCTGGGCA GTGG CA GC	
		TCGACCCGT CACC GT CG	
		AC AC A	
GAM1697	FLJ10346	5' GCGTGAGCCACCGCGCCCGGC 36044	ACA
		GCTGGGC GTGGCTCACGC	
		CGGCCCG CACCGAGTGCG	
		CGC	
GAM1697	FLJ10520	3' GCGTGAGCCACTGCACCCGGC 36212	CA
		GCTGGG CAGTGGCTCACGC	
		CGGCCG GTCACCGAGTGCG	
		AC	
GAM1697	FLJ10535	3' GCATGAGCCACCACACCCAGC 36240	CACA C
		GCTGGG GTGGCTCA GC	
		CGACCC CACCGAGT CG	
		ACAC A	
GAM1697	FLJ10535	3' TGAGCCACCACGCTTGGCCGG 36253	A TG ACA
		TC GC GGC GTGGCTCA	
		GG CG TCG CACCGAGT	
		C GT CAC	
GAM1697	FLJ10560	3' GCGTGAGCCACCGTGCCAGC 36279	A
		GCTGGGCAC GTGGCTCACGC	
		CGACCCGTG CACCGAGTGCG	
		C	
GAM1697	FLJ10737	3' GCGTGAGCCACTTCTGCAGTCC 36522	AC_____
	A	TGGGC AGTGGCTCACGC	
		ACCTG TCACCGAGTGCG	
		ACGTCT	
GAM1697	FLJ10846	3' GCACCTGCCACCATGCCAGCT 36739	CA TCAC
		AGCTGGGCA GTGGC GC	
		TCGACCCGT CACCG CG	
		AC TCCA	
GAM1697	FLJ10846	3' GCGTGAGCCACTGCGCCTGGC 36741	TG A
		GC GGC CAGTGGCTCACGC	
		CG CCG GTCACCGAGTGCG	
		GT C	
GAM1697	FLJ10847	3' GCCACCATGCCAGCTGG 36749	CA
		TCAGCTGGGCA GTGGC	

		GGTCGACCCGT CACCG			
		AC			
GAM1697	FLJ10847	3' GCGTGTGCCACCACGCCTAGCT 36750	ACA	T	
		AGCTGGGC GTGGC CACGC			
		TCGATCCG CACCG GTGCG			
		CAC T			
GAM1697	FLJ11186	3' GCATGAGCCACTGTGCCTGGC 37142	TG		C
		GC GGCACAGTGGCTCA GC			
		CG CCGTGTACCGAGT CG			
		GT A			
GAM1697	FLJ11715	3' TGAGCCACCGCGCCCAGC 44678	ACA		
		GCTGGGC GTGGCTCA			
		CGACCCG CACCGAGT			
		CGC			
GAM1697	FLJ11800	3' GCATGGGGCCACCACAGCCAGCT 46428	GCACA		C
	GA	TCAGCTGG GTGGCTCA GC			
		AGTCGACC CACCGGGT CG			
		GACAC A			
GAM1697	FLJ12363	3' GCATGAGCCACCACGCCAGC 49681	ACA		C
		GCTGGGC GTGGCTCA GC			
		CGACCCG CACCGAGT CG			
		CAC A			
GAM1697	FLJ12581	3' GCGTGAGCCACCGCGCCCTGC 45878	T	ACA	
		GC GGGC GTGGCTCACGC			
		CG CCCG CACCGAGTGCG			
		T CGC			
GAM1697	FLJ12649	3' GTGAGCCACTGCACCCAGC 44782	CA		
		GCTGGG CAGTGGCTCAC			
		CGACCC GTCACCGAGTG			
		AC			
GAM1697	FLJ12668	3' GCCACCATGCCCGGCT 46517	CA		
		AGCTGGGCA GTGGC			
		TCGGCCCGT CACCG			
		AC			
GAM1697	FLJ12668	3' GCGTAAGCCACCATGCCTGGC 46518	TG	CA	C
		GC GGCA GTGGCT ACGC			
		CG CCGT CACCGA TGCG			
		GT AC A			
GAM1697	FLJ12687	3' GCGTGAGCCACCACACCCCGC 46195	T	CACA	
		GC GGG GTGGCTCACGC			

		CG CCC CACCGAGTGCG		
		C ACAC		
GAM1697	FLJ12687	3' GCGTGCCACCATGCCCGGCT 46196	CA	TC
		AGCTGGGCA GTGGC ACGC		
		TCGGCCCGT CACCG TGCG		
		AC —		
GAM1697	FLJ12747	3' GCGTGAGCCACCATGCCTGCCC 49718	—	—
		AGC GCTGGGCA CA GTGGCTCACGC		
		CGACCCGT GT CACCGAGTGCG		
		CC AC		
GAM1697	FLJ12876	3' GCGCCCGCCACCACGCCCGGCT 42786	ACA	TCA
		AGCTGGGC GTGGC CGC		
		TCGGCCCG CACCG GCG		
		CAC CCC		
GAM1697	FLJ12876	3' GCGTGAGCCACCGCACCCGGC 42787	CACA	
		GCTGGG GTGGCTCACGC		
		CGGCC CACCGAGTGCG		
		ACGC		
GAM1697	FLJ12888	3' GCATGTACCACCATGCCCAGCT 46319	CA	CT C
		AGCTGGGCA GTGG CA GC		
		TCGACCCGT CACC GT CG		
		AC AT A		
GAM1697	FLJ12903	3' GCATGAGCCACTGCACCTGGCC 42774	A TG CA	C
		GG TC GC GG CAGTGGCTCA GC		
		GG CG CC GTCACCGAGT CG		
		C GT AC A		
GAM1697	FLJ12973	3' GCGTGAGCCACCATGCCTGGC 46105	TG	CA
		GC GGCA GTGGCTCACGC		
		CG CCGT CACCGAGTGCG		
		GT AC		
GAM1697	FLJ12975	3' CGTGAGCCACTGCGTCCGG 69582	A	
		CTGGGC CAGTGGCTCACG		
		GGCCTG GTCACCGAGTGC		
		C		
GAM1697	FLJ12975	3' GCATGAGCCACCGCACCCGGC 69585	CACA	C
		GCTGGG GTGGCTCA GC		
		CGGCC CACCGAGT CG		
		ACGC A		
GAM1697	FLJ12975	3' GCATGCACCACCGACCCGGCT 69586	ACA	CT C
		AGCTGGGC GTGG CA GC		

		TCGGCCCG CACC GT CG		
		CAC AC A		
GAM1697	FLJ13072	5' GTGAGCCACCACACCCGGC 89821	CACA	
		GCTGGG GTGGCTCAC		
		CGGCCC CACCGAGTG		
		ACAC		
GAM1697	FLJ13102	3' GCATGAGCCACCATGCCAG 46012	G CA C	
		CTGG CA GTGGCTCA GC		
		GACC GT CACCGAGT CG		
		_ AC A		
GAM1697	FLJ13114	3' GCGTGAGCCACCACACCCAGC 44599	CACA	
		GCTGGG GTGGCTCACGC		
		CGACCC CACCGAGTGCG		
		ACAC		
GAM1697	FLJ13114	3' GCGTGTGCCACGCCCGGCT 44600	ACA T	
		AGCTGGGC GTGGC CACGC		
		TCGGCCCG CACCG GTGCG		
		___ T		
GAM1697	FLJ13193	3' CCACCACGCCCAGCTGA 49761	ACA	
		TCAGCTGGGC GTGG		
		AGTCGACCCG CACC		
		CAC		
GAM1697	FLJ13197	3' GCGTGAGCCACTGCGCCTGGC 44855	TG A	
		GC GGC CAGTGGCTCACGC		
		CG CCG GTCACCGAGTGCG		
		GT C		
GAM1697	FLJ13305	5' GCATGAACCACTGTGCCTGGC 90128	TG C C	
		GC GGCACAGTGG TCA GC		
		CG CCGTGTCAACC AGT CG		
		GT A A		
GAM1697	FLJ13798	5' GCGACTCGACACCGTCCAGCT 87107	C A GCTCA_	
	GA	TCAGCTGGG AC GTG CGC		
		AGTCGACCC TG CAC GCG		
		_ C AGCTCA		
GAM1697	FLJ13952	3' GCGTGAGCCACCGTGCTCGGC 45617	A	
		GCTGGGCAC GTGGCTCACGC		
		CGGCTCGTG CACCGAGTGCG		
		C		
GAM1697	FLJ14824	3' GCGTGAGCCACCGTGCCTGGC 51645	TG A	
		GC GGCAC GTGGCTCACGC		

CG CCGTG CACCGAGTGCG  
GT C

GAM1697 FLJ14957 3' GCGCATGAGCCACCACGCCAG 51751 \_ ACA C III  
CCATTGA GCTGGGC GTGGCTCA GC GC  
||||| ||||| || ||  
CGACCCG CACCGAGT CG CG  
C CAC A III

GAM1697 FLJ20034 3' GCATGTGTCACCATGCCCGGCT 34372 CA T C  
AGCTGGGCA GTGGC CA GC  
||||||| |||| || ||  
TCGGCCCGT CACTG GT CG  
AC T A

GAM1697 FLJ20045 3' GCATGAGCCACCACGCCTGGC 34419 TG ACA C  
GC GGC GTGGCTCA GC  
|| ||| ||||| ||  
CG CCG CACCGAGT CG  
GT CAC A

GAM1697 FLJ20045 3' GCCACCATGCTCAGCT 34420 CA  
AGCTGGGCA GTGGC  
||||||| ||||  
TCGACTCGT CACCG  
AC

GAM1697 FLJ20136 3' GCATGAGCCACCACGGCCCGC 34612 T ACA\_ C  
GC GGGC GTGGCTCA GC  
|| ||| ||||| ||  
CG CCCG CACCGAGT CG  
\_ GCAC A

GAM1697 FLJ20147 3' GCATGAGCCACCACACCTGGC 34639 TG CACA C  
GC GG GTGGCTCA GC  
|| || ||||| ||  
CG CC CACCGAGT CG  
GT ACAC A

GAM1697 FLJ20208 3' GCATGAGCCACTGCACCCAGC 34744 CA C  
GCTGGG CAGTGGCTCA GC  
||||| ||||| ||  
CGACCC GTCACCGAGT CG  
AC A

GAM1697 FLJ20342 3' GCGTGAGCCACTCCACCCAGC 34990 CAC  
GCTGGG AGTGGCTCACGC  
||||| ||||| ||  
CGACCC TCACCGAGTGCG  
ACC

GAM1697 FLJ20344 3' GCATGAGCCACTGCACCCGGCT 35012 CA C  
AGCTGGG CAGTGGCTCA GC  
||||| ||||| ||  
TCGGCCC GTCACCGAGT CG  
AC A

GAM1697 FLJ20436 5' CTCCTGTGCCAGCTGA 35169 G TG  
TCAGCTGG CACAG G  
||||||| |||| |

AGTCGACC GTGTC C  
 \_ CT  
 GAM1697 FLJ20452 3' CGCGTAAGCCACTGCGCCCAGC 35198 A C III  
 GCTGGGC CAGTGGCT ACGC G  
 ||||| ||||| ||| I  
 CGACCCG GTCACCGA TGCG C  
 C A III  
 GAM1697 FLJ20485 3' GCGCACCACCACGCCTAGCTGA 38766 ACA CTCA  
 TCAGCTGGGC GTGG CGC  
 ||||| ||| |||  
 AGTCGATCCG CACC GCG  
 CAC AC\_\_  
 GAM1697 FLJ20507 3' GCATGAACCACCGTGCCTGGC 35288 TG A C C  
 GC GGCAC GTGG TCA GC  
 || |||| ||| |||  
 CG CCGTG CACC AGT CG  
 GT C A A  
 GAM1697 FLJ20507 3' GCATGAACCACCGTGCCTGGC 60223 TG A C C  
 GC GGCAC GTGG TCA GC  
 || |||| ||| |||  
 CG CCGTG CACC AGT CG  
 GT C A A  
 GAM1697 FLJ20508 3' GCATGAGCCACTGCTCCTGA 35307 CT CA C  
 TCAG GGGCA GTGGCTCA GC  
 ||| |||| ||||| ||  
 AGTC CTCGT CACCGAGT CG  
 \_ \_ A  
 GAM1697 FLJ20511 3' GCGCCCGCCACCATGCCAGCT 35325 CA TCA  
 AGCTGGGCA GTGGC CGC  
 ||||| |||| |||  
 TCGACCCGT CACCG GCG  
 AC CCC  
 GAM1697 FLJ20511 3' GCGTGAGCCACCGCGCGC 35326 T G ACA  
 GC G GC GTGGCTCACGC  
 || || |||||  
 CG C CG CACCGAGTGCG  
 \_ G C\_  
 GAM1697 FLJ20700 3' GCGTGAGCCACCGCGGCCCA 35577 ACA\_  
 TGGGC GTGGCTCACGC  
 |||| |||||  
 ACCCG CACCGAGTGCG  
 GCGC  
 GAM1697 FLJ20700 3' GTGAGCCACCACCCAGC 35583 CACA  
 GCTGGG GTGGCTCAC  
 |||| |||||  
 CGACCC CACCGAGTG  
 ACAC  
 GAM1697 FLJ20718 3' GCGTGAGCCACCGTGCCTGGC 35607 TG A  
 GC GGCAC GTGGCTCACGC  
 || |||| |||||

CG CCGTG CACCGAGTGCG  
GT C

GAM1697 FLJ20958 3' CGTGAACCACTGTGTCCAG 42057 C  
CTGGGCACAGTGG TCACG  
||||||| ||||  
GACCTGTGTCACC AGTGC  
A

GAM1697 FLJ20958 3' GCGTGAGCCACCACACCCAGC 42058 CACA  
GCTGGG GTGGCTCACGC  
|||| | |||||  
CGACCC CACCGAGTGCG  
ACAC

GAM1697 FLJ21324 5' GCATGCGCCACCACGCTCAGCT 91204 ACA T C  
GA TCAGCTGGGC GTGGC CA GC  
|||||| | ||| ||  
AGTCGACTCG CACCG GT CG  
CAC C A

GAM1697 FLJ21603 3' CGTGAGCCACTGCTCCTGG 45423 TG CA  
C GG CAGTGGCTCACG  
| || |||||  
G CC GTCACCGAGTGC  
GT TC

GAM1697 FLJ21916 3' AGCCATGGACCCAGCTGA 43640 CA G  
TCAGCTGGG CA TGGCT  
|||||| || ||||  
AGTCGACCC GT ACCGA  
AG \_

GAM1697 FLJ22316 5' CTGAGCCACTGCACAG 46920 GGCA C  
CTG CAGTGGCTCA G  
|| | ||||| |  
GAC GTCACCGAGT C  
AC\_ A

GAM1697 FLJ22329 3' GCATGAGCCACTGTGCCAGC 45071 C  
GCTGGGCACAGTGGCTCA GC  
||||||| ||||| ||  
CGACCCGTGTCACCGAGT CG  
A

GAM1697 FLJ22529 3' GCATGAGCCACCGCACTCGGC 45570 CACA C  
GCTGGG GTGGCTCA GC  
|||| | ||||| ||  
CGGCTC CACCGAGT CG  
ACGC A

GAM1697 FLJ22529 3' GCGTGAGCCACTGTGGCCA 45571 G  
TGG CACAGTGGCTCACGC  
|| | |||||  
ACC GTGTCACCGAGTGCG  
G

GAM1697 FLJ22684 3' GCATGAGCCACCACATCTGGC 46795 TG CACA C  
GC GG GTGGCTCA GC  
|| || ||||| ||



		CG CT CACCGAGT CG		
		GT ACAC A		
GAM1697	FLJ23323	3' GCGTGAGCCACCGCGCCCGGC 45053	ACA	
		GCTGGGC GTGGCTCACGC		
		CGGCCCG CACCGAGTGCG		
		CGC		
GAM1697	FLJ23356	3' GCGTGAGCCACTGCGCCCGGC 49939	A	
		GCTGGGC CAGTGGCTCACGC		
		CGGCCCG GTCACCGAGTGCG		
		C		
GAM1697	FLJ23392	3' GCATGAGCCACCGCGCCAGCT 45534	ACA	C
	G	CAGCTGGGC GTGGCTCA GC		
		GTCGACCCG CACCGAGT CG		
		CGC A		
GAM1697	FLJ23392	3' GCGTGAGCCACCATGCCAGC 45536	CA	
		GCTGGGCA GTGGCTCACGC		
		CGACCCGT CACCGAGTGCG		
		AC		
GAM1697	FLJ23519	3' GCGTGAGCCACCACGCCTGGC 49966	TG	ACA
		GC GGC GTGGCTCACGC		
		CG CCG CACCGAGTGCG		
		GT CAC		
GAM1697	FLJ23556	3' GCGTGAGCCACTACACCAGC 45950	CAC	
		GCTGGG AGTGGCTCACGC		
		CGACCC TCACCGAGTGCG		
		ACA		
GAM1697	FLJ23563	3' GCCACCATGCTCAGCT 67594	CA	
		AGCTGGGCA GTGGC		
		TCGACTCGT CACCG		
		AC		
GAM1697	FLJ30532	3' GCGTGAGTCACCGCGCCAGCT 58548	ACA	
	GG	TCAGCTGGGC GTGGCTCACGC		
		GGTCGACCCG CACTGAGTGCG		
		CGC		
GAM1697	FLJ31101	3' GCACCTGCCACCACGCCAGCT 35711	ACA	TCAC
		AGCTGGGC GTGGC GC		
		TCGACCCG CACCG CG		
		CAC TCCA		
GAM1697	FLJ32865	3' GCATGCACCACCACGCCAGCT 58174	ACA	CT C
		AGCTGGGC GTGG CA GC		

			TCGACCCG CACC GT CG	
			CAC AC A	
GAM1697	FLJ32865	3'	GCGTGAGCCACTGCACCCGGCT 58175	CA
			AGCTGGG CAGTGGCTCACGC	
			TCGGCCC GTCACCGAGTGCG	
			AC	
GAM1697	GAL3ST-4	3'	CGTGAGCCACTAGGCCT 44937	AC
			GGGC AGTGGCTCACG	
			TCCG TCACCGAGTGC	
			GA	
GAM1697	GGA2	3'	GCGTGAGCCACCGCACCCGGC 56883	CACA
			GCTGGG GTGGCTCACGC	
			CGGCC CACCGAGTGCG	
			ACGC	
GAM1697	GGA2	3'	GCGTGAGCCAGCACGCCAGCT 56884	ACAG
			AGCTGGGC TGGCTCACGC	
			TCGACCCG ACCGAGTGCG	
			CACG	
GAM1697	GGA2	3'	GCGTGAGCCACCGCACCCGGC 30469	CACA
			GCTGGG GTGGCTCACGC	
			CGGCC CACCGAGTGCG	
			ACGC	
GAM1697	GGA2	3'	GCGTGAGCCAGCACGCCAGCT 30470	ACAG
			AGCTGGGC TGGCTCACGC	
			TCGACCCG ACCGAGTGCG	
			CACG	
GAM1697	GMPPB	5'	CGCCCACCACACGCCCGGCT 95730	ACA CTCA
			AGCTGGGC GTGG CG	
			TCGGCCCG CACC GC	
			CAC ACCC	
GAM1697	GMPPB	5'	GCGTGAGCCACCGCGCCCGGC 95742	ACA
			GCTGGGC GTGGCTCACGC	
			CGGCCCG CACCGAGTGCG	
			CGC	
GAM1697	GNG4	3'	GCGTGAGCCACCACCCGGC 15616	CACA
			GCTGGG GTGGCTCACGC	
			CGGCC CACCGAGTGCG	
			ACAC	
GAM1697	GREB1	3'	GCGCCCACCACACGCCCGGCT 27873	ACA CTCA
			AGCTGGGC GTGG CGC	

			TCGGCCCG CACC GCG		
			CAC ACCC		
GAM1697 GREB1	3'	GCGCCCACCACCATGCCAGCT 27874		CA	CTCA
		AGCTGGGCA GTGG CGC			
		TCGACCCGT CACC GCG			
		AC ACCC			
GAM1697 GREB1	3'	GCGTGAGCCACCGTGCCTGC 27876	T	A	
		GC GGGCAC GTGGCTCACGC			
		CG TCCGTG CACCGAGTGCG			
		— C			
GAM1697 GRWD	3'	GCGTGAGCCACCGCGTCCGGCT 48967		ACA	
		AGCTGGGC GTGGCTCACGC			
		TCGGCCTG CACCGAGTGCG			
		CGC			
GAM1697 GTF2H3	3'	GCGTGAGCCACCGCACCCGGC 7705		CACA	
		GCTGGG GTGGCTCACGC			
		CGGCC CACCGAGTGCG			
		ACGC			
GAM1697 H2AV	3'	GCCACCATGCCAGCT 56854		CA	
		AGCTGGGCA GTGGC			
		TCGACCCGT CACCG			
		AC			
GAM1697 HCA4	3'	GCATGAGCCACCTCGCCCAGC 77586		ACA	C
		GCTGGGC GTGGCTCA GC			
		CGACCCG CACCGAGT CG			
		CTC A			
GAM1697 HSMPP8	3'	GCATGAGCCACCGCACCCAGC 93477		CACA	C
		GCTGGG GTGGCTCA GC			
		CGACCC CACCGAGT CG			
		ACGC A			
GAM1697 HSNV1	3'	TGTGGCCCCACGCCAGCT 34017		ACAGT	T
		AGCTGGGC GGC CACG			
		TCGACCCG CCG GTGT			
		CACC_ _			
GAM1697 HSPC065	3'	GCCACCATGCCAGCT 26303		CA	
		AGCTGGGCA GTGGC			
		TCGACCCGT CACCG			
		AC			
GAM1697 HSPC065	3'	GCGTGAGCCACTGCACCCGGC 26305		CA	
		GCTGGG CAGTGGCTCACGC			

		CGGCCC GTCACCGAGTGCG		
		AC		
GAM1697	HSPC232	3' GCGTGAGCCACCGCTCCCTGC 33231	T	CACA
		GC GGG GTGGCTCACGC		
		CG CCC CACCGAGTGCG		
		T TCGC		
GAM1697	HSPF2	5' GCGTGAGCCACCGCGCCTGTCC 18642	CA	_____
	AG	CTGGGCA GTGGCTCACGC		
		GACCTGT CACCGAGTGCG		
		CCGCGC		
GAM1697	HT002	3' GCGTGAGCCACCATGCCCGGCT 25943	CA	
		AGCTGGGCA GTGGCTCACGC		
		TCGGCCCGT CACCGAGTGCG		
		AC		
GAM1697	ICK	3' GCATGAGCCACTGCACCCAGC 29931	CA	C
		GCTGGG CAGTGGCTCA GC		
		CGACCC GTCACCGAGT CG		
		AC A		
GAM1697	ICK	3' GCGCCCGCCACCACGCCAGCT 29932	ACA	TCA
		AGCTGGGC GTGGC CGC		
		TCGACCCG CACCG GCG		
		CAC CCC		
GAM1697	JM11	3' GCCACCATGCCCGGCT 53260	CA	
		AGCTGGGCA GTGGC		
		TCGGCCCGT CACCG		
		AC		
GAM1697	KCNS1	3' GCACATCTAGGCCAGCTGA 9576	AC	_ _ _ _
		TCAGCTGGGC AG TG GC		
		AGTCGACCCG TC AC CG		
		GA T A		
GAM1697	KIAA0022	3' GCGTGAGCCACCACACTTGGC 29666	TG	CACA
		GC GG GTGGCTCACGC		
		CG TC CACCGAGTGCG		
		GT ACAC		
GAM1697	KIAA0063	3' GCGTGAGCCACCGCACCCGGC 29630	CACA	
		GCTGGG GTGGCTCACGC		
		CGGCCC CACCGAGTGCG		
		ACGC		
GAM1697	KIAA0087	3' GCATGAGCCACGCGCCAGC 28698	ACA	C
		GCTGGGC GTGGCTCA GC		

			CGACCCG CACCGAGT CG		
			CG_ A		
GAM1697	KIAA0090	3'	GCGTGCGCCACCATGCCCGGCT 88445	CA	T
			AGCTGGGCA GTGGC CACGC		
			TCGGCCCGT CACCG GTGCG		
			AC C		
GAM1697	KIAA0152	3'	CCACTGAGCCCAGCTGA 28295	A	
			TCAGCTGGGC CAGTGG		
			AGTCGACCCG GTCACC		
			A		
GAM1697	KIAA0186	3'	GCGTGAGCCACTGCACCCG 40753	CA	
			TGGG CAGTGGCTCACGC		
			GCCC GTCACCGAGTGCG		
			AC		
GAM1697	KIAA0205	3'	GCGTGAGCCACCACGCCCGGC 29585	ACA	
			GCTGGGC GTGGCTCACGC		
			CGGCCCG CACCGAGTGCG		
			CAC		
GAM1697	KIAA0349	3'	GCGTGGGACTGACTCACCCAGC 92305	CAC	_ _
			TGA TCAGCTGGG AGT GG CTCACGC		
			AGTCGACCC TCA TC GGGTGCG		
			AC_ G A		
GAM1697	KIAA0426	3'	GCATGAGCCACCATGCCCGGCT 28258	CA	C
			G CAGCTGGGCA GTGGCTCA GC		
			GTCGGCCCGT CACCGAGT CG		
			AC A		
GAM1697	KIAA0435	5'	GCGTGAGCCACCGTGCTCAGC 28977	A	
			GCTGGGCAC GTGGCTCACGC		
			CGACTCGTG CACCGAGTGCG		
			C		
GAM1697	KIAA0446	5'	CGTGAGCCACTGTGTCCAG 68863		
			CTGGGCACAGTGGCTCACG		
			GACCTGTGTCACCGAGTGC		
GAM1697	KIAA0469	3'	GCGTGAACCACCACGCCAGCT 29336	ACA	C
			GG TCAGCTGGGC GTGG TCACGC		
			GGTCGACCCG CACC AGTGCG		
			CAC A		
GAM1697	KIAA0472	5'	GTGAGCCACCACCCAGC 71868	CACA	
			GCTGGG GTGGCTCAC		

		CGACCC CACCGAGTG	
		ACAC	
GAM1697 KIAA0475	3'	GCATGAGCCACCGTGGCCGGC 29492	G A C
		GCTGG CAC GTGGCTCA GC	
		CGGCC GTG CACCGAGT CG	
		G C A	
GAM1697 KIAA0475	3'	GCGCCCGCCATCGTGCCCAGCT 29495	A TCA
		AGCTGGGCAC GTGGC CGC	
		TCGACCCGTG TACCG GCG	
		C CCC	
GAM1697 KIAA0478	3'	GCGTGAGCCACCACTGCTGGCC 29549	G _ _
	AG	CTGG CA CAGT GGCTCACGC	
		GACC GT GTCA CCGAGTGCG	
		G C CCA	
GAM1697 KIAA0478	3'	TGAGCCACTACGCCTGGC 29562	TG AC
		GC GGC AGTGGCTCA	
		CG CCG TCACCGAGT	
		GT CA	
GAM1697 KIAA0495	3'	GCGTGAGCCACCATGCTCGGC 62591	CA
		GCTGGGCA GTGGCTCACGC	
		CGGCTCGT CACCGAGTGCG	
		AC	
GAM1697 KIAA0513	5'	CGTGAGCCACTGCCCCCAG 28351	CA
		CTGGG CAGTGGCTCACG	
		GACCC GTCACCGAGTGC	
		CC	
GAM1697 KIAA0513	5'	GCACCTGCCACCACGCCCGGCT 28360	ACA TCAC
	GA	TCAGCTGGGC GTGGC GC	
		AGTCGGCCCG CACCG CG	
		CAC TCCA	
GAM1697 KIAA0527	3'	GCATGCACCACCATGCCAGCT 95800	CA CT C
		AGCTGGGCA GTGG CA GC	
		TCGACCCGT CACC GT CG	
		AC AC A	
GAM1697 KIAA0557	3'	GCGTGAGCCACCGCGCCCGGC 77998	ACA
		GCTGGGC GTGGCTCACGC	
		CGGCCCG CACCGAGTGCG	
		CGC	
GAM1697 KIAA0561	3'	GCGTGAGCCACTGGGCCAGC 65890	A
		GCTGGGC CAGTGGCTCACGC	

		CGACCCG GTCACCGAGTGCG		
		G		
GAM1697 KIAA0561	3'	GCGCCCACCACTATGCCAGCT 65888	C	CTCA
		AGCTGGGCA AGTGG CGC		
		TCGACCCGT TCACC GCG		
		A ACCC		
GAM1697 KIAA0562	3'	GCATGAGCCACCGCGCCCGGC 28154	ACA	C
		GCTGGGC GTGGCTCA GC		
		CGGCCCG CACCGAGT CG		
		CGC A		
GAM1697 KIAA0594	3'	GCGTGAGCCCOCTGCACCCGGC 64898	CA	T
		GCTGGG CAG GGCTCACGC		
		CGGCCG GTC CCGAGTGCG		
		AC C		
GAM1697 KIAA0599	3'	GCATGAGCCACCACACCCAGCT 77181	CACA	C
		AGCTGGG GTGGCTCA GC		
		TCGACCC CACCGAGT CG		
		ACAC A		
GAM1697 KIAA0630	5'	CCACGCACACAAGGCTTGCCAG 89390	___ ACA	___ TCAC
	CTGA	GCTGG GC GTG GC G		
		CGACC CG CAC CG C		
		GTT GAA A    CACT		
GAM1697 KIAA0737	3'	GCATGAGCCACCGCACCCAGC 29137	CACA	C
		GCTGGG GTGGCTCA GC		
		CGACCC CACCGAGT CG		
		ACGC A		
GAM1697 KIAA0737	3'	GCGCCCGCCACTACGCCAGCT 29139	AC	TCA
		AGCTGGGC AGTGGC CGC		
		TCGACCCG TCACCG GCG		
		CA CCC		
GAM1697 KIAA0831	3'	GCACCTGCCATCATGCCAGCT 29976	CA	TCAC
		AGCTGGGCA GTGGC GC		
		TCGACCCGT TACCG CG		
		AC TCCA		
GAM1697 KIAA0831	5'	GCGTGAGCCACCGCACTGGC 29978	TG_ ACA	
		GC G GC GTGGCTCACGC		
		CG C CG CACCGAGTGCG		
		GT A C__		
GAM1697 KIAA0841	3'	GCATGAGCCACCGCGCCT 71385	ACA	C
		GGGC GTGGCTCA GC		

TCCG CACCGAGT CG  
 CGC A  
 GAM1697 KIAA0861 3' GCGCCCGCCACCACGCCCCGGCT 88925 ACA TCA  
 AGCTGGGC GTGGC CGC  
 ||||| ||| ||  
 TCGGCCCG CACCG GCG  
 CAC CCC  
 GAM1697 KIAA0861 3' GCGTGAGCCACCGCGCCCAGCC 88927 A ACA  
 GG TC GCTGGGC GTGGCTCACGC  
 || ||||| |||||  
 GG CGACCCG CACCGAGTGCG  
 C CGC  
 GAM1697 KIAA0889 3' GCGCCTGCCACCATGCCCCGGCT 31139 CA TCA  
 AGCTGGGCA GTGGC CGC  
 ||||| ||| ||  
 TCGGCCCGT CACCG GCG  
 AC TCC  
 GAM1697 KIAA0889 3' GCGTGAGCCACCGCGCCTGGC 31140 TG ACA  
 GC GGC GTGGCTCACGC  
 || || |||||  
 CG CCG CACCGAGTGCG  
 GT CGC  
 GAM1697 KIAA0924 3' GCGTGAGCCACCACGTCCAAC 29716 C ACA  
 G CAG TGGGC GTGGCTCACGC  
 || ||| |||||  
 GTC ACCTG CACCGAGTGCG  
 A CAC  
 GAM1697 KIAA0961 3' GCGTGAGCCACCATGCCCCGGCT 29734 CA  
 AGCTGGGCA GTGGCTCACGC  
 ||||| |||||  
 TCGGCCCGT CACCGAGTGCG  
 AC  
 GAM1697 KIAA1026 3' TGAGCCACTGCACCTGGC 71216 TG CA  
 GC GG CAGTGGCTCA  
 || || |||||  
 CG CC GTCACCGAGT  
 GT AC  
 GAM1697 KIAA1040 3' GCCTGAGCCACTGCGCCCAGC 72229 A C  
 GCTGGGC CAGTGGCTCA GC  
 ||||| ||||| ||  
 CGACCCG GTCACCGAGT CG  
 C C  
 GAM1697 KIAA1041 3' TGAGCCACTGCGCCTGGC 30143 TG A  
 GC GGC CAGTGGCTCA  
 || || |||||  
 CG CCG GTCACCGAGT  
 GT C  
 GAM1697 KIAA1054 3' GCATGCGCCACCACGCCCAGCT 68438 ACA T C  
 AGCTGGGC GTGGC CA GC  
 ||||| ||| ||



		TCGACCCG CACCG GT CG		
		CAC C A		
GAM1697 KIAA1145	3'	AGCCACCATGCCTGGCTG 65618	TG CA	
		CAGC GGCA GTGGCT		
		GTCG CCGT CACCGA		
		GT AC		
GAM1697 KIAA1161	5'	GCATGAGCCACCACGCCAGC 81752	G ACA C	
		GCTGG C GTGGCTCA GC		
		CGACC G CACCGAGT CG		
		_CAC A		
GAM1697 KIAA1193	3'	GCGCCCGCCACCATGCCCAGCT 67639	CA TCA	
		AGCTGGGCA GTGGC CGC		
		TCGACCCGT CACCG GCG		
		AC CCC		
GAM1697 KIAA1193	3'	GCGTGAGACATCGCGCCCGGCT 67641	ACA G	
	GA	TCAGCTGGGC GTG CTCACGC		
		AGTCGGCCCG TAC GAGTGCG		
		CGC A		
GAM1697 KIAA1198	3'	GCGTGAGCCACCACACCCGGC 63312	CACA	
		GCTGGG GTGGCTCACGC		
		CGGCCC CACCGAGTGCG		
		ACAC		
GAM1697 KIAA1198	3'	GCGTGAGCCACCGCGCCCGGC 63313	ACA	
		GCTGGGC GTGGCTCACGC		
		CGGCCC CACCGAGTGCG		
		CGC		
GAM1697 KIAA1200	3'	GCATGAGCCATCGCCCAGC 62376	ACA C	
		GCTGGGC GTGGCTCA GC		
		CGACCCG TACCGAGT CG		
		C_ A		
GAM1697 KIAA1200	3'	GCCACCATGCCCGGCT 62377	CA	
		AGCTGGGCA GTGGC		
		TCGGCCCGT CACCG		
		AC		
GAM1697 KIAA1209	3'	GCATGAGCCACTGCGCCCGGC 60757	A C	
		GCTGGGC CAGTGGCTCA GC		
		CGGCCC GTACCGAGT CG		
		C A		
GAM1697 KIAA1210	3'	GCGTGAGCCACCGCGCCCGGC 96332	ACA	
		GCTGGGC GTGGCTCACGC		

		CGGCCCG CACCGAGTGCG		
		CGC		
GAM1697	KIAA1257	3' GCGTGAGCCACCGTACCCGGC 62743	C	A
		GCTGGG AC GTGGCTCACGC		
		CGGCCCG TG CACCGAGTGCG		
		A C		
GAM1697	KIAA1320	5' CGTGAGCCACCATCTCCGG 69301	CACA	
		CTGGG GTGGCTCACG		
		GGCCT CACCGAGTGC		
		CTAC		
GAM1697	KIAA1328	5' CGTGAGCCACTGCACCTGGC 61645	TG	CA
		GC GG CAGTGGCTCACG		
		CG CC GTCACCGAGTGC		
		GT AC		
GAM1697	KIAA1349	5' GCATGAGCCACTGTGCCAGCT 70756		C
	GA	TCAGCTGGGCACAGTGGCTCA GC		
		AGTCGACCCGTGTCACCGAGT CG		
		A		
GAM1697	KIAA1364	3' CCACTGTGCCAGATGA 63589	G	
		TCA CTGGGCACAGTGG		
		AGT GACCCGTGTCACC		
		A		
GAM1697	KIAA1373	3' GCATGAGCCACCATGCCTGGCT 70937	TG	CA C
		AGC GGCA GTGGCTCA GC		
		TCG CCGT CACCGAGT CG		
		GT AC A		
GAM1697	KIAA1373	3' GCGTGACCAACCACGCCAGCT 70940	ACA	CT
		AGCTGGGC GTGG CACGC		
		TCGACCCG CACC GTGCG		
		CAC AC		
GAM1697	KIAA1373	3' TGAGCCACTGTGCCCTGC 70956	T	
		GC GGGCACAGTGGCTCA		
		CG CCCGTGTCACCGAGT		
		T		
GAM1697	KIAA1443	3' GCATGAGCCACCGTGCCCGGCT 63831	A	C
		AGCTGGGCAC GTGGCTCA GC		
		TCGGCCCGTG CACCGAGT CG		
		C A		
GAM1697	KIAA1456	3' GCGTGAGCCACCGCGCCCGGC 66998	ACA	
		GCTGGGC GTGGCTCACGC		

		CGGCCCG CACCGAGTGCG		
		CGC		
GAM1697 KIAA1467	3'	GCGTGAGCCACCATGCCCCGGCT 71609	CA	
	GG	TCAGCTGGGCA GTGGCTCACGC		
		GGTCGGCCCGT CACCGAGTGCG		
		AC		
GAM1697 KIAA1497	5'	CGTACCACCACGCCTAGCT 67507	ACA	CTC
		AGCTGGGC GTGG ACG		
		TCGATCCG CACC TGC		
		CAC A__		
GAM1697 KIAA1497	5'	GCGTGAGCCACCGCGCCCGGC 67510	ACA	
		GCTGGGC GTGGCTCACGC		
		CGGCCCG CACCGAGTGCG		
		CGC		
GAM1697 KIAA1508	3'	GCGTGAGCCACCATGTCCGG 61882	CA	
		CTGGGCA GTGGCTCACG		
		GGCCTGT CACCGAGTGC		
		AC		
GAM1697 KIAA1530	3'	GCGCACCACCACGCCAGCT 67953	ACA	CTCA
		AGCTGGGC GTGG CGC		
		TCGACCCG CACC GCG		
		CAC AC__		
GAM1697 KIAA1530	3'	GTGAGCCACCGCACTCAGCTGA 67957	CACA	
		TCAGCTGGG GTGGCTCAC		
		AGTCGACTC CACCGAGTG		
		ACGC		
GAM1697 KIAA1559	3'	TGAGCCACCACACCCAGC 73076	CACA	
		GCTGGG GTGGCTCA		
		CGACCC CACCGAGT		
		ACAC		
GAM1697 KIAA1571	3'	GCGTGCGCCACCATGCCCCGGCT 60954	CA	T
		AGCTGGGCA GTGGC CACGC		
		TCGGCCCGT CACCG GTGCG		
		AC C		
GAM1697 KIAA1571	3'	TGAGCCACCATGCCCAGC 60964	CA	
		GCTGGGCA GTGGCTCA		
		CGACCCGT CACCGAGT		
		AC		
GAM1697 KIAA1615	3'	GCATGAGCCACCACGCCTGTCC 68714	CA_____	C
	GG	CTGGGCA GTGGCTCA GC		

GGCCTGT CACCGAGT CG  
 CCGCAC A  
 GAM1697 KIAA1615 3' GCATGAGCCACCGCACCCAGCC 68716 \_ CACA C  
 TGG TCAG CTGGG GTGGCTCA GC  
 |||| |||| ||||| ||  
 GGTC GACCC CACCGAGT CG  
 C ACGC A  
 GAM1697 KIAA1615 3' GCATGCGCCACCATGCCCAGCT 68717 CA T C  
 AGCTGGGCA GTGGC CA GC  
 ||||| |||| ||  
 TCGACCCGT CACCG GT CG  
 AC C A  
 GAM1697 KIAA1649 5' CCATCACGCCCAGCTGG 50251 ACA  
 TCAGCTGGGC GTGG  
 ||||| ||  
 GGTCGACCCG TACC  
 CAC  
 GAM1697 KIAA1649 3' GCATGAGCCACTGCTCCCCA 50264 CA\_ C  
 TGGG CAGTGGCTCA GC  
 ||| ||||| ||  
 ACCC GTCACCGAGT CG  
 CTC A  
 GAM1697 KIAA1649 3' GCGTGAGCCACCACGCCCAGC 50269 ACA  
 GCTGGGC GTGGCTCACGC  
 ||||| |||||  
 CGACCCG CACCGAGTGCG  
 CAC  
 GAM1697 KIAA1655 3' GCGTGAGCCACTGCACCCAGC 66614 CA  
 GCTGGG CAGTGGCTCACGC  
 ||||| |||||  
 CGACCC GTCACCGAGTGCG  
 AC  
 GAM1697 KIAA1668 3' GCGTGAGCCACCACGCCCCGC 66474 ACA  
 GCTGGGC GTGGCTCACGC  
 ||||| |||||  
 CGGCCCCG CACCGAGTGCG  
 CAC  
 GAM1697 KIAA1671 3' CCACGCCCAGCTGA 65667 ACA  
 TCAGCTGGGC GTGG  
 ||||| ||  
 AGTCGACCCG CACC  
 —  
 GAM1697 KIAA1671 3' GCCTGAGCCACCATGCCCAGCT 65677 CA C  
 GA TCAGCTGGGCA GTGGCTCA GC  
 ||||| ||||| ||  
 AGTCGACCCGT CACCGAGT CG  
 AC C  
 GAM1697 KIAA1671 3' TGAGCCACTGCACCTGGC 65697 TG CA  
 GC GG CAGTGGCTCA  
 || || |||||

	CG CC GTCACCGAGT	
	GT AC	
GAM1697 KIAA1712	3' GCATGCACCACCATGCCAGCT 67538	CA CT C
	AGCTGGGCA GTGG CA GC	
	TCGACCCGT CACC GT CG	
	AC AC A	
GAM1697 KIAA1713	3' GCATGGGACTCATGCCAGC 72348	C_ GG C
	GCTGGGCA AGT CTCA GC	
	CGACCCGT TCA GGGT CG	
	AC _ A	
GAM1697 KIAA1737	3' GCCACCATGCCAGCT 67357	CA
	AGCTGGGCA GTGGC	
	TCGACCCGT CACCG	
	AC	
GAM1697 KIAA1784	3' CGCTGCCACGCCAGCTGA 65147	ACA TCA
	TCAGCTGGGC GTGGC CG	
	AGTCGACCCG CACCG GC	
	_ TC_	
GAM1697 KIAA1821	3' GCATGAGCCACCATGCCTGGC 71785	TG CA C
	GC GGCA GTGGCTCA GC	
	CG CCGT CACCGAGT CG	
	GT AC A	
GAM1697 KIAA1821	3' GCATGCACCACCACGCCAGCT 71786	ACA CT C
	AGCTGGGC GTGG CA GC	
	TCGACCCG CACC GT CG	
	CAC AC A	
GAM1697 KIAA1829	3' GCGTGAGCCACCGCGCCTGGC 61950	TG ACA
	GC GGC GTGGCTCACGC	
	CG CCG CACCGAGTGCG	
	GT CGC	
GAM1697 KIAA1871	3' GCATGAGCCACTGCACCAGC 61233	GCA C
	GCTGG CAGTGGCTCA GC	
	CGACC GTCACCGAGT CG	
	AC_ A	
GAM1697 KIAA1872	5' GCGTGAGCGATGCCAGCTG 62937	CAG G
	CAGCTGGGCA T GCTCACGC	
	GTCGACCCGT A CGAGTGCG	
	_ G	
GAM1697 KIAA1924	3' GCATGAGCCACTGTGCCAGC 73676	C
	GCTGGGCACAGTGGCTCA GC	

			CGACCCGTGTCACCGAGT CG		
			A		
GAM1697 KIAA1971	3'	GCATGAGCCACCGTGCCTGGCT 74219	TG A C		
	GA	TCAGC GGCAC GTGGCTCA GC			
		AGTCG CCGTG CACCGAGT CG			
		GT C A			
GAM1697 KLK7	3'	GCATGAGCCACCACGGCCAGC 17291	G ACA_ C		
		GCTGG C GTGGCTCA GC			
		CGACC G CACCGAGT CG			
		_GCAC A			
GAM1697 KLK7	3'	GCATGAGCCACCACGGCCAGC 57731	G ACA_ C		
		GCTGG C GTGGCTCA GC			
		CGACC G CACCGAGT CG			
		_GCAC A			
GAM1697 LIECG3	3'	GCATGAGCCACTGCACCCAGC 87410	CA C		
		GCTGGG CAGTGGCTCA GC			
		CGACCC GTCACCGAGT CG			
		AC A			
GAM1697 LY75	3'	GCCACCATGCCCGGCT 9840	CA		
		AGCTGGGCA GTGGC			
		TCGGCCCGT CACCG			
		AC			
GAM1697 MAP-1	3'	GCATGTGCCACCACGCCAGCT 42179	ACA T C		
		AGCTGGGC GTGGC CA GC			
		TCGACCCG CACCG GT CG			
		CAC T A			
GAM1697 MCLC	3'	GCATGAGCCATTGTGCCAGC 30685	C		
		GCTGGGCACAGTGGCTCA GC			
		CGACCCGTGTTACCGAGT CG			
		A			
GAM1697 MCM10	3'	CGTGACCAAGCCCAGCT 37571	ACAG C		
		AGCTGGGC TGG TCACG			
		TCGACCCG ACC AGTGC			
		A_ _			
GAM1697 MEF-2	3'	GCGCGAGCCACCACCCGGCT 64387	CACA A		
	GG	TCAGCTGGG GTGGCTC CGC			
		GGTCGGCCC CACCGAG GCG			
		ACAC C			
GAM1697 MGC11386	3'	GCATGAGCCACTGCACCCGGC 51952	CA C		
		GCTGGG CAGTGGCTCA GC			

			CGGCCC GTCACCGAGT CG		
			AC A		
GAM1697	MGC12466	3'	GCCACCATGCTCAGCT 79033	CA	
			AGCTGGGCA GTGGC		
			TCGACTCGT CACCG		
			AC		
GAM1697	MGC12518	3'	GCATGAGCCACAGTGCCCGGC 64080	A	C
			GCTGGGCAC GTGGCTCA GC		
			CGGCCCCGTG CACCGAGT CG		
			A A		
GAM1697	MGC14289	3'	GCATGAGCCACTGCACCCAGC 54703	CA	C
			GCTGGG CAGTGGCTCA GC		
			CGACCC GTCACCGAGT CG		
			AC A		
GAM1697	MGC15563	3'	GCGTAAGCCACTGTGTCTGGC 51795	TG	C
			GC GGCACAGTGGCT ACGC		
			CG CTGTGTCACCGA TGCG		
			GT A		
GAM1697	MGC1842	3'	GCCACCATGCCCCGGCT 65651	CA	
			AGCTGGGCA GTGGC		
			TCGGCCCCGT CACCG		
			AC		
GAM1697	MGC21675	3'	GCATGAACCACTGTGCCCAGCC 53483	A	C C
	GA		TC GCTGGGCACAGTGG TCA GC		
			AG CGACCCGTGTCACC AGT CG		
			C A A		
GAM1697	MGC2474	3'	GCACCTGCCACTATGCCCCGGCT 43726	C	TCAC
			AGCTGGGCA AGTGGC GC		
			TCGGCCCCGT TCACCG CG		
			A TCCA		
GAM1697	MGC2603	3'	GCATGCGCCACCACGCCAGCT 43860	ACA	T C
			AGCTGGGC GTGGC CA GC		
			TCGACCCG CACCG GT CG		
			CAC C A		
GAM1697	MGC29898	3'	GCGTGTGCCACCATGCCCCAGCT 58928	CA	T
			AGCTGGGCA GTGGC CACGC		
			TCGACCCGT CACCG GTGCG		
			AC T		
GAM1697	MGC3771	3'	GCGTGAGCCACCGCGCCCAGC 48246	ACA	
			GCTGGGC GTGGCTCACGC		

			CGACCCG CACCGAGTGCG		
			CGC		
GAM1697	MGC4638	3'	GCGTGAGCCACCGCGCCTGGCT 48942	TG	ACA
			AGC GGC GTGGCTCACGC		
			TCG CCG CACCGAGTGCG		
			GT CGC		
GAM1697	MGC5149	3'	CGTGCCACCACGCCAGCT 72290	ACA	TC
			AGCTGGGC GTGGC ACG		
			TCGACCCG CACCG TGC		
			CAC —		
GAM1697	MGC5149	3'	GCGTGAGCCACCGCGCCAAGC 72291	G	ACA
			GCT GGC GTGGCTCACGC		
			CGA CCG CACCGAGTGCG		
			A CGC		
GAM1697	MGC9912	3'	GCATGAGCCACCGTGCCCGGC 54718	A	C
			GCTGGGCAC GTGGCTCA GC		
			CGGCCCGTG CACCGAGT CG		
			C A		
GAM1697	MKRN4	3'	GCTACAATGCCAGCT 47749	CA	
			AGCTGGGCA GTGGC		
			TCGACCCGT CATCG		
			AA		
GAM1697	MLZE	5'	CGTGAGCCACCGTGCCCGGC 48619	A	
			GCTGGGCAC GTGGCTCACG		
			CGGCCCGTG CACCGAGTGC		
			C		
GAM1697	MMPL1	3'	GCATGAGCCACCACACCCAGCT 14719	CACA	C
			AGCTGGG GTGGCTCA GC		
			TCGACCC CACCGAGT CG		
			ACAC A		
GAM1697	moblak	3'	GCGTGAGCCACTGTGCCCGGC 55502		
			GCTGGGCACAGTGGCTCACGC		
			CGGCCCGTGTCACCGAGTGCG		
GAM1697	MOCS3	3'	GCGTGAGCCACCACACCC 27151	CACA	
			GGG GTGGCTCACGC		
			CCC CACCGAGTGCG		
			ACAC		
GAM1697	MRPL20	3'	GCGTGAGACACCGTGCCAGCT 35737	A	G
	GG		TCAGCTGGGCAC GTG CTCACGC		



GGTCGACCCGTG CAC GAGTGCG  
C A  
GAM1697 MRPS27 3' GCGTGAGCCACCACACCCGGC 30637 CACA  
GCTGGG GTGGCTCACGC  
||||| |||||  
CGGCC CACCGAGTGCG  
ACAC  
GAM1697 MT-ACT48 3' GCATGAGCCACTGCACCCGGCC 24689 A CA C  
GG TC GCTGGG CAGTGGCTCA GC  
|| ||||| ||||| ||  
GG CGGCC GTCACCGAGT CG  
C AC A  
GAM1697 MtFMT 3' CGTGAGCCACCGTGCCTGGC 57653 TG A  
GC GGCAC GTGGCTCACG  
|| ||||| |||||  
CG CCGTG CACCGAGTGCG  
GT C  
GAM1697 MYO5C 3' GCACCTGCCACCACGCCAGCT 38107 ACA TCAC  
AGCTGGGC GTGGC GC  
||||| ||||| ||  
TCGACCCG CACCG CG  
CAC TCCA  
GAM1697 NDP52 3' GCGTGAGCCACTGTGCTGGGC 19532 G  
GCT GGCACAGTGGCTCACGC  
||| |||||  
CGG TCGTGTACCGAGTGCG  
G  
GAM1697 NDUFC2 3' GCCACGACGCCAGCTGA 15834 ACA  
TCAGCTGGGC GTGGC  
||||| |||||  
AGTCGACCCG CACCG  
CAG  
GAM1697 NDUFC2 3' GCGTGAGCCACCGCGCCTGGT 15835 TG ACA  
GC GGC GTGGCTCACGC  
|| ||| |||||  
TG CCG CACCGAGTGCG  
GT CGC  
GAM1697 NICN1 3' GCATGAGCCACCGCGCCCGGC 50291 ACA C  
GCTGGGC GTGGCTCA GC  
||||| ||||| ||  
CGGCCCG CACCGAGT CG  
CGC A  
GAM1697 NIN283 3' CGTGAGCCAGGGCCAGCGGA 50069 A G ACAG  
TC GCTGG C TGGCTCACG  
|| ||||| |||||  
AG CGACC G ACCGAGTGCG  
G \_GG\_  
GAM1697 NINJ2 3' GCATGAGCCACTGCGCCTGGCC 33285 A TG A C  
GA TC GC GGC CAGTGGCTCA GC  
|| || ||| ||||| ||

AG CG CCG GTCACCGAGT CG  
 C GT C A  
 GAM1697 OSBPL2 3' GCGTGAGCCACTGCGCCTGGC 57865 TG A  
 GC GGC CAGTGGCTCACGC  
 || ||| |||||  
 CG CCG GTCACCGAGTGCG  
 GT C  
 GAM1697 OSBPL2 3' GCGTGAGCCACTGCGCCTGGC 29214 TG A  
 GC GGC CAGTGGCTCACGC  
 || ||| |||||  
 CG CCG GTCACCGAGTGCG  
 GT C  
 GAM1697 PELI1 5' CGTGAGCCACTGCTCCCAG 40261 CA  
 CTGGG CAGTGGCTCACG  
 ||||| |||||  
 GACCC GTCACCGAGTGC  
 TC  
 GAM1697 PELI1 5' GCATGTGCCACCACGCCCGGCT 40269 ACA T C  
 AGCTGGGC GTGGC CA GC  
 ||||| ||||| ||  
 TCGGCCCG CACCG GT CG  
 CAC T A  
 GAM1697 PPIL3 5' GCGTGAGCCACCACGCCCGGC 55657 ACA  
 GCTGGGC GTGGCTCACGC  
 ||||| |||||  
 CGGCCCG CACCGAGTGCG  
 CAC  
 GAM1697 PRO0365 5' GCACCTGCCACCACGCCCAGCT 26158 ACA TCAC  
 AGCTGGGC GTGGC GC  
 ||||| ||||| ||  
 TCGACCCG CACCG CG  
 CAC TCCA  
 GAM1697 PRO0365 5' GCGTGAGCCACCACGCCCAGCT 26159 ACA  
 GG TCAGCTGGGC GTGGCTCACGC  
 ||||| |||||  
 GGTCGACCCG CACCGAGTGCG  
 CAC  
 GAM1697 PRO1048 3' CGTGAACCACTGTGTCCA 37514 C  
 TGGGCACAGTGG TCACG  
 ||||| |||||  
 ACCTGTGTCACC AGTGC  
 A  
 GAM1697 PRO2955 3' GCGTGAGCCACTGCGCCCGGC 37638 A  
 GCTGGGC CAGTGGCTCACGC  
 ||||| |||||  
 CGGCCCG GTCACCGAGTGCG  
 C  
 GAM1697 PSMD12 3' GCATGAGCCACTGCACCCAACT 11000 C CA C  
 AG TGGG CAGTGGCTCA GC  
 || ||| ||||| ||

			TC ACCC GTCACCGAGT CG		
			A AC A		
GAM1697	PSTPIP2	3'	GCGTGAGCCACTGCGCCCGGC 44390	A	
			GCTGGGC CAGTGGCTCACGC		
			CGGCCCG GTCACCGAGTGCG		
			C		
GAM1697	RAB21	3'	GCGTGAGCCACCGTGCCCGGC 30387	A	
			GCTGGGCAC GTGGCTCACGC		
			CGGCCCGTG CACCGAGTGCG		
			C		
GAM1697	RAB33B	3'	GTCACTGCACCCAGCCGA 48502	A	CA
			TC GCTGGG CAGTGGC		
			AG CGACCC GTCACTG		
			C AC		
GAM1697	RAB39	3'	GCCACCATGCCCGGCT 76633		CA
			AGCTGGGCA GTGGC		
			TCGGCCCGT CACCG		
			AC		
GAM1697	RAI	5'	GCGTGTGCCACCACGCCCGGCT 21882	ACA	T
			AGCTGGGC GTGGC CACGC		
			TCGGCCCG CACCG GTGCG		
			CAC T		
GAM1697	RASSF2	3'	GCGTGAGCCACTGTGCCCAGC 28437		
			GCTGGGCACAGTGGCTCACGC		
			CGACCCGTGTCACCGAGTGCG		
GAM1697	RES4-25	3'	TGTGCCACCACGCCCAGCT 64655	ACA	T
			AGCTGGGC GTGGC CA		
			TCGACCCG CACCG GT		
			CAC T		
GAM1697	RGC32	5'	CGCGCCGGGCCCAGCTGA 25922	ACAG	TCA
			TCAGCTGGGC TGGC CG		
			AGTCGACCCG GCCG GC		
			G__ C__		
GAM1697	RNF8	3'	GCGTGAGCCACCACGCCCAGC 14227	ACA	
			GCTGGGC GTGGCTCACGC		
			CGACCCG CACCGAGTGCG		
			CAC		
GAM1697	SCYA16	3'	GCGTGAGCCACCACATCCGGC 15960	CACA	
			GCTGGG GTGGCTCACGC		

			CGGCCT CACCGAGTGCG			
			ACAC			
GAM1697	SCYA28	3'	GCATGAGCCACTGCACCTGGC 39058	TG CA		C
			GC GG CAGTGGCTCA GC			
			CG CC GTCACCGAGT CG			
			GT AC A			
GAM1697	SERF1B	3'	GCGCCTGCCACCACGCCAGCT 43415	ACA TCA		
			AGCTGGGC GTGGC CGC			
			TCGACCCG CACCG GCG			
			CAC TCC			
GAM1697	SFXN2	3'	GCATGAGCCACCACACCCAGC 73947	CACA C		
			GCTGGG GTGGCTCA GC			
			CGACCC CACCGAGT CG			
			ACAC A			
GAM1697	SIAT4B	3'	GCGTCTGCTGTGCCCCGC 22656	T TG CTC		
			GC GGGCACAG G ACGC			
			CG CCCGTGTC C TGCG			
			C GT _			
GAM1697	SIRPB1	3'	GCATGAGCCACCATGCCTAGC 20253	CA C		
			GCTGGGCA GTGGCTCA GC			
			CGATCCGT CACCGAGT CG			
			AC A			
GAM1697	SLC11A1	3'	GCGCGCCACCACGCCAGCT 59459	ACA TCA		
			AGCTGGGC GTGGC CGC			
			TCGACCCG CACCG GCG			
			CAC C _			
GAM1697	SLC12A8	3'	GCGTGAGCCACCATGCCTGGC 44900	TG CA		
			GC GGCA GTGGCTCACGC			
			CG CCGT CACCGAGTGCG			
			GT AC			
GAM1697	SLC19A3	3'	GCGTGAGCCACCATGCCTGGC 47491	TG CA		
			GC GGCA GTGGCTCACGC			
			CG CCGT CACCGAGTGCG			
			GT AC			
GAM1697	SREC	3'	GCATGAGCCACCACGCCTGGT 13502	TG ACA C		
			GC GGC GTGGCTCA GC			
			TG CCG CACCGAGT CG			
			GT CAC A			
GAM1697	SS-56	3'	GCATGAGCCACTGCGCCCGGC 59604	A C		
			GCTGGGC CAGTGGCTCA GC			

			CGGCCCG GTCACCGAGT CG	
			C A	
GAM1697	TADA3L	3'	GCGTGAGCCACTGCGCCTGGC 55995	TG A
			GC GGC CAGTGGCTCACGC	
			CG CCG GTCACCGAGTGCG	
			GT C	
GAM1697	TCL6	5'	GCGTGAGCCGCTGCACCCAGC 40136	CA
			GCTGGG CAGTGGCTCACGC	
			CGACCC GTCGCCGAGTGCG	
			AC	
GAM1697	TCL6	5'	GCGTGAGCCGCTGCACCCAGC 40159	CA
			GCTGGG CAGTGGCTCACGC	
			CGACCC GTCGCCGAGTGCG	
			AC	
GAM1697	TCL6	3'	GCGTGAGCCACCACGCCCGGT 24981	ACA
			GCTGGGC GTGGCTCACGC	
			TGGCCCG CACCGAGTGCG	
			CAC	
GAM1697	TCL6	3'	GCGTGAGCCACCACGCCCGGT 26997	ACA
			GCTGGGC GTGGCTCACGC	
			TGGCCCG CACCGAGTGCG	
			CAC	
GAM1697	TM4-B	3'	GCGTGAGCCACCACGCTGGGC 24970	G ACA
			GCT GGC GTGGCTCACGC	
			CGG TCG CACCGAGTGCG	
			G CAC	
GAM1697	TOB2	5'	TGAGCCACTGGTGGGACAG 32773	GG_ _
			CTG CAC AGTGGCTCA	
			GAC GTG TCACCGAGT	
			AGG G	
GAM1697	TOR1B	3'	GCATGAGCCACTGTGCCCAGCT 27200	C
	GG		TCAGCTGGGCACAGTGGCTCA GC	
			GGTCGACCCGTGTCACCGAGT CG	
			A	
GAM1697	TRIM16	3'	GCGTGAGCCACTGCGCCCTGC 21340	T A
			GC GGGC CAGTGGCTCACGC	
			CG CCCG GTCACCGAGTGCG	
			T C	
GAM1697	TU12B1-TY	3'	GCATGAGCCACCGTGCCCAGC 33386	A C
			GCTGGGCAC GTGGCTCA GC	

		CGACCCGTG CACCGAGT CG		
		C A		
GAM1697 TUSP	3'	CGTGAGCCACCACTCCCGG 39632	CACA	
		CTGGG GTGGCTCACG		
		GGCCC CACCGAGTGC		
		TCAC		
GAM1697 UBCE7IP5	3'	GCATGAGCCACTTCGCCTAGC 30153	AC	C
		GCTGGGC AGTGGCTCA GC		
		CGATCCG TCACCGAGT CG		
		CT A		
GAM1697 UBCE7IP5	3'	GCATGTGCCACCATGCCCAGCT 30154	CA	T C
		AGCTGGGCA GTGGC CA GC		
		TCGACCCGT CACCG GT CG		
		AC T A		
GAM1697 USP22	3'	GCGTGAGCCACCGCACCTGGC 68014	TG	CACA
		GC GG GTGGCTCACGC		
		CG CC CACCGAGTGCG		
		GT ACGC		
GAM1697 VDU1	3'	GCACCTGCCACCATGCCCCGGCT 30419	CA	TCAC
		AGCTGGGCA GTGGC GC		
		TCGGCCCGT CACCG CG		
		AC TCCA		
GAM1697 ZNF17	3'	GCATGAGCCACCGTGCCCCGGC 82391	A	C
		GCTGGGCAC GTGGCTCA GC		
		CGGCCCCGTG CACCGAGT CG		
		C A		
GAM1697 ZNF339	3'	GCCACTATGCCCAGCT 41119	C	
		AGCTGGGCA AGTGGC		
		TCGACCCGT TCACCG		
		A		
GAM1697 LOC112687	3'	GCATGTGTCACCACGCCCGGCT 72860	ACA	T C
		AGCTGGGC GTGGC CA GC		
		TCGGCCCG CACTG GT CG		
		CAC T A		
GAM1697 LOC112817	3'	GCGCCTGCCACCACGCCCAGCT 56513	ACA	TCA
		AGCTGGGC GTGGC CGC		
		TCGACCCG CACCG GCG		
		CAC TCC		
GAM1697 LOC113730	5'	CCCTGCCCCAGCTGA 73106	CA	T
		TCAGCTGGG CAG GG		

AGTCGACCC GTC CC  
 C\_ \_  
 GAM1697 LOC115648 3' CGTGAGCCACCACCCCGG 59297 CACA  
 CTGGG GTGGCTCACG  
 |||| |||||  
 GGCCC CACCGAGTGC  
 CCAC  
 GAM1697 LOC115648 3' GCGTGAGCCACCATGCCCAGC 59300 CA  
 GCTGGGCA GTGGCTCACGC  
 ||||| |||||  
 CGACCCGT CACCGAGTGCG  
 AC  
 GAM1697 LOC119392 3' GCGCCCGCCACCATGCCCCGGCT 59136 CA TCA  
 AGCTGGGCA GTGGC CGC  
 ||||| ||| ||  
 TCGGCCCGT CACCG GCG  
 AC CCC  
 GAM1697 LOC120114 3' GCATGAGCCACCGTGCCCAGC 75529 A C  
 GCTGGGCAC GTGGCTCA GC  
 ||||| ||||| ||  
 CGACCCGTG CACCGAGT CG  
 C A  
 GAM1697 LOC120114 3' TGAGCCACCGTGCCCAGC 75542 A  
 GCTGGGCAC GTGGCTCA  
 ||||| |||||  
 CGACCCGTG CACCGAGT  
 C  
 GAM1697 LOC120939 3' GCCACCGTGCCCAGCT 76256 A  
 AGCTGGGCAC GTGGC  
 ||||| |||||  
 TCGACCCGTG CACCG  
 C  
 GAM1697 LOC121504 3' GCGTGAGCCACCACGCTTGGT 74098 TG ACA  
 GC GGC GTGGCTCACGC  
 || ||| |||||  
 TG TCG CACCGAGTGCG  
 GT CAC  
 GAM1697 LOC122622 3' GGTTCGCGTGCCAGCCGA 74137 A A TG  
 TC GCTGGGCAC G GCT  
 || ||||| | |||  
 AG CGACCTGTG C TGG  
 C \_GT  
 GAM1697 LOC124216 3' GTGAGCCACCACACCCAGC 74265 CACA  
 GCTGGG GTGGCTCAC  
 |||| |||||  
 CGACCC CACCGAGTG  
 ACAC  
 GAM1697 LOC124871 3' GCATGAGCCACTGTGCCAGGC 74347 G C  
 GCT GGCACAGTGGCTCA GC  
 || ||||| ||||| ||

		CGG CCGTGTACACCGAGT CG		
		A A		
GAM1697	LOC126272 3'	GCGTGAGCCACCGCGCCCGGCC 76089	A	ACA
	GA	TC GCTGGGC GTGGCTCACGC		
		AG CGGCCCG CACCGAGTGCG		
		C CGC		
GAM1697	LOC126661 3'	GTGAGCCACCATGCCCAGC 74556	CA	
		GCTGGGCA GTGGCTCAC		
		CGACCCGT CACCGAGTG		
		AC		
GAM1697	LOC126669 3'	GCATGAGCCACTGCACCCGGC 75406	CA	C
		GCTGGG CAGTGGCTCA GC		
		CGGCCG GTCACCGAGT CG		
		AC A		
GAM1697	LOC128989 3'	GCGTGAGCCACCACGCCTGGCC 74811	A TG	ACA
	GA	TC GC GGC GTGGCTCACGC		
		AG CG CCG CACCGAGTGCG		
		C GT CAC		
GAM1697	LOC128989 3'	GCGTGTGCCACCATGCCCAGCT 74813	CA	T
		AGCTGGGCA GTGGC CACGC		
		TCGACCCGT CACCG GTGCG		
		AC T		
GAM1697	LOC128989 3'	GCCACCATGCCCAGCT 74810	CA	
		AGCTGGGCA GTGGC		
		TCGACCCGT CACCG		
		AC		
GAM1697	LOC132241 5'	GCGTGAGCCACCGCGCCCGGC 75049	ACA	
		GCTGGGC GTGGCTCACGC		
		CGGCCCG CACCGAGTGCG		
		CGC		
GAM1697	LOC133686 3'	GCATGAGCCACCATGCCCAGC 75122	CA	C
		GCTGGGCA GTGGCTCA GC		
		CGGCCCGT CACCGAGT CG		
		AC A		
GAM1697	LOC135154 3'	GTGAGCCACCACGCCCAGC 75220	ACA	
		GCTGGGC GTGGCTCAC		
		CGACCCG CACCGAGTG		
		CAC		
GAM1697	LOC135293 3'	GCATGAGCCACCGCACCCGGC 76181	CACA	C
		GCTGGG GTGGCTCA GC		



	CGGCCC CACCGAGT CG		
	ACGC A		
GAM1697 LOC135293 3'	GCGCACCATGCCCAGCT 76183	CA	_____
	AGCTGGGCA GTG GC		
	TCGACCCGT CAC CG		
	AC GIII		
GAM1697 LOC135818 3'	GCGTGAGCCACCACACCTGGCT 75238	TG	CACA
	AGC GG GTGGCTCACGC		
	TCG CC CACCGAGTGCG		
	GT ACAC		
GAM1697 LOC139046 5'	GCCGCCCGTGCCCAGCCGA 75813	A	A_
	TC GCTGGGCAC GTGGC		
	AG CGACCCGTG CGCCG		
	C CC		
GAM1697 LOC142949 5'	CCACCGTGCCCAGCTGA 82893	A	
	TCAGCTGGGCAC GTGG		
	AGTCGACCCGTG CACC		
	C		
GAM1697 LOC144317 5'	GCCTGACACCACGCCAGCT 76793	ACA	C_ C
	AGCTGGGC GTGG TCA GC		
	TCGACCCG CACC AGT CG		
	_____ AC C		
GAM1697 LOC144519 5'	GCGCACCATGCCCAGCT 76871	CA	CTCA
	AGCTGGGCA GTGG CGC		
	TCGACCCGT CACC GCG		
	AC AC_		
GAM1697 LOC144667 3'	GTGAGCCACTTCGCCCAGCTGA 83171	AC	
	TCAGCTGGGC AGTGGCTCAC		
	AGTCGACCCG TCACCGAGTG		
	CT		
GAM1697 LOC144742 5'	GTTACCATGCCCAGCT 76946	CA	
	AGCTGGGCA GTGGC		
	TCGACCCGT CATTG		
	AC		
GAM1697 LOC144871 3'	GCGTGAGCCACTGCGCCTGGC 83200	TG	A
	GC GGC CAGTGGCTCACGC		
	CG CCG GTCACCGAGTGCG		
	GT C		
GAM1697 LOC145082 5'	GCATGAGCCACCACACCTGACT 83239	CT	CACA C
	AG GGG GTGGCTCA GC		

		TC TCC CACCGAGT CG		
		AG ACAC A		
GAM1697	LOC145082 5'	GCATGAGCCACCACATCTGGC 83240	TG CACA	C
		GC GG GTGGCTCA GC		
		CG CT CACCGAGT CG		
		GT ACAC A		
GAM1697	LOC145268 5'	GCGTGAGCCACCACACCTGGC 77058	TG CACA	
		GC GG GTGGCTCACGC		
		CG CC CACCGAGTGCG		
		GT ACAC		
GAM1697	LOC145453 5'	GCATGAGCCACCACGCCAGC 77142	ACA	C
		GCTGGGC GTGGCTCA GC		
		CGACCCG CACCGAGT CG		
		CAC A		
GAM1697	LOC145622 3'	GCGTGAGCCACTGTGCCTGGC 77302	TG	
		GC GGCACAGTGGCTCACGC		
		CG CCGTGTACCGAGTGCG		
		GT		
GAM1697	LOC146050 3'	GCATGCGCCACCATGCCAGCT 77638	CA	T C
		AGCTGGGCA GTGGC CA GC		
		TCGACCCGT CACCG GT CG		
		AC C A		
GAM1697	LOC146108 3'	GCATGAGCCACCATGCCAGC 77665	CA	C
		GCTGGGCA GTGGCTCA GC		
		CGACCCGT CACCGAGT CG		
		AC A		
GAM1697	LOC146229 3'	GCGTGAGTCACCATGCCCTGCT 77753	T CA	
		AGC GGGCA GTGGCTCACGC		
		TCG CCCGT CACTGAGTGCG		
		T AC		
GAM1697	LOC146337 5'	GCATGAGCCACCGTGCCCGGCC 83659	A A	C
	GG	TC GCTGGGCAC GTGGCTCA GC		
		GG CGGCCCGTG CACCGAGT CG		
		C C A		
GAM1697	LOC146346 5'	GCGTGAGCCACCACGCCCGGC 77843	ACA	
		GCTGGGC GTGGCTCACGC		
		CGGCCCG CACCGAGTGCG		
		CAC		
GAM1697	LOC146438 3'	GCGTGAGCCACCGCGCCCAGC 77891	ACA	
		GCTGGGC GTGGCTCACGC		

	CGACCCG CACCGAGTGCG		
	CGC		
GAM1697 LOC146603 5'	GCGTGAGCCACCGCGCCGGGC 78017	G	ACA
	GCT GGC GTGGCTCACGC		
	CGG CCG CACCGAGTGCG		
	G CGC		
GAM1697 LOC146784 5'	GCATGAGCCACCACGCCAGC 78116	ACA	C
	GCTGGGC GTGGCTCA GC		
	CGACCCG CACCGAGT CG		
	CAC A		
GAM1697 LOC146784 5'	GCGTGCCACCACACCCAGCT 78118	CACA	TC
	AGCTGGG GTGGC ACGC		
	TCGACCC CACCG TGCG		
	ACAC —		
GAM1697 LOC146894 3'	CTGAGCCACTGTGTCTGG 59189	TG	C
	C GGCACAGTGGCTCA G		
	G CTGTGTCACCGAGT C		
	GT A		
GAM1697 LOC146901 3'	GCATGAGCCACCGCACCTGGTC 83840	_ TG	CACA C
TG	CAG C GG GTGGCTCA GC		
	GTC G CC CACCGAGT CG		
	T GT ACGC A		
GAM1697 LOC146909 3'	GCGTGAGCCACTGCGCCCGGC 78175	A	
	GCTGGGC CAGTGGCTCACGC		
	CGGCCCG GTCACCGAGTGCG		
	C		
GAM1697 LOC146952 5'	GCCACCCTGCCAGCT 83867	CA	
	AGCTGGGCA GTGGC		
	TCGACCCGT CACCG		
	CC		
GAM1697 LOC147054 3'	GCGTGAGTCACCGCGCCCAGCC 83921	A	ACA
GG	TC GCTGGGC GTGGCTCACGC		
	GG CGACCCG CACTGAGTGCG		
	C CGC		
GAM1697 LOC147080 5'	GCGTGAGCCACCGCGCCCG 83934	ACA	
	TGGGC GTGGCTCACGC		
	GCCCG CACCGAGTGCG		
	CGC		
GAM1697 LOC147160 5'	GCGCACGTGTGCCAGTCGA 83966	A	— —
	TC GCTGGGCACA GTG GC		

AG TGACCCGTGT CAC CG  
 C G GIII  
 GAM1697 LOC147166 3' GCGTGAGCCACTGCGCCCTGC 78287 T A  
 GC GGGC CAGTGGCTCACGC  
 || ||| |||||  
 CG CCCG GTCACCGAGTGCG  
 T C  
 GAM1697 LOC147276 3' GCATGAGCCACTGCGCCAGGC 78334 G A C  
 GCT GGC CAGTGGCTCA GC  
 ||| ||| ||||| ||  
 CGG CCG GTCACCGAGT CG  
 A C A  
 GAM1697 LOC147429 3' GCGTGAGCCACCGCGCCCGGC 78360 ACA  
 GCTGGGC GTGGCTCACGC  
 ||||| |||||  
 CGGCCCG CACCGAGTGCG  
 CGC  
 GAM1697 LOC147694 3' GCGTGAGCCACCGCGCCTGGC 78451 TG ACA  
 GC GGC GTGGCTCACGC  
 || ||| |||||  
 CG CCG CACCGAGTGCG  
 GT CGC  
 GAM1697 LOC147817 3' AGCCACTGCACCCAGC 78489 CA  
 GCTGGG CAGTGGCT  
 ||||| |||||  
 CGACCC GTCACCGA  
 AC  
 GAM1697 LOC147817 3' CTGAGCCACTGCATCCAG 78498 CA C  
 CTGGG CAGTGGCTCA G  
 ||||| ||||| |  
 GACCT GTCACCGAGT C  
 AC A  
 GAM1697 LOC147841 3' GCGTGAGCCATCGTGCCCAGCT 78528 A  
 AGCTGGGCAC GTGGCTCACGC  
 ||||| |||||  
 TCGACCCGTG TACCGAGTGCG  
 C  
 GAM1697 LOC147990 3' GCGTGAGCCACTGCGTCCAGC 84094 A  
 GCTGGGC CAGTGGCTCACGC  
 ||||| |||||  
 CGACCTG GTCACCGAGTGCG  
 C  
 GAM1697 LOC148137 3' GCGTGAGCCACCGTGCTGGGC 58432 G A  
 GCT GGCAC GTGGCTCACGC  
 ||| ||||| |||||  
 CGG TCGTG CACCGAGTGCG  
 G C  
 GAM1697 LOC148189 5' GCATGCGCCACCACGCCAGCT 78710 ACA T C  
 GA TCAGCTGGGC GTGGC CA GC  
 ||||| ||||| |||

AGTCGACCCG CACCG GT CG  
 CAC C A  
 GAM1697 LOC148189 5' GCGTGAGCCACCATGCCTGGC 78711 TG CA  
 GC GGCA GTGGCTCACGC  
 || ||| |||||  
 CG CCGT CACCGAGTGCG  
 GT AC  
 GAM1697 LOC148887 5' GCGTGAGCCACCGCGCCCGGCC 84240 A ACA  
 GG TC GCTGGGC GTGGCTCACGC  
 || ||||| |||||  
 GG CGGCCCG CACCGAGTGCG  
 C CGC  
 GAM1697 LOC148918 5' GCATGAGCCACTGTGCCT 79072 C  
 GGGCACAGTGGCTCA GC  
 ||||| ||  
 TCCGTGTCACCGAGT CG  
 A  
 GAM1697 LOC149113 3' CCACGCGCATCACCATGTCCAG 79162 CA \_\_\_\_\_ TCAC  
 CTGA GCTGGGCA GTG GC G  
 ||||| || || |  
 CGACCTGT CAC CG C  
 AC TACG||| CACT  
 GAM1697 LOC149421 3' GCATGAGCCACTGCGCCCGGC 79359 A C  
 GCTGGGC CAGTGGCTCA GC  
 ||||| ||||| ||  
 CGGCCCG GTCACCGAGT CG  
 C A  
 GAM1697 LOC149506 3' GCATGAGCCACTGTGCCCAGC 84468 C  
 GCTGGGCACAGTGGCTCA GC  
 ||||| ||||| ||  
 CGACCCGTGTCACCGAGT CG  
 A  
 GAM1697 LOC149577 3' GCCACCATGCCAGCT 84514 CA  
 AGCTGGGCA GTGGC  
 ||||| ||||  
 TCGACCCGT CACCG  
 AC  
 GAM1697 LOC149692 3' CTGAGCCACCGCTCCTGG 84586 CT ACA C  
 TCAG GGC GTGGCTCA G  
 ||| ||| ||||| |  
 GGTC CTCG CACCGAGT C  
 \_ C \_ A  
 GAM1697 LOC149692 3' GCGTGAGCCACTGCGCCCGGC 84587 A  
 GCTGGGC CAGTGGCTCACGC  
 ||||| |||||  
 CGGCCCG GTCACCGAGTGCG  
 C  
 GAM1697 LOC149703 5' GCGTGAGCCACTGCACCCAGC 84654 CA  
 GCTGGG CAGTGGCTCACGC  
 ||||| |||||

		CGACCC GTCACCGAGTGCG			
		AC			
GAM1697	LOC149821 5'	GCGTGAGCCACTGCGCCCGGC 84764	A		
		GCTGGGC CAGTGGCTCACGC			
		CGGCCCG GTCACCGAGTGCG			
		C			
GAM1697	LOC150054 5'	GCATATGCCACCACGCCCGGCT 84833	ACA	TCAC	
		AGCTGGGC GTGGC GC			
		TCGGCCCG CACCG CG			
		CAC TATA			
GAM1697	LOC150054 5'	GCATGAGCCACTGCACCTGGC 84834	TG CA	C	
		GC GG CAGTGGCTCA GC			
		CG CC GTCACCGAGT CG			
		GT AC A			
GAM1697	LOC150166 5'	GCGTGACCACTGTGCCCCGGCT 84885		CT	
		AGCTGGGCACAGTGG CACGC			
		TCGGCCCGTGTACC GTGCG			
		AC			
GAM1697	LOC150282 5'	GCATGAGCCACCGTGCCCCGGCT 79726	A	C	
	G	CAGCTGGGCAC GTGGCTCA GC			
		GTCGGCCCGTG CACCGAGT CG			
		C A			
GAM1697	LOC150282 5'	GCGCCCGCCACCACGCCCGGCT 79728	ACA	TCA	
		AGCTGGGC GTGGC CGC			
		TCGGCCCG CACCG GCG			
		CAC CCC			
GAM1697	LOC150397 3'	GCGTGAGCCACCGTGCTGGGC 79846	G A		
		GCT GGCAC GTGGCTCACGC			
		CGG TCGTG CACCGAGTGCG			
		G C			
GAM1697	LOC150407 3'	AGCCACTGTGCCAGC 79816			
		GCTGGGCACAGTGGCT			
		CGACCCGTGTCACCGA			
GAM1697	LOC150407 3'	GCGTGAGCCACCGCATCTGGC 79826	TG CACA		
		GC GG GTGGCTCACGC			
		CG CT CACCGAGTGCG			
		GT ACGC			
GAM1697	LOC150587 3'	GCATGAGCCACCATGCCTGGCC 85062	_ TG CA	C	
	TG	CAG C GGCA GTGGCTCA GC			

	GTC G CCGT CACCGAGT CG		
	C GT AC A		
GAM1697 LOC150630 5'	GCGCCCCG CACTGCGCCCGGCT 85106	A	TCA
	AGCTGGGC CAGTGGC CGC		
	TCGGCCCCG GTCACCG GCG		
	C CCC		
GAM1697 LOC150630 5'	GCGTGAGCCACCGCGCCCGGC 85107	ACA	
	GCTGGGC GTGGCTCACGC		
	CGGCCCG CACCGAGTGCG		
	CGC		
GAM1697 LOC150960 3'	GCATGAGCCACCGCACCCAGC 80062	CACA	C
	GCTGGG GTGGCTCA GC		
	CGACCC CACCGAGT CG		
	ACGC A		
GAM1697 LOC151057 3'	CGTGCCACCACGCCCGGCT 85211	ACA	TC
	AGCTGGGC GTGGC ACG		
	TCGGCCCCG CACCG TGC		
	CAC —		
GAM1697 LOC151201 3'	GCGTGAGCCACCACGCCAGC 85280	ACA	
	GCTGGGC GTGGCTCACGC		
	CGACCCG CACCGAGTGCG		
	CAC		
GAM1697 LOC151475 5'	GCATGAGCCACCGCGCCTGGC 85406	TG ACA	C
	GC GGC GTGGCTCA GC		
	CG CCG CACCGAGT CG		
	GT CGC A		
GAM1697 LOC151826 3'	GCATGAGCCACCATGCCTGGC 80357	TG CA	C
	GC GGCA GTGGCTCA GC		
	CG CCGT CACCGAGT CG		
	GT AC A		
GAM1697 LOC152300 3'	GCTTGAGCCACCGCACCCGGCC 80547	A CACA	C
GA	TC GCTGGG GTGGCTCA GC		
	AG CGGCC CACCGAGT CG		
	C ACGC T		
GAM1697 LOC152343 3'	GCCACCATGCTCAGCT 80566	CA	
	AGCTGGGCA GTGGC		
	TCGACTCGT CACCG		
	AC		
GAM1697 LOC152445 3'	GCATGAGCCACTGCGCCTGGC 85751	TG A	C
	GC GGC CAGTGGCTCA GC		

		CG CCG GTCACCGAGT CG			
		GT C A			
GAM1697	LOC152445 3'	GCGTGAGCCACTGCGCCCGGC	85752	A	
		GCTGGGC CAGTGGCTCACGC			
		CGGCCCG GTCACCGAGTGCG			
		C			
GAM1697	LOC152719 5'	GCATGAGCCACCGCGCCCGGC	85850	ACA	C
		GCTGGGC GTGGCTCA GC			
		CGGCCCG CACCGAGT CG			
		CGC A			
GAM1697	LOC152794 5'	GCATGAGCCACCGCGCCCTGC	80678	T ACA	C
		GC GGC GTGGCTCA GC			
		CG CCG CACCGAGT CG			
		T CGC A			
GAM1697	LOC152851 3'	GCATGCACCACCACGCCCGGCT	80711	ACA	CT C
		AGCTGGGC GTGG CA GC			
		TCGGCCCG CACC GT CG			
		CAC AC A			
GAM1697	LOC152851 3'	GCGTGAGCCACCGCACCTGGC	80712	TG CACA	
		GC GG GTGGCTCACGC			
		CG CC CACCGAGTGCG			
		GT ACGC			
GAM1697	LOC153577 3'	GCAACTACTGCCAGCCGA	86059	A C_	G
		TC GCTGGGCA AGT GC			
		AG CGACCCGT TCA CG			
		C CA A			
GAM1697	LOC153688 3'	GCGTGAGCCACTGTGCCAGC	86111		
		GCTGGGCACAGTGGCTCACGC			
		CGACCCGTGTCACCGAGTGCG			
GAM1697	LOC154141 5'	GCGTGAGCCACCGCGCCCGGCC	86170	A ACA	
	GG	TC GCTGGGC GTGGCTCACGC			
		GG CGGCCCG CACCGAGTGCG			
		C CGC			
GAM1697	LOC154282 5'	CTGAGCCACTGCATCCGG	86198	CA	C
		CTGGG CAGTGGCTCA G			
		GGCCT GTCACCGAGT C			
		AC A			
GAM1697	LOC154403 3'	CCACGCGCATCACCATGTCCAG	81070	CA	TCAC
	CTGA	GCTGGGCA GTG GC G			



		CGACCTGT CAC CG C		
		AC TACGIII CACT		
GAM1697	LOC154726 5'	GCATGAGCCACCGTGCCTGGC	81106	TG A C
		GC GGCAC GTGGCTCA GC		
		CG CCGTG CACCGAGT CG		
		GT C A		
GAM1697	LOC154726 3'	TGAGCCACCACGCCAGC	81111	ACA
		GCTGGGC GTGGCTCA		
		CGACCCG CACCGAGT		
		CAC		
GAM1697	LOC154739 5'	GCATGAGCCACCATGCCTGGC	86232	TG CA C
		GC GGCA GTGGCTCA GC		
		CG CCGT CACCGAGT CG		
		GT AC A		
GAM1697	LOC154877 3'	CGTGAGCCACTGCATCTGG	86292	TG CA
		C GG CAGTGGCTCACG		
		G CT GTCACCGAGTGC		
		GT AC		
GAM1697	LOC154877 3'	GCGTGAGCCACCACACCCGGCT	86296	CACA
		AGCTGGG GTGGCTCACGC		
		TCGGCCC CACCGAGTGCG		
		ACAC		
GAM1697	LOC154930 3'	GTGAGCCACTGTTCCCAGC	81180	C
		GCTGGG ACAGTGGCTCAC		
		CGACCC TGTACCGAGTG		
		T		
GAM1697	LOC154992 3'	CCACGCGCATCACCATGTCCAG	81212	CA _____ TCAC
	CTGA	GCTGGGCA GTG GC G		
		CGACCTGT CAC CG C		
		AC TACGIII CACT		
GAM1697	LOC157247 5'	GCATGAACCACCGTGCCCGGC	81367	A C C
		GCTGGGCAC GTGG TCA GC		
		CGGCCCGTG CACC AGT CG		
		C A A		
GAM1697	LOC157506 3'	GCATGAGCCACTGCACCCAGC	81441	CA C
		GCTGGG CAGTGGCTCA GC		
		CGACCC GTCACCGAGT CG		
		AC A		
GAM1697	LOC157506 3'	GCATGCGCCACCACGCCAGCT	81442	ACA T C
		AGCTGGGC GTGGC CA GC		

	TCGACCCG CACCG GT CG		
	CAC C A		
GAM1697 LOC157507 5'	GCATGAGCCACCAAACCCAGC 81457	CACA	C
	GCTGGG GTGGCTCA GC		
	CGACCC CACCGAGT CG		
	AAAC A		
GAM1697 LOC157623 3'	GCATGAGCCACTGTGCCT 81499	C	
	GGGCACAGTGGCTCA GC		
	TCCGTGTCACCGAGT CG		
	A		
GAM1697 LOC157798 5'	GCATGAGCCACTGCGCCCGGC 86549	A	C
	GCTGGGC CAGTGGCTCA GC		
	CGGCCCG GTCACCGAGT CG		
	C A		
GAM1697 LOC158055 5'	GGCTACTCCGCCAGCTGA 81670	AC	
	TCAGCTGGGC AGTGGCT		
	AGTCGACCCG TCATCGG		
	CC		
GAM1697 LOC158310 5'	AGCCACTGCGCCCGGC 86748	A	
	GCTGGGC CAGTGGCT		
	CGGCCCG GTCACCGA		
	C		
GAM1697 LOC158402 5'	CTGAGCCACCGAGGCTGG 86805	GGGCACA	C
	TCAGCT GTGGCTCA G		
	GGTCGG CACCGAGT C		
	AGC_____ A		
GAM1697 LOC158476 3'	CGTGAGCCACCATGCCAGC 86843	CA	
	GCTGGGCA GTGGCTCACG		
	CGACCCGT CACCGAGTGC		
	AC		
GAM1697 LOC158476 3'	GCATGAGCCACCACGCCCGC 86846	T ACA	C
	GC GGC GTGGCTCA GC		
	CG CCG CACCGAGT CG		
	_ CAC A		
GAM1697 LOC158709 3'	GCGTGAGCCACCGCACCCAGC 81981	CACA	
	GCTGGG GTGGCTCACGC		
	CGACCC CACCGAGTGCG		
	ACGC		
GAM1697 LOC158865 5'	GCGTGAGCCACCATGTCCAGC 86936	CA	
	GCTGGGCA GTGGCTCACGC		

	CGACCTGT CACCGAGTGCG		
	AC		
GAM1697 LOC158943 5'	CGACCACCGACCCAGCTGA 60531	CACA	CTCA
	TCAGCTGGG GTGG CG		
	AGTCGACCC CACC GC		
	AGC_ A__		
GAM1697 LOC160391 3'	GAGCCACTGTGCCCGGC 87064		
	GCTGGGCACAGTGCGTC		
	CGGCCCGTGTACCGAG		
GAM1697 LOC160646 3'	GCGTGAGCCACCGTGCCCGGC 82228	A	
	GCTGGGCAC GTGGCTCACGC		
	CGGCCCGTG CACCGAGTGCG		
	C		
GAM1697 LOC161829 3'	GCGTGCCACCACGCCCGGCT 82315	ACA	TC
	AGCTGGGC GTGGC ACGC		
	TCGGCCCG CACCG TGCG		
	CAC _		
GAM1697 LOC169611 3'	GCATGAGCCACCACGCCTGGC 82765	TG	ACA C
	GC GGC GTGGCTCA GC		
	CG CCG CACCGAGT CG		
	GT CAC A		
GAM1697 LOC169611 3'	GCATGAGCCACTGCGCCTGGC 82766	TG	A C
	GC GGC CAGTGGCTCA GC		
	CG CCG GTCACCGAGT CG		
	GT C A		
GAM1697 LOC196047 5'	TGAGCCACCACGCCCGGC 89613	ACA	
	GCTGGGC GTGGCTCA		
	CGGCCCG CACCGAGT		
	CAC		
GAM1697 LOC196264 3'	GCATGAGCCACTGTGCTTGGC 87605	TG	C
	GC GGCACAGTGGCTCA GC		
	CG TCGTGTACCGAGT CG		
	GT A		
GAM1697 LOC196411 3'	GCGCCCGCCACCACGCCAGCT 87673	ACA	TCA
	AGCTGGGC GTGGC CGC		
	TCGACCCG CACCG GCG		
	CAC CCC		
GAM1697 LOC196529 3'	GCGTGAGCAACCGCACCCAGCT 87774	CACA	G
	AGCTGGG GT GCTCACGC		

	TCGACCC	CA	CGAGTGCG			
	ACGC	A				
GAM1697	LOC197358	3'	GCCACCATGCCCGGCT	88037	CA	
			AGCTGGGCA	GTGGC		
			TCGGCCCGT	CACCG		
			AC			
GAM1697	LOC199699	3'	GCCACCATGCCCAGCT	88307	CA	
			AGCTGGGCA	GTGGC		
			TCGACCCGT	CACCG		
			AC			
GAM1697	LOC199725	5'	GCATGAGCCACTGCACCCAGC	89838	CA	C
			GCTGGG	CAGTGGCTCA	GC	
			CGACCC	GTCACCGAGT	CG	
			AC	A		
GAM1697	LOC199775	5'	GCGTGAGCCACCGTGCCCGAGC	88357	A	
			GCTGGGCAC	GTGGCTCACGC		
			CGACCCGTG	CACCGAGTGCG		
			C			
GAM1697	LOC199786	3'	GCATGAGCCACCGCACCCGGC	88384	CACA	C
			GCTGGG	GTGGCTCA	GC	
			CGGCC	CACCGAGT	CG	
			ACGC	A		
GAM1697	LOC200169	5'	GCATGAGCCACCGCGCCTGGC	89950	TG	ACA C
			GC	GGC	GTGGCTCA	GC
			CG	CCG	CACCGAGT	CG
			GT	CGC	A	
GAM1697	LOC200301	5'	GCGCCCGCCACCAACGCCAGCT	88745	ACA	TCA
			AGCTGGGC	GTGGC	CGC	
			TCGACCCG	CACCG	GCG	
			CAC	CCC		
GAM1697	LOC200310	3'	GCATGTGCCACCGCGCCCGGCT	65736	ACA	T C
			AGCTGGGC	GTGGC	CA	GC
			TCGGCCCG	CACCG	GT	CG
			CGC	T	A	
GAM1697	LOC200310	3'	GCGTGAGCCACCGTGCCTGGC	65737	TG	A
			GC	GGCAC	GTGGCTCACGC	
			CG	CCGTG	CACCGAGTGCG	
			GT	C		
GAM1697	LOC200316	5'	GCGTGAGCCACCGTGCCCGGCC	88769	A	A
	GG		TC	GCTGGGCAC	GTGGCTCACGC	

		GG CGGCCCGTG CACCGAGTGCG		
		C C		
GAM1697	LOC200845 5'	GCATGAGCCACTGCGCCCAGC 88900	A	C
		GCTGGGC CAGTGGCTCA GC		
		CGACCCG GTCACCGAGT CG		
		C A		
GAM1697	LOC200860 3'	GCGTGAGCCACCACGCCCGACC 90165	C_	ACA
	TG	CAG TGGGC GTGGCTCACGC		
		GTC GCCCG CACCGAGTGCG		
		CA CAC		
GAM1697	LOC201294 3'	GCGTGAGCCACCACGCCCGGCC 88211	_	ACA
	TGG	TCAG CTGGGC GTGGCTCACGC		
		GGTC GGCCCG CACCGAGTGCG		
		C CAC		
GAM1697	LOC201411 3'	GCCACCATGCCAGCT 62955	CA	
		AGCTGGGCA GTGGC		
		TCGACCCGT CACCG		
		AC		
GAM1697	LOC201411 3'	GCGTGAGCCACTGTGCCTGGC 62956	TG	
		GC GGCACAGTGGCTCACGC		
		CG CCGTGTACCGAGTGCG		
		GT		
GAM1697	LOC201510 3'	GCATGAGCCACTGTACCCTGC 88251	T C	C
		GC GGG ACAGTGGCTCA GC		
		CG CCC TGTCACCGAGT CG		
		T A A		
GAM1697	LOC201626 3'	GCGTGAGCCACCGCACCCGGC 88991	CACA	
		GCTGGG GTGGCTCACGC		
		CGGCC CACCGAGTGCG		
		ACGC		
GAM1697	LOC201705 5'	GCGTGAGCCACCGCGTCCAGC 90252	ACA	
		GCTGGGC GTGGCTCACGC		
		CGACCTG CACCGAGTGCG		
		CGC		
GAM1697	LOC201868 3'	CCACGCGCATCACCATGTCCAG 89075	CA	_____ TCAC
	CTGA	GCTGGGCA GTG GC G		
		CGACCTGT CAC CG C		
		AC TACG    CACT		
GAM1697	LOC202934 3'	GCGTGAGCCACCACACTTGGC 90414	TG	CACA
		GC GG GTGGCTCACGC		

		CG TC CACCGAGTGCG		
		GT ACAC		
GAM1697	LOC203246 3'	GCGTGAGCCACCGCGCCCGGCC 89307	A	ACA
	GG	TC GCTGGGC GTGGCTCACGC		
		GG CGGCCCCG CACCGAGTGCG		
		C CGC		
GAM1697	LOC203350 3'	GCATGAGCCACTGTACCCGGC 90569	C	C
		GCTGGG ACAGTGGCTCA GC		
		CGGCCC TGTCACCGAGT CG		
		A A		
GAM1697	LOC203369 3'	GCGCCCGCCACCATGCCCGGCT 89341	CA	TCA
		AGCTGGGCA GTGGC CGC		
		TCGGCCCGT CACCG GCG		
		AC CCC		
GAM1697	LOC203369 3'	GCGTGAGCCACCACGCCCGGC 89342	ACA	
		GCTGGGC GTGGCTCACGC		
		CGGCCCCG CACCGAGTGCG		
		CAC		
GAM1697	LOC205251 5'	GCATGAGCTGTGCGACTCAGC 90670	CACA TG	C
		GCTGGG G GCTCA GC		
		C GACTC T CGAGT CG		
		ACGC GT A		
GAM1697	LOC219294 3'	GCGTGAGCCACTGTACCTGGC 93007	TG C	
		GC GG ACAGTGGCTCACGC		
		CG CC TGTCACCGAGTGCG		
		GT A		
GAM1697	LOC219295 3'	GCGTGAGCCACTGTACCTGGC 92991	TG C	
		GC GG ACAGTGGCTCACGC		
		CG CC TGTCACCGAGTGCG		
		GT A		
GAM1697	LOC219649 5'	CGTCCACCATGCCCAGCTGG 92955	CA	CTC
		TCAGCTGGGCA GTGG ACG		
		GGTCGACCCGT CACC TGC		
		AC ____		
GAM1697	LOC219731 5'	AGTCACCATGCCCAGCCGG 93089	A	CA
		TC GCTGGGCA GTGGCT		
		GG CGACCCGT CACTGA		
		C AC		
GAM1697	LOC219735 3'	GCATGAGCCACCGCACCTGA 93110	CTGG ACA	C
		TCAG GC GTGGCTCA GC		

		AGTC CG CACCGAGT CG		
		CA__ C__ A		
GAM1697	LOC220064 3'	CTGAGCCACCACTCCCGG 93425	CACA	C
		CTGGG GTGGCTCA G		
		GGCCC CACCGAGT C		
		TCAC A		
GAM1697	LOC220074 3'	GCGTGAGCCACACGCCCAGC 59275	ACA	
		GCTGGGC GTGGCTCACGC		
		CGACCCG CACCGAGTGCG		
		CAC		
GAM1697	LOC220575 3'	GCATGGGCCACACACCCAGCT 76313	CACA	C
	GA	TCAGCTGGG GTGGCTCA GC		
		AGTCGACCC CACCGGGT CG		
		ACAC A		
GAM1697	LOC221035 3'	GCGTGAGCCACCGCACCCAGC 93164	CACA	
		GCTGGG GTGGCTCACGC		
		CGACCC CACCGAGTGCG		
		ACGC		
GAM1697	LOC221060 3'	GGGCCACCAAGCCCAGCT 93215	ACA	
		AGCTGGGC GTGGCTC		
		TCGACCCG CACCGGG		
		AC_		
GAM1697	LOC221271 3'	GCATGAGCCACTGTGCCCAGC 91859		C
		GCTGGGCACAGTGGCTCA GC		
		CGACCCGTGTCACCGAGT CG		
		A		
GAM1697	LOC221271 3'	GCATGCGCCACCATGCCCAGCT 91860	CA	T C
		AGCTGGGCA GTGGC CA GC		
		TCGACCCGT CACCG GT CG		
		AC C A		
GAM1697	LOC221271 3'	GCCACCATGCCCAGCT 91861	CA	
		AGCTGGGCA GTGGC		
		TCGACCCGT CACCG		
		AC		
GAM1697	LOC221296 3'	GCGCGCCGCCACGCCCGGCT 91964	ACA	TCA
		AGCTGGGC GTGGC CGC		
		TCGGCCCG CGCCG GCG		
		CAC C__		
GAM1697	LOC221431 5'	GCATGAGCCACCGCACCCGGC 92101	CACA	C
		GCTGGG GTGGCTCA GC		

		CGGCCC CACCGAGT CG		
		ACGC A		
GAM1697	LOC221663 5'	GCATGAGCCACTGCACCCAGAC 93815	_	CA C
	T	AG CTGGG CAGTGGCTCA GC		
		TC GACCC GTCACCGAGT CG		
		A AC A		
GAM1697	LOC221814 5'	GCATGCACCACCATGCCCAGCT 93943	CA	CT C
		AGCTGGGCA GTGG CA GC		
		TCGACCCGT CACC GT CG		
		AC AC A		
GAM1697	LOC221815 5'	GCATGCACCACCATGCCCAGCT 93937	CA	CT C
		AGCTGGGCA GTGG CA GC		
		TCGACCCGT CACC GT CG		
		AC AC A		
GAM1697	LOC221964 3'	GCGTGAGTCACAGCACCCGGCT 93982	CACA	
		AGCTGGG GTGGCTCACGC		
		TCGGCCC CACTGAGTGCG		
		ACGA		
GAM1697	LOC222031 3'	GCGCCCGCCACCATGCCCAGCT 94024	CA	TCA
		AGCTGGGCA GTGGC CGC		
		TCGACCCGT CACCG GCG		
		AC CCC		
GAM1697	LOC222070 5'	GCGTGAGCCCCCGTGCCCAGC 94155	AGT	
		GCTGGGCAC GGCTCACGC		
		CGACCCGTG CCGAGTGCG		
		CCC		
GAM1697	LOC222159 5'	TGAGCCATCCAACTGA 94081	C GCACA	
		TCAG TGG GTGGCTCA		
		AGTC ACC TACCGAGT		
		A _____		
GAM1697	LOC222224 5'	GCATGAGCCACCATGCCTGGC 94197	TG CA C	
		GC GGCA GTGGCTCA GC		
		CG CCGT CACCGAGT CG		
		GT AC A		
GAM1697	LOC253664 3'	GCATGCACCACACGCCCCGGCT 94811	ACA	CT C
		AGCTGGGC GTGG CA GC		
		TCGGCCCCG CACC GT CG		
		CAC AC A		
GAM1697	LOC253778 3'	GCGTGAGCCACCGCGCCCAGC 94872	ACA	
		GCTGGGC GTGGCTCACGC		



	CGACCCG CACCGAGTGCG	
	CGC	
GAM1697 LOC253842 5'	GCGTGAGCCACTGCACCCAGCC 97388	A CA
GA	TC GCTGGG CAGTGGCTCACGC	
	AG CGACCC GTCACCGAGTGCG	
	C AC	
GAM1697 LOC253956 5'	GCGTGAGCCACTGTGCCCGGC 96032	
	GCTGGGCACAGTGGCTCACGC	
	CGGCCCGTGTACCGAGTGCG	
GAM1697 LOC254018 5'	GCGTGAGCCACTGTGCCCAGC 96968	
	GCTGGGCACAGTGGCTCACGC	
	CGACCCGTGTACCGAGTGCG	
GAM1697 LOC254351 3'	GCGTGAGCCACCGCGCCCCCGG 94994	__ ACA
T	GCT GGGC GTGGCTCACGC	
	TGG CCCG CACCGAGTGCG	
	CC CGC	
GAM1697 LOC254351 5'	GCGTGAGCCACCGTGCCCCCGG 94995	__ A
T	GCT GGGCAC GTGGCTCACGC	
	TGG CCCGTG CACCGAGTGCG	
	CC C	
GAM1697 LOC255465 3'	CGTGCAACCATGCCCAGCT 97287	CAG CT_
	AGCTGGGCA TGG CACG	
	TCGACCCGT ACC GTGC	
	__ AAC	
GAM1697 LOC255465 3'	GCGTGAGCCACCACACTTGGC 97290	TG CACA
	GC GG GTGGCTCACGC	
	CG TC CACCGAGTGCG	
	GT ACAC	
GAM1697 LOC255707 3'	GCGTGAGCCACCAAACCCAGC 96959	CACA
	GCTGGG GTGGCTCACGC	
	CGACCC CACCGAGTGCG	
	AAAC	
GAM1697 LOC255919 3'	GCCACCATGCCCAGCT 95036	CA
	AGCTGGGCA GTGGC	
	TCGACCCGT CACCG	
	AC	
GAM1697 LOC255927 3'	CGTGAGCCACCGCGCCCGGC 96009	ACA
	GCTGGGC GTGGCTCACG	

	CGGCCCG CACCGAGTGC		
	CGC		
GAM1697 LOC255981 3'	GCATGAGCCACCGCGCCCGGC 97132	ACA	C
	GCTGGGC GTGGCTCA GC		
	CGGCCCG CACCGAGT CG		
	CGC A		
GAM1697 LOC255991 3'	GCCACTGTGCCCAGCTGA 97249		
	TCAGCTGGGCACAGTGGC		
	AGTCGACCCGTGTCACCG		
GAM1697 LOC256221 3'	GACCACGCCCGGCTGA 95210	ACA	C
	TCAGCTGGGC GTGG TC		
	AGTCGGCCCG CACC AG		
GAM1697 LOC256364 5'	GCATGAGCCACTGCACCTGGC 94800	TG CA	C
	GC GG CAGTGGCTCA GC		
	CG CC GTCACCGAGT CG		
	GT AC A		
GAM1697 LOC257277 5'	GCGTGCTGGTCGCGCCAGCTG 95262	ACA	—
	CAGCTGGGC GTGGCT CACGC		
	GTCGACCCG CGCTGG GTGCG		
	TC		
GAM1697 LOC257463 3'	GCATGAGCCACCATGCCAGC 71069	CA	C
	GCTGGGCA GTGGCTCA GC		
	CGACCCGT CACCGAGT CG		
	AC A		
GAM1697 LOC257465 3'	CTGAGCCACCGTGTCCAG 81592	A	C
	CTGGGCAC GTGGCTCA G		
	GACCTGTG CACCGAGT C		
	C A		
GAM1697 LOC257465 3'	GCGTGCCACCACGCCAGCT 81594	ACA	TC
	AGCTGGGC GTGGC ACGC		
	TCGACCCG CACCG TGCG		
	CAC —		
GAM1697 LOC257486 3'	GCGTGAGCCACCGCGCCCGGC 69247	ACA	
	GCTGGGC GTGGCTCACGC		
	CGGCCCG CACCGAGTGCG		
	CGC		
GAM1697 LOC51193 5'	GCATGTGCCACCACGCCCGGCT 32906	ACA	T C
	AGCTGGGC GTGGC CA GC		

				TCGGCCCG	CACCG GT CG			
				CAC	T A			
GAM1697	LOC51219	5'	GCATGAGCCACCGCGCTTGGC	33121		TG	ACA	C
			GC GGC GTGGCTCA GC					
			CG TCG CACCGAGT CG					
			GT CGC A					
GAM1697	LOC51275	5'	GCGTGAGCCACCGTGCCTGGCT	33292		TG	A	
	GA		TCAGC GGCAC GTGGCTCACGC					
			AGTCG CCGTG CACCGAGTGCG					
			GT C					
GAM1697	LOC57146	3'	GCGTGAGCCACTGTGCCCAGC	39921				
			GCTGGGCACAGTGGCTCACGC					
			CGACCCGTGTCACCGAGTGCG					
GAM1697	LOC81034	3'	GCGTGAGCCACTGCGCCTGGC	47851		TG	A	
			GC GGC CAGTGGCTCACGC					
			CG CCG GTCACCGAGTGCG					
			GT C					
GAM1697	LOC89932	3'	GCATGAGCCACCACGCCCAGC	60801		ACA		C
			GCTGGGC GTGGCTCA GC					
			CGACCCG CACCGAGT CG					
			CAC A					
GAM1697	LOC89932	3'	GTGAGCCACTGTGCCCAGC	60812				
			GCTGGGCACAGTGGCTCAC					
			CGACCCGTGTCACCGAGTG					
GAM1697	LOC90072	3'	GCGTGAGCCACCGCGCCTGGC	61298		TG	ACA	
			GC GGC GTGGCTCACGC					
			CG CCG CACCGAGTGCG					
			GT CGC					
GAM1697	LOC90288	3'	CGTGCCACCATGCCCGGCT	62088		CA	TC	
			AGCTGGGCA GTGGC ACG					
			TCGGCCCGT CACCG TGC					
			AC —					
GAM1697	LOC90288	3'	GCGTGAGCCACCGCGCCTGGCT	62097		TG	ACA	
			AGC GGC GTGGCTCACGC					
			TCG CCG CACCGAGTGCG					
			GT CGC					
GAM1697	LOC90459	3'	CGTGAGCCACTGCGCTCAGC	62885		A		
			GCTGGGC CAGTGGCTCACG					

			CGACTCG GTCACCGAGTGC		
			C		
GAM1697	LOC90485	3'	GCATGAGCCACCGCGCCCAGC 63018	ACA	C
			GCTGGGC GTGGCTCA GC		
			CGACCCG CACCGAGT CG		
			CGC A		
GAM1697	LOC90591	3'	GCATGAGCCACTGCACCCAGCT 63425	CA	C
	G		CAGCTGGG CAGTGGCTCA GC		
			GTCGACCC GTCACCGAGT CG		
			AC A		
GAM1697	LOC90591	3'	GCATGAGCCACTGCACCCGGC 63426	CA	C
			GCTGGG CAGTGGCTCA GC		
			CGGCCC GTCACCGAGT CG		
			AC A		
GAM1697	LOC90591	3'	GCCACCACACCCGGCTGA 63427	CACA	
			TCAGCTGGG GTGGC		
			AGTCGGCCC CACCG		
			ACAC		
GAM1697	LOC90918	3'	AGCCACTGCACCCAGC 64349	CA	
			GCTGGG CAGTGGCT		
			CGACCC GTCACCGA		
			AC		
GAM1697	LOC91012	5'	GCATGAGCCACCATGCCTGGC 64640	TG CA	C
			GC GGCA GTGGCTCA GC		
			CG CCGT CACCGAGT CG		
			GT AC A		
GAM1697	LOC91115	3'	GCATGAGCCACGACGCCCAGC 64936	ACA	C
			GCTGGGC GTGGCTCA GC		
			CGACCCG CACCGAGT CG		
			CAG A		
GAM1697	LOC91115	3'	GCCACCATGCCCCGGT 64937	CA	
			AGCTGGGCA GTGGC		
			TCGGCCCGT CACCG		
			AC		
GAM1697	LOC91115	3'	GCGTGAGCCACCGCACCTGGC 64939	TG CACA	
			GC GG GTGGCTCACGC		
			CG CC CACCGAGTGCG		
			GT ACGC		
GAM1697	LOC91308	3'	CGTGAGCCACCACCCCGG 65558	CACA	
			CTGGG GTGGCTCACG		

		GGCCC CACCGAGTGC		
		CCAC		
GAM1697	LOC91561	5' GCGTGAGCCACTGCACCCGGC	66450	CA
		GCTGGG CAGTGGCTCACGC		
		CGGCCC GTCACCGAGTGCG		
		AC		
GAM1697	LOC92148	5' GTGAGCCACCGCACCCAGC	68335	CACA
		GCTGGG GTGGCTCAC		
		CGACCC CACCGAGTG		
		ACGC		
GAM1697	LOC92267	3' CTGAGCCACCAAGCCCA	68611	ACA C
		TGGGC GTGGCTCA G		
		ACCCG CACCGAGT C		
		AAC A		
GAM1697	LOC92283	3' GCGCAGCCACTATGCCCGGC	68746	C CA
		GCTGGGCA AGTGGCT CGC		
		CGGCCCGT TCACCGA GCG		
		A C_		
GAM1697	LOC92609	3' GTGAGCTACTGTGCCAGCT	72850	
		AGCTGGGCACAGTGGCTCAC		
		TCGACCCGTGTCATCGAGTG		
GAM1697	LOC92697	5' GCATGAGCCACCGCACCCGGC	70270	CACA C
		GCTGGG GTGGCTCA GC		
		CGGCCC CACCGAGT CG		
		ACGC A		
GAM1697	LOC92697	5' GCATGTGCCACCACGCCCGGCT	70271	ACA T C
		AGCTGGGC GTGGC CA GC		
		TCGGCCCG CACCG GT CG		
		CAC T A		
GAM1697	LOC92841	3' GCATGAGCCACCGTGCCT	70710	A C
		GGGCAC GTGGCTCA GC		
		TCCGTG CACCGAGT CG		
		C A		
GAM1697	LOC93132	5' GCCACCATGCCCAGCT	71489	CA
		AGCTGGGCA GTGGC		
		TCGACCCGT CACCG		
		AC		
GAM1697	LOC93166	3' CGCAGGCCACCCAGCTGA	71624	CACAG CA
		TCAGCTGGG TGGCT CG		

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AGTCGACCC ACCGG GC
      _____ AC
GAM1697 LOC93349 3' GCCACCATGCCCAGCT 56459 CA
      AGCTGGGCA GTGGC
      ||||| |||
      TCGACCCGT CACCG
      AC
GAM1697 LOC93356 3' GCGTGAGCCACTGCACCCAGC 72077 CA
      GCTGGG CAGTGGCTCACGC
      |||| |||||
      CGACCC GTCACCGAGTGCG
      AC
GAM1697 LOC93496 3' GCGTGAGCCACCACGCCCGGC 72435 ACA
      GCTGGGC GTGGCTCACGC
      |||| |||||
      CGGCCCG CACCGAGTGCG
      CAC
GAM1698 ARHGEF6 3' CAAACTTGAAGCCAGGC 68198 ACCA
      GCCTGG CAAGTTTG
      |||| |||||
      CGGACC GTTCAAAC
      GAA_
GAM1698 BIG1 3' TCAAACCTGCAACACTCCAG 21205 CCA___
      CTGGA CAAGTTTGA
      |||| |||||
      GACCT GTTCAAAC
      CACAAC
GAM1698 CABC1 5' TCAAGCTGACCCAGGCGG 39658 ACCACA
      TCGCCTGG AGTTTGA
      ||||| |||||
      GGCGGACC TCGAACT
      CAG___
GAM1698 CORO2A 3' TCAAACCTGTGGTCCAGAGA 53403 GC A
      TC CTGGACCACA GTTTGA
      || ||||| |||||
      AG GACCTGGTGT CAAACT
      A_ _
GAM1698 CORO2A 3' TCAAACCTGTGGTCCAGAGA 12647 GC A
      TC CTGGACCACA GTTTGA
      || ||||| |||||
      AG GACCTGGTGT CAAACT
      A_ _
GAM1698 DISC1 3' TCAAACCTCCTGACCTCAGGCGA 37892 _AC CA
      TCGCCTG G CA AGTTTGA
      ||||| | || |||||
      AGCGGAC C GT TCAAAC
      T CA CC
GAM1698 EN2 5' CGGGCGGCCAGGCGG 7459 A ACAA
      TCGCCTGG CC GTTTG
      ||||| || |||||

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			GGCGGACC GG CGGGC		
			C ____		
GAM1698	FOXD2	5'	CAGAGGGGGCCCAGGCGA 15562	A	ACAAG
			TCGCCTGG CC TTTG		
			AGCGGACC GG AGAC		
			C GGG__		
GAM1698	GPX3	5'	TCAGGCAGCGGCTCAGGCGA 9125	GA	ACAA
			TCGCCTG CC GTTTGA		
			AGCGGAC GG CGGACT		
			TC CGA_		
GAM1698	HNF3G	3'	AACTCTGGTCCAGGAGA 72339	G	CA
			TC CCTGGACCA AGTT		
			AG GGACCTGGT TCAA		
			A C_		
GAM1698	IL13RA1	3'	TCAAACCTTGAGTCACAAAGA 7778	GCC _	CA
			TC TG GAC CAAGTTTGA		
			AG AC CTG GTTCAAAC		
			AA_ A A_		
GAM1698	KCNS2	3'	CAAACCTTGATTGAAGGGA 68300	G	GGACC
			TC CCT ACAAGTTTG		
			AG GGA TGTCAAAC		
			_ AGTTA		
GAM1698	LMO4	5'	CAAACCTTGACAGCAGCGA 22251	_	GACCA
			TCGC CTG CAAGTTTG		
			AGCG GAC GTTCAAAC		
			AC ____		
GAM1698	LZTS1	3'	TCAAACCTTGTTGGCCTCAAGC 40695	CT__	A
			GC GG CCACAAGTTTGA		
			CG CC GGTGTTCAAAC		
			AACT _		
GAM1698	MATK	3'	CAAGGAGGGTCCAGGCGG 57816		ACAAG
			TCGCCTGGACC TTTG		
			GGCGGACCTGG GAAC		
			GAG__		
GAM1698	MATK	3'	CAAGGAGGGTCCAGGCGG 57819		ACAAG
			TCGCCTGGACC TTTG		
			GGCGGACCTGG GAAC		
			GAG__		
GAM1698	MATK	3'	CAAGGAGGGTCCAGGCGG 9915		ACAAG
			TCGCCTGGACC TTTG		

			GGCGGACCTGG	GAAC	
			GAG__		
GAM1698	MIR16	3'	TCAAACCTTGTGGCCA	33565	A
			TGG CCACAAGTTTGA		
			ACC GGTGTTCAAAC		
			—		
GAM1698	PIK3C2B	3'	AGCTCGGTCCAGGTGA	10559	ACA
			TCGCCTGGACC AGTT		
			AGTGGACCTGG TCGA		
			C__		
GAM1698	PLCG2	5'	CAAACCCGGGGCAGGCGG	72463	GA ACAA
			TCGCCTG CC GTTTG		
			GGCGGAC GG CAAAC		
			GG CC__		
GAM1698	PLIN	3'	CAAACCTTGTGGCCAAAAGA	10640	GCC A
			TC TGG CCACAAGTTTG		
			AG ACC GGTGTTCAAAC		
			AAA _		
GAM1698	POU2AF1	3'	CAGATTTACAGTCCAGGC	20648	CAC
			GCCTGGAC AAGTTTG		
			CGGACCTG TTTAGAC		
			ACA		
GAM1698	SLC6A12	3'	CGAATGTGCTCCAGGCGA	11734	C AG
			TCGCCTGGA CACA TTTG		
			AGCGGACCT GTGT AAGC		
			C _		
GAM1698	STARD4	3'	TCAAACCTGTAGTACTACAGA	57516	GCC _ C
			TC TGG AC ACAAGTTTGA		
			AG ATC TG TGTTCAAAC		
			AC_ A A		
GAM1698	TP53	3'	TCAAACCTCCTGGGCTCAGGCGA	5043	A_ CA
			TCGCCTGG CCA AGTTTGA		
			AGCGGACT GGT TCAAAC		
			CG CC		
GAM1698	TR2	5'	CAAACCTTCCAGGC	72314	CCAC
			GCCTGGA AAGTTTG		
			CGGACCT TTCAAAC		
			—		
GAM1698	C21orf42	5'	TCAAACCTGTAGCTGTATGA	54207	CC ACC
			TCG TGG ACAAGTTTGA		



AGT GTC TGTTCAAACT  
 AT GA\_  
 GAM1698 DAZAP1 3' CAAACTTGTGAACTCGTGA 38536 CT AC  
 TCGC GG CACAAGTTTG  
 |||| || |||||  
 AGTG TC GTGTTCAAAC  
 C\_ AA  
 GAM1698 DBR1 3' AACTCCTGACCTCAGGCGA 32523 \_AC CA  
 TCGCCTG G CA AGTT  
 ||||| | || |||  
 AGCGGAC C GT TCAA  
 T CA CC  
 GAM1698 DC-TM4F2 3' CAAACTTGTGACTGC 48171 CT AC  
 GC GG CACAAGTTTG  
 || || |||||  
 CG TC GTGTTCAAAC  
 \_ A\_  
 GAM1698 DKFZp434N2030 5' TCAAACCTTGTCTCGC 65525 CT CAC  
 GC GGAC AAGTTTGA  
 || ||| |||||  
 CG CCTG TTCAAAC  
 CT \_  
 GAM1698 DKFZP564I1171 3' TCAGAAGCTGAGTCCAGGC 71592 \_ CAAG  
 GCCTGGAC CA TTTGA  
 ||||| || |||  
 CGGACCTG GT AGACT  
 A CGA\_  
 GAM1698 DKFZP564O0423 3' TCAAACCTCCTGGCCTCAGGCGA 91699 \_A CA  
 TCGCCTG G CCA AGTTTGA  
 ||||| | ||| |||||  
 AGCGGAC C GGT TCAAAC  
 T C CC  
 GAM1698 EPN2 5' CAAACTTGTGGACAGG 30321 GA  
 CCTG CCACAAGTTTG  
 ||| |||||  
 GGAC GGTGTTCAAAC  
 A\_  
 GAM1698 EREG 3' TCAAACCTTATGGGCAGGGA 7510 G GA C  
 TC CCTG CCA AAGTTTGA  
 || ||| || |||||  
 AG GGAC GGT TTCAAAC  
 \_ G\_ A  
 GAM1698 FLJ10718 3' TCAAACCTCTTAGGCTCAGGCGA 36496 GA ACA\_  
 TCGCCTG CC AGTTTGA  
 ||||| || |||||  
 AGCGGAC GG TCAAAC  
 TC ATTC  
 GAM1698 FLJ10803 3' TCAAACCTTGTATGGATGA 36671 \_ TGGACC  
 TCG CC ACAAGTTTGA  
 ||| || |||||

AGT GG    TGTTCAAAC  
           A TA\_\_\_\_  
 GAM1698 FLJ20312 5' TCAAACCTGTGTGCTGAGG 34928    \_ AC  
                   CCT GG CACAAGTTTGA  
                   ||| || |||||  
                   GGA TC GTGTTCAAAC  
                   G GT  
 GAM1698 FLJ23420 3' CAAGTGGGTCCAGGC 46846    A AG  
                   GCCTGGACC CA TTTG  
                   ||||||| || |||  
                   CGGACCTGG GT GAAC  
  
 GAM1698        — —  
 GAM1698    FREQ    3' TCAGCTGCTGGCCCGGGCGA 26585    A CA T  
                   TCGCCTGG CCA AGTT GA  
                   ||||||| ||| ||| ||  
                   AGCGGGCC GGT TCGA CT  
                   C CG \_  
 GAM1698 H2AV    3' TCAAACCTCCTGACCTCAGGCGA 56858    \_AC CA  
                   TCGCCTG G CA AGTTTGA  
                   ||||||| | || |||||  
                   AGCGGAC C GT TCAAAC  
                   T CA CC  
 GAM1698 HSA249128 5' GGCGCGGTCCAGGCGG 34153    ACAA  
                   TCGCCTGGACC GTT  
                   ||||||| |||  
                   GGCGGACCTGG CGG  
                   CG\_\_\_\_  
 GAM1698 KIAA0089 5' AAGCACGGTCCAGGCGG 69960    ACAA  
                   TCGCCTGGACC GTTT  
                   ||||||| |||  
                   GGCGGACCTGG CGAA  
                   CA\_\_\_\_  
 GAM1698 KIAA0256 3' CAAACCTGTCTCCTGAGTGC 64417    \_ \_ CAC  
                   GC CT GGAC AAGTTTG  
                   || || ||| |||||  
                   CG GA CCTG TTCAAAC  
                   T GT \_\_\_\_  
 GAM1698 KIAA1026 3' TCAACCTCCTGACCTCAGGCGA 71207    \_AC CA T  
                   TCGCCTG G CA AGTT GA  
                   ||||||| | || ||| ||  
                   AGCGGAC C GT TCAA CT  
                   T CA CC \_  
 GAM1698 KIAA1981 3' CAGAGGATGATTCAGGCGA 88341    C CAAG  
                   TCGCCTGGA CA TTTG  
                   ||||||| || |||  
                   AGCGGACTT GT AGAC  
                   A AGG\_  
 GAM1698 MGC13090 5' TCAAACCTGTCCGCCAAGT 51141    C ACC  
                   GC TGG ACAAGTTTGA  
                   || ||| |||||

			TG ACC TGTTCAAACT		
			A GCC		
GAM1698	MGC2452	5'	TCAAGGAGATGTGGTCCAGG	50990	AG__
			CCTGGACCACA TTTGA		
			GGACCTGGTGT GAACT		
			AGAG		
GAM1698	MYT1L	5'	TCAAACCTTGTGGTGG	66825	TGG
			CC ACCACAAGTTTGA		
			GG TGGTGTTCAAACT		
			_____		
GAM1698	NUDT13	3'	TCAGTTTGTGACCCAGGGA	63215	G AC AGT
			TC CCTGG CACA TTGA		
			AG GGACC GTGT GACT		
			_ CA TT_		
GAM1698	PCDH17	3'	CAAACCTTGTATTAGG	27087	ACC
			CCTGG ACAAGTTTG		
			GGATT TGTTCAAAC		
			A__		
GAM1698	PGRMC1	3'	TCAAACCTTGTAATTGTGGT	21895	TG CC
			GCC GA ACAAGTTTGA		
			TGG TT TGTTCAAACT		
			TG AA		
GAM1698	PTDSS2	3'	CATGGTGTGGTCCAGGC	47884	AGTT
			GCCTGGACCACA TG		
			CGGACCTGGTGT AC		
			GGT_		
GAM1698	RPS6KB1	3'	TCAAACCTTTTCCAGGC	12038	ACCAC
			GCCTGG AAGTTTGA		
			CGGACC TTCAAAC		
			CTT_		
GAM1698	USP22	3'	TCAAACCTCCTGACCTCAGGCGA	68023	_ AC CA
			TCGCCTG G CA AGTTTGA		
			AGCGGAC C GT TCAAAC		
			T CA CC		
GAM1698	LOC129011	5'	CAGACCTGCGGTCCAGGC	74865	A A
			GCCTGGACC CA GTTTG		
			CGGACCTGG GT CAGAC		
			C C		
GAM1698	LOC130595	5'	CAGGCTCAGTCCAGGC	75748	CACA
			GCCTGGAC AGTTTG		

CGGACCTG TCGGAC  
 AC\_\_  
 GAM1698 LOC131873 5' CTGGTGGTCCAGGAGA 75879 G A  
 TC CCTGGACCAC AG  
 || ||||| ||  
 AG GGACCTGGTG TC  
 A G  
 GAM1698 LOC145978 3' TCAAACCTTTAACAGGTGA 77600 GACCAC  
 TCGCCTG AAGTTTGA  
 ||||| |||||  
 AGTGGAC TTCAAAC  
 AAT\_\_  
 GAM1698 LOC146890 5' TCAGAAGTAGTCAGGCGA 83854 G C AAG  
 TCGCCTG AC AC TTTGA  
 ||||| || || |||||  
 AGCGGAC TG TG AGACT  
 \_ A A\_\_  
 GAM1698 LOC150622 5' CTGGTGGTCCAGGGA 79957 G A  
 TC CCTGGACCAC AG  
 || ||||| ||  
 AG GGACCTGGTG TC  
 \_ G  
 GAM1698 LOC152002 3' CAAACCAGCTCCAGGTGA 80431 CCACAA  
 TCGCCTGGA GTTTG  
 ||||| |||||  
 AGTGGACCT CAAAC  
 CGAC\_\_  
 GAM1698 LOC153474 3' TCAGAAGCTGAGTCCAGGC 80847 \_ CAAG  
 GCCTGGAC CA TTTGA  
 ||||| || |||||  
 CGGACCTG GT AGACT  
 A CGA\_  
 GAM1698 LOC154007 3' TCAAACCTCCTAGGCTCAGGCGA 81021 GA ACA\_  
 TCGCCTG CC AGTTTGA  
 ||||| || |||||  
 AGCGGAC GG TCAAAC  
 TC ATCC  
 GAM1698 LOC154789 5' TCAAACCTTGAGCAGGC 81141 GACCA  
 GCCTG CAAGTTTGA  
 |||| |||||  
 CGGAC GTTCAAAC  
 GA\_\_  
 GAM1698 LOC158301 3' CAAACCTGTGGTTCCA 81869 \_ A  
 TGGA CCACA GTTTG  
 |||| |||||  
 ACCT GGTGT CAAAC  
 T C  
 GAM1698 LOC199906 3' TCAAACCTCCTGACCTCAGGCGA 88487 \_ AC CA  
 TCGCCTG G CA AGTTTGA  
 ||||| | || |||||

AGCGGAC C GT TCAAAC  
 T CA CC  
 GAM1698 LOC199991 5' TCAGAGCGTTCCAGGCGA 89916 CC AAG  
 TCGCCTGGA AC TTTGA  
 ||||| || ||||  
 AGCGGACCT TG AGACT  
 \_ CG\_  
 GAM1698 LOC219529 5' TCAAACCTCCTGAGCCCAGGTGA 92974 AC\_ CA  
 TCGCCTGG CA AGTTTGA  
 ||||| || |||||  
 AGTGGACC GT TCAAAC  
 CGA CC  
 GAM1698 LOC220753 3' CAAACTTGTAGAGGTGGGC 92941 GG \_  
 GCCT ACC ACAAGTTTG  
 ||| ||| |||||  
 CGGG TGG TGTTCAAAC  
 \_ AGA  
 GAM1698 LOC221718 3' TCAAACCTTATTGGTGAAG 93632 GG C\_  
 CT ACCA AAGTTTGA  
 || ||| |||||  
 GA TGGT TTCAAAC  
 AG TA  
 GAM1698 LOC253927 3' TCAAACCTTAGACTTCAGGC 95025 CCAC  
 GCCTGGA AAGTTTGA  
 ||||| |||||  
 CGGACTT TTCAAAC  
 CAGA  
 GAM1698 LOC51028 3' CAAATATGGTCCAGG 32179 CAA  
 CCTGGACCA GTTTG  
 ||||| ||||  
 GGACCTGGT TAAAC  
 A\_  
 GAM1699 ADAM21 3' TGAGCACATTTCTGACCA 13763 ACA G  
 TG AGAAATGTG TCG  
 || ||||| |||  
 AC TCTTTACAC AGT  
 CAG G  
 GAM1699 AP1S1 3' TCAGGGCACTTCTTGTG 54035 AT G G  
 GACAAGAA GTG TC TGA  
 ||||| ||| |||  
 CTGTTCTT CAC GG ACT  
 \_ \_ G  
 GAM1699 AQP3 3' TCACGATCCACCCTTTC 59592 T\_ \_  
 GAAA GTGG TCGTGA  
 ||| ||| |||||  
 CTTT CACC AGCACT  
 CC T  
 GAM1699 CHML 5' TCACACCTCATTTCTTTCA 8431 C T C  
 TGA AAGAAATG GGT GTGA  
 ||| ||||| ||| |||

			ACT TTCTTTAC CCA CACT		
			— T —		
GAM1699	CHRNA3	3'	TCGTTACCCATTTCTT 5611	T	CG
			AAGAAATG GGT TGA		
			TTCTTTAC CCA GCT		
			— TT		
GAM1699	FBXL7	3'	CATGGACATTCTTGTCA 24545	AAT	GT
			TGACAAGA GTG CGTG		
			ACTGTTCT TAC GTAC		
			— AG		
GAM1699	FGF20	3'	CACAACCATTTCTTTCTTGTCA 39069	T_	C
			TGACAAGAAA GTGGT GTG		
			ACTGTTCTTT TACCA CAC		
			CT A		
GAM1699	IGFBP1	3'	TCATGAAACACTTCTCATCA 5181	CA	A GG
			TGA AGAA TGT TCGTGA		
			ACT TCTT ACA AGTACT		
			AC C A_		
GAM1699	KERA	3'	TCATTACCATTCTTGT 22871	AT	C
			ACAAGAA GTGGT GTGA		
			TGTTCTT TACCA TACT		
			— T		
GAM1699	MICB	3'	TCACGACTGCTCCTGCCA 19831	A A	AAT TG
			TG CA GA G GTCGTGA		
			AC GT CT C CAGCACT		
			C C — GT		
GAM1699	OLR1	3'	TCACAACAGTTCTTGTTA 10340	ATGTG	C
			TGACAAGAA GT GTGA		
			ATTGTTCTT CA CACT		
			GA — A		
GAM1699	PLAUR	5'	CACATTCATATTTACCGTCA 10616	AAG	TC
			TGAC AAATGTGG GTG		
			ACTG TTTATACT CAC		
			CCA TA		
GAM1699	POU4F1	3'	CACTGAAAACATTTTGTCA 20661	A	GG _
			TGACAAGAA TGT TC GTG		
			ACTGTTTTT ACA AG CAC		
			— AA T		
GAM1699	PTPN1	3'	TCACGACTCTTCCTGCA 11051	A A	ATGT
			TG CA GAA GGTCGTGA		

			AC GT CTT TCAGCACT		
			_ C C_		
GAM1699	SCN7A	3'	CACTTACCACCTCTTTTCA 11440	C AAT C_	
			TGA AAGA GTGGT GTG		
			ACT TTCT CACCA CAC		
			T C_ TT		
GAM1699	SLC4A4	3'	CCACTTATTTTTGTCA 13634	_	
			TGACAAGAAAT GTGG		
			ACTGTTTTTTA CACC		
			TT		
GAM1699	SMP1	3'	TCACATGAATAATTTTTGTCA 26703	A GGTC	
			TGACAAGAA TGT GTGA		
			ACTGTTTTT ATA CACT		
			A AGTA		
GAM1699	7h3	3'	CACGATTGGCCTCTAGTCA 52271	A AATGT	
			TGAC AGA GGTCGTG		
			ACTG TCT TTAGCAC		
			A CCGG_		
GAM1699	ADMP	3'	TCACAAATCATATTCTGTCA 58870	A A C_	
			TGACA GAA TGTGGT GTGA		
			ACTGT CTT ATACTA CACT		
			_ _ AA		
GAM1699	C6orf35	3'	TCAAGAGCCTTTCTTGTCA 37452	TGT CG_	
			TGACAAGAAA GGT TGA		
			ACTGTTCTTT CCG ACT		
			_ AGA		
GAM1699	CAPNS2	3'	TCACAACCCTACATATTTCTGA 50322	CA _ C	
	TCA		TGA AGAAATGT GGT GTGA		
			ACT TCTTTATA CCA CACT		
			AG CATC A		
GAM1699	CLIC4	3'	ACCAATTTCTTGCA 25627	A G	
			TG CAAGAAAT TGGT		
			AC GTTCTTTA ACCA		
			_ _		
GAM1699	DCOHM	3'	TCACAATCTTTTCTTGTC 49611	TGT C	
			GACAAGAAA GGT GTGA		
			CTGTTCTTT CTA CACT		
			T_ A		
GAM1699	GORASP2	3'	CACGCAACATTTCTTGT 31382	G T	
			ACAAGAAATGT G CGTG		

			TGTTCTTTACA C GCAC		
			A _		
GAM1699	GTF2E1	3'	TACAGACCTCTTGTCA 18617	AATGT	_
			TGACAAGA GGTC GTG		
			ACTGTTCT CCAG CAT		
			_____ A		
GAM1699	KIAA0336	3'	CCACAATTCTTTTGTCA 27588	__	A
			TGACA AGAA TGTGG		
			ACTGT TCTT ACACC		
			TT A		
GAM1699	KIAA0475	3'	TCATGGCCATTTCCTG 29505	A	AT
			CA GAA GTGGTCGTGA		
			GT CTT TACCGGTACT		
			C _		
GAM1699	KIAA0475	3'	CAGCTTTGCATTTCTGTCA 29486	A	TG TCG
			TGACA GAAATG G TG		
			ACTGT CTTTAC T AC		
			_ GT TCG		
GAM1699	KIAA0635	5'	TCACACAAATTTCTTGTC 27698	GTG	C
			GACAAGAAAT GT GTGA		
			CTGTTCTTTA CA CACT		
			AA_ _		
GAM1699	KIAA1320	5'	CCACATTTTGTAATTTCTTGTC 69299	_____	
	A		TGACAAGAA ATGTGG		
			ACTGTTCTT TACACC		
			TAATGTTT		
GAM1699	KIAA1813	3'	TCACACTGTAAATTTCTTGT 70307	__	TG C
			ACAAGAAAT G GT GTGA		
			TGTTCTTTA T CA CACT		
			AA GT _		
GAM1699	KIAA1821	3'	CAGAATACATTTCTTGT 71778	G	G
			ACAAGAAATGTG TC TG		
			TGTTCTTTACAT AG AC		
			A _		
GAM1699	KIAA1951	3'	CAGGCTTCTCTTGTCA 73758	AATGT	G
			TGACAAGA GGTC TG		
			ACTGTTCT TCGG AC		
			CT_ _		
GAM1699	MGC2306	3'	CACAGCCTGTCTTGTCA 50956	AATGT	C
			TGACAAGA GGT GTG		



		ACTGTTCT	CCG CAC		
		GT__	A		
GAM1699	NRN1	3'	CACTGCACATTTCTCCTCA	33433	CA GTC
			TGA AGAAATGTG GTG		
			ACT TCTTTACAC CAC		
			CC GT_		
GAM1699	PTPN9	3'	TCATGTCTCCTCTTGTCA	11081	AATGT T
			TGACAAGA GG CGTGA		
			ACTGTTCT TC GTACT		
			CC__ T		
GAM1699	RA-GEF-2	3'	CCACAGGGTTTCTTGTCA	32954	__
			TGACAAGAAA TGTGG		
			ACTGTTCTTT ACACC		
			GGG		
GAM1699	SERF2	5'	CACGTGCTTTTTCTTGTG	19307	TGT _
			GACAAGAAA GGT CGTG		
			CTGTTCTTT TCG GCAC		
			T__ T		
GAM1699	SGKL	3'	TCACAGAAGCATTCT	25147	GG _
			AGAAATGT TC GTGA		
			TCTTTACG AG CACT		
			A_ A		
GAM1699	TACTILE	5'	CACATTACTTTTCTGTC	19468	A T C
			GACA GAAA GTGGT GTG		
			CTGT CTTT CATTA CAC		
			C _ _		
GAM1699	WBP4	3'	TCACAAAATTACATTCT	23232	C__
			AGAAATGTGGT GTGA		
			TCTTTACATTA CACT		
			AAA		
GAM1699	LOC115219	3'	CACGACAACGGGTCCTCA	73296	CAA AA G
			TGA GA TGT GTCGTG		
			ACT CT GCA CAGCAC		
			C__ GG A		
GAM1699	LOC115294	3'	TCATTGCATATTTCTTGTCA	73018	G C
			TGACAAGAAATGTG T GTGA		
			ACTGTTCTTTATAC G TACT		
			_T		
GAM1699	LOC128499	3'	CACGACCACATCCTCT	74762	A_
			AGA ATGTGGTCGTG		

	TCT TACACCAGCAC		
	CC		
GAM1699 LOC132946 3'	TCACGACTGAGATGTCA 75074	AGAAATG	
	TGACA TGGTCGTGA		
	ACTGT GTCAGCACT		
	AGA____		
GAM1699 LOC148426 5'	CAGGACACAATTTCTTGCCA 84150	A GTG G	
	TG CAAGAAAT GTC TG		
	AC GTTCTTTA CAG AC		
	C ACA G		
GAM1699 LOC151195 3'	CATGTTGCATTTCTTGT 80168	TG T	
	ACAAGAAATG G CGTG		
	TGTTCTTTAC T GTAC		
	GT _		
GAM1699 LOC152317 5'	TCACACTGACTTTTGTCA 85650	AATG C	
	TGACAAGA TGGT GTGA		
	ACTGTTTT GTCA CACT		
	CA__ _		
GAM1699 LOC152674 3'	TCAACCCACCCTCTTGTCA 85839	AAT TCG	
	TGACAAGA GTGG TGA		
	ACTGTTCT CACC ACT		
	CC_ CA_		
GAM1699 LOC154428 5'	CACGTGTGCACATTTCTGACCA 86215	ACA GT__	
	TG AGAAATGTG CGTG		
	AC TCTTTACAC GCAC		
	CAG GTGT		
GAM1699 LOC154743 3'	CCACATTGTCTTGTCA 81115	_	
	TGACAAGA AATGTGG		
	ACTGTTCT TTACACC		
	G		
GAM1699 LOC155435 3'	TCACATTCTCTTGTCA 81354	_	
	TGACAAGA AATGTGG		
	ACTGTTCT TTACACT		
	C		
GAM1699 LOC158263 3'	CGCCCACTTCTTGTCA 81844	AT T	
	TGACAAGAA GTGG CG		
	ACTGTTCTT CACC GC		
	_ C		
GAM1699 LOC164955 3'	TCATGACCATTCTT 82460	AT	
	AAGAA GTGGTCGTGA		

TTCTT TACCAGTACT

GAM1699 LOC221069 5' TCACAGTTCGTTTCTTCTCA 93202 C T TC  
TGA AAGAAATG GG GTGA  
||| ||||| || |||  
ACT TTCTTTGC TT CACT  
C \_ GA

GAM1699 LOC253228 5' TCAGGAGCATTCTTTCA 95941 C GG G  
TGA AAGAAATGT TC TGA  
||| ||||| || |||  
ACT TTCTTTACG AG ACT  
\_ \_ G

GAM1699 LOC255919 3' TCATTCTTACATTCTAATCA 95041 CA TC  
TGA AGAAATGTGG GTGA  
||| ||||| |||  
ACT TCTTTACATT TACT  
AA CT

GAM1699 LOC56920 3' TCAGAGCACATTTCTTGT 39392 G G  
ACAAGAAATGTG TC TGA  
||||||| || |||  
TGTTCTTTACAC AG ACT  
G \_

GAM1699 LOC91115 3' TCACGACCCTCTCATGCA 64948 A A AATGT  
TG CA GA GGTCGTGA  
|| || || |||||  
AC GT CT CCAGCACT  
\_ A CTC\_

GAM1699 LOC91768 3' CAAGGGCCATTCTTCTCA 67111 C AT G\_  
TGA AAGAA GTGGTC TG  
||| |||| ||||| ||  
ACT TTCTT TACCGG AC  
C \_ GA